



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:35 PM UTC

PDB ID : 4V5W / pdb_00004v5w
Title : Grapevine Fanleaf virus
Authors : Schellenberger, P.; Demangeat, G.; Ritzenthaler, C.; Lorber, B.; Sauter, C.
Deposited on : 2011-05-10
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

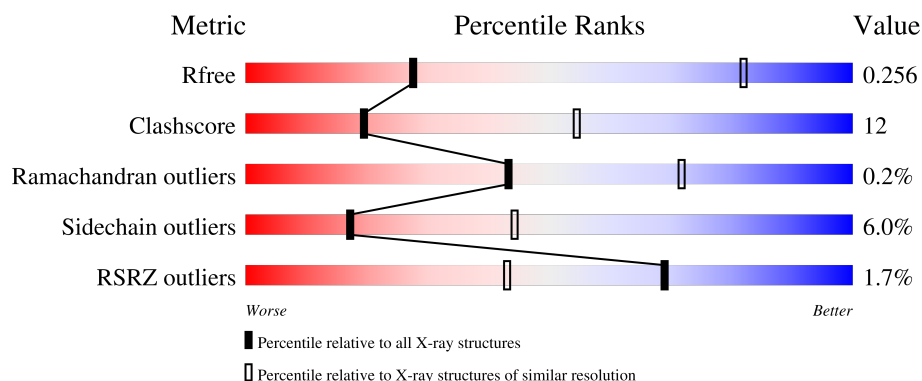
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 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.



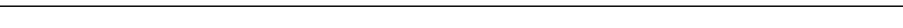
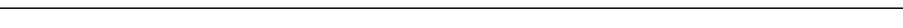
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1131 (3.80-3.60)
Clashscore	190562	1171 (3.80-3.60)
Ramachandran outliers	187476	1129 (3.80-3.60)
Sidechain outliers	187428	1126 (3.80-3.60)
RSRZ outliers	180081	1130 (3.80-3.60)

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

Mol	Chain	Length	Quality of chain
1	AA	504	79% 19% .
1	AB	504	78% 18% .
1	AC	504	79% 18% .
1	AD	504	81% 17% .
1	AE	504	81% 17% .

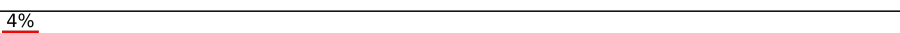
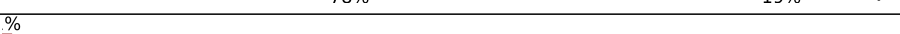
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Mol	Chain	Length	Quality of chain
1	AF	504	 79% 19% .
1	AG	504	 76% 19% 5% .
1	AH	504	 77% 20% .
1	AI	504	 78% 18% .
1	AJ	504	 78% 19% .
1	AK	504	 78% 19% .
1	AL	504	 79% 19% .
1	AM	504	 80% 18% .
1	AN	504	 77% 20% .
1	AO	504	 77% 19% .
1	AP	504	 80% 17% .
1	AQ	504	 77% 20% .
1	AR	504	 79% 18% .
1	AS	504	 81% 16% .
1	AT	504	 80% 18% .
1	BA	504	 2% 79% 19% .
1	BB	504	 4% 81% 16% .
1	BC	504	 5% 79% 18% .
1	BD	504	 3% 79% 18% .
1	BE	504	 1% 79% 18% .
1	BF	504	 2% 77% 20% .
1	BG	504	 2% 80% 18% .
1	BH	504	 2% 80% 17% .
1	BI	504	 2% 81% 17% .
1	BJ	504	 3% 80% 17% .

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Mol	Chain	Length	Quality of chain
1	BK	504	 82% 16% .
1	BL	504	 79% 18% .
1	BM	504	 80% 17% .
1	BN	504	 80% 17% .
1	BO	504	 79% 18% .
1	BP	504	 9% 81% 16% .
1	BQ	504	 5% 81% 17% .
1	BR	504	 5% 80% 17% .
1	BS	504	 4% 80% 18% .
1	BT	504	 8% 79% 19% .
1	CA	504	 4% 81% 16% .
1	CB	504	 4% 79% 18% .
1	CC	504	 3% 81% 16% .
1	CD	504	 4% 80% 17% .
1	CE	504	 4% 78% 19% .
1	CF	504	 % 80% 17% .
1	CG	504	 2% 80% 18% .
1	CH	504	 % 78% 19% .
1	CI	504	 2% 77% 19% .
1	CJ	504	 78% 19% .
1	CK	504	 2% 79% 19% .
1	CL	504	 2% 81% 17% .
1	CM	504	 3% 79% 19% .
1	CN	504	 % 81% 17% .
1	CO	504	 % 79% 19% .

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Mol	Chain	Length	Quality of chain
1	CP	504	80%17%
1	CQ	504	%80%18%
1	CR	504	%77%20%
1	CS	504	%80%17%
1	CT	504	81%16%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 237060 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AB	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AC	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AD	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AE	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AF	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AG	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AH	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AI	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AJ	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AK	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AL	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AM	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AN	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AO	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AP	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AQ	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AR	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AS	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AT	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BA	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BB	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BC	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BD	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BE	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BF	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BG	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BH	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BI	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BJ	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BK	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BL	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BM	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BN	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BO	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BP	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BQ	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BR	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BS	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BT	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CA	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CB	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CC	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CD	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CE	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CF	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CG	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CH	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CI	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CJ	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CK	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CL	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CM	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CN	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CO	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CP	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CQ	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CR	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			

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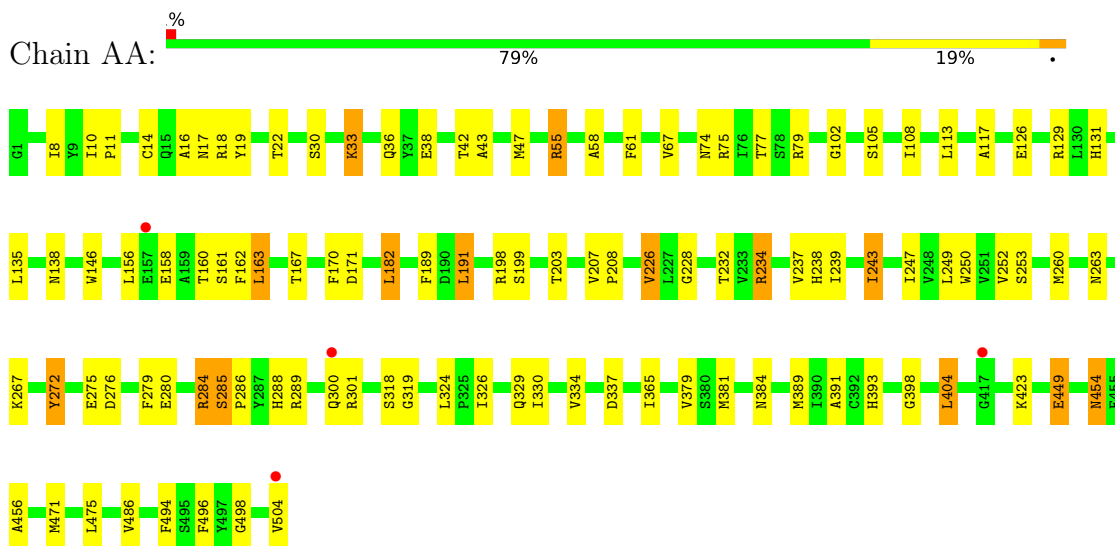
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	CS	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CT	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			

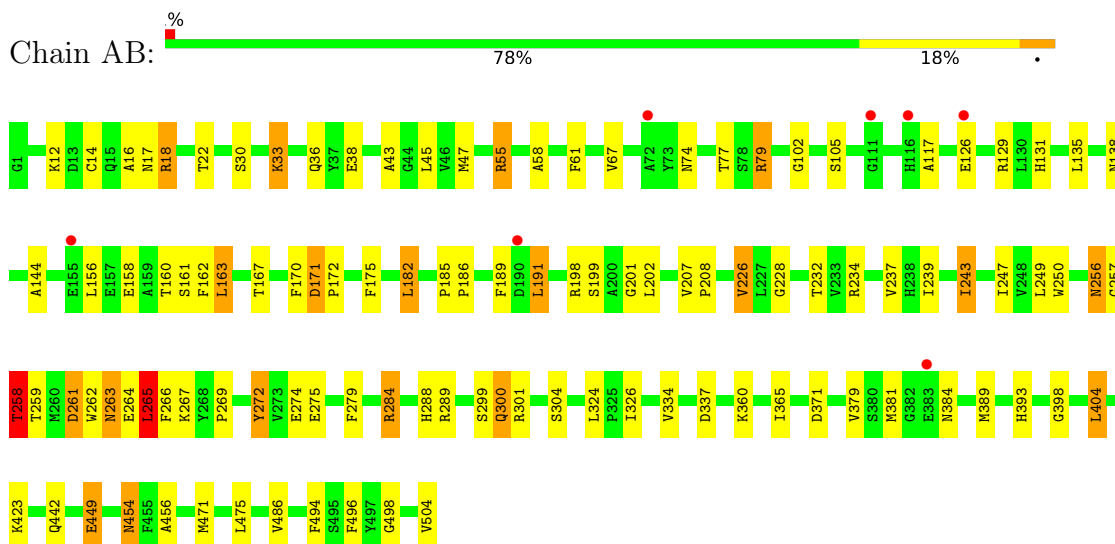
3 Residue-property plots [i](#)

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

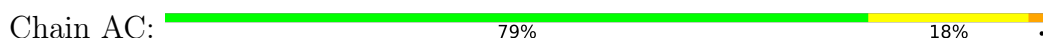
• Molecule 1: COAT PROTEIN

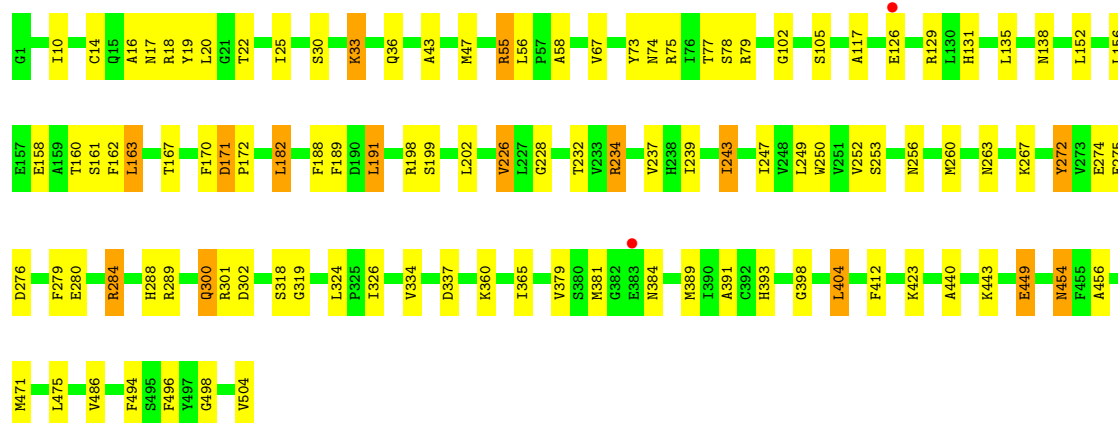


• Molecule 1: COAT PROTEIN



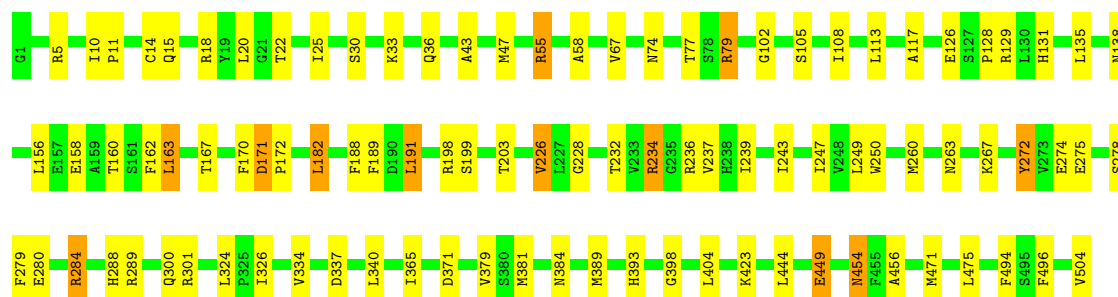
• Molecule 1: COAT PROTEIN





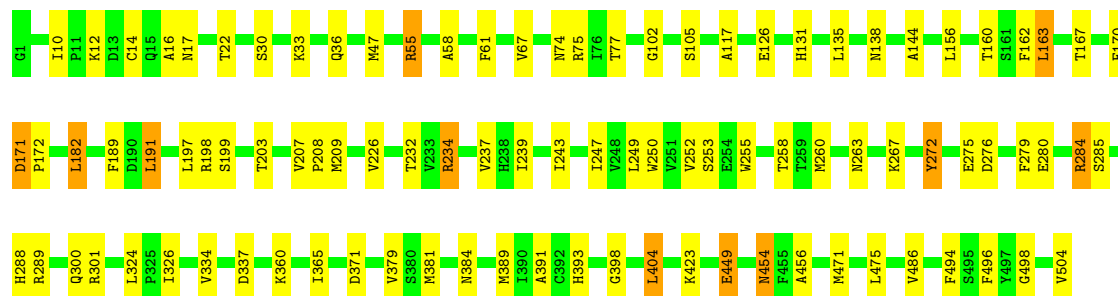
• Molecule 1: COAT PROTEIN

Chain AD: 81% 17%



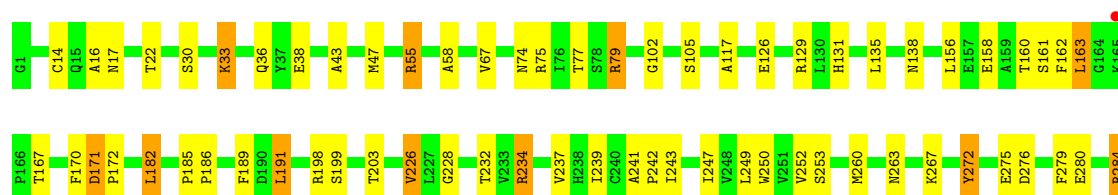
• Molecule 1: COAT PROTEIN

Chain AE: 81% 17%



• Molecule 1: COAT PROTEIN

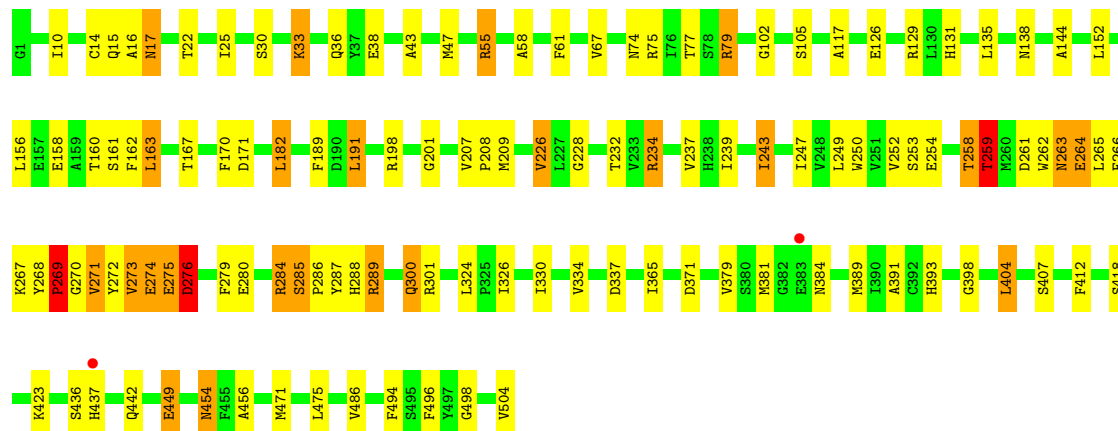
Chain AF: 79% 19%





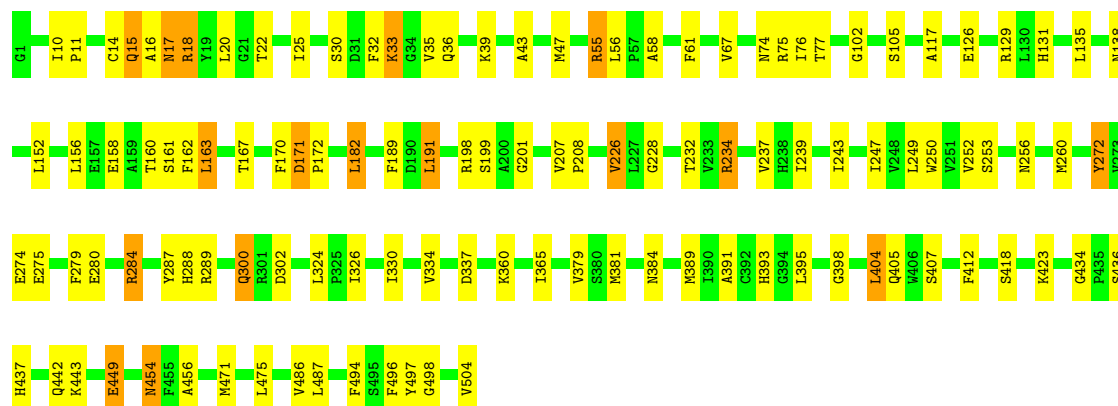
• Molecule 1: COAT PROTEIN

Chain AG: 76% 19% 5% •



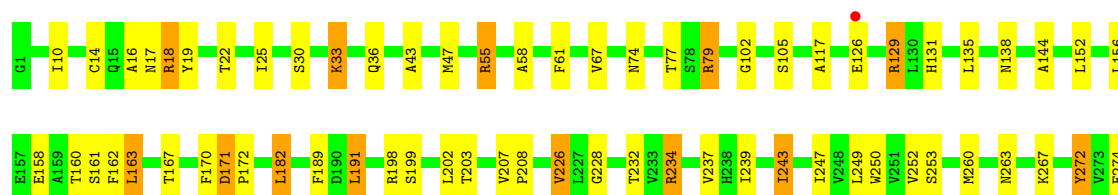
• Molecule 1: COAT PROTEIN

Chain AH: 77% 20% •



• Molecule 1: COAT PROTEIN

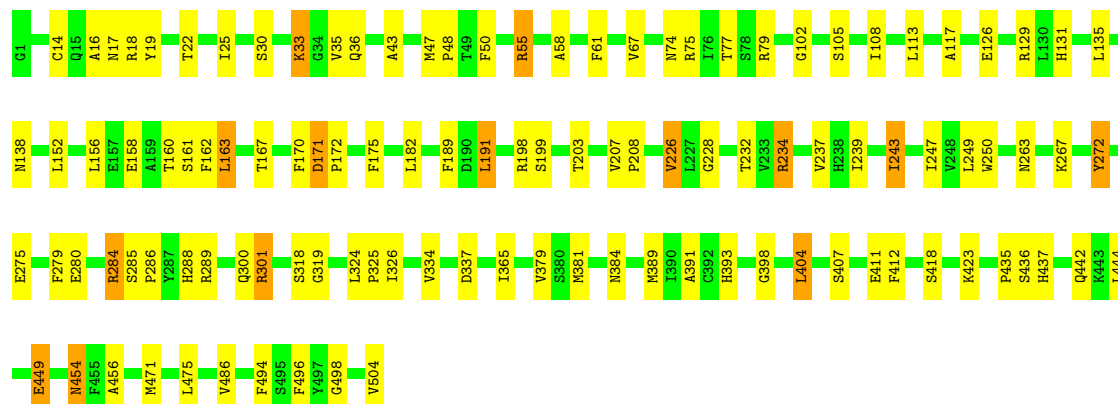
Chain AI: 78% 18% •





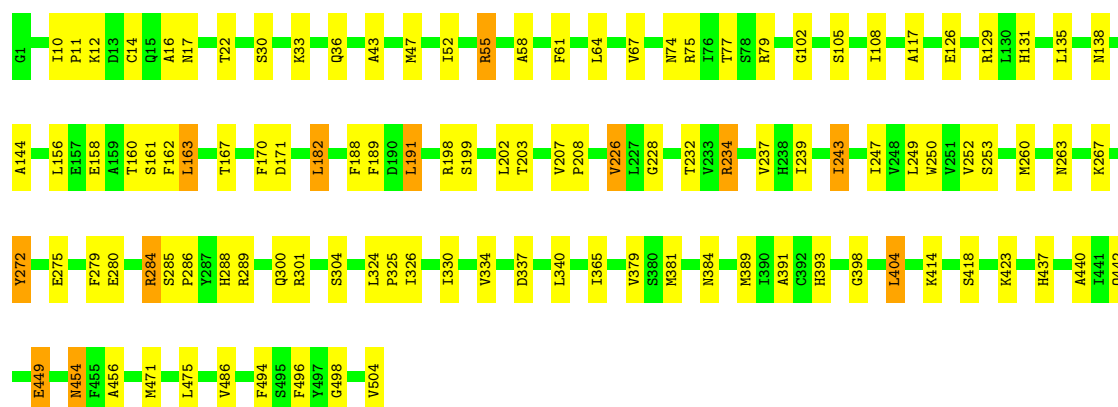
• Molecule 1: COAT PROTEIN

Chain AJ: 78% 19% .



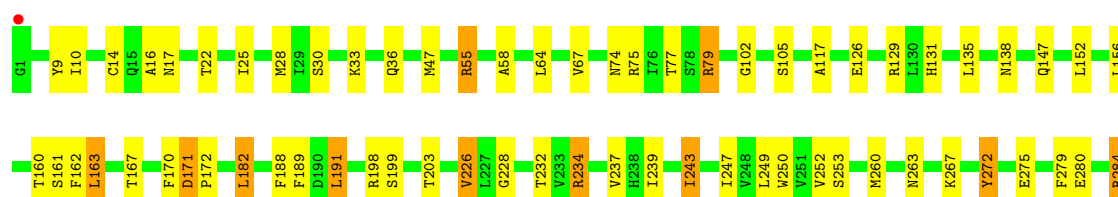
• Molecule 1: COAT PROTEIN

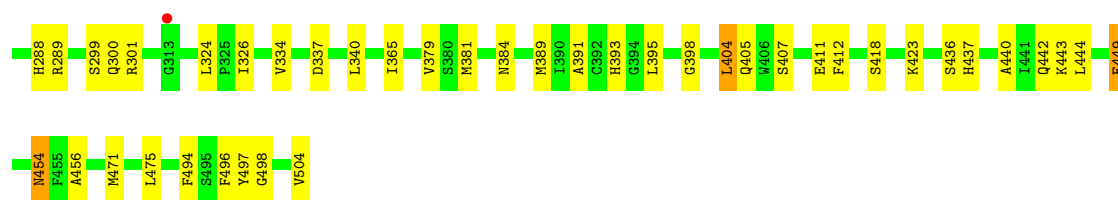
Chain AK: 78% 19% .



• Molecule 1: COAT PROTEIN

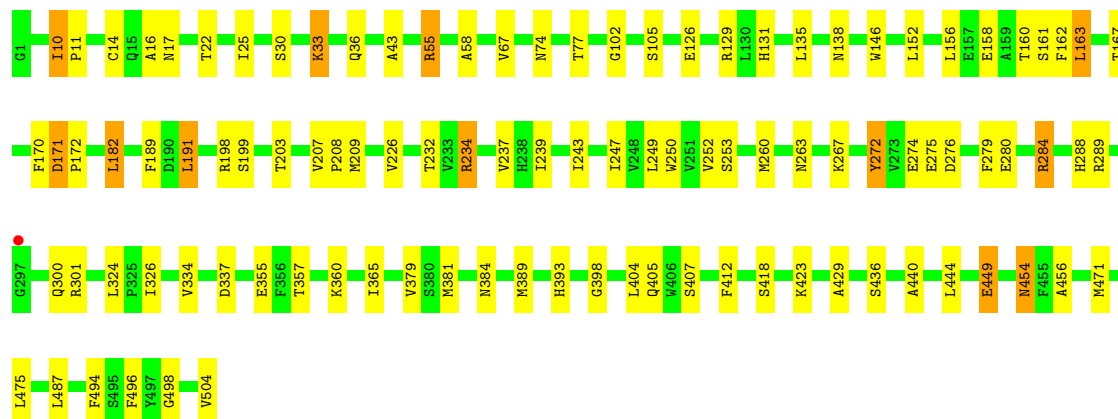
Chain AL: 79% 19% .





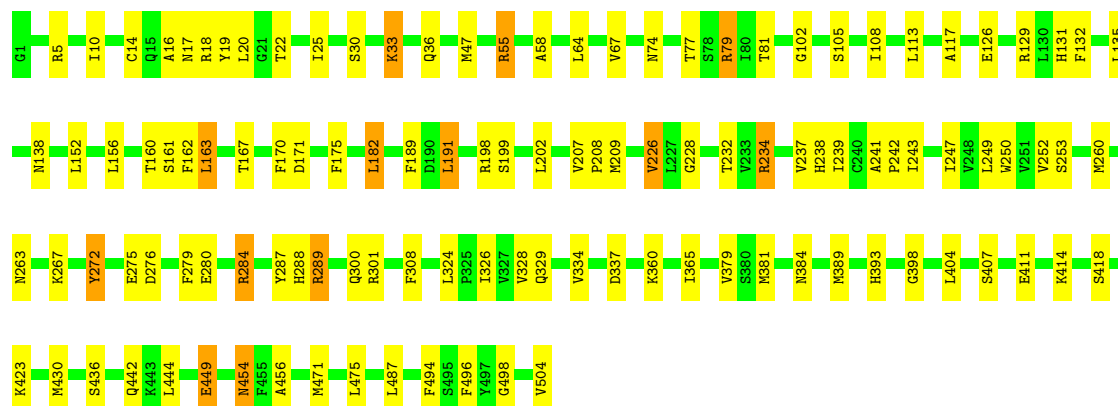
• Molecule 1: COAT PROTEIN

Chain AM: 80% 18% .



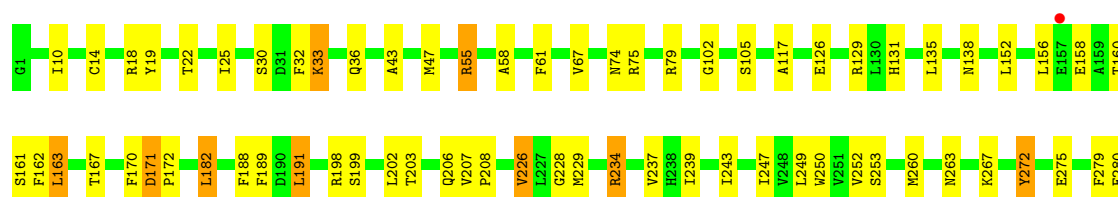
• Molecule 1: COAT PROTEIN

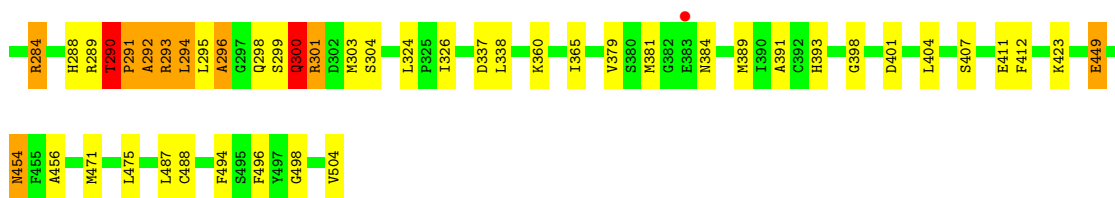
Chain AN: 77% 20% .



• Molecule 1: COAT PROTEIN

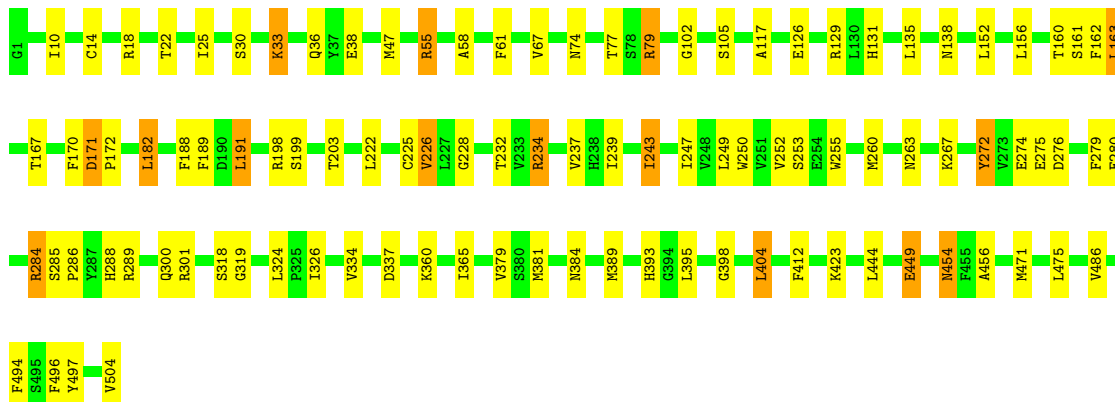
Chain AO: 77% 19% .





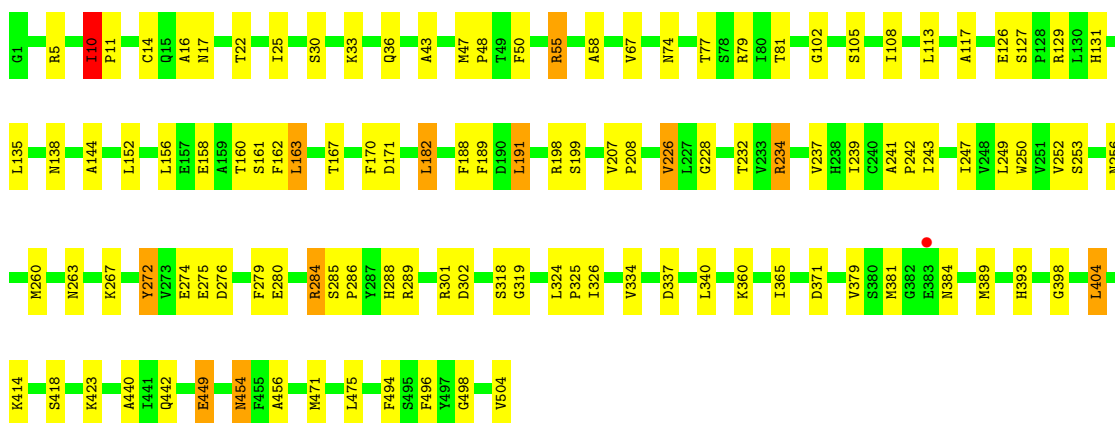
• Molecule 1: COAT PROTEIN

Chain AP: 80% 17% .



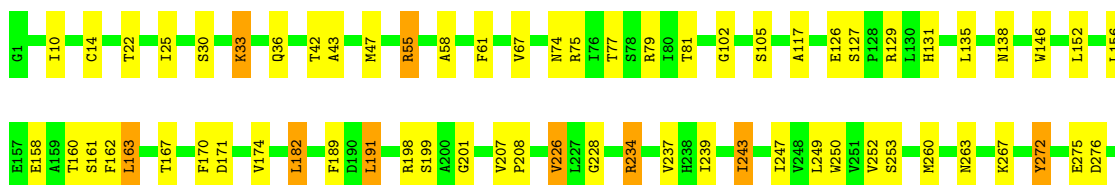
• Molecule 1: COAT PROTEIN

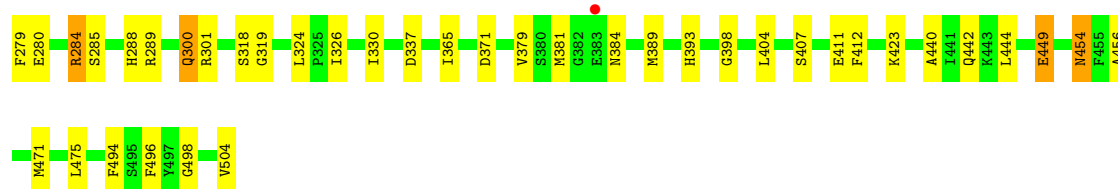
Chain AQ: 77% 20% .



• Molecule 1: COAT PROTEIN

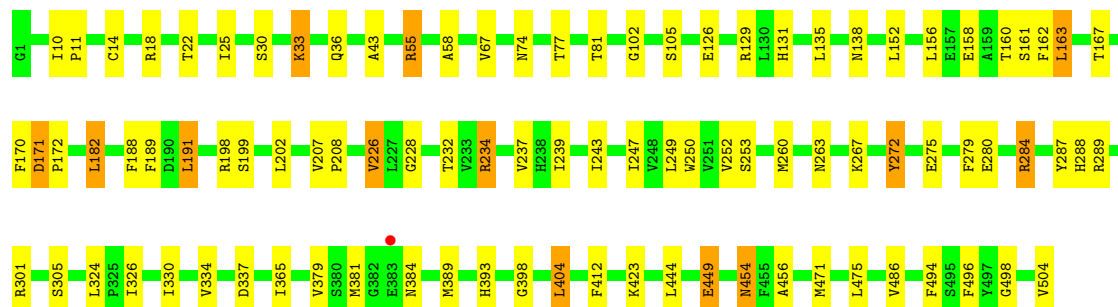
Chain AR: 79% 18% .





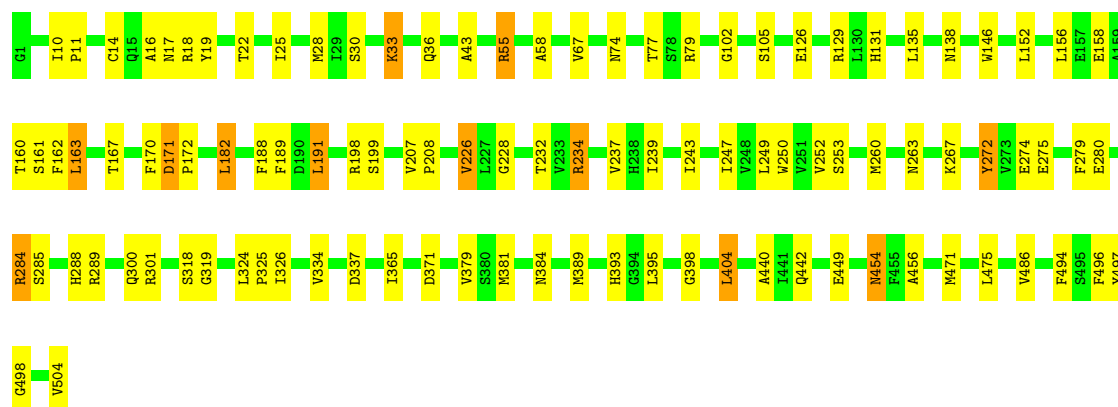
• Molecule 1: COAT PROTEIN

Chain AS: 81% 16% .



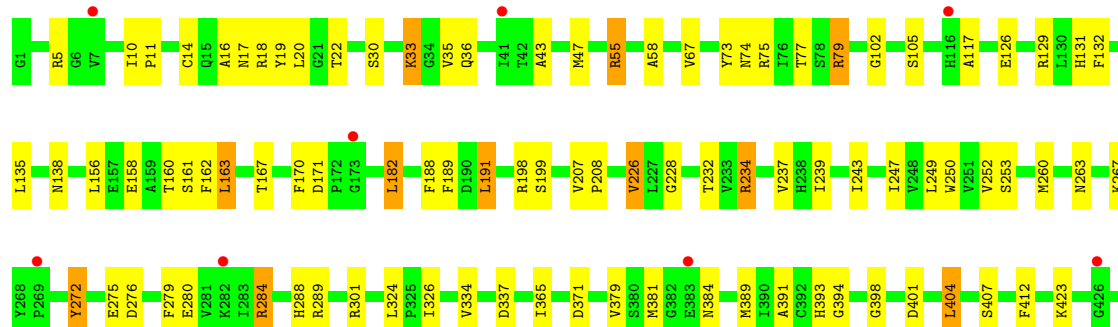
• Molecule 1: COAT PROTEIN

Chain AT: 80% 18% .



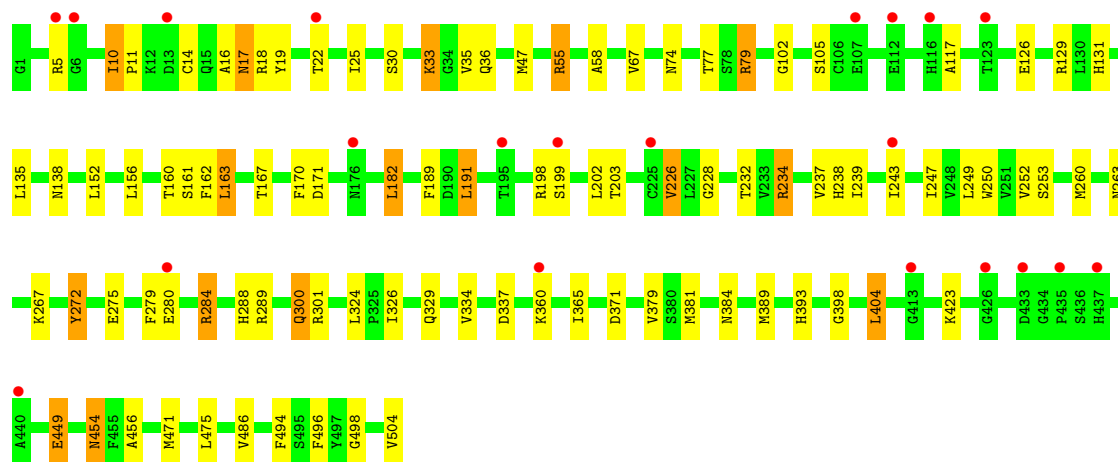
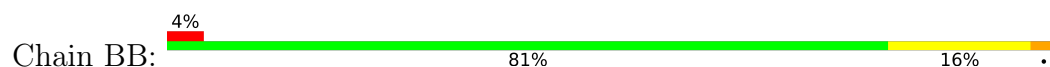
• Molecule 1: COAT PROTEIN

Chain BA: 2% 79% 19% .

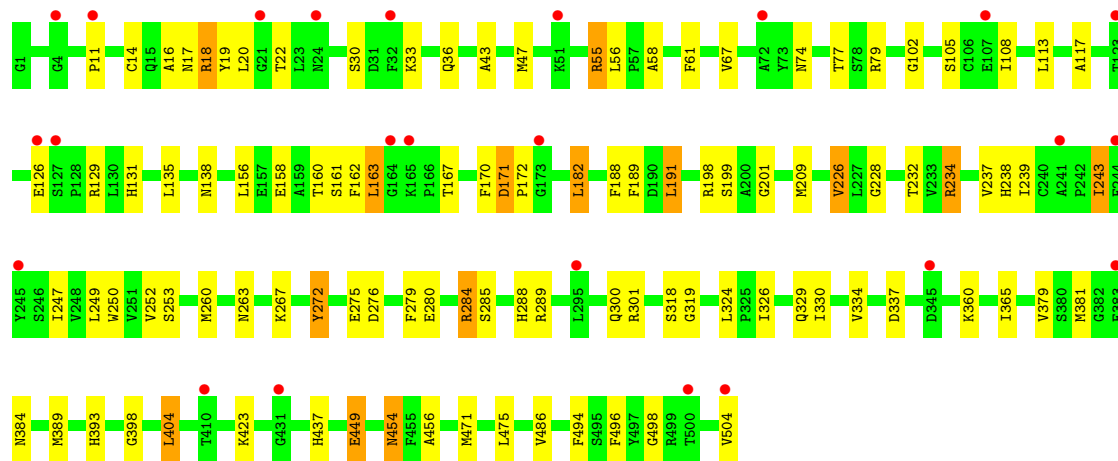
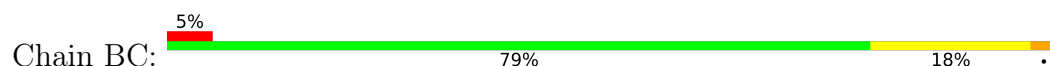




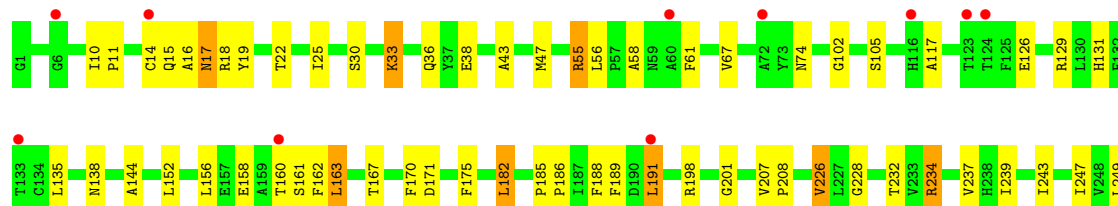
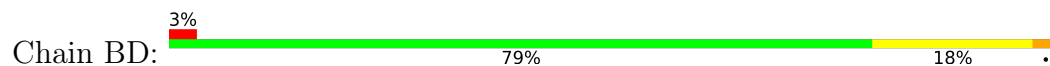
• Molecule 1: COAT PROTEIN

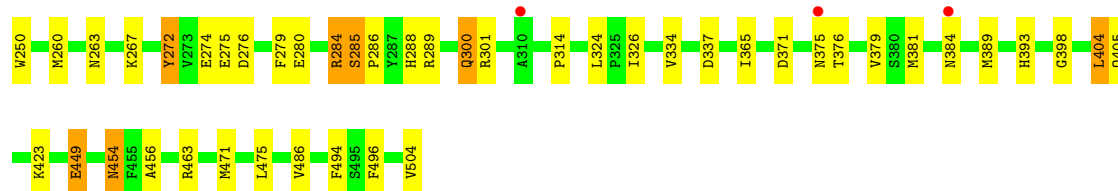


• Molecule 1: COAT PROTEIN

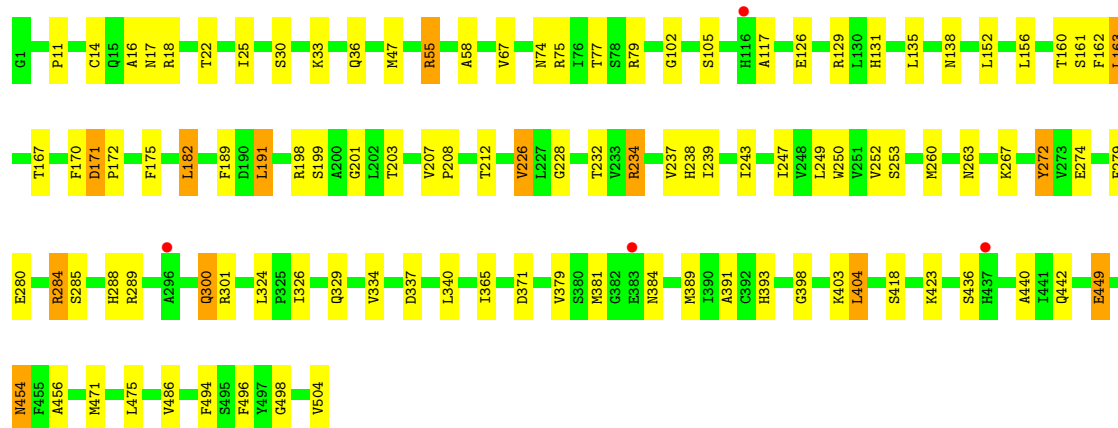
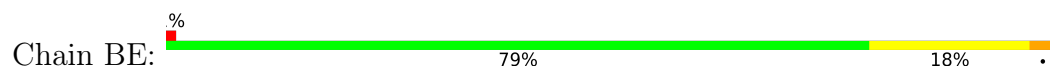


• Molecule 1: COAT PROTEIN

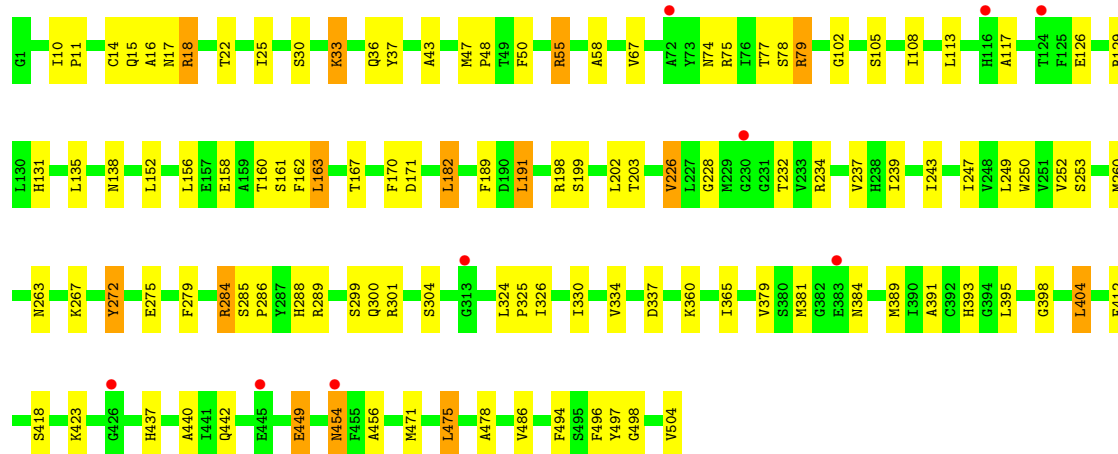
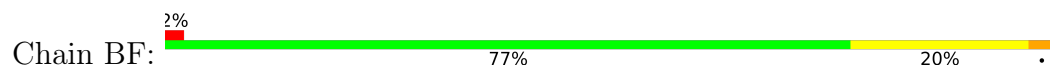




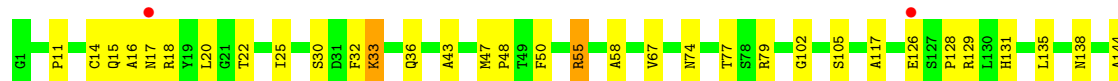
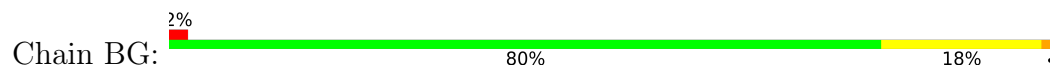
• Molecule 1: COAT PROTEIN

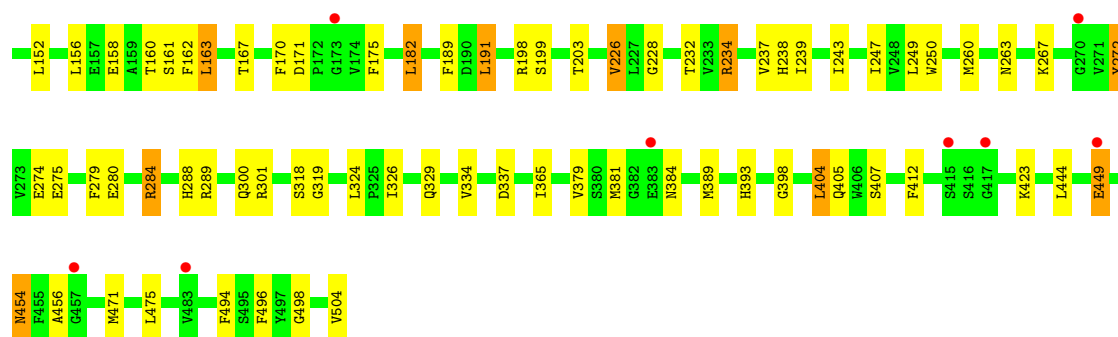


• Molecule 1: COAT PROTEIN

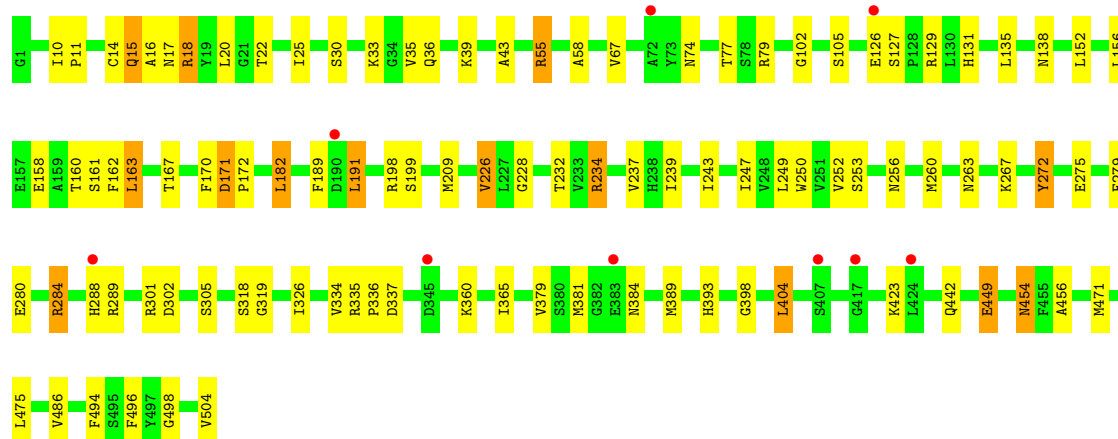
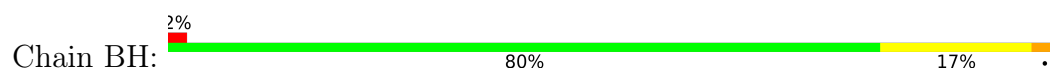


• Molecule 1: COAT PROTEIN

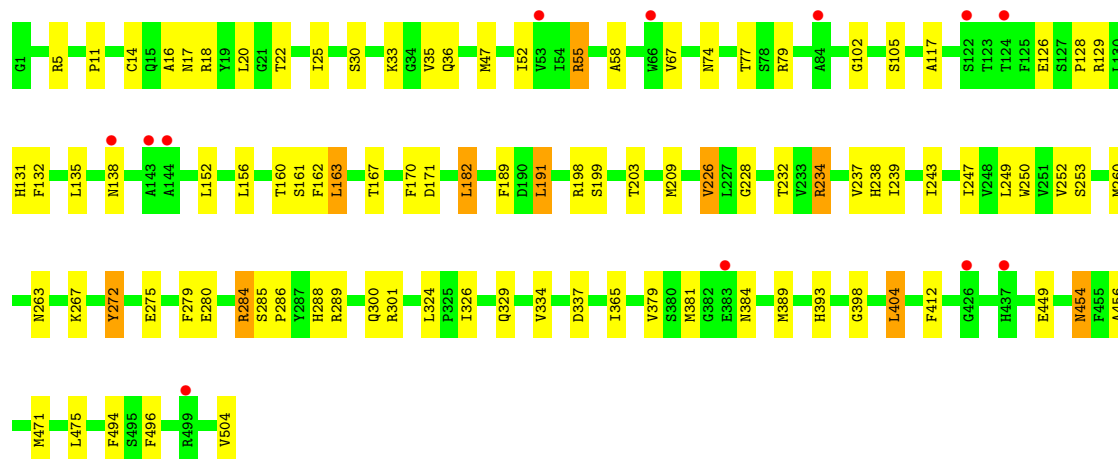
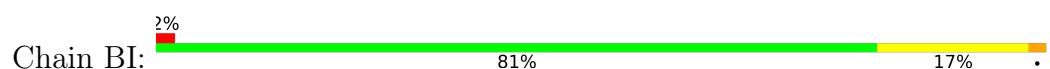




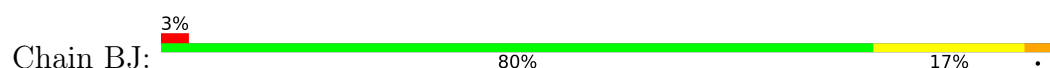
• Molecule 1: COAT PROTEIN

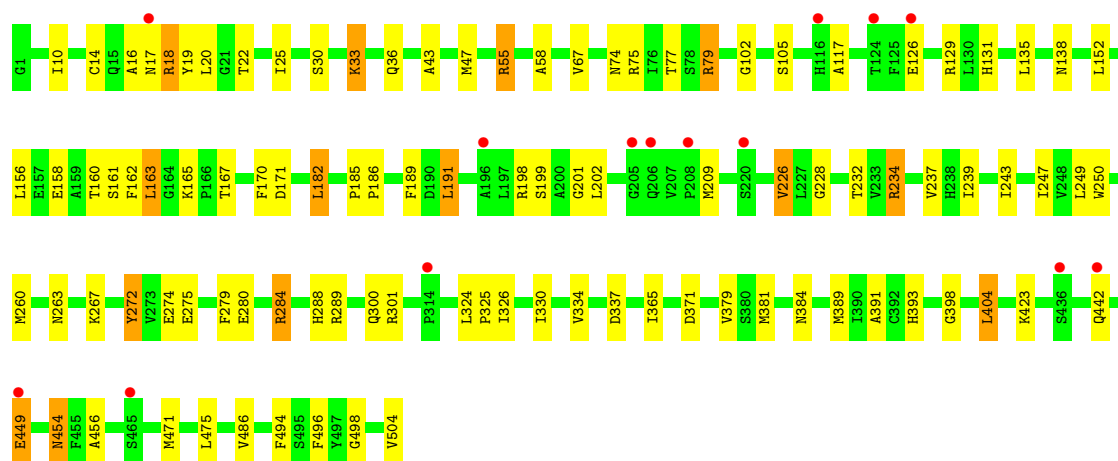


• Molecule 1: COAT PROTEIN



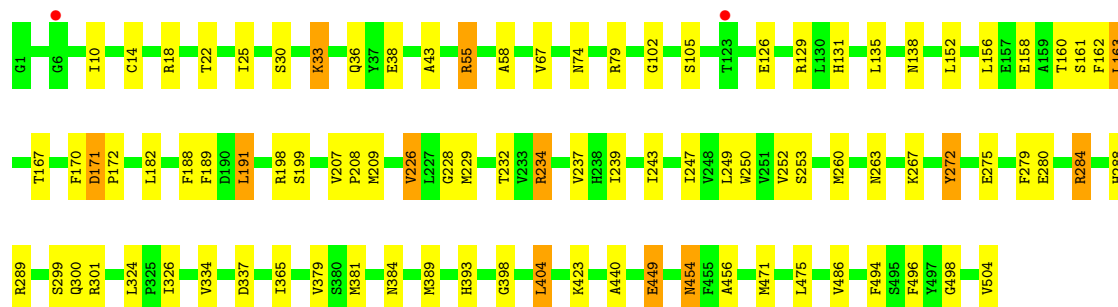
• Molecule 1: COAT PROTEIN





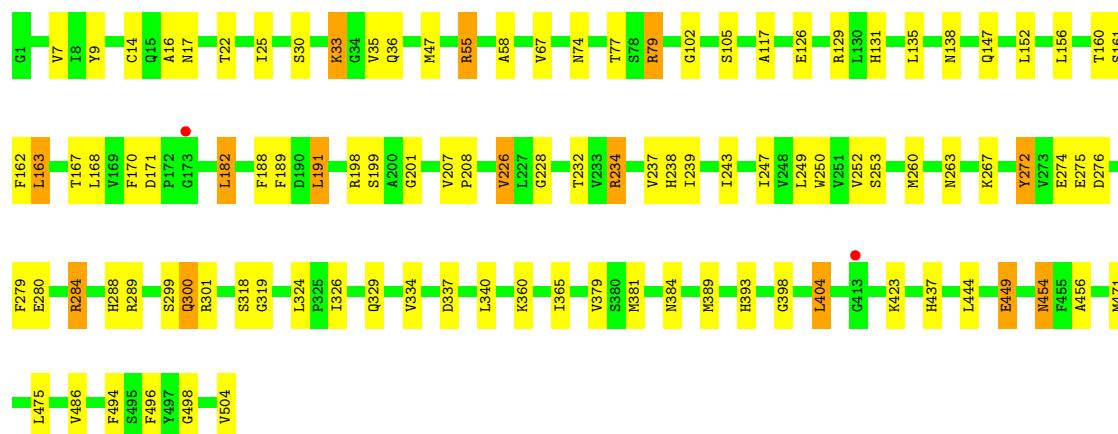
• Molecule 1: COAT PROTEIN

Chain BK: 82% 16%



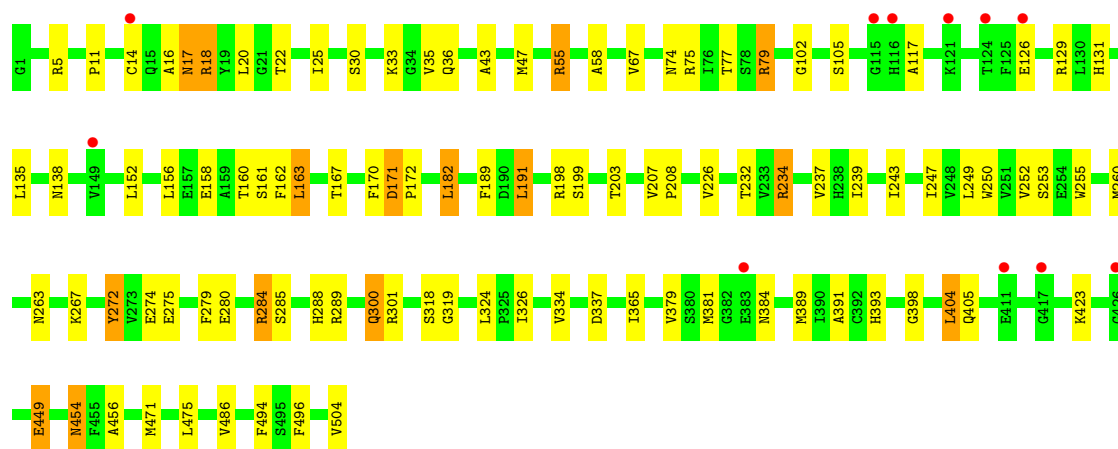
• Molecule 1: COAT PROTEIN

Chain BL: 79% 18%

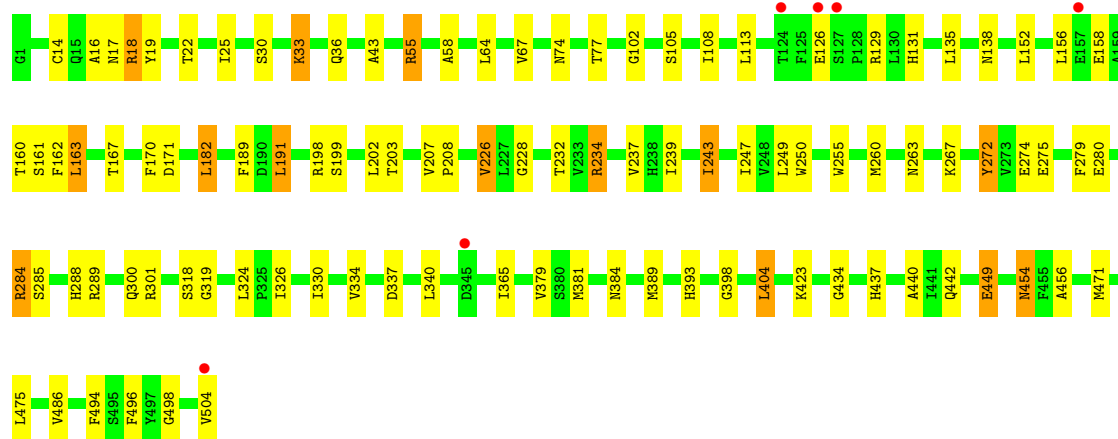
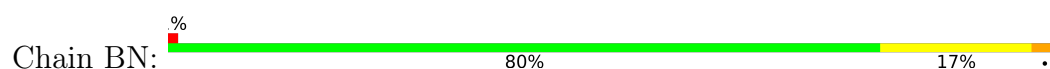


• Molecule 1: COAT PROTEIN

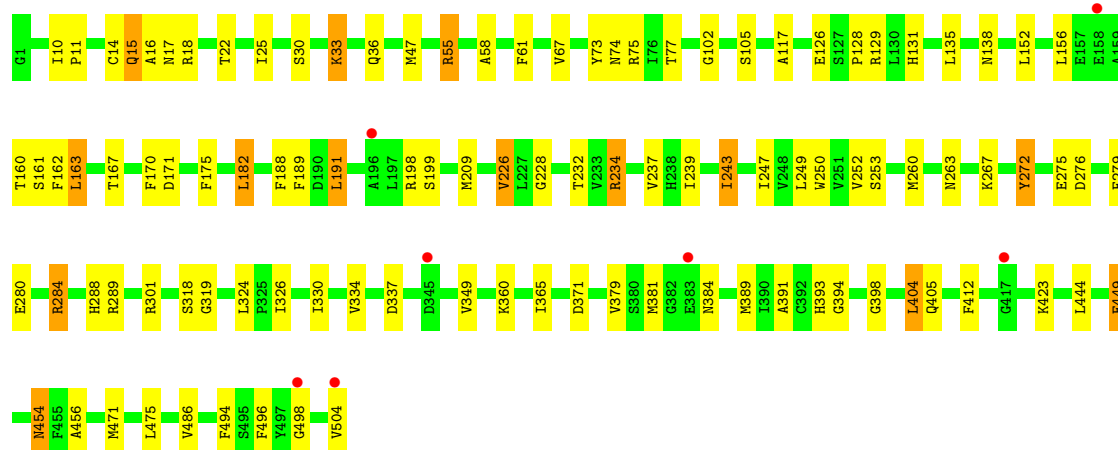
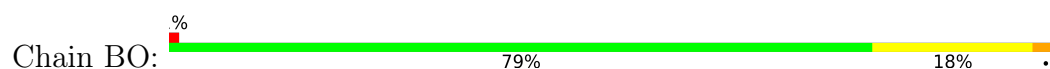
Chain BM: 2% 80% 17%



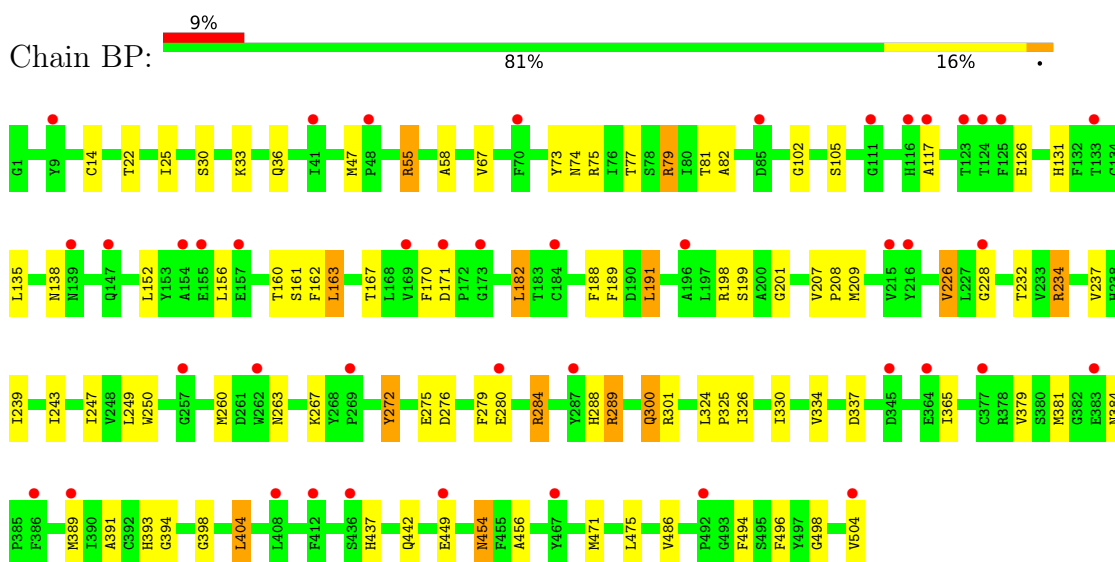
• Molecule 1: COAT PROTEIN



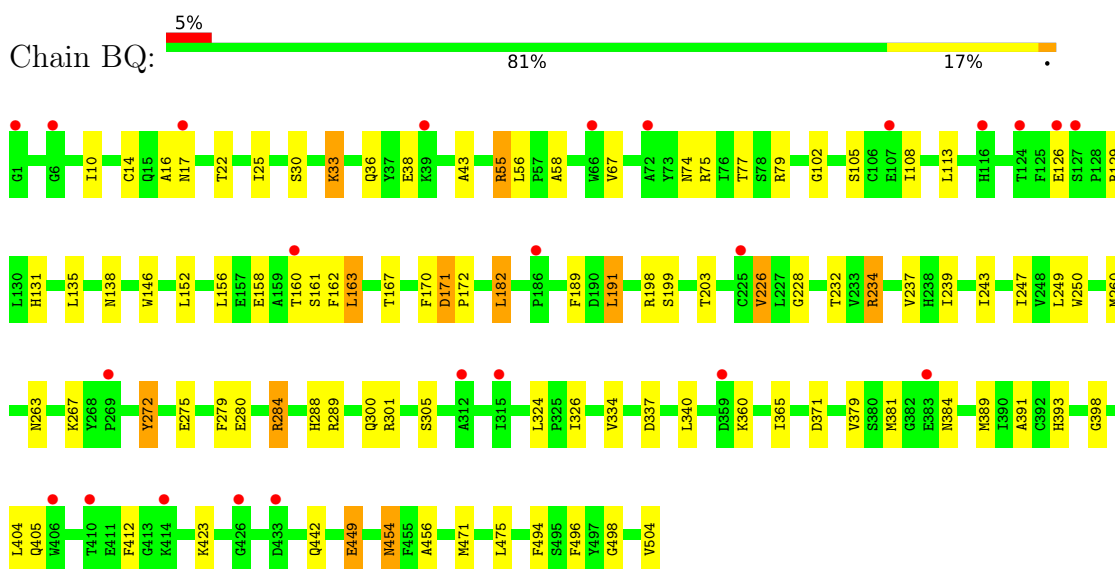
• Molecule 1: COAT PROTEIN



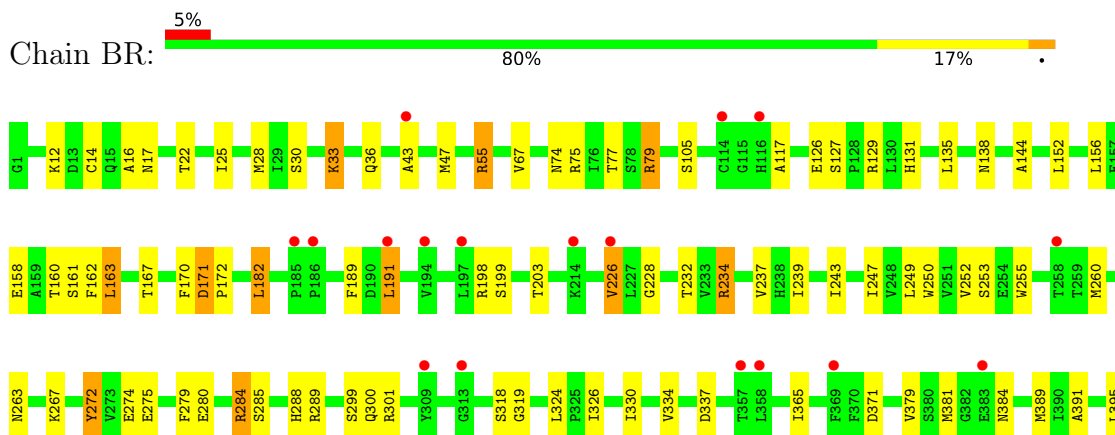
• Molecule 1: COAT PROTEIN

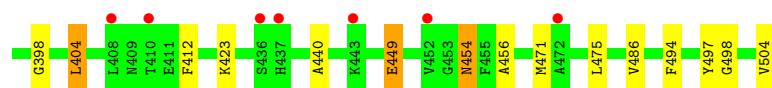


• Molecule 1: COAT PROTEIN

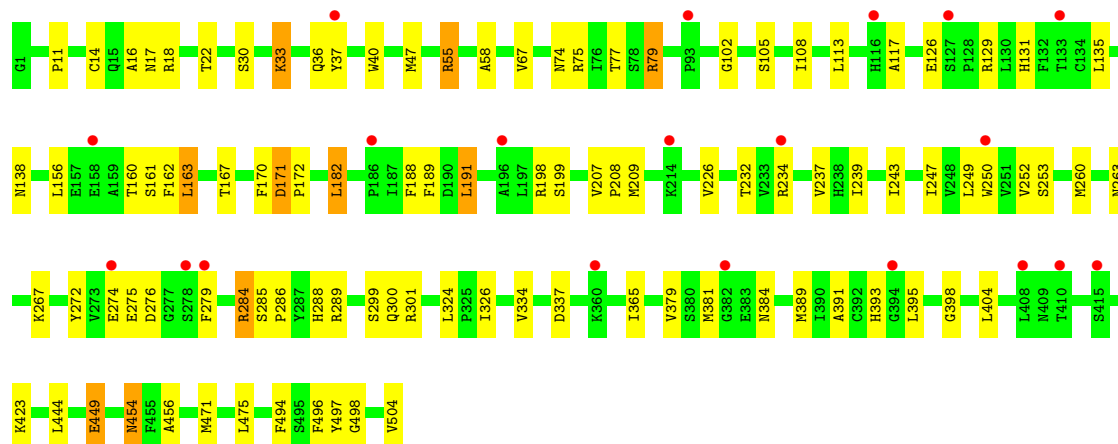
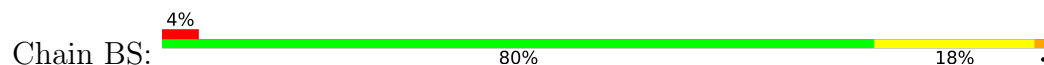


• Molecule 1: COAT PROTEIN

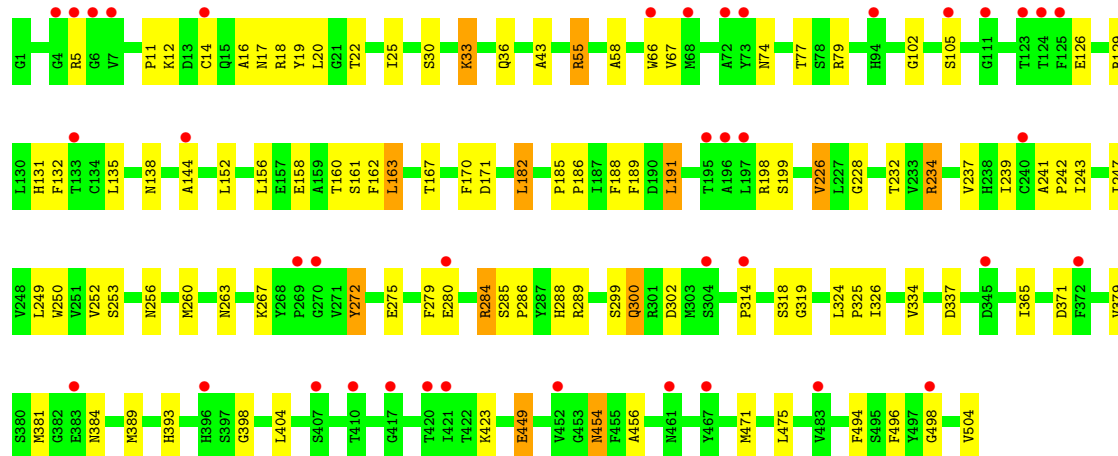
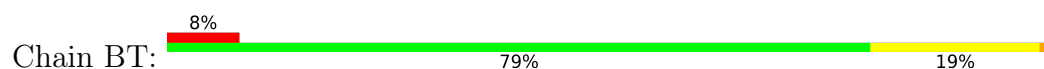




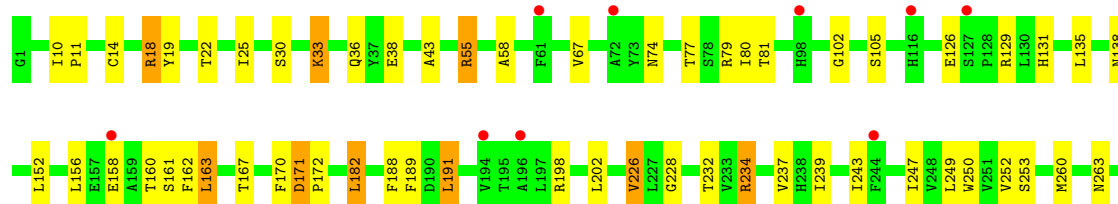
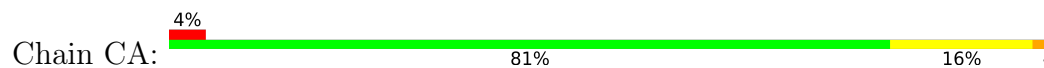
• Molecule 1: COAT PROTEIN

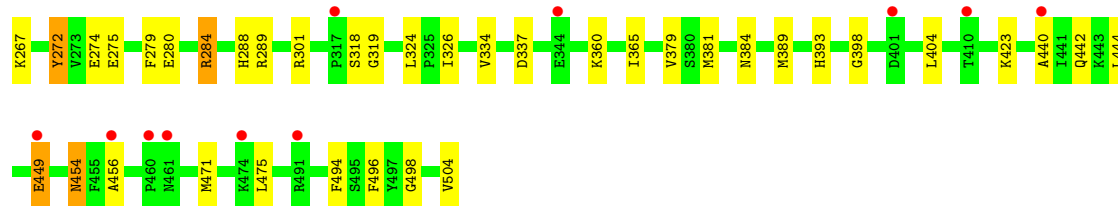


• Molecule 1: COAT PROTEIN

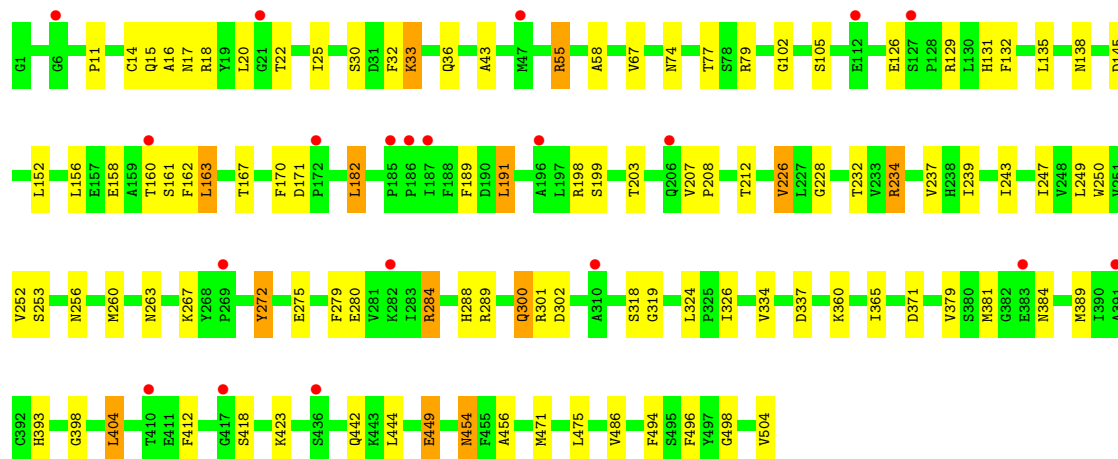
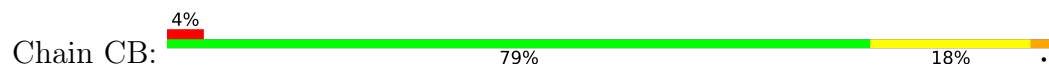


• Molecule 1: COAT PROTEIN

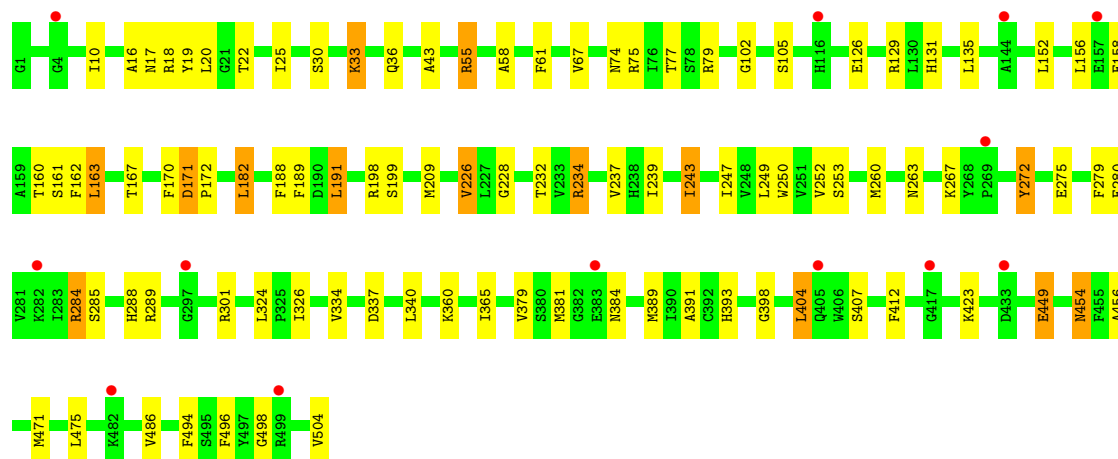
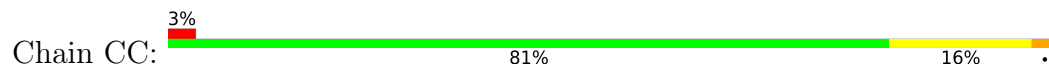




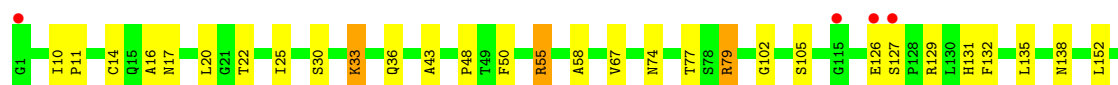
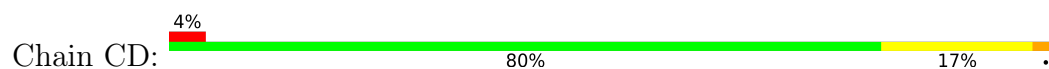
• Molecule 1: COAT PROTEIN

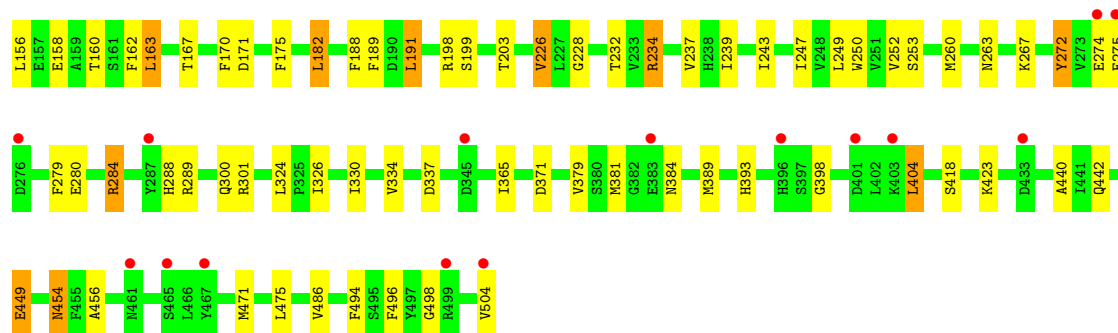


• Molecule 1: COAT PROTEIN

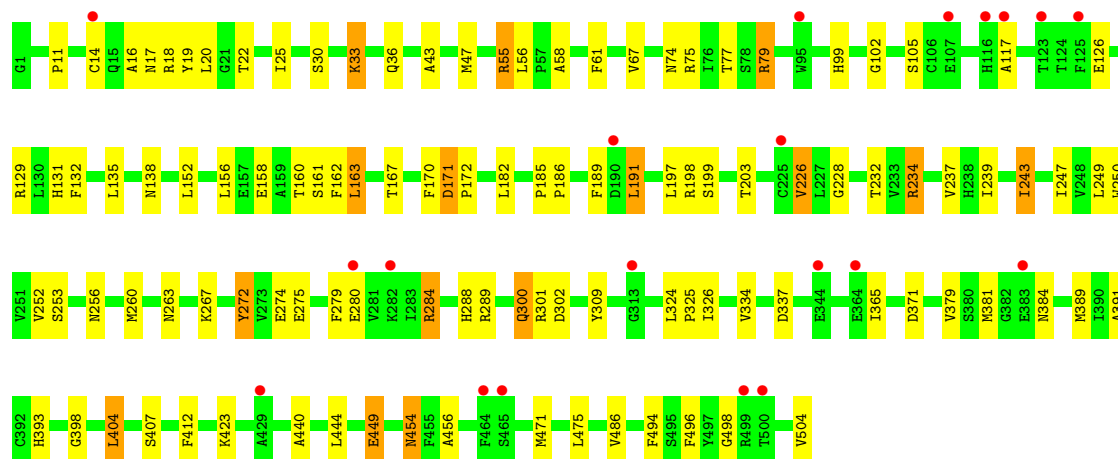
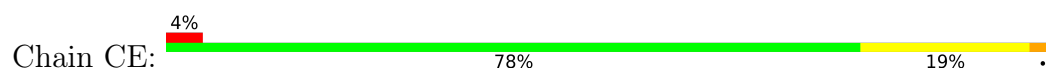


• Molecule 1: COAT PROTEIN

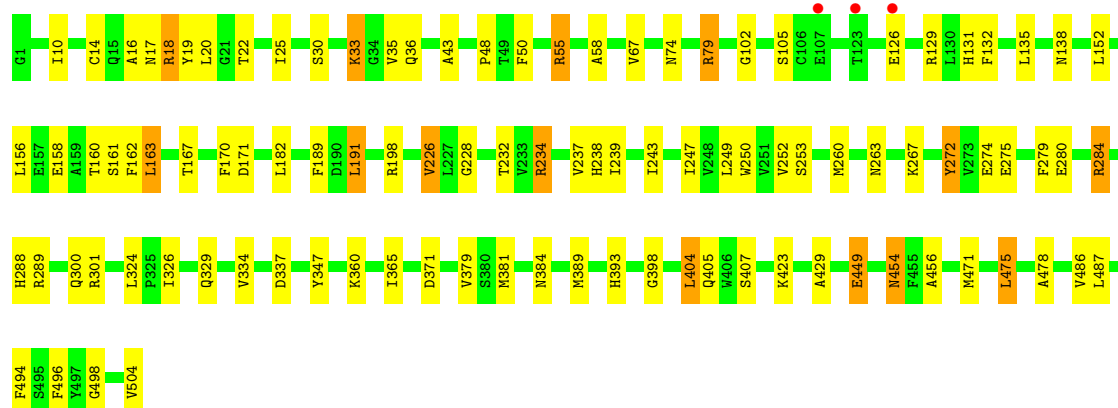
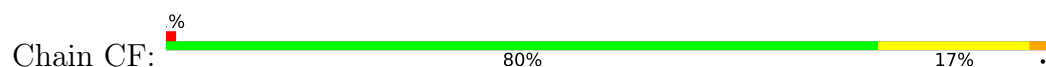




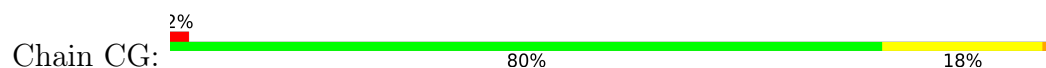
● Molecule 1: COAT PROTEIN

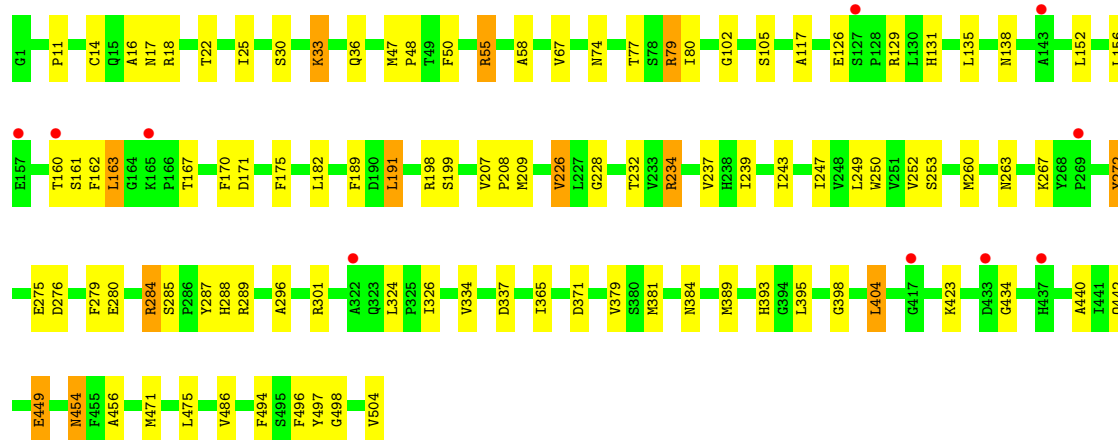


● Molecule 1: COAT PROTEIN

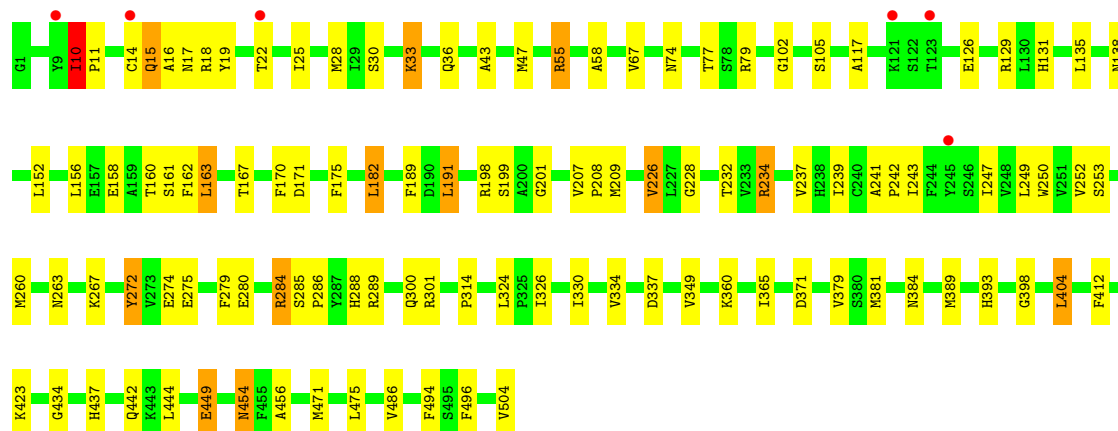
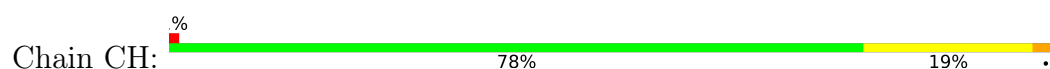


● Molecule 1: COAT PROTEIN

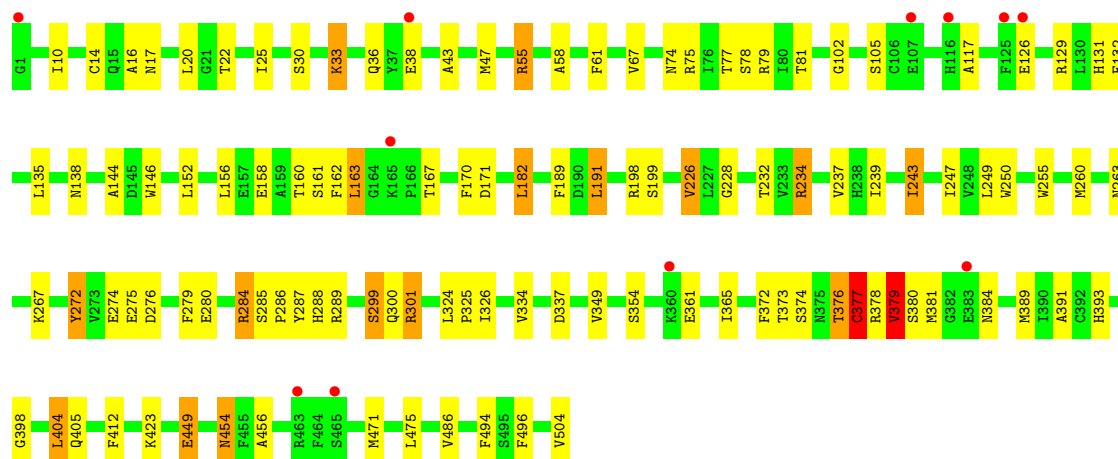
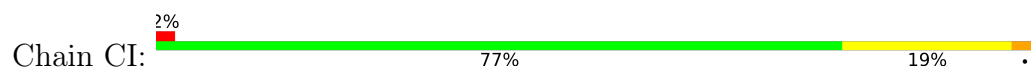




• Molecule 1: COAT PROTEIN

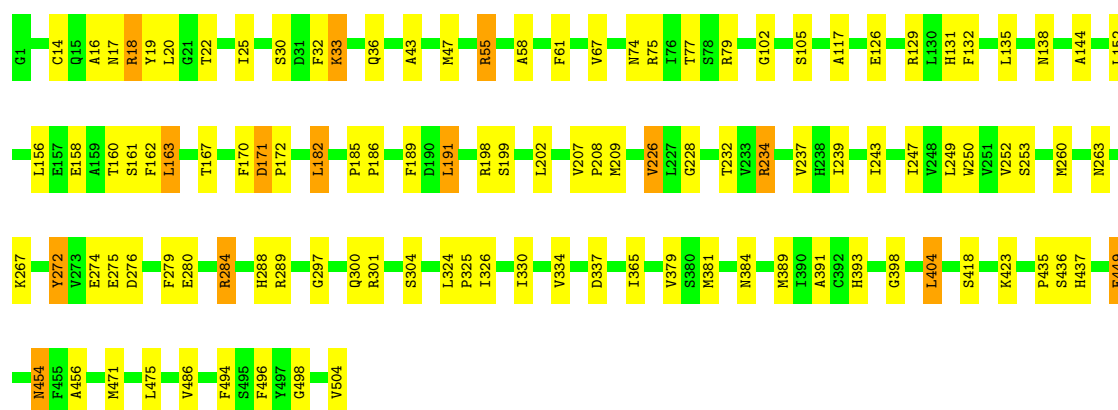


• Molecule 1: COAT PROTEIN



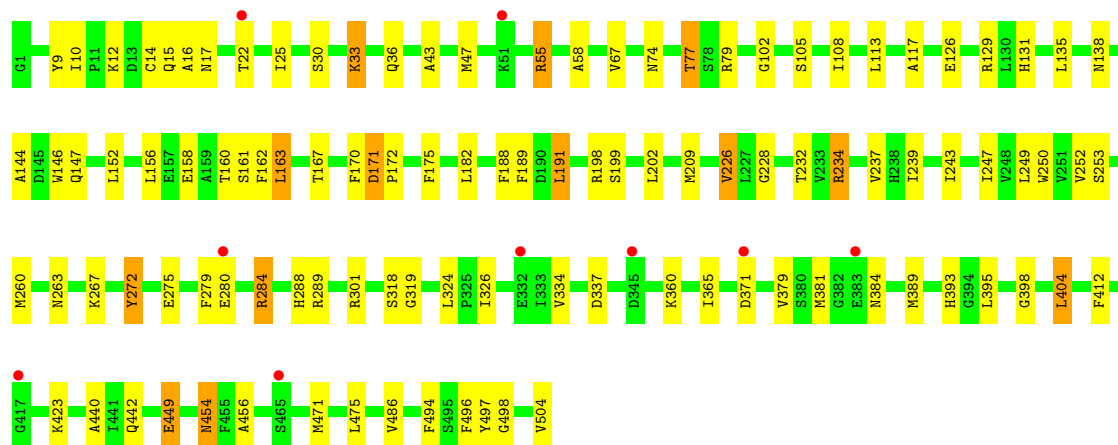
• Molecule 1: COAT PROTEIN

Chain CJ:  78% 19%



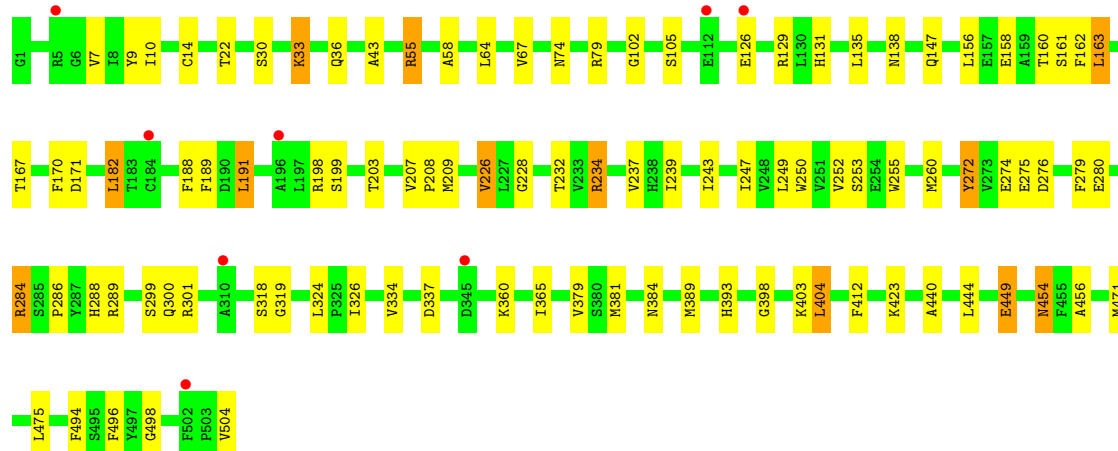
• Molecule 1: COAT PROTEIN

Chain CK:  79% 19%

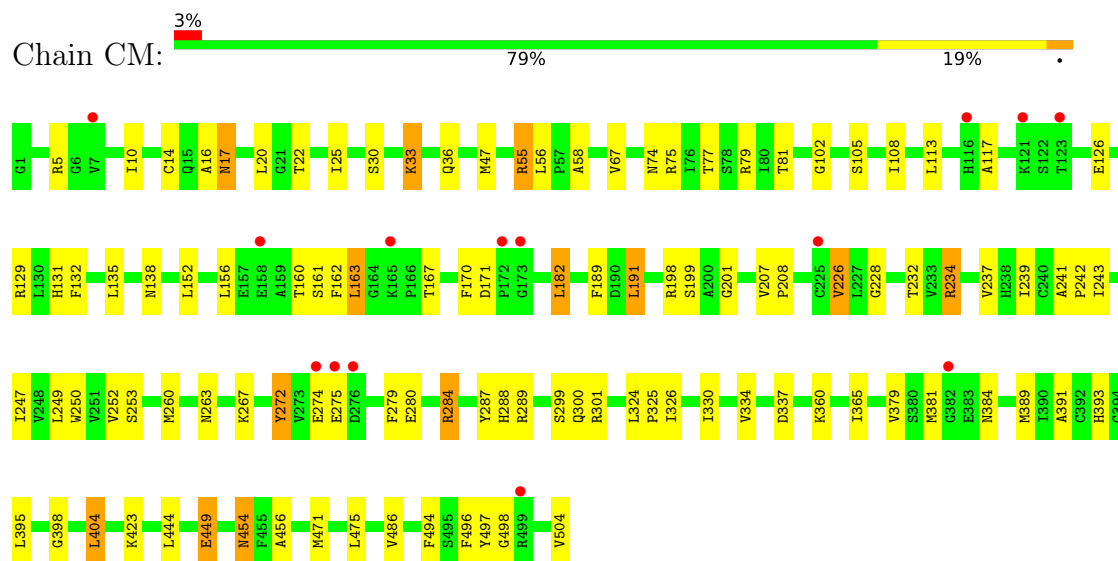


• Molecule 1: COAT PROTEIN

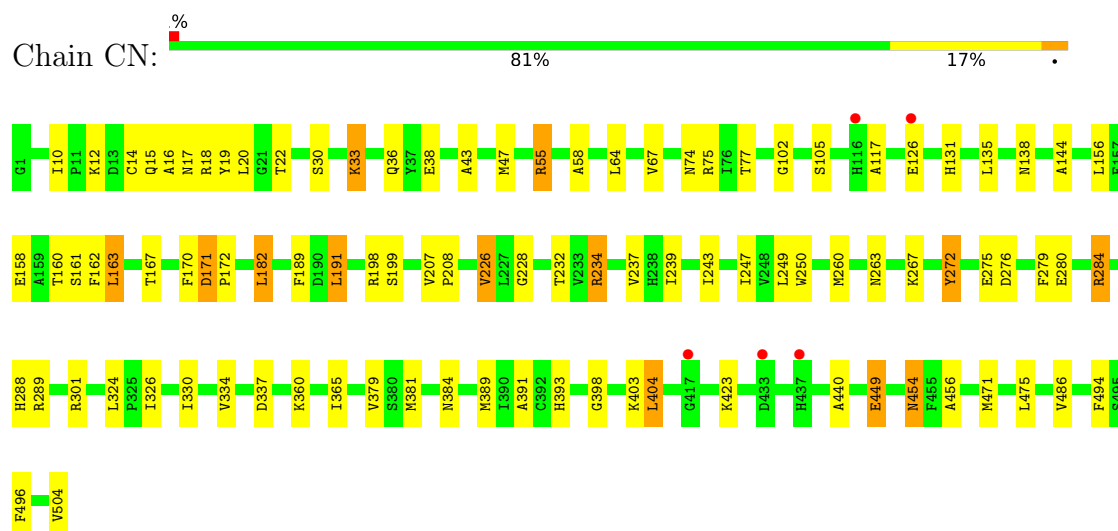
Chain CL:  81% 17%



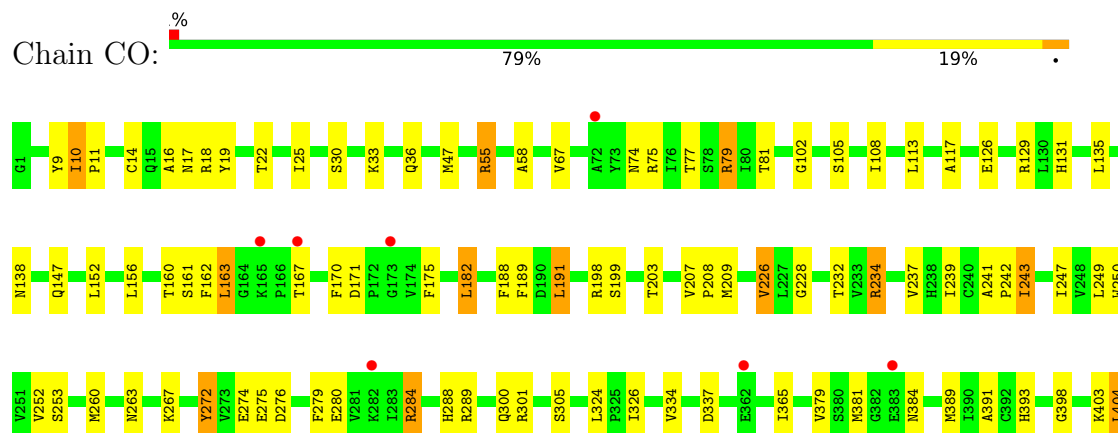
• Molecule 1: COAT PROTEIN

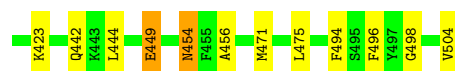


• Molecule 1: COAT PROTEIN



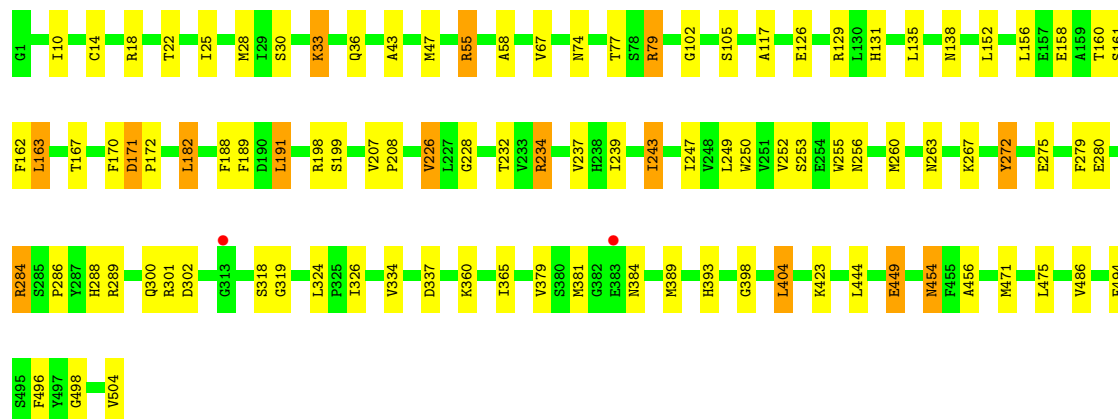
• Molecule 1: COAT PROTEIN





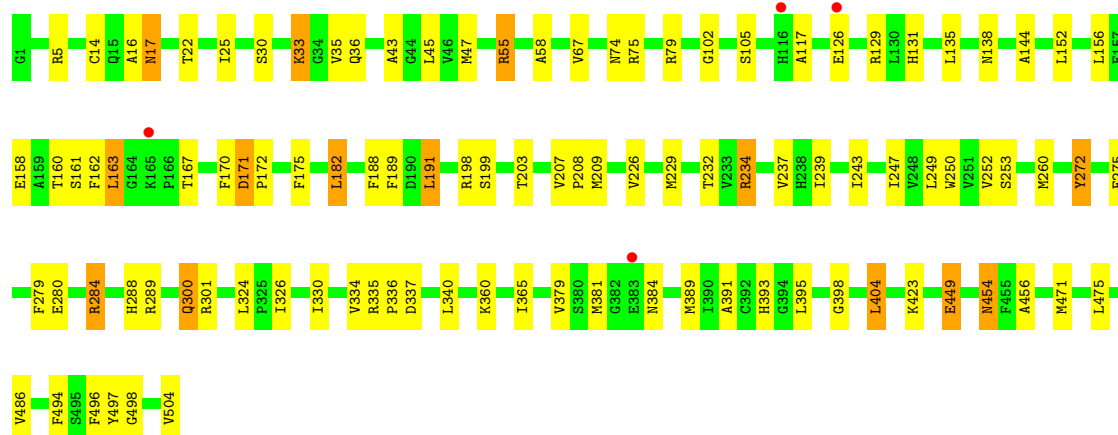
• Molecule 1: COAT PROTEIN

Chain CP: 80% 17%



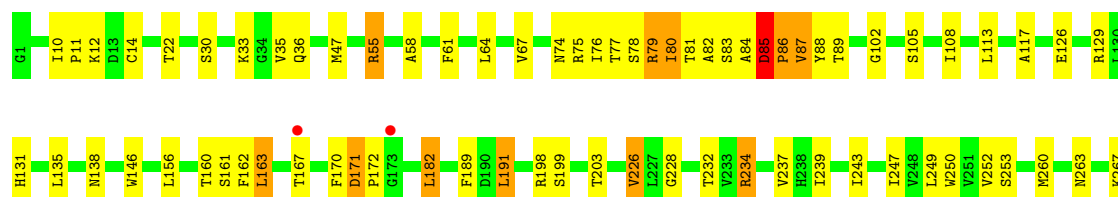
• Molecule 1: COAT PROTEIN

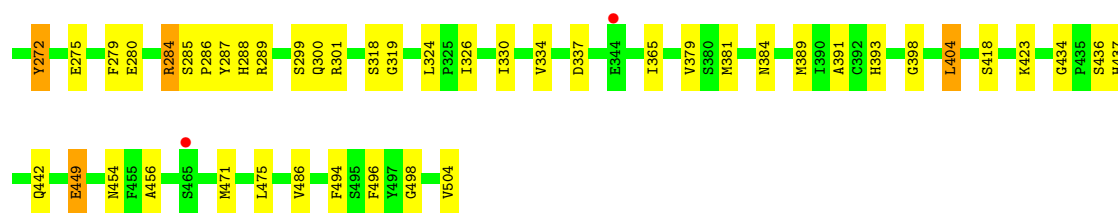
Chain CQ: 80% 18%



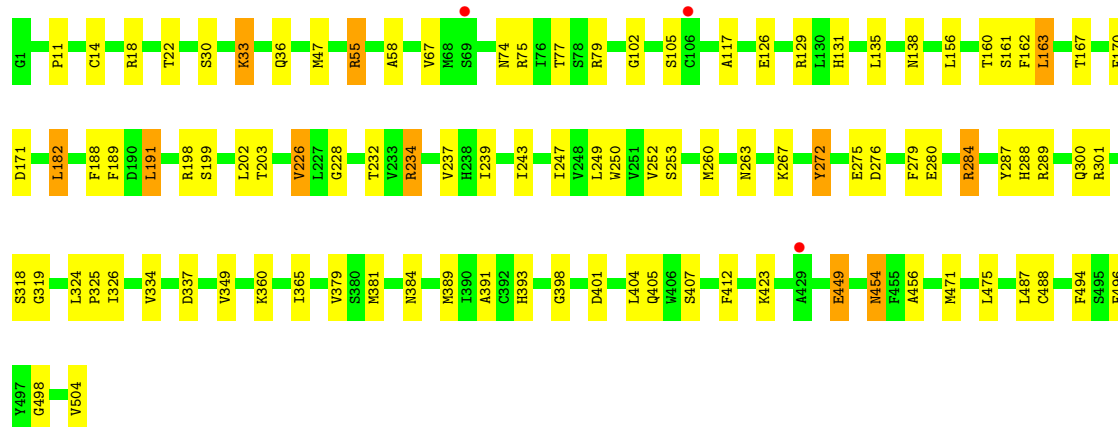
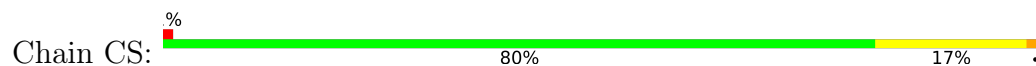
• Molecule 1: COAT PROTEIN

Chain CR: 77% 20%

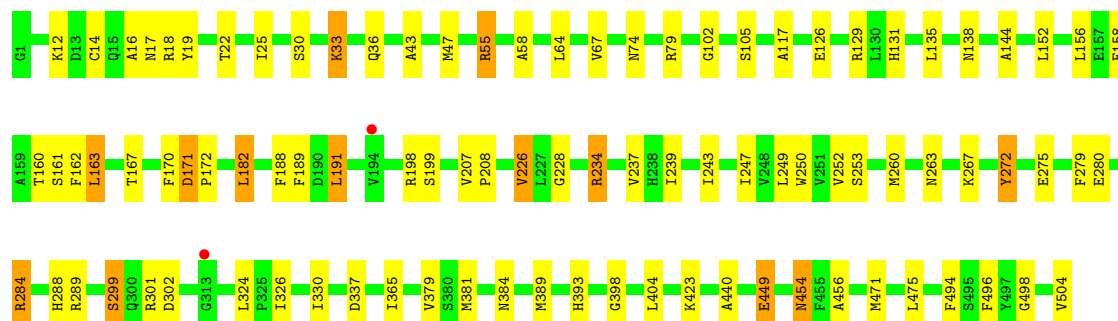
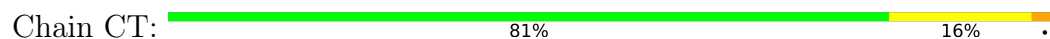




● Molecule 1: COAT PROTEIN



● Molecule 1: COAT PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	283.60Å 295.50Å 394.30Å 90.00° 91.60° 90.00°	Depositor
Resolution (Å)	49.80 – 3.70 49.80 – 3.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (49.80-3.70) 99.0 (49.80-3.70)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 3.67Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.232 , 0.247 0.244 , 0.256	Depositor DCC
R_{free} test set	34196 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	66.2	Xtriage
Anisotropy	0.406	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 81.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.088 for -k,-h,-l 0.087 for k,h,-l 0.089 for h,-k,-l	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	237060	wwPDB-VP
Average B, all atoms (Å ²)	91.0	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.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.57	0/4058	0.88	4/5517 (0.1%)
1	AB	0.65	1/4058 (0.0%)	0.91	5/5517 (0.1%)
1	AC	0.57	0/4058	0.88	3/5517 (0.1%)
1	AD	0.57	0/4058	0.88	2/5517 (0.0%)
1	AE	0.63	0/4058	0.90	2/5517 (0.0%)
1	AF	0.57	0/4058	0.89	2/5517 (0.0%)
1	AG	0.69	2/4058 (0.0%)	0.94	9/5517 (0.2%)
1	AH	0.58	0/4058	0.89	3/5517 (0.1%)
1	AI	0.58	0/4058	0.89	4/5517 (0.1%)
1	AJ	0.56	0/4058	0.87	2/5517 (0.0%)
1	AK	0.55	0/4058	0.88	2/5517 (0.0%)
1	AL	0.59	0/4058	0.89	2/5517 (0.0%)
1	AM	0.60	0/4058	0.89	4/5517 (0.1%)
1	AN	0.58	0/4058	0.89	2/5517 (0.0%)
1	AO	0.69	3/4058 (0.1%)	0.92	8/5517 (0.1%)
1	AP	0.60	0/4058	0.89	4/5517 (0.1%)
1	AQ	0.57	0/4058	0.89	5/5517 (0.1%)
1	AR	0.60	0/4058	0.89	7/5517 (0.1%)
1	AS	0.58	0/4058	0.87	2/5517 (0.0%)
1	AT	0.56	0/4058	0.87	4/5517 (0.1%)
1	BA	0.56	0/4058	0.88	2/5517 (0.0%)
1	BB	0.58	0/4058	0.90	4/5517 (0.1%)
1	BC	0.55	0/4058	0.88	4/5517 (0.1%)
1	BD	0.55	0/4058	0.88	6/5517 (0.1%)
1	BE	0.57	0/4058	0.88	4/5517 (0.1%)
1	BF	0.57	0/4058	0.89	2/5517 (0.0%)
1	BG	0.56	0/4058	0.87	2/5517 (0.0%)
1	BH	0.58	0/4058	0.88	4/5517 (0.1%)
1	BI	0.61	0/4058	0.89	2/5517 (0.0%)
1	BJ	0.56	0/4058	0.88	3/5517 (0.1%)
1	BK	0.56	0/4058	0.87	4/5517 (0.1%)
1	BL	0.59	0/4058	0.89	2/5517 (0.0%)
1	BM	0.62	0/4058	0.90	2/5517 (0.0%)
1	BN	0.58	0/4058	0.89	2/5517 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BO	0.60	0/4058	0.89	4/5517 (0.1%)
1	BP	0.62	0/4058	0.91	2/5517 (0.0%)
1	BQ	0.58	0/4058	0.89	2/5517 (0.0%)
1	BR	0.58	0/4058	0.89	4/5517 (0.1%)
1	BS	0.57	0/4058	0.89	2/5517 (0.0%)
1	BT	0.56	0/4058	0.87	2/5517 (0.0%)
1	CA	0.56	0/4058	0.89	3/5517 (0.1%)
1	CB	0.56	0/4058	0.88	2/5517 (0.0%)
1	CC	0.56	0/4058	0.87	4/5517 (0.1%)
1	CD	0.57	0/4058	0.88	2/5517 (0.0%)
1	CE	0.58	1/4058 (0.0%)	0.89	2/5517 (0.0%)
1	CF	0.55	0/4058	0.88	3/5517 (0.1%)
1	CG	0.56	0/4058	0.89	6/5517 (0.1%)
1	CH	0.55	0/4058	0.88	4/5517 (0.1%)
1	CI	0.64	2/4058 (0.0%)	0.90	2/5517 (0.0%)
1	CJ	0.57	0/4058	0.89	2/5517 (0.0%)
1	CK	0.56	0/4058	0.87	2/5517 (0.0%)
1	CL	0.58	0/4058	0.89	4/5517 (0.1%)
1	CM	0.59	0/4058	0.87	2/5517 (0.0%)
1	CN	0.59	0/4058	0.89	2/5517 (0.0%)
1	CO	0.59	0/4058	0.89	4/5517 (0.1%)
1	CP	0.61	0/4058	0.89	2/5517 (0.0%)
1	CQ	0.58	0/4058	0.89	2/5517 (0.0%)
1	CR	0.67	0/4058	0.93	8/5517 (0.1%)
1	CS	0.58	0/4058	0.89	2/5517 (0.0%)
1	CT	0.58	0/4058	0.87	2/5517 (0.0%)
All	All	0.59	9/243480 (0.0%)	0.89	195/331020 (0.1%)

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	AA	0	2
1	AB	0	2
1	AC	0	2
1	AD	0	1
1	AE	0	1
1	AF	0	2
1	AG	0	2
1	AH	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	AI	0	2
1	AJ	0	2
1	AK	0	1
1	AL	0	1
1	AM	0	2
1	AN	0	2
1	AO	0	2
1	AP	0	2
1	AQ	0	1
1	AR	0	2
1	AS	0	2
1	AT	0	2
1	BA	0	2
1	BB	0	2
1	BC	0	1
1	BD	0	2
1	BE	0	1
1	BF	0	2
1	BG	0	2
1	BH	0	1
1	BI	0	1
1	BJ	0	2
1	BK	0	2
1	BL	0	2
1	BM	0	1
1	BN	0	2
1	BO	0	2
1	BP	0	1
1	BQ	0	2
1	BR	0	2
1	BS	0	2
1	BT	0	2
1	CA	0	2
1	CB	0	2
1	CC	0	2
1	CD	0	2
1	CE	0	2
1	CF	0	2
1	CG	0	2
1	CH	0	2
1	CI	0	3
1	CJ	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	CK	0	2
1	CL	0	2
1	CM	0	2
1	CN	0	2
1	CO	0	1
1	CP	0	2
1	CQ	0	2
1	CR	0	1
1	CS	0	2
1	CT	0	2
All	All	0	108

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CI	379	VAL	CA-CB	-10.58	1.44	1.55
1	AG	271	VAL	CA-CB	-6.26	1.46	1.55
1	AO	290	THR	CA-CB	-6.10	1.42	1.54
1	AG	259	THR	CA-C	-5.78	1.45	1.53
1	AO	292	ALA	CA-CB	-5.76	1.43	1.53
1	CI	376	THR	CA-CB	-5.61	1.45	1.53
1	AO	291	PRO	CA-C	-5.43	1.46	1.52
1	CE	99	HIS	ND1-CE1	-5.11	1.27	1.32
1	AB	256	ASN	CA-C	-5.08	1.46	1.53

All (195) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AG	263	ASN	N-CA-C	-11.97	98.23	111.28
1	AG	259	THR	N-CA-C	-9.31	98.24	110.43
1	AB	258	THR	N-CA-C	-8.29	96.11	108.79
1	AB	263	ASN	N-CA-C	-7.61	102.13	111.33
1	CR	80	ILE	N-CA-C	7.54	118.33	110.72
1	CR	85	ASP	N-CA-C	-7.27	99.07	109.62
1	CN	171	ASP	CA-C-N	7.05	126.88	119.05
1	CN	171	ASP	C-N-CA	7.05	126.88	119.05
1	CS	171	ASP	CA-C-N	7.05	126.88	119.05
1	CS	171	ASP	C-N-CA	7.05	126.88	119.05
1	AE	171	ASP	CA-C-N	7.03	126.85	119.05
1	AE	171	ASP	C-N-CA	7.03	126.85	119.05
1	AO	300	GLN	N-CA-C	-7.01	103.82	112.38
1	CK	171	ASP	CA-C-N	6.99	126.81	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CK	171	ASP	C-N-CA	6.99	126.81	119.05
1	BN	171	ASP	CA-C-N	6.96	126.77	119.05
1	BN	171	ASP	C-N-CA	6.96	126.77	119.05
1	CR	171	ASP	CA-C-N	6.95	126.77	119.05
1	CR	171	ASP	C-N-CA	6.95	126.77	119.05
1	AT	171	ASP	CA-C-N	6.93	126.74	119.05
1	AT	171	ASP	C-N-CA	6.93	126.74	119.05
1	BB	10	ILE	CA-C-N	6.91	126.90	119.78
1	BB	10	ILE	C-N-CA	6.91	126.90	119.78
1	AP	10	ILE	CA-C-N	6.88	126.87	119.78
1	AP	10	ILE	C-N-CA	6.88	126.87	119.78
1	AF	171	ASP	CA-C-N	6.85	126.66	119.05
1	AF	171	ASP	C-N-CA	6.85	126.66	119.05
1	BL	171	ASP	CA-C-N	6.85	126.65	119.05
1	BL	171	ASP	C-N-CA	6.85	126.65	119.05
1	CR	86	PRO	CA-C-N	-6.82	109.69	121.97
1	CR	86	PRO	C-N-CA	-6.82	109.69	121.97
1	CT	171	ASP	CA-C-N	6.80	126.60	119.05
1	CT	171	ASP	C-N-CA	6.80	126.60	119.05
1	BB	171	ASP	CA-C-N	6.79	126.59	119.05
1	BB	171	ASP	C-N-CA	6.79	126.59	119.05
1	CO	171	ASP	CA-C-N	6.79	126.59	119.05
1	CO	171	ASP	C-N-CA	6.79	126.59	119.05
1	BF	171	ASP	CA-C-N	6.76	126.56	119.05
1	BF	171	ASP	C-N-CA	6.76	126.56	119.05
1	CE	171	ASP	CA-C-N	6.76	126.56	119.05
1	CE	171	ASP	C-N-CA	6.76	126.56	119.05
1	BM	171	ASP	CA-C-N	6.75	126.54	119.05
1	BM	171	ASP	C-N-CA	6.75	126.54	119.05
1	BR	171	ASP	CA-C-N	6.74	126.53	119.05
1	BR	171	ASP	C-N-CA	6.74	126.53	119.05
1	CD	171	ASP	CA-C-N	6.74	126.53	119.05
1	CD	171	ASP	C-N-CA	6.74	126.53	119.05
1	AR	171	ASP	CA-C-N	6.71	126.50	119.05
1	AR	171	ASP	C-N-CA	6.71	126.50	119.05
1	CG	171	ASP	CA-C-N	6.67	126.45	119.05
1	CG	171	ASP	C-N-CA	6.67	126.45	119.05
1	BT	171	ASP	CA-C-N	6.64	126.42	119.05
1	BT	171	ASP	C-N-CA	6.64	126.42	119.05
1	AN	171	ASP	CA-C-N	6.64	126.42	119.05
1	AN	171	ASP	C-N-CA	6.64	126.42	119.05
1	CA	171	ASP	CA-C-N	6.62	126.40	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	171	ASP	C-N-CA	6.62	126.40	119.05
1	BO	171	ASP	CA-C-N	6.62	126.39	119.05
1	BO	171	ASP	C-N-CA	6.62	126.39	119.05
1	BE	171	ASP	CA-C-N	6.60	126.38	119.05
1	BE	171	ASP	C-N-CA	6.60	126.38	119.05
1	BD	171	ASP	CA-C-N	6.58	126.36	119.05
1	BD	171	ASP	C-N-CA	6.58	126.36	119.05
1	CQ	171	ASP	CA-C-N	6.54	126.31	119.05
1	CQ	171	ASP	C-N-CA	6.54	126.31	119.05
1	AP	171	ASP	CA-C-N	6.54	126.31	119.05
1	AP	171	ASP	C-N-CA	6.54	126.31	119.05
1	CM	171	ASP	CA-C-N	6.50	126.27	119.05
1	CM	171	ASP	C-N-CA	6.50	126.27	119.05
1	AM	171	ASP	CA-C-N	6.48	126.24	119.05
1	AM	171	ASP	C-N-CA	6.48	126.24	119.05
1	AK	171	ASP	CA-C-N	6.47	126.23	119.05
1	AK	171	ASP	C-N-CA	6.47	126.23	119.05
1	BC	171	ASP	CA-C-N	6.46	126.22	119.05
1	BC	171	ASP	C-N-CA	6.46	126.22	119.05
1	AH	171	ASP	CA-C-N	6.46	126.22	119.05
1	AH	171	ASP	C-N-CA	6.46	126.22	119.05
1	BQ	171	ASP	CA-C-N	6.46	126.22	119.05
1	BQ	171	ASP	C-N-CA	6.46	126.22	119.05
1	CH	171	ASP	CA-C-N	6.45	126.21	119.05
1	CH	171	ASP	C-N-CA	6.45	126.21	119.05
1	AQ	171	ASP	CA-C-N	6.44	126.19	119.05
1	AQ	171	ASP	C-N-CA	6.44	126.19	119.05
1	AD	171	ASP	CA-C-N	6.43	126.19	119.05
1	AD	171	ASP	C-N-CA	6.43	126.19	119.05
1	AS	171	ASP	CA-C-N	6.43	126.19	119.05
1	AS	171	ASP	C-N-CA	6.43	126.19	119.05
1	AG	171	ASP	CA-C-N	6.42	126.17	119.05
1	AG	171	ASP	C-N-CA	6.42	126.17	119.05
1	AJ	171	ASP	CA-C-N	6.40	126.15	119.05
1	AJ	171	ASP	C-N-CA	6.40	126.15	119.05
1	AI	171	ASP	CA-C-N	6.39	126.14	119.05
1	AI	171	ASP	C-N-CA	6.39	126.14	119.05
1	CI	171	ASP	CA-C-N	6.38	126.14	119.05
1	CI	171	ASP	C-N-CA	6.38	126.14	119.05
1	BK	171	ASP	CA-C-N	6.38	126.13	119.05
1	BK	171	ASP	C-N-CA	6.38	126.13	119.05
1	CB	171	ASP	CA-C-N	6.37	126.12	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CB	171	ASP	C-N-CA	6.37	126.12	119.05
1	AO	171	ASP	CA-C-N	6.36	126.11	119.05
1	AO	171	ASP	C-N-CA	6.36	126.11	119.05
1	CF	171	ASP	CA-C-N	6.35	126.09	119.05
1	CF	171	ASP	C-N-CA	6.35	126.09	119.05
1	BH	171	ASP	CA-C-N	6.34	126.09	119.05
1	BH	171	ASP	C-N-CA	6.34	126.09	119.05
1	AG	274	GLU	N-CA-C	6.32	118.17	111.28
1	AO	296	ALA	N-CA-C	-6.32	101.75	110.35
1	CC	171	ASP	CA-C-N	6.31	126.05	119.05
1	CC	171	ASP	C-N-CA	6.31	126.05	119.05
1	AC	171	ASP	CA-C-N	6.28	126.02	119.05
1	AC	171	ASP	C-N-CA	6.28	126.02	119.05
1	AL	171	ASP	CA-C-N	6.28	126.02	119.05
1	AL	171	ASP	C-N-CA	6.28	126.02	119.05
1	BP	171	ASP	CA-C-N	6.26	126.00	119.05
1	BP	171	ASP	C-N-CA	6.26	126.00	119.05
1	CR	80	ILE	CB-CA-C	-6.24	103.60	112.22
1	AO	290	THR	CB-CA-C	-6.19	99.24	109.15
1	AB	171	ASP	CA-C-N	6.19	125.92	119.05
1	AB	171	ASP	C-N-CA	6.19	125.92	119.05
1	BI	171	ASP	CA-C-N	6.17	125.90	119.05
1	BI	171	ASP	C-N-CA	6.17	125.90	119.05
1	CL	171	ASP	CA-C-N	6.15	125.88	119.05
1	CL	171	ASP	C-N-CA	6.15	125.88	119.05
1	BJ	171	ASP	CA-C-N	6.14	125.87	119.05
1	BJ	171	ASP	C-N-CA	6.14	125.87	119.05
1	BG	171	ASP	CA-C-N	6.12	125.85	119.05
1	BG	171	ASP	C-N-CA	6.12	125.85	119.05
1	AO	293	ARG	N-CA-C	6.12	118.15	108.79
1	CP	171	ASP	CA-C-N	6.05	125.77	119.05
1	CP	171	ASP	C-N-CA	6.05	125.77	119.05
1	BA	171	ASP	CA-C-N	6.05	125.76	119.05
1	BA	171	ASP	C-N-CA	6.05	125.76	119.05
1	CJ	171	ASP	CA-C-N	6.02	125.73	119.05
1	CJ	171	ASP	C-N-CA	6.02	125.73	119.05
1	AA	171	ASP	CA-C-N	6.00	125.71	119.05
1	AA	171	ASP	C-N-CA	6.00	125.71	119.05
1	BS	171	ASP	CA-C-N	6.00	125.71	119.05
1	BS	171	ASP	C-N-CA	6.00	125.71	119.05
1	AI	10	ILE	CA-C-N	5.99	125.75	119.76
1	AI	10	ILE	C-N-CA	5.99	125.75	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AQ	10	ILE	N-CA-C	5.98	114.47	107.77
1	AG	276	ASP	N-CA-C	-5.93	102.28	110.35
1	CG	80	ILE	CB-CA-C	-5.86	104.49	110.93
1	AO	291	PRO	CA-C-O	-5.83	114.66	121.95
1	CR	82	ALA	N-CA-C	-5.70	105.06	111.28
1	CG	80	ILE	N-CA-C	5.64	118.57	113.10
1	CL	10	ILE	CA-C-N	5.51	125.98	120.14
1	CL	10	ILE	C-N-CA	5.51	125.98	120.14
1	AR	285	SER	CA-C-N	5.39	125.06	119.56
1	AR	285	SER	C-N-CA	5.39	125.06	119.56
1	AG	285	SER	CA-C-N	5.37	125.04	119.56
1	AG	285	SER	C-N-CA	5.37	125.04	119.56
1	AR	127	SER	CA-C-N	5.35	125.60	119.83
1	AR	127	SER	C-N-CA	5.35	125.60	119.83
1	AR	174	VAL	N-CA-C	5.30	116.05	106.61
1	CA	80	ILE	CB-CA-C	-5.27	105.48	110.70
1	CO	10	ILE	CA-C-N	5.27	125.72	120.14
1	CO	10	ILE	C-N-CA	5.27	125.72	120.14
1	AO	291	PRO	N-CA-C	-5.24	103.23	111.34
1	BJ	165	LYS	N-CA-C	-5.23	103.10	110.31
1	BD	10	ILE	CA-C-N	5.22	125.12	119.85
1	BD	10	ILE	C-N-CA	5.22	125.12	119.85
1	AH	76	ILE	N-CA-C	5.19	117.88	112.90
1	BK	10	ILE	CA-C-N	5.19	125.09	119.85
1	BK	10	ILE	C-N-CA	5.19	125.09	119.85
1	AQ	127	SER	CA-C-N	5.16	125.41	119.83
1	AQ	127	SER	C-N-CA	5.16	125.41	119.83
1	BD	285	SER	CA-C-N	5.15	124.81	119.56
1	BD	285	SER	C-N-CA	5.15	124.81	119.56
1	CG	285	SER	CA-C-N	5.14	124.80	119.56
1	CG	285	SER	C-N-CA	5.14	124.80	119.56
1	AB	265	LEU	N-CA-C	-5.11	105.71	111.28
1	AM	10	ILE	CA-C-N	5.10	125.00	119.85
1	AM	10	ILE	C-N-CA	5.10	125.00	119.85
1	AT	285	SER	CA-C-N	5.09	124.75	119.56
1	AT	285	SER	C-N-CA	5.09	124.75	119.56
1	BR	127	SER	CA-C-N	5.08	125.31	119.83
1	BR	127	SER	C-N-CA	5.08	125.31	119.83
1	CC	285	SER	CA-C-N	5.08	124.74	119.56
1	CC	285	SER	C-N-CA	5.08	124.74	119.56
1	AA	285	SER	CA-C-N	5.08	124.74	119.56
1	AA	285	SER	C-N-CA	5.08	124.74	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BO	10	ILE	CA-C-N	5.07	124.97	119.85
1	BO	10	ILE	C-N-CA	5.07	124.97	119.85
1	BE	285	SER	CA-C-N	5.05	124.72	119.56
1	BE	285	SER	C-N-CA	5.05	124.72	119.56
1	CH	10	ILE	CA-C-N	5.03	124.93	119.85
1	CH	10	ILE	C-N-CA	5.03	124.93	119.85
1	BH	127	SER	CA-C-N	5.03	125.26	119.83
1	BH	127	SER	C-N-CA	5.03	125.26	119.83
1	BC	285	SER	CA-C-N	5.03	124.69	119.56
1	BC	285	SER	C-N-CA	5.03	124.69	119.56
1	AC	243	ILE	CB-CA-C	-5.02	104.72	112.05
1	CF	10	ILE	CB-CA-C	-5.01	105.22	110.53
1	AG	264	GLU	CB-CA-C	-5.01	102.33	110.85

There are no chirality outliers.

All (108) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	33	LYS	Peptide
1	AA	55	ARG	Peptide
1	AB	33	LYS	Peptide
1	AB	55	ARG	Peptide
1	AC	33	LYS	Peptide
1	AC	55	ARG	Peptide
1	AD	55	ARG	Peptide
1	AE	55	ARG	Peptide
1	AF	33	LYS	Peptide
1	AF	55	ARG	Peptide
1	AG	33	LYS	Peptide
1	AG	55	ARG	Peptide
1	AH	33	LYS	Peptide
1	AH	55	ARG	Peptide
1	AI	33	LYS	Peptide
1	AI	55	ARG	Peptide
1	AJ	33	LYS	Peptide
1	AJ	55	ARG	Peptide
1	AK	55	ARG	Peptide
1	AL	55	ARG	Peptide
1	AM	33	LYS	Peptide
1	AM	55	ARG	Peptide
1	AN	33	LYS	Peptide
1	AN	55	ARG	Peptide

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Mol	Chain	Res	Type	Group
1	AO	33	LYS	Peptide
1	AO	55	ARG	Peptide
1	AP	33	LYS	Peptide
1	AP	55	ARG	Peptide
1	AQ	55	ARG	Peptide
1	AR	33	LYS	Peptide
1	AR	55	ARG	Peptide
1	AS	33	LYS	Peptide
1	AS	55	ARG	Peptide
1	AT	33	LYS	Peptide
1	AT	55	ARG	Peptide
1	BA	33	LYS	Peptide
1	BA	55	ARG	Peptide
1	BB	33	LYS	Peptide
1	BB	55	ARG	Peptide
1	BC	55	ARG	Peptide
1	BD	33	LYS	Peptide
1	BD	55	ARG	Peptide
1	BE	55	ARG	Peptide
1	BF	33	LYS	Peptide
1	BF	55	ARG	Peptide
1	BG	33	LYS	Peptide
1	BG	55	ARG	Peptide
1	BH	55	ARG	Peptide
1	BI	55	ARG	Peptide
1	BJ	33	LYS	Peptide
1	BJ	55	ARG	Peptide
1	BK	33	LYS	Peptide
1	BK	55	ARG	Peptide
1	BL	33	LYS	Peptide
1	BL	55	ARG	Peptide
1	BM	55	ARG	Peptide
1	BN	33	LYS	Peptide
1	BN	55	ARG	Peptide
1	BO	33	LYS	Peptide
1	BO	55	ARG	Peptide
1	BP	55	ARG	Peptide
1	BQ	33	LYS	Peptide
1	BQ	55	ARG	Peptide
1	BR	33	LYS	Peptide
1	BR	55	ARG	Peptide
1	BS	33	LYS	Peptide

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Mol	Chain	Res	Type	Group
1	BS	55	ARG	Peptide
1	BT	33	LYS	Peptide
1	BT	55	ARG	Peptide
1	CA	33	LYS	Peptide
1	CA	55	ARG	Peptide
1	CB	33	LYS	Peptide
1	CB	55	ARG	Peptide
1	CC	33	LYS	Peptide
1	CC	55	ARG	Peptide
1	CD	33	LYS	Peptide
1	CD	55	ARG	Peptide
1	CE	33	LYS	Peptide
1	CE	55	ARG	Peptide
1	CF	33	LYS	Peptide
1	CF	55	ARG	Peptide
1	CG	33	LYS	Peptide
1	CG	55	ARG	Peptide
1	CH	33	LYS	Peptide
1	CH	55	ARG	Peptide
1	CI	33	LYS	Peptide
1	CI	372	PHE	Peptide
1	CI	55	ARG	Peptide
1	CJ	33	LYS	Peptide
1	CJ	55	ARG	Peptide
1	CK	33	LYS	Peptide
1	CK	55	ARG	Peptide
1	CL	33	LYS	Peptide
1	CL	55	ARG	Peptide
1	CM	33	LYS	Peptide
1	CM	55	ARG	Peptide
1	CN	33	LYS	Peptide
1	CN	55	ARG	Peptide
1	CO	55	ARG	Peptide
1	CP	33	LYS	Peptide
1	CP	55	ARG	Peptide
1	CQ	33	LYS	Peptide
1	CQ	55	ARG	Peptide
1	CR	55	ARG	Peptide
1	CS	33	LYS	Peptide
1	CS	55	ARG	Peptide
1	CT	33	LYS	Peptide
1	CT	55	ARG	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	3951	0	3909	103	0
1	AB	3951	0	3909	124	0
1	AC	3951	0	3909	97	0
1	AD	3951	0	3909	96	0
1	AE	3951	0	3909	96	0
1	AF	3951	0	3909	105	0
1	AG	3951	0	3907	155	1
1	AH	3951	0	3909	114	0
1	AI	3951	0	3909	119	5
1	AJ	3951	0	3909	116	1
1	AK	3951	0	3909	113	0
1	AL	3951	0	3909	116	0
1	AM	3951	0	3909	100	5
1	AN	3951	0	3909	119	1
1	AO	3951	0	3909	132	0
1	AP	3951	0	3909	92	0
1	AQ	3951	0	3909	107	0
1	AR	3951	0	3909	103	0
1	AS	3951	0	3909	97	0
1	AT	3951	0	3909	100	0
1	BA	3951	0	3909	106	0
1	BB	3951	0	3909	95	0
1	BC	3951	0	3909	88	0
1	BD	3951	0	3909	93	2
1	BE	3951	0	3909	99	1
1	BF	3951	0	3909	106	0
1	BG	3951	0	3909	112	2
1	BH	3951	0	3909	95	0
1	BI	3951	0	3909	92	0
1	BJ	3951	0	3909	100	0
1	BK	3951	0	3909	78	0
1	BL	3951	0	3909	101	0
1	BM	3951	0	3909	95	0
1	BN	3951	0	3909	95	0
1	BO	3951	0	3909	107	0
1	BP	3951	0	3909	102	0
1	BQ	3951	0	3909	90	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BR	3951	0	3909	102	0
1	BS	3951	0	3909	89	0
1	BT	3951	0	3909	95	0
1	CA	3951	0	3909	93	0
1	CB	3951	0	3909	100	3
1	CC	3951	0	3909	91	0
1	CD	3951	0	3909	100	0
1	CE	3951	0	3909	112	0
1	CF	3951	0	3909	106	0
1	CG	3951	0	3909	94	0
1	CH	3951	0	3909	104	0
1	CI	3951	0	3909	122	1
1	CJ	3951	0	3909	116	2
1	CK	3951	0	3909	92	0
1	CL	3951	0	3909	92	0
1	CM	3951	0	3909	94	0
1	CN	3951	0	3909	92	0
1	CO	3951	0	3909	104	0
1	CP	3951	0	3909	98	0
1	CQ	3951	0	3909	96	0
1	CR	3951	0	3909	129	0
1	CS	3951	0	3909	92	0
1	CT	3951	0	3909	84	0
All	All	237060	0	234538	5473	12

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (5473) 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:AG:263:ASN:ND2	1:BG:32:PHE:CA	1.68	1.50
1:AG:272:TYR:CE2	1:BG:55:ARG:CZ	2.02	1.43
1:AG:272:TYR:HE2	1:BG:55:ARG:NE	1.23	1.37
1:AN:430:MET:CE	1:AO:296:ALA:HB2	1.62	1.29
1:AG:272:TYR:HE2	1:BG:55:ARG:CZ	1.36	1.25
1:AN:430:MET:HE3	1:AO:296:ALA:CB	1.70	1.21
1:CR:86:PRO:O	1:CR:88:TYR:N	1.74	1.19
1:CR:79:ARG:CG	1:CR:79:ARG:HH11	1.57	1.15
1:AB:265:LEU:C	1:AB:265:LEU:HD12	1.62	1.15
1:AG:263:ASN:ND2	1:BG:32:PHE:HA	0.78	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:265:LEU:O	1:AG:265:LEU:HD12	1.50	1.11
1:AG:272:TYR:CE2	1:BG:55:ARG:NE	2.11	1.09
1:AG:272:TYR:HD2	1:BG:55:ARG:NH1	1.51	1.08
1:AB:250:TRP:HE1	1:AB:265:LEU:HD11	1.09	1.07
1:AG:272:TYR:CD2	1:BG:55:ARG:NH1	2.23	1.07
1:CF:79:ARG:HH11	1:CF:79:ARG:HG3	1.18	1.06
1:AB:265:LEU:C	1:AB:265:LEU:CD1	2.30	1.04
1:CR:79:ARG:HH11	1:CR:79:ARG:HG2	1.19	1.04
1:AL:272:TYR:CE2	1:CJ:55:ARG:NE	2.26	1.04
1:AG:272:TYR:CD2	1:BG:55:ARG:CZ	2.40	1.04
1:CR:86:PRO:O	1:CR:87:VAL:C	1.97	1.04
1:AO:295:LEU:HB2	1:AO:298:GLN:OE1	1.58	1.03
1:CC:250:TRP:CZ3	1:CC:272:TYR:HE1	1.77	1.01
1:AI:272:TYR:CE2	1:AO:55:ARG:NE	2.30	0.99
1:AA:38:GLU:OE1	1:AB:267:LYS:NZ	1.96	0.99
1:AH:55:ARG:NE	1:AK:272:TYR:CE2	2.31	0.99
1:AO:290:THR:HG23	1:AO:290:THR:O	1.63	0.97
1:AN:430:MET:HE3	1:AO:296:ALA:HB2	0.97	0.97
1:CI:376:THR:O	1:CI:377:CYS:HB3	1.62	0.96
1:AN:55:ARG:NE	1:AS:272:TYR:CE2	2.33	0.95
1:BO:250:TRP:CZ3	1:BO:272:TYR:HE1	1.83	0.95
1:AL:272:TYR:CE2	1:CJ:55:ARG:CD	2.49	0.95
1:CC:250:TRP:CZ3	1:CC:272:TYR:CE1	2.54	0.95
1:AN:430:MET:CE	1:AO:296:ALA:CB	2.39	0.94
1:BS:79:ARG:HG3	1:BS:79:ARG:HH11	1.31	0.94
1:AB:250:TRP:NE1	1:AB:265:LEU:HD11	1.83	0.94
1:CJ:272:TYR:HE2	1:CQ:55:ARG:NE	1.67	0.93
1:AJ:191:LEU:HD23	1:AJ:191:LEU:H	1.34	0.93
1:BJ:250:TRP:CZ3	1:BJ:272:TYR:HE1	1.85	0.93
1:BI:55:ARG:NE	1:BR:272:TYR:CE2	2.36	0.93
1:CD:79:ARG:HG3	1:CD:79:ARG:HH11	1.34	0.93
1:CJ:272:TYR:CE2	1:CQ:55:ARG:NE	2.37	0.93
1:BP:272:TYR:CE2	1:CE:55:ARG:NE	2.35	0.93
1:AO:295:LEU:O	1:AO:298:GLN:HB2	1.69	0.92
1:BO:272:TYR:CE2	1:BR:55:ARG:NE	2.37	0.92
1:AN:55:ARG:NE	1:AS:272:TYR:HE2	1.66	0.92
1:AS:250:TRP:CZ3	1:AS:272:TYR:HE1	1.87	0.92
1:CO:272:TYR:CE2	1:CR:55:ARG:NE	2.38	0.92
1:BJ:191:LEU:H	1:BJ:191:LEU:HD23	1.34	0.92
1:BP:250:TRP:CZ3	1:BP:272:TYR:HE1	1.86	0.92
1:AL:272:TYR:HE2	1:CJ:55:ARG:CD	1.82	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BO:250:TRP:CZ3	1:BO:272:TYR:CE1	2.58	0.91
1:BJ:250:TRP:CZ3	1:BJ:272:TYR:CE1	2.58	0.91
1:AG:265:LEU:HD12	1:AG:265:LEU:C	1.80	0.90
1:AC:191:LEU:H	1:AC:191:LEU:HD23	1.36	0.90
1:AG:79:ARG:HH11	1:AG:79:ARG:HG3	1.36	0.90
1:BJ:79:ARG:HH11	1:BJ:79:ARG:HG3	1.35	0.90
1:CI:377:CYS:SG	1:CI:378:ARG:N	2.43	0.90
1:CI:377:CYS:SG	1:CI:378:ARG:O	2.30	0.90
1:AB:191:LEU:HD23	1:AB:191:LEU:H	1.37	0.90
1:BL:9:TYR:CE1	1:BL:147:GLN:NE2	2.40	0.90
1:BE:191:LEU:HD23	1:BE:191:LEU:H	1.36	0.90
1:BP:272:TYR:HE2	1:CE:55:ARG:CD	1.84	0.90
1:BP:272:TYR:HE2	1:CE:55:ARG:NE	1.70	0.90
1:CE:272:TYR:CE2	1:CM:55:ARG:NE	2.40	0.89
1:AR:191:LEU:HD23	1:AR:191:LEU:H	1.38	0.89
1:AS:250:TRP:CZ3	1:AS:272:TYR:CE1	2.59	0.89
1:AL:191:LEU:HD23	1:AL:191:LEU:H	1.37	0.89
1:AB:265:LEU:HD12	1:AB:265:LEU:O	1.73	0.89
1:CC:191:LEU:HD23	1:CC:191:LEU:H	1.38	0.89
1:BP:250:TRP:CZ3	1:BP:272:TYR:CE1	2.60	0.89
1:CP:191:LEU:HD23	1:CP:191:LEU:H	1.38	0.89
1:BP:191:LEU:HD23	1:BP:191:LEU:H	1.37	0.88
1:AP:191:LEU:HD23	1:AP:191:LEU:H	1.36	0.88
1:CI:191:LEU:H	1:CI:191:LEU:HD23	1.37	0.88
1:BJ:272:TYR:CE2	1:BQ:55:ARG:NE	2.41	0.88
1:BO:191:LEU:HD23	1:BO:191:LEU:H	1.38	0.88
1:AQ:191:LEU:HD23	1:AQ:191:LEU:H	1.39	0.88
1:AO:191:LEU:HD23	1:AO:191:LEU:H	1.37	0.88
1:AE:55:ARG:NE	1:CP:272:TYR:CE2	2.42	0.88
1:AG:191:LEU:HD23	1:AG:191:LEU:H	1.38	0.88
1:AO:292:ALA:O	1:AO:293:ARG:HG2	1.73	0.88
1:CQ:191:LEU:HD23	1:CQ:191:LEU:H	1.37	0.88
1:BB:191:LEU:HD23	1:BB:191:LEU:H	1.39	0.88
1:CF:191:LEU:HD23	1:CF:191:LEU:H	1.39	0.88
1:CI:378:ARG:HG3	1:CI:379:VAL:N	1.88	0.88
1:BD:191:LEU:HD23	1:BD:191:LEU:H	1.39	0.87
1:AD:191:LEU:HD23	1:AD:191:LEU:H	1.40	0.87
1:BM:191:LEU:H	1:BM:191:LEU:HD23	1.38	0.87
1:AK:191:LEU:HD23	1:AK:191:LEU:H	1.38	0.87
1:AE:191:LEU:HD23	1:AE:191:LEU:H	1.39	0.87
1:CD:191:LEU:HD23	1:CD:191:LEU:H	1.39	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CO:250:TRP:CZ3	1:CO:272:TYR:CE1	2.63	0.87
1:BF:191:LEU:HD23	1:BF:191:LEU:H	1.40	0.86
1:BJ:189:PHE:HE1	1:BJ:198:ARG:HG3	1.40	0.86
1:BQ:191:LEU:HD23	1:BQ:191:LEU:H	1.40	0.86
1:AN:79:ARG:HH11	1:AN:79:ARG:HG3	1.38	0.86
1:AA:191:LEU:HD23	1:AA:191:LEU:H	1.37	0.86
1:AM:191:LEU:HD23	1:AM:191:LEU:H	1.38	0.86
1:AO:250:TRP:CZ3	1:AO:272:TYR:CE1	2.63	0.86
1:CE:191:LEU:HD23	1:CE:191:LEU:H	1.39	0.86
1:AJ:272:TYR:CE2	1:AQ:55:ARG:NE	2.44	0.86
1:BT:191:LEU:HD23	1:BT:191:LEU:H	1.40	0.86
1:CG:191:LEU:HD23	1:CG:191:LEU:H	1.40	0.86
1:CJ:250:TRP:CZ3	1:CJ:272:TYR:HE1	1.94	0.86
1:CQ:250:TRP:CZ3	1:CQ:272:TYR:CE1	2.64	0.86
1:CR:191:LEU:HD23	1:CR:191:LEU:H	1.41	0.86
1:BH:191:LEU:HD23	1:BH:191:LEU:H	1.40	0.86
1:BO:272:TYR:HE2	1:BR:55:ARG:NE	1.73	0.86
1:CJ:250:TRP:CZ3	1:CJ:272:TYR:CE1	2.63	0.86
1:AH:55:ARG:CD	1:AK:272:TYR:CE2	2.59	0.86
1:AP:272:TYR:CE2	1:BE:55:ARG:CD	2.59	0.86
1:BG:191:LEU:HD23	1:BG:191:LEU:H	1.39	0.86
1:CM:191:LEU:HD23	1:CM:191:LEU:H	1.39	0.86
1:AF:79:ARG:HG3	1:AF:79:ARG:HH11	1.38	0.86
1:BK:191:LEU:HD23	1:BK:191:LEU:H	1.41	0.86
1:CK:191:LEU:HD23	1:CK:191:LEU:H	1.40	0.86
1:CO:272:TYR:HE2	1:CR:55:ARG:CD	1.89	0.86
1:CN:191:LEU:HD23	1:CN:191:LEU:H	1.40	0.86
1:BP:272:TYR:CE2	1:CE:55:ARG:CD	2.58	0.85
1:BS:191:LEU:HD23	1:BS:191:LEU:H	1.40	0.85
1:BT:55:ARG:NE	1:CA:272:TYR:CE2	2.44	0.85
1:AL:79:ARG:HG3	1:AL:79:ARG:HH11	1.39	0.85
1:AL:272:TYR:CD2	1:CJ:55:ARG:HD3	2.10	0.85
1:CL:191:LEU:H	1:CL:191:LEU:HD23	1.39	0.85
1:CH:191:LEU:HD23	1:CH:191:LEU:H	1.39	0.85
1:BH:15:GLN:HE21	1:BH:15:GLN:HA	1.38	0.85
1:BN:191:LEU:HD23	1:BN:191:LEU:H	1.41	0.85
1:CR:79:ARG:CG	1:CR:79:ARG:NH1	2.30	0.85
1:AT:250:TRP:CZ3	1:AT:272:TYR:CE1	2.65	0.85
1:CD:272:TYR:CE2	1:CS:55:ARG:NE	2.44	0.85
1:CG:189:PHE:HE1	1:CG:198:ARG:CG	1.90	0.85
1:CA:191:LEU:HD23	1:CA:191:LEU:H	1.41	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:250:TRP:CZ3	1:CM:272:TYR:CE1	2.64	0.85
1:CR:189:PHE:HE1	1:CR:198:ARG:CG	1.89	0.85
1:BC:191:LEU:HD23	1:BC:191:LEU:H	1.40	0.85
1:CB:191:LEU:HD23	1:CB:191:LEU:H	1.40	0.85
1:CO:250:TRP:CZ3	1:CO:272:TYR:HE1	1.95	0.85
1:AO:250:TRP:CZ3	1:AO:272:TYR:HE1	1.95	0.85
1:CB:189:PHE:HE1	1:CB:198:ARG:CG	1.90	0.84
1:CO:191:LEU:HD23	1:CO:191:LEU:H	1.42	0.84
1:CO:272:TYR:HE2	1:CR:55:ARG:NE	1.74	0.84
1:AO:272:TYR:HE2	1:AR:55:ARG:CD	1.88	0.84
1:BE:189:PHE:HE1	1:BE:198:ARG:CG	1.91	0.84
1:BI:191:LEU:HD23	1:BI:191:LEU:H	1.40	0.84
1:CS:454:ASN:HD22	1:CS:456:ALA:H	1.24	0.84
1:CP:250:TRP:CZ3	1:CP:272:TYR:CE1	2.65	0.84
1:CR:79:ARG:HH11	1:CR:79:ARG:HG3	1.42	0.84
1:CR:79:ARG:HG2	1:CR:79:ARG:NH1	1.86	0.84
1:AH:191:LEU:HD23	1:AH:191:LEU:H	1.43	0.84
1:CN:189:PHE:HE1	1:CN:198:ARG:HG3	1.41	0.84
1:AB:250:TRP:CZ3	1:AB:272:TYR:CE1	2.66	0.84
1:AG:263:ASN:ND2	1:BG:32:PHE:CB	2.41	0.84
1:BN:189:PHE:HE1	1:BN:198:ARG:CG	1.91	0.84
1:AS:191:LEU:HD23	1:AS:191:LEU:H	1.42	0.84
1:CS:191:LEU:HD23	1:CS:191:LEU:H	1.42	0.84
1:AF:191:LEU:HD23	1:AF:191:LEU:H	1.42	0.83
1:AI:191:LEU:HD23	1:AI:191:LEU:H	1.40	0.83
1:AE:189:PHE:HE1	1:AE:198:ARG:HG3	1.42	0.83
1:AI:272:TYR:CE2	1:AO:55:ARG:CD	2.62	0.83
1:AN:189:PHE:HE1	1:AN:198:ARG:CG	1.91	0.83
1:AN:191:LEU:H	1:AN:191:LEU:HD23	1.42	0.83
1:AP:272:TYR:CE2	1:BE:55:ARG:NE	2.46	0.83
1:AR:189:PHE:HE1	1:AR:198:ARG:HG3	1.42	0.83
1:CF:250:TRP:CZ3	1:CF:272:TYR:CE1	2.66	0.83
1:BB:189:PHE:HE1	1:BB:198:ARG:CG	1.92	0.83
1:AI:189:PHE:HE1	1:AI:198:ARG:CG	1.91	0.83
1:AT:191:LEU:HD23	1:AT:191:LEU:H	1.42	0.83
1:CJ:191:LEU:HD23	1:CJ:191:LEU:H	1.42	0.83
1:AF:454:ASN:HD22	1:AF:456:ALA:H	1.27	0.83
1:AN:189:PHE:HE1	1:AN:198:ARG:HG3	1.44	0.83
1:CJ:189:PHE:HE1	1:CJ:198:ARG:CG	1.92	0.83
1:BR:191:LEU:HD23	1:BR:191:LEU:H	1.42	0.83
1:CC:250:TRP:CE3	1:CC:272:TYR:CE1	2.66	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CD:250:TRP:CZ3	1:CD:272:TYR:CE1	2.65	0.83
1:CE:189:PHE:HE1	1:CE:198:ARG:HG3	1.44	0.83
1:BA:191:LEU:HD23	1:BA:191:LEU:H	1.42	0.83
1:BT:250:TRP:CZ3	1:BT:272:TYR:CE1	2.65	0.83
1:CJ:189:PHE:HE1	1:CJ:198:ARG:HG3	1.43	0.83
1:AF:38:GLU:OE1	1:AG:267:LYS:HE2	1.79	0.83
1:AJ:189:PHE:HE1	1:AJ:198:ARG:CG	1.92	0.83
1:BL:9:TYR:HE1	1:BL:147:GLN:HE21	1.25	0.83
1:AM:454:ASN:HD22	1:AM:456:ALA:H	1.26	0.83
1:AO:272:TYR:CE2	1:AR:55:ARG:NE	2.47	0.83
1:AR:250:TRP:CZ3	1:AR:272:TYR:CE1	2.67	0.83
1:BG:250:TRP:CZ3	1:BG:272:TYR:CE1	2.67	0.83
1:CR:85:ASP:OD1	1:CR:86:PRO:HD2	1.78	0.83
1:AI:189:PHE:HE1	1:AI:198:ARG:HG3	1.42	0.82
1:CG:250:TRP:CZ3	1:CG:272:TYR:CE1	2.67	0.82
1:AG:269:PRO:HG2	1:AG:269:PRO:O	1.78	0.82
1:AL:272:TYR:CE2	1:CJ:55:ARG:HD3	2.15	0.82
1:CM:189:PHE:HE1	1:CM:198:ARG:CG	1.91	0.82
1:CT:191:LEU:HD23	1:CT:191:LEU:H	1.41	0.82
1:AR:189:PHE:HE1	1:AR:198:ARG:CG	1.91	0.82
1:BP:79:ARG:CG	1:BP:79:ARG:HH11	1.90	0.82
1:CN:250:TRP:CZ3	1:CN:272:TYR:CE1	2.67	0.82
1:AP:272:TYR:CD2	1:BE:55:ARG:HD3	2.14	0.82
1:BB:250:TRP:CZ3	1:BB:272:TYR:CE1	2.68	0.82
1:BD:250:TRP:CZ3	1:BD:272:TYR:CE1	2.67	0.82
1:AO:291:PRO:O	1:AO:291:PRO:HD2	1.79	0.82
1:BA:250:TRP:CZ3	1:BA:272:TYR:CE1	2.67	0.82
1:BL:191:LEU:HD23	1:BL:191:LEU:H	1.43	0.82
1:AN:250:TRP:CZ3	1:AN:272:TYR:CE1	2.68	0.82
1:BB:55:ARG:NE	1:CB:272:TYR:CE2	2.48	0.82
1:BH:189:PHE:HE1	1:BH:198:ARG:CG	1.92	0.82
1:CF:189:PHE:HE1	1:CF:198:ARG:CG	1.92	0.82
1:CG:189:PHE:HE1	1:CG:198:ARG:HG3	1.44	0.82
1:BA:79:ARG:HH11	1:BA:79:ARG:HG3	1.43	0.82
1:BB:454:ASN:HD22	1:BB:456:ALA:H	1.26	0.82
1:BK:454:ASN:HD22	1:BK:456:ALA:H	1.27	0.82
1:BO:15:GLN:HA	1:BO:15:GLN:HE21	1.43	0.82
1:CR:250:TRP:CZ3	1:CR:272:TYR:CE1	2.68	0.82
1:AC:250:TRP:CZ3	1:AC:272:TYR:CE1	2.67	0.82
1:CF:454:ASN:HD22	1:CF:456:ALA:H	1.26	0.82
1:BR:79:ARG:HH11	1:BR:79:ARG:HG3	1.45	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:189:PHE:HE1	1:CM:198:ARG:HG3	1.45	0.81
1:CT:250:TRP:CZ3	1:CT:272:TYR:CE1	2.68	0.81
1:AB:189:PHE:HE1	1:AB:198:ARG:CG	1.93	0.81
1:AI:79:ARG:HG3	1:AI:79:ARG:HH11	1.43	0.81
1:CE:250:TRP:CZ3	1:CE:272:TYR:CE1	2.68	0.81
1:CF:79:ARG:HH11	1:CF:79:ARG:CG	1.91	0.81
1:AC:55:ARG:NE	1:AT:272:TYR:CE2	2.49	0.81
1:AG:272:TYR:C	1:AG:273:VAL:HG23	2.05	0.81
1:BK:250:TRP:CZ3	1:BK:272:TYR:CE1	2.68	0.81
1:BN:250:TRP:CZ3	1:BN:272:TYR:CE1	2.69	0.81
1:CH:79:ARG:HH11	1:CH:79:ARG:HG3	1.45	0.81
1:CK:250:TRP:CZ3	1:CK:272:TYR:CE1	2.68	0.81
1:CN:189:PHE:HE1	1:CN:198:ARG:CG	1.92	0.81
1:CQ:454:ASN:HD22	1:CQ:456:ALA:H	1.27	0.81
1:BI:250:TRP:CZ3	1:BI:272:TYR:CE1	2.69	0.81
1:BJ:272:TYR:HE2	1:BQ:55:ARG:NE	1.78	0.81
1:CI:376:THR:O	1:CI:376:THR:HG23	1.79	0.81
1:AH:55:ARG:HD3	1:AK:272:TYR:CD2	2.15	0.81
1:BG:189:PHE:HE1	1:BG:198:ARG:HG3	1.45	0.81
1:AH:189:PHE:HE1	1:AH:198:ARG:CG	1.93	0.81
1:AM:189:PHE:HE1	1:AM:198:ARG:CG	1.94	0.81
1:BH:250:TRP:CZ3	1:BH:272:TYR:CE1	2.69	0.81
1:BI:454:ASN:HD22	1:BI:456:ALA:H	1.26	0.81
1:BL:9:TYR:HE1	1:BL:147:GLN:NE2	1.79	0.81
1:CH:250:TRP:CZ3	1:CH:272:TYR:CE1	2.68	0.81
1:CM:454:ASN:HD22	1:CM:456:ALA:H	1.29	0.81
1:AE:250:TRP:CZ3	1:AE:272:TYR:CE1	2.69	0.81
1:AH:272:TYR:CE2	1:CF:55:ARG:NE	2.48	0.81
1:AM:189:PHE:HE1	1:AM:198:ARG:HG3	1.45	0.81
1:BI:189:PHE:HE1	1:BI:198:ARG:HG3	1.45	0.81
1:CE:272:TYR:HE2	1:CM:55:ARG:NE	1.78	0.81
1:BB:189:PHE:HE1	1:BB:198:ARG:HG3	1.45	0.80
1:CI:250:TRP:CZ3	1:CI:272:TYR:CE1	2.69	0.80
1:CS:250:TRP:CZ3	1:CS:272:TYR:CE1	2.69	0.80
1:AL:250:TRP:CZ3	1:AL:272:TYR:CE1	2.69	0.80
1:CD:454:ASN:HD22	1:CD:456:ALA:H	1.30	0.80
1:CH:189:PHE:HE1	1:CH:198:ARG:HG3	1.46	0.80
1:CI:189:PHE:HE1	1:CI:198:ARG:HG3	1.45	0.80
1:CR:85:ASP:OD1	1:CR:86:PRO:CD	2.30	0.80
1:BM:250:TRP:CZ3	1:BM:272:TYR:CE1	2.69	0.80
1:BP:454:ASN:HD22	1:BP:456:ALA:H	1.27	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:189:PHE:HE1	1:CF:198:ARG:HG3	1.46	0.80
1:CI:378:ARG:O	1:CI:379:VAL:HG23	1.81	0.80
1:BF:189:PHE:HE1	1:BF:198:ARG:CG	1.95	0.80
1:CR:454:ASN:HD22	1:CR:456:ALA:H	1.27	0.80
1:AF:189:PHE:HE1	1:AF:198:ARG:HG3	1.43	0.80
1:AH:250:TRP:CZ3	1:AH:272:TYR:CE1	2.68	0.80
1:AI:55:ARG:HD3	1:AR:272:TYR:CD2	2.17	0.80
1:AP:272:TYR:HE2	1:BE:55:ARG:CD	1.93	0.80
1:BG:272:TYR:CE2	1:CG:55:ARG:NE	2.49	0.80
1:CB:250:TRP:CZ3	1:CB:272:TYR:CE1	2.70	0.80
1:AF:250:TRP:CZ3	1:AF:272:TYR:CE1	2.70	0.80
1:AG:189:PHE:HE1	1:AG:198:ARG:CG	1.95	0.80
1:AI:272:TYR:CD2	1:AO:55:ARG:HD3	2.16	0.80
1:AK:250:TRP:CZ3	1:AK:272:TYR:CE1	2.69	0.80
1:AO:272:TYR:CE2	1:AR:55:ARG:CD	2.65	0.80
1:BL:250:TRP:CZ3	1:BL:272:TYR:CE1	2.70	0.80
1:CC:55:ARG:NE	1:CT:272:TYR:CE2	2.50	0.80
1:CL:454:ASN:HD22	1:CL:456:ALA:H	1.29	0.80
1:AG:189:PHE:HE1	1:AG:198:ARG:HG3	1.46	0.80
1:AR:454:ASN:HD22	1:AR:456:ALA:H	1.29	0.80
1:CB:189:PHE:HE1	1:CB:198:ARG:HG3	1.44	0.80
1:AH:55:ARG:CD	1:AK:272:TYR:HE2	1.95	0.80
1:AO:290:THR:OG1	1:AO:291:PRO:CD	2.30	0.80
1:AO:292:ALA:O	1:AO:293:ARG:CG	2.30	0.80
1:BM:189:PHE:HE1	1:BM:198:ARG:CG	1.94	0.80
1:AO:290:THR:OG1	1:AO:291:PRO:HD2	1.81	0.79
1:BO:250:TRP:CE3	1:BO:272:TYR:CE1	2.70	0.79
1:CI:376:THR:O	1:CI:377:CYS:CB	2.29	0.79
1:AG:265:LEU:O	1:AG:265:LEU:CD1	2.30	0.79
1:CH:189:PHE:HE1	1:CH:198:ARG:CG	1.95	0.79
1:AM:250:TRP:CZ3	1:AM:272:TYR:CE1	2.70	0.79
1:BH:189:PHE:HE1	1:BH:198:ARG:HG3	1.45	0.79
1:CR:86:PRO:O	1:CR:89:THR:N	2.14	0.79
1:AN:454:ASN:HD22	1:AN:456:ALA:H	1.31	0.79
1:CL:250:TRP:CZ3	1:CL:272:TYR:CE1	2.70	0.79
1:AC:454:ASN:HD22	1:AC:456:ALA:H	1.31	0.79
1:BE:189:PHE:HE1	1:BE:198:ARG:HG3	1.46	0.79
1:BF:250:TRP:CZ3	1:BF:272:TYR:CE1	2.70	0.79
1:BR:189:PHE:HE1	1:BR:198:ARG:HG3	1.46	0.79
1:CJ:272:TYR:HE2	1:CQ:55:ARG:CD	1.95	0.79
1:CN:454:ASN:HD22	1:CN:456:ALA:H	1.30	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CO:272:TYR:CE2	1:CR:55:ARG:CD	2.66	0.79
1:AB:259:THR:CG2	1:AB:259:THR:O	2.30	0.79
1:AJ:189:PHE:HE1	1:AJ:198:ARG:HG3	1.48	0.79
1:CR:189:PHE:HE1	1:CR:198:ARG:HG3	1.47	0.79
1:AQ:250:TRP:CZ3	1:AQ:272:TYR:CE1	2.71	0.79
1:BJ:189:PHE:HE1	1:BJ:198:ARG:CG	1.96	0.79
1:AH:189:PHE:HE1	1:AH:198:ARG:HG3	1.49	0.78
1:AG:272:TYR:O	1:AG:273:VAL:HG23	1.83	0.78
1:BQ:189:PHE:HE1	1:BQ:198:ARG:HG3	1.49	0.78
1:AN:55:ARG:CD	1:AS:272:TYR:HE2	1.96	0.78
1:BQ:250:TRP:CZ3	1:BQ:272:TYR:CE1	2.71	0.78
1:CD:250:TRP:CZ3	1:CD:272:TYR:HE1	2.02	0.78
1:CI:189:PHE:HE1	1:CI:198:ARG:CG	1.96	0.78
1:CK:454:ASN:HD22	1:CK:456:ALA:H	1.28	0.78
1:BA:189:PHE:HE1	1:BA:198:ARG:HG3	1.49	0.78
1:AD:250:TRP:CZ3	1:AD:272:TYR:CE1	2.72	0.78
1:AG:55:ARG:CD	1:CG:272:TYR:CE2	2.66	0.78
1:AK:55:ARG:NE	1:CF:272:TYR:CE2	2.52	0.78
1:BR:454:ASN:HD22	1:BR:456:ALA:H	1.31	0.78
1:CO:79:ARG:HG3	1:CO:79:ARG:HH11	1.49	0.78
1:AO:289:ARG:NH1	1:AO:337:ASP:C	2.42	0.78
1:BM:454:ASN:HD22	1:BM:456:ALA:H	1.31	0.78
1:CO:189:PHE:HE1	1:CO:198:ARG:HG3	1.49	0.78
1:AA:250:TRP:CZ3	1:AA:272:TYR:CE1	2.72	0.78
1:AG:272:TYR:O	1:AG:273:VAL:CG2	2.32	0.78
1:BO:272:TYR:HE2	1:BR:55:ARG:CD	1.97	0.78
1:CD:272:TYR:HE2	1:CS:55:ARG:CD	1.97	0.78
1:AD:454:ASN:HD22	1:AD:456:ALA:H	1.32	0.78
1:BH:454:ASN:HD22	1:BH:456:ALA:H	1.30	0.78
1:BL:454:ASN:HD22	1:BL:456:ALA:H	1.31	0.78
1:BR:250:TRP:CZ3	1:BR:272:TYR:CE1	2.71	0.78
1:BG:189:PHE:HE1	1:BG:198:ARG:CG	1.96	0.77
1:BO:272:TYR:CE2	1:BR:55:ARG:CD	2.67	0.77
1:AG:55:ARG:HD3	1:CG:272:TYR:CE2	2.19	0.77
1:BF:272:TYR:CE2	1:CK:55:ARG:NE	2.52	0.77
1:AD:272:TYR:CE2	1:AS:55:ARG:NE	2.52	0.77
1:BI:55:ARG:CD	1:BR:272:TYR:CE2	2.67	0.77
1:CE:272:TYR:HE2	1:CM:55:ARG:CD	1.97	0.77
1:AG:272:TYR:CE2	1:BG:55:ARG:NH2	2.52	0.77
1:BT:55:ARG:CD	1:CA:272:TYR:HE2	1.97	0.77
1:BA:454:ASN:HD22	1:BA:456:ALA:H	1.32	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:250:TRP:CE3	1:BP:272:TYR:CE1	2.73	0.77
1:BS:454:ASN:HD22	1:BS:456:ALA:H	1.30	0.77
1:CE:250:TRP:CZ3	1:CE:272:TYR:HE1	2.03	0.77
1:CP:250:TRP:CZ3	1:CP:272:TYR:HE1	2.01	0.77
1:AE:454:ASN:HD22	1:AE:456:ALA:H	1.31	0.77
1:AO:272:TYR:CE2	1:AR:55:ARG:HD3	2.19	0.77
1:AB:189:PHE:HE1	1:AB:198:ARG:HG3	1.49	0.77
1:BF:454:ASN:HD22	1:BF:456:ALA:H	1.31	0.77
1:BJ:250:TRP:CE3	1:BJ:272:TYR:CE1	2.73	0.77
1:CA:250:TRP:CZ3	1:CA:272:TYR:CE1	2.71	0.77
1:CJ:454:ASN:HD22	1:CJ:456:ALA:H	1.31	0.77
1:CJ:272:TYR:CE2	1:CQ:55:ARG:CZ	2.68	0.77
1:BP:22:THR:OG1	1:BP:131:HIS:HD2	1.68	0.77
1:BT:454:ASN:HD22	1:BT:456:ALA:H	1.31	0.77
1:CD:22:THR:OG1	1:CD:131:HIS:HD2	1.68	0.77
1:AA:454:ASN:HD22	1:AA:456:ALA:H	1.30	0.77
1:AP:250:TRP:CZ3	1:AP:272:TYR:CE1	2.73	0.77
1:AH:272:TYR:CE2	1:CF:55:ARG:CD	2.68	0.76
1:BE:250:TRP:CZ3	1:BE:272:TYR:CE1	2.73	0.76
1:BQ:284:ARG:HH11	1:BQ:284:ARG:CG	1.98	0.76
1:AE:189:PHE:HE1	1:AE:198:ARG:CG	1.98	0.76
1:BF:79:ARG:HH11	1:BF:79:ARG:HG3	1.48	0.76
1:BI:55:ARG:CD	1:BR:272:TYR:HE2	1.97	0.76
1:BT:55:ARG:CD	1:CA:272:TYR:CE2	2.68	0.76
1:AP:22:THR:OG1	1:AP:131:HIS:HD2	1.68	0.76
1:BS:250:TRP:CZ3	1:BS:272:TYR:CE1	2.73	0.76
1:CH:454:ASN:HD22	1:CH:456:ALA:H	1.32	0.76
1:AO:291:PRO:O	1:AO:291:PRO:CD	2.30	0.76
1:BP:189:PHE:HE1	1:BP:198:ARG:HG3	1.50	0.76
1:CC:79:ARG:HH11	1:CC:79:ARG:HG3	1.51	0.76
1:AO:454:ASN:HD22	1:AO:456:ALA:H	1.33	0.76
1:BN:454:ASN:HD22	1:BN:456:ALA:H	1.33	0.76
1:CE:189:PHE:HE1	1:CE:198:ARG:CG	1.98	0.76
1:BL:7:VAL:HG11	1:BL:9:TYR:CZ	2.21	0.76
1:AB:259:THR:O	1:AB:259:THR:HG23	1.85	0.76
1:AG:55:ARG:HD3	1:CG:272:TYR:CD2	2.21	0.76
1:AN:55:ARG:CD	1:AS:272:TYR:CE2	2.69	0.76
1:AO:289:ARG:NH1	1:AO:337:ASP:O	2.19	0.76
1:AP:272:TYR:CE2	1:BE:55:ARG:HD3	2.20	0.76
1:AE:22:THR:OG1	1:AE:131:HIS:HD2	1.69	0.75
1:AF:189:PHE:HE1	1:AF:198:ARG:CG	1.98	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:189:PHE:HE1	1:AK:198:ARG:HG3	1.51	0.75
1:BG:74:ASN:HB3	1:BG:126:GLU:HG2	1.68	0.75
1:BJ:454:ASN:HD22	1:BJ:456:ALA:H	1.32	0.75
1:CD:272:TYR:CE2	1:CS:55:ARG:CD	2.68	0.75
1:CE:22:THR:OG1	1:CE:131:HIS:HD2	1.68	0.75
1:AL:454:ASN:HD22	1:AL:456:ALA:H	1.30	0.75
1:BC:454:ASN:HD22	1:BC:456:ALA:H	1.31	0.75
1:BT:79:ARG:HH11	1:BT:79:ARG:HG3	1.51	0.75
1:CR:77:THR:O	1:CR:80:ILE:CG1	2.33	0.75
1:AI:272:TYR:HE2	1:AO:55:ARG:CD	1.99	0.75
1:BP:272:TYR:CD2	1:CE:55:ARG:HD3	2.22	0.75
1:CC:454:ASN:HD22	1:CC:456:ALA:H	1.34	0.75
1:BL:189:PHE:HE1	1:BL:198:ARG:HG3	1.51	0.75
1:AI:55:ARG:CD	1:AR:272:TYR:CE2	2.69	0.75
1:AJ:55:ARG:NE	1:BL:272:TYR:CE2	2.55	0.75
1:AB:265:LEU:CD1	1:AB:265:LEU:O	2.30	0.75
1:BC:22:THR:OG1	1:BC:131:HIS:HD2	1.69	0.75
1:AP:454:ASN:HD22	1:AP:456:ALA:H	1.32	0.75
1:BF:189:PHE:HE1	1:BF:198:ARG:HG3	1.51	0.75
1:BS:189:PHE:HE1	1:BS:198:ARG:HG3	1.52	0.75
1:CB:11:PRO:HG2	1:CB:18:ARG:CD	2.17	0.75
1:CI:74:ASN:HB3	1:CI:126:GLU:HG2	1.67	0.75
1:CI:272:TYR:CE2	1:CO:55:ARG:NE	2.55	0.75
1:AE:272:TYR:CE2	1:AM:55:ARG:NE	2.55	0.75
1:AJ:250:TRP:CZ3	1:AJ:272:TYR:CE1	2.75	0.75
1:BN:189:PHE:HE1	1:BN:198:ARG:HG3	1.51	0.75
1:AF:22:THR:OG1	1:AF:131:HIS:HD2	1.70	0.75
1:AM:284:ARG:HG2	1:AM:284:ARG:HH11	1.51	0.75
1:BQ:36:GLN:NE2	1:BQ:156:LEU:H	1.85	0.75
1:BT:170:PHE:HD1	1:BT:389:MET:HE1	1.51	0.75
1:CD:55:ARG:NE	1:CN:272:TYR:CE2	2.55	0.75
1:BA:33:LYS:HG2	1:BA:33:LYS:O	1.87	0.74
1:BE:454:ASN:HD22	1:BE:456:ALA:H	1.35	0.74
1:BI:189:PHE:HE1	1:BI:198:ARG:CG	2.00	0.74
1:CB:11:PRO:HG2	1:CB:18:ARG:NE	2.02	0.74
1:CI:454:ASN:HD22	1:CI:456:ALA:H	1.35	0.74
1:AF:55:ARG:NE	1:BH:272:TYR:CE2	2.55	0.74
1:AG:261:ASP:C	1:AG:261:ASP:OD1	2.30	0.74
1:AP:33:LYS:HG2	1:AP:33:LYS:O	1.86	0.74
1:AR:22:THR:OG1	1:AR:131:HIS:HD2	1.70	0.74
1:CN:170:PHE:HD1	1:CN:389:MET:HE1	1.51	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:170:PHE:HD1	1:CR:389:MET:HE1	1.51	0.74
1:AM:284:ARG:HH11	1:AM:284:ARG:CG	2.00	0.74
1:AT:170:PHE:HD1	1:AT:389:MET:HE1	1.52	0.74
1:BB:33:LYS:O	1:BB:33:LYS:HG2	1.87	0.74
1:BP:272:TYR:CE2	1:CE:55:ARG:HD3	2.22	0.74
1:CJ:22:THR:OG1	1:CJ:131:HIS:HD2	1.70	0.74
1:CL:189:PHE:HE1	1:CL:198:ARG:HG3	1.52	0.74
1:AB:201:GLY:HA3	1:AB:300:GLN:HG2	1.70	0.74
1:BA:22:THR:OG1	1:BA:131:HIS:HD2	1.70	0.74
1:AC:55:ARG:CD	1:AT:272:TYR:HE2	2.01	0.74
1:AE:55:ARG:CD	1:CP:272:TYR:CE2	2.70	0.74
1:AF:272:TYR:CE2	1:BK:55:ARG:NE	2.55	0.74
1:BQ:284:ARG:HH11	1:BQ:284:ARG:HG2	1.52	0.74
1:AE:55:ARG:CD	1:CP:272:TYR:HE2	2.00	0.74
1:AI:250:TRP:CZ3	1:AI:272:TYR:CE1	2.76	0.74
1:CA:170:PHE:HD1	1:CA:389:MET:HE1	1.52	0.74
1:CG:79:ARG:HG3	1:CG:79:ARG:HH11	1.52	0.74
1:BK:189:PHE:HE1	1:BK:198:ARG:HG3	1.52	0.74
1:AG:55:ARG:CD	1:CG:272:TYR:HE2	2.00	0.74
1:BR:189:PHE:HE1	1:BR:198:ARG:CG	2.00	0.74
1:CT:454:ASN:HD22	1:CT:456:ALA:H	1.33	0.74
1:AG:262:TRP:O	1:AG:263:ASN:C	2.29	0.74
1:AJ:454:ASN:HD22	1:AJ:456:ALA:H	1.35	0.74
1:AT:454:ASN:HD22	1:AT:456:ALA:H	1.36	0.74
1:BJ:170:PHE:HD1	1:BJ:389:MET:HE1	1.52	0.74
1:CB:454:ASN:HD22	1:CB:456:ALA:H	1.35	0.74
1:CJ:170:PHE:HD1	1:CJ:389:MET:HE1	1.53	0.74
1:AH:272:TYR:HE2	1:CF:55:ARG:CD	1.99	0.74
1:AS:250:TRP:CE3	1:AS:272:TYR:CE1	2.75	0.74
1:AT:250:TRP:CZ3	1:AT:272:TYR:HE1	2.06	0.74
1:BP:79:ARG:HH11	1:BP:79:ARG:HG3	1.52	0.74
1:CG:22:THR:OG1	1:CG:131:HIS:HD2	1.71	0.74
1:AA:189:PHE:HE1	1:AA:198:ARG:HG3	1.53	0.73
1:AB:261:ASP:C	1:AB:261:ASP:OD1	2.28	0.73
1:AS:454:ASN:HD22	1:AS:456:ALA:H	1.35	0.73
1:CG:33:LYS:O	1:CG:33:LYS:HG2	1.88	0.73
1:AR:250:TRP:CZ3	1:AR:272:TYR:HE1	2.06	0.73
1:AT:33:LYS:O	1:AT:33:LYS:HG2	1.88	0.73
1:AR:170:PHE:HD1	1:AR:389:MET:HE1	1.54	0.73
1:AT:189:PHE:HE1	1:AT:198:ARG:HG3	1.54	0.73
1:BA:14:CYS:H	1:BA:138:ASN:HD21	1.35	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BE:33:LYS:O	1:BE:33:LYS:HG2	1.88	0.73
1:CC:55:ARG:CD	1:CT:272:TYR:CE2	2.72	0.73
1:AA:55:ARG:NE	1:CC:272:TYR:HE2	1.86	0.73
1:AE:272:TYR:CE2	1:AM:55:ARG:CD	2.72	0.73
1:BJ:189:PHE:CE1	1:BJ:198:ARG:HG3	2.24	0.73
1:AK:170:PHE:HD1	1:AK:389:MET:HE1	1.53	0.73
1:AK:454:ASN:HD22	1:AK:456:ALA:H	1.34	0.73
1:AN:430:MET:SD	1:AO:296:ALA:HB2	2.28	0.73
1:BA:74:ASN:HB3	1:BA:126:GLU:HG2	1.69	0.73
1:BC:250:TRP:CZ3	1:BC:272:TYR:CE1	2.76	0.73
1:CR:77:THR:O	1:CR:80:ILE:HG13	1.89	0.73
1:AF:272:TYR:CE2	1:BK:55:ARG:CD	2.72	0.73
1:AN:55:ARG:CZ	1:AS:272:TYR:CE2	2.71	0.73
1:AT:55:ARG:NE	1:BA:272:TYR:CE2	2.56	0.73
1:BD:33:LYS:HG2	1:BD:33:LYS:O	1.89	0.73
1:BH:170:PHE:HD1	1:BH:389:MET:HE1	1.52	0.73
1:BK:33:LYS:O	1:BK:33:LYS:HG2	1.88	0.73
1:CA:454:ASN:HD22	1:CA:456:ALA:H	1.34	0.73
1:CD:170:PHE:HD1	1:CD:389:MET:HE1	1.54	0.73
1:AI:55:ARG:HD3	1:AR:272:TYR:HD2	1.53	0.73
1:CO:454:ASN:HD22	1:CO:456:ALA:H	1.34	0.73
1:AC:55:ARG:CD	1:AT:272:TYR:CE2	2.71	0.73
1:AF:33:LYS:O	1:AF:33:LYS:HG2	1.88	0.73
1:AI:272:TYR:CD2	1:AO:55:ARG:CZ	2.72	0.73
1:AJ:55:ARG:CD	1:BL:272:TYR:CE2	2.72	0.73
1:AO:206:GLN:HE22	1:AO:294:LEU:HB2	1.53	0.73
1:BD:55:ARG:CD	1:BN:272:TYR:CE2	2.72	0.73
1:BD:272:TYR:CE2	1:BS:55:ARG:NE	2.57	0.73
1:BN:170:PHE:HD1	1:BN:389:MET:HE1	1.54	0.73
1:BS:74:ASN:HB3	1:BS:126:GLU:HG2	1.71	0.73
1:CP:79:ARG:HH11	1:CP:79:ARG:HG3	1.54	0.73
1:CQ:250:TRP:CZ3	1:CQ:272:TYR:HE1	2.05	0.73
1:CR:86:PRO:C	1:CR:88:TYR:N	2.47	0.73
1:AB:250:TRP:CZ3	1:AB:272:TYR:HE1	2.06	0.73
1:AG:189:PHE:HE2	1:AG:249:LEU:HD21	1.54	0.73
1:BL:74:ASN:HB3	1:BL:126:GLU:HG2	1.71	0.73
1:BO:33:LYS:HG2	1:BO:33:LYS:O	1.87	0.73
1:CC:33:LYS:HG2	1:CC:33:LYS:O	1.88	0.73
1:CN:189:PHE:CE1	1:CN:198:ARG:HG3	2.23	0.73
1:CT:33:LYS:HG2	1:CT:33:LYS:O	1.88	0.73
1:AM:22:THR:OG1	1:AM:131:HIS:HD2	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:284:ARG:CG	1:BB:284:ARG:HH11	2.02	0.72
1:BD:250:TRP:CZ3	1:BD:272:TYR:HE1	2.06	0.72
1:BJ:191:LEU:H	1:BJ:191:LEU:CD2	2.02	0.72
1:CE:454:ASN:HD22	1:CE:456:ALA:H	1.37	0.72
1:CG:454:ASN:HD22	1:CG:456:ALA:H	1.34	0.72
1:CL:284:ARG:CG	1:CL:284:ARG:HH11	2.01	0.72
1:AD:55:ARG:NE	1:AN:272:TYR:CE2	2.56	0.72
1:AD:79:ARG:HH11	1:AD:79:ARG:HG3	1.54	0.72
1:AD:189:PHE:HE1	1:AD:198:ARG:HG3	1.54	0.72
1:CD:284:ARG:HG2	1:CD:284:ARG:HH11	1.55	0.72
1:CI:55:ARG:CD	1:CR:272:TYR:CE2	2.72	0.72
1:CJ:272:TYR:CE2	1:CQ:55:ARG:CD	2.72	0.72
1:CM:250:TRP:CZ3	1:CM:272:TYR:HE1	2.06	0.72
1:AK:55:ARG:CD	1:CF:272:TYR:CE2	2.71	0.72
1:CH:36:GLN:NE2	1:CH:156:LEU:H	1.88	0.72
1:CL:74:ASN:HB3	1:CL:126:GLU:HG2	1.71	0.72
1:CI:189:PHE:HE2	1:CI:249:LEU:HD21	1.53	0.72
1:AI:55:ARG:NE	1:AR:272:TYR:CE2	2.57	0.72
1:BE:16:ALA:O	1:BE:17:ASN:HB2	1.89	0.72
1:CP:33:LYS:O	1:CP:33:LYS:HG2	1.89	0.72
1:AL:74:ASN:HB3	1:AL:126:GLU:HG2	1.70	0.72
1:AN:22:THR:OG1	1:AN:131:HIS:HD2	1.72	0.72
1:BL:33:LYS:HG2	1:BL:33:LYS:O	1.87	0.72
1:BO:454:ASN:HD22	1:BO:456:ALA:H	1.37	0.72
1:AF:74:ASN:HB3	1:AF:126:GLU:HG2	1.72	0.72
1:BM:284:ARG:CG	1:BM:284:ARG:HH11	2.02	0.72
1:BN:55:ARG:NE	1:BS:272:TYR:CE2	2.57	0.72
1:CI:378:ARG:CG	1:CI:379:VAL:N	2.52	0.72
1:AG:454:ASN:HD22	1:AG:456:ALA:H	1.36	0.72
1:AJ:33:LYS:O	1:AJ:33:LYS:HG2	1.90	0.72
1:BB:191:LEU:H	1:BB:191:LEU:CD2	2.03	0.72
1:BQ:33:LYS:O	1:BQ:33:LYS:HG2	1.89	0.72
1:CI:22:THR:OG1	1:CI:131:HIS:HD2	1.72	0.72
1:AH:454:ASN:HD22	1:AH:456:ALA:H	1.35	0.72
1:AQ:22:THR:OG1	1:AQ:131:HIS:HD2	1.72	0.72
1:BG:33:LYS:HG2	1:BG:33:LYS:O	1.88	0.72
1:BI:33:LYS:O	1:BI:33:LYS:HG2	1.90	0.72
1:BR:33:LYS:HG2	1:BR:33:LYS:O	1.90	0.72
1:BS:170:PHE:HD1	1:BS:389:MET:HE1	1.55	0.72
1:CM:22:THR:OG1	1:CM:131:HIS:HD2	1.73	0.72
1:AE:189:PHE:HE2	1:AE:249:LEU:HD21	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:22:THR:OG1	1:AS:131:HIS:HD2	1.73	0.72
1:AS:33:LYS:HG2	1:AS:33:LYS:O	1.90	0.72
1:BH:33:LYS:O	1:BH:33:LYS:HG2	1.90	0.72
1:CC:284:ARG:HG2	1:CC:284:ARG:HH11	1.55	0.72
1:AA:55:ARG:NE	1:CC:272:TYR:CE2	2.58	0.71
1:AB:256:ASN:CG	1:AB:256:ASN:O	2.30	0.71
1:AC:284:ARG:CG	1:AC:284:ARG:HH11	2.02	0.71
1:AK:55:ARG:HD3	1:CF:272:TYR:CD2	2.25	0.71
1:BC:189:PHE:HE1	1:BC:198:ARG:HG3	1.55	0.71
1:BQ:454:ASN:HD22	1:BQ:456:ALA:H	1.36	0.71
1:CL:33:LYS:O	1:CL:33:LYS:HG2	1.88	0.71
1:AB:454:ASN:HD22	1:AB:456:ALA:H	1.38	0.71
1:AQ:33:LYS:O	1:AQ:33:LYS:HG2	1.89	0.71
1:BF:170:PHE:HD1	1:BF:389:MET:HE1	1.54	0.71
1:AD:170:PHE:HD1	1:AD:389:MET:HE1	1.55	0.71
1:AG:250:TRP:CZ3	1:AG:272:TYR:HE1	2.08	0.71
1:AI:170:PHE:HD1	1:AI:389:MET:HE1	1.54	0.71
1:AQ:170:PHE:HD1	1:AQ:389:MET:HE1	1.55	0.71
1:BM:79:ARG:HH11	1:BM:79:ARG:HG3	1.55	0.71
1:BO:74:ASN:HB3	1:BO:126:GLU:HG2	1.73	0.71
1:BO:284:ARG:HH11	1:BO:284:ARG:CG	2.02	0.71
1:BR:74:ASN:HB3	1:BR:126:GLU:HG2	1.72	0.71
1:CC:55:ARG:CD	1:CT:272:TYR:HE2	2.02	0.71
1:CK:36:GLN:NE2	1:CK:156:LEU:H	1.88	0.71
1:CT:189:PHE:HE1	1:CT:198:ARG:HG3	1.55	0.71
1:AB:284:ARG:HG2	1:AB:284:ARG:HH11	1.55	0.71
1:AL:22:THR:OG1	1:AL:131:HIS:HD2	1.72	0.71
1:AR:33:LYS:O	1:AR:33:LYS:HG2	1.88	0.71
1:BH:22:THR:OG1	1:BH:131:HIS:HD2	1.73	0.71
1:CB:22:THR:OG1	1:CB:131:HIS:HD2	1.73	0.71
1:CG:79:ARG:HH11	1:CG:79:ARG:CG	2.03	0.71
1:AG:273:VAL:O	1:AG:273:VAL:HG12	1.91	0.71
1:AQ:74:ASN:HB3	1:AQ:126:GLU:HG2	1.72	0.71
1:AR:189:PHE:HE2	1:AR:249:LEU:HD21	1.53	0.71
1:AR:189:PHE:CE1	1:AR:198:ARG:HG3	2.25	0.71
1:BT:33:LYS:O	1:BT:33:LYS:HG2	1.90	0.71
1:CR:85:ASP:OD1	1:CR:85:ASP:C	2.29	0.71
1:CT:284:ARG:HH11	1:CT:284:ARG:CG	2.04	0.71
1:AC:250:TRP:CZ3	1:AC:272:TYR:HE1	2.08	0.71
1:AK:14:CYS:H	1:AK:138:ASN:HD21	1.39	0.71
1:BC:36:GLN:NE2	1:BC:156:LEU:H	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:22:THR:OG1	1:BD:131:HIS:HD2	1.73	0.71
1:BN:22:THR:OG1	1:BN:131:HIS:HD2	1.74	0.71
1:CN:74:ASN:HB3	1:CN:126:GLU:HG2	1.73	0.71
1:CN:250:TRP:CZ3	1:CN:272:TYR:HE1	2.08	0.71
1:CO:33:LYS:O	1:CO:33:LYS:HG2	1.90	0.71
1:CQ:170:PHE:HD1	1:CQ:389:MET:HE1	1.56	0.71
1:AB:74:ASN:HB3	1:AB:126:GLU:HG2	1.72	0.71
1:AB:79:ARG:HH11	1:AB:79:ARG:HG3	1.56	0.71
1:AF:272:TYR:CD2	1:BK:55:ARG:HD3	2.25	0.71
1:AJ:272:TYR:CE2	1:AQ:55:ARG:CD	2.73	0.71
1:BG:454:ASN:HD22	1:BG:456:ALA:H	1.39	0.71
1:BP:33:LYS:O	1:BP:33:LYS:HG2	1.90	0.71
1:CA:33:LYS:O	1:CA:33:LYS:HG2	1.90	0.71
1:CC:284:ARG:HH11	1:CC:284:ARG:CG	2.04	0.71
1:CD:55:ARG:CD	1:CN:272:TYR:CE2	2.74	0.71
1:CE:33:LYS:O	1:CE:33:LYS:HG2	1.89	0.71
1:CO:272:TYR:CE2	1:CR:55:ARG:HD3	2.26	0.71
1:CS:74:ASN:HB3	1:CS:126:GLU:HG2	1.72	0.71
1:AO:295:LEU:CB	1:AO:298:GLN:OE1	2.35	0.71
1:CD:284:ARG:HH11	1:CD:284:ARG:CG	2.04	0.71
1:CH:170:PHE:HD1	1:CH:389:MET:HE1	1.56	0.71
1:CN:36:GLN:NE2	1:CN:156:LEU:H	1.88	0.71
1:CT:14:CYS:H	1:CT:138:ASN:HD21	1.38	0.71
1:CT:16:ALA:O	1:CT:17:ASN:HB2	1.91	0.71
1:AM:33:LYS:HG2	1:AM:33:LYS:O	1.91	0.71
1:BD:191:LEU:H	1:BD:191:LEU:CD2	2.04	0.71
1:BS:22:THR:OG1	1:BS:131:HIS:HD2	1.74	0.71
1:CE:272:TYR:CE2	1:CM:55:ARG:CZ	2.73	0.71
1:CJ:14:CYS:H	1:CJ:138:ASN:HD21	1.38	0.71
1:CR:33:LYS:O	1:CR:33:LYS:HG2	1.90	0.71
1:CS:189:PHE:HE1	1:CS:198:ARG:HG3	1.56	0.71
1:AN:55:ARG:CZ	1:AS:272:TYR:CD2	2.74	0.71
1:BA:284:ARG:HH11	1:BA:284:ARG:CG	2.03	0.71
1:BF:22:THR:OG1	1:BF:131:HIS:HD2	1.74	0.71
1:BM:189:PHE:HE2	1:BM:249:LEU:HD21	1.54	0.71
1:CP:22:THR:OG1	1:CP:131:HIS:HD2	1.74	0.71
1:CQ:191:LEU:H	1:CQ:191:LEU:CD2	2.04	0.71
1:AB:191:LEU:H	1:AB:191:LEU:CD2	2.04	0.70
1:AC:33:LYS:O	1:AC:33:LYS:HG2	1.90	0.70
1:AE:272:TYR:HE2	1:AM:55:ARG:CD	2.03	0.70
1:AI:189:PHE:CE1	1:AI:198:ARG:HG3	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:284:ARG:HH11	1:AS:284:ARG:CG	2.04	0.70
1:BC:33:LYS:O	1:BC:33:LYS:HG2	1.91	0.70
1:CL:284:ARG:HH11	1:CL:284:ARG:HG2	1.56	0.70
1:CS:33:LYS:O	1:CS:33:LYS:HG2	1.91	0.70
1:AN:33:LYS:HG2	1:AN:33:LYS:O	1.90	0.70
1:BI:22:THR:OG1	1:BI:131:HIS:HD2	1.73	0.70
1:BM:189:PHE:HE1	1:BM:198:ARG:HG3	1.55	0.70
1:CJ:189:PHE:CE1	1:CJ:198:ARG:HG3	2.25	0.70
1:CP:189:PHE:HE1	1:CP:198:ARG:HG3	1.56	0.70
1:AN:74:ASN:HB3	1:AN:126:GLU:HG2	1.72	0.70
1:BQ:272:TYR:CE2	1:CL:55:ARG:NE	2.59	0.70
1:CL:22:THR:OG1	1:CL:131:HIS:HD2	1.73	0.70
1:AG:284:ARG:HH11	1:AG:284:ARG:CG	2.04	0.70
1:AP:170:PHE:HD1	1:AP:389:MET:HE1	1.56	0.70
1:BD:55:ARG:HD3	1:BN:272:TYR:CD2	2.26	0.70
1:CF:74:ASN:HB3	1:CF:126:GLU:HG2	1.73	0.70
1:CH:33:LYS:O	1:CH:33:LYS:HG2	1.91	0.70
1:AA:33:LYS:O	1:AA:33:LYS:HG2	1.92	0.70
1:AO:79:ARG:HH11	1:AO:79:ARG:HG3	1.56	0.70
1:AQ:454:ASN:HD22	1:AQ:456:ALA:H	1.36	0.70
1:BF:272:TYR:CE2	1:CK:55:ARG:CD	2.75	0.70
1:CB:33:LYS:O	1:CB:33:LYS:HG2	1.91	0.70
1:CF:170:PHE:HD1	1:CF:389:MET:HE1	1.55	0.70
1:CK:33:LYS:HG2	1:CK:33:LYS:O	1.90	0.70
1:AJ:74:ASN:HB3	1:AJ:126:GLU:HG2	1.73	0.70
1:AJ:170:PHE:HD1	1:AJ:389:MET:HE1	1.56	0.70
1:BL:22:THR:OG1	1:BL:131:HIS:HD2	1.73	0.70
1:BO:284:ARG:HH11	1:BO:284:ARG:HG2	1.54	0.70
1:BT:189:PHE:HE1	1:BT:198:ARG:HG3	1.56	0.70
1:CT:284:ARG:HH11	1:CT:284:ARG:HG2	1.56	0.70
1:AI:33:LYS:O	1:AI:33:LYS:HG2	1.92	0.70
1:AN:189:PHE:HE2	1:AN:249:LEU:HD21	1.56	0.70
1:BE:272:TYR:CE2	1:BM:55:ARG:NE	2.59	0.70
1:BK:36:GLN:NE2	1:BK:156:LEU:H	1.89	0.70
1:CF:22:THR:OG1	1:CF:131:HIS:HD2	1.73	0.70
1:CG:189:PHE:CE1	1:CG:198:ARG:HG3	2.27	0.70
1:AA:272:TYR:CE2	1:CT:55:ARG:NE	2.60	0.70
1:AB:33:LYS:HG2	1:AB:33:LYS:O	1.90	0.70
1:AF:189:PHE:HE2	1:AF:249:LEU:HD21	1.56	0.70
1:AG:284:ARG:HH11	1:AG:284:ARG:HG2	1.56	0.70
1:AJ:272:TYR:HE2	1:AQ:55:ARG:CD	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:191:LEU:H	1:AO:191:LEU:CD2	2.05	0.70
1:AS:189:PHE:HE1	1:AS:198:ARG:HG3	1.57	0.70
1:BF:284:ARG:HH11	1:BF:284:ARG:CG	2.04	0.70
1:BJ:272:TYR:CE2	1:BQ:55:ARG:CD	2.74	0.70
1:BM:170:PHE:HD1	1:BM:389:MET:HE1	1.57	0.70
1:BP:191:LEU:H	1:BP:191:LEU:CD2	2.05	0.70
1:BP:284:ARG:HG2	1:BP:284:ARG:HH11	1.56	0.70
1:BT:22:THR:OG1	1:BT:131:HIS:HD2	1.74	0.70
1:CB:79:ARG:HH11	1:CB:79:ARG:HG3	1.56	0.70
1:CD:55:ARG:HD3	1:CN:272:TYR:CD2	2.27	0.70
1:AH:15:GLN:HA	1:AH:15:GLN:HE21	1.57	0.70
1:AL:284:ARG:HH11	1:AL:284:ARG:CG	2.05	0.70
1:BA:250:TRP:CZ3	1:BA:272:TYR:HE1	2.10	0.70
1:BB:189:PHE:HE2	1:BB:249:LEU:HD21	1.56	0.70
1:BF:284:ARG:HH11	1:BF:284:ARG:HG2	1.57	0.70
1:BO:191:LEU:H	1:BO:191:LEU:CD2	2.05	0.70
1:CA:284:ARG:HG2	1:CA:284:ARG:HH11	1.57	0.70
1:CI:38:GLU:HB2	1:CQ:35:VAL:HG22	1.74	0.70
1:CN:284:ARG:HG2	1:CN:284:ARG:HH11	1.56	0.70
1:CO:189:PHE:CE1	1:CO:198:ARG:HG3	2.26	0.70
1:CP:74:ASN:HB3	1:CP:126:GLU:HG2	1.74	0.70
1:AD:55:ARG:CD	1:AN:272:TYR:CE2	2.75	0.70
1:AK:74:ASN:HB3	1:AK:126:GLU:HG2	1.72	0.70
1:AM:272:TYR:CE2	1:CP:55:ARG:NE	2.60	0.70
1:BH:284:ARG:CG	1:BH:284:ARG:HH11	2.04	0.70
1:BJ:22:THR:OG1	1:BJ:131:HIS:HD2	1.75	0.70
1:BK:74:ASN:HB3	1:BK:126:GLU:HG2	1.74	0.70
1:BT:250:TRP:CZ3	1:BT:272:TYR:HE1	2.08	0.70
1:CJ:250:TRP:CE3	1:CJ:272:TYR:CE1	2.80	0.70
1:CN:33:LYS:HG2	1:CN:33:LYS:O	1.91	0.70
1:CT:74:ASN:HB3	1:CT:126:GLU:HG2	1.73	0.70
1:AH:33:LYS:HG2	1:AH:33:LYS:O	1.92	0.69
1:BD:284:ARG:HH11	1:BD:284:ARG:CG	2.05	0.69
1:BN:74:ASN:HB3	1:BN:126:GLU:HG2	1.74	0.69
1:CD:272:TYR:CD2	1:CS:55:ARG:HD3	2.26	0.69
1:AA:22:THR:OG1	1:AA:131:HIS:HD2	1.74	0.69
1:AG:33:LYS:O	1:AG:33:LYS:HG2	1.91	0.69
1:AI:284:ARG:CG	1:AI:284:ARG:HH11	2.05	0.69
1:BO:22:THR:OG1	1:BO:131:HIS:HD2	1.75	0.69
1:CG:189:PHE:HE2	1:CG:249:LEU:HD21	1.57	0.69
1:CK:170:PHE:HD1	1:CK:389:MET:HE1	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:170:PHE:HD1	1:AA:389:MET:HE1	1.57	0.69
1:AE:74:ASN:HB3	1:AE:126:GLU:HG2	1.74	0.69
1:AH:284:ARG:HH11	1:AH:284:ARG:CG	2.05	0.69
1:AJ:79:ARG:HH11	1:AJ:79:ARG:HG3	1.56	0.69
1:AO:284:ARG:HH11	1:AO:284:ARG:CG	2.05	0.69
1:BI:284:ARG:HH11	1:BI:284:ARG:CG	2.05	0.69
1:BJ:36:GLN:NE2	1:BJ:156:LEU:H	1.89	0.69
1:CE:16:ALA:O	1:CE:17:ASN:HB2	1.92	0.69
1:AB:284:ARG:HH11	1:AB:284:ARG:CG	2.05	0.69
1:AD:74:ASN:HB3	1:AD:126:GLU:HG2	1.73	0.69
1:AF:284:ARG:CG	1:AF:284:ARG:HH11	2.05	0.69
1:AH:55:ARG:HD3	1:AK:272:TYR:HD2	1.58	0.69
1:AN:189:PHE:CE1	1:AN:198:ARG:HG3	2.26	0.69
1:CB:74:ASN:HB3	1:CB:126:GLU:HG2	1.74	0.69
1:CI:33:LYS:HG2	1:CI:33:LYS:O	1.90	0.69
1:CI:55:ARG:HD3	1:CR:272:TYR:CD2	2.26	0.69
1:CI:284:ARG:HG2	1:CI:284:ARG:HH11	1.57	0.69
1:AD:284:ARG:HH11	1:AD:284:ARG:CG	2.05	0.69
1:AL:191:LEU:H	1:AL:191:LEU:CD2	2.06	0.69
1:AR:191:LEU:H	1:AR:191:LEU:CD2	2.06	0.69
1:BI:191:LEU:H	1:BI:191:LEU:CD2	2.06	0.69
1:CA:36:GLN:NE2	1:CA:156:LEU:H	1.89	0.69
1:CN:189:PHE:HE2	1:CN:249:LEU:HD21	1.58	0.69
1:AH:250:TRP:CZ3	1:AH:272:TYR:HE1	2.11	0.69
1:AK:33:LYS:HG2	1:AK:33:LYS:O	1.93	0.69
1:AO:250:TRP:CE3	1:AO:272:TYR:CE1	2.81	0.69
1:BL:79:ARG:HH11	1:BL:79:ARG:HG3	1.57	0.69
1:BP:55:ARG:NE	1:CM:272:TYR:CE2	2.61	0.69
1:CJ:74:ASN:HB3	1:CJ:126:GLU:HG2	1.74	0.69
1:CQ:74:ASN:HB3	1:CQ:126:GLU:HG2	1.74	0.69
1:AD:55:ARG:CD	1:AN:272:TYR:HE2	2.06	0.69
1:AO:74:ASN:HB3	1:AO:126:GLU:HG2	1.75	0.69
1:AT:22:THR:OG1	1:AT:131:HIS:HD2	1.76	0.69
1:BJ:74:ASN:HB3	1:BJ:126:GLU:HG2	1.73	0.69
1:CC:22:THR:OG1	1:CC:131:HIS:HD2	1.75	0.69
1:CE:272:TYR:CE2	1:CM:55:ARG:CD	2.74	0.69
1:CE:284:ARG:HH11	1:CE:284:ARG:CG	2.06	0.69
1:CG:250:TRP:CZ3	1:CG:272:TYR:HE1	2.10	0.69
1:CT:170:PHE:HD1	1:CT:389:MET:HE1	1.57	0.69
1:AA:191:LEU:H	1:AA:191:LEU:CD2	2.05	0.69
1:AJ:191:LEU:H	1:AJ:191:LEU:CD2	2.04	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:442:GLN:HE21	1:AL:412:PHE:HB2	1.58	0.69
1:AO:206:GLN:NE2	1:AO:294:LEU:HB2	2.07	0.69
1:AO:284:ARG:HH11	1:AO:284:ARG:HG2	1.57	0.69
1:AT:79:ARG:HG3	1:AT:79:ARG:HH11	1.58	0.69
1:BB:284:ARG:HH11	1:BB:284:ARG:HG2	1.57	0.69
1:BH:189:PHE:HE2	1:BH:249:LEU:HD21	1.56	0.69
1:BM:16:ALA:O	1:BM:17:ASN:HB2	1.92	0.69
1:BQ:170:PHE:HD1	1:BQ:389:MET:HE1	1.58	0.69
1:CB:191:LEU:H	1:CB:191:LEU:CD2	2.06	0.69
1:CI:55:ARG:HD3	1:CR:272:TYR:CE2	2.27	0.69
1:CI:191:LEU:H	1:CI:191:LEU:CD2	2.05	0.69
1:CM:191:LEU:H	1:CM:191:LEU:CD2	2.06	0.69
1:CM:284:ARG:HH11	1:CM:284:ARG:CG	2.06	0.69
1:CN:191:LEU:H	1:CN:191:LEU:CD2	2.06	0.69
1:CQ:22:THR:OG1	1:CQ:131:HIS:HD2	1.76	0.69
1:AA:284:ARG:HG2	1:AA:284:ARG:HH11	1.58	0.69
1:AD:284:ARG:HH11	1:AD:284:ARG:HG2	1.57	0.69
1:AG:74:ASN:HB3	1:AG:126:GLU:HG2	1.75	0.69
1:AH:189:PHE:HE2	1:AH:249:LEU:HD21	1.56	0.69
1:AI:14:CYS:H	1:AI:138:ASN:HD21	1.41	0.69
1:AK:191:LEU:H	1:AK:191:LEU:CD2	2.05	0.69
1:AM:191:LEU:H	1:AM:191:LEU:CD2	2.05	0.69
1:AP:284:ARG:HH11	1:AP:284:ARG:CG	2.06	0.69
1:BI:284:ARG:HH11	1:BI:284:ARG:HG2	1.57	0.69
1:CA:79:ARG:HG3	1:CA:79:ARG:HH11	1.58	0.69
1:CA:191:LEU:H	1:CA:191:LEU:CD2	2.06	0.69
1:CE:189:PHE:CE1	1:CE:198:ARG:HG3	2.27	0.69
1:CH:15:GLN:HA	1:CH:15:GLN:HE21	1.57	0.69
1:CJ:189:PHE:HE2	1:CJ:249:LEU:HD21	1.58	0.69
1:AD:33:LYS:O	1:AD:33:LYS:HG2	1.93	0.69
1:AD:272:TYR:CE2	1:AS:55:ARG:CD	2.76	0.69
1:AE:14:CYS:H	1:AE:138:ASN:HD21	1.39	0.69
1:AF:55:ARG:CD	1:BH:272:TYR:CE2	2.76	0.69
1:AI:22:THR:OG1	1:AI:131:HIS:HD2	1.75	0.69
1:BA:170:PHE:HD1	1:BA:389:MET:HE1	1.58	0.69
1:BB:189:PHE:CE1	1:BB:198:ARG:HG3	2.28	0.69
1:BB:250:TRP:CZ3	1:BB:272:TYR:HE1	2.11	0.69
1:CF:250:TRP:CZ3	1:CF:272:TYR:HE1	2.09	0.69
1:CG:191:LEU:H	1:CG:191:LEU:CD2	2.06	0.69
1:AA:284:ARG:HH11	1:AA:284:ARG:CG	2.06	0.68
1:AG:36:GLN:NE2	1:AG:156:LEU:H	1.91	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:14:CYS:H	1:AL:138:ASN:HD21	1.40	0.68
1:AL:79:ARG:HH11	1:AL:79:ARG:CG	2.06	0.68
1:AL:272:TYR:CE2	1:CJ:55:ARG:CZ	2.75	0.68
1:BC:272:TYR:CD2	1:CA:55:ARG:HD3	2.27	0.68
1:BJ:272:TYR:HE2	1:BQ:55:ARG:CD	2.05	0.68
1:CB:189:PHE:CE1	1:CB:198:ARG:HG3	2.28	0.68
1:CK:284:ARG:HH11	1:CK:284:ARG:CG	2.06	0.68
1:CQ:284:ARG:HH11	1:CQ:284:ARG:CG	2.06	0.68
1:CR:189:PHE:HE2	1:CR:249:LEU:HD21	1.57	0.68
1:AC:22:THR:OG1	1:AC:131:HIS:HD2	1.76	0.68
1:AL:272:TYR:CD2	1:CJ:55:ARG:CZ	2.76	0.68
1:AM:189:PHE:CE1	1:AM:198:ARG:HG3	2.28	0.68
1:AT:55:ARG:CD	1:BA:272:TYR:CE2	2.76	0.68
1:BC:284:ARG:HH11	1:BC:284:ARG:CG	2.07	0.68
1:BH:74:ASN:HB3	1:BH:126:GLU:HG2	1.74	0.68
1:BQ:189:PHE:CE1	1:BQ:198:ARG:HG3	2.29	0.68
1:BT:74:ASN:HB3	1:BT:126:GLU:HG2	1.74	0.68
1:CI:284:ARG:HH11	1:CI:284:ARG:CG	2.06	0.68
1:CP:191:LEU:H	1:CP:191:LEU:CD2	2.05	0.68
1:CR:22:THR:OG1	1:CR:131:HIS:HD2	1.76	0.68
1:AJ:22:THR:OG1	1:AJ:131:HIS:HD2	1.76	0.68
1:BF:191:LEU:H	1:BF:191:LEU:CD2	2.05	0.68
1:BI:189:PHE:CE1	1:BI:198:ARG:HG3	2.28	0.68
1:BK:284:ARG:HG2	1:BK:284:ARG:HH11	1.57	0.68
1:CJ:33:LYS:O	1:CJ:33:LYS:HG2	1.91	0.68
1:CK:191:LEU:H	1:CK:191:LEU:CD2	2.07	0.68
1:CM:33:LYS:O	1:CM:33:LYS:HG2	1.93	0.68
1:CO:22:THR:OG1	1:CO:131:HIS:HD2	1.75	0.68
1:AA:36:GLN:NE2	1:AA:156:LEU:H	1.92	0.68
1:AF:189:PHE:CE1	1:AF:198:ARG:HG3	2.26	0.68
1:AJ:55:ARG:HD3	1:BL:272:TYR:CD2	2.28	0.68
1:AK:284:ARG:HH11	1:AK:284:ARG:CG	2.06	0.68
1:AP:191:LEU:H	1:AP:191:LEU:CD2	2.05	0.68
1:AQ:272:TYR:CE2	1:BL:55:ARG:NE	2.62	0.68
1:BD:55:ARG:CD	1:BN:272:TYR:HE2	2.07	0.68
1:BG:189:PHE:HE2	1:BG:249:LEU:HD21	1.57	0.68
1:BH:55:ARG:NE	1:BK:272:TYR:CE2	2.61	0.68
1:CG:170:PHE:HD1	1:CG:389:MET:HE1	1.59	0.68
1:CH:284:ARG:HG2	1:CH:284:ARG:HH11	1.59	0.68
1:CO:272:TYR:CE2	1:CR:55:ARG:CZ	2.76	0.68
1:AN:170:PHE:HD1	1:AN:389:MET:HE1	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:250:TRP:CZ3	1:AN:272:TYR:HE1	2.10	0.68
1:AO:272:TYR:CD2	1:AR:55:ARG:HD3	2.29	0.68
1:BB:16:ALA:O	1:BB:17:ASN:HB2	1.92	0.68
1:BC:284:ARG:HH11	1:BC:284:ARG:HG2	1.59	0.68
1:CH:189:PHE:HE2	1:CH:249:LEU:HD21	1.59	0.68
1:CK:189:PHE:HE1	1:CK:198:ARG:HG3	1.58	0.68
1:CL:189:PHE:CE1	1:CL:198:ARG:HG3	2.28	0.68
1:CN:284:ARG:HH11	1:CN:284:ARG:CG	2.06	0.68
1:AK:189:PHE:CE1	1:AK:198:ARG:HG3	2.28	0.68
1:AO:33:LYS:O	1:AO:33:LYS:HG2	1.94	0.68
1:AS:74:ASN:HB3	1:AS:126:GLU:HG2	1.74	0.68
1:BM:22:THR:OG1	1:BM:131:HIS:HD2	1.76	0.68
1:BP:189:PHE:CE1	1:BP:198:ARG:HG3	2.28	0.68
1:BR:170:PHE:HD1	1:BR:389:MET:HE1	1.58	0.68
1:CB:250:TRP:CZ3	1:CB:272:TYR:HE1	2.11	0.68
1:CE:189:PHE:HE2	1:CE:249:LEU:HD21	1.59	0.68
1:CH:191:LEU:H	1:CH:191:LEU:CD2	2.07	0.68
1:CL:191:LEU:H	1:CL:191:LEU:CD2	2.06	0.68
1:CS:22:THR:OG1	1:CS:131:HIS:HD2	1.76	0.68
1:AE:250:TRP:CZ3	1:AE:272:TYR:HE1	2.11	0.68
1:AH:272:TYR:CE2	1:CF:55:ARG:HD3	2.28	0.68
1:AI:36:GLN:NE2	1:AI:156:LEU:H	1.92	0.68
1:AI:191:LEU:H	1:AI:191:LEU:CD2	2.07	0.68
1:AI:454:ASN:HD22	1:AI:456:ALA:H	1.39	0.68
1:AL:189:PHE:HE1	1:AL:198:ARG:HG3	1.58	0.68
1:BB:55:ARG:NE	1:CB:272:TYR:HE2	1.92	0.68
1:BB:55:ARG:CD	1:CB:272:TYR:HE2	2.07	0.68
1:BK:22:THR:OG1	1:BK:131:HIS:HD2	1.76	0.68
1:BT:284:ARG:HH11	1:BT:284:ARG:CG	2.07	0.68
1:CG:189:PHE:CE1	1:CG:198:ARG:CG	2.77	0.68
1:CN:22:THR:OG1	1:CN:131:HIS:HD2	1.76	0.68
1:AE:33:LYS:HG2	1:AE:33:LYS:O	1.92	0.68
1:AI:189:PHE:HE2	1:AI:249:LEU:HD21	1.58	0.68
1:AL:33:LYS:O	1:AL:33:LYS:HG2	1.94	0.68
1:AT:36:GLN:NE2	1:AT:156:LEU:H	1.92	0.68
1:BD:189:PHE:HE1	1:BD:198:ARG:HG3	1.58	0.68
1:BN:284:ARG:HH11	1:BN:284:ARG:CG	2.06	0.68
1:BR:284:ARG:HG2	1:BR:284:ARG:HH11	1.59	0.68
1:BS:33:LYS:O	1:BS:33:LYS:HG2	1.92	0.68
1:CA:22:THR:OG1	1:CA:131:HIS:HD2	1.75	0.68
1:CA:189:PHE:HE1	1:CA:198:ARG:HG3	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:33:LYS:HG2	1:CF:33:LYS:O	1.94	0.68
1:CH:74:ASN:HB3	1:CH:126:GLU:HG2	1.74	0.68
1:CK:284:ARG:HH11	1:CK:284:ARG:HG2	1.59	0.68
1:AC:74:ASN:HB3	1:AC:126:GLU:HG2	1.75	0.68
1:AC:284:ARG:HH11	1:AC:284:ARG:HG2	1.59	0.68
1:AE:189:PHE:CE1	1:AE:198:ARG:HG3	2.26	0.68
1:AI:272:TYR:HD2	1:AO:55:ARG:HD3	1.56	0.68
1:BE:74:ASN:HB3	1:BE:126:GLU:HG2	1.74	0.68
1:BM:284:ARG:HH11	1:BM:284:ARG:HG2	1.59	0.68
1:BT:191:LEU:H	1:BT:191:LEU:CD2	2.06	0.68
1:CO:284:ARG:HG2	1:CO:284:ARG:HH11	1.58	0.68
1:CP:454:ASN:HD22	1:CP:456:ALA:H	1.40	0.68
1:AE:55:ARG:NE	1:CP:272:TYR:HE2	1.88	0.68
1:AG:189:PHE:CE1	1:AG:198:ARG:HG3	2.29	0.68
1:AG:259:THR:CG2	1:AG:268:TYR:OH	2.42	0.68
1:AO:170:PHE:HD1	1:AO:389:MET:HE1	1.59	0.68
1:AT:284:ARG:HG2	1:AT:284:ARG:HH11	1.59	0.68
1:BA:189:PHE:CE1	1:BA:198:ARG:HG3	2.29	0.68
1:BD:272:TYR:HE2	1:BS:55:ARG:CD	2.06	0.68
1:CI:189:PHE:CE1	1:CI:198:ARG:HG3	2.28	0.68
1:AB:262:TRP:O	1:AB:263:ASN:C	2.30	0.67
1:AD:14:CYS:H	1:AD:138:ASN:HD21	1.42	0.67
1:AR:284:ARG:HH11	1:AR:284:ARG:CG	2.06	0.67
1:BE:189:PHE:CE1	1:BE:198:ARG:HG3	2.29	0.67
1:BG:284:ARG:HH11	1:BG:284:ARG:HG2	1.60	0.67
1:BO:272:TYR:CD2	1:BR:55:ARG:HD3	2.29	0.67
1:CF:189:PHE:HE2	1:CF:249:LEU:HD21	1.59	0.67
1:AF:272:TYR:HE2	1:BK:55:ARG:CD	2.07	0.67
1:AH:272:TYR:CD2	1:CF:55:ARG:HD3	2.28	0.67
1:AJ:55:ARG:CD	1:BL:272:TYR:HE2	2.07	0.67
1:AM:16:ALA:O	1:AM:17:ASN:HB2	1.92	0.67
1:AM:189:PHE:HE2	1:AM:249:LEU:HD21	1.58	0.67
1:AO:36:GLN:NE2	1:AO:156:LEU:H	1.92	0.67
1:BA:79:ARG:HH11	1:BA:79:ARG:CG	2.06	0.67
1:BD:170:PHE:HD1	1:BD:389:MET:HE1	1.58	0.67
1:BG:284:ARG:HH11	1:BG:284:ARG:CG	2.06	0.67
1:BH:191:LEU:H	1:BH:191:LEU:CD2	2.07	0.67
1:BJ:33:LYS:HG2	1:BJ:33:LYS:O	1.94	0.67
1:BQ:191:LEU:H	1:BQ:191:LEU:CD2	2.07	0.67
1:AG:16:ALA:O	1:AG:17:ASN:HB2	1.94	0.67
1:BE:22:THR:OG1	1:BE:131:HIS:HD2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:55:ARG:NE	1:CH:272:TYR:CE2	2.63	0.67
1:CB:16:ALA:O	1:CB:17:ASN:HB2	1.93	0.67
1:CB:36:GLN:NE2	1:CB:156:LEU:H	1.92	0.67
1:CF:191:LEU:H	1:CF:191:LEU:CD2	2.07	0.67
1:CO:284:ARG:HH11	1:CO:284:ARG:CG	2.07	0.67
1:CQ:33:LYS:HG2	1:CQ:33:LYS:O	1.93	0.67
1:BD:55:ARG:HD3	1:BN:272:TYR:CE2	2.28	0.67
1:BJ:55:ARG:NE	1:CL:272:TYR:CE2	2.62	0.67
1:BL:284:ARG:HH11	1:BL:284:ARG:CG	2.07	0.67
1:BM:33:LYS:HG2	1:BM:33:LYS:O	1.93	0.67
1:CL:170:PHE:HD1	1:CL:389:MET:HE1	1.59	0.67
1:CM:189:PHE:HE2	1:CM:249:LEU:HD21	1.58	0.67
1:AA:272:TYR:CD2	1:CT:55:ARG:HD3	2.29	0.67
1:AD:191:LEU:H	1:AD:191:LEU:CD2	2.07	0.67
1:AG:22:THR:OG1	1:AG:131:HIS:HD2	1.77	0.67
1:AK:55:ARG:CD	1:CF:272:TYR:HE2	2.08	0.67
1:CD:55:ARG:CD	1:CN:272:TYR:HE2	2.08	0.67
1:CE:79:ARG:HH11	1:CE:79:ARG:HG3	1.60	0.67
1:AD:272:TYR:HE2	1:AS:55:ARG:CD	2.08	0.67
1:AP:74:ASN:HB3	1:AP:126:GLU:HG2	1.76	0.67
1:AQ:189:PHE:HE1	1:AQ:198:ARG:HG3	1.60	0.67
1:BD:55:ARG:NE	1:BN:272:TYR:CE2	2.63	0.67
1:BE:191:LEU:H	1:BE:191:LEU:CD2	2.06	0.67
1:BE:284:ARG:CG	1:BE:284:ARG:HH11	2.07	0.67
1:CC:74:ASN:HB3	1:CC:126:GLU:HG2	1.75	0.67
1:CE:74:ASN:HB3	1:CE:126:GLU:HG2	1.76	0.67
1:AB:22:THR:OG1	1:AB:131:HIS:HD2	1.78	0.67
1:AG:270:GLY:C	1:AG:271:VAL:HG13	2.19	0.67
1:AH:170:PHE:HD1	1:AH:389:MET:HE1	1.60	0.67
1:AJ:189:PHE:HE2	1:AJ:249:LEU:HD21	1.59	0.67
1:AT:74:ASN:HB3	1:AT:126:GLU:HG2	1.75	0.67
1:BC:191:LEU:H	1:BC:191:LEU:CD2	2.08	0.67
1:BM:191:LEU:H	1:BM:191:LEU:CD2	2.06	0.67
1:BO:170:PHE:HD1	1:BO:389:MET:HE1	1.60	0.67
1:CD:36:GLN:NE2	1:CD:156:LEU:H	1.93	0.67
1:CG:284:ARG:CG	1:CG:284:ARG:HH11	2.07	0.67
1:AF:170:PHE:HD1	1:AF:389:MET:HE1	1.60	0.67
1:BE:189:PHE:HE2	1:BE:249:LEU:HD21	1.59	0.67
1:BI:189:PHE:HE2	1:BI:249:LEU:HD21	1.59	0.67
1:BK:284:ARG:HH11	1:BK:284:ARG:CG	2.07	0.67
1:BP:170:PHE:HD1	1:BP:389:MET:HE1	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:272:TYR:CE2	1:CL:55:ARG:CD	2.78	0.67
1:CC:189:PHE:HE1	1:CC:198:ARG:HG3	1.59	0.67
1:CD:33:LYS:O	1:CD:33:LYS:HG2	1.95	0.67
1:CF:189:PHE:CE1	1:CF:198:ARG:HG3	2.29	0.67
1:CS:170:PHE:HD1	1:CS:389:MET:HE1	1.60	0.67
1:CT:191:LEU:H	1:CT:191:LEU:CD2	2.08	0.67
1:AI:284:ARG:HH11	1:AI:284:ARG:HG2	1.58	0.67
1:AK:36:GLN:NE2	1:AK:156:LEU:H	1.92	0.67
1:AS:284:ARG:HH11	1:AS:284:ARG:HG2	1.58	0.67
1:BD:454:ASN:HD22	1:BD:456:ALA:H	1.43	0.67
1:BJ:284:ARG:HH11	1:BJ:284:ARG:CG	2.08	0.67
1:BQ:284:ARG:HG2	1:BQ:284:ARG:NH1	2.09	0.67
1:BS:284:ARG:CG	1:BS:284:ARG:HH11	2.08	0.67
1:CS:250:TRP:CZ3	1:CS:272:TYR:HE1	2.12	0.67
1:AE:55:ARG:HD3	1:CP:272:TYR:CD2	2.30	0.67
1:AI:74:ASN:HB3	1:AI:126:GLU:HG2	1.76	0.67
1:AR:284:ARG:HH11	1:AR:284:ARG:HG2	1.60	0.67
1:AT:55:ARG:CD	1:BA:272:TYR:HE2	2.08	0.67
1:AT:284:ARG:HH11	1:AT:284:ARG:CG	2.08	0.67
1:BC:272:TYR:CE2	1:CA:55:ARG:CD	2.78	0.67
1:BH:189:PHE:CE1	1:BH:198:ARG:HG3	2.28	0.67
1:CR:189:PHE:CE1	1:CR:198:ARG:HG3	2.29	0.67
1:AE:191:LEU:H	1:AE:191:LEU:CD2	2.08	0.66
1:AE:284:ARG:HH11	1:AE:284:ARG:CG	2.08	0.66
1:AH:55:ARG:CZ	1:AK:272:TYR:CD2	2.79	0.66
1:BC:170:PHE:HD1	1:BC:389:MET:HE1	1.60	0.66
1:BE:170:PHE:HD1	1:BE:389:MET:HE1	1.59	0.66
1:BF:55:ARG:HD3	1:CH:272:TYR:CD2	2.31	0.66
1:BF:272:TYR:HE2	1:CK:55:ARG:CD	2.08	0.66
1:BN:33:LYS:O	1:BN:33:LYS:HG2	1.93	0.66
1:CE:170:PHE:HD1	1:CE:389:MET:HE1	1.59	0.66
1:CH:284:ARG:HH11	1:CH:284:ARG:CG	2.08	0.66
1:CK:74:ASN:HB3	1:CK:126:GLU:HG2	1.76	0.66
1:CM:74:ASN:HB3	1:CM:126:GLU:HG2	1.77	0.66
1:AR:14:CYS:H	1:AR:138:ASN:HD21	1.42	0.66
1:BC:189:PHE:CE1	1:BC:198:ARG:HG3	2.30	0.66
1:BR:284:ARG:HH11	1:BR:284:ARG:CG	2.07	0.66
1:BT:55:ARG:HD3	1:CA:272:TYR:CE2	2.30	0.66
1:CB:284:ARG:HH11	1:CB:284:ARG:CG	2.08	0.66
1:CG:74:ASN:HB3	1:CG:126:GLU:HG2	1.78	0.66
1:AC:191:LEU:H	1:AC:191:LEU:CD2	2.06	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:191:LEU:H	1:BA:191:LEU:CD2	2.08	0.66
1:BI:170:PHE:HD1	1:BI:389:MET:HE1	1.60	0.66
1:AB:189:PHE:CE1	1:AB:198:ARG:HG3	2.31	0.66
1:AE:36:GLN:NE2	1:AE:156:LEU:H	1.94	0.66
1:AL:55:ARG:NE	1:CQ:272:TYR:CE2	2.64	0.66
1:BL:191:LEU:H	1:BL:191:LEU:CD2	2.09	0.66
1:BN:55:ARG:CD	1:BS:272:TYR:CE2	2.78	0.66
1:CO:250:TRP:CE3	1:CO:272:TYR:CE1	2.83	0.66
1:CR:80:ILE:O	1:CR:83:SER:C	2.38	0.66
1:CT:22:THR:OG1	1:CT:131:HIS:HD2	1.78	0.66
1:AN:189:PHE:HE2	1:AN:249:LEU:CD2	2.08	0.66
1:BA:284:ARG:HH11	1:BA:284:ARG:HG2	1.61	0.66
1:BI:55:ARG:CZ	1:BR:272:TYR:CE2	2.78	0.66
1:CD:79:ARG:HH11	1:CD:79:ARG:CG	2.07	0.66
1:CH:250:TRP:CZ3	1:CH:272:TYR:HE1	2.12	0.66
1:CN:14:CYS:H	1:CN:138:ASN:HD21	1.41	0.66
1:CP:250:TRP:CE3	1:CP:272:TYR:CE1	2.84	0.66
1:CP:284:ARG:HH11	1:CP:284:ARG:CG	2.07	0.66
1:CR:191:LEU:H	1:CR:191:LEU:CD2	2.09	0.66
1:AE:272:TYR:CD2	1:AM:55:ARG:HD3	2.30	0.66
1:AH:36:GLN:NE2	1:AH:156:LEU:H	1.94	0.66
1:BI:55:ARG:HD3	1:BR:272:TYR:CD2	2.31	0.66
1:BJ:189:PHE:HE2	1:BJ:249:LEU:HD21	1.61	0.66
1:BM:11:PRO:HG2	1:BM:18:ARG:HD3	1.76	0.66
1:CD:74:ASN:HB3	1:CD:126:GLU:HG2	1.77	0.66
1:CH:22:THR:OG1	1:CH:131:HIS:HD2	1.79	0.66
1:CI:74:ASN:CB	1:CI:126:GLU:HG2	2.26	0.66
1:CI:378:ARG:HG3	1:CI:379:VAL:H	1.61	0.66
1:CM:189:PHE:CE1	1:CM:198:ARG:HG3	2.28	0.66
1:CM:284:ARG:HH11	1:CM:284:ARG:HG2	1.60	0.66
1:CO:74:ASN:HB3	1:CO:126:GLU:HG2	1.76	0.66
1:CO:191:LEU:H	1:CO:191:LEU:CD2	2.07	0.66
1:AL:170:PHE:HD1	1:AL:389:MET:HE1	1.60	0.66
1:AN:284:ARG:HH11	1:AN:284:ARG:CG	2.08	0.66
1:BF:33:LYS:O	1:BF:33:LYS:HG2	1.96	0.66
1:BS:79:ARG:HH11	1:BS:79:ARG:CG	2.04	0.66
1:BS:189:PHE:CE1	1:BS:198:ARG:HG3	2.31	0.66
1:CA:250:TRP:CZ3	1:CA:272:TYR:HE1	2.14	0.66
1:CB:284:ARG:HH11	1:CB:284:ARG:HG2	1.59	0.66
1:CG:16:ALA:O	1:CG:17:ASN:HB2	1.95	0.66
1:CN:74:ASN:ND2	1:CN:77:THR:OG1	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:86:PRO:HG2	1:CR:87:VAL:H	1.60	0.66
1:BD:272:TYR:CE2	1:BS:55:ARG:CD	2.78	0.66
1:BK:250:TRP:CZ3	1:BK:272:TYR:HE1	2.13	0.66
1:CC:191:LEU:H	1:CC:191:LEU:CD2	2.07	0.66
1:CN:189:PHE:CE1	1:CN:198:ARG:CG	2.79	0.66
1:AD:250:TRP:CZ3	1:AD:272:TYR:HE1	2.14	0.66
1:AK:22:THR:OG1	1:AK:131:HIS:HD2	1.79	0.66
1:BL:189:PHE:CE1	1:BL:198:ARG:HG3	2.31	0.66
1:CR:250:TRP:CZ3	1:CR:272:TYR:HE1	2.14	0.66
1:AH:189:PHE:CE1	1:AH:198:ARG:HG3	2.31	0.65
1:AO:272:TYR:HE2	1:AR:55:ARG:NE	1.89	0.65
1:BN:36:GLN:NE2	1:BN:156:LEU:H	1.94	0.65
1:CA:284:ARG:HH11	1:CA:284:ARG:CG	2.09	0.65
1:CL:79:ARG:HG3	1:CL:79:ARG:HH11	1.59	0.65
1:AP:284:ARG:HH11	1:AP:284:ARG:HG2	1.62	0.65
1:BB:74:ASN:HB3	1:BB:126:GLU:HG2	1.79	0.65
1:BE:189:PHE:CE1	1:BE:198:ARG:CG	2.78	0.65
1:CC:170:PHE:HD1	1:CC:389:MET:HE1	1.60	0.65
1:CT:250:TRP:CZ3	1:CT:272:TYR:HE1	2.14	0.65
1:AB:189:PHE:HE2	1:AB:249:LEU:HD21	1.59	0.65
1:BJ:284:ARG:HH11	1:BJ:284:ARG:HG2	1.62	0.65
1:BN:284:ARG:HH11	1:BN:284:ARG:HG2	1.62	0.65
1:CB:170:PHE:HD1	1:CB:389:MET:HE1	1.60	0.65
1:CD:191:LEU:H	1:CD:191:LEU:CD2	2.09	0.65
1:AL:284:ARG:HH11	1:AL:284:ARG:HG2	1.60	0.65
1:AO:189:PHE:HE1	1:AO:198:ARG:HG3	1.61	0.65
1:AQ:191:LEU:H	1:AQ:191:LEU:CD2	2.08	0.65
1:AR:189:PHE:HE2	1:AR:249:LEU:CD2	2.09	0.65
1:AS:170:PHE:HD1	1:AS:389:MET:HE1	1.59	0.65
1:BD:74:ASN:HB3	1:BD:126:GLU:HG2	1.77	0.65
1:BQ:272:TYR:HE2	1:CL:55:ARG:CD	2.09	0.65
1:BR:189:PHE:HE2	1:BR:249:LEU:HD21	1.61	0.65
1:CB:189:PHE:HE2	1:CB:249:LEU:HD21	1.61	0.65
1:CD:272:TYR:CE2	1:CS:55:ARG:HD3	2.30	0.65
1:CI:55:ARG:CD	1:CR:272:TYR:HE2	2.08	0.65
1:AD:36:GLN:NE2	1:AD:156:LEU:H	1.95	0.65
1:AT:379:VAL:HG11	1:AT:381:MET:HE1	1.79	0.65
1:BK:189:PHE:CE1	1:BK:198:ARG:HG3	2.32	0.65
1:CG:284:ARG:HH11	1:CG:284:ARG:HG2	1.62	0.65
1:CS:284:ARG:HH11	1:CS:284:ARG:CG	2.09	0.65
1:AD:22:THR:OG1	1:AD:131:HIS:HD2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:170:PHE:HD1	1:AE:389:MET:HE1	1.61	0.65
1:AF:55:ARG:CD	1:BH:272:TYR:HE2	2.10	0.65
1:AH:191:LEU:H	1:AH:191:LEU:CD2	2.10	0.65
1:AI:272:TYR:CD2	1:AO:55:ARG:CD	2.79	0.65
1:BH:284:ARG:HH11	1:BH:284:ARG:HG2	1.61	0.65
1:CN:16:ALA:O	1:CN:17:ASN:HB2	1.97	0.65
1:AB:256:ASN:O	1:AB:256:ASN:ND2	2.30	0.65
1:AB:262:TRP:O	1:AB:265:LEU:N	2.30	0.65
1:AF:284:ARG:HH11	1:AF:284:ARG:HG2	1.61	0.65
1:BF:55:ARG:CD	1:CH:272:TYR:CE2	2.80	0.65
1:BF:189:PHE:HE2	1:BF:249:LEU:HD21	1.62	0.65
1:CD:284:ARG:HG2	1:CD:284:ARG:NH1	2.12	0.65
1:CF:288:HIS:HD2	1:CF:337:ASP:OD2	1.79	0.65
1:CI:36:GLN:NE2	1:CI:156:LEU:H	1.94	0.65
1:AA:272:TYR:CE2	1:CT:55:ARG:CD	2.80	0.65
1:AB:36:GLN:NE2	1:AB:156:LEU:H	1.94	0.65
1:AJ:189:PHE:CE1	1:AJ:198:ARG:HG3	2.30	0.65
1:BB:22:THR:OG1	1:BB:131:HIS:HD2	1.80	0.65
1:BG:189:PHE:CE1	1:BG:198:ARG:HG3	2.29	0.65
1:BO:189:PHE:HE1	1:BO:198:ARG:HG3	1.61	0.65
1:CL:14:CYS:H	1:CL:138:ASN:HD21	1.45	0.65
1:CR:80:ILE:O	1:CR:83:SER:N	2.30	0.65
1:AK:250:TRP:CZ3	1:AK:272:TYR:HE1	2.14	0.65
1:AP:250:TRP:CZ3	1:AP:272:TYR:HE1	2.14	0.65
1:AS:36:GLN:NE2	1:AS:156:LEU:H	1.95	0.65
1:BB:189:PHE:CE1	1:BB:198:ARG:CG	2.78	0.65
1:BF:36:GLN:NE2	1:BF:156:LEU:H	1.94	0.65
1:BK:191:LEU:H	1:BK:191:LEU:CD2	2.09	0.65
1:CC:189:PHE:CE1	1:CC:198:ARG:HG3	2.32	0.65
1:AN:191:LEU:H	1:AN:191:LEU:CD2	2.10	0.65
1:AS:189:PHE:CE1	1:AS:198:ARG:HG3	2.32	0.65
1:AT:189:PHE:CE1	1:AT:198:ARG:HG3	2.32	0.65
1:BS:36:GLN:NE2	1:BS:156:LEU:H	1.95	0.65
1:CH:55:ARG:NE	1:CK:272:TYR:CE2	2.65	0.65
1:CH:189:PHE:CE1	1:CH:198:ARG:HG3	2.30	0.65
1:AC:55:ARG:HD3	1:AT:272:TYR:CE2	2.32	0.64
1:BB:170:PHE:HD1	1:BB:389:MET:HE1	1.62	0.64
1:BG:22:THR:OG1	1:BG:131:HIS:HD2	1.80	0.64
1:BJ:272:TYR:CD2	1:BQ:55:ARG:HD3	2.32	0.64
1:BO:272:TYR:CD2	1:BR:55:ARG:CZ	2.80	0.64
1:AJ:189:PHE:CE1	1:AJ:198:ARG:CG	2.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:284:ARG:HH11	1:AJ:284:ARG:CG	2.10	0.64
1:AM:74:ASN:HB3	1:AM:126:GLU:HG2	1.78	0.64
1:CC:55:ARG:HD3	1:CT:272:TYR:CD2	2.32	0.64
1:CO:170:PHE:HD1	1:CO:389:MET:HE1	1.60	0.64
1:CQ:16:ALA:O	1:CQ:17:ASN:HB2	1.95	0.64
1:AG:55:ARG:NE	1:CG:272:TYR:CE2	2.66	0.64
1:AQ:36:GLN:NE2	1:AQ:156:LEU:H	1.94	0.64
1:BI:55:ARG:CZ	1:BR:272:TYR:CD2	2.80	0.64
1:BL:74:ASN:CB	1:BL:126:GLU:HG2	2.27	0.64
1:BN:189:PHE:HE2	1:BN:249:LEU:HD21	1.61	0.64
1:CC:284:ARG:HG2	1:CC:284:ARG:NH1	2.12	0.64
1:CK:14:CYS:H	1:CK:138:ASN:HD21	1.44	0.64
1:CM:16:ALA:O	1:CM:17:ASN:HB2	1.95	0.64
1:AF:189:PHE:HE2	1:AF:249:LEU:CD2	2.10	0.64
1:AN:74:ASN:CB	1:AN:126:GLU:HG2	2.28	0.64
1:AN:79:ARG:HH11	1:AN:79:ARG:CG	2.11	0.64
1:BE:272:TYR:HE2	1:BM:55:ARG:CD	2.10	0.64
1:BM:189:PHE:HE2	1:BM:249:LEU:CD2	2.10	0.64
1:BR:191:LEU:H	1:BR:191:LEU:CD2	2.09	0.64
1:CH:189:PHE:HE2	1:CH:249:LEU:CD2	2.10	0.64
1:CL:250:TRP:CZ3	1:CL:272:TYR:HE1	2.15	0.64
1:CN:18:ARG:HG3	1:CN:19:TYR:N	2.12	0.64
1:AG:284:ARG:HG2	1:AG:284:ARG:NH1	2.12	0.64
1:AJ:36:GLN:NE2	1:AJ:156:LEU:H	1.96	0.64
1:AM:250:TRP:CZ3	1:AM:272:TYR:HE1	2.16	0.64
1:BA:74:ASN:CB	1:BA:126:GLU:HG2	2.28	0.64
1:BG:36:GLN:NE2	1:BG:156:LEU:H	1.95	0.64
1:BG:250:TRP:CZ3	1:BG:272:TYR:HE1	2.13	0.64
1:BG:272:TYR:HE2	1:CG:55:ARG:CD	2.10	0.64
1:CF:79:ARG:HG3	1:CF:79:ARG:NH1	2.00	0.64
1:CF:284:ARG:HH11	1:CF:284:ARG:CG	2.10	0.64
1:CJ:284:ARG:HH11	1:CJ:284:ARG:CG	2.10	0.64
1:AA:74:ASN:HB3	1:AA:126:GLU:HG2	1.78	0.64
1:AC:189:PHE:HE1	1:AC:198:ARG:HG3	1.63	0.64
1:AF:250:TRP:CZ3	1:AF:272:TYR:HE1	2.15	0.64
1:AR:379:VAL:HG11	1:AR:381:MET:HE1	1.79	0.64
1:AT:191:LEU:H	1:AT:191:LEU:CD2	2.08	0.64
1:CI:170:PHE:HD1	1:CI:389:MET:HE1	1.63	0.64
1:CI:377:CYS:HG	1:CI:378:ARG:N	1.94	0.64
1:AN:16:ALA:O	1:AN:17:ASN:HB2	1.97	0.64
1:BB:239:ILE:HG12	1:BB:326:ILE:CD1	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:74:ASN:HB3	1:BC:126:GLU:HG2	1.78	0.64
1:BE:284:ARG:HH11	1:BE:284:ARG:HG2	1.61	0.64
1:BF:74:ASN:HB3	1:BF:126:GLU:HG2	1.80	0.64
1:BF:250:TRP:CZ3	1:BF:272:TYR:HE1	2.14	0.64
1:BF:272:TYR:CD2	1:CK:55:ARG:HD3	2.32	0.64
1:BI:55:ARG:HD3	1:BR:272:TYR:CE2	2.33	0.64
1:BP:74:ASN:HB3	1:BP:126:GLU:HG2	1.80	0.64
1:CM:170:PHE:HD1	1:CM:389:MET:HE1	1.62	0.64
1:CP:189:PHE:CE1	1:CP:198:ARG:HG3	2.33	0.64
1:AG:263:ASN:O	1:BG:32:PHE:CE1	2.51	0.64
1:AI:55:ARG:CD	1:AR:272:TYR:HE2	2.11	0.64
1:AM:189:PHE:CE1	1:AM:198:ARG:CG	2.80	0.64
1:BB:55:ARG:CZ	1:CB:272:TYR:CE2	2.81	0.64
1:BK:170:PHE:HD1	1:BK:389:MET:HE1	1.61	0.64
1:BL:16:ALA:O	1:BL:17:ASN:HB2	1.98	0.64
1:BL:170:PHE:HD1	1:BL:389:MET:HE1	1.63	0.64
1:BL:284:ARG:HH11	1:BL:284:ARG:HG2	1.63	0.64
1:BM:74:ASN:HB3	1:BM:126:GLU:HG2	1.80	0.64
1:CK:22:THR:OG1	1:CK:131:HIS:HD2	1.81	0.64
1:CN:55:ARG:CD	1:CS:272:TYR:CE2	2.80	0.64
1:CR:85:ASP:OD1	1:CR:86:PRO:N	2.31	0.64
1:AF:55:ARG:HD3	1:BH:272:TYR:CD2	2.33	0.64
1:AG:269:PRO:O	1:AG:269:PRO:CG	2.46	0.64
1:AJ:272:TYR:CD2	1:AQ:55:ARG:HD3	2.32	0.64
1:AN:284:ARG:HH11	1:AN:284:ARG:HG2	1.63	0.64
1:AR:36:GLN:NE2	1:AR:156:LEU:H	1.95	0.64
1:BH:250:TRP:CZ3	1:BH:272:TYR:HE1	2.15	0.64
1:BJ:189:PHE:CE1	1:BJ:198:ARG:CG	2.81	0.64
1:BR:189:PHE:CE1	1:BR:198:ARG:HG3	2.29	0.64
1:CA:67:VAL:HG23	1:CA:135:LEU:HB2	1.79	0.64
1:CL:9:TYR:CE1	1:CL:147:GLN:NE2	2.65	0.64
1:CR:74:ASN:HB3	1:CR:126:GLU:HG2	1.79	0.64
1:AJ:55:ARG:HD3	1:BL:272:TYR:CE2	2.32	0.64
1:AM:284:ARG:HG2	1:AM:284:ARG:NH1	2.09	0.64
1:BI:250:TRP:CZ3	1:BI:272:TYR:HE1	2.16	0.64
1:CE:189:PHE:CE1	1:CE:198:ARG:CG	2.81	0.64
1:CQ:284:ARG:HH11	1:CQ:284:ARG:HG2	1.62	0.64
1:CR:80:ILE:HA	1:CR:83:SER:O	1.98	0.64
1:AB:74:ASN:CB	1:AB:126:GLU:HG2	2.29	0.63
1:AG:170:PHE:HD1	1:AG:389:MET:HE1	1.61	0.63
1:BE:36:GLN:NE2	1:BE:156:LEU:H	1.96	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:272:TYR:CE2	1:CE:55:ARG:CZ	2.81	0.63
1:BR:250:TRP:CZ3	1:BR:272:TYR:HE1	2.15	0.63
1:BT:55:ARG:HD3	1:CA:272:TYR:CD2	2.32	0.63
1:CF:284:ARG:HH11	1:CF:284:ARG:HG2	1.63	0.63
1:CI:250:TRP:CZ3	1:CI:272:TYR:HE1	2.15	0.63
1:CQ:14:CYS:H	1:CQ:138:ASN:HD21	1.43	0.63
1:CQ:189:PHE:HE1	1:CQ:198:ARG:HG3	1.62	0.63
1:AG:191:LEU:H	1:AG:191:LEU:CD2	2.07	0.63
1:AG:259:THR:HG21	1:AG:268:TYR:OH	1.98	0.63
1:AI:379:VAL:HG11	1:AI:381:MET:HE1	1.80	0.63
1:AL:36:GLN:NE2	1:AL:156:LEU:H	1.95	0.63
1:AM:36:GLN:NE2	1:AM:156:LEU:H	1.96	0.63
1:AM:272:TYR:CE2	1:CP:55:ARG:CD	2.81	0.63
1:BB:14:CYS:H	1:BB:138:ASN:HD21	1.45	0.63
1:BG:79:ARG:HH11	1:BG:79:ARG:HG3	1.62	0.63
1:BT:14:CYS:H	1:BT:138:ASN:HD21	1.46	0.63
1:BT:74:ASN:CB	1:BT:126:GLU:HG2	2.28	0.63
1:CE:250:TRP:CE3	1:CE:272:TYR:CE1	2.86	0.63
1:CK:189:PHE:CE1	1:CK:198:ARG:HG3	2.33	0.63
1:AC:55:ARG:HD3	1:AT:272:TYR:CD2	2.32	0.63
1:BH:14:CYS:H	1:BH:138:ASN:HD21	1.46	0.63
1:BQ:22:THR:OG1	1:BQ:131:HIS:HD2	1.81	0.63
1:CC:55:ARG:HD3	1:CT:272:TYR:CE2	2.33	0.63
1:CD:442:GLN:HE21	1:CE:412:PHE:HB2	1.63	0.63
1:CF:454:ASN:HD22	1:CF:456:ALA:N	1.96	0.63
1:BG:191:LEU:H	1:BG:191:LEU:CD2	2.08	0.63
1:CD:250:TRP:CE3	1:CD:272:TYR:CE1	2.86	0.63
1:CE:272:TYR:CD2	1:CM:55:ARG:CZ	2.81	0.63
1:CL:36:GLN:NE2	1:CL:156:LEU:H	1.97	0.63
1:CM:189:PHE:HE2	1:CM:249:LEU:CD2	2.11	0.63
1:AG:250:TRP:CE3	1:AG:272:TYR:CE1	2.86	0.63
1:AH:22:THR:OG1	1:AH:131:HIS:HD2	1.81	0.63
1:AH:55:ARG:CD	1:AK:272:TYR:CD2	2.81	0.63
1:AT:55:ARG:HD3	1:BA:272:TYR:CD2	2.33	0.63
1:BB:36:GLN:NE2	1:BB:156:LEU:H	1.96	0.63
1:BG:189:PHE:CE1	1:BG:198:ARG:CG	2.81	0.63
1:BP:284:ARG:HH11	1:BP:284:ARG:CG	2.12	0.63
1:BS:191:LEU:H	1:BS:191:LEU:CD2	2.08	0.63
1:BT:284:ARG:HH11	1:BT:284:ARG:HG2	1.63	0.63
1:CT:284:ARG:HG2	1:CT:284:ARG:NH1	2.13	0.63
1:AA:55:ARG:CD	1:CC:272:TYR:HE2	2.11	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:170:PHE:HD1	1:AB:389:MET:HE1	1.62	0.63
1:AC:272:TYR:CE2	1:BA:55:ARG:NE	2.66	0.63
1:AD:55:ARG:HD3	1:AN:272:TYR:CD2	2.34	0.63
1:AH:284:ARG:HH11	1:AH:284:ARG:HG2	1.63	0.63
1:BH:36:GLN:NE2	1:BH:156:LEU:H	1.96	0.63
1:BL:239:ILE:HG12	1:BL:326:ILE:CD1	2.29	0.63
1:BS:74:ASN:CB	1:BS:126:GLU:HG2	2.28	0.63
1:CE:14:CYS:H	1:CE:138:ASN:HD21	1.45	0.63
1:AO:22:THR:OG1	1:AO:131:HIS:HD2	1.82	0.63
1:BB:55:ARG:CD	1:CB:272:TYR:CE2	2.82	0.63
1:BE:79:ARG:HG3	1:BE:79:ARG:HH11	1.63	0.63
1:CS:189:PHE:CE1	1:CS:198:ARG:HG3	2.34	0.63
1:AA:14:CYS:H	1:AA:138:ASN:HD21	1.45	0.63
1:AF:191:LEU:H	1:AF:191:LEU:CD2	2.11	0.63
1:AH:55:ARG:HD3	1:AK:272:TYR:CE2	2.31	0.63
1:BB:79:ARG:HG3	1:BB:79:ARG:HH11	1.64	0.63
1:BF:67:VAL:HG23	1:BF:135:LEU:HB2	1.80	0.63
1:BF:379:VAL:HG11	1:BF:381:MET:HE1	1.79	0.63
1:BI:272:TYR:CE2	1:BO:55:ARG:CD	2.81	0.63
1:BR:36:GLN:NE2	1:BR:156:LEU:H	1.97	0.63
1:CK:250:TRP:CZ3	1:CK:272:TYR:HE1	2.13	0.63
1:AB:261:ASP:OD1	1:AB:263:ASN:N	2.31	0.63
1:AC:170:PHE:HD1	1:AC:389:MET:HE1	1.63	0.63
1:AD:189:PHE:CE1	1:AD:198:ARG:HG3	2.34	0.63
1:AE:272:TYR:CE2	1:AM:55:ARG:HD3	2.34	0.63
1:AF:79:ARG:HH11	1:AF:79:ARG:CG	2.10	0.63
1:AG:272:TYR:CE2	1:BG:55:ARG:CD	2.81	0.63
1:AH:74:ASN:HB3	1:AH:126:GLU:HG2	1.79	0.63
1:BC:74:ASN:ND2	1:BC:77:THR:OG1	2.32	0.63
1:BO:284:ARG:HG2	1:BO:284:ARG:NH1	2.12	0.63
1:CN:189:PHE:HE2	1:CN:249:LEU:CD2	2.12	0.63
1:AG:263:ASN:ND2	1:BG:32:PHE:CD1	2.67	0.62
1:AN:36:GLN:NE2	1:AN:156:LEU:H	1.96	0.62
1:AP:36:GLN:NE2	1:AP:156:LEU:H	1.97	0.62
1:AR:74:ASN:HB3	1:AR:126:GLU:HG2	1.81	0.62
1:BA:189:PHE:HE1	1:BA:198:ARG:CG	2.11	0.62
1:BI:272:TYR:CE2	1:BO:55:ARG:HD3	2.34	0.62
1:BN:189:PHE:CE1	1:BN:198:ARG:CG	2.79	0.62
1:CD:272:TYR:HE2	1:CS:55:ARG:NE	1.91	0.62
1:CE:36:GLN:NE2	1:CE:156:LEU:H	1.97	0.62
1:CT:189:PHE:CE1	1:CT:198:ARG:HG3	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:274:GLU:OE1	1:AG:274:GLU:N	2.30	0.62
1:AM:454:ASN:ND2	1:AM:456:ALA:H	1.96	0.62
1:AR:201:GLY:HA3	1:AR:300:GLN:HG2	1.81	0.62
1:BD:284:ARG:HH11	1:BD:284:ARG:HG2	1.64	0.62
1:BG:15:GLN:HA	1:BG:15:GLN:HE21	1.64	0.62
1:BI:74:ASN:HB3	1:BI:126:GLU:HG2	1.79	0.62
1:BI:239:ILE:HG12	1:BI:326:ILE:CD1	2.30	0.62
1:BS:284:ARG:HH11	1:BS:284:ARG:HG2	1.64	0.62
1:CN:55:ARG:NE	1:CS:272:TYR:CE2	2.67	0.62
1:AD:272:TYR:CD2	1:AS:55:ARG:HD3	2.33	0.62
1:AG:264:GLU:O	1:AG:267:LYS:HB2	1.99	0.62
1:AK:284:ARG:HH11	1:AK:284:ARG:HG2	1.64	0.62
1:BB:288:HIS:HD2	1:BB:337:ASP:OD2	1.82	0.62
1:BP:14:CYS:H	1:BP:138:ASN:HD21	1.47	0.62
1:CC:36:GLN:NE2	1:CC:156:LEU:H	1.98	0.62
1:CG:189:PHE:HE2	1:CG:249:LEU:CD2	2.12	0.62
1:AO:284:ARG:HG2	1:AO:284:ARG:NH1	2.15	0.62
1:BN:55:ARG:CD	1:BS:272:TYR:HE2	2.11	0.62
1:CM:189:PHE:CE1	1:CM:198:ARG:CG	2.79	0.62
1:AI:272:TYR:CD2	1:AO:55:ARG:NE	2.67	0.62
1:AL:250:TRP:CZ3	1:AL:272:TYR:HE1	2.14	0.62
1:CO:272:TYR:CD2	1:CR:55:ARG:HD3	2.34	0.62
1:CP:74:ASN:CB	1:CP:126:GLU:HG2	2.30	0.62
1:CT:36:GLN:NE2	1:CT:156:LEU:H	1.97	0.62
1:AB:250:TRP:HE1	1:AB:265:LEU:CD1	2.00	0.62
1:AF:36:GLN:NE2	1:AF:156:LEU:H	1.97	0.62
1:AK:74:ASN:CB	1:AK:126:GLU:HG2	2.29	0.62
1:AR:189:PHE:CE1	1:AR:198:ARG:CG	2.79	0.62
1:BG:272:TYR:CE2	1:CG:55:ARG:CD	2.83	0.62
1:BI:189:PHE:HE2	1:BI:249:LEU:CD2	2.12	0.62
1:BI:272:TYR:CE2	1:BO:55:ARG:NE	2.68	0.62
1:BN:189:PHE:CE1	1:BN:198:ARG:HG3	2.34	0.62
1:BO:36:GLN:NE2	1:BO:156:LEU:H	1.96	0.62
1:BQ:250:TRP:CZ3	1:BQ:272:TYR:HE1	2.16	0.62
1:CD:14:CYS:H	1:CD:138:ASN:HD21	1.46	0.62
1:CR:284:ARG:CG	1:CR:284:ARG:HH11	2.12	0.62
1:AD:55:ARG:HD3	1:AN:272:TYR:CE2	2.35	0.62
1:AD:284:ARG:HG2	1:AD:284:ARG:NH1	2.14	0.62
1:AL:189:PHE:CE1	1:AL:198:ARG:HG3	2.33	0.62
1:BB:284:ARG:HG2	1:BB:284:ARG:NH1	2.14	0.62
1:BC:272:TYR:CE2	1:CA:55:ARG:NE	2.68	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:55:ARG:CD	1:CL:272:TYR:CE2	2.82	0.62
1:BN:250:TRP:CZ3	1:BN:272:TYR:HE1	2.15	0.62
1:CD:189:PHE:HE1	1:CD:198:ARG:HG3	1.64	0.62
1:CH:189:PHE:CE1	1:CH:198:ARG:CG	2.81	0.62
1:CL:284:ARG:HG2	1:CL:284:ARG:NH1	2.14	0.62
1:AB:263:ASN:HD22	1:CB:32:PHE:HA	1.64	0.62
1:AL:272:TYR:CD2	1:CJ:55:ARG:CD	2.80	0.62
1:AL:272:TYR:HD2	1:CJ:55:ARG:HD3	1.62	0.62
1:BF:14:CYS:H	1:BF:138:ASN:HD21	1.47	0.62
1:BF:365:ILE:HD12	1:BF:471:MET:HE2	1.81	0.62
1:CA:74:ASN:HB3	1:CA:126:GLU:HG2	1.81	0.62
1:CB:74:ASN:CB	1:CB:126:GLU:HG2	2.30	0.62
1:CE:191:LEU:H	1:CE:191:LEU:CD2	2.09	0.62
1:AF:272:TYR:CE2	1:BK:55:ARG:HD3	2.35	0.62
1:AQ:79:ARG:HG3	1:AQ:79:ARG:HH11	1.64	0.62
1:BF:284:ARG:HG2	1:BF:284:ARG:NH1	2.13	0.62
1:BO:14:CYS:H	1:BO:138:ASN:HD21	1.48	0.62
1:CF:379:VAL:HG11	1:CF:381:MET:HE1	1.81	0.62
1:CS:379:VAL:HG11	1:CS:381:MET:HE1	1.81	0.62
1:AB:272:TYR:CE2	1:CB:55:ARG:NE	2.67	0.62
1:AQ:284:ARG:CG	1:AQ:284:ARG:HH11	2.11	0.62
1:BD:250:TRP:CE3	1:BD:272:TYR:CE1	2.88	0.62
1:BJ:272:TYR:CD2	1:BQ:55:ARG:CZ	2.82	0.62
1:CJ:36:GLN:NE2	1:CJ:156:LEU:H	1.98	0.62
1:CQ:36:GLN:NE2	1:CQ:156:LEU:H	1.98	0.62
1:AB:55:ARG:HD3	1:BB:272:TYR:CE2	2.36	0.61
1:AG:189:PHE:HE2	1:AG:249:LEU:CD2	2.12	0.61
1:AJ:284:ARG:HH11	1:AJ:284:ARG:HG2	1.65	0.61
1:AL:16:ALA:O	1:AL:17:ASN:HB2	1.98	0.61
1:AM:272:TYR:HE2	1:CP:55:ARG:CD	2.12	0.61
1:AN:55:ARG:HD3	1:AS:272:TYR:CD2	2.34	0.61
1:AO:298:GLN:NE2	1:AO:303:MET:HE1	2.14	0.61
1:BB:189:PHE:HE2	1:BB:249:LEU:CD2	2.13	0.61
1:BC:74:ASN:CB	1:BC:126:GLU:HG2	2.30	0.61
1:BE:272:TYR:CE2	1:BM:55:ARG:CD	2.83	0.61
1:BQ:272:TYR:CE2	1:CL:55:ARG:HD3	2.35	0.61
1:CC:379:VAL:HG11	1:CC:381:MET:HE1	1.82	0.61
1:CH:74:ASN:CB	1:CH:126:GLU:HG2	2.30	0.61
1:CP:170:PHE:HD1	1:CP:389:MET:HE1	1.64	0.61
1:AE:189:PHE:CE1	1:AE:198:ARG:CG	2.83	0.61
1:AH:67:VAL:HG23	1:AH:135:LEU:HB2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:189:PHE:HE2	1:AM:249:LEU:CD2	2.13	0.61
1:AT:250:TRP:CE3	1:AT:272:TYR:CE1	2.88	0.61
1:CB:189:PHE:CE1	1:CB:198:ARG:CG	2.79	0.61
1:CG:379:VAL:HG11	1:CG:381:MET:HE1	1.82	0.61
1:CI:284:ARG:HG2	1:CI:284:ARG:NH1	2.15	0.61
1:CJ:272:TYR:CD2	1:CQ:55:ARG:CZ	2.83	0.61
1:CM:79:ARG:HH11	1:CM:79:ARG:HG3	1.64	0.61
1:CN:55:ARG:HD3	1:CS:272:TYR:CE2	2.35	0.61
1:AB:58:ALA:HB2	1:AB:102:GLY:HA3	1.83	0.61
1:AB:265:LEU:HD12	1:AB:266:PHE:N	2.12	0.61
1:BI:189:PHE:CE1	1:BI:198:ARG:CG	2.83	0.61
1:BQ:189:PHE:HE1	1:BQ:198:ARG:CG	2.13	0.61
1:BR:22:THR:OG1	1:BR:131:HIS:HD2	1.82	0.61
1:CD:454:ASN:HD22	1:CD:456:ALA:N	1.98	0.61
1:CH:55:ARG:CD	1:CK:272:TYR:CE2	2.84	0.61
1:AL:55:ARG:HD3	1:CQ:272:TYR:CD2	2.35	0.61
1:BD:189:PHE:CE1	1:BD:198:ARG:HG3	2.34	0.61
1:BG:379:VAL:HG11	1:BG:381:MET:HE1	1.82	0.61
1:BQ:74:ASN:HB3	1:BQ:126:GLU:HG2	1.81	0.61
1:CG:14:CYS:H	1:CG:138:ASN:HD21	1.48	0.61
1:CI:38:GLU:HB3	1:CQ:35:VAL:HG23	1.83	0.61
1:CK:454:ASN:HD22	1:CK:456:ALA:N	1.98	0.61
1:CO:284:ARG:HG2	1:CO:284:ARG:NH1	2.15	0.61
1:CQ:250:TRP:CE3	1:CQ:272:TYR:CE1	2.89	0.61
1:CS:284:ARG:HH11	1:CS:284:ARG:HG2	1.63	0.61
1:AF:74:ASN:CB	1:AF:126:GLU:HG2	2.30	0.61
1:AN:288:HIS:HD2	1:AN:337:ASP:OD2	1.84	0.61
1:BD:379:VAL:HG11	1:BD:381:MET:HE1	1.83	0.61
1:BQ:272:TYR:CD2	1:CL:55:ARG:HD3	2.35	0.61
1:CI:189:PHE:HE2	1:CI:249:LEU:CD2	2.12	0.61
1:CK:379:VAL:HG11	1:CK:381:MET:HE1	1.82	0.61
1:CP:284:ARG:HH11	1:CP:284:ARG:HG2	1.66	0.61
1:BD:36:GLN:NE2	1:BD:156:LEU:H	1.98	0.61
1:BJ:55:ARG:HD3	1:CL:272:TYR:CD2	2.35	0.61
1:CI:376:THR:O	1:CI:376:THR:CG2	2.48	0.61
1:CR:284:ARG:HH11	1:CR:284:ARG:HG2	1.64	0.61
1:AR:79:ARG:HH11	1:AR:79:ARG:HG3	1.64	0.61
1:AS:284:ARG:HG2	1:AS:284:ARG:NH1	2.15	0.61
1:BN:191:LEU:H	1:BN:191:LEU:CD2	2.10	0.61
1:BP:454:ASN:HD22	1:BP:456:ALA:N	1.99	0.61
1:CJ:189:PHE:CE1	1:CJ:198:ARG:CG	2.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP:36:GLN:NE2	1:CP:156:LEU:H	1.98	0.61
1:CQ:74:ASN:CB	1:CQ:126:GLU:HG2	2.30	0.61
1:AA:250:TRP:CZ3	1:AA:272:TYR:HE1	2.17	0.61
1:AF:189:PHE:CE1	1:AF:198:ARG:CG	2.82	0.61
1:AG:79:ARG:HG3	1:AG:79:ARG:NH1	2.10	0.61
1:AH:189:PHE:CE1	1:AH:198:ARG:CG	2.81	0.61
1:CD:189:PHE:CE1	1:CD:198:ARG:HG3	2.36	0.61
1:CI:14:CYS:H	1:CI:138:ASN:HD21	1.47	0.61
1:CK:284:ARG:HG2	1:CK:284:ARG:NH1	2.15	0.61
1:CN:284:ARG:HG2	1:CN:284:ARG:NH1	2.15	0.61
1:AB:250:TRP:CE3	1:AB:272:TYR:CE1	2.89	0.61
1:AC:36:GLN:NE2	1:AC:156:LEU:H	1.98	0.61
1:AI:55:ARG:CD	1:AR:272:TYR:CD2	2.83	0.61
1:AL:55:ARG:CD	1:CQ:272:TYR:CE2	2.83	0.61
1:AO:67:VAL:HG23	1:AO:135:LEU:HB2	1.83	0.61
1:AQ:250:TRP:CZ3	1:AQ:272:TYR:HE1	2.17	0.61
1:BA:288:HIS:HD2	1:BA:337:ASP:OD2	1.83	0.61
1:BE:74:ASN:CB	1:BE:126:GLU:HG2	2.30	0.61
1:BH:398:GLY:HA3	1:BH:494:PHE:CD2	2.36	0.61
1:BK:14:CYS:H	1:BK:138:ASN:HD21	1.49	0.61
1:BK:379:VAL:HG11	1:BK:381:MET:HE1	1.83	0.61
1:BN:16:ALA:O	1:BN:17:ASN:HB2	2.01	0.61
1:BR:74:ASN:CB	1:BR:126:GLU:HG2	2.31	0.61
1:BS:250:TRP:CZ3	1:BS:272:TYR:HE1	2.19	0.61
1:CF:189:PHE:CE1	1:CF:198:ARG:CG	2.79	0.61
1:CJ:74:ASN:CB	1:CJ:126:GLU:HG2	2.31	0.61
1:CP:379:VAL:HG11	1:CP:381:MET:HE1	1.83	0.61
1:CR:77:THR:O	1:CR:80:ILE:HG12	1.99	0.61
1:AE:55:ARG:CZ	1:CP:272:TYR:CD2	2.84	0.61
1:AE:284:ARG:HH11	1:AE:284:ARG:HG2	1.66	0.61
1:AG:261:ASP:O	1:AG:264:GLU:HB3	2.01	0.61
1:AI:189:PHE:HE2	1:AI:249:LEU:CD2	2.14	0.61
1:AJ:203:THR:HB	1:AJ:300:GLN:HG3	1.82	0.61
1:AN:189:PHE:CE1	1:AN:198:ARG:CG	2.79	0.61
1:AR:284:ARG:HG2	1:AR:284:ARG:NH1	2.16	0.61
1:BA:36:GLN:NE2	1:BA:156:LEU:H	1.99	0.61
1:BE:379:VAL:HG11	1:BE:381:MET:HE1	1.82	0.61
1:BG:189:PHE:HE2	1:BG:249:LEU:CD2	2.14	0.61
1:BI:272:TYR:HE2	1:BO:55:ARG:CD	2.12	0.61
1:BO:74:ASN:CB	1:BO:126:GLU:HG2	2.31	0.61
1:CH:284:ARG:HG2	1:CH:284:ARG:NH1	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:74:ASN:CB	1:CM:126:GLU:HG2	2.31	0.61
1:CM:284:ARG:HG2	1:CM:284:ARG:NH1	2.15	0.61
1:CS:191:LEU:H	1:CS:191:LEU:CD2	2.10	0.61
1:AE:379:VAL:HG11	1:AE:381:MET:HE1	1.82	0.60
1:BA:284:ARG:HG2	1:BA:284:ARG:NH1	2.15	0.60
1:BI:55:ARG:NE	1:BR:272:TYR:HE2	1.89	0.60
1:CE:189:PHE:HE2	1:CE:249:LEU:CD2	2.13	0.60
1:CF:74:ASN:CB	1:CF:126:GLU:HG2	2.31	0.60
1:AA:189:PHE:CE1	1:AA:198:ARG:HG3	2.33	0.60
1:AC:284:ARG:HG2	1:AC:284:ARG:NH1	2.13	0.60
1:AD:74:ASN:CB	1:AD:126:GLU:HG2	2.31	0.60
1:AF:454:ASN:HD22	1:AF:456:ALA:N	1.99	0.60
1:BG:170:PHE:HD1	1:BG:389:MET:HE1	1.65	0.60
1:BS:379:VAL:HG11	1:BS:381:MET:HE1	1.83	0.60
1:CA:189:PHE:CE1	1:CA:198:ARG:HG3	2.34	0.60
1:CO:379:VAL:HG11	1:CO:381:MET:HE1	1.83	0.60
1:CR:76:ILE:O	1:CR:80:ILE:HG12	2.02	0.60
1:AA:55:ARG:CD	1:CC:272:TYR:CE2	2.85	0.60
1:AB:256:ASN:ND2	1:AB:256:ASN:C	2.54	0.60
1:AH:55:ARG:CZ	1:AK:272:TYR:CE2	2.84	0.60
1:AO:294:LEU:HD11	1:AO:299:SER:HA	1.84	0.60
1:AT:379:VAL:CG1	1:AT:381:MET:HE1	2.31	0.60
1:BE:250:TRP:CZ3	1:BE:272:TYR:HE1	2.18	0.60
1:CH:379:VAL:HG11	1:CH:381:MET:HE1	1.82	0.60
1:BL:250:TRP:CZ3	1:BL:272:TYR:HE1	2.20	0.60
1:BO:16:ALA:O	1:BO:17:ASN:HB2	2.00	0.60
1:CI:272:TYR:CE2	1:CO:55:ARG:CD	2.84	0.60
1:AA:189:PHE:HE1	1:AA:198:ARG:CG	2.13	0.60
1:AE:74:ASN:CB	1:AE:126:GLU:HG2	2.31	0.60
1:AP:189:PHE:HE1	1:AP:198:ARG:HG3	1.67	0.60
1:AT:74:ASN:CB	1:AT:126:GLU:HG2	2.31	0.60
1:BF:454:ASN:HD22	1:BF:456:ALA:N	2.00	0.60
1:BH:55:ARG:CD	1:BK:272:TYR:CE2	2.85	0.60
1:BQ:74:ASN:ND2	1:BQ:77:THR:OG1	2.34	0.60
1:BT:36:GLN:NE2	1:BT:156:LEU:H	1.99	0.60
1:CB:284:ARG:HG2	1:CB:284:ARG:NH1	2.16	0.60
1:CN:55:ARG:CD	1:CS:272:TYR:HE2	2.13	0.60
1:CN:55:ARG:HD3	1:CS:272:TYR:CD2	2.36	0.60
1:CQ:189:PHE:CE1	1:CQ:198:ARG:HG3	2.37	0.60
1:AA:454:ASN:HD22	1:AA:456:ALA:N	1.99	0.60
1:AE:203:THR:HB	1:AE:300:GLN:HG3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:74:ASN:ND2	1:AH:77:THR:OG1	2.34	0.60
1:AJ:365:ILE:HD12	1:AJ:471:MET:HE2	1.84	0.60
1:AQ:74:ASN:CB	1:AQ:126:GLU:HG2	2.31	0.60
1:AS:191:LEU:H	1:AS:191:LEU:CD2	2.12	0.60
1:BF:189:PHE:CE1	1:BF:198:ARG:HG3	2.35	0.60
1:BM:250:TRP:CZ3	1:BM:272:TYR:HE1	2.17	0.60
1:BP:379:VAL:HG11	1:BP:381:MET:HE1	1.84	0.60
1:BR:284:ARG:HG2	1:BR:284:ARG:NH1	2.16	0.60
1:AB:189:PHE:HE2	1:AB:249:LEU:CD2	2.14	0.60
1:AB:284:ARG:HG2	1:AB:284:ARG:NH1	2.13	0.60
1:AE:55:ARG:HD3	1:CP:272:TYR:CE2	2.36	0.60
1:AG:74:ASN:CB	1:AG:126:GLU:HG2	2.32	0.60
1:BJ:79:ARG:HG3	1:BJ:79:ARG:NH1	2.13	0.60
1:CE:272:TYR:CE2	1:CM:55:ARG:HD3	2.36	0.60
1:CE:284:ARG:HH11	1:CE:284:ARG:HG2	1.66	0.60
1:CJ:191:LEU:H	1:CJ:191:LEU:CD2	2.10	0.60
1:CR:86:PRO:HG2	1:CR:87:VAL:N	2.17	0.60
1:CR:189:PHE:HE2	1:CR:249:LEU:CD2	2.15	0.60
1:AE:189:PHE:HE2	1:AE:249:LEU:CD2	2.14	0.60
1:AH:189:PHE:HE2	1:AH:249:LEU:CD2	2.15	0.60
1:AH:398:GLY:HA3	1:AH:494:PHE:CD2	2.37	0.60
1:AI:272:TYR:CE2	1:AO:55:ARG:CZ	2.84	0.60
1:AJ:189:PHE:HE2	1:AJ:249:LEU:CD2	2.15	0.60
1:AO:289:ARG:HH12	1:AO:337:ASP:C	2.10	0.60
1:BD:272:TYR:CE2	1:BS:55:ARG:HD3	2.36	0.60
1:BG:284:ARG:HG2	1:BG:284:ARG:NH1	2.15	0.60
1:BL:189:PHE:HE1	1:BL:198:ARG:CG	2.14	0.60
1:CA:284:ARG:HG2	1:CA:284:ARG:NH1	2.15	0.60
1:CH:365:ILE:HD12	1:CH:471:MET:HE2	1.84	0.60
1:CM:379:VAL:HG11	1:CM:381:MET:HE1	1.83	0.60
1:CN:379:VAL:HG11	1:CN:381:MET:HE1	1.83	0.60
1:CR:14:CYS:H	1:CR:138:ASN:HD21	1.50	0.60
1:AB:379:VAL:HG11	1:AB:381:MET:HE1	1.83	0.60
1:AQ:379:VAL:HG11	1:AQ:381:MET:HE1	1.82	0.60
1:AT:55:ARG:HD3	1:BA:272:TYR:CE2	2.37	0.60
1:BQ:67:VAL:HG23	1:BQ:135:LEU:HB2	1.84	0.60
1:CE:74:ASN:ND2	1:CE:77:THR:OG1	2.35	0.60
1:AA:365:ILE:HD12	1:AA:471:MET:HE2	1.84	0.60
1:AC:454:ASN:HD22	1:AC:456:ALA:N	2.00	0.60
1:AJ:272:TYR:HE2	1:AQ:55:ARG:NE	2.00	0.60
1:BF:272:TYR:CE2	1:CK:55:ARG:HD3	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:15:GLN:HA	1:BH:15:GLN:NE2	2.15	0.60
1:BO:272:TYR:CE2	1:BR:55:ARG:CZ	2.85	0.60
1:CD:74:ASN:CB	1:CD:126:GLU:HG2	2.32	0.60
1:CE:74:ASN:CB	1:CE:126:GLU:HG2	2.32	0.60
1:CL:74:ASN:CB	1:CL:126:GLU:HG2	2.32	0.60
1:AB:55:ARG:CD	1:BB:272:TYR:CE2	2.85	0.59
1:AE:55:ARG:CZ	1:CP:272:TYR:CE2	2.85	0.59
1:AH:284:ARG:HG2	1:AH:284:ARG:NH1	2.17	0.59
1:AN:379:VAL:HG11	1:AN:381:MET:HE1	1.84	0.59
1:AP:284:ARG:HG2	1:AP:284:ARG:NH1	2.17	0.59
1:BA:189:PHE:HE2	1:BA:249:LEU:HD21	1.67	0.59
1:BC:284:ARG:HG2	1:BC:284:ARG:NH1	2.16	0.59
1:BJ:189:PHE:HE2	1:BJ:249:LEU:CD2	2.14	0.59
1:BM:239:ILE:HG12	1:BM:326:ILE:CD1	2.32	0.59
1:BM:250:TRP:HZ3	1:BM:272:TYR:CE1	2.20	0.59
1:BO:398:GLY:HA3	1:BO:494:PHE:CD2	2.37	0.59
1:BP:55:ARG:CD	1:CM:272:TYR:HE2	2.15	0.59
1:BR:16:ALA:O	1:BR:17:ASN:HB2	2.02	0.59
1:CI:144:ALA:HB3	1:CR:191:LEU:O	2.02	0.59
1:CM:454:ASN:HD22	1:CM:456:ALA:N	1.99	0.59
1:CR:189:PHE:CE1	1:CR:198:ARG:CG	2.78	0.59
1:CS:14:CYS:H	1:CS:138:ASN:HD21	1.49	0.59
1:AT:250:TRP:HZ3	1:AT:272:TYR:CE1	2.20	0.59
1:BT:55:ARG:CZ	1:CA:272:TYR:CE2	2.85	0.59
1:BT:250:TRP:CE3	1:BT:272:TYR:CE1	2.90	0.59
1:BT:379:VAL:HG11	1:BT:381:MET:HE1	1.84	0.59
1:CT:74:ASN:CB	1:CT:126:GLU:HG2	2.31	0.59
1:AG:79:ARG:HH11	1:AG:79:ARG:CG	2.13	0.59
1:AG:250:TRP:CZ3	1:AG:272:TYR:CE1	2.89	0.59
1:AS:74:ASN:CB	1:AS:126:GLU:HG2	2.31	0.59
1:BN:55:ARG:HD3	1:BS:272:TYR:CE2	2.37	0.59
1:BO:379:VAL:HG11	1:BO:381:MET:HE1	1.83	0.59
1:BR:189:PHE:CE1	1:BR:198:ARG:CG	2.84	0.59
1:AH:14:CYS:H	1:AH:138:ASN:HD21	1.50	0.59
1:AJ:74:ASN:CB	1:AJ:126:GLU:HG2	2.32	0.59
1:BF:189:PHE:CE1	1:BF:198:ARG:CG	2.81	0.59
1:BH:189:PHE:HE2	1:BH:249:LEU:CD2	2.16	0.59
1:CG:36:GLN:NE2	1:CG:156:LEU:H	1.99	0.59
1:AA:284:ARG:HG2	1:AA:284:ARG:NH1	2.15	0.59
1:AG:379:VAL:HG11	1:AG:381:MET:HE1	1.84	0.59
1:AI:189:PHE:CE1	1:AI:198:ARG:CG	2.79	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:454:ASN:HD22	1:AM:456:ALA:N	1.97	0.59
1:BD:272:TYR:CD2	1:BS:55:ARG:HD3	2.38	0.59
1:BG:272:TYR:CE2	1:CG:55:ARG:CZ	2.86	0.59
1:BH:74:ASN:CB	1:BH:126:GLU:HG2	2.31	0.59
1:CF:250:TRP:CE3	1:CF:272:TYR:CE1	2.91	0.59
1:CO:74:ASN:CB	1:CO:126:GLU:HG2	2.31	0.59
1:CS:74:ASN:CB	1:CS:126:GLU:HG2	2.32	0.59
1:AO:162:PHE:CD2	1:AO:163:LEU:HD13	2.38	0.59
1:AR:250:TRP:CE3	1:AR:272:TYR:CE1	2.91	0.59
1:AG:258:THR:O	1:AG:259:THR:C	2.40	0.59
1:AM:170:PHE:HD1	1:AM:389:MET:HE1	1.68	0.59
1:AS:365:ILE:HD12	1:AS:471:MET:HE2	1.84	0.59
1:BC:379:VAL:HG11	1:BC:381:MET:HE1	1.85	0.59
1:BI:284:ARG:HG2	1:BI:284:ARG:NH1	2.15	0.59
1:BK:189:PHE:HE1	1:BK:198:ARG:CG	2.15	0.59
1:BN:189:PHE:HE2	1:BN:249:LEU:CD2	2.16	0.59
1:CD:379:VAL:HG11	1:CD:381:MET:HE1	1.85	0.59
1:CJ:284:ARG:HH11	1:CJ:284:ARG:HG2	1.66	0.59
1:CP:79:ARG:HH11	1:CP:79:ARG:CG	2.16	0.59
1:CS:36:GLN:NE2	1:CS:156:LEU:H	2.01	0.59
1:AN:454:ASN:HD22	1:AN:456:ALA:N	2.00	0.59
1:AP:272:TYR:HD2	1:BE:55:ARG:HD3	1.64	0.59
1:AP:365:ILE:HD12	1:AP:471:MET:HE2	1.84	0.59
1:AP:379:VAL:HG11	1:AP:381:MET:HE1	1.84	0.59
1:BA:189:PHE:HE2	1:BA:249:LEU:CD2	2.16	0.59
1:BK:74:ASN:CB	1:BK:126:GLU:HG2	2.32	0.59
1:AG:189:PHE:CE1	1:AG:198:ARG:CG	2.81	0.59
1:AK:379:VAL:HG11	1:AK:381:MET:HE1	1.85	0.59
1:BF:74:ASN:CB	1:BF:126:GLU:HG2	2.33	0.59
1:BI:74:ASN:CB	1:BI:126:GLU:HG2	2.32	0.59
1:BS:189:PHE:HE1	1:BS:198:ARG:CG	2.15	0.59
1:CF:189:PHE:HE2	1:CF:249:LEU:CD2	2.15	0.59
1:CG:454:ASN:HD22	1:CG:456:ALA:N	2.01	0.59
1:CK:74:ASN:CB	1:CK:126:GLU:HG2	2.33	0.59
1:AA:74:ASN:ND2	1:AA:77:THR:OG1	2.36	0.59
1:AC:250:TRP:CE3	1:AC:272:TYR:CE1	2.91	0.59
1:AG:14:CYS:H	1:AG:138:ASN:HD21	1.49	0.59
1:AI:74:ASN:CB	1:AI:126:GLU:HG2	2.33	0.59
1:BA:454:ASN:HD22	1:BA:456:ALA:N	2.01	0.59
1:BK:288:HIS:HD2	1:BK:337:ASP:OD2	1.86	0.59
1:BT:189:PHE:CE1	1:BT:198:ARG:HG3	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:79:ARG:HG3	1:CH:79:ARG:NH1	2.17	0.59
1:CJ:379:VAL:HG11	1:CJ:381:MET:HE1	1.84	0.59
1:AB:16:ALA:O	1:AB:17:ASN:HB2	2.02	0.58
1:AC:74:ASN:CB	1:AC:126:GLU:HG2	2.32	0.58
1:AD:189:PHE:HE1	1:AD:198:ARG:CG	2.15	0.58
1:AG:264:GLU:O	1:AG:267:LYS:N	2.30	0.58
1:AI:272:TYR:CE2	1:AO:55:ARG:HD3	2.36	0.58
1:AK:55:ARG:HD3	1:CF:272:TYR:CE2	2.37	0.58
1:AP:79:ARG:HH11	1:AP:79:ARG:HG3	1.66	0.58
1:BP:189:PHE:HE1	1:BP:198:ARG:CG	2.16	0.58
1:CB:379:VAL:HG11	1:CB:381:MET:HE1	1.85	0.58
1:CC:74:ASN:CB	1:CC:126:GLU:HG2	2.32	0.58
1:CI:55:ARG:NE	1:CR:272:TYR:CE2	2.71	0.58
1:CJ:272:TYR:CE2	1:CQ:55:ARG:HD3	2.38	0.58
1:CJ:454:ASN:HD22	1:CJ:456:ALA:N	2.00	0.58
1:AE:454:ASN:HD22	1:AE:456:ALA:N	2.01	0.58
1:AP:58:ALA:HB2	1:AP:102:GLY:HA3	1.84	0.58
1:AQ:284:ARG:HH11	1:AQ:284:ARG:HG2	1.68	0.58
1:AT:189:PHE:HE1	1:AT:198:ARG:CG	2.16	0.58
1:BE:284:ARG:HG2	1:BE:284:ARG:NH1	2.17	0.58
1:BH:189:PHE:CE1	1:BH:198:ARG:CG	2.80	0.58
1:BL:365:ILE:HD12	1:BL:471:MET:HE2	1.85	0.58
1:BP:284:ARG:HG2	1:BP:284:ARG:NH1	2.17	0.58
1:BS:454:ASN:HD22	1:BS:456:ALA:N	2.01	0.58
1:CA:43:ALA:HB1	1:CA:158:GLU:HA	1.86	0.58
1:CN:250:TRP:CE3	1:CN:272:TYR:CE1	2.91	0.58
1:CS:288:HIS:HD2	1:CS:337:ASP:OD2	1.86	0.58
1:AG:38:GLU:HB2	1:CF:35:VAL:HG22	1.84	0.58
1:AG:272:TYR:N	1:AG:272:TYR:HD1	2.00	0.58
1:AT:74:ASN:ND2	1:AT:77:THR:OG1	2.35	0.58
1:BA:189:PHE:CE1	1:BA:198:ARG:CG	2.86	0.58
1:BJ:379:VAL:HG11	1:BJ:381:MET:HE1	1.84	0.58
1:BR:379:VAL:HG11	1:BR:381:MET:HE1	1.85	0.58
1:CE:379:VAL:HG11	1:CE:381:MET:HE1	1.85	0.58
1:CO:272:TYR:CD2	1:CR:55:ARG:CZ	2.87	0.58
1:AD:272:TYR:CE2	1:AS:55:ARG:HD3	2.38	0.58
1:AF:203:THR:HB	1:AF:300:GLN:HG3	1.85	0.58
1:AJ:379:VAL:HG11	1:AJ:381:MET:HE1	1.85	0.58
1:AM:379:VAL:HG11	1:AM:381:MET:HE1	1.84	0.58
1:BC:14:CYS:H	1:BC:138:ASN:HD21	1.51	0.58
1:BC:454:ASN:HD22	1:BC:456:ALA:N	2.00	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:454:ASN:HD22	1:BT:456:ALA:N	2.01	0.58
1:AB:262:TRP:N	1:AB:262:TRP:CD1	2.70	0.58
1:AC:189:PHE:CE1	1:AC:198:ARG:HG3	2.39	0.58
1:AF:379:VAL:HG11	1:AF:381:MET:HE1	1.84	0.58
1:AO:239:ILE:HG12	1:AO:326:ILE:CD1	2.33	0.58
1:BD:14:CYS:H	1:BD:138:ASN:HD21	1.51	0.58
1:CB:189:PHE:HE2	1:CB:249:LEU:CD2	2.17	0.58
1:CG:284:ARG:HG2	1:CG:284:ARG:NH1	2.17	0.58
1:CN:74:ASN:CB	1:CN:126:GLU:HG2	2.32	0.58
1:AB:288:HIS:HD2	1:AB:337:ASP:OD2	1.86	0.58
1:AI:284:ARG:HG2	1:AI:284:ARG:NH1	2.15	0.58
1:AO:454:ASN:HD22	1:AO:456:ALA:N	2.00	0.58
1:BG:74:ASN:CB	1:BG:126:GLU:HG2	2.31	0.58
1:BP:55:ARG:CD	1:CM:272:TYR:CE2	2.87	0.58
1:BQ:43:ALA:HB1	1:BQ:158:GLU:HA	1.86	0.58
1:BR:365:ILE:HD12	1:BR:471:MET:HE2	1.85	0.58
1:CI:365:ILE:HD12	1:CI:471:MET:HE2	1.85	0.58
1:CQ:250:TRP:HZ3	1:CQ:272:TYR:CE1	2.19	0.58
1:AA:67:VAL:HG23	1:AA:135:LEU:HB2	1.85	0.58
1:AL:55:ARG:CD	1:CQ:272:TYR:HE2	2.17	0.58
1:AL:454:ASN:HD22	1:AL:456:ALA:N	2.01	0.58
1:BB:74:ASN:CB	1:BB:126:GLU:HG2	2.34	0.58
1:BD:284:ARG:HG2	1:BD:284:ARG:NH1	2.18	0.58
1:BG:11:PRO:HG2	1:BG:18:ARG:HD2	1.85	0.58
1:BJ:79:ARG:HH11	1:BJ:79:ARG:CG	2.10	0.58
1:BN:74:ASN:CB	1:BN:126:GLU:HG2	2.34	0.58
1:BP:272:TYR:CD2	1:CE:55:ARG:CZ	2.87	0.58
1:BR:454:ASN:HD22	1:BR:456:ALA:N	2.01	0.58
1:CC:365:ILE:HD12	1:CC:471:MET:HE2	1.86	0.58
1:CJ:263:ASN:HD22	1:CQ:5:ARG:HD3	1.68	0.58
1:AB:264:GLU:O	1:AB:265:LEU:C	2.45	0.58
1:AJ:14:CYS:H	1:AJ:138:ASN:HD21	1.51	0.58
1:AL:74:ASN:CB	1:AL:126:GLU:HG2	2.32	0.58
1:AN:284:ARG:HG2	1:AN:284:ARG:NH1	2.18	0.58
1:AQ:189:PHE:HE2	1:AQ:249:LEU:CD2	2.17	0.58
1:BM:36:GLN:NE2	1:BM:156:LEU:H	2.02	0.58
1:BM:284:ARG:HG2	1:BM:284:ARG:NH1	2.15	0.58
1:CE:365:ILE:HD12	1:CE:471:MET:HE2	1.84	0.58
1:CO:365:ILE:HD12	1:CO:471:MET:HE2	1.86	0.58
1:CR:379:VAL:HG11	1:CR:381:MET:HE1	1.84	0.58
1:CT:365:ILE:HD12	1:CT:471:MET:HE2	1.83	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:239:ILE:HG12	1:AN:326:ILE:CD1	2.34	0.58
1:BF:189:PHE:HE2	1:BF:249:LEU:CD2	2.17	0.58
1:BH:55:ARG:CD	1:BK:272:TYR:HE2	2.17	0.58
1:BJ:74:ASN:CB	1:BJ:126:GLU:HG2	2.33	0.58
1:BN:67:VAL:HG23	1:BN:135:LEU:HB2	1.86	0.58
1:BS:284:ARG:HG2	1:BS:284:ARG:NH1	2.19	0.58
1:BT:284:ARG:HG2	1:BT:284:ARG:NH1	2.18	0.58
1:CB:454:ASN:HD22	1:CB:456:ALA:N	2.01	0.58
1:CH:43:ALA:HB1	1:CH:158:GLU:HA	1.86	0.58
1:CL:9:TYR:HE1	1:CL:147:GLN:HE21	1.50	0.58
1:CO:239:ILE:HG12	1:CO:326:ILE:CD1	2.34	0.58
1:AA:398:GLY:HA3	1:AA:494:PHE:CD2	2.38	0.58
1:AD:189:PHE:HE2	1:AD:249:LEU:CD2	2.17	0.58
1:AJ:272:TYR:CE2	1:AQ:55:ARG:HD3	2.39	0.58
1:AP:74:ASN:CB	1:AP:126:GLU:HG2	2.34	0.58
1:BN:55:ARG:HD3	1:BS:272:TYR:CD2	2.39	0.58
1:BP:454:ASN:ND2	1:BP:456:ALA:H	2.00	0.58
1:CM:250:TRP:CE3	1:CM:272:TYR:CE1	2.91	0.58
1:CR:36:GLN:NE2	1:CR:156:LEU:H	2.02	0.58
1:AG:250:TRP:CE3	1:AG:272:TYR:HE1	2.22	0.57
1:AH:379:VAL:HG11	1:AH:381:MET:HE1	1.84	0.57
1:AI:365:ILE:HD12	1:AI:471:MET:HE2	1.86	0.57
1:AN:55:ARG:HD3	1:AS:272:TYR:CE2	2.38	0.57
1:AO:289:ARG:NH1	1:AO:338:LEU:C	2.62	0.57
1:AP:74:ASN:ND2	1:AP:77:THR:OG1	2.37	0.57
1:AQ:272:TYR:CE2	1:BL:55:ARG:CD	2.87	0.57
1:AR:379:VAL:CG1	1:AR:381:MET:HE1	2.34	0.57
1:BA:379:VAL:HG11	1:BA:381:MET:HE1	1.85	0.57
1:BC:239:ILE:HG12	1:BC:326:ILE:CD1	2.33	0.57
1:BH:79:ARG:HG3	1:BH:79:ARG:HH11	1.67	0.57
1:BL:284:ARG:HG2	1:BL:284:ARG:NH1	2.19	0.57
1:BN:365:ILE:HD12	1:BN:471:MET:HE2	1.85	0.57
1:CF:284:ARG:HG2	1:CF:284:ARG:NH1	2.19	0.57
1:CQ:284:ARG:HG2	1:CQ:284:ARG:NH1	2.17	0.57
1:CS:454:ASN:ND2	1:CS:456:ALA:H	1.98	0.57
1:AA:189:PHE:CE1	1:AA:198:ARG:CG	2.87	0.57
1:AK:284:ARG:HG2	1:AK:284:ARG:NH1	2.17	0.57
1:AP:189:PHE:CE1	1:AP:198:ARG:HG3	2.38	0.57
1:AR:74:ASN:CB	1:AR:126:GLU:HG2	2.34	0.57
1:BF:379:VAL:CG1	1:BF:381:MET:HE1	2.34	0.57
1:BN:284:ARG:HG2	1:BN:284:ARG:NH1	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:18:ARG:HG3	1:CF:19:TYR:N	2.19	0.57
1:CT:454:ASN:HD22	1:CT:456:ALA:N	2.01	0.57
1:AT:189:PHE:CE1	1:AT:198:ARG:CG	2.87	0.57
1:BE:272:TYR:CE2	1:BM:55:ARG:HD3	2.39	0.57
1:BF:55:ARG:CD	1:CH:272:TYR:HE2	2.16	0.57
1:BJ:284:ARG:HG2	1:BJ:284:ARG:NH1	2.18	0.57
1:BN:189:PHE:HE1	1:BN:198:ARG:HG2	1.68	0.57
1:CI:454:ASN:HD22	1:CI:456:ALA:N	2.02	0.57
1:AA:74:ASN:CB	1:AA:126:GLU:HG2	2.34	0.57
1:AB:189:PHE:CE1	1:AB:198:ARG:CG	2.81	0.57
1:AF:284:ARG:HG2	1:AF:284:ARG:NH1	2.17	0.57
1:AH:11:PRO:HG2	1:AH:18:ARG:HD2	1.87	0.57
1:AL:379:VAL:HG11	1:AL:381:MET:HE1	1.85	0.57
1:AN:250:TRP:CE3	1:AN:272:TYR:CE1	2.92	0.57
1:BE:365:ILE:HD12	1:BE:471:MET:HE2	1.86	0.57
1:BH:284:ARG:HG2	1:BH:284:ARG:NH1	2.16	0.57
1:BP:189:PHE:CE1	1:BP:198:ARG:CG	2.88	0.57
1:CF:36:GLN:NE2	1:CF:156:LEU:H	2.03	0.57
1:CF:379:VAL:CG1	1:CF:381:MET:HE1	2.33	0.57
1:CG:250:TRP:CE3	1:CG:272:TYR:CE1	2.92	0.57
1:CH:288:HIS:HD2	1:CH:337:ASP:OD2	1.88	0.57
1:CQ:454:ASN:ND2	1:CQ:456:ALA:H	2.00	0.57
1:AL:284:ARG:HG2	1:AL:284:ARG:NH1	2.16	0.57
1:BQ:288:HIS:HD2	1:BQ:337:ASP:OD2	1.87	0.57
1:CQ:379:VAL:HG11	1:CQ:381:MET:HE1	1.86	0.57
1:AT:454:ASN:HD22	1:AT:456:ALA:N	2.02	0.57
1:BI:454:ASN:ND2	1:BI:456:ALA:H	2.01	0.57
1:BN:454:ASN:HD22	1:BN:456:ALA:N	2.02	0.57
1:BO:272:TYR:CE2	1:BR:55:ARG:HD3	2.40	0.57
1:BR:79:ARG:HH11	1:BR:79:ARG:CG	2.16	0.57
1:BS:14:CYS:H	1:BS:138:ASN:HD21	1.52	0.57
1:CF:454:ASN:ND2	1:CF:456:ALA:H	2.00	0.57
1:CI:79:ARG:HH11	1:CI:79:ARG:HG3	1.68	0.57
1:CL:189:PHE:CE1	1:CL:198:ARG:CG	2.88	0.57
1:CL:379:VAL:HG11	1:CL:381:MET:HE1	1.86	0.57
1:AF:14:CYS:H	1:AF:138:ASN:HD21	1.52	0.57
1:AM:272:TYR:CE2	1:CP:55:ARG:HD3	2.40	0.57
1:AN:379:VAL:CG1	1:AN:381:MET:HE1	2.35	0.57
1:AO:189:PHE:CE1	1:AO:198:ARG:HG3	2.40	0.57
1:BE:454:ASN:HD22	1:BE:456:ALA:N	2.02	0.57
1:BK:284:ARG:HG2	1:BK:284:ARG:NH1	2.15	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:189:PHE:CE1	1:BL:198:ARG:CG	2.87	0.57
1:BP:36:GLN:NE2	1:BP:156:LEU:H	2.02	0.57
1:CK:9:TYR:HE1	1:CK:147:GLN:HE21	1.53	0.57
1:CR:189:PHE:HE1	1:CR:198:ARG:HG2	1.67	0.57
1:AB:272:TYR:HE2	1:CB:55:ARG:CD	2.18	0.57
1:AH:75:ARG:NH2	1:AH:391:ALA:O	2.37	0.57
1:AM:398:GLY:HA3	1:AM:494:PHE:CD2	2.39	0.57
1:AP:454:ASN:HD22	1:AP:456:ALA:N	2.02	0.57
1:AT:288:HIS:HD2	1:AT:337:ASP:OD2	1.88	0.57
1:BB:250:TRP:CE3	1:BB:272:TYR:CE1	2.92	0.57
1:BD:398:GLY:HA3	1:BD:494:PHE:CD2	2.40	0.57
1:BG:16:ALA:O	1:BG:17:ASN:HB2	2.03	0.57
1:BH:379:VAL:HG11	1:BH:381:MET:HE1	1.86	0.57
1:BJ:272:TYR:CE2	1:BQ:55:ARG:CZ	2.88	0.57
1:CC:250:TRP:CE3	1:CC:272:TYR:CD1	2.92	0.57
1:CM:36:GLN:NE2	1:CM:156:LEU:H	2.02	0.57
1:CT:250:TRP:HZ3	1:CT:272:TYR:CE1	2.22	0.57
1:AC:365:ILE:HD12	1:AC:471:MET:HE2	1.86	0.57
1:AH:288:HIS:HD2	1:AH:337:ASP:OD2	1.88	0.57
1:AM:272:TYR:CD2	1:CP:55:ARG:HD3	2.40	0.57
1:BB:250:TRP:HZ3	1:BB:272:TYR:CE1	2.23	0.57
1:BE:74:ASN:ND2	1:BE:77:THR:OG1	2.38	0.57
1:BJ:55:ARG:CD	1:CL:272:TYR:HE2	2.17	0.57
1:BM:284:ARG:CG	1:BM:284:ARG:NH1	2.67	0.57
1:BS:79:ARG:CG	1:BS:79:ARG:NH1	2.66	0.57
1:BT:365:ILE:HD12	1:BT:471:MET:HE2	1.85	0.57
1:CD:55:ARG:HD3	1:CN:272:TYR:CE2	2.40	0.57
1:CJ:284:ARG:HG2	1:CJ:284:ARG:NH1	2.20	0.57
1:CK:379:VAL:CG1	1:CK:381:MET:HE1	2.34	0.57
1:CM:365:ILE:HD12	1:CM:471:MET:HE2	1.87	0.57
1:AE:284:ARG:HG2	1:AE:284:ARG:NH1	2.20	0.57
1:AG:272:TYR:N	1:AG:272:TYR:CD1	2.67	0.57
1:AK:454:ASN:HD22	1:AK:456:ALA:N	2.03	0.57
1:AP:55:ARG:NE	1:BM:272:TYR:CE2	2.73	0.57
1:AQ:189:PHE:CE1	1:AQ:198:ARG:HG3	2.39	0.57
1:BA:232:THR:HB	1:BA:334:VAL:HG23	1.87	0.57
1:BC:79:ARG:HH11	1:BC:79:ARG:HG3	1.70	0.57
1:BN:170:PHE:CD1	1:BN:389:MET:HE1	2.39	0.57
1:BO:189:PHE:CE1	1:BO:198:ARG:HG3	2.39	0.57
1:AA:189:PHE:HE2	1:AA:249:LEU:CD2	2.18	0.56
1:AO:290:THR:O	1:AO:290:THR:CG2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AQ:379:VAL:CG1	1:AQ:381:MET:HE1	2.35	0.56
1:AS:398:GLY:HA3	1:AS:494:PHE:CD2	2.40	0.56
1:BB:379:VAL:HG11	1:BB:381:MET:HE1	1.87	0.56
1:BM:189:PHE:CE1	1:BM:198:ARG:CG	2.82	0.56
1:BM:189:PHE:CE1	1:BM:198:ARG:HG3	2.38	0.56
1:BQ:365:ILE:HD12	1:BQ:471:MET:HE2	1.87	0.56
1:CP:284:ARG:HG2	1:CP:284:ARG:NH1	2.20	0.56
1:CS:284:ARG:HG2	1:CS:284:ARG:NH1	2.19	0.56
1:AB:55:ARG:HD3	1:BB:272:TYR:CD2	2.40	0.56
1:AC:379:VAL:HG11	1:AC:381:MET:HE1	1.86	0.56
1:AJ:250:TRP:CZ3	1:AJ:272:TYR:HE1	2.23	0.56
1:BG:272:TYR:CD2	1:CG:55:ARG:CZ	2.88	0.56
1:BS:189:PHE:CE1	1:BS:198:ARG:CG	2.88	0.56
1:CM:14:CYS:H	1:CM:138:ASN:HD21	1.51	0.56
1:CM:239:ILE:HG12	1:CM:326:ILE:CD1	2.35	0.56
1:CS:250:TRP:CE3	1:CS:272:TYR:CE1	2.93	0.56
1:CS:398:GLY:HA3	1:CS:494:PHE:CD2	2.40	0.56
1:AB:55:ARG:CD	1:BB:272:TYR:HE2	2.19	0.56
1:AD:365:ILE:HD12	1:AD:471:MET:HE2	1.86	0.56
1:AD:379:VAL:HG11	1:AD:381:MET:HE1	1.87	0.56
1:AH:16:ALA:O	1:AH:17:ASN:HB2	2.04	0.56
1:AH:250:TRP:CE3	1:AH:272:TYR:CE1	2.93	0.56
1:AJ:454:ASN:HD22	1:AJ:456:ALA:N	2.03	0.56
1:AK:365:ILE:HD12	1:AK:471:MET:HE2	1.87	0.56
1:AP:250:TRP:CE3	1:AP:272:TYR:CE1	2.93	0.56
1:BB:454:ASN:ND2	1:BB:456:ALA:H	2.00	0.56
1:BM:365:ILE:HD12	1:BM:471:MET:HE2	1.88	0.56
1:BM:398:GLY:HA3	1:BM:494:PHE:CD2	2.40	0.56
1:BN:189:PHE:CE1	1:BN:198:ARG:HG2	2.41	0.56
1:BP:74:ASN:CB	1:BP:126:GLU:HG2	2.35	0.56
1:BQ:74:ASN:CB	1:BQ:126:GLU:HG2	2.35	0.56
1:CB:191:LEU:HD23	1:CB:191:LEU:N	2.18	0.56
1:CB:250:TRP:CE3	1:CB:272:TYR:CE1	2.93	0.56
1:CC:454:ASN:HD22	1:CC:456:ALA:N	2.02	0.56
1:CI:378:ARG:CG	1:CI:379:VAL:H	2.17	0.56
1:CJ:189:PHE:HE2	1:CJ:249:LEU:CD2	2.18	0.56
1:CK:74:ASN:ND2	1:CK:77:THR:OG1	2.38	0.56
1:CR:284:ARG:HG2	1:CR:284:ARG:NH1	2.20	0.56
1:AA:272:TYR:HE2	1:CT:55:ARG:CD	2.18	0.56
1:AI:442:GLN:HE21	1:AJ:412:PHE:HB2	1.70	0.56
1:AI:454:ASN:HD22	1:AI:456:ALA:N	2.03	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:454:ASN:ND2	1:AN:456:ALA:H	2.03	0.56
1:BE:288:HIS:HD2	1:BE:337:ASP:OD2	1.89	0.56
1:BJ:250:TRP:HZ3	1:BJ:272:TYR:CE1	2.22	0.56
1:CN:250:TRP:HZ3	1:CN:272:TYR:CE1	2.23	0.56
1:CO:14:CYS:H	1:CO:138:ASN:HD21	1.53	0.56
1:CR:250:TRP:HZ3	1:CR:272:TYR:CE1	2.23	0.56
1:AD:189:PHE:CE1	1:AD:198:ARG:CG	2.89	0.56
1:AD:398:GLY:HA3	1:AD:494:PHE:CD2	2.40	0.56
1:AF:454:ASN:ND2	1:AF:456:ALA:H	2.01	0.56
1:AJ:79:ARG:HG3	1:AJ:79:ARG:NH1	2.21	0.56
1:AQ:67:VAL:HG23	1:AQ:135:LEU:HB2	1.88	0.56
1:AQ:442:GLN:HE21	1:AR:412:PHE:HB2	1.71	0.56
1:AS:454:ASN:HD22	1:AS:456:ALA:N	2.03	0.56
1:BE:189:PHE:HE2	1:BE:249:LEU:CD2	2.18	0.56
1:BF:79:ARG:HH11	1:BF:79:ARG:CG	2.18	0.56
1:BL:288:HIS:HD2	1:BL:337:ASP:OD2	1.89	0.56
1:BQ:189:PHE:CE1	1:BQ:198:ARG:CG	2.88	0.56
1:CE:454:ASN:HD22	1:CE:456:ALA:N	2.03	0.56
1:CR:365:ILE:HD12	1:CR:471:MET:HE2	1.87	0.56
1:AM:288:HIS:HD2	1:AM:337:ASP:OD2	1.89	0.56
1:AR:365:ILE:HD12	1:AR:471:MET:HE2	1.86	0.56
1:BA:250:TRP:CE3	1:BA:272:TYR:CE1	2.93	0.56
1:BA:379:VAL:CG1	1:BA:381:MET:HE1	2.36	0.56
1:BH:55:ARG:HD3	1:BK:272:TYR:CD2	2.41	0.56
1:BR:189:PHE:HE2	1:BR:249:LEU:CD2	2.18	0.56
1:BR:454:ASN:ND2	1:BR:456:ALA:H	2.03	0.56
1:BT:288:HIS:HD2	1:BT:337:ASP:OD2	1.89	0.56
1:CH:55:ARG:CD	1:CK:272:TYR:HE2	2.17	0.56
1:CJ:18:ARG:HD2	1:CJ:19:TYR:O	2.05	0.56
1:CM:75:ARG:NH2	1:CM:391:ALA:O	2.38	0.56
1:CR:74:ASN:CB	1:CR:126:GLU:HG2	2.35	0.56
1:AL:14:CYS:H	1:AL:138:ASN:ND2	2.03	0.56
1:BA:365:ILE:HD12	1:BA:471:MET:HE2	1.88	0.56
1:BM:189:PHE:HE1	1:BM:198:ARG:HG2	1.70	0.56
1:BQ:14:CYS:H	1:BQ:138:ASN:HD21	1.53	0.56
1:BS:79:ARG:HG3	1:BS:79:ARG:NH1	2.10	0.56
1:BT:79:ARG:HG3	1:BT:79:ARG:NH1	2.21	0.56
1:CF:239:ILE:HG12	1:CF:326:ILE:CD1	2.35	0.56
1:CI:189:PHE:CE1	1:CI:198:ARG:CG	2.83	0.56
1:CO:36:GLN:NE2	1:CO:156:LEU:H	2.03	0.56
1:AH:43:ALA:HB1	1:AH:158:GLU:HA	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:288:HIS:HD2	1:AL:337:ASP:OD2	1.89	0.56
1:BN:442:GLN:HE21	1:BO:412:PHE:HB2	1.71	0.56
1:CE:284:ARG:HG2	1:CE:284:ARG:NH1	2.21	0.56
1:CM:250:TRP:HZ3	1:CM:272:TYR:CE1	2.19	0.56
1:CN:454:ASN:HD22	1:CN:456:ALA:N	2.00	0.56
1:CT:189:PHE:HE2	1:CT:249:LEU:CD2	2.19	0.56
1:AE:250:TRP:CE3	1:AE:272:TYR:CE1	2.94	0.56
1:AN:14:CYS:H	1:AN:138:ASN:HD21	1.53	0.56
1:AO:379:VAL:HG11	1:AO:381:MET:HE1	1.88	0.56
1:AP:14:CYS:H	1:AP:138:ASN:HD21	1.53	0.56
1:BN:379:VAL:HG11	1:BN:381:MET:HE1	1.88	0.56
1:BP:79:ARG:HH11	1:BP:79:ARG:HG2	1.70	0.56
1:CI:272:TYR:CD2	1:CO:55:ARG:HD3	2.40	0.56
1:CR:250:TRP:CE3	1:CR:272:TYR:CE1	2.94	0.56
1:AG:288:HIS:HD2	1:AG:337:ASP:OD2	1.89	0.56
1:AK:191:LEU:HD23	1:AK:191:LEU:N	2.17	0.56
1:AM:74:ASN:ND2	1:AM:77:THR:OG1	2.39	0.56
1:AQ:288:HIS:HD2	1:AQ:337:ASP:OD2	1.89	0.56
1:BB:74:ASN:ND2	1:BB:77:THR:OG1	2.39	0.56
1:BF:74:ASN:ND2	1:BF:77:THR:OG1	2.38	0.56
1:BG:250:TRP:HZ3	1:BG:272:TYR:CE1	2.20	0.56
1:BH:250:TRP:HZ3	1:BH:272:TYR:CE1	2.22	0.56
1:BK:250:TRP:HZ3	1:BK:272:TYR:CE1	2.23	0.56
1:BK:398:GLY:HA3	1:BK:494:PHE:CD2	2.40	0.56
1:CH:454:ASN:HD22	1:CH:456:ALA:N	2.02	0.56
1:AA:379:VAL:HG11	1:AA:381:MET:HE1	1.86	0.55
1:AB:191:LEU:HD23	1:AB:191:LEU:N	2.16	0.55
1:AD:67:VAL:HG23	1:AD:135:LEU:HB2	1.87	0.55
1:AH:55:ARG:NE	1:AK:272:TYR:CD2	2.74	0.55
1:AJ:284:ARG:HG2	1:AJ:284:ARG:NH1	2.22	0.55
1:AT:284:ARG:HG2	1:AT:284:ARG:NH1	2.16	0.55
1:BB:67:VAL:HG23	1:BB:135:LEU:HB2	1.88	0.55
1:BG:67:VAL:HG23	1:BG:135:LEU:HB2	1.88	0.55
1:BG:365:ILE:HD12	1:BG:471:MET:HE2	1.88	0.55
1:BO:365:ILE:HD12	1:BO:471:MET:HE2	1.88	0.55
1:BT:189:PHE:HE1	1:BT:198:ARG:CG	2.18	0.55
1:AI:144:ALA:HB3	1:AR:191:LEU:O	2.06	0.55
1:AP:55:ARG:CD	1:BM:272:TYR:CE2	2.90	0.55
1:BB:11:PRO:HG2	1:BB:18:ARG:HD2	1.88	0.55
1:BJ:365:ILE:HD12	1:BJ:471:MET:HE2	1.88	0.55
1:BM:14:CYS:H	1:BM:138:ASN:HD21	1.52	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:74:ASN:CB	1:BM:126:GLU:HG2	2.36	0.55
1:CH:55:ARG:HD3	1:CK:272:TYR:CD2	2.41	0.55
1:CI:272:TYR:HE2	1:CO:55:ARG:CD	2.18	0.55
1:CK:454:ASN:ND2	1:CK:456:ALA:H	2.01	0.55
1:CL:189:PHE:HE1	1:CL:198:ARG:CG	2.19	0.55
1:CN:365:ILE:HD12	1:CN:471:MET:HE2	1.87	0.55
1:CQ:288:HIS:HD2	1:CQ:337:ASP:OD2	1.89	0.55
1:AC:272:TYR:HE2	1:BA:55:ARG:CD	2.19	0.55
1:AD:250:TRP:CE3	1:AD:272:TYR:CE1	2.95	0.55
1:AE:379:VAL:CG1	1:AE:381:MET:HE1	2.37	0.55
1:AQ:454:ASN:HD22	1:AQ:456:ALA:N	2.04	0.55
1:BC:16:ALA:O	1:BC:17:ASN:HB2	2.06	0.55
1:BC:272:TYR:CE2	1:CA:55:ARG:HD3	2.42	0.55
1:BQ:189:PHE:HE2	1:BQ:249:LEU:HD21	1.71	0.55
1:BS:288:HIS:HD2	1:BS:337:ASP:OD2	1.89	0.55
1:CD:55:ARG:HD3	1:CN:272:TYR:HD2	1.70	0.55
1:CD:454:ASN:ND2	1:CD:456:ALA:H	2.02	0.55
1:CQ:189:PHE:HE2	1:CQ:249:LEU:CD2	2.20	0.55
1:CT:379:VAL:HG11	1:CT:381:MET:HE1	1.88	0.55
1:AA:16:ALA:O	1:AA:17:ASN:HB2	2.07	0.55
1:AE:288:HIS:HD2	1:AE:337:ASP:OD2	1.90	0.55
1:AH:365:ILE:HD12	1:AH:471:MET:HE2	1.88	0.55
1:AI:379:VAL:CG1	1:AI:381:MET:HE1	2.36	0.55
1:AM:74:ASN:CB	1:AM:126:GLU:HG2	2.35	0.55
1:AR:10:ILE:HG21	1:AR:146:TRP:CZ2	2.41	0.55
1:AR:58:ALA:HB2	1:AR:102:GLY:HA3	1.88	0.55
1:AS:67:VAL:HG23	1:AS:135:LEU:HB2	1.88	0.55
1:BA:232:THR:HB	1:BA:334:VAL:CG2	2.37	0.55
1:BJ:67:VAL:HG23	1:BJ:135:LEU:HB2	1.89	0.55
1:BK:189:PHE:HE2	1:BK:249:LEU:CD2	2.18	0.55
1:BP:75:ARG:NH2	1:BP:391:ALA:O	2.39	0.55
1:CH:11:PRO:HG2	1:CH:18:ARG:HD2	1.88	0.55
1:AA:272:TYR:HD2	1:CT:55:ARG:HD3	1.72	0.55
1:AJ:272:TYR:CE2	1:AQ:55:ARG:CZ	2.89	0.55
1:AQ:272:TYR:HE2	1:BL:55:ARG:CD	2.19	0.55
1:BL:250:TRP:HZ3	1:BL:272:TYR:CE1	2.22	0.55
1:BM:67:VAL:HG23	1:BM:135:LEU:HB2	1.88	0.55
1:BQ:189:PHE:HE2	1:BQ:249:LEU:CD2	2.20	0.55
1:CA:454:ASN:HD22	1:CA:456:ALA:N	2.04	0.55
1:CP:288:HIS:HD2	1:CP:337:ASP:OD2	1.90	0.55
1:AI:74:ASN:ND2	1:AI:77:THR:OG1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:67:VAL:HG23	1:BD:135:LEU:HB2	1.88	0.55
1:BD:365:ILE:HD12	1:BD:471:MET:HE2	1.88	0.55
1:BF:170:PHE:CD1	1:BF:389:MET:HE1	2.41	0.55
1:BH:288:HIS:HD2	1:BH:337:ASP:OD2	1.90	0.55
1:BK:250:TRP:CE3	1:BK:272:TYR:CE1	2.94	0.55
1:BK:454:ASN:ND2	1:BK:456:ALA:H	2.02	0.55
1:CG:398:GLY:HA3	1:CG:494:PHE:CD2	2.41	0.55
1:CK:250:TRP:CE3	1:CK:272:TYR:CE1	2.94	0.55
1:CS:189:PHE:HE1	1:CS:198:ARG:CG	2.19	0.55
1:CS:239:ILE:HG12	1:CS:326:ILE:CD1	2.37	0.55
1:AG:379:VAL:CG1	1:AG:381:MET:HE1	2.37	0.55
1:AI:272:TYR:HE2	1:AO:55:ARG:NE	1.92	0.55
1:AN:430:MET:HE3	1:AO:296:ALA:HB1	1.81	0.55
1:BB:55:ARG:CZ	1:CB:272:TYR:CD2	2.90	0.55
1:BG:454:ASN:HD22	1:BG:456:ALA:N	2.04	0.55
1:BM:288:HIS:HD2	1:BM:337:ASP:OD2	1.90	0.55
1:BM:454:ASN:HD22	1:BM:456:ALA:N	2.00	0.55
1:BQ:379:VAL:HG11	1:BQ:381:MET:HE1	1.88	0.55
1:CA:74:ASN:CB	1:CA:126:GLU:HG2	2.37	0.55
1:AA:191:LEU:HD23	1:AA:191:LEU:N	2.16	0.55
1:AC:398:GLY:HA3	1:AC:494:PHE:CD2	2.42	0.55
1:BF:55:ARG:HD3	1:CH:272:TYR:CE2	2.42	0.55
1:BH:365:ILE:HD12	1:BH:471:MET:HE2	1.88	0.55
1:BK:189:PHE:CE1	1:BK:198:ARG:CG	2.89	0.55
1:CB:14:CYS:H	1:CB:138:ASN:HD21	1.54	0.55
1:CI:250:TRP:HZ3	1:CI:272:TYR:CE1	2.22	0.55
1:CQ:454:ASN:HD22	1:CQ:456:ALA:N	2.00	0.55
1:CR:67:VAL:HG23	1:CR:135:LEU:HB2	1.89	0.55
1:AB:14:CYS:H	1:AB:138:ASN:HD21	1.52	0.55
1:AH:272:TYR:CE2	1:CF:55:ARG:CZ	2.90	0.55
1:AQ:284:ARG:HG2	1:AQ:284:ARG:NH1	2.20	0.55
1:BA:74:ASN:ND2	1:BA:77:THR:OG1	2.40	0.55
1:BK:454:ASN:HD22	1:BK:456:ALA:N	1.99	0.55
1:BR:379:VAL:CG1	1:BR:381:MET:HE1	2.37	0.55
1:CA:379:VAL:HG11	1:CA:381:MET:HE1	1.88	0.55
1:CJ:79:ARG:HH11	1:CJ:79:ARG:HG3	1.72	0.55
1:CJ:454:ASN:ND2	1:CJ:456:ALA:H	2.04	0.55
1:CS:454:ASN:HD22	1:CS:456:ALA:N	1.98	0.55
1:AS:379:VAL:HG11	1:AS:381:MET:HE1	1.88	0.55
1:BD:189:PHE:HE2	1:BD:249:LEU:CD2	2.20	0.55
1:BE:379:VAL:CG1	1:BE:381:MET:HE1	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:272:TYR:CD2	1:BO:55:ARG:HD3	2.41	0.55
1:BL:36:GLN:NE2	1:BL:156:LEU:H	2.05	0.55
1:BQ:398:GLY:HA3	1:BQ:494:PHE:CD2	2.41	0.55
1:CH:250:TRP:CE3	1:CH:272:TYR:CE1	2.93	0.55
1:CI:74:ASN:ND2	1:CI:77:THR:OG1	2.40	0.55
1:CM:288:HIS:HD2	1:CM:337:ASP:OD2	1.90	0.55
1:CO:189:PHE:CE1	1:CO:198:ARG:CG	2.90	0.55
1:AE:365:ILE:HD12	1:AE:471:MET:HE2	1.88	0.54
1:AH:454:ASN:HD22	1:AH:456:ALA:N	2.03	0.54
1:AO:365:ILE:HD12	1:AO:471:MET:HE2	1.89	0.54
1:AQ:16:ALA:O	1:AQ:17:ASN:HB2	2.07	0.54
1:AR:288:HIS:HD2	1:AR:337:ASP:OD2	1.90	0.54
1:BD:74:ASN:CB	1:BD:126:GLU:HG2	2.36	0.54
1:BI:250:TRP:HZ3	1:BI:272:TYR:CE1	2.23	0.54
1:BI:454:ASN:HD22	1:BI:456:ALA:N	1.99	0.54
1:BJ:18:ARG:HD2	1:BJ:19:TYR:O	2.06	0.54
1:BL:379:VAL:HG11	1:BL:381:MET:HE1	1.88	0.54
1:BS:189:PHE:HE2	1:BS:249:LEU:CD2	2.20	0.54
1:CE:288:HIS:HD2	1:CE:337:ASP:OD2	1.90	0.54
1:CH:67:VAL:HG23	1:CH:135:LEU:HB2	1.90	0.54
1:CP:379:VAL:CG1	1:CP:381:MET:HE1	2.37	0.54
1:CS:189:PHE:CE1	1:CS:198:ARG:CG	2.90	0.54
1:AA:58:ALA:HB2	1:AA:102:GLY:HA3	1.89	0.54
1:AB:250:TRP:HZ3	1:AB:272:TYR:CE1	2.22	0.54
1:AB:454:ASN:HD22	1:AB:456:ALA:N	2.03	0.54
1:AF:405:GLN:NE2	1:AJ:437:HIS:CE1	2.76	0.54
1:AG:365:ILE:HD12	1:AG:471:MET:HE2	1.88	0.54
1:AH:162:PHE:CD2	1:AH:163:LEU:HD13	2.43	0.54
1:AJ:272:TYR:CD2	1:AQ:55:ARG:CZ	2.90	0.54
1:AS:288:HIS:HD2	1:AS:337:ASP:OD2	1.91	0.54
1:BH:170:PHE:CD1	1:BH:389:MET:HE1	2.39	0.54
1:BP:189:PHE:HE2	1:BP:249:LEU:CD2	2.20	0.54
1:BT:55:ARG:NE	1:CA:272:TYR:HE2	1.96	0.54
1:BT:189:PHE:HE2	1:BT:249:LEU:CD2	2.20	0.54
1:CG:74:ASN:CB	1:CG:126:GLU:HG2	2.37	0.54
1:CJ:250:TRP:HZ3	1:CJ:272:TYR:CE1	2.25	0.54
1:CS:365:ILE:HD12	1:CS:471:MET:HE2	1.88	0.54
1:AB:272:TYR:CE2	1:CB:55:ARG:CD	2.90	0.54
1:AG:398:GLY:HA3	1:AG:494:PHE:CD2	2.43	0.54
1:AL:250:TRP:CE3	1:AL:272:TYR:CE1	2.95	0.54
1:AQ:256:ASN:HD22	1:AQ:302:ASP:HA	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AR:398:GLY:HA3	1:AR:494:PHE:CD2	2.42	0.54
1:BA:250:TRP:HZ3	1:BA:272:TYR:CE1	2.22	0.54
1:BC:365:ILE:HD12	1:BC:471:MET:HE2	1.88	0.54
1:BI:398:GLY:HA3	1:BI:494:PHE:CD2	2.41	0.54
1:BS:58:ALA:HB2	1:BS:102:GLY:HA3	1.88	0.54
1:CF:365:ILE:HD12	1:CF:471:MET:HE2	1.89	0.54
1:CL:454:ASN:HD22	1:CL:456:ALA:N	2.01	0.54
1:AB:398:GLY:HA3	1:AB:494:PHE:CD2	2.43	0.54
1:AH:284:ARG:CG	1:AH:284:ARG:NH1	2.70	0.54
1:AK:442:GLN:NE2	1:AL:412:PHE:HB2	2.23	0.54
1:BG:250:TRP:CE3	1:BG:272:TYR:CE1	2.95	0.54
1:BI:379:VAL:HG11	1:BI:381:MET:HE1	1.90	0.54
1:BJ:74:ASN:ND2	1:BJ:77:THR:OG1	2.40	0.54
1:BP:365:ILE:HD12	1:BP:471:MET:HE2	1.89	0.54
1:BS:170:PHE:CD1	1:BS:389:MET:HE1	2.41	0.54
1:CE:226:VAL:HG13	1:CE:228:GLY:H	1.73	0.54
1:CJ:272:TYR:CD2	1:CQ:55:ARG:HD3	2.43	0.54
1:CK:250:TRP:HZ3	1:CK:272:TYR:CE1	2.22	0.54
1:CM:454:ASN:ND2	1:CM:456:ALA:H	2.02	0.54
1:CQ:454:ASN:HD21	1:CQ:456:ALA:HB3	1.72	0.54
1:CS:203:THR:HB	1:CS:300:GLN:HG3	1.88	0.54
1:AG:258:THR:C	1:AG:259:THR:O	2.41	0.54
1:AG:275:GLU:O	1:AG:276:ASP:C	2.44	0.54
1:AG:454:ASN:HD22	1:AG:456:ALA:N	2.04	0.54
1:AJ:67:VAL:HG23	1:AJ:135:LEU:HB2	1.90	0.54
1:AM:67:VAL:HG23	1:AM:135:LEU:HB2	1.89	0.54
1:AO:74:ASN:CB	1:AO:126:GLU:HG2	2.37	0.54
1:BA:189:PHE:HD2	1:BA:247:ILE:HD11	1.73	0.54
1:BD:288:HIS:HD2	1:BD:337:ASP:OD2	1.90	0.54
1:BI:14:CYS:H	1:BI:138:ASN:HD21	1.56	0.54
1:BM:379:VAL:HG11	1:BM:381:MET:HE1	1.88	0.54
1:BN:250:TRP:CE3	1:BN:272:TYR:CE1	2.96	0.54
1:BP:398:GLY:HA3	1:BP:494:PHE:CD2	2.43	0.54
1:CC:79:ARG:HG3	1:CC:79:ARG:NH1	2.21	0.54
1:CP:454:ASN:HD22	1:CP:456:ALA:N	2.06	0.54
1:AF:16:ALA:O	1:AF:17:ASN:HB2	2.07	0.54
1:AG:58:ALA:HB2	1:AG:102:GLY:HA3	1.89	0.54
1:BB:454:ASN:HD22	1:BB:456:ALA:N	1.99	0.54
1:BF:250:TRP:CE3	1:BF:272:TYR:CE1	2.95	0.54
1:BJ:454:ASN:HD21	1:BJ:456:ALA:HB3	1.73	0.54
1:BO:250:TRP:CE3	1:BO:272:TYR:CD1	2.95	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:162:PHE:CD2	1:BQ:163:LEU:HD13	2.43	0.54
1:CB:398:GLY:HA3	1:CB:494:PHE:CD2	2.43	0.54
1:CD:379:VAL:CG1	1:CD:381:MET:HE1	2.38	0.54
1:CF:30:SER:O	1:CF:33:LYS:HB2	2.08	0.54
1:CT:189:PHE:HE1	1:CT:198:ARG:CG	2.19	0.54
1:CT:250:TRP:CE3	1:CT:272:TYR:CE1	2.96	0.54
1:AH:379:VAL:CG1	1:AH:381:MET:HE1	2.38	0.54
1:AK:379:VAL:CG1	1:AK:381:MET:HE1	2.38	0.54
1:AL:365:ILE:HD12	1:AL:471:MET:HE2	1.88	0.54
1:BG:14:CYS:H	1:BG:138:ASN:HD21	1.54	0.54
1:BH:454:ASN:HD22	1:BH:456:ALA:N	2.02	0.54
1:BP:77:THR:O	1:BP:81:THR:HG23	2.07	0.54
1:BT:250:TRP:HZ3	1:BT:272:TYR:CE1	2.22	0.54
1:CC:67:VAL:HG23	1:CC:135:LEU:HB2	1.90	0.54
1:CF:250:TRP:HZ3	1:CF:272:TYR:CE1	2.21	0.54
1:CJ:272:TYR:CD2	1:CQ:55:ARG:NH1	2.75	0.54
1:AF:55:ARG:HD3	1:BH:272:TYR:CE2	2.43	0.54
1:AI:250:TRP:CZ3	1:AI:272:TYR:HE1	2.22	0.54
1:AK:58:ALA:HB2	1:AK:102:GLY:HA3	1.89	0.54
1:AN:55:ARG:NH1	1:AS:272:TYR:CD2	2.76	0.54
1:AT:365:ILE:HD12	1:AT:471:MET:HE2	1.88	0.54
1:BC:398:GLY:HA3	1:BC:494:PHE:CD2	2.43	0.54
1:BT:189:PHE:CE1	1:BT:198:ARG:CG	2.91	0.54
1:BT:454:ASN:ND2	1:BT:456:ALA:H	2.03	0.54
1:CA:11:PRO:HG2	1:CA:18:ARG:HD2	1.90	0.54
1:CB:67:VAL:HG23	1:CB:135:LEU:HB2	1.89	0.54
1:CS:379:VAL:CG1	1:CS:381:MET:HE1	2.37	0.54
1:CT:189:PHE:HD2	1:CT:247:ILE:HD11	1.73	0.54
1:AH:74:ASN:CB	1:AH:126:GLU:HG2	2.37	0.54
1:AH:250:TRP:HZ3	1:AH:272:TYR:CE1	2.24	0.54
1:AI:43:ALA:HB1	1:AI:158:GLU:HA	1.89	0.54
1:AI:418:SER:HB3	1:AJ:407:SER:HB3	1.90	0.54
1:AQ:189:PHE:HE2	1:AQ:249:LEU:HD21	1.71	0.54
1:BO:15:GLN:HA	1:BO:15:GLN:NE2	2.18	0.54
1:CD:67:VAL:HG23	1:CD:135:LEU:HB2	1.88	0.54
1:CF:170:PHE:CD1	1:CF:389:MET:HE1	2.42	0.54
1:CK:67:VAL:HG23	1:CK:135:LEU:HB2	1.89	0.54
1:CR:379:VAL:CG1	1:CR:381:MET:HE1	2.38	0.54
1:AD:272:TYR:HE2	1:AS:55:ARG:NE	2.06	0.54
1:AF:288:HIS:HD2	1:AF:337:ASP:OD2	1.91	0.54
1:AG:267:LYS:C	1:AG:268:TYR:O	2.45	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:191:LEU:O	1:AQ:144:ALA:HB3	2.09	0.54
1:AO:203:THR:CG2	1:AO:293:ARG:HA	2.38	0.54
1:CE:203:THR:HB	1:CE:300:GLN:HG3	1.90	0.54
1:CS:79:ARG:HH11	1:CS:79:ARG:HG3	1.73	0.54
1:AL:442:GLN:HE21	1:AM:412:PHE:HB2	1.73	0.53
1:AO:272:TYR:CE2	1:AR:55:ARG:CZ	2.91	0.53
1:AO:398:GLY:HA3	1:AO:494:PHE:CD2	2.42	0.53
1:BA:398:GLY:HA3	1:BA:494:PHE:CD2	2.42	0.53
1:BJ:14:CYS:H	1:BJ:138:ASN:HD21	1.54	0.53
1:BJ:288:HIS:HD2	1:BJ:337:ASP:OD2	1.91	0.53
1:BM:189:PHE:CE1	1:BM:198:ARG:HG2	2.43	0.53
1:BO:454:ASN:HD22	1:BO:456:ALA:N	2.06	0.53
1:BP:379:VAL:CG1	1:BP:381:MET:HE1	2.38	0.53
1:BR:398:GLY:HA3	1:BR:494:PHE:CD2	2.43	0.53
1:CH:16:ALA:O	1:CH:17:ASN:HB2	2.08	0.53
1:CN:454:ASN:ND2	1:CN:456:ALA:H	2.02	0.53
1:CT:67:VAL:HG23	1:CT:135:LEU:HB2	1.89	0.53
1:AO:288:HIS:HD2	1:AO:337:ASP:OD2	1.91	0.53
1:AP:379:VAL:CG1	1:AP:381:MET:HE1	2.38	0.53
1:CR:398:GLY:HA3	1:CR:494:PHE:CD2	2.42	0.53
1:AC:47:MET:HE2	1:AC:117:ALA:N	2.23	0.53
1:AI:79:ARG:HG3	1:AI:79:ARG:NH1	2.18	0.53
1:AK:288:HIS:HD2	1:AK:337:ASP:OD2	1.90	0.53
1:AT:11:PRO:HG2	1:AT:18:ARG:HD2	1.89	0.53
1:AT:189:PHE:HE2	1:AT:249:LEU:CD2	2.21	0.53
1:AT:398:GLY:HA3	1:AT:494:PHE:CD2	2.42	0.53
1:BA:239:ILE:HG12	1:BA:326:ILE:CD1	2.39	0.53
1:BF:189:PHE:CE1	1:BF:198:ARG:HG2	2.43	0.53
1:BJ:454:ASN:HD22	1:BJ:456:ALA:N	2.03	0.53
1:BM:203:THR:HB	1:BM:300:GLN:HG3	1.91	0.53
1:BS:191:LEU:HD23	1:BS:191:LEU:N	2.19	0.53
1:CL:250:TRP:CE3	1:CL:272:TYR:CE1	2.95	0.53
1:CQ:365:ILE:HD12	1:CQ:471:MET:HE2	1.90	0.53
1:CT:189:PHE:CE1	1:CT:198:ARG:CG	2.91	0.53
1:AI:67:VAL:HG23	1:AI:135:LEU:HB2	1.89	0.53
1:AK:250:TRP:CE3	1:AK:272:TYR:CE1	2.96	0.53
1:AR:67:VAL:HG23	1:AR:135:LEU:HB2	1.91	0.53
1:BC:272:TYR:HE2	1:CA:55:ARG:CD	2.21	0.53
1:BH:250:TRP:CE3	1:BH:272:TYR:CE1	2.97	0.53
1:BT:398:GLY:HA3	1:BT:494:PHE:CD2	2.43	0.53
1:CC:379:VAL:CG1	1:CC:381:MET:HE1	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CD:272:TYR:CD2	1:CS:55:ARG:CZ	2.92	0.53
1:CE:454:ASN:HD21	1:CE:456:ALA:HB3	1.73	0.53
1:CJ:288:HIS:HD2	1:CJ:337:ASP:OD2	1.91	0.53
1:CO:67:VAL:HG23	1:CO:135:LEU:HB2	1.90	0.53
1:CP:250:TRP:HZ3	1:CP:272:TYR:CE1	2.25	0.53
1:AA:250:TRP:CE3	1:AA:272:TYR:CE1	2.97	0.53
1:AK:14:CYS:H	1:AK:138:ASN:ND2	2.05	0.53
1:AL:74:ASN:ND2	1:AL:77:THR:OG1	2.41	0.53
1:AM:250:TRP:CE3	1:AM:272:TYR:CE1	2.96	0.53
1:AQ:250:TRP:CE3	1:AQ:272:TYR:CE1	2.97	0.53
1:BB:162:PHE:CD2	1:BB:163:LEU:HD13	2.44	0.53
1:BC:454:ASN:ND2	1:BC:456:ALA:H	2.03	0.53
1:BG:379:VAL:CG1	1:BG:381:MET:HE1	2.38	0.53
1:BN:18:ARG:HG3	1:BN:19:TYR:N	2.22	0.53
1:CA:250:TRP:CE3	1:CA:272:TYR:CE1	2.95	0.53
1:CC:75:ARG:NH2	1:CC:391:ALA:O	2.41	0.53
1:CE:67:VAL:HG23	1:CE:135:LEU:HB2	1.91	0.53
1:CG:379:VAL:CG1	1:CG:381:MET:HE1	2.39	0.53
1:CH:14:CYS:H	1:CH:138:ASN:HD21	1.56	0.53
1:CK:288:HIS:HD2	1:CK:337:ASP:OD2	1.92	0.53
1:AB:365:ILE:HD12	1:AB:471:MET:HE2	1.90	0.53
1:AC:288:HIS:HD2	1:AC:337:ASP:OD2	1.92	0.53
1:AG:266:PHE:N	1:AG:266:PHE:HD1	2.07	0.53
1:AG:270:GLY:C	1:AG:271:VAL:CG1	2.81	0.53
1:AK:55:ARG:HD3	1:CF:272:TYR:HD2	1.69	0.53
1:AK:170:PHE:CD1	1:AK:389:MET:HE1	2.40	0.53
1:AL:272:TYR:CD2	1:CJ:55:ARG:NE	2.77	0.53
1:AO:30:SER:O	1:AO:33:LYS:HB2	2.09	0.53
1:BE:14:CYS:H	1:BE:138:ASN:HD21	1.57	0.53
1:BI:250:TRP:CE3	1:BI:272:TYR:CE1	2.96	0.53
1:BT:67:VAL:HG23	1:BT:135:LEU:HB2	1.89	0.53
1:CD:272:TYR:CE2	1:CS:55:ARG:CZ	2.91	0.53
1:CL:365:ILE:HD12	1:CL:471:MET:HE2	1.90	0.53
1:CN:379:VAL:CG1	1:CN:381:MET:HE1	2.38	0.53
1:CT:43:ALA:HB1	1:CT:158:GLU:HA	1.90	0.53
1:AA:239:ILE:HG12	1:AA:326:ILE:CD1	2.39	0.53
1:AC:67:VAL:HG23	1:AC:135:LEU:HB2	1.90	0.53
1:AF:79:ARG:HG3	1:AF:79:ARG:NH1	2.17	0.53
1:AF:487:LEU:HD21	1:AJ:436:SER:O	2.09	0.53
1:AL:272:TYR:CD2	1:CJ:55:ARG:NH1	2.76	0.53
1:AP:412:PHE:HB2	1:AT:442:GLN:HE21	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AR:454:ASN:ND2	1:AR:456:ALA:H	2.03	0.53
1:BK:365:ILE:HD12	1:BK:471:MET:HE2	1.90	0.53
1:BK:379:VAL:CG1	1:BK:381:MET:HE1	2.38	0.53
1:BL:454:ASN:HD22	1:BL:456:ALA:N	2.03	0.53
1:BR:250:TRP:CE3	1:BR:272:TYR:CE1	2.96	0.53
1:CA:14:CYS:H	1:CA:138:ASN:HD21	1.57	0.53
1:CC:288:HIS:HD2	1:CC:337:ASP:OD2	1.92	0.53
1:CH:250:TRP:HZ3	1:CH:272:TYR:CE1	2.22	0.53
1:CJ:58:ALA:HB2	1:CJ:102:GLY:HA3	1.89	0.53
1:CP:189:PHE:HE2	1:CP:249:LEU:CD2	2.22	0.53
1:AA:30:SER:O	1:AA:33:LYS:HB2	2.09	0.53
1:AH:55:ARG:NE	1:AK:272:TYR:HE2	1.92	0.53
1:AI:243:ILE:HD13	1:AO:61:PHE:CZ	2.44	0.53
1:AM:203:THR:HB	1:AM:300:GLN:HG3	1.91	0.53
1:AN:79:ARG:HG3	1:AN:79:ARG:NH1	2.18	0.53
1:AQ:43:ALA:HB1	1:AQ:158:GLU:HA	1.91	0.53
1:BA:58:ALA:HB2	1:BA:102:GLY:HA3	1.90	0.53
1:BG:272:TYR:HE2	1:CG:55:ARG:NE	1.99	0.53
1:BI:191:LEU:HD23	1:BI:191:LEU:N	2.18	0.53
1:BJ:272:TYR:N	1:BJ:272:TYR:HD1	2.06	0.53
1:BK:67:VAL:HG23	1:BK:135:LEU:HB2	1.90	0.53
1:BM:79:ARG:HH11	1:BM:79:ARG:CG	2.22	0.53
1:BM:191:LEU:HD23	1:BM:191:LEU:N	2.17	0.53
1:BN:250:TRP:HZ3	1:BN:272:TYR:CE1	2.24	0.53
1:CB:288:HIS:HD2	1:CB:337:ASP:OD2	1.92	0.53
1:CO:79:ARG:HG3	1:CO:79:ARG:NH1	2.23	0.53
1:AB:47:MET:HE2	1:AB:117:ALA:N	2.24	0.53
1:AD:288:HIS:HD2	1:AD:337:ASP:OD2	1.92	0.53
1:AD:454:ASN:HD22	1:AD:456:ALA:N	2.02	0.53
1:AF:67:VAL:HG23	1:AF:135:LEU:HB2	1.91	0.53
1:AF:250:TRP:CE3	1:AF:272:TYR:CE1	2.97	0.53
1:AK:74:ASN:ND2	1:AK:77:THR:OG1	2.42	0.53
1:AK:189:PHE:CE1	1:AK:198:ARG:CG	2.92	0.53
1:BM:25:ILE:HG23	1:BM:152:LEU:HD11	1.91	0.53
1:CC:398:GLY:HA3	1:CC:494:PHE:CD2	2.44	0.53
1:CD:58:ALA:HB2	1:CD:102:GLY:HA3	1.91	0.53
1:CD:188:PHE:C	1:CD:189:PHE:HD1	2.17	0.53
1:CI:288:HIS:HD2	1:CI:337:ASP:OD2	1.90	0.53
1:CL:189:PHE:HE2	1:CL:249:LEU:CD2	2.22	0.53
1:CO:189:PHE:HE2	1:CO:249:LEU:CD2	2.22	0.53
1:CR:189:PHE:CE1	1:CR:198:ARG:HG2	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:189:PHE:HE2	1:AL:249:LEU:CD2	2.22	0.53
1:AO:191:LEU:CD2	1:AO:191:LEU:N	2.72	0.53
1:AR:250:TRP:HZ3	1:AR:272:TYR:CE1	2.23	0.53
1:AR:454:ASN:HD21	1:AR:456:ALA:HB3	1.73	0.53
1:AT:43:ALA:HB1	1:AT:158:GLU:HA	1.90	0.53
1:BA:14:CYS:H	1:BA:138:ASN:ND2	2.03	0.53
1:BC:288:HIS:HD2	1:BC:337:ASP:OD2	1.92	0.53
1:BF:43:ALA:HB1	1:BF:158:GLU:HA	1.91	0.53
1:BK:189:PHE:HD2	1:BK:247:ILE:HD11	1.74	0.53
1:BP:58:ALA:HB2	1:BP:102:GLY:HA3	1.91	0.53
1:BP:250:TRP:CE3	1:BP:272:TYR:CD1	2.97	0.53
1:BT:74:ASN:ND2	1:BT:77:THR:OG1	2.41	0.53
1:CD:288:HIS:HD2	1:CD:337:ASP:OD2	1.92	0.53
1:CE:379:VAL:CG1	1:CE:381:MET:HE1	2.40	0.53
1:CG:189:PHE:CE1	1:CG:198:ARG:HG2	2.44	0.53
1:CR:170:PHE:CD1	1:CR:389:MET:HE1	2.40	0.53
1:AD:79:ARG:HH11	1:AD:79:ARG:CG	2.21	0.52
1:AG:284:ARG:CG	1:AG:284:ARG:NH1	2.69	0.52
1:AK:75:ARG:NH2	1:AK:391:ALA:O	2.42	0.52
1:AK:398:GLY:HA3	1:AK:494:PHE:CD2	2.43	0.52
1:AL:55:ARG:HD3	1:CQ:272:TYR:CE2	2.44	0.52
1:BD:454:ASN:HD22	1:BD:456:ALA:N	2.06	0.52
1:BI:36:GLN:NE2	1:BI:156:LEU:H	2.07	0.52
1:BO:288:HIS:HD2	1:BO:337:ASP:OD2	1.92	0.52
1:BS:365:ILE:HD12	1:BS:471:MET:HE2	1.89	0.52
1:CC:272:TYR:N	1:CC:272:TYR:HD1	2.07	0.52
1:CL:398:GLY:HA3	1:CL:494:PHE:CD2	2.45	0.52
1:CP:284:ARG:CG	1:CP:284:ARG:NH1	2.72	0.52
1:AF:379:VAL:CG1	1:AF:381:MET:HE1	2.39	0.52
1:AH:437:HIS:CE1	1:AI:405:GLN:NE2	2.77	0.52
1:AJ:191:LEU:CD2	1:AJ:191:LEU:N	2.70	0.52
1:AO:226:VAL:HG13	1:AO:228:GLY:H	1.74	0.52
1:AO:250:TRP:HZ3	1:AO:272:TYR:CE1	2.25	0.52
1:AQ:239:ILE:HG12	1:AQ:326:ILE:CD1	2.40	0.52
1:BB:30:SER:O	1:BB:33:LYS:HB2	2.09	0.52
1:BT:55:ARG:CZ	1:CA:272:TYR:CD2	2.92	0.52
1:BT:170:PHE:CD1	1:BT:389:MET:HE1	2.38	0.52
1:CA:189:PHE:CE1	1:CA:198:ARG:CG	2.93	0.52
1:CH:379:VAL:CG1	1:CH:381:MET:HE1	2.39	0.52
1:CJ:14:CYS:H	1:CJ:138:ASN:ND2	2.07	0.52
1:CN:288:HIS:HD2	1:CN:337:ASP:OD2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CS:189:PHE:HE2	1:CS:249:LEU:CD2	2.20	0.52
1:AA:272:TYR:CE2	1:CT:55:ARG:HD3	2.43	0.52
1:AA:288:HIS:HD2	1:AA:337:ASP:OD2	1.92	0.52
1:AG:266:PHE:N	1:AG:266:PHE:CD1	2.77	0.52
1:AR:189:PHE:CE2	1:AR:249:LEU:HD21	2.41	0.52
1:BA:79:ARG:CG	1:BA:79:ARG:NH1	2.71	0.52
1:BG:288:HIS:HD2	1:BG:337:ASP:OD2	1.92	0.52
1:BH:74:ASN:ND2	1:BH:77:THR:OG1	2.42	0.52
1:CC:250:TRP:HZ3	1:CC:272:TYR:CE1	2.20	0.52
1:CF:398:GLY:HA3	1:CF:494:PHE:CD2	2.45	0.52
1:CR:86:PRO:O	1:CR:88:TYR:C	2.52	0.52
1:CT:14:CYS:H	1:CT:138:ASN:ND2	2.04	0.52
1:AD:284:ARG:CG	1:AD:284:ARG:NH1	2.70	0.52
1:AF:250:TRP:HZ3	1:AF:272:TYR:CE1	2.25	0.52
1:AS:189:PHE:HE2	1:AS:249:LEU:CD2	2.22	0.52
1:BC:189:PHE:CE1	1:BC:198:ARG:CG	2.92	0.52
1:BF:398:GLY:HA3	1:BF:494:PHE:CD2	2.45	0.52
1:BH:232:THR:HB	1:BH:334:VAL:CG2	2.40	0.52
1:BJ:398:GLY:HA3	1:BJ:494:PHE:CD2	2.44	0.52
1:BL:79:ARG:HH11	1:BL:79:ARG:CG	2.23	0.52
1:BL:398:GLY:HA3	1:BL:494:PHE:CD2	2.44	0.52
1:BO:191:LEU:CD2	1:BO:191:LEU:N	2.73	0.52
1:BO:284:ARG:CG	1:BO:284:ARG:NH1	2.68	0.52
1:CA:189:PHE:HE2	1:CA:249:LEU:CD2	2.23	0.52
1:CA:288:HIS:HD2	1:CA:337:ASP:OD2	1.92	0.52
1:CB:379:VAL:CG1	1:CB:381:MET:HE1	2.40	0.52
1:CG:226:VAL:HG13	1:CG:228:GLY:H	1.75	0.52
1:CK:454:ASN:HD21	1:CK:456:ALA:HB3	1.75	0.52
1:CL:454:ASN:ND2	1:CL:456:ALA:H	2.03	0.52
1:AB:379:VAL:CG1	1:AB:381:MET:HE1	2.39	0.52
1:AJ:189:PHE:HE1	1:AJ:198:ARG:HG2	1.74	0.52
1:AK:250:TRP:HZ3	1:AK:272:TYR:CE1	2.23	0.52
1:AL:379:VAL:CG1	1:AL:381:MET:HE1	2.39	0.52
1:AN:250:TRP:HZ3	1:AN:272:TYR:CE1	2.24	0.52
1:AR:454:ASN:HD22	1:AR:456:ALA:N	2.01	0.52
1:BE:189:PHE:CE1	1:BE:198:ARG:HG2	2.43	0.52
1:BF:30:SER:O	1:BF:33:LYS:HB2	2.09	0.52
1:BG:272:TYR:CE2	1:CG:55:ARG:HD3	2.43	0.52
1:BJ:250:TRP:CE3	1:BJ:272:TYR:CD1	2.97	0.52
1:BN:288:HIS:HD2	1:BN:337:ASP:OD2	1.92	0.52
1:CA:30:SER:O	1:CA:33:LYS:HB2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:272:TYR:CD2	1:CM:55:ARG:HD3	2.44	0.52
1:CE:398:GLY:HA3	1:CE:494:PHE:CD2	2.44	0.52
1:CI:250:TRP:CE3	1:CI:272:TYR:CE1	2.97	0.52
1:CK:365:ILE:HD12	1:CK:471:MET:HE2	1.91	0.52
1:CM:454:ASN:HD21	1:CM:456:ALA:HB3	1.74	0.52
1:CP:365:ILE:HD12	1:CP:471:MET:HE2	1.91	0.52
1:CS:75:ARG:NH2	1:CS:391:ALA:O	2.42	0.52
1:AC:239:ILE:HG12	1:AC:326:ILE:CD1	2.38	0.52
1:AI:170:PHE:CD1	1:AI:389:MET:HE1	2.40	0.52
1:AJ:16:ALA:O	1:AJ:17:ASN:HB2	2.10	0.52
1:AO:203:THR:HG21	1:AO:294:LEU:HD23	1.92	0.52
1:BE:58:ALA:HB2	1:BE:102:GLY:HA3	1.92	0.52
1:BJ:43:ALA:HB1	1:BJ:158:GLU:HA	1.92	0.52
1:BQ:25:ILE:HG23	1:BQ:152:LEU:HD11	1.91	0.52
1:BR:162:PHE:CD2	1:BR:163:LEU:HD13	2.44	0.52
1:CE:272:TYR:N	1:CE:272:TYR:HD1	2.08	0.52
1:CF:487:LEU:HD21	1:CJ:436:SER:O	2.09	0.52
1:CG:162:PHE:CD2	1:CG:163:LEU:HD13	2.45	0.52
1:CL:7:VAL:HG11	1:CL:9:TYR:CZ	2.44	0.52
1:CO:75:ARG:NH2	1:CO:391:ALA:O	2.43	0.52
1:AA:454:ASN:ND2	1:AA:456:ALA:H	2.03	0.52
1:AC:162:PHE:CD2	1:AC:163:LEU:HD13	2.44	0.52
1:AD:189:PHE:HE2	1:AD:249:LEU:HD21	1.75	0.52
1:AI:398:GLY:HA3	1:AI:494:PHE:CD2	2.44	0.52
1:AL:58:ALA:HB2	1:AL:102:GLY:HA3	1.92	0.52
1:AL:191:LEU:CD2	1:AL:191:LEU:N	2.72	0.52
1:AL:284:ARG:CG	1:AL:284:ARG:NH1	2.70	0.52
1:AT:14:CYS:H	1:AT:138:ASN:HD21	1.56	0.52
1:BA:189:PHE:CE2	1:BA:249:LEU:HD21	2.45	0.52
1:BB:55:ARG:HD3	1:CB:272:TYR:CE2	2.44	0.52
1:BO:67:VAL:HG23	1:BO:135:LEU:HB2	1.90	0.52
1:BQ:454:ASN:HD22	1:BQ:456:ALA:N	2.03	0.52
1:BS:379:VAL:CG1	1:BS:381:MET:HE1	2.39	0.52
1:CB:189:PHE:HE1	1:CB:198:ARG:HG2	1.73	0.52
1:CB:365:ILE:HD12	1:CB:471:MET:HE2	1.91	0.52
1:CR:454:ASN:HD22	1:CR:456:ALA:N	2.02	0.52
1:AL:189:PHE:CE1	1:AL:198:ARG:CG	2.92	0.52
1:AL:267:LYS:HG2	1:CJ:32:PHE:CZ	2.45	0.52
1:AO:75:ARG:NH2	1:AO:391:ALA:O	2.41	0.52
1:AQ:398:GLY:HA3	1:AQ:494:PHE:CD2	2.44	0.52
1:BB:18:ARG:HG3	1:BB:19:TYR:N	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:43:ALA:HB1	1:BC:158:GLU:HA	1.92	0.52
1:BC:250:TRP:HZ3	1:BC:272:TYR:CE1	2.28	0.52
1:BJ:226:VAL:HG13	1:BJ:228:GLY:H	1.75	0.52
1:BO:191:LEU:HD23	1:BO:191:LEU:N	2.17	0.52
1:BO:379:VAL:CG1	1:BO:381:MET:HE1	2.40	0.52
1:BS:250:TRP:CE3	1:BS:272:TYR:CE1	2.98	0.52
1:BT:191:LEU:HD23	1:BT:191:LEU:N	2.19	0.52
1:CC:74:ASN:ND2	1:CC:77:THR:OG1	2.43	0.52
1:CG:67:VAL:HG23	1:CG:135:LEU:HB2	1.90	0.52
1:CI:38:GLU:HB2	1:CQ:35:VAL:CG2	2.38	0.52
1:CJ:365:ILE:HD12	1:CJ:471:MET:HE2	1.90	0.52
1:CR:288:HIS:HD2	1:CR:337:ASP:OD2	1.92	0.52
1:AB:272:TYR:CD1	1:AB:272:TYR:N	2.78	0.52
1:AP:55:ARG:CD	1:BM:272:TYR:HE2	2.23	0.52
1:AP:55:ARG:HD3	1:BM:272:TYR:CD2	2.44	0.52
1:AP:191:LEU:CD2	1:AP:191:LEU:N	2.72	0.52
1:AQ:189:PHE:HE1	1:AQ:198:ARG:CG	2.22	0.52
1:BC:58:ALA:HB2	1:BC:102:GLY:HA3	1.92	0.52
1:BE:272:TYR:CE2	1:BM:55:ARG:CZ	2.93	0.52
1:BJ:272:TYR:N	1:BJ:272:TYR:CD1	2.78	0.52
1:BQ:16:ALA:O	1:BQ:17:ASN:HB2	2.10	0.52
1:BT:379:VAL:CG1	1:BT:381:MET:HE1	2.40	0.52
1:CJ:75:ARG:NH2	1:CJ:391:ALA:O	2.42	0.52
1:CO:398:GLY:HA3	1:CO:494:PHE:CD2	2.44	0.52
1:CP:74:ASN:ND2	1:CP:77:THR:OG1	2.43	0.52
1:BI:288:HIS:HD2	1:BI:337:ASP:OD2	1.93	0.52
1:BN:43:ALA:HB1	1:BN:158:GLU:HA	1.91	0.52
1:BN:398:GLY:HA3	1:BN:494:PHE:CD2	2.45	0.52
1:BQ:442:GLN:HE21	1:BR:412:PHE:HB2	1.75	0.52
1:CF:162:PHE:CD2	1:CF:163:LEU:HD13	2.45	0.52
1:CJ:67:VAL:HG23	1:CJ:135:LEU:HB2	1.92	0.52
1:CO:79:ARG:HH11	1:CO:79:ARG:CG	2.20	0.52
1:CS:11:PRO:HG2	1:CS:18:ARG:HD2	1.92	0.52
1:CS:250:TRP:HZ3	1:CS:272:TYR:CE1	2.26	0.52
1:AC:272:TYR:CE2	1:BA:55:ARG:CD	2.92	0.51
1:AD:454:ASN:ND2	1:AD:456:ALA:H	2.05	0.51
1:AG:270:GLY:O	1:AG:271:VAL:CG1	2.58	0.51
1:AI:288:HIS:HD2	1:AI:337:ASP:OD2	1.92	0.51
1:AK:67:VAL:HG23	1:AK:135:LEU:HB2	1.92	0.51
1:AN:191:LEU:HD23	1:AN:191:LEU:N	2.20	0.51
1:AN:239:ILE:HG23	1:AN:324:LEU:HD21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:398:GLY:HA3	1:AN:494:PHE:CD2	2.43	0.51
1:AS:232:THR:HB	1:AS:334:VAL:HG23	1.92	0.51
1:BC:379:VAL:CG1	1:BC:381:MET:HE1	2.40	0.51
1:BD:191:LEU:CD2	1:BD:191:LEU:N	2.73	0.51
1:BQ:250:TRP:CE3	1:BQ:272:TYR:CE1	2.97	0.51
1:BR:67:VAL:HG23	1:BR:135:LEU:HB2	1.91	0.51
1:CD:398:GLY:HA3	1:CD:494:PHE:CD2	2.45	0.51
1:CF:79:ARG:CG	1:CF:79:ARG:NH1	2.60	0.51
1:CJ:170:PHE:CD1	1:CJ:389:MET:HE1	2.40	0.51
1:CT:58:ALA:HB2	1:CT:102:GLY:HA3	1.92	0.51
1:AE:14:CYS:H	1:AE:138:ASN:ND2	2.05	0.51
1:AR:239:ILE:HG12	1:AR:326:ILE:CD1	2.41	0.51
1:BC:250:TRP:CZ3	1:BC:272:TYR:HE1	2.26	0.51
1:BI:30:SER:O	1:BI:33:LYS:HB2	2.10	0.51
1:BK:79:ARG:HH11	1:BK:79:ARG:HG3	1.75	0.51
1:BL:250:TRP:CE3	1:BL:272:TYR:CE1	2.98	0.51
1:BR:43:ALA:HB1	1:BR:158:GLU:HA	1.91	0.51
1:CE:18:ARG:HG3	1:CE:19:TYR:N	2.25	0.51
1:CG:365:ILE:HD12	1:CG:471:MET:HE2	1.92	0.51
1:CL:250:TRP:HZ3	1:CL:272:TYR:CE1	2.24	0.51
1:CM:67:VAL:HG23	1:CM:135:LEU:HB2	1.91	0.51
1:CN:43:ALA:HB1	1:CN:158:GLU:HA	1.92	0.51
1:CS:67:VAL:HG23	1:CS:135:LEU:HB2	1.92	0.51
1:CT:288:HIS:HD2	1:CT:337:ASP:OD2	1.92	0.51
1:AC:454:ASN:HD21	1:AC:456:ALA:HB3	1.75	0.51
1:AE:454:ASN:ND2	1:AE:456:ALA:H	2.03	0.51
1:AI:58:ALA:HB2	1:AI:102:GLY:HA3	1.92	0.51
1:AL:250:TRP:HZ3	1:AL:272:TYR:CE1	2.22	0.51
1:AS:43:ALA:HB1	1:AS:158:GLU:HA	1.92	0.51
1:BC:188:PHE:C	1:BC:189:PHE:HD1	2.17	0.51
1:BJ:272:TYR:HD2	1:BQ:55:ARG:HD3	1.75	0.51
1:BL:7:VAL:CG1	1:BL:9:TYR:CZ	2.93	0.51
1:BO:272:TYR:CD2	1:BR:55:ARG:CD	2.94	0.51
1:CA:74:ASN:ND2	1:CA:77:THR:OG1	2.43	0.51
1:CA:250:TRP:HZ3	1:CA:272:TYR:CE1	2.26	0.51
1:CE:272:TYR:CD2	1:CM:55:ARG:NH1	2.78	0.51
1:CF:191:LEU:HD23	1:CF:191:LEU:N	2.18	0.51
1:CK:191:LEU:HD23	1:CK:191:LEU:N	2.19	0.51
1:CO:250:TRP:HZ3	1:CO:272:TYR:CE1	2.23	0.51
1:AB:265:LEU:O	1:AB:265:LEU:HD13	2.10	0.51
1:AD:379:VAL:CG1	1:AD:381:MET:HE1	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:189:PHE:CE2	1:AG:249:LEU:HD21	2.42	0.51
1:AH:189:PHE:HE1	1:AH:198:ARG:HG2	1.75	0.51
1:AM:250:TRP:HZ3	1:AM:272:TYR:CE1	2.24	0.51
1:AO:292:ALA:C	1:AO:293:ARG:CG	2.80	0.51
1:AQ:25:ILE:HG23	1:AQ:152:LEU:HD11	1.92	0.51
1:AS:162:PHE:CD2	1:AS:163:LEU:HD13	2.45	0.51
1:AS:250:TRP:HZ3	1:AS:272:TYR:CE1	2.23	0.51
1:BE:250:TRP:CE3	1:BE:272:TYR:CE1	2.98	0.51
1:BH:58:ALA:HB2	1:BH:102:GLY:HA3	1.92	0.51
1:BI:365:ILE:HD12	1:BI:471:MET:HE2	1.92	0.51
1:BL:189:PHE:HE2	1:BL:249:LEU:CD2	2.24	0.51
1:BQ:239:ILE:HG12	1:BQ:326:ILE:CD1	2.41	0.51
1:CF:14:CYS:H	1:CF:138:ASN:HD21	1.57	0.51
1:CJ:272:TYR:N	1:CJ:272:TYR:HD1	2.07	0.51
1:CP:189:PHE:CE1	1:CP:198:ARG:CG	2.93	0.51
1:AD:239:ILE:HG12	1:AD:326:ILE:CD1	2.41	0.51
1:AF:412:PHE:HB2	1:AJ:442:GLN:HE21	1.74	0.51
1:AJ:288:HIS:HD2	1:AJ:337:ASP:OD2	1.93	0.51
1:AK:189:PHE:HE2	1:AK:249:LEU:CD2	2.23	0.51
1:AN:232:THR:HB	1:AN:334:VAL:CG2	2.40	0.51
1:AO:189:PHE:HE2	1:AO:249:LEU:CD2	2.24	0.51
1:BC:272:TYR:HD2	1:CA:55:ARG:HD3	1.73	0.51
1:BH:232:THR:HB	1:BH:334:VAL:HG23	1.93	0.51
1:BO:58:ALA:HB2	1:BO:102:GLY:HA3	1.93	0.51
1:CF:67:VAL:HG23	1:CF:135:LEU:HB2	1.91	0.51
1:CG:239:ILE:HG12	1:CG:326:ILE:CD1	2.40	0.51
1:CR:80:ILE:O	1:CR:83:SER:CA	2.59	0.51
1:AJ:189:PHE:CE1	1:AJ:198:ARG:HG2	2.45	0.51
1:AJ:379:VAL:CG1	1:AJ:381:MET:HE1	2.40	0.51
1:AK:189:PHE:HE1	1:AK:198:ARG:CG	2.21	0.51
1:AQ:189:PHE:HD2	1:AQ:247:ILE:HD11	1.76	0.51
1:AS:272:TYR:N	1:AS:272:TYR:HD1	2.08	0.51
1:BB:189:PHE:CE1	1:BB:198:ARG:HG2	2.46	0.51
1:BD:18:ARG:HG3	1:BD:19:TYR:N	2.26	0.51
1:BD:144:ALA:HB3	1:BN:191:LEU:O	2.10	0.51
1:BE:191:LEU:CD2	1:BE:191:LEU:N	2.74	0.51
1:BI:79:ARG:HH11	1:BI:79:ARG:HG3	1.75	0.51
1:BI:226:VAL:HG13	1:BI:228:GLY:H	1.76	0.51
1:BK:239:ILE:HG12	1:BK:326:ILE:CD1	2.41	0.51
1:BN:170:PHE:HD1	1:BN:389:MET:CE	2.21	0.51
1:BN:454:ASN:ND2	1:BN:456:ALA:H	2.05	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BO:189:PHE:CE1	1:BO:198:ARG:CG	2.94	0.51
1:CC:188:PHE:C	1:CC:189:PHE:HD1	2.19	0.51
1:CF:347:TYR:O	1:CJ:435:PRO:HB3	2.11	0.51
1:CG:30:SER:O	1:CG:33:LYS:HB2	2.11	0.51
1:CI:38:GLU:CB	1:CQ:35:VAL:CG2	2.88	0.51
1:CI:354:SER:O	1:CI:378:ARG:CB	2.58	0.51
1:CQ:14:CYS:H	1:CQ:138:ASN:ND2	2.09	0.51
1:CQ:239:ILE:HG12	1:CQ:326:ILE:CD1	2.41	0.51
1:CR:74:ASN:ND2	1:CR:77:THR:OG1	2.43	0.51
1:AA:8:ILE:HG22	1:AA:10:ILE:HD11	1.92	0.51
1:AA:55:ARG:HD3	1:CC:272:TYR:CD2	2.45	0.51
1:AG:272:TYR:C	1:AG:273:VAL:CG2	2.71	0.51
1:AL:189:PHE:HE2	1:AL:249:LEU:HD21	1.75	0.51
1:AM:58:ALA:HB2	1:AM:102:GLY:HA3	1.93	0.51
1:AP:67:VAL:HG23	1:AP:135:LEU:HB2	1.93	0.51
1:AP:226:VAL:HG13	1:AP:228:GLY:H	1.75	0.51
1:AQ:189:PHE:CE1	1:AQ:198:ARG:CG	2.94	0.51
1:AQ:272:TYR:CD2	1:BL:55:ARG:HD3	2.45	0.51
1:AR:191:LEU:CD2	1:AR:191:LEU:N	2.73	0.51
1:BE:162:PHE:CD2	1:BE:163:LEU:HD13	2.46	0.51
1:BJ:379:VAL:CG1	1:BJ:381:MET:HE1	2.41	0.51
1:BO:30:SER:O	1:BO:33:LYS:HB2	2.11	0.51
1:CC:404:LEU:HD22	1:CC:486:VAL:HG22	1.92	0.51
1:CN:38:GLU:HB2	1:CR:35:VAL:HG22	1.92	0.51
1:CT:263:ASN:O	1:CT:267:LYS:HG3	2.11	0.51
1:AD:170:PHE:CD1	1:AD:389:MET:HE1	2.41	0.51
1:AD:263:ASN:O	1:AD:267:LYS:HG3	2.10	0.51
1:AF:191:LEU:HD23	1:AF:191:LEU:N	2.21	0.51
1:AK:43:ALA:HB1	1:AK:158:GLU:HA	1.93	0.51
1:AN:365:ILE:HD12	1:AN:471:MET:HE2	1.93	0.51
1:AQ:14:CYS:H	1:AQ:138:ASN:HD21	1.58	0.51
1:BK:454:ASN:HD21	1:BK:456:ALA:HB3	1.76	0.51
1:BM:454:ASN:ND2	1:BM:456:ALA:H	2.04	0.51
1:BO:272:TYR:N	1:BO:272:TYR:HD1	2.08	0.51
1:CA:365:ILE:HD12	1:CA:471:MET:HE2	1.91	0.51
1:CB:43:ALA:HB1	1:CB:158:GLU:HA	1.92	0.51
1:CD:250:TRP:HZ3	1:CD:272:TYR:CE1	2.26	0.51
1:CE:30:SER:O	1:CE:33:LYS:HB2	2.11	0.51
1:CK:189:PHE:CE1	1:CK:198:ARG:CG	2.94	0.51
1:CO:189:PHE:HE1	1:CO:198:ARG:CG	2.19	0.51
1:CP:189:PHE:HE1	1:CP:198:ARG:CG	2.23	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:80:ILE:O	1:CR:83:SER:O	2.29	0.51
1:CR:86:PRO:O	1:CR:88:TYR:CA	2.56	0.51
1:AA:189:PHE:HE2	1:AA:249:LEU:HD21	1.74	0.51
1:AC:250:TRP:HZ3	1:AC:272:TYR:CE1	2.26	0.51
1:AG:262:TRP:O	1:AG:265:LEU:N	2.43	0.51
1:AH:454:ASN:HD21	1:AH:456:ALA:HB3	1.76	0.51
1:AO:43:ALA:HB1	1:AO:158:GLU:HA	1.91	0.51
1:BF:55:ARG:HD3	1:CH:272:TYR:HD2	1.75	0.51
1:BJ:30:SER:O	1:BJ:33:LYS:HB2	2.09	0.51
1:BP:55:ARG:HD3	1:CM:272:TYR:CE2	2.46	0.51
1:BS:74:ASN:ND2	1:BS:77:THR:OG1	2.44	0.51
1:CL:288:HIS:HD2	1:CL:337:ASP:OD2	1.94	0.51
1:CN:14:CYS:H	1:CN:138:ASN:ND2	2.09	0.51
1:CQ:398:GLY:HA3	1:CQ:494:PHE:CD2	2.46	0.51
1:AB:261:ASP:CG	1:AB:261:ASP:O	2.51	0.51
1:AF:58:ALA:HB2	1:AF:102:GLY:HA3	1.93	0.51
1:AF:239:ILE:HG12	1:AF:326:ILE:CD1	2.41	0.51
1:AF:324:LEU:C	1:AF:324:LEU:HD23	2.36	0.51
1:AN:67:VAL:HG23	1:AN:135:LEU:HB2	1.93	0.51
1:AO:299:SER:C	1:AO:301:ARG:N	2.68	0.51
1:AP:288:HIS:HD2	1:AP:337:ASP:OD2	1.94	0.51
1:BB:398:GLY:HA3	1:BB:494:PHE:CD2	2.46	0.51
1:BD:30:SER:O	1:BD:33:LYS:HB2	2.10	0.51
1:BL:189:PHE:HD2	1:BL:247:ILE:HD11	1.76	0.51
1:BP:191:LEU:CD2	1:BP:191:LEU:N	2.73	0.51
1:BT:30:SER:O	1:BT:33:LYS:HB2	2.11	0.51
1:CB:232:THR:HB	1:CB:334:VAL:CG2	2.41	0.51
1:CB:250:TRP:HZ3	1:CB:272:TYR:CE1	2.25	0.51
1:AD:14:CYS:H	1:AD:138:ASN:ND2	2.09	0.50
1:AG:75:ARG:NH2	1:AG:391:ALA:O	2.45	0.50
1:AG:263:ASN:O	1:BG:32:PHE:HE1	1.93	0.50
1:AL:398:GLY:HA3	1:AL:494:PHE:CD2	2.46	0.50
1:AM:191:LEU:CD2	1:AM:191:LEU:N	2.73	0.50
1:AR:14:CYS:H	1:AR:138:ASN:ND2	2.07	0.50
1:BH:55:ARG:HD3	1:BK:272:TYR:CE2	2.45	0.50
1:BJ:239:ILE:HG12	1:BJ:326:ILE:CD1	2.41	0.50
1:BM:250:TRP:CE3	1:BM:272:TYR:CE1	2.99	0.50
1:BQ:30:SER:O	1:BQ:33:LYS:HB2	2.12	0.50
1:BS:162:PHE:CD2	1:BS:163:LEU:HD13	2.46	0.50
1:BT:191:LEU:CD2	1:BT:191:LEU:N	2.74	0.50
1:CC:55:ARG:CZ	1:CT:272:TYR:CE2	2.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:25:ILE:HG23	1:CG:152:LEU:HD11	1.93	0.50
1:CH:191:LEU:CD2	1:CH:191:LEU:N	2.75	0.50
1:CH:398:GLY:HA3	1:CH:494:PHE:CD2	2.45	0.50
1:CI:58:ALA:HB2	1:CI:102:GLY:HA3	1.93	0.50
1:CI:404:LEU:HD22	1:CI:486:VAL:HG22	1.92	0.50
1:CL:170:PHE:CD1	1:CL:389:MET:HE1	2.44	0.50
1:CP:239:ILE:HG12	1:CP:326:ILE:CD1	2.41	0.50
1:CQ:191:LEU:CD2	1:CQ:191:LEU:N	2.73	0.50
1:AB:79:ARG:HH11	1:AB:79:ARG:CG	2.22	0.50
1:AD:5:ARG:HD3	1:AN:263:ASN:HD22	1.75	0.50
1:AD:170:PHE:HD1	1:AD:389:MET:CE	2.24	0.50
1:AD:454:ASN:HD21	1:AD:456:ALA:HB3	1.75	0.50
1:AG:38:GLU:HB3	1:CF:35:VAL:HG23	1.93	0.50
1:AH:436:SER:O	1:AI:487:LEU:HD21	2.11	0.50
1:AI:79:ARG:HH11	1:AI:79:ARG:CG	2.19	0.50
1:AJ:189:PHE:HD2	1:AJ:247:ILE:CD1	2.24	0.50
1:AL:418:SER:HB3	1:AM:407:SER:HB3	1.93	0.50
1:AM:365:ILE:HD12	1:AM:471:MET:HE2	1.94	0.50
1:AO:25:ILE:HG23	1:AO:152:LEU:HD11	1.93	0.50
1:AP:454:ASN:ND2	1:AP:456:ALA:H	2.05	0.50
1:AS:250:TRP:CE3	1:AS:272:TYR:CD1	2.99	0.50
1:AT:67:VAL:HG23	1:AT:135:LEU:HB2	1.93	0.50
1:BD:272:TYR:HE2	1:BS:55:ARG:NE	2.04	0.50
1:BI:67:VAL:HG23	1:BI:135:LEU:HB2	1.93	0.50
1:BM:162:PHE:CD2	1:BM:163:LEU:HD13	2.46	0.50
1:CC:191:LEU:CD2	1:CC:191:LEU:N	2.74	0.50
1:CM:379:VAL:CG1	1:CM:381:MET:HE1	2.40	0.50
1:AA:191:LEU:CD2	1:AA:191:LEU:N	2.74	0.50
1:AC:30:SER:O	1:AC:33:LYS:HB2	2.11	0.50
1:AI:14:CYS:H	1:AI:138:ASN:ND2	2.08	0.50
1:AJ:74:ASN:ND2	1:AJ:77:THR:OG1	2.44	0.50
1:AL:30:SER:O	1:AL:33:LYS:HB2	2.12	0.50
1:AP:55:ARG:HD3	1:BM:272:TYR:CE2	2.47	0.50
1:BA:191:LEU:HD23	1:BA:191:LEU:N	2.21	0.50
1:BB:58:ALA:HB2	1:BB:102:GLY:HA3	1.92	0.50
1:BJ:16:ALA:O	1:BJ:17:ASN:HB2	2.11	0.50
1:BR:288:HIS:HD2	1:BR:337:ASP:OD2	1.93	0.50
1:BT:189:PHE:HE2	1:BT:249:LEU:HD21	1.76	0.50
1:BT:234:ARG:HG2	1:BT:280:GLU:HG2	1.94	0.50
1:CJ:272:TYR:N	1:CJ:272:TYR:CD1	2.80	0.50
1:CK:14:CYS:H	1:CK:138:ASN:ND2	2.08	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:43:ALA:HB1	1:CK:158:GLU:HA	1.93	0.50
1:CL:67:VAL:HG23	1:CL:135:LEU:HB2	1.93	0.50
1:CS:30:SER:O	1:CS:33:LYS:HB2	2.12	0.50
1:AE:191:LEU:CD2	1:AE:191:LEU:N	2.74	0.50
1:BG:398:GLY:HA3	1:BG:494:PHE:CD2	2.47	0.50
1:BL:454:ASN:ND2	1:BL:456:ALA:H	2.06	0.50
1:BO:272:TYR:CD1	1:BO:272:TYR:N	2.79	0.50
1:BR:250:TRP:HZ3	1:BR:272:TYR:CE1	2.27	0.50
1:CA:189:PHE:HE1	1:CA:198:ARG:CG	2.24	0.50
1:CD:170:PHE:CD1	1:CD:389:MET:HE1	2.42	0.50
1:CG:250:TRP:HZ3	1:CG:272:TYR:CE1	2.23	0.50
1:CJ:74:ASN:ND2	1:CJ:77:THR:OG1	2.44	0.50
1:CM:272:TYR:N	1:CM:272:TYR:CD1	2.79	0.50
1:CM:272:TYR:N	1:CM:272:TYR:HD1	2.09	0.50
1:AB:239:ILE:HG12	1:AB:326:ILE:CD1	2.41	0.50
1:AB:261:ASP:OD1	1:AB:261:ASP:O	2.30	0.50
1:AC:191:LEU:CD2	1:AC:191:LEU:N	2.73	0.50
1:AG:259:THR:HG21	1:AG:268:TYR:CZ	2.45	0.50
1:AH:272:TYR:CD2	1:CF:55:ARG:CZ	2.94	0.50
1:AI:239:ILE:HG12	1:AI:326:ILE:CD1	2.42	0.50
1:AJ:170:PHE:CD1	1:AJ:389:MET:HE1	2.43	0.50
1:AK:16:ALA:O	1:AK:17:ASN:HB2	2.12	0.50
1:AS:189:PHE:CE1	1:AS:198:ARG:CG	2.95	0.50
1:BM:43:ALA:HB1	1:BM:158:GLU:HA	1.92	0.50
1:BN:263:ASN:O	1:BN:267:LYS:HG3	2.12	0.50
1:BP:47:MET:HE2	1:BP:117:ALA:N	2.25	0.50
1:CB:189:PHE:CE1	1:CB:198:ARG:HG2	2.46	0.50
1:CD:365:ILE:HD12	1:CD:471:MET:HE2	1.93	0.50
1:CI:226:VAL:HG13	1:CI:228:GLY:H	1.76	0.50
1:CI:454:ASN:ND2	1:CI:456:ALA:H	2.08	0.50
1:CR:58:ALA:HB2	1:CR:102:GLY:HA3	1.94	0.50
1:CS:324:LEU:HD23	1:CS:324:LEU:C	2.36	0.50
1:AC:58:ALA:HB2	1:AC:102:GLY:HA3	1.94	0.50
1:AH:226:VAL:HG13	1:AH:228:GLY:H	1.76	0.50
1:AI:226:VAL:HG13	1:AI:228:GLY:H	1.76	0.50
1:AO:272:TYR:N	1:AO:272:TYR:HD1	2.10	0.50
1:AR:442:GLN:HE21	1:AS:412:PHE:HB2	1.76	0.50
1:AT:162:PHE:CD2	1:AT:163:LEU:HD13	2.47	0.50
1:BA:454:ASN:HD21	1:BA:456:ALA:HB3	1.77	0.50
1:BB:272:TYR:N	1:BB:272:TYR:CD1	2.79	0.50
1:BC:55:ARG:NE	1:BT:272:TYR:CE2	2.79	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BO:189:PHE:HD2	1:BO:247:ILE:HD11	1.77	0.50
1:BS:250:TRP:HZ3	1:BS:272:TYR:CE1	2.27	0.50
1:CC:58:ALA:HB2	1:CC:102:GLY:HA3	1.94	0.50
1:CI:191:LEU:HD23	1:CI:191:LEU:N	2.17	0.50
1:CJ:379:VAL:CG1	1:CJ:381:MET:HE1	2.42	0.50
1:CN:189:PHE:HD2	1:CN:247:ILE:CD1	2.24	0.50
1:CQ:67:VAL:HG23	1:CQ:135:LEU:HB2	1.94	0.50
1:CQ:232:THR:HB	1:CQ:334:VAL:CG2	2.42	0.50
1:AB:61:PHE:CD2	1:AB:243:ILE:HD11	2.47	0.50
1:AC:55:ARG:CZ	1:AT:272:TYR:CE2	2.95	0.50
1:AC:379:VAL:CG1	1:AC:381:MET:HE1	2.42	0.50
1:AC:454:ASN:ND2	1:AC:456:ALA:H	2.06	0.50
1:AI:284:ARG:CG	1:AI:284:ARG:NH1	2.71	0.50
1:AK:189:PHE:HD2	1:AK:247:ILE:HD11	1.77	0.50
1:AN:189:PHE:CE2	1:AN:249:LEU:HD21	2.42	0.50
1:AO:79:ARG:HG3	1:AO:79:ARG:NH1	2.24	0.50
1:AO:189:PHE:CE1	1:AO:198:ARG:CG	2.95	0.50
1:BE:284:ARG:CG	1:BE:284:ARG:NH1	2.72	0.50
1:BI:58:ALA:HB2	1:BI:102:GLY:HA3	1.92	0.50
1:BS:398:GLY:HA3	1:BS:494:PHE:CD2	2.47	0.50
1:CD:442:GLN:NE2	1:CE:412:PHE:HB2	2.27	0.50
1:CL:324:LEU:HD23	1:CL:324:LEU:C	2.37	0.50
1:AA:226:VAL:HG13	1:AA:228:GLY:H	1.77	0.50
1:AB:272:TYR:N	1:AB:272:TYR:HD1	2.09	0.50
1:AF:272:TYR:HD2	1:BK:55:ARG:HD3	1.72	0.50
1:AJ:203:THR:CB	1:AJ:300:GLN:HG3	2.42	0.50
1:AL:226:VAL:HG13	1:AL:228:GLY:H	1.77	0.50
1:AN:14:CYS:HB3	1:AN:64:LEU:HD21	1.94	0.50
1:BD:170:PHE:HD1	1:BD:389:MET:CE	2.24	0.50
1:BD:250:TRP:HZ3	1:BD:272:TYR:CE1	2.27	0.50
1:BD:379:VAL:CG1	1:BD:381:MET:HE1	2.42	0.50
1:BE:67:VAL:HG23	1:BE:135:LEU:HB2	1.94	0.50
1:BF:162:PHE:CD2	1:BF:163:LEU:HD13	2.47	0.50
1:BG:30:SER:O	1:BG:33:LYS:HB2	2.10	0.50
1:BP:67:VAL:HG23	1:BP:135:LEU:HB2	1.93	0.50
1:CB:191:LEU:CD2	1:CB:191:LEU:N	2.74	0.50
1:CF:16:ALA:O	1:CF:17:ASN:HB2	2.12	0.50
1:CO:16:ALA:O	1:CO:17:ASN:HB2	2.11	0.50
1:CQ:79:ARG:HH11	1:CQ:79:ARG:HG3	1.77	0.50
1:CQ:232:THR:HB	1:CQ:334:VAL:HG23	1.93	0.50
1:AE:58:ALA:HB2	1:AE:102:GLY:HA3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:67:VAL:HG23	1:AE:135:LEU:HB2	1.93	0.50
1:AE:197:LEU:HD12	1:AE:198:ARG:N	2.26	0.50
1:AF:398:GLY:HA3	1:AF:494:PHE:CD2	2.46	0.50
1:AK:454:ASN:ND2	1:AK:456:ALA:H	2.07	0.50
1:AL:272:TYR:HE2	1:CJ:55:ARG:NE	1.87	0.50
1:AQ:232:THR:HB	1:AQ:334:VAL:HG23	1.94	0.50
1:BA:16:ALA:O	1:BA:17:ASN:HB2	2.11	0.50
1:BE:239:ILE:HG12	1:BE:326:ILE:CD1	2.42	0.50
1:BF:170:PHE:HD1	1:BF:389:MET:CE	2.24	0.50
1:BF:272:TYR:CD2	1:CK:55:ARG:CZ	2.95	0.50
1:BH:15:GLN:HE21	1:BH:15:GLN:CA	2.09	0.50
1:BO:189:PHE:HE2	1:BO:249:LEU:CD2	2.24	0.50
1:BQ:58:ALA:HB2	1:BQ:102:GLY:HA3	1.94	0.50
1:BS:191:LEU:CD2	1:BS:191:LEU:N	2.75	0.50
1:CB:454:ASN:ND2	1:CB:456:ALA:H	2.08	0.50
1:CH:18:ARG:HG3	1:CH:19:TYR:N	2.26	0.50
1:CH:55:ARG:HD3	1:CK:272:TYR:CE2	2.47	0.50
1:CL:14:CYS:HB3	1:CL:64:LEU:HD21	1.93	0.50
1:CN:170:PHE:HD1	1:CN:389:MET:CE	2.23	0.50
1:CT:379:VAL:CG1	1:CT:381:MET:HE1	2.42	0.50
1:AF:30:SER:O	1:AF:33:LYS:HB2	2.12	0.49
1:AL:454:ASN:ND2	1:AL:456:ALA:H	2.05	0.49
1:BA:47:MET:HE2	1:BA:117:ALA:N	2.27	0.49
1:BE:189:PHE:HE1	1:BE:198:ARG:HG2	1.73	0.49
1:BF:189:PHE:HE1	1:BF:198:ARG:HG2	1.75	0.49
1:BN:14:CYS:H	1:BN:138:ASN:HD21	1.58	0.49
1:BO:74:ASN:ND2	1:BO:77:THR:OG1	2.45	0.49
1:BS:454:ASN:ND2	1:BS:456:ALA:H	2.03	0.49
1:BT:189:PHE:HD2	1:BT:247:ILE:HD11	1.77	0.49
1:CB:25:ILE:HG23	1:CB:152:LEU:HD11	1.94	0.49
1:CD:418:SER:HB3	1:CE:407:SER:HB3	1.93	0.49
1:CE:272:TYR:N	1:CE:272:TYR:CD1	2.80	0.49
1:CG:239:ILE:HD12	1:CG:275:GLU:HA	1.94	0.49
1:CH:454:ASN:ND2	1:CH:456:ALA:H	2.06	0.49
1:CP:189:PHE:HD2	1:CP:247:ILE:HD11	1.77	0.49
1:AI:55:ARG:HD3	1:AR:272:TYR:CE2	2.44	0.49
1:AK:79:ARG:HH11	1:AK:79:ARG:HG3	1.77	0.49
1:AO:189:PHE:HE1	1:AO:198:ARG:CG	2.24	0.49
1:AS:182:LEU:C	1:AS:182:LEU:HD12	2.37	0.49
1:BJ:191:LEU:CD2	1:BJ:191:LEU:N	2.70	0.49
1:BJ:404:LEU:HD22	1:BJ:486:VAL:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:75:ARG:NH2	1:BQ:391:ALA:O	2.43	0.49
1:BS:189:PHE:HE2	1:BS:249:LEU:HD21	1.77	0.49
1:CA:170:PHE:CD1	1:CA:389:MET:HE1	2.39	0.49
1:CB:74:ASN:ND2	1:CB:77:THR:OG1	2.44	0.49
1:CB:232:THR:HB	1:CB:334:VAL:HG23	1.93	0.49
1:CB:454:ASN:HD21	1:CB:456:ALA:HB3	1.77	0.49
1:CD:189:PHE:CE1	1:CD:198:ARG:CG	2.96	0.49
1:CH:189:PHE:HD2	1:CH:247:ILE:CD1	2.25	0.49
1:CL:203:THR:HB	1:CL:300:GLN:HG3	1.94	0.49
1:CN:67:VAL:HG23	1:CN:135:LEU:HB2	1.94	0.49
1:CQ:189:PHE:HE2	1:CQ:249:LEU:HD21	1.77	0.49
1:AB:189:PHE:HD2	1:AB:247:ILE:CD1	2.25	0.49
1:AC:79:ARG:HG3	1:AC:79:ARG:HH11	1.76	0.49
1:AE:16:ALA:O	1:AE:17:ASN:HB2	2.11	0.49
1:AE:398:GLY:HA3	1:AE:494:PHE:CD2	2.47	0.49
1:AN:58:ALA:HB2	1:AN:102:GLY:HA3	1.94	0.49
1:AP:239:ILE:HG12	1:AP:326:ILE:CD1	2.42	0.49
1:AQ:418:SER:HB3	1:AR:407:SER:HB3	1.94	0.49
1:BG:189:PHE:CE2	1:BG:249:LEU:HD21	2.44	0.49
1:BG:191:LEU:CD2	1:BG:191:LEU:N	2.75	0.49
1:BJ:454:ASN:ND2	1:BJ:456:ALA:H	2.07	0.49
1:BR:79:ARG:HG3	1:BR:79:ARG:NH1	2.22	0.49
1:CF:454:ASN:HD21	1:CF:456:ALA:HB3	1.78	0.49
1:CG:191:LEU:CD2	1:CG:191:LEU:N	2.75	0.49
1:CK:239:ILE:HD12	1:CK:275:GLU:HA	1.94	0.49
1:CN:30:SER:O	1:CN:33:LYS:HB2	2.11	0.49
1:CO:77:THR:O	1:CO:81:THR:HG23	2.11	0.49
1:CO:284:ARG:CG	1:CO:284:ARG:NH1	2.72	0.49
1:CO:288:HIS:HD2	1:CO:337:ASP:OD2	1.95	0.49
1:CO:379:VAL:CG1	1:CO:381:MET:HE1	2.40	0.49
1:AA:75:ARG:NH2	1:AA:391:ALA:O	2.45	0.49
1:AB:30:SER:O	1:AB:33:LYS:HB2	2.12	0.49
1:AC:189:PHE:CE1	1:AC:198:ARG:CG	2.95	0.49
1:AF:365:ILE:HD12	1:AF:471:MET:HE2	1.95	0.49
1:AG:74:ASN:ND2	1:AG:77:THR:OG1	2.46	0.49
1:AL:75:ARG:NH2	1:AL:391:ALA:O	2.46	0.49
1:AM:162:PHE:CD2	1:AM:163:LEU:HD13	2.48	0.49
1:AQ:454:ASN:HD21	1:AQ:456:ALA:HB3	1.78	0.49
1:AR:30:SER:O	1:AR:33:LYS:HB2	2.12	0.49
1:BB:18:ARG:NH1	1:BB:18:ARG:HB2	2.27	0.49
1:BD:189:PHE:HD2	1:BD:247:ILE:HD11	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:272:TYR:N	1:BD:272:TYR:HD1	2.10	0.49
1:BF:16:ALA:O	1:BF:17:ASN:HB2	2.11	0.49
1:BH:191:LEU:HD23	1:BH:191:LEU:N	2.19	0.49
1:BP:162:PHE:CD2	1:BP:163:LEU:HD13	2.47	0.49
1:BR:170:PHE:CD1	1:BR:389:MET:HE1	2.43	0.49
1:CC:272:TYR:CD1	1:CC:272:TYR:N	2.78	0.49
1:CE:189:PHE:CE2	1:CE:249:LEU:HD21	2.45	0.49
1:CI:191:LEU:CD2	1:CI:191:LEU:N	2.73	0.49
1:CK:191:LEU:CD2	1:CK:191:LEU:N	2.75	0.49
1:CK:239:ILE:HG12	1:CK:326:ILE:CD1	2.42	0.49
1:CS:189:PHE:HE2	1:CS:249:LEU:HD21	1.77	0.49
1:AA:252:VAL:HG22	1:AA:253:SER:N	2.28	0.49
1:AB:262:TRP:HA	1:AB:265:LEU:HB3	1.95	0.49
1:AF:162:PHE:CD2	1:AF:163:LEU:HD13	2.47	0.49
1:AR:162:PHE:CD2	1:AR:163:LEU:HD13	2.46	0.49
1:AS:272:TYR:N	1:AS:272:TYR:CD1	2.80	0.49
1:AT:58:ALA:HB2	1:AT:102:GLY:HA3	1.93	0.49
1:BA:272:TYR:CD1	1:BA:272:TYR:N	2.80	0.49
1:BC:189:PHE:HE2	1:BC:249:LEU:CD2	2.26	0.49
1:BD:189:PHE:CE1	1:BD:198:ARG:CG	2.95	0.49
1:BI:55:ARG:NH1	1:BR:272:TYR:CD2	2.81	0.49
1:BP:55:ARG:HD3	1:CM:272:TYR:CD2	2.47	0.49
1:CD:191:LEU:HD23	1:CD:191:LEU:N	2.18	0.49
1:CF:189:PHE:HD2	1:CF:247:ILE:CD1	2.26	0.49
1:CH:442:GLN:HE21	1:CI:412:PHE:HB2	1.77	0.49
1:CJ:30:SER:O	1:CJ:33:LYS:HB2	2.12	0.49
1:CK:189:PHE:HE2	1:CK:249:LEU:CD2	2.25	0.49
1:CP:191:LEU:CD2	1:CP:191:LEU:N	2.73	0.49
1:CP:272:TYR:N	1:CP:272:TYR:HD1	2.10	0.49
1:CT:454:ASN:ND2	1:CT:456:ALA:H	2.06	0.49
1:AC:16:ALA:O	1:AC:17:ASN:HB2	2.13	0.49
1:AD:272:TYR:CD2	1:AS:55:ARG:CZ	2.96	0.49
1:AH:30:SER:O	1:AH:33:LYS:HB2	2.12	0.49
1:AL:189:PHE:HE1	1:AL:198:ARG:CG	2.24	0.49
1:AM:379:VAL:CG1	1:AM:381:MET:HE1	2.42	0.49
1:AO:284:ARG:CG	1:AO:284:ARG:NH1	2.71	0.49
1:AQ:232:THR:HB	1:AQ:334:VAL:CG2	2.43	0.49
1:AQ:239:ILE:HD12	1:AQ:275:GLU:HA	1.94	0.49
1:BB:189:PHE:HD2	1:BB:247:ILE:CD1	2.24	0.49
1:BC:67:VAL:HG23	1:BC:135:LEU:HB2	1.94	0.49
1:BE:170:PHE:CD1	1:BE:389:MET:HE1	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:250:TRP:HZ3	1:BF:272:TYR:CE1	2.26	0.49
1:BI:162:PHE:CD2	1:BI:163:LEU:HD13	2.47	0.49
1:CI:398:GLY:HA3	1:CI:494:PHE:CD2	2.47	0.49
1:CO:18:ARG:HG3	1:CO:19:TYR:N	2.27	0.49
1:AC:55:ARG:NE	1:AT:272:TYR:HE2	2.02	0.49
1:AR:189:PHE:HD2	1:AR:247:ILE:CD1	2.26	0.49
1:BJ:55:ARG:HD3	1:CL:272:TYR:CE2	2.46	0.49
1:CC:189:PHE:CE1	1:CC:198:ARG:CG	2.96	0.49
1:CG:189:PHE:HD2	1:CG:247:ILE:HD11	1.77	0.49
1:CJ:16:ALA:O	1:CJ:17:ASN:HB2	2.11	0.49
1:CL:454:ASN:HD21	1:CL:456:ALA:HB3	1.77	0.49
1:CM:189:PHE:CE1	1:CM:198:ARG:HG2	2.47	0.49
1:CM:191:LEU:CD2	1:CM:191:LEU:N	2.74	0.49
1:CP:398:GLY:HA3	1:CP:494:PHE:CD2	2.48	0.49
1:CR:454:ASN:HD21	1:CR:456:ALA:HB3	1.77	0.49
1:AG:189:PHE:HD2	1:AG:247:ILE:CD1	2.25	0.49
1:AH:189:PHE:CE2	1:AH:249:LEU:HD21	2.44	0.49
1:AI:191:LEU:HD23	1:AI:191:LEU:N	2.19	0.49
1:AI:250:TRP:CE3	1:AI:272:TYR:CE1	3.01	0.49
1:AJ:30:SER:O	1:AJ:33:LYS:HB2	2.13	0.49
1:AK:284:ARG:CG	1:AK:284:ARG:NH1	2.70	0.49
1:AM:189:PHE:CE2	1:AM:249:LEU:HD21	2.45	0.49
1:AQ:170:PHE:CD1	1:AQ:389:MET:HE1	2.42	0.49
1:AQ:272:TYR:CE2	1:BL:55:ARG:HD3	2.48	0.49
1:AR:272:TYR:N	1:AR:272:TYR:CD1	2.80	0.49
1:AS:188:PHE:C	1:AS:189:PHE:HD1	2.20	0.49
1:BB:365:ILE:HD12	1:BB:471:MET:HE2	1.94	0.49
1:BH:191:LEU:CD2	1:BH:191:LEU:N	2.76	0.49
1:BI:189:PHE:HD2	1:BI:247:ILE:HD11	1.76	0.49
1:BI:454:ASN:HD21	1:BI:456:ALA:HB3	1.78	0.49
1:BJ:58:ALA:HB2	1:BJ:102:GLY:HA3	1.94	0.49
1:BM:189:PHE:CE2	1:BM:249:LEU:HD21	2.42	0.49
1:BP:263:ASN:O	1:BP:267:LYS:HG3	2.13	0.49
1:BS:67:VAL:HG23	1:BS:135:LEU:HB2	1.95	0.49
1:CG:288:HIS:HD2	1:CG:337:ASP:OD2	1.95	0.49
1:AB:189:PHE:HE1	1:AB:198:ARG:HG2	1.74	0.49
1:AH:170:PHE:CD1	1:AH:389:MET:HE1	2.46	0.49
1:AL:67:VAL:HG23	1:AL:135:LEU:HB2	1.94	0.49
1:BD:272:TYR:N	1:BD:272:TYR:CD1	2.81	0.49
1:BJ:272:TYR:CE2	1:BQ:55:ARG:HD3	2.48	0.49
1:BO:272:TYR:HD2	1:BR:55:ARG:HD3	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:191:LEU:CD2	1:BQ:191:LEU:N	2.76	0.49
1:BQ:379:VAL:CG1	1:BQ:381:MET:HE1	2.43	0.49
1:BR:75:ARG:NH2	1:BR:391:ALA:O	2.46	0.49
1:BT:12:LYS:HB3	1:BT:144:ALA:C	2.37	0.49
1:CE:14:CYS:H	1:CE:138:ASN:ND2	2.11	0.49
1:CF:58:ALA:HB2	1:CF:102:GLY:HA3	1.94	0.49
1:CF:189:PHE:CE1	1:CF:198:ARG:HG2	2.47	0.49
1:CK:188:PHE:C	1:CK:189:PHE:HD1	2.21	0.49
1:CM:189:PHE:HD2	1:CM:247:ILE:CD1	2.25	0.49
1:CN:454:ASN:HD21	1:CN:456:ALA:HB3	1.77	0.49
1:CO:189:PHE:HE2	1:CO:249:LEU:HD21	1.78	0.49
1:CO:393:HIS:CG	1:CO:496:PHE:HB3	2.48	0.49
1:CO:454:ASN:HD22	1:CO:456:ALA:N	2.06	0.49
1:CR:454:ASN:ND2	1:CR:456:ALA:H	2.02	0.49
1:CS:74:ASN:ND2	1:CS:77:THR:OG1	2.46	0.49
1:CT:299:SER:O	1:CT:302:ASP:HB2	2.13	0.49
1:AG:162:PHE:CD2	1:AG:163:LEU:HD13	2.48	0.49
1:AS:58:ALA:HB2	1:AS:102:GLY:HA3	1.95	0.49
1:AS:232:THR:HB	1:AS:334:VAL:CG2	2.43	0.49
1:BA:454:ASN:ND2	1:BA:456:ALA:H	2.05	0.49
1:BB:272:TYR:N	1:BB:272:TYR:HD1	2.11	0.49
1:BC:404:LEU:HD22	1:BC:486:VAL:HG22	1.95	0.49
1:BE:272:TYR:CD2	1:BM:55:ARG:HD3	2.47	0.49
1:BE:398:GLY:HA3	1:BE:494:PHE:CD2	2.48	0.49
1:BH:379:VAL:CG1	1:BH:381:MET:HE1	2.43	0.49
1:BK:189:PHE:HE2	1:BK:249:LEU:HD21	1.78	0.49
1:CA:170:PHE:HD1	1:CA:389:MET:CE	2.23	0.49
1:CA:239:ILE:HG12	1:CA:326:ILE:CD1	2.43	0.49
1:CC:454:ASN:ND2	1:CC:456:ALA:H	2.06	0.49
1:CN:191:LEU:HD23	1:CN:191:LEU:N	2.19	0.49
1:AH:189:PHE:HD2	1:AH:247:ILE:CD1	2.26	0.48
1:AL:324:LEU:C	1:AL:324:LEU:HD23	2.38	0.48
1:AO:18:ARG:HG3	1:AO:19:TYR:N	2.28	0.48
1:BB:191:LEU:HD23	1:BB:191:LEU:N	2.17	0.48
1:BH:239:ILE:HG12	1:BH:326:ILE:CD1	2.42	0.48
1:BJ:272:TYR:CD2	1:BQ:55:ARG:CD	2.95	0.48
1:BM:191:LEU:CD2	1:BM:191:LEU:N	2.74	0.48
1:BP:272:TYR:N	1:BP:272:TYR:HD1	2.11	0.48
1:CE:250:TRP:HZ3	1:CE:272:TYR:CE1	2.29	0.48
1:CO:272:TYR:CD2	1:CR:55:ARG:NH1	2.81	0.48
1:CR:30:SER:O	1:CR:33:LYS:HB2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CS:272:TYR:N	1:CS:272:TYR:HD1	2.11	0.48
1:CT:189:PHE:HE2	1:CT:249:LEU:HD21	1.78	0.48
1:AB:162:PHE:CD2	1:AB:163:LEU:HD13	2.48	0.48
1:AB:262:TRP:N	1:AB:262:TRP:HD1	2.11	0.48
1:AD:30:SER:O	1:AD:33:LYS:HB2	2.13	0.48
1:AH:443:LYS:HE2	1:AI:444:LEU:HB2	1.95	0.48
1:AQ:170:PHE:HD1	1:AQ:389:MET:CE	2.25	0.48
1:AT:170:PHE:HD1	1:AT:389:MET:CE	2.25	0.48
1:BC:226:VAL:HG13	1:BC:228:GLY:H	1.77	0.48
1:BD:43:ALA:HB1	1:BD:158:GLU:HA	1.94	0.48
1:BF:191:LEU:CD2	1:BF:191:LEU:N	2.74	0.48
1:BK:43:ALA:HB1	1:BK:158:GLU:HA	1.95	0.48
1:BN:454:ASN:HD21	1:BN:456:ALA:HB3	1.78	0.48
1:BP:189:PHE:HE2	1:BP:249:LEU:HD21	1.79	0.48
1:CB:324:LEU:HD23	1:CB:324:LEU:C	2.37	0.48
1:CD:440:ALA:HB3	1:CE:444:LEU:HD13	1.95	0.48
1:CH:189:PHE:CE2	1:CH:249:LEU:HD21	2.45	0.48
1:CJ:43:ALA:HB1	1:CJ:158:GLU:HA	1.95	0.48
1:CJ:170:PHE:HD1	1:CJ:389:MET:CE	2.23	0.48
1:CM:398:GLY:HA3	1:CM:494:PHE:CD2	2.48	0.48
1:CT:398:GLY:HA3	1:CT:494:PHE:CD2	2.47	0.48
1:AA:55:ARG:CZ	1:CC:272:TYR:CE2	2.96	0.48
1:AD:272:TYR:CE2	1:AS:55:ARG:CZ	2.96	0.48
1:AH:324:LEU:HD23	1:AH:324:LEU:C	2.38	0.48
1:AT:191:LEU:CD2	1:AT:191:LEU:N	2.76	0.48
1:BG:226:VAL:HG13	1:BG:228:GLY:H	1.78	0.48
1:BH:67:VAL:HG23	1:BH:135:LEU:HB2	1.96	0.48
1:BR:74:ASN:ND2	1:BR:77:THR:OG1	2.46	0.48
1:CB:263:ASN:O	1:CB:267:LYS:HG3	2.12	0.48
1:CD:74:ASN:ND2	1:CD:77:THR:OG1	2.46	0.48
1:CD:272:TYR:HD2	1:CS:55:ARG:HD3	1.75	0.48
1:CD:393:HIS:CG	1:CD:496:PHE:HB3	2.48	0.48
1:AB:67:VAL:HG23	1:AB:135:LEU:HB2	1.96	0.48
1:AG:259:THR:HG22	1:AG:268:TYR:OH	2.14	0.48
1:AJ:35:VAL:HG22	1:BK:38:GLU:HB2	1.94	0.48
1:AJ:239:ILE:HD12	1:AJ:275:GLU:HA	1.94	0.48
1:AN:232:THR:HB	1:AN:334:VAL:HG23	1.96	0.48
1:AO:454:ASN:ND2	1:AO:456:ALA:H	2.06	0.48
1:AP:22:THR:OG1	1:AP:131:HIS:CD2	2.58	0.48
1:BA:67:VAL:HG23	1:BA:135:LEU:HB2	1.94	0.48
1:BA:272:TYR:N	1:BA:272:TYR:HD1	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:454:ASN:HD21	1:BF:456:ALA:HB3	1.78	0.48
1:BH:189:PHE:CE2	1:BH:249:LEU:HD21	2.44	0.48
1:BN:74:ASN:ND2	1:BN:77:THR:OG1	2.45	0.48
1:BT:16:ALA:O	1:BT:17:ASN:HB2	2.14	0.48
1:CA:191:LEU:CD2	1:CA:191:LEU:N	2.74	0.48
1:CD:272:TYR:N	1:CD:272:TYR:CD1	2.82	0.48
1:CH:162:PHE:CD2	1:CH:163:LEU:HD13	2.49	0.48
1:CH:239:ILE:HG12	1:CH:326:ILE:CD1	2.42	0.48
1:CI:189:PHE:HD2	1:CI:247:ILE:CD1	2.25	0.48
1:CM:239:ILE:HD12	1:CM:275:GLU:HA	1.94	0.48
1:CS:11:PRO:HG2	1:CS:18:ARG:CD	2.43	0.48
1:CT:272:TYR:N	1:CT:272:TYR:CD1	2.82	0.48
1:AA:250:TRP:HZ3	1:AA:272:TYR:CE1	2.28	0.48
1:AB:189:PHE:CE1	1:AB:198:ARG:HG2	2.49	0.48
1:AC:188:PHE:C	1:AC:189:PHE:HD1	2.20	0.48
1:AG:67:VAL:HG23	1:AG:135:LEU:HB2	1.96	0.48
1:AK:55:ARG:CD	1:CF:272:TYR:CD2	2.94	0.48
1:AK:440:ALA:HB3	1:AL:444:LEU:HD13	1.96	0.48
1:AP:272:TYR:CD2	1:BE:55:ARG:CD	2.88	0.48
1:AS:284:ARG:CG	1:AS:284:ARG:NH1	2.70	0.48
1:AT:189:PHE:HD2	1:AT:247:ILE:HD11	1.78	0.48
1:BB:234:ARG:HG2	1:BB:280:GLU:HG2	1.95	0.48
1:BD:170:PHE:CD1	1:BD:389:MET:HE1	2.43	0.48
1:BE:263:ASN:HD22	1:BM:5:ARG:HD3	1.78	0.48
1:BG:272:TYR:N	1:BG:272:TYR:CD1	2.82	0.48
1:BO:189:PHE:HE1	1:BO:198:ARG:CG	2.24	0.48
1:BO:239:ILE:HG12	1:BO:326:ILE:CD1	2.44	0.48
1:BT:239:ILE:HG12	1:BT:326:ILE:CD1	2.43	0.48
1:CC:30:SER:O	1:CC:33:LYS:HB2	2.13	0.48
1:CH:284:ARG:CG	1:CH:284:ARG:NH1	2.73	0.48
1:CI:16:ALA:O	1:CI:17:ASN:HB2	2.13	0.48
1:CJ:226:VAL:HG13	1:CJ:228:GLY:H	1.78	0.48
1:CN:189:PHE:HD2	1:CN:247:ILE:HD11	1.77	0.48
1:CO:162:PHE:CD2	1:CO:163:LEU:HD13	2.47	0.48
1:CO:189:PHE:HD2	1:CO:247:ILE:HD11	1.78	0.48
1:CR:191:LEU:HD23	1:CR:191:LEU:N	2.19	0.48
1:AO:14:CYS:H	1:AO:138:ASN:HD21	1.60	0.48
1:AO:289:ARG:NH1	1:AO:338:LEU:O	2.47	0.48
1:AQ:250:TRP:HZ3	1:AQ:272:TYR:CE1	2.26	0.48
1:BA:30:SER:O	1:BA:33:LYS:HB2	2.13	0.48
1:BA:75:ARG:NH2	1:BA:391:ALA:O	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:5:ARG:HD3	1:CB:263:ASN:HD22	1.79	0.48
1:BC:252:VAL:HG22	1:BC:253:SER:N	2.28	0.48
1:BD:189:PHE:HE2	1:BD:249:LEU:HD21	1.79	0.48
1:BE:250:TRP:HZ3	1:BE:272:TYR:CE1	2.29	0.48
1:BN:58:ALA:HB2	1:BN:102:GLY:HA3	1.96	0.48
1:BO:75:ARG:NH2	1:BO:391:ALA:O	2.46	0.48
1:BQ:189:PHE:HD2	1:BQ:247:ILE:HD11	1.79	0.48
1:BS:189:PHE:HD2	1:BS:247:ILE:HD11	1.79	0.48
1:CC:162:PHE:CD2	1:CC:163:LEU:HD13	2.49	0.48
1:CL:189:PHE:HD2	1:CL:247:ILE:HD11	1.77	0.48
1:CL:379:VAL:CG1	1:CL:381:MET:HE1	2.43	0.48
1:CN:170:PHE:CD1	1:CN:389:MET:HE1	2.39	0.48
1:CP:272:TYR:N	1:CP:272:TYR:CD1	2.81	0.48
1:CR:189:PHE:HD2	1:CR:247:ILE:CD1	2.25	0.48
1:AB:191:LEU:CD2	1:AB:191:LEU:N	2.72	0.48
1:AE:55:ARG:HD3	1:CP:272:TYR:HD2	1.77	0.48
1:AG:276:ASP:OD1	1:AG:276:ASP:N	2.30	0.48
1:AG:454:ASN:ND2	1:AG:456:ALA:H	2.08	0.48
1:AI:170:PHE:HD1	1:AI:389:MET:CE	2.24	0.48
1:AJ:250:TRP:CE3	1:AJ:272:TYR:CE1	3.01	0.48
1:AJ:398:GLY:HA3	1:AJ:494:PHE:CD2	2.48	0.48
1:AJ:404:LEU:HD22	1:AJ:486:VAL:HG22	1.95	0.48
1:AK:418:SER:HB3	1:AL:407:SER:HB3	1.94	0.48
1:AM:454:ASN:HD22	1:AM:454:ASN:C	2.22	0.48
1:BB:14:CYS:H	1:BB:138:ASN:ND2	2.12	0.48
1:BF:440:ALA:CB	1:BG:444:LEU:HD13	2.43	0.48
1:BN:189:PHE:HD2	1:BN:247:ILE:CD1	2.26	0.48
1:BP:272:TYR:CD2	1:CE:55:ARG:CD	2.93	0.48
1:BQ:324:LEU:HD23	1:BQ:324:LEU:C	2.39	0.48
1:BS:239:ILE:HG12	1:BS:326:ILE:CD1	2.44	0.48
1:CG:272:TYR:N	1:CG:272:TYR:CD1	2.82	0.48
1:CI:144:ALA:CB	1:CR:191:LEU:O	2.61	0.48
1:CI:324:LEU:HD23	1:CI:324:LEU:C	2.38	0.48
1:CJ:189:PHE:HD2	1:CJ:247:ILE:CD1	2.26	0.48
1:CK:16:ALA:O	1:CK:17:ASN:HB2	2.14	0.48
1:CO:182:LEU:C	1:CO:182:LEU:HD12	2.38	0.48
1:CS:234:ARG:HG2	1:CS:280:GLU:HG2	1.94	0.48
1:AA:379:VAL:CG1	1:AA:381:MET:HE1	2.43	0.48
1:AB:239:ILE:HD12	1:AB:275:GLU:HA	1.96	0.48
1:AE:250:TRP:HZ3	1:AE:272:TYR:CE1	2.28	0.48
1:AE:272:TYR:HD2	1:AM:55:ARG:HD3	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:191:LEU:CD2	1:AG:191:LEU:N	2.74	0.48
1:AL:189:PHE:HD2	1:AL:247:ILE:HD11	1.79	0.48
1:AO:189:PHE:HD2	1:AO:247:ILE:HD11	1.79	0.48
1:AP:404:LEU:HD22	1:AP:486:VAL:HG22	1.94	0.48
1:AQ:191:LEU:CD2	1:AQ:191:LEU:N	2.75	0.48
1:AQ:393:HIS:CG	1:AQ:496:PHE:HB3	2.49	0.48
1:AQ:442:GLN:NE2	1:AR:412:PHE:HB2	2.29	0.48
1:AR:189:PHE:CE1	1:AR:198:ARG:HG2	2.49	0.48
1:AS:234:ARG:HG2	1:AS:280:GLU:HG2	1.96	0.48
1:AT:189:PHE:HE2	1:AT:249:LEU:HD21	1.79	0.48
1:BF:412:PHE:HB2	1:BJ:442:GLN:HE21	1.79	0.48
1:BH:43:ALA:HB1	1:BH:158:GLU:HA	1.95	0.48
1:BK:58:ALA:HB2	1:BK:102:GLY:HA3	1.95	0.48
1:BM:47:MET:HE2	1:BM:117:ALA:N	2.29	0.48
1:BQ:250:TRP:HZ3	1:BQ:272:TYR:CE1	2.27	0.48
1:CF:232:THR:HB	1:CF:334:VAL:CG2	2.43	0.48
1:CG:14:CYS:H	1:CG:138:ASN:ND2	2.10	0.48
1:CH:58:ALA:HB2	1:CH:102:GLY:HA3	1.96	0.48
1:CJ:162:PHE:CD2	1:CJ:163:LEU:HD13	2.49	0.48
1:CJ:324:LEU:C	1:CJ:324:LEU:HD23	2.39	0.48
1:AA:272:TYR:N	1:AA:272:TYR:CD1	2.82	0.48
1:AC:239:ILE:HD12	1:AC:275:GLU:HA	1.94	0.48
1:AD:272:TYR:HD1	1:AD:272:TYR:N	2.12	0.48
1:AF:55:ARG:HD3	1:BH:272:TYR:HD2	1.77	0.48
1:AL:79:ARG:CG	1:AL:79:ARG:NH1	2.71	0.48
1:AP:444:LEU:HD13	1:AT:440:ALA:HB3	1.95	0.48
1:AT:284:ARG:CG	1:AT:284:ARG:NH1	2.73	0.48
1:BB:454:ASN:HD21	1:BB:456:ALA:HB3	1.77	0.48
1:BD:38:GLU:HB2	1:BM:35:VAL:HG22	1.96	0.48
1:BD:201:GLY:HA3	1:BD:300:GLN:HG2	1.96	0.48
1:BE:11:PRO:HG2	1:BE:18:ARG:HD3	1.95	0.48
1:BF:239:ILE:HG12	1:BF:326:ILE:CD1	2.44	0.48
1:BM:170:PHE:CD1	1:BM:389:MET:HE1	2.44	0.48
1:BN:239:ILE:HG12	1:BN:326:ILE:CD1	2.44	0.48
1:BO:189:PHE:HE2	1:BO:249:LEU:HD21	1.79	0.48
1:BO:404:LEU:HD22	1:BO:486:VAL:HG22	1.96	0.48
1:BR:440:ALA:CB	1:BS:444:LEU:HD13	2.44	0.48
1:BS:232:THR:HB	1:BS:334:VAL:HG23	1.96	0.48
1:BT:162:PHE:CD2	1:BT:163:LEU:HD13	2.48	0.48
1:CA:398:GLY:HA3	1:CA:494:PHE:CD2	2.49	0.48
1:CD:272:TYR:N	1:CD:272:TYR:HD1	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:189:PHE:CE1	1:CH:198:ARG:HG2	2.49	0.48
1:CH:454:ASN:HD21	1:CH:456:ALA:HB3	1.79	0.48
1:CN:10:ILE:HD13	1:CN:20:LEU:HD13	1.95	0.48
1:CQ:189:PHE:CE1	1:CQ:198:ARG:CG	2.96	0.48
1:CR:237:VAL:HG23	1:CR:279:PHE:CD2	2.48	0.48
1:AD:189:PHE:HD2	1:AD:247:ILE:HD11	1.79	0.48
1:AF:79:ARG:CG	1:AF:79:ARG:NH1	2.72	0.48
1:AH:25:ILE:HG23	1:AH:152:LEU:HD11	1.96	0.48
1:AI:263:ASN:O	1:AI:267:LYS:HG3	2.13	0.48
1:AM:252:VAL:HG22	1:AM:253:SER:N	2.29	0.48
1:BB:239:ILE:HG23	1:BB:324:LEU:HD21	1.96	0.48
1:BF:454:ASN:ND2	1:BF:456:ALA:H	2.05	0.48
1:BM:182:LEU:HD12	1:BM:182:LEU:C	2.39	0.48
1:BN:239:ILE:HD12	1:BN:275:GLU:HA	1.95	0.48
1:BR:232:THR:HB	1:BR:334:VAL:HG23	1.96	0.48
1:BT:170:PHE:HD1	1:BT:389:MET:CE	2.22	0.48
1:CA:25:ILE:HG23	1:CA:152:LEU:HD11	1.96	0.48
1:CA:442:GLN:HE21	1:CB:412:PHE:HB2	1.78	0.48
1:CB:189:PHE:HD2	1:CB:247:ILE:CD1	2.27	0.48
1:CC:189:PHE:HE2	1:CC:249:LEU:CD2	2.26	0.48
1:CC:239:ILE:HG12	1:CC:326:ILE:CD1	2.44	0.48
1:CI:272:TYR:N	1:CI:272:TYR:CD1	2.81	0.48
1:CJ:284:ARG:CG	1:CJ:284:ARG:NH1	2.74	0.48
1:CJ:398:GLY:HA3	1:CJ:494:PHE:CD2	2.49	0.48
1:CN:58:ALA:HB2	1:CN:102:GLY:HA3	1.96	0.48
1:CO:188:PHE:C	1:CO:189:PHE:HD1	2.22	0.48
1:CT:454:ASN:HD21	1:CT:456:ALA:HB3	1.79	0.48
1:AD:58:ALA:HB2	1:AD:102:GLY:HA3	1.96	0.47
1:AG:258:THR:O	1:AG:258:THR:OG1	2.29	0.47
1:AK:272:TYR:N	1:AK:272:TYR:CD1	2.81	0.47
1:AN:191:LEU:CD2	1:AN:191:LEU:N	2.77	0.47
1:AO:272:TYR:N	1:AO:272:TYR:CD1	2.81	0.47
1:BC:55:ARG:CD	1:BT:272:TYR:CE2	2.96	0.47
1:BC:237:VAL:HG23	1:BC:279:PHE:CD2	2.49	0.47
1:BC:250:TRP:CE3	1:BC:272:TYR:CE1	3.02	0.47
1:BH:263:ASN:O	1:BH:267:LYS:HG3	2.14	0.47
1:BJ:393:HIS:CG	1:BJ:496:PHE:HB3	2.49	0.47
1:BQ:79:ARG:HH11	1:BQ:79:ARG:HG3	1.79	0.47
1:BT:381:MET:HE2	1:BT:381:MET:HB2	1.68	0.47
1:CB:20:LEU:HB2	1:CB:132:PHE:O	2.14	0.47
1:CF:324:LEU:HD23	1:CF:324:LEU:C	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:189:PHE:HD2	1:CG:247:ILE:CD1	2.26	0.47
1:CM:30:SER:O	1:CM:33:LYS:HB2	2.14	0.47
1:CP:162:PHE:CD2	1:CP:163:LEU:HD13	2.48	0.47
1:AB:55:ARG:NE	1:BB:272:TYR:CE2	2.82	0.47
1:AE:203:THR:CB	1:AE:300:GLN:HG3	2.43	0.47
1:AG:272:TYR:O	1:AG:273:VAL:HG22	2.10	0.47
1:AH:201:GLY:HA3	1:AH:300:GLN:HG2	1.96	0.47
1:AH:454:ASN:ND2	1:AH:456:ALA:H	2.08	0.47
1:AQ:365:ILE:HD12	1:AQ:471:MET:HE2	1.96	0.47
1:AR:263:ASN:O	1:AR:267:LYS:HG3	2.13	0.47
1:BG:58:ALA:HB2	1:BG:102:GLY:HA3	1.95	0.47
1:BG:272:TYR:CD2	1:CG:55:ARG:HD3	2.48	0.47
1:BH:454:ASN:HD21	1:BH:456:ALA:HB3	1.78	0.47
1:BJ:189:PHE:CE2	1:BJ:249:LEU:HD21	2.47	0.47
1:BO:272:TYR:CD2	1:BR:55:ARG:NE	2.82	0.47
1:BT:5:ARG:HD3	1:CA:263:ASN:HD22	1.78	0.47
1:BT:182:LEU:C	1:BT:182:LEU:HD12	2.39	0.47
1:CB:30:SER:O	1:CB:33:LYS:HB2	2.14	0.47
1:CC:381:MET:HE2	1:CC:381:MET:HB2	1.64	0.47
1:CE:189:PHE:HD2	1:CE:247:ILE:CD1	2.27	0.47
1:CE:232:THR:HB	1:CE:334:VAL:HG23	1.95	0.47
1:CI:379:VAL:CG1	1:CI:380:SER:N	2.70	0.47
1:CL:226:VAL:HG13	1:CL:228:GLY:H	1.79	0.47
1:CO:454:ASN:ND2	1:CO:456:ALA:H	2.09	0.47
1:CR:239:ILE:HD12	1:CR:275:GLU:HA	1.96	0.47
1:AB:226:VAL:HG13	1:AB:228:GLY:H	1.80	0.47
1:AG:254:GLU:OE1	1:AG:259:THR:HG22	2.14	0.47
1:AH:61:PHE:CZ	1:AK:243:ILE:HD13	2.49	0.47
1:AI:191:LEU:CD2	1:AI:191:LEU:N	2.76	0.47
1:AI:414:LYS:HA	1:AJ:411:GLU:HB3	1.95	0.47
1:AJ:18:ARG:HD2	1:AJ:19:TYR:O	2.13	0.47
1:AK:442:GLN:HG2	1:AL:412:PHE:CD1	2.49	0.47
1:AM:239:ILE:HG12	1:AM:326:ILE:CD1	2.44	0.47
1:AO:300:GLN:HE21	1:AO:300:GLN:HB2	1.47	0.47
1:AP:79:ARG:HH11	1:AP:79:ARG:CG	2.27	0.47
1:AP:454:ASN:HD21	1:AP:456:ALA:HB3	1.78	0.47
1:BB:79:ARG:HH11	1:BB:79:ARG:CG	2.26	0.47
1:BF:284:ARG:CG	1:BF:284:ARG:NH1	2.70	0.47
1:BH:170:PHE:HD1	1:BH:389:MET:CE	2.23	0.47
1:BH:454:ASN:ND2	1:BH:456:ALA:H	2.04	0.47
1:BI:393:HIS:CG	1:BI:496:PHE:HB3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:237:VAL:HG23	1:BN:279:PHE:CD2	2.49	0.47
1:CA:188:PHE:C	1:CA:189:PHE:HD1	2.21	0.47
1:CJ:237:VAL:HG23	1:CJ:279:PHE:CD2	2.50	0.47
1:CK:398:GLY:HA3	1:CK:494:PHE:CD2	2.48	0.47
1:CL:252:VAL:HG22	1:CL:253:SER:N	2.28	0.47
1:CP:30:SER:O	1:CP:33:LYS:HB2	2.14	0.47
1:CQ:379:VAL:CG1	1:CQ:381:MET:HE1	2.44	0.47
1:CR:404:LEU:HD22	1:CR:486:VAL:HG22	1.94	0.47
1:AD:191:LEU:CD2	1:AD:191:LEU:N	2.74	0.47
1:AF:237:VAL:HG23	1:AF:279:PHE:CD2	2.49	0.47
1:AG:262:TRP:C	1:AG:264:GLU:N	2.67	0.47
1:AJ:189:PHE:CE2	1:AJ:249:LEU:HD21	2.46	0.47
1:AK:162:PHE:CD2	1:AK:163:LEU:HD13	2.49	0.47
1:BA:162:PHE:CD2	1:BA:163:LEU:HD13	2.49	0.47
1:BA:324:LEU:HD23	1:BA:324:LEU:C	2.39	0.47
1:BC:300:GLN:HE21	1:BC:300:GLN:HB2	1.55	0.47
1:BF:272:TYR:CE2	1:CK:55:ARG:CZ	2.97	0.47
1:BI:74:ASN:ND2	1:BI:77:THR:OG1	2.48	0.47
1:BJ:55:ARG:HD3	1:CL:272:TYR:HD2	1.78	0.47
1:BQ:232:THR:HB	1:BQ:334:VAL:HG23	1.96	0.47
1:CA:454:ASN:HD21	1:CA:456:ALA:HB3	1.79	0.47
1:CA:454:ASN:ND2	1:CA:456:ALA:H	2.08	0.47
1:CB:170:PHE:CD1	1:CB:389:MET:HE1	2.46	0.47
1:CE:263:ASN:HD22	1:CM:5:ARG:HD3	1.79	0.47
1:CH:170:PHE:CD1	1:CH:389:MET:HE1	2.43	0.47
1:CH:189:PHE:HD2	1:CH:247:ILE:HD11	1.79	0.47
1:CI:61:PHE:CD2	1:CI:243:ILE:HD11	2.49	0.47
1:CJ:239:ILE:HG12	1:CJ:326:ILE:CD1	2.43	0.47
1:AD:74:ASN:ND2	1:AD:77:THR:OG1	2.48	0.47
1:AF:189:PHE:HD2	1:AF:247:ILE:CD1	2.27	0.47
1:AF:407:SER:HB3	1:AJ:418:SER:HB3	1.96	0.47
1:AH:18:ARG:HG2	1:AH:20:LEU:HD23	1.96	0.47
1:AI:272:TYR:N	1:AI:272:TYR:CD1	2.83	0.47
1:AJ:55:ARG:HD3	1:BL:272:TYR:HD2	1.78	0.47
1:AJ:170:PHE:HD1	1:AJ:389:MET:CE	2.24	0.47
1:AJ:454:ASN:ND2	1:AJ:456:ALA:H	2.09	0.47
1:AM:182:LEU:C	1:AM:182:LEU:HD12	2.39	0.47
1:AO:47:MET:HE2	1:AO:117:ALA:N	2.28	0.47
1:AP:398:GLY:HA3	1:AP:494:PHE:CD2	2.49	0.47
1:AS:239:ILE:HG12	1:AS:326:ILE:CD1	2.44	0.47
1:BB:404:LEU:HD22	1:BB:486:VAL:HG22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:284:ARG:CG	1:BC:284:ARG:NH1	2.72	0.47
1:BC:393:HIS:CG	1:BC:496:PHE:HB3	2.49	0.47
1:BD:162:PHE:CD2	1:BD:163:LEU:HD13	2.49	0.47
1:BD:191:LEU:HD23	1:BD:191:LEU:N	2.17	0.47
1:BD:239:ILE:HG12	1:BD:326:ILE:CD1	2.45	0.47
1:BG:162:PHE:CD2	1:BG:163:LEU:HD13	2.50	0.47
1:BG:239:ILE:HG12	1:BG:326:ILE:CD1	2.45	0.47
1:BM:189:PHE:HD2	1:BM:247:ILE:CD1	2.28	0.47
1:BO:170:PHE:CD1	1:BO:389:MET:HE1	2.46	0.47
1:BP:30:SER:O	1:BP:33:LYS:HB2	2.13	0.47
1:CA:189:PHE:HD2	1:CA:247:ILE:HD11	1.80	0.47
1:CB:58:ALA:HB2	1:CB:102:GLY:HA3	1.96	0.47
1:CB:162:PHE:CD2	1:CB:163:LEU:HD13	2.50	0.47
1:CE:393:HIS:CG	1:CE:496:PHE:HB3	2.49	0.47
1:CK:170:PHE:CD1	1:CK:389:MET:HE1	2.44	0.47
1:CK:189:PHE:HE1	1:CK:198:ARG:CG	2.27	0.47
1:CN:75:ARG:NH2	1:CN:391:ALA:O	2.47	0.47
1:CO:203:THR:HB	1:CO:300:GLN:HG3	1.96	0.47
1:CQ:170:PHE:CD1	1:CQ:389:MET:HE1	2.43	0.47
1:AC:272:TYR:HE2	1:BA:55:ARG:NE	2.12	0.47
1:AG:226:VAL:HG13	1:AG:228:GLY:H	1.80	0.47
1:AG:258:THR:O	1:AG:259:THR:O	2.33	0.47
1:AL:243:ILE:HD13	1:CJ:61:PHE:CZ	2.48	0.47
1:AQ:182:LEU:HD12	1:AQ:182:LEU:C	2.40	0.47
1:AS:189:PHE:HD2	1:AS:247:ILE:HD11	1.78	0.47
1:BE:454:ASN:ND2	1:BE:456:ALA:H	2.08	0.47
1:BF:189:PHE:HD2	1:BF:247:ILE:CD1	2.28	0.47
1:BH:234:ARG:HG2	1:BH:280:GLU:HG2	1.97	0.47
1:BQ:454:ASN:ND2	1:BQ:456:ALA:H	2.09	0.47
1:BS:393:HIS:CG	1:BS:496:PHE:HB3	2.50	0.47
1:BT:239:ILE:HD12	1:BT:275:GLU:HA	1.96	0.47
1:CA:234:ARG:HG2	1:CA:280:GLU:HG2	1.97	0.47
1:CB:239:ILE:HD12	1:CB:275:GLU:HA	1.97	0.47
1:CE:58:ALA:HB2	1:CE:102:GLY:HA3	1.96	0.47
1:CE:232:THR:HB	1:CE:334:VAL:CG2	2.45	0.47
1:CG:58:ALA:HB2	1:CG:102:GLY:HA3	1.97	0.47
1:CH:79:ARG:HH11	1:CH:79:ARG:CG	2.19	0.47
1:CJ:393:HIS:CG	1:CJ:496:PHE:HB3	2.50	0.47
1:CK:170:PHE:HD1	1:CK:389:MET:CE	2.26	0.47
1:CM:232:THR:HB	1:CM:334:VAL:CG2	2.45	0.47
1:CS:272:TYR:N	1:CS:272:TYR:CD1	2.81	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:162:PHE:CD2	1:AE:163:LEU:HD13	2.50	0.47
1:AE:189:PHE:HD2	1:AE:247:ILE:HD11	1.80	0.47
1:AE:189:PHE:CE2	1:AE:249:LEU:HD21	2.43	0.47
1:AF:226:VAL:HG13	1:AF:228:GLY:H	1.78	0.47
1:AG:265:LEU:C	1:AG:265:LEU:CD1	2.51	0.47
1:AG:437:HIS:CE1	1:AH:405:GLN:NE2	2.83	0.47
1:AI:30:SER:O	1:AI:33:LYS:HB2	2.14	0.47
1:AI:162:PHE:CD2	1:AI:163:LEU:HD13	2.49	0.47
1:AI:234:ARG:HG2	1:AI:280:GLU:HG2	1.97	0.47
1:AJ:47:MET:HE2	1:AJ:117:ALA:N	2.30	0.47
1:AK:47:MET:HE2	1:AK:117:ALA:N	2.29	0.47
1:AK:191:LEU:CD2	1:AK:191:LEU:N	2.74	0.47
1:AL:170:PHE:HD1	1:AL:389:MET:CE	2.28	0.47
1:AM:324:LEU:HD23	1:AM:324:LEU:C	2.40	0.47
1:AN:272:TYR:N	1:AN:272:TYR:CD1	2.83	0.47
1:AP:188:PHE:C	1:AP:189:PHE:HD1	2.22	0.47
1:AQ:162:PHE:CD2	1:AQ:163:LEU:HD13	2.50	0.47
1:AQ:234:ARG:HG2	1:AQ:280:GLU:HG2	1.94	0.47
1:AR:272:TYR:N	1:AR:272:TYR:HD1	2.12	0.47
1:AS:189:PHE:HE2	1:AS:249:LEU:HD21	1.80	0.47
1:AS:226:VAL:HG13	1:AS:228:GLY:H	1.80	0.47
1:BA:43:ALA:HB1	1:BA:158:GLU:HA	1.95	0.47
1:BB:55:ARG:HD3	1:CB:272:TYR:CD2	2.49	0.47
1:BD:16:ALA:O	1:BD:17:ASN:HB2	2.14	0.47
1:BE:454:ASN:HD21	1:BE:456:ALA:HB3	1.79	0.47
1:BF:288:HIS:HD2	1:BF:337:ASP:OD2	1.97	0.47
1:BG:324:LEU:HD23	1:BG:324:LEU:C	2.40	0.47
1:BH:30:SER:O	1:BH:33:LYS:HB2	2.14	0.47
1:BH:189:PHE:HD2	1:BH:247:ILE:CD1	2.27	0.47
1:BI:182:LEU:C	1:BI:182:LEU:HD12	2.40	0.47
1:BJ:47:MET:HE2	1:BJ:117:ALA:N	2.30	0.47
1:BJ:189:PHE:HD2	1:BJ:247:ILE:HD11	1.80	0.47
1:BK:30:SER:O	1:BK:33:LYS:HB2	2.15	0.47
1:BL:232:THR:HB	1:BL:334:VAL:CG2	2.45	0.47
1:BM:379:VAL:CG1	1:BM:381:MET:HE1	2.45	0.47
1:BO:47:MET:HE2	1:BO:117:ALA:N	2.29	0.47
1:BR:239:ILE:HD12	1:BR:275:GLU:HA	1.96	0.47
1:BT:189:PHE:CE2	1:BT:249:LEU:HD21	2.49	0.47
1:BT:256:ASN:HD22	1:BT:302:ASP:HA	1.79	0.47
1:CA:171:ASP:HA	1:CA:172:PRO:HD3	1.77	0.47
1:CB:252:VAL:HG22	1:CB:253:SER:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:272:TYR:CD2	1:CO:55:ARG:CZ	2.97	0.47
1:CI:393:HIS:CG	1:CI:496:PHE:HB3	2.50	0.47
1:CK:263:ASN:O	1:CK:267:LYS:HG3	2.15	0.47
1:CK:442:GLN:HE21	1:CL:412:PHE:HB2	1.78	0.47
1:CO:272:TYR:N	1:CO:272:TYR:HD1	2.13	0.47
1:CR:234:ARG:HG2	1:CR:280:GLU:HG2	1.97	0.47
1:CR:324:LEU:C	1:CR:324:LEU:HD23	2.40	0.47
1:CS:189:PHE:HD2	1:CS:247:ILE:HD11	1.80	0.47
1:CT:189:PHE:CE2	1:CT:249:LEU:HD21	2.50	0.47
1:AC:55:ARG:CZ	1:AT:272:TYR:CD2	2.98	0.47
1:AG:61:PHE:CD2	1:AG:243:ILE:HD11	2.50	0.47
1:AH:189:PHE:CE1	1:AH:198:ARG:HG2	2.48	0.47
1:AI:189:PHE:CE2	1:AI:249:LEU:HD21	2.46	0.47
1:AJ:232:THR:HB	1:AJ:334:VAL:HG23	1.97	0.47
1:AK:324:LEU:HD23	1:AK:324:LEU:C	2.40	0.47
1:AM:189:PHE:CE1	1:AM:198:ARG:HG2	2.50	0.47
1:AM:234:ARG:HG2	1:AM:280:GLU:HG2	1.96	0.47
1:AO:295:LEU:O	1:AO:296:ALA:C	2.57	0.47
1:AR:22:THR:OG1	1:AR:131:HIS:CD2	2.60	0.47
1:AT:454:ASN:ND2	1:AT:456:ALA:H	2.09	0.47
1:BB:189:PHE:HD2	1:BB:247:ILE:HD11	1.79	0.47
1:BC:55:ARG:CD	1:BT:272:TYR:HE2	2.28	0.47
1:BH:162:PHE:CD2	1:BH:163:LEU:HD13	2.50	0.47
1:BK:191:LEU:HD23	1:BK:191:LEU:N	2.19	0.47
1:BL:201:GLY:HA3	1:BL:300:GLN:HG2	1.96	0.47
1:BL:379:VAL:CG1	1:BL:381:MET:HE1	2.45	0.47
1:BL:393:HIS:CG	1:BL:496:PHE:HB3	2.50	0.47
1:BM:170:PHE:HD1	1:BM:389:MET:CE	2.27	0.47
1:BS:454:ASN:HD21	1:BS:456:ALA:HB3	1.79	0.47
1:CB:404:LEU:HD22	1:CB:486:VAL:HG22	1.96	0.47
1:CE:239:ILE:HG12	1:CE:326:ILE:CD1	2.44	0.47
1:CF:232:THR:HB	1:CF:334:VAL:HG23	1.97	0.47
1:CG:234:ARG:HG2	1:CG:280:GLU:HG2	1.97	0.47
1:AA:11:PRO:HG2	1:AA:18:ARG:HD2	1.96	0.47
1:AB:272:TYR:CE2	1:CB:55:ARG:HD3	2.50	0.47
1:AD:250:TRP:HZ3	1:AD:272:TYR:CE1	2.29	0.47
1:AE:239:ILE:HG12	1:AE:326:ILE:CD1	2.45	0.47
1:AF:189:PHE:CE2	1:AF:249:LEU:HD21	2.42	0.47
1:AH:191:LEU:HD23	1:AH:191:LEU:N	2.22	0.47
1:AJ:237:VAL:HG23	1:AJ:279:PHE:CD2	2.50	0.47
1:AL:170:PHE:CD1	1:AL:389:MET:HE1	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:239:ILE:HD12	1:AO:275:GLU:HA	1.97	0.47
1:AP:30:SER:O	1:AP:33:LYS:HB2	2.14	0.47
1:BC:191:LEU:CD2	1:BC:191:LEU:N	2.76	0.47
1:BC:437:HIS:CE1	1:BD:405:GLN:NE2	2.83	0.47
1:BD:188:PHE:C	1:BD:189:PHE:HD1	2.23	0.47
1:BE:272:TYR:HE2	1:BM:55:ARG:NE	2.09	0.47
1:BK:232:THR:HB	1:BK:334:VAL:HG23	1.97	0.47
1:BL:191:LEU:CD2	1:BL:191:LEU:N	2.76	0.47
1:BP:22:THR:OG1	1:BP:131:HIS:CD2	2.58	0.47
1:BP:272:TYR:CD1	1:BP:272:TYR:N	2.83	0.47
1:BQ:10:ILE:HG21	1:BQ:146:TRP:CZ2	2.50	0.47
1:CD:170:PHE:HD1	1:CD:389:MET:CE	2.25	0.47
1:CD:239:ILE:HG12	1:CD:326:ILE:CD1	2.45	0.47
1:CH:239:ILE:HD12	1:CH:275:GLU:HA	1.96	0.47
1:CL:239:ILE:HG12	1:CL:326:ILE:CD1	2.45	0.47
1:CO:30:SER:O	1:CO:33:LYS:HB2	2.15	0.47
1:CQ:189:PHE:CE2	1:CQ:249:LEU:HD21	2.50	0.47
1:CQ:272:TYR:N	1:CQ:272:TYR:CD1	2.83	0.47
1:CR:10:ILE:HG21	1:CR:146:TRP:CZ2	2.49	0.47
1:AB:61:PHE:CE2	1:AB:243:ILE:HD11	2.50	0.47
1:AB:272:TYR:CD2	1:CB:55:ARG:HD3	2.49	0.47
1:AD:272:TYR:N	1:AD:272:TYR:CD1	2.82	0.47
1:AE:454:ASN:HD21	1:AE:456:ALA:HB3	1.80	0.47
1:AF:239:ILE:HD12	1:AF:275:GLU:HA	1.96	0.47
1:AF:442:GLN:HE21	1:AG:412:PHE:HB2	1.80	0.47
1:AG:30:SER:O	1:AG:33:LYS:HB2	2.14	0.47
1:AK:55:ARG:CZ	1:CF:272:TYR:CD2	2.98	0.47
1:AL:393:HIS:CG	1:AL:496:PHE:HB3	2.50	0.47
1:AN:25:ILE:HG23	1:AN:152:LEU:HD11	1.96	0.47
1:BB:25:ILE:HG23	1:BB:152:LEU:HD11	1.97	0.47
1:BC:30:SER:O	1:BC:33:LYS:HB2	2.15	0.47
1:BD:324:LEU:HD23	1:BD:324:LEU:C	2.40	0.47
1:BE:182:LEU:C	1:BE:182:LEU:HD12	2.40	0.47
1:BH:256:ASN:HD22	1:BH:302:ASP:HA	1.80	0.47
1:BI:272:TYR:N	1:BI:272:TYR:CD1	2.83	0.47
1:BN:440:ALA:HB3	1:BO:444:LEU:HD13	1.97	0.47
1:CA:226:VAL:HG13	1:CA:228:GLY:H	1.79	0.47
1:CD:324:LEU:C	1:CD:324:LEU:HD23	2.40	0.47
1:CE:234:ARG:HG2	1:CE:280:GLU:HG2	1.97	0.47
1:CG:324:LEU:C	1:CG:324:LEU:HD23	2.40	0.47
1:CM:263:ASN:O	1:CM:267:LYS:HG3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:393:HIS:CG	1:CM:496:PHE:HB3	2.50	0.47
1:CT:191:LEU:CD2	1:CT:191:LEU:N	2.76	0.47
1:CT:239:ILE:HG12	1:CT:326:ILE:CD1	2.45	0.47
1:AA:55:ARG:HD3	1:CC:272:TYR:CE2	2.50	0.46
1:AI:189:PHE:HD2	1:AI:247:ILE:CD1	2.28	0.46
1:AI:381:MET:HE2	1:AI:381:MET:HB2	1.67	0.46
1:AJ:75:ARG:NH2	1:AJ:391:ALA:O	2.47	0.46
1:AN:393:HIS:CG	1:AN:496:PHE:HB3	2.50	0.46
1:AN:454:ASN:HD21	1:AN:456:ALA:HB3	1.80	0.46
1:AO:239:ILE:HG23	1:AO:324:LEU:HD21	1.96	0.46
1:AO:454:ASN:HD21	1:AO:456:ALA:HB3	1.80	0.46
1:AP:263:ASN:O	1:AP:267:LYS:HG3	2.15	0.46
1:AS:379:VAL:CG1	1:AS:381:MET:HE1	2.45	0.46
1:AS:393:HIS:CG	1:AS:496:PHE:HB3	2.50	0.46
1:BB:379:VAL:CG1	1:BB:381:MET:HE1	2.45	0.46
1:BE:30:SER:O	1:BE:33:LYS:HB2	2.15	0.46
1:BP:189:PHE:HD2	1:BP:247:ILE:HD11	1.80	0.46
1:BT:232:THR:HB	1:BT:334:VAL:CG2	2.44	0.46
1:CC:250:TRP:CZ3	1:CC:272:TYR:CD1	3.03	0.46
1:CG:454:ASN:HD21	1:CG:456:ALA:HB3	1.80	0.46
1:CI:67:VAL:HG23	1:CI:135:LEU:HB2	1.96	0.46
1:CI:162:PHE:CD2	1:CI:163:LEU:HD13	2.49	0.46
1:CK:79:ARG:HH11	1:CK:79:ARG:HG3	1.80	0.46
1:CM:182:LEU:C	1:CM:182:LEU:HD12	2.40	0.46
1:CP:43:ALA:HB1	1:CP:158:GLU:HA	1.96	0.46
1:AB:232:THR:HB	1:AB:334:VAL:HG23	1.97	0.46
1:AD:162:PHE:CD2	1:AD:163:LEU:HD13	2.50	0.46
1:AE:75:ARG:NH2	1:AE:391:ALA:O	2.47	0.46
1:AF:252:VAL:HG22	1:AF:253:SER:N	2.29	0.46
1:AG:263:ASN:ND2	1:BG:32:PHE:HD1	2.14	0.46
1:AH:393:HIS:CG	1:AH:496:PHE:HB3	2.50	0.46
1:AI:454:ASN:HD21	1:AI:456:ALA:HB3	1.80	0.46
1:AL:436:SER:O	1:AM:487:LEU:HD21	2.15	0.46
1:AN:5:ARG:HD3	1:AS:263:ASN:HD22	1.80	0.46
1:AN:18:ARG:HG3	1:AN:19:TYR:N	2.30	0.46
1:AN:170:PHE:CD1	1:AN:389:MET:HE1	2.45	0.46
1:AN:189:PHE:HD2	1:AN:247:ILE:CD1	2.27	0.46
1:AP:25:ILE:HG23	1:AP:152:LEU:HD11	1.97	0.46
1:AS:263:ASN:O	1:AS:267:LYS:HG3	2.15	0.46
1:BA:170:PHE:CD1	1:BA:389:MET:HE1	2.44	0.46
1:BC:189:PHE:HD2	1:BC:247:ILE:HD11	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BE:75:ARG:NH2	1:BE:391:ALA:O	2.49	0.46
1:BG:47:MET:HE2	1:BG:117:ALA:N	2.31	0.46
1:BR:454:ASN:HD21	1:BR:456:ALA:HB3	1.79	0.46
1:CD:20:LEU:HB2	1:CD:132:PHE:O	2.16	0.46
1:CE:191:LEU:CD2	1:CE:191:LEU:N	2.75	0.46
1:CF:405:GLN:NE2	1:CJ:437:HIS:CE1	2.83	0.46
1:CK:237:VAL:HG23	1:CK:279:PHE:CD2	2.49	0.46
1:CL:188:PHE:C	1:CL:189:PHE:HD1	2.22	0.46
1:CL:189:PHE:HE2	1:CL:249:LEU:HD21	1.80	0.46
1:CP:232:THR:HB	1:CP:334:VAL:CG2	2.45	0.46
1:AB:189:PHE:CE2	1:AB:249:LEU:HD21	2.46	0.46
1:AC:189:PHE:HE2	1:AC:249:LEU:CD2	2.28	0.46
1:AD:55:ARG:CZ	1:AN:272:TYR:CE2	2.99	0.46
1:AG:264:GLU:O	1:AG:267:LYS:CB	2.64	0.46
1:AM:239:ILE:HD12	1:AM:275:GLU:HA	1.97	0.46
1:AP:444:LEU:HD13	1:AT:440:ALA:CB	2.45	0.46
1:AQ:189:PHE:CE2	1:AQ:249:LEU:HD21	2.49	0.46
1:AR:189:PHE:HD2	1:AR:247:ILE:HD11	1.79	0.46
1:AR:423:LYS:HE2	1:AR:449:GLU:O	2.15	0.46
1:BA:371:ASP:OD1	1:BA:381:MET:HG2	2.16	0.46
1:BH:189:PHE:CE1	1:BH:198:ARG:HG2	2.48	0.46
1:BH:272:TYR:N	1:BH:272:TYR:CD1	2.83	0.46
1:BH:442:GLN:HE21	1:BI:412:PHE:HB2	1.80	0.46
1:BL:14:CYS:H	1:BL:138:ASN:HD21	1.62	0.46
1:BR:226:VAL:HG13	1:BR:228:GLY:H	1.80	0.46
1:BS:170:PHE:HD1	1:BS:389:MET:CE	2.25	0.46
1:CJ:250:TRP:CE3	1:CJ:272:TYR:CD1	3.03	0.46
1:CL:404:LEU:N	1:CL:404:LEU:HD23	2.31	0.46
1:CP:58:ALA:HB2	1:CP:102:GLY:HA3	1.98	0.46
1:CR:442:GLN:HE21	1:CS:412:PHE:HB2	1.78	0.46
1:AC:43:ALA:HB1	1:AC:158:GLU:HA	1.98	0.46
1:AC:272:TYR:CE2	1:BA:55:ARG:HD3	2.50	0.46
1:AD:226:VAL:HG13	1:AD:228:GLY:H	1.80	0.46
1:AG:162:PHE:CD1	1:AH:287:TYR:HA	2.50	0.46
1:AG:189:PHE:CE1	1:AG:198:ARG:HG2	2.50	0.46
1:AH:239:ILE:HD12	1:AH:275:GLU:HA	1.98	0.46
1:AJ:58:ALA:HB2	1:AJ:102:GLY:HA3	1.97	0.46
1:AJ:284:ARG:CG	1:AJ:284:ARG:NH1	2.75	0.46
1:AJ:454:ASN:HD21	1:AJ:456:ALA:HB3	1.81	0.46
1:AL:239:ILE:HD12	1:AL:275:GLU:HA	1.98	0.46
1:AM:232:THR:HB	1:AM:334:VAL:CG2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:237:VAL:HG23	1:AN:279:PHE:CD2	2.51	0.46
1:BC:263:ASN:O	1:BC:267:LYS:HG3	2.16	0.46
1:BF:442:GLN:HE21	1:BG:412:PHE:HB2	1.80	0.46
1:BG:18:ARG:HG2	1:BG:20:LEU:HD23	1.98	0.46
1:BG:43:ALA:HB1	1:BG:158:GLU:HA	1.97	0.46
1:BI:47:MET:HE2	1:BI:117:ALA:N	2.30	0.46
1:BK:171:ASP:HA	1:BK:172:PRO:HD3	1.81	0.46
1:BL:239:ILE:HD12	1:BL:275:GLU:HA	1.98	0.46
1:BP:324:LEU:C	1:BP:324:LEU:HD23	2.40	0.46
1:BR:232:THR:HB	1:BR:334:VAL:CG2	2.45	0.46
1:CB:203:THR:HB	1:CB:300:GLN:HG3	1.97	0.46
1:CB:239:ILE:HG12	1:CB:326:ILE:CD1	2.46	0.46
1:CD:79:ARG:CG	1:CD:79:ARG:NH1	2.71	0.46
1:CF:234:ARG:HG2	1:CF:280:GLU:HG2	1.98	0.46
1:CF:237:VAL:HG23	1:CF:279:PHE:CD2	2.50	0.46
1:CI:10:ILE:HG21	1:CI:146:TRP:CZ2	2.50	0.46
1:CK:12:LYS:HB3	1:CK:144:ALA:C	2.41	0.46
1:CO:25:ILE:HG23	1:CO:152:LEU:HD11	1.97	0.46
1:CO:170:PHE:HD1	1:CO:389:MET:CE	2.29	0.46
1:CP:188:PHE:C	1:CP:189:PHE:HD1	2.24	0.46
1:CQ:182:LEU:C	1:CQ:182:LEU:HD12	2.41	0.46
1:CT:18:ARG:HG3	1:CT:19:TYR:N	2.30	0.46
1:AG:79:ARG:NH1	1:AG:79:ARG:CG	2.72	0.46
1:AJ:203:THR:HB	1:AJ:300:GLN:CG	2.45	0.46
1:AP:47:MET:HE2	1:AP:117:ALA:N	2.31	0.46
1:AS:237:VAL:HG23	1:AS:279:PHE:CD2	2.50	0.46
1:BA:393:HIS:CG	1:BA:496:PHE:HB3	2.50	0.46
1:BD:404:LEU:HD22	1:BD:486:VAL:HG22	1.96	0.46
1:BF:393:HIS:CG	1:BF:496:PHE:HB3	2.50	0.46
1:BM:189:PHE:HD2	1:BM:247:ILE:HD11	1.80	0.46
1:BP:14:CYS:H	1:BP:138:ASN:ND2	2.11	0.46
1:CA:162:PHE:CD2	1:CA:163:LEU:HD13	2.51	0.46
1:CD:454:ASN:HD21	1:CD:456:ALA:HB3	1.79	0.46
1:CK:272:TYR:CD1	1:CK:272:TYR:N	2.84	0.46
1:CL:170:PHE:HD1	1:CL:389:MET:CE	2.28	0.46
1:CL:234:ARG:HG2	1:CL:280:GLU:HG2	1.97	0.46
1:CP:189:PHE:HE2	1:CP:249:LEU:HD21	1.80	0.46
1:CS:454:ASN:HD21	1:CS:456:ALA:HB3	1.81	0.46
1:AC:263:ASN:HD22	1:BA:5:ARG:HD3	1.80	0.46
1:AG:234:ARG:HG2	1:AG:280:GLU:HG2	1.98	0.46
1:AG:393:HIS:CG	1:AG:496:PHE:HB3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:442:GLN:HE21	1:AI:412:PHE:HB2	1.81	0.46
1:AJ:272:TYR:HD2	1:AQ:55:ARG:HD3	1.78	0.46
1:AK:170:PHE:HD1	1:AK:389:MET:CE	2.24	0.46
1:AL:162:PHE:CD2	1:AL:163:LEU:HD13	2.51	0.46
1:AP:272:TYR:CD2	1:BE:55:ARG:CZ	2.98	0.46
1:AR:234:ARG:HG2	1:AR:280:GLU:HG2	1.98	0.46
1:AT:454:ASN:HD21	1:AT:456:ALA:HB3	1.80	0.46
1:BB:189:PHE:CE2	1:BB:249:LEU:HD21	2.43	0.46
1:BF:58:ALA:HB2	1:BF:102:GLY:HA3	1.97	0.46
1:BF:272:TYR:HE2	1:CK:55:ARG:NE	2.10	0.46
1:BI:252:VAL:HG22	1:BI:253:SER:N	2.30	0.46
1:BK:365:ILE:CD1	1:BK:471:MET:HE2	2.45	0.46
1:BL:232:THR:HB	1:BL:334:VAL:HG23	1.97	0.46
1:BM:30:SER:O	1:BM:33:LYS:HB2	2.15	0.46
1:BN:379:VAL:CG1	1:BN:381:MET:HE1	2.46	0.46
1:BQ:239:ILE:HD12	1:BQ:275:GLU:HA	1.97	0.46
1:BR:30:SER:O	1:BR:33:LYS:HB2	2.15	0.46
1:BR:191:LEU:CD2	1:BR:191:LEU:N	2.77	0.46
1:BR:263:ASN:O	1:BR:267:LYS:HG3	2.14	0.46
1:BT:43:ALA:HB1	1:BT:158:GLU:HA	1.97	0.46
1:BT:393:HIS:CG	1:BT:496:PHE:HB3	2.51	0.46
1:BT:423:LYS:HE2	1:BT:449:GLU:O	2.16	0.46
1:CE:61:PHE:CD2	1:CE:243:ILE:HD11	2.50	0.46
1:CE:75:ARG:NH2	1:CE:391:ALA:O	2.48	0.46
1:CG:442:GLN:HE21	1:CH:412:PHE:HB2	1.81	0.46
1:CJ:454:ASN:HD21	1:CJ:456:ALA:HB3	1.80	0.46
1:CM:162:PHE:CD2	1:CM:163:LEU:HD13	2.50	0.46
1:CN:207:VAL:HA	1:CN:208:PRO:HD3	1.80	0.46
1:CP:14:CYS:H	1:CP:138:ASN:HD21	1.62	0.46
1:CP:324:LEU:HD23	1:CP:324:LEU:C	2.40	0.46
1:AA:162:PHE:CD2	1:AA:163:LEU:HD13	2.51	0.46
1:AD:237:VAL:HG23	1:AD:279:PHE:CD2	2.50	0.46
1:AE:239:ILE:HD12	1:AE:275:GLU:HA	1.98	0.46
1:AH:189:PHE:HD2	1:AH:247:ILE:HD11	1.79	0.46
1:AJ:43:ALA:HB1	1:AJ:158:GLU:HA	1.98	0.46
1:AR:237:VAL:HG23	1:AR:279:PHE:CD2	2.50	0.46
1:AS:404:LEU:HD22	1:AS:486:VAL:HG22	1.98	0.46
1:AT:170:PHE:CD1	1:AT:389:MET:HE1	2.40	0.46
1:AT:239:ILE:HD12	1:AT:275:GLU:HA	1.98	0.46
1:AT:324:LEU:C	1:AT:324:LEU:HD23	2.40	0.46
1:BA:284:ARG:CG	1:BA:284:ARG:NH1	2.68	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:365:ILE:CD1	1:BL:471:MET:HE2	2.46	0.46
1:BM:272:TYR:N	1:BM:272:TYR:CD1	2.82	0.46
1:BM:454:ASN:HD21	1:BM:456:ALA:HB3	1.80	0.46
1:BN:182:LEU:HG	1:BN:330:ILE:HB	1.97	0.46
1:CB:182:LEU:C	1:CB:182:LEU:HD12	2.40	0.46
1:CE:263:ASN:O	1:CE:267:LYS:HG3	2.16	0.46
1:CF:191:LEU:CD2	1:CF:191:LEU:N	2.75	0.46
1:CI:61:PHE:CE2	1:CI:243:ILE:HD11	2.50	0.46
1:CK:189:PHE:HD2	1:CK:247:ILE:HD11	1.80	0.46
1:CP:393:HIS:CG	1:CP:496:PHE:HB3	2.51	0.46
1:CQ:393:HIS:CG	1:CQ:496:PHE:HB3	2.51	0.46
1:AC:237:VAL:HG23	1:AC:279:PHE:CD2	2.50	0.46
1:AF:189:PHE:HD2	1:AF:247:ILE:HD11	1.80	0.46
1:AG:270:GLY:O	1:AG:271:VAL:HG13	2.16	0.46
1:AH:234:ARG:HG2	1:AH:280:GLU:HG2	1.98	0.46
1:AK:234:ARG:HG2	1:AK:280:GLU:HG2	1.98	0.46
1:AM:232:THR:HB	1:AM:334:VAL:HG23	1.98	0.46
1:AM:454:ASN:HD21	1:AM:456:ALA:HB3	1.80	0.46
1:AP:61:PHE:CD2	1:AP:243:ILE:HD11	2.51	0.46
1:AS:14:CYS:H	1:AS:138:ASN:HD21	1.64	0.46
1:BD:189:PHE:CE2	1:BD:249:LEU:HD21	2.50	0.46
1:BD:226:VAL:HG13	1:BD:228:GLY:H	1.80	0.46
1:BH:16:ALA:O	1:BH:17:ASN:HB2	2.15	0.46
1:BJ:170:PHE:CD1	1:BJ:389:MET:HE1	2.41	0.46
1:BK:191:LEU:CD2	1:BK:191:LEU:N	2.76	0.46
1:BM:252:VAL:HG22	1:BM:253:SER:N	2.31	0.46
1:BO:250:TRP:CZ3	1:BO:272:TYR:CD1	3.04	0.46
1:CC:250:TRP:HE3	1:CC:272:TYR:CD1	2.33	0.46
1:CD:30:SER:O	1:CD:33:LYS:HB2	2.15	0.46
1:CI:189:PHE:CE2	1:CI:249:LEU:HD21	2.41	0.46
1:CK:234:ARG:HG2	1:CK:280:GLU:HG2	1.96	0.46
1:AA:189:PHE:HD2	1:AA:247:ILE:HD11	1.81	0.46
1:AA:393:HIS:CG	1:AA:496:PHE:HB3	2.51	0.46
1:AE:272:TYR:CD1	1:AE:272:TYR:N	2.84	0.46
1:AH:191:LEU:CD2	1:AH:191:LEU:N	2.77	0.46
1:AI:18:ARG:NH1	1:AI:18:ARG:HB2	2.31	0.46
1:AK:188:PHE:C	1:AK:189:PHE:HD1	2.24	0.46
1:AK:203:THR:HB	1:AK:300:GLN:HG3	1.97	0.46
1:AL:14:CYS:HB3	1:AL:64:LEU:HD21	1.98	0.46
1:AL:25:ILE:HG23	1:AL:152:LEU:HD11	1.97	0.46
1:AM:14:CYS:H	1:AM:138:ASN:HD21	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:162:PHE:CD2	1:AN:163:LEU:HD13	2.51	0.46
1:AO:393:HIS:CG	1:AO:496:PHE:HB3	2.51	0.46
1:AP:189:PHE:CE1	1:AP:198:ARG:CG	2.99	0.46
1:AQ:188:PHE:C	1:AQ:189:PHE:HD1	2.24	0.46
1:AQ:454:ASN:ND2	1:AQ:456:ALA:H	2.10	0.46
1:AS:171:ASP:HA	1:AS:172:PRO:HD3	1.77	0.46
1:AT:171:ASP:HA	1:AT:172:PRO:HD3	1.76	0.46
1:AT:263:ASN:O	1:AT:267:LYS:HG3	2.15	0.46
1:BA:234:ARG:HG2	1:BA:280:GLU:HG2	1.97	0.46
1:BE:272:TYR:N	1:BE:272:TYR:CD1	2.84	0.46
1:BG:232:THR:HB	1:BG:334:VAL:CG2	2.45	0.46
1:BI:5:ARG:HD3	1:BR:263:ASN:HD22	1.81	0.46
1:BL:25:ILE:HG23	1:BL:152:LEU:HD11	1.98	0.46
1:BL:237:VAL:HG23	1:BL:279:PHE:CD2	2.50	0.46
1:BN:30:SER:O	1:BN:33:LYS:HB2	2.15	0.46
1:BN:255:TRP:CE3	1:BN:285:SER:HB2	2.51	0.46
1:BO:11:PRO:HG2	1:BO:18:ARG:CD	2.46	0.46
1:BT:18:ARG:HG3	1:BT:19:TYR:N	2.31	0.46
1:CC:55:ARG:CZ	1:CT:272:TYR:CD2	2.98	0.46
1:CG:272:TYR:N	1:CG:272:TYR:HD1	2.13	0.46
1:CG:454:ASN:ND2	1:CG:456:ALA:H	2.08	0.46
1:CI:373:THR:HG22	1:CI:374:SER:N	2.29	0.46
1:CJ:239:ILE:HD12	1:CJ:275:GLU:HA	1.98	0.46
1:CK:30:SER:O	1:CK:33:LYS:HB2	2.15	0.46
1:CL:79:ARG:HH11	1:CL:79:ARG:CG	2.27	0.46
1:CM:226:VAL:HG13	1:CM:228:GLY:H	1.80	0.46
1:CR:182:LEU:HG	1:CR:330:ILE:HB	1.97	0.46
1:CR:393:HIS:CG	1:CR:496:PHE:HB3	2.51	0.46
1:CT:272:TYR:N	1:CT:272:TYR:HD1	2.14	0.46
1:AC:324:LEU:HD23	1:AC:324:LEU:C	2.42	0.46
1:AC:393:HIS:CG	1:AC:496:PHE:HB3	2.51	0.46
1:AE:189:PHE:HD2	1:AE:247:ILE:CD1	2.28	0.46
1:AG:47:MET:HE2	1:AG:117:ALA:N	2.30	0.46
1:AG:263:ASN:ND2	1:BG:32:PHE:CG	2.83	0.46
1:AH:239:ILE:HG12	1:AH:326:ILE:CD1	2.46	0.46
1:AI:171:ASP:HA	1:AI:172:PRO:HD3	1.77	0.46
1:AI:182:LEU:C	1:AI:182:LEU:HD12	2.41	0.46
1:AL:188:PHE:C	1:AL:189:PHE:HD1	2.24	0.46
1:AL:437:HIS:CE1	1:AM:405:GLN:NE2	2.84	0.46
1:AN:189:PHE:CE1	1:AN:198:ARG:HG2	2.49	0.46
1:AQ:30:SER:O	1:AQ:33:LYS:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:381:MET:HE2	1:BD:381:MET:HB2	1.74	0.46
1:BG:25:ILE:HG23	1:BG:152:LEU:HD11	1.96	0.46
1:BG:189:PHE:CE1	1:BG:198:ARG:HG2	2.51	0.46
1:BG:393:HIS:CG	1:BG:496:PHE:HB3	2.51	0.46
1:BH:189:PHE:HE1	1:BH:198:ARG:HG2	1.77	0.46
1:BH:239:ILE:HD12	1:BH:275:GLU:HA	1.96	0.46
1:BJ:250:TRP:CZ3	1:BJ:272:TYR:CD1	3.04	0.46
1:BJ:263:ASN:O	1:BJ:267:LYS:HG3	2.16	0.46
1:BO:170:PHE:HD1	1:BO:389:MET:CE	2.28	0.46
1:CC:252:VAL:HG22	1:CC:253:SER:N	2.31	0.46
1:CI:272:TYR:N	1:CI:272:TYR:HD1	2.14	0.46
1:CK:162:PHE:CD2	1:CK:163:LEU:HD13	2.50	0.46
1:CK:171:ASP:HA	1:CK:172:PRO:HD3	1.79	0.46
1:CN:232:THR:HB	1:CN:334:VAL:CG2	2.46	0.46
1:CR:162:PHE:CD2	1:CR:163:LEU:HD13	2.51	0.46
1:CR:191:LEU:CD2	1:CR:191:LEU:N	2.76	0.46
1:CT:170:PHE:CD1	1:CT:389:MET:HE1	2.45	0.46
1:AA:237:VAL:HG23	1:AA:279:PHE:CD2	2.51	0.45
1:AB:269:PRO:O	1:AB:269:PRO:HG2	2.16	0.45
1:AD:189:PHE:CE2	1:AD:249:LEU:HD21	2.51	0.45
1:AF:454:ASN:HD21	1:AF:456:ALA:HB3	1.80	0.45
1:AG:182:LEU:C	1:AG:182:LEU:HD12	2.40	0.45
1:AH:182:LEU:C	1:AH:182:LEU:HD12	2.41	0.45
1:AH:381:MET:HE2	1:AH:381:MET:HB2	1.72	0.45
1:AH:418:SER:HB3	1:AI:407:SER:HB3	1.98	0.45
1:AN:239:ILE:HD12	1:AN:275:GLU:HA	1.97	0.45
1:AP:272:TYR:N	1:AP:272:TYR:HD1	2.15	0.45
1:AQ:284:ARG:CG	1:AQ:284:ARG:NH1	2.74	0.45
1:AT:226:VAL:HG13	1:AT:228:GLY:H	1.81	0.45
1:AT:272:TYR:N	1:AT:272:TYR:CD1	2.83	0.45
1:AT:395:LEU:HB2	1:AT:497:TYR:HB2	1.98	0.45
1:AT:404:LEU:HD22	1:AT:486:VAL:HG22	1.97	0.45
1:BB:393:HIS:CG	1:BB:496:PHE:HB3	2.51	0.45
1:BE:25:ILE:HG23	1:BE:152:LEU:HD11	1.98	0.45
1:BG:79:ARG:HG3	1:BG:79:ARG:NH1	2.30	0.45
1:BG:272:TYR:N	1:BG:272:TYR:HD1	2.14	0.45
1:BI:189:PHE:HD2	1:BI:247:ILE:CD1	2.29	0.45
1:BK:189:PHE:CE2	1:BK:249:LEU:HD21	2.51	0.45
1:BM:272:TYR:N	1:BM:272:TYR:HD1	2.14	0.45
1:BN:182:LEU:C	1:BN:182:LEU:HD12	2.41	0.45
1:BO:162:PHE:CD2	1:BO:163:LEU:HD13	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:324:LEU:HD23	1:BR:324:LEU:C	2.41	0.45
1:CA:444:LEU:HD13	1:CE:440:ALA:CB	2.46	0.45
1:CB:318:SER:HA	1:CB:319:GLY:HA2	1.76	0.45
1:CF:272:TYR:N	1:CF:272:TYR:CD1	2.85	0.45
1:CF:393:HIS:CG	1:CF:496:PHE:HB3	2.52	0.45
1:CF:404:LEU:HD22	1:CF:486:VAL:HG22	1.98	0.45
1:CJ:263:ASN:O	1:CJ:267:LYS:HG3	2.16	0.45
1:CK:226:VAL:HG13	1:CK:228:GLY:H	1.81	0.45
1:CL:162:PHE:CD2	1:CL:163:LEU:HD13	2.51	0.45
1:CO:47:MET:HE2	1:CO:117:ALA:N	2.31	0.45
1:CO:170:PHE:CD1	1:CO:389:MET:HE1	2.46	0.45
1:CT:381:MET:HB2	1:CT:381:MET:HE2	1.62	0.45
1:AA:239:ILE:HD12	1:AA:275:GLU:HA	1.97	0.45
1:AC:189:PHE:HD2	1:AC:247:ILE:HD11	1.80	0.45
1:AE:324:LEU:HD23	1:AE:324:LEU:C	2.41	0.45
1:AG:442:GLN:HE21	1:AH:412:PHE:HB2	1.81	0.45
1:AI:16:ALA:O	1:AI:17:ASN:HB2	2.17	0.45
1:AI:144:ALA:CB	1:AR:191:LEU:O	2.64	0.45
1:AK:263:ASN:O	1:AK:267:LYS:HG3	2.15	0.45
1:AK:272:TYR:N	1:AK:272:TYR:HD1	2.13	0.45
1:AN:189:PHE:HD2	1:AN:247:ILE:HD11	1.80	0.45
1:AS:30:SER:O	1:AS:33:LYS:HB2	2.16	0.45
1:BB:423:LYS:HE2	1:BB:449:GLU:O	2.16	0.45
1:BF:324:LEU:HD23	1:BF:324:LEU:C	2.42	0.45
1:BF:440:ALA:HB3	1:BG:444:LEU:HD13	1.98	0.45
1:BH:393:HIS:CG	1:BH:496:PHE:HB3	2.51	0.45
1:BI:324:LEU:HD23	1:BI:324:LEU:C	2.40	0.45
1:BO:454:ASN:HD21	1:BO:456:ALA:HB3	1.80	0.45
1:BP:73:TYR:CZ	1:BP:394:GLY:HA3	2.51	0.45
1:BP:272:TYR:CD2	1:CE:55:ARG:NH1	2.84	0.45
1:BR:189:PHE:CE2	1:BR:249:LEU:HD21	2.48	0.45
1:BS:30:SER:O	1:BS:33:LYS:HB2	2.16	0.45
1:CA:232:THR:HB	1:CA:334:VAL:CG2	2.46	0.45
1:CA:324:LEU:C	1:CA:324:LEU:HD23	2.41	0.45
1:CA:393:HIS:CG	1:CA:496:PHE:HB3	2.52	0.45
1:CH:201:GLY:HA3	1:CH:300:GLN:HG2	1.98	0.45
1:CJ:234:ARG:HG2	1:CJ:280:GLU:HG2	1.98	0.45
1:CN:232:THR:HB	1:CN:334:VAL:HG23	1.99	0.45
1:CR:263:ASN:O	1:CR:267:LYS:HG3	2.16	0.45
1:CS:58:ALA:HB2	1:CS:102:GLY:HA3	1.97	0.45
1:AD:182:LEU:C	1:AD:182:LEU:HD12	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:144:ALA:HB3	1:CG:191:LEU:O	2.17	0.45
1:AG:201:GLY:HA3	1:AG:300:GLN:HG2	1.99	0.45
1:AG:263:ASN:ND2	1:BG:32:PHE:N	2.51	0.45
1:AL:203:THR:HB	1:AL:300:GLN:HG3	1.98	0.45
1:AN:381:MET:HE2	1:AN:381:MET:HB2	1.66	0.45
1:AO:250:TRP:CE3	1:AO:272:TYR:CD1	3.04	0.45
1:AP:18:ARG:CG	1:AP:18:ARG:HH11	2.29	0.45
1:AP:18:ARG:HH11	1:AP:18:ARG:HG3	1.81	0.45
1:AT:318:SER:HA	1:AT:319:GLY:HA2	1.78	0.45
1:BE:237:VAL:HG23	1:BE:279:PHE:CD2	2.52	0.45
1:BH:25:ILE:HG23	1:BH:152:LEU:HD11	1.98	0.45
1:BI:239:ILE:HD12	1:BI:275:GLU:HA	1.98	0.45
1:BL:58:ALA:HB2	1:BL:102:GLY:HA3	1.98	0.45
1:BL:162:PHE:CD2	1:BL:163:LEU:HD13	2.51	0.45
1:BP:79:ARG:CG	1:BP:79:ARG:NH1	2.60	0.45
1:BP:182:LEU:HD12	1:BP:182:LEU:C	2.42	0.45
1:BP:454:ASN:HD21	1:BP:456:ALA:HB3	1.81	0.45
1:BS:75:ARG:NH2	1:BS:391:ALA:O	2.49	0.45
1:BT:237:VAL:HG23	1:BT:279:PHE:CD2	2.51	0.45
1:CF:162:PHE:CD1	1:CG:287:TYR:HA	2.51	0.45
1:CG:232:THR:HB	1:CG:334:VAL:HG23	1.97	0.45
1:CH:182:LEU:C	1:CH:182:LEU:HD12	2.40	0.45
1:CO:226:VAL:HG13	1:CO:228:GLY:H	1.81	0.45
1:CO:234:ARG:HG2	1:CO:280:GLU:HG2	1.97	0.45
1:CT:30:SER:O	1:CT:33:LYS:HB2	2.16	0.45
1:CT:324:LEU:HD23	1:CT:324:LEU:C	2.41	0.45
1:AC:189:PHE:HE1	1:AC:198:ARG:CG	2.27	0.45
1:AF:182:LEU:C	1:AF:182:LEU:HD12	2.42	0.45
1:AF:232:THR:HB	1:AF:334:VAL:CG2	2.46	0.45
1:AI:18:ARG:HG3	1:AI:19:TYR:O	2.16	0.45
1:AK:226:VAL:HG13	1:AK:228:GLY:H	1.81	0.45
1:AK:239:ILE:HG12	1:AK:326:ILE:CD1	2.46	0.45
1:AM:171:ASP:HA	1:AM:172:PRO:HD3	1.79	0.45
1:AP:170:PHE:CD1	1:AP:389:MET:HE1	2.45	0.45
1:AT:232:THR:HB	1:AT:334:VAL:HG23	1.98	0.45
1:AT:381:MET:HE2	1:AT:381:MET:HB2	1.62	0.45
1:BC:454:ASN:HD21	1:BC:456:ALA:HB3	1.82	0.45
1:BD:393:HIS:CG	1:BD:496:PHE:HB3	2.52	0.45
1:BG:239:ILE:HD12	1:BG:275:GLU:HA	1.99	0.45
1:BI:16:ALA:O	1:BI:17:ASN:HB2	2.16	0.45
1:BL:454:ASN:HD21	1:BL:456:ALA:HB3	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:14:CYS:HB3	1:BN:64:LEU:HD21	1.97	0.45
1:BN:381:MET:HE2	1:BN:381:MET:HB2	1.67	0.45
1:BO:234:ARG:HG2	1:BO:280:GLU:HG2	1.97	0.45
1:BO:252:VAL:HG22	1:BO:253:SER:N	2.31	0.45
1:CC:234:ARG:HG2	1:CC:280:GLU:HG2	1.99	0.45
1:CD:440:ALA:CB	1:CE:444:LEU:HD13	2.46	0.45
1:CH:232:THR:HB	1:CH:334:VAL:HG23	1.99	0.45
1:CI:454:ASN:HD21	1:CI:456:ALA:HB3	1.81	0.45
1:CQ:189:PHE:HD2	1:CQ:247:ILE:HD11	1.81	0.45
1:CT:226:VAL:HG13	1:CT:228:GLY:H	1.81	0.45
1:AA:189:PHE:CE2	1:AA:249:LEU:HD21	2.51	0.45
1:AC:73:TYR:O	1:AC:75:ARG:HG2	2.16	0.45
1:AJ:226:VAL:HG13	1:AJ:228:GLY:H	1.82	0.45
1:AJ:234:ARG:HG2	1:AJ:280:GLU:HG2	1.98	0.45
1:AN:272:TYR:N	1:AN:272:TYR:HD1	2.14	0.45
1:AO:324:LEU:HD23	1:AO:324:LEU:C	2.41	0.45
1:AQ:207:VAL:HA	1:AQ:208:PRO:HD3	1.84	0.45
1:BC:55:ARG:HD3	1:BT:272:TYR:CE2	2.51	0.45
1:BC:55:ARG:HD3	1:BT:272:TYR:CD2	2.52	0.45
1:BD:14:CYS:H	1:BD:138:ASN:ND2	2.14	0.45
1:BD:237:VAL:HG23	1:BD:279:PHE:CD2	2.51	0.45
1:BE:324:LEU:C	1:BE:324:LEU:HD23	2.42	0.45
1:BG:234:ARG:HG2	1:BG:280:GLU:HG2	1.99	0.45
1:BH:404:LEU:HD22	1:BH:486:VAL:HG22	1.99	0.45
1:BO:324:LEU:HD23	1:BO:324:LEU:C	2.41	0.45
1:BP:442:GLN:HE21	1:BQ:412:PHE:HB2	1.82	0.45
1:BQ:232:THR:HB	1:BQ:334:VAL:CG2	2.46	0.45
1:BR:189:PHE:HD2	1:BR:247:ILE:HD11	1.81	0.45
1:BR:454:ASN:HD22	1:BR:454:ASN:C	2.25	0.45
1:CA:232:THR:HB	1:CA:334:VAL:HG23	1.99	0.45
1:CF:263:ASN:O	1:CF:267:LYS:HG3	2.16	0.45
1:CH:30:SER:O	1:CH:33:LYS:HB2	2.16	0.45
1:CI:354:SER:O	1:CI:378:ARG:HB3	2.16	0.45
1:CJ:189:PHE:HE1	1:CJ:198:ARG:HG2	1.79	0.45
1:CM:234:ARG:HG2	1:CM:280:GLU:HG2	1.98	0.45
1:CN:189:PHE:CE1	1:CN:198:ARG:HG2	2.51	0.45
1:CN:239:ILE:HD12	1:CN:275:GLU:HA	1.97	0.45
1:CQ:272:TYR:N	1:CQ:272:TYR:HD1	2.15	0.45
1:CS:263:ASN:O	1:CS:267:LYS:HG3	2.16	0.45
1:CT:14:CYS:HB3	1:CT:64:LEU:HD21	1.97	0.45
1:AB:74:ASN:ND2	1:AB:77:THR:OG1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:18:ARG:HG2	1:AC:20:LEU:HD23	1.98	0.45
1:AC:272:TYR:N	1:AC:272:TYR:CD1	2.85	0.45
1:AE:30:SER:O	1:AE:33:LYS:HB2	2.16	0.45
1:AE:182:LEU:C	1:AE:182:LEU:HD12	2.42	0.45
1:AF:75:ARG:NH2	1:AF:391:ALA:O	2.49	0.45
1:AJ:189:PHE:HD2	1:AJ:247:ILE:HD11	1.82	0.45
1:AO:188:PHE:C	1:AO:189:PHE:HD1	2.23	0.45
1:AR:393:HIS:CG	1:AR:496:PHE:HB3	2.52	0.45
1:AS:189:PHE:CE2	1:AS:249:LEU:HD21	2.51	0.45
1:AT:234:ARG:HG2	1:AT:280:GLU:HG2	1.97	0.45
1:AT:272:TYR:N	1:AT:272:TYR:HD1	2.14	0.45
1:BE:226:VAL:HG13	1:BE:228:GLY:H	1.81	0.45
1:BJ:237:VAL:HG23	1:BJ:279:PHE:CD2	2.51	0.45
1:BN:393:HIS:CG	1:BN:496:PHE:HB3	2.51	0.45
1:CB:371:ASP:OD1	1:CB:381:MET:HG2	2.16	0.45
1:CE:79:ARG:HH11	1:CE:79:ARG:CG	2.28	0.45
1:CE:365:ILE:CD1	1:CE:471:MET:HE2	2.47	0.45
1:CG:263:ASN:O	1:CG:267:LYS:HG3	2.15	0.45
1:CH:237:VAL:HG23	1:CH:279:PHE:CD2	2.51	0.45
1:CI:361:GLU:OE1	1:CI:376:THR:HG23	2.17	0.45
1:CJ:20:LEU:HB2	1:CJ:132:PHE:O	2.16	0.45
1:CJ:207:VAL:HA	1:CJ:208:PRO:HD3	1.83	0.45
1:CK:393:HIS:CG	1:CK:496:PHE:HB3	2.52	0.45
1:CL:22:THR:OG1	1:CL:131:HIS:CD2	2.63	0.45
1:CP:18:ARG:HH11	1:CP:18:ARG:HG3	1.82	0.45
1:CQ:30:SER:O	1:CQ:33:LYS:HB2	2.16	0.45
1:AA:381:MET:HE2	1:AA:381:MET:HB2	1.65	0.45
1:AD:203:THR:HB	1:AD:300:GLN:HG3	1.99	0.45
1:AG:324:LEU:HD23	1:AG:324:LEU:C	2.42	0.45
1:AG:371:ASP:OD1	1:AG:381:MET:HG2	2.17	0.45
1:AH:232:THR:HB	1:AH:334:VAL:HG23	1.99	0.45
1:AI:393:HIS:CG	1:AI:496:PHE:HB3	2.52	0.45
1:AJ:162:PHE:CD2	1:AJ:163:LEU:HD13	2.52	0.45
1:AM:272:TYR:CD1	1:AM:272:TYR:N	2.85	0.45
1:AM:440:ALA:CB	1:AN:444:LEU:HD13	2.47	0.45
1:AO:379:VAL:CG1	1:AO:381:MET:HE1	2.47	0.45
1:AP:412:PHE:HB2	1:AT:442:GLN:NE2	2.31	0.45
1:AQ:252:VAL:HG22	1:AQ:253:SER:N	2.32	0.45
1:AR:61:PHE:CD2	1:AR:243:ILE:HD11	2.52	0.45
1:BC:189:PHE:HE1	1:BC:198:ARG:CG	2.26	0.45
1:BE:393:HIS:CG	1:BE:496:PHE:HB3	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:272:TYR:CD1	1:BL:272:TYR:N	2.85	0.45
1:BL:381:MET:HE2	1:BL:381:MET:HB2	1.72	0.45
1:BM:75:ARG:NH2	1:BM:391:ALA:O	2.50	0.45
1:BP:74:ASN:ND2	1:BP:77:THR:OG1	2.50	0.45
1:BP:189:PHE:CE2	1:BP:249:LEU:HD21	2.52	0.45
1:BQ:237:VAL:HG23	1:BQ:279:PHE:CD2	2.52	0.45
1:BQ:272:TYR:N	1:BQ:272:TYR:CD1	2.84	0.45
1:BT:25:ILE:HG23	1:BT:152:LEU:HD11	1.99	0.45
1:CE:197:LEU:HD13	1:CE:309:TYR:CZ	2.51	0.45
1:CH:263:ASN:O	1:CH:267:LYS:HG3	2.17	0.45
1:CI:43:ALA:HB1	1:CI:158:GLU:HA	1.97	0.45
1:CI:189:PHE:HD2	1:CI:247:ILE:HD11	1.81	0.45
1:CK:324:LEU:HD23	1:CK:324:LEU:C	2.42	0.45
1:CL:237:VAL:HG23	1:CL:279:PHE:CD2	2.52	0.45
1:CP:237:VAL:HG23	1:CP:279:PHE:CD2	2.51	0.45
1:CQ:25:ILE:HG23	1:CQ:152:LEU:HD11	1.98	0.45
1:CQ:58:ALA:HB2	1:CQ:102:GLY:HA3	1.98	0.45
1:CR:85:ASP:O	1:CR:86:PRO:C	2.57	0.45
1:CS:162:PHE:CD2	1:CS:163:LEU:HD13	2.51	0.45
1:AA:79:ARG:HH11	1:AA:79:ARG:HG3	1.82	0.45
1:AB:256:ASN:C	1:AB:256:ASN:HD22	2.22	0.45
1:AB:393:HIS:CG	1:AB:496:PHE:HB3	2.51	0.45
1:AD:324:LEU:HD23	1:AD:324:LEU:C	2.41	0.45
1:AE:170:PHE:CD1	1:AE:389:MET:HE1	2.48	0.45
1:AE:207:VAL:HA	1:AE:208:PRO:HD3	1.82	0.45
1:AF:171:ASP:HA	1:AF:172:PRO:HD3	1.79	0.45
1:AG:404:LEU:HD22	1:AG:486:VAL:HG22	1.98	0.45
1:AH:170:PHE:HD1	1:AH:389:MET:CE	2.26	0.45
1:AH:232:THR:HB	1:AH:334:VAL:CG2	2.47	0.45
1:AI:189:PHE:CE1	1:AI:198:ARG:HG2	2.51	0.45
1:AJ:25:ILE:HG23	1:AJ:152:LEU:HD11	1.99	0.45
1:AK:418:SER:HB3	1:AL:407:SER:CB	2.47	0.45
1:AL:234:ARG:HG2	1:AL:280:GLU:HG2	1.99	0.45
1:AM:43:ALA:HB1	1:AM:158:GLU:HA	1.99	0.45
1:AP:203:THR:HB	1:AP:300:GLN:HG3	1.97	0.45
1:AP:272:TYR:N	1:AP:272:TYR:CD1	2.85	0.45
1:AQ:74:ASN:ND2	1:AQ:77:THR:OG1	2.49	0.45
1:BA:237:VAL:HG23	1:BA:279:PHE:CD2	2.51	0.45
1:BC:162:PHE:CD2	1:BC:163:LEU:HD13	2.52	0.45
1:BD:58:ALA:HB2	1:BD:102:GLY:HA3	1.99	0.45
1:BF:404:LEU:HD22	1:BF:486:VAL:HG22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:189:PHE:HD2	1:BG:247:ILE:HD11	1.82	0.45
1:BM:234:ARG:HG2	1:BM:280:GLU:HG2	1.97	0.45
1:BN:232:THR:HB	1:BN:334:VAL:CG2	2.47	0.45
1:BN:318:SER:HA	1:BN:319:GLY:HA2	1.80	0.45
1:BO:263:ASN:O	1:BO:267:LYS:HG3	2.17	0.45
1:BR:272:TYR:N	1:BR:272:TYR:CD1	2.85	0.45
1:BS:16:ALA:O	1:BS:17:ASN:HB2	2.16	0.45
1:BS:182:LEU:C	1:BS:182:LEU:HD12	2.41	0.45
1:CC:232:THR:HB	1:CC:334:VAL:HG23	1.99	0.45
1:CG:189:PHE:CE2	1:CG:249:LEU:HD21	2.44	0.45
1:CH:226:VAL:HG13	1:CH:228:GLY:H	1.82	0.45
1:CH:371:ASP:OD1	1:CH:381:MET:HG2	2.16	0.45
1:CJ:189:PHE:CE1	1:CJ:198:ARG:HG2	2.52	0.45
1:CM:77:THR:O	1:CM:81:THR:HG23	2.16	0.45
1:CP:67:VAL:HG23	1:CP:135:LEU:HB2	1.98	0.45
1:AJ:393:HIS:CG	1:AJ:496:PHE:HB3	2.51	0.45
1:AO:189:PHE:HE2	1:AO:249:LEU:HD21	1.82	0.45
1:AO:207:VAL:HA	1:AO:208:PRO:HD3	1.86	0.45
1:AP:324:LEU:HD23	1:AP:324:LEU:C	2.42	0.45
1:AS:25:ILE:HG23	1:AS:152:LEU:HD11	1.98	0.45
1:AS:250:TRP:CZ3	1:AS:272:TYR:CD1	3.05	0.45
1:BA:381:MET:HE2	1:BA:381:MET:HB2	1.65	0.45
1:BB:237:VAL:HG23	1:BB:279:PHE:CD2	2.51	0.45
1:BB:371:ASP:OD1	1:BB:381:MET:HG2	2.17	0.45
1:BD:61:PHE:CZ	1:BN:243:ILE:HD13	2.51	0.45
1:BE:189:PHE:HD2	1:BE:247:ILE:CD1	2.30	0.45
1:BH:10:ILE:HD13	1:BH:20:LEU:HD13	1.99	0.45
1:BH:226:VAL:HG13	1:BH:228:GLY:H	1.82	0.45
1:BL:182:LEU:C	1:BL:182:LEU:HD12	2.42	0.45
1:BP:237:VAL:HG23	1:BP:279:PHE:CD2	2.51	0.45
1:BR:189:PHE:HD2	1:BR:247:ILE:CD1	2.30	0.45
1:BT:454:ASN:HD21	1:BT:456:ALA:HB3	1.82	0.45
1:CB:442:GLN:HE21	1:CC:412:PHE:HB2	1.82	0.45
1:CE:324:LEU:HD23	1:CE:324:LEU:C	2.42	0.45
1:CF:238:HIS:HE1	1:CF:329:GLN:OE1	2.00	0.45
1:CG:207:VAL:HA	1:CG:208:PRO:HD3	1.82	0.45
1:CI:38:GLU:CB	1:CQ:35:VAL:HG23	2.46	0.45
1:CJ:79:ARG:HH11	1:CJ:79:ARG:CG	2.29	0.45
1:CM:22:THR:OG1	1:CM:131:HIS:CD2	2.63	0.45
1:CM:189:PHE:CE2	1:CM:249:LEU:HD21	2.45	0.45
1:CM:300:GLN:HE21	1:CM:300:GLN:HB2	1.54	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:395:LEU:HB2	1:CM:497:TYR:HB2	1.99	0.45
1:CN:440:ALA:CB	1:CO:444:LEU:HD13	2.47	0.45
1:CN:454:ASN:HD22	1:CN:454:ASN:C	2.25	0.45
1:CO:252:VAL:HG22	1:CO:253:SER:N	2.32	0.45
1:CR:77:THR:O	1:CR:81:THR:CG2	2.65	0.45
1:CR:437:HIS:CE1	1:CS:405:GLN:NE2	2.85	0.45
1:AA:272:TYR:CD2	1:CT:55:ARG:CD	2.99	0.45
1:AC:423:LYS:HE2	1:AC:449:GLU:O	2.17	0.45
1:AD:234:ARG:HG2	1:AD:280:GLU:HG2	1.98	0.45
1:AE:171:ASP:HA	1:AE:172:PRO:HD3	1.79	0.45
1:AH:182:LEU:HG	1:AH:330:ILE:HB	1.98	0.45
1:AI:237:VAL:HG23	1:AI:279:PHE:CD2	2.52	0.45
1:AL:263:ASN:O	1:AL:267:LYS:HG3	2.17	0.45
1:AO:299:SER:O	1:AO:301:ARG:N	2.50	0.45
1:AQ:47:MET:HE2	1:AQ:117:ALA:N	2.32	0.45
1:AT:239:ILE:HG12	1:AT:326:ILE:CD1	2.47	0.45
1:BD:234:ARG:HG2	1:BD:280:GLU:HG2	1.99	0.45
1:BE:47:MET:HE2	1:BE:117:ALA:N	2.32	0.45
1:BI:170:PHE:HD1	1:BI:389:MET:CE	2.30	0.45
1:BJ:163:LEU:HD12	1:BJ:163:LEU:HA	1.84	0.45
1:BJ:232:THR:HB	1:BJ:334:VAL:HG23	1.98	0.45
1:BK:170:PHE:CD1	1:BK:389:MET:HE1	2.48	0.45
1:BK:232:THR:HB	1:BK:334:VAL:CG2	2.46	0.45
1:BL:252:VAL:HG22	1:BL:253:SER:N	2.31	0.45
1:BM:263:ASN:O	1:BM:267:LYS:HG3	2.17	0.45
1:BM:423:LYS:HE2	1:BM:449:GLU:O	2.17	0.45
1:BP:188:PHE:C	1:BP:189:PHE:HD1	2.25	0.45
1:BQ:182:LEU:C	1:BQ:182:LEU:HD12	2.42	0.45
1:CA:163:LEU:HD12	1:CA:163:LEU:HA	1.86	0.45
1:CA:182:LEU:HD12	1:CA:182:LEU:C	2.42	0.45
1:CD:16:ALA:O	1:CD:17:ASN:HB2	2.16	0.45
1:CE:162:PHE:CD2	1:CE:163:LEU:HD13	2.52	0.45
1:CF:381:MET:HE2	1:CF:381:MET:HB2	1.70	0.45
1:CH:74:ASN:ND2	1:CH:77:THR:OG1	2.50	0.45
1:CI:47:MET:HE2	1:CI:117:ALA:N	2.32	0.45
1:CJ:232:THR:HB	1:CJ:334:VAL:HG23	1.99	0.45
1:CS:423:LYS:HE2	1:CS:449:GLU:O	2.17	0.45
1:CT:393:HIS:CG	1:CT:496:PHE:HB3	2.51	0.45
1:AE:47:MET:HE2	1:AE:117:ALA:N	2.32	0.44
1:AF:170:PHE:CD1	1:AF:389:MET:HE1	2.48	0.44
1:AH:237:VAL:HG23	1:AH:279:PHE:CD2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:30:SER:O	1:AK:33:LYS:HB2	2.17	0.44
1:AK:182:LEU:HG	1:AK:330:ILE:HB	1.99	0.44
1:AO:234:ARG:HG2	1:AO:280:GLU:HG2	1.99	0.44
1:AP:393:HIS:CG	1:AP:496:PHE:HB3	2.51	0.44
1:AR:10:ILE:HG21	1:AR:146:TRP:CE2	2.52	0.44
1:AR:25:ILE:HG23	1:AR:152:LEU:HD11	1.99	0.44
1:AS:207:VAL:HA	1:AS:208:PRO:HD3	1.83	0.44
1:AS:454:ASN:HD21	1:AS:456:ALA:HB3	1.82	0.44
1:BA:239:ILE:HD12	1:BA:275:GLU:HA	1.98	0.44
1:BB:324:LEU:HD23	1:BB:324:LEU:C	2.42	0.44
1:BE:234:ARG:HG2	1:BE:280:GLU:HG2	1.98	0.44
1:BH:423:LYS:HE2	1:BH:449:GLU:O	2.16	0.44
1:BJ:232:THR:HB	1:BJ:334:VAL:CG2	2.47	0.44
1:BJ:239:ILE:HD12	1:BJ:275:GLU:HA	2.00	0.44
1:BL:74:ASN:ND2	1:BL:77:THR:OG1	2.50	0.44
1:BN:162:PHE:CD2	1:BN:163:LEU:HD13	2.52	0.44
1:BO:182:LEU:C	1:BO:182:LEU:HD12	2.42	0.44
1:BQ:203:THR:HB	1:BQ:300:GLN:HG3	1.99	0.44
1:CC:25:ILE:HG23	1:CC:152:LEU:HD11	1.99	0.44
1:CC:324:LEU:HD23	1:CC:324:LEU:C	2.42	0.44
1:CD:79:ARG:HG3	1:CD:79:ARG:NH1	2.14	0.44
1:CD:191:LEU:CD2	1:CD:191:LEU:N	2.77	0.44
1:CG:275:GLU:O	1:CG:276:ASP:C	2.60	0.44
1:CN:324:LEU:HD23	1:CN:324:LEU:C	2.42	0.44
1:CO:239:ILE:HD12	1:CO:275:GLU:HA	2.00	0.44
1:CO:275:GLU:O	1:CO:276:ASP:C	2.60	0.44
1:CP:232:THR:HB	1:CP:334:VAL:HG23	1.98	0.44
1:AA:18:ARG:HG3	1:AA:19:TYR:N	2.32	0.44
1:AE:237:VAL:HG23	1:AE:279:PHE:CD2	2.53	0.44
1:AH:35:VAL:O	1:AH:39:LYS:HG3	2.18	0.44
1:AK:414:LYS:HA	1:AL:411:GLU:HB3	1.99	0.44
1:AR:162:PHE:CD1	1:AS:287:TYR:HA	2.53	0.44
1:BB:47:MET:HE2	1:BB:117:ALA:N	2.32	0.44
1:BC:47:MET:HE2	1:BC:117:ALA:N	2.33	0.44
1:BC:239:ILE:HD12	1:BC:275:GLU:HA	1.99	0.44
1:BE:207:VAL:HA	1:BE:208:PRO:HD3	1.83	0.44
1:BE:232:THR:HB	1:BE:334:VAL:CG2	2.47	0.44
1:BG:263:ASN:O	1:BG:267:LYS:HG3	2.17	0.44
1:BI:234:ARG:HG2	1:BI:280:GLU:HG2	1.98	0.44
1:BM:58:ALA:HB2	1:BM:102:GLY:HA3	1.99	0.44
1:BM:207:VAL:HA	1:BM:208:PRO:HD3	1.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:393:HIS:CG	1:BM:496:PHE:HB3	2.52	0.44
1:BN:272:TYR:N	1:BN:272:TYR:CD1	2.86	0.44
1:BO:188:PHE:C	1:BO:189:PHE:HD1	2.25	0.44
1:BO:189:PHE:CE2	1:BO:249:LEU:HD21	2.52	0.44
1:BP:232:THR:HB	1:BP:334:VAL:CG2	2.47	0.44
1:BP:250:TRP:CZ3	1:BP:272:TYR:CD1	3.05	0.44
1:BR:203:THR:HB	1:BR:300:GLN:HG3	1.99	0.44
1:BS:232:THR:HB	1:BS:334:VAL:CG2	2.46	0.44
1:CA:272:TYR:N	1:CA:272:TYR:CD1	2.85	0.44
1:CA:379:VAL:CG1	1:CA:381:MET:HE1	2.47	0.44
1:CB:170:PHE:HD1	1:CB:389:MET:CE	2.28	0.44
1:CB:272:TYR:N	1:CB:272:TYR:CD1	2.85	0.44
1:CC:18:ARG:HG3	1:CC:19:TYR:N	2.31	0.44
1:CK:423:LYS:HE2	1:CK:449:GLU:O	2.17	0.44
1:CL:393:HIS:CG	1:CL:496:PHE:HB3	2.52	0.44
1:CN:239:ILE:HG12	1:CN:326:ILE:CD1	2.47	0.44
1:CQ:162:PHE:CD2	1:CQ:163:LEU:HD13	2.52	0.44
1:CS:47:MET:HE2	1:CS:117:ALA:N	2.32	0.44
1:CS:239:ILE:HD12	1:CS:275:GLU:HA	1.99	0.44
1:AA:207:VAL:HA	1:AA:208:PRO:HD3	1.82	0.44
1:AE:234:ARG:HG2	1:AE:280:GLU:HG2	1.99	0.44
1:AG:423:LYS:HE2	1:AG:449:GLU:O	2.17	0.44
1:AI:272:TYR:N	1:AI:272:TYR:HD1	2.15	0.44
1:AJ:108:ILE:HG23	1:AJ:113:LEU:HD12	2.00	0.44
1:AK:232:THR:HB	1:AK:334:VAL:HG23	1.99	0.44
1:AM:207:VAL:HA	1:AM:208:PRO:HD3	1.82	0.44
1:AT:79:ARG:HH11	1:AT:79:ARG:CG	2.29	0.44
1:BB:55:ARG:NH1	1:CB:272:TYR:CD2	2.85	0.44
1:BB:182:LEU:HD12	1:BB:182:LEU:C	2.41	0.44
1:BC:234:ARG:HG2	1:BC:280:GLU:HG2	2.00	0.44
1:BF:11:PRO:HG2	1:BF:18:ARG:CD	2.48	0.44
1:BG:454:ASN:ND2	1:BG:456:ALA:H	2.11	0.44
1:BJ:75:ARG:NH2	1:BJ:391:ALA:O	2.49	0.44
1:BJ:272:TYR:CD2	1:BQ:55:ARG:NE	2.83	0.44
1:BJ:324:LEU:HD23	1:BJ:324:LEU:C	2.42	0.44
1:BN:191:LEU:CD2	1:BN:191:LEU:N	2.77	0.44
1:BO:250:TRP:HZ3	1:BO:272:TYR:CE1	2.25	0.44
1:BO:393:HIS:CG	1:BO:496:PHE:HB3	2.52	0.44
1:BQ:272:TYR:N	1:BQ:272:TYR:HD1	2.15	0.44
1:BT:188:PHE:C	1:BT:189:PHE:HD1	2.25	0.44
1:CB:207:VAL:HA	1:CB:208:PRO:HD3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:371:ASP:OD1	1:CF:381:MET:HG2	2.17	0.44
1:CG:423:LYS:HE2	1:CG:449:GLU:O	2.17	0.44
1:CM:241:ALA:HB1	1:CM:242:PRO:HD2	1.99	0.44
1:CN:263:ASN:O	1:CN:267:LYS:HG3	2.18	0.44
1:CO:324:LEU:C	1:CO:324:LEU:HD23	2.42	0.44
1:CP:239:ILE:HD12	1:CP:275:GLU:HA	1.98	0.44
1:CQ:300:GLN:HE21	1:CQ:300:GLN:HB2	1.58	0.44
1:AA:42:THR:OG1	1:AB:267:LYS:O	2.26	0.44
1:AA:324:LEU:HD23	1:AA:324:LEU:C	2.43	0.44
1:AC:75:ARG:NH2	1:AC:391:ALA:O	2.51	0.44
1:AC:275:GLU:O	1:AC:276:ASP:C	2.61	0.44
1:AE:272:TYR:N	1:AE:272:TYR:HD1	2.15	0.44
1:AG:55:ARG:HD3	1:CG:272:TYR:HD2	1.76	0.44
1:AG:189:PHE:HD2	1:AG:247:ILE:HD11	1.81	0.44
1:AL:171:ASP:HA	1:AL:172:PRO:HD3	1.79	0.44
1:AM:423:LYS:HE2	1:AM:449:GLU:O	2.18	0.44
1:AN:436:SER:O	1:AO:487:LEU:HD21	2.17	0.44
1:AP:162:PHE:CD2	1:AP:163:LEU:HD13	2.53	0.44
1:AQ:272:TYR:CD2	1:BL:55:ARG:CZ	3.01	0.44
1:AS:423:LYS:HE2	1:AS:449:GLU:O	2.18	0.44
1:BA:170:PHE:HD1	1:BA:389:MET:CE	2.26	0.44
1:BC:61:PHE:CD2	1:BC:243:ILE:HD11	2.53	0.44
1:BE:171:ASP:HA	1:BE:172:PRO:HD3	1.78	0.44
1:BF:202:LEU:HB2	1:BF:304:SER:O	2.17	0.44
1:BH:11:PRO:HG2	1:BH:18:ARG:HD2	1.99	0.44
1:BL:30:SER:O	1:BL:33:LYS:HB2	2.16	0.44
1:BL:238:HIS:HE1	1:BL:329:GLN:OE1	2.01	0.44
1:BM:18:ARG:HG2	1:BM:20:LEU:HD23	2.00	0.44
1:BM:74:ASN:ND2	1:BM:77:THR:OG1	2.51	0.44
1:BO:22:THR:OG1	1:BO:131:HIS:CD2	2.65	0.44
1:BO:318:SER:HA	1:BO:319:GLY:HA2	1.80	0.44
1:BQ:170:PHE:CD1	1:BQ:389:MET:HE1	2.46	0.44
1:BS:237:VAL:HG23	1:BS:279:PHE:CD2	2.53	0.44
1:CA:189:PHE:HE2	1:CA:249:LEU:HD21	1.82	0.44
1:CB:234:ARG:HG2	1:CB:280:GLU:HG2	2.00	0.44
1:CF:407:SER:HB3	1:CJ:418:SER:HB3	1.99	0.44
1:CG:11:PRO:HG2	1:CG:18:ARG:HD2	2.00	0.44
1:CG:393:HIS:CG	1:CG:496:PHE:HB3	2.52	0.44
1:CG:434:GLY:O	1:CH:349:VAL:HG23	2.18	0.44
1:CH:252:VAL:HG22	1:CH:253:SER:N	2.33	0.44
1:CI:14:CYS:H	1:CI:138:ASN:ND2	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:30:SER:O	1:CI:33:LYS:HB2	2.18	0.44
1:CK:25:ILE:HG23	1:CK:152:LEU:HD11	1.99	0.44
1:CP:404:LEU:HD22	1:CP:486:VAL:HG22	1.99	0.44
1:CR:318:SER:HA	1:CR:319:GLY:HA2	1.81	0.44
1:CS:191:LEU:CD2	1:CS:191:LEU:N	2.77	0.44
1:AA:14:CYS:H	1:AA:138:ASN:ND2	2.12	0.44
1:AA:263:ASN:O	1:AA:267:LYS:HG3	2.17	0.44
1:AD:232:THR:HB	1:AD:334:VAL:HG23	2.00	0.44
1:AD:393:HIS:CG	1:AD:496:PHE:HB3	2.52	0.44
1:AE:404:LEU:HD22	1:AE:486:VAL:HG22	1.98	0.44
1:AH:252:VAL:HG22	1:AH:253:SER:N	2.32	0.44
1:AI:404:LEU:HD22	1:AI:486:VAL:HG22	1.99	0.44
1:AK:393:HIS:CG	1:AK:496:PHE:HB3	2.52	0.44
1:AL:237:VAL:HG23	1:AL:279:PHE:CD2	2.52	0.44
1:AM:189:PHE:HD2	1:AM:247:ILE:CD1	2.31	0.44
1:AN:234:ARG:HG2	1:AN:280:GLU:HG2	1.99	0.44
1:AO:237:VAL:HG23	1:AO:279:PHE:CD2	2.53	0.44
1:AP:272:TYR:CE2	1:BE:55:ARG:CZ	3.00	0.44
1:BC:182:LEU:HG	1:BC:330:ILE:HB	1.98	0.44
1:BE:232:THR:HB	1:BE:334:VAL:HG23	2.00	0.44
1:BF:203:THR:HB	1:BF:300:GLN:HG3	1.99	0.44
1:BI:25:ILE:HG23	1:BI:152:LEU:HD11	1.99	0.44
1:BM:232:THR:HB	1:BM:334:VAL:HG23	2.00	0.44
1:BM:237:VAL:HG23	1:BM:279:PHE:CD2	2.52	0.44
1:BN:234:ARG:HG2	1:BN:280:GLU:HG2	2.00	0.44
1:BP:234:ARG:HG2	1:BP:280:GLU:HG2	2.00	0.44
1:BP:239:ILE:HD12	1:BP:275:GLU:HA	2.00	0.44
1:BR:237:VAL:HG23	1:BR:279:PHE:CD2	2.52	0.44
1:CB:237:VAL:HG23	1:CB:279:PHE:CD2	2.53	0.44
1:CC:43:ALA:HB1	1:CC:158:GLU:HA	1.99	0.44
1:CD:203:THR:HB	1:CD:300:GLN:HG3	1.98	0.44
1:CF:170:PHE:HD1	1:CF:389:MET:CE	2.25	0.44
1:CH:234:ARG:HG2	1:CH:280:GLU:HG2	2.00	0.44
1:CJ:191:LEU:O	1:CQ:144:ALA:HB3	2.17	0.44
1:CK:272:TYR:N	1:CK:272:TYR:HD1	2.16	0.44
1:CN:398:GLY:HA3	1:CN:494:PHE:CD2	2.52	0.44
1:CS:189:PHE:CE2	1:CS:249:LEU:HD21	2.53	0.44
1:CT:162:PHE:CD2	1:CT:163:LEU:HD13	2.53	0.44
1:AE:232:THR:HB	1:AE:334:VAL:CG2	2.48	0.44
1:AF:263:ASN:O	1:AF:267:LYS:HG3	2.16	0.44
1:AF:393:HIS:CG	1:AF:496:PHE:HB3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:14:CYS:H	1:AG:138:ASN:ND2	2.15	0.44
1:AK:454:ASN:HD21	1:AK:456:ALA:HB3	1.83	0.44
1:AL:191:LEU:O	1:CJ:144:ALA:HB3	2.18	0.44
1:AN:207:VAL:HA	1:AN:208:PRO:HD3	1.83	0.44
1:AT:189:PHE:CE2	1:AT:249:LEU:HD21	2.52	0.44
1:BA:263:ASN:O	1:BA:267:LYS:HG3	2.17	0.44
1:BB:10:ILE:HA	1:BB:11:PRO:HD3	1.80	0.44
1:BE:263:ASN:O	1:BE:267:LYS:HG3	2.18	0.44
1:BK:239:ILE:HD12	1:BK:275:GLU:HA	2.00	0.44
1:BN:203:THR:HB	1:BN:300:GLN:CD	2.43	0.44
1:BN:440:ALA:CB	1:BO:444:LEU:HD13	2.47	0.44
1:BP:226:VAL:HG13	1:BP:228:GLY:H	1.82	0.44
1:BQ:263:ASN:O	1:BQ:267:LYS:HG3	2.17	0.44
1:BQ:393:HIS:CG	1:BQ:496:PHE:HB3	2.53	0.44
1:BS:188:PHE:C	1:BS:189:PHE:HD1	2.25	0.44
1:CA:189:PHE:CE2	1:CA:249:LEU:HD21	2.53	0.44
1:CB:393:HIS:CG	1:CB:496:PHE:HB3	2.53	0.44
1:CC:393:HIS:CG	1:CC:496:PHE:HB3	2.52	0.44
1:CE:189:PHE:HD2	1:CE:247:ILE:HD11	1.81	0.44
1:CF:239:ILE:HD12	1:CF:275:GLU:HA	1.99	0.44
1:CH:423:LYS:HE2	1:CH:449:GLU:O	2.18	0.44
1:CK:381:MET:HE2	1:CK:381:MET:HB2	1.64	0.44
1:CO:79:ARG:NH1	1:CO:79:ARG:CG	2.79	0.44
1:CO:191:LEU:CD2	1:CO:191:LEU:N	2.76	0.44
1:CQ:171:ASP:HA	1:CQ:172:PRO:HD3	1.78	0.44
1:CQ:188:PHE:C	1:CQ:189:PHE:HD1	2.25	0.44
1:CS:182:LEU:C	1:CS:182:LEU:HD12	2.42	0.44
1:CT:79:ARG:HH11	1:CT:79:ARG:HG3	1.83	0.44
1:CT:171:ASP:HA	1:CT:172:PRO:HD3	1.79	0.44
1:CT:207:VAL:HA	1:CT:208:PRO:HD3	1.84	0.44
1:CT:423:LYS:HE2	1:CT:449:GLU:O	2.18	0.44
1:AD:365:ILE:CD1	1:AD:471:MET:HE2	2.46	0.44
1:AE:232:THR:HB	1:AE:334:VAL:HG23	1.98	0.44
1:AG:252:VAL:HG22	1:AG:253:SER:N	2.33	0.44
1:AM:30:SER:O	1:AM:33:LYS:HB2	2.16	0.44
1:AP:38:GLU:HB2	1:BL:35:VAL:HG22	2.00	0.44
1:AS:324:LEU:HD23	1:AS:324:LEU:C	2.43	0.44
1:AT:393:HIS:CG	1:AT:496:PHE:HB3	2.52	0.44
1:BC:18:ARG:HG3	1:BC:19:TYR:N	2.31	0.44
1:BC:182:LEU:C	1:BC:182:LEU:HD12	2.42	0.44
1:BF:25:ILE:HG23	1:BF:152:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:423:LYS:HE2	1:BF:449:GLU:O	2.17	0.44
1:BG:74:ASN:ND2	1:BG:77:THR:OG1	2.51	0.44
1:BI:191:LEU:CD2	1:BI:191:LEU:N	2.74	0.44
1:BJ:182:LEU:HG	1:BJ:330:ILE:HB	1.99	0.44
1:BJ:189:PHE:HD2	1:BJ:247:ILE:CD1	2.30	0.44
1:BK:162:PHE:CD2	1:BK:163:LEU:HD13	2.53	0.44
1:BK:393:HIS:CG	1:BK:496:PHE:HB3	2.52	0.44
1:BL:170:PHE:CD1	1:BL:389:MET:HE1	2.49	0.44
1:BL:404:LEU:HD22	1:BL:486:VAL:HG22	1.99	0.44
1:BP:289:ARG:NH1	1:BP:337:ASP:OD1	2.51	0.44
1:BQ:234:ARG:HG2	1:BQ:280:GLU:HG2	2.00	0.44
1:BT:272:TYR:N	1:BT:272:TYR:CD1	2.86	0.44
1:CB:189:PHE:CE2	1:CB:249:LEU:HD21	2.48	0.44
1:CC:170:PHE:CD1	1:CC:389:MET:HE1	2.47	0.44
1:CC:189:PHE:HD2	1:CC:247:ILE:HD11	1.82	0.44
1:CD:226:VAL:HG13	1:CD:228:GLY:H	1.82	0.44
1:CD:237:VAL:HG23	1:CD:279:PHE:CD2	2.53	0.44
1:CI:299:SER:OG	1:CI:301:ARG:HG2	2.18	0.44
1:CK:58:ALA:HB2	1:CK:102:GLY:HA3	1.99	0.44
1:CP:189:PHE:CE2	1:CP:249:LEU:HD21	2.53	0.44
1:CQ:75:ARG:NH2	1:CQ:391:ALA:O	2.48	0.44
1:CQ:239:ILE:HD12	1:CQ:275:GLU:HA	1.99	0.44
1:CQ:252:VAL:HG22	1:CQ:253:SER:N	2.33	0.44
1:CR:239:ILE:HG12	1:CR:326:ILE:CD1	2.48	0.44
1:AA:170:PHE:CD1	1:AA:389:MET:HE1	2.46	0.44
1:AA:272:TYR:N	1:AA:272:TYR:HD1	2.15	0.44
1:AC:182:LEU:HD12	1:AC:182:LEU:C	2.43	0.44
1:AF:162:PHE:CD1	1:AG:287:TYR:HA	2.53	0.44
1:AF:272:TYR:N	1:AF:272:TYR:CD1	2.84	0.44
1:AH:423:LYS:HE2	1:AH:449:GLU:O	2.18	0.44
1:AI:25:ILE:HG23	1:AI:152:LEU:HD11	1.98	0.44
1:AI:250:TRP:HZ3	1:AI:272:TYR:CE1	2.31	0.44
1:AI:272:TYR:CD2	1:AO:55:ARG:NH1	2.86	0.44
1:AJ:55:ARG:CZ	1:BL:272:TYR:CE2	3.01	0.44
1:AJ:232:THR:HB	1:AJ:334:VAL:CG2	2.47	0.44
1:AJ:239:ILE:HG12	1:AJ:326:ILE:CD1	2.48	0.44
1:AJ:250:TRP:HZ3	1:AJ:272:TYR:CE1	2.29	0.44
1:AP:381:MET:HE2	1:AP:381:MET:HB2	1.69	0.44
1:BB:170:PHE:CD1	1:BB:389:MET:HE1	2.49	0.44
1:BB:239:ILE:HD12	1:BB:275:GLU:HA	2.00	0.44
1:BB:381:MET:HE2	1:BB:381:MET:HB2	1.61	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:272:TYR:N	1:BC:272:TYR:CD1	2.85	0.44
1:BE:170:PHE:HD1	1:BE:389:MET:CE	2.28	0.44
1:BN:434:GLY:O	1:BO:349:VAL:HG23	2.18	0.44
1:BP:288:HIS:HD2	1:BP:337:ASP:OD2	2.00	0.44
1:BQ:423:LYS:HE2	1:BQ:449:GLU:O	2.18	0.44
1:BR:170:PHE:HD1	1:BR:389:MET:CE	2.27	0.44
1:BS:263:ASN:O	1:BS:267:LYS:HG3	2.18	0.44
1:BT:58:ALA:HB2	1:BT:102:GLY:HA3	2.00	0.44
1:CA:239:ILE:HD12	1:CA:275:GLU:HA	2.00	0.44
1:CC:423:LYS:HE2	1:CC:449:GLU:O	2.18	0.44
1:CF:189:PHE:HD2	1:CF:247:ILE:HD11	1.81	0.44
1:CI:170:PHE:CD1	1:CI:389:MET:HE1	2.48	0.44
1:CI:237:VAL:HG23	1:CI:279:PHE:CD2	2.53	0.44
1:CO:74:ASN:ND2	1:CO:77:THR:OG1	2.51	0.44
1:CS:393:HIS:CG	1:CS:496:PHE:HB3	2.53	0.44
1:AC:232:THR:HB	1:AC:334:VAL:HG23	2.00	0.44
1:AC:381:MET:HB2	1:AC:381:MET:HE2	1.66	0.44
1:AC:440:ALA:CB	1:AD:444:LEU:HD13	2.48	0.44
1:AD:55:ARG:CZ	1:AN:272:TYR:CD2	3.01	0.44
1:AE:393:HIS:CG	1:AE:496:PHE:HB3	2.53	0.44
1:AF:234:ARG:HG2	1:AF:280:GLU:HG2	1.99	0.44
1:AF:272:TYR:N	1:AF:272:TYR:HD1	2.16	0.44
1:AH:272:TYR:N	1:AH:272:TYR:CD1	2.85	0.44
1:AK:423:LYS:HE2	1:AK:449:GLU:O	2.18	0.44
1:AM:25:ILE:HG23	1:AM:152:LEU:HD11	2.00	0.44
1:AO:171:ASP:HA	1:AO:172:PRO:HD3	1.81	0.44
1:AO:252:VAL:HG22	1:AO:253:SER:N	2.33	0.44
1:BA:404:LEU:HD22	1:BA:486:VAL:HG22	1.98	0.44
1:BA:444:LEU:HD13	1:BE:440:ALA:CB	2.48	0.44
1:BB:16:ALA:O	1:BB:17:ASN:CB	2.64	0.44
1:BB:234:ARG:CG	1:BB:280:GLU:HG2	2.48	0.44
1:BD:163:LEU:HD12	1:BD:163:LEU:HA	1.87	0.44
1:BE:11:PRO:HG2	1:BE:18:ARG:CD	2.48	0.44
1:BL:47:MET:HE2	1:BL:117:ALA:N	2.33	0.44
1:BM:239:ILE:HD12	1:BM:275:GLU:HA	1.99	0.44
1:BO:275:GLU:O	1:BO:276:ASP:C	2.61	0.44
1:BS:189:PHE:CE2	1:BS:249:LEU:HD21	2.53	0.44
1:CD:232:THR:HB	1:CD:334:VAL:CG2	2.48	0.44
1:CD:381:MET:HE2	1:CD:381:MET:HB2	1.63	0.44
1:CH:365:ILE:CD1	1:CH:471:MET:HE2	2.47	0.44
1:CI:182:LEU:C	1:CI:182:LEU:HD12	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:14:CYS:H	1:CL:138:ASN:ND2	2.12	0.44
1:CL:272:TYR:N	1:CL:272:TYR:CD1	2.84	0.44
1:CN:365:ILE:CD1	1:CN:471:MET:HE2	2.48	0.44
1:CN:423:LYS:HE2	1:CN:449:GLU:O	2.17	0.44
1:CQ:43:ALA:HB1	1:CQ:158:GLU:HA	1.99	0.44
1:CR:86:PRO:HA	1:CR:89:THR:OG1	2.17	0.44
1:CT:188:PHE:C	1:CT:189:PHE:HD1	2.26	0.44
1:AB:454:ASN:ND2	1:AB:456:ALA:H	2.10	0.43
1:AE:275:GLU:O	1:AE:276:ASP:C	2.61	0.43
1:AI:207:VAL:HA	1:AI:208:PRO:HD3	1.84	0.43
1:AI:232:THR:HB	1:AI:334:VAL:HG23	1.98	0.43
1:AK:239:ILE:HD12	1:AK:275:GLU:HA	2.00	0.43
1:AL:189:PHE:CE2	1:AL:249:LEU:HD21	2.50	0.43
1:AN:238:HIS:HE1	1:AN:329:GLN:OE1	2.01	0.43
1:AQ:272:TYR:CE2	1:BL:55:ARG:CZ	3.01	0.43
1:BB:250:TRP:HZ3	1:BB:272:TYR:HE1	1.63	0.43
1:BH:272:TYR:N	1:BH:272:TYR:HD1	2.15	0.43
1:BI:203:THR:HB	1:BI:300:GLN:HG3	2.00	0.43
1:BK:272:TYR:N	1:BK:272:TYR:CD1	2.86	0.43
1:BK:404:LEU:HD22	1:BK:486:VAL:HG22	1.99	0.43
1:BM:232:THR:HB	1:BM:334:VAL:CG2	2.47	0.43
1:BN:108:ILE:HG23	1:BN:113:LEU:HD12	2.00	0.43
1:BO:14:CYS:H	1:BO:138:ASN:ND2	2.14	0.43
1:BR:25:ILE:HG23	1:BR:152:LEU:HD11	2.00	0.43
1:BT:232:THR:HB	1:BT:334:VAL:HG23	2.00	0.43
1:CC:171:ASP:HA	1:CC:172:PRO:HD3	1.79	0.43
1:CE:239:ILE:HD12	1:CE:275:GLU:HA	2.00	0.43
1:CH:272:TYR:N	1:CH:272:TYR:CD1	2.86	0.43
1:CI:272:TYR:HD2	1:CO:55:ARG:HD3	1.82	0.43
1:CK:252:VAL:HG22	1:CK:253:SER:N	2.33	0.43
1:CO:272:TYR:N	1:CO:272:TYR:CD1	2.84	0.43
1:CR:226:VAL:HG13	1:CR:228:GLY:H	1.83	0.43
1:CS:188:PHE:C	1:CS:189:PHE:HD1	2.26	0.43
1:AB:442:GLN:HE21	1:AC:412:PHE:HB2	1.83	0.43
1:AC:404:LEU:HD22	1:AC:486:VAL:HG22	1.99	0.43
1:AE:170:PHE:HD1	1:AE:389:MET:CE	2.29	0.43
1:AL:22:THR:OG1	1:AL:131:HIS:CD2	2.63	0.43
1:AL:47:MET:HE2	1:AL:117:ALA:N	2.33	0.43
1:AL:440:ALA:HB3	1:AM:444:LEU:HD13	2.00	0.43
1:AM:22:THR:OG1	1:AM:131:HIS:CD2	2.63	0.43
1:AN:30:SER:O	1:AN:33:LYS:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:263:ASN:O	1:AN:267:LYS:HG3	2.17	0.43
1:AP:239:ILE:HD12	1:AP:275:GLU:HA	2.00	0.43
1:AR:324:LEU:HD23	1:AR:324:LEU:C	2.43	0.43
1:AT:55:ARG:HD3	1:BA:272:TYR:HD2	1.81	0.43
1:BB:232:THR:HB	1:BB:334:VAL:CG2	2.48	0.43
1:BC:108:ILE:HG23	1:BC:113:LEU:HD12	2.00	0.43
1:BF:252:VAL:HG22	1:BF:253:SER:N	2.33	0.43
1:BI:379:VAL:CG1	1:BI:381:MET:HE1	2.47	0.43
1:BJ:191:LEU:HD23	1:BJ:191:LEU:N	2.13	0.43
1:BN:324:LEU:HD23	1:BN:324:LEU:C	2.44	0.43
1:BO:239:ILE:HD12	1:BO:275:GLU:HA	1.99	0.43
1:BR:182:LEU:C	1:BR:182:LEU:HD12	2.43	0.43
1:BS:395:LEU:HB2	1:BS:497:TYR:HB2	2.00	0.43
1:CA:18:ARG:HG3	1:CA:19:TYR:N	2.32	0.43
1:CA:58:ALA:HB2	1:CA:102:GLY:HA3	2.00	0.43
1:CD:182:LEU:C	1:CD:182:LEU:HD12	2.43	0.43
1:CG:79:ARG:CG	1:CG:79:ARG:NH1	2.70	0.43
1:CL:30:SER:O	1:CL:33:LYS:HB2	2.17	0.43
1:CL:381:MET:HE2	1:CL:381:MET:HB2	1.69	0.43
1:CN:15:GLN:OE1	1:CN:15:GLN:HA	2.17	0.43
1:CO:454:ASN:HD21	1:CO:456:ALA:HB3	1.82	0.43
1:CQ:237:VAL:HG23	1:CQ:279:PHE:CD2	2.52	0.43
1:CR:272:TYR:N	1:CR:272:TYR:CD1	2.86	0.43
1:CT:237:VAL:HG23	1:CT:279:PHE:CD2	2.53	0.43
1:AA:43:ALA:HB1	1:AA:158:GLU:HA	2.00	0.43
1:AB:38:GLU:HB2	1:BA:35:VAL:HG22	2.00	0.43
1:AB:202:LEU:HB2	1:AB:304:SER:O	2.19	0.43
1:AC:22:THR:OG1	1:AC:131:HIS:CD2	2.66	0.43
1:AC:272:TYR:N	1:AC:272:TYR:HD1	2.16	0.43
1:AG:237:VAL:HG23	1:AG:279:PHE:CD2	2.54	0.43
1:AI:324:LEU:C	1:AI:324:LEU:HD23	2.44	0.43
1:AQ:371:ASP:OD1	1:AQ:381:MET:HG2	2.18	0.43
1:AR:77:THR:O	1:AR:81:THR:HG23	2.18	0.43
1:AS:191:LEU:CD2	1:AS:191:LEU:N	2.79	0.43
1:AT:163:LEU:HD12	1:AT:163:LEU:HA	1.85	0.43
1:BB:226:VAL:HG13	1:BB:228:GLY:H	1.84	0.43
1:BC:239:ILE:HG23	1:BC:324:LEU:HD21	2.00	0.43
1:BF:237:VAL:HG23	1:BF:279:PHE:CD2	2.54	0.43
1:BF:365:ILE:CD1	1:BF:471:MET:HE2	2.46	0.43
1:BH:14:CYS:H	1:BH:138:ASN:ND2	2.13	0.43
1:BH:163:LEU:HD12	1:BH:163:LEU:HA	1.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:35:VAL:HG22	1:BQ:38:GLU:HB2	1.99	0.43
1:BJ:209:MET:HE2	1:BJ:209:MET:HB3	1.93	0.43
1:BL:67:VAL:HG23	1:BL:135:LEU:HB2	1.98	0.43
1:CA:237:VAL:HG23	1:CA:279:PHE:CD2	2.53	0.43
1:CE:170:PHE:HD1	1:CE:389:MET:CE	2.29	0.43
1:CE:171:ASP:HA	1:CE:172:PRO:HD3	1.80	0.43
1:CF:189:PHE:HE1	1:CF:198:ARG:HG2	1.76	0.43
1:CG:237:VAL:HG23	1:CG:279:PHE:CD2	2.53	0.43
1:CH:404:LEU:HD22	1:CH:486:VAL:HG22	1.99	0.43
1:CI:234:ARG:HG2	1:CI:280:GLU:HG2	1.99	0.43
1:CI:239:ILE:HG12	1:CI:326:ILE:CD1	2.48	0.43
1:CJ:209:MET:HE2	1:CJ:209:MET:HB3	1.91	0.43
1:CJ:232:THR:HB	1:CJ:334:VAL:CG2	2.47	0.43
1:CR:232:THR:HB	1:CR:334:VAL:HG23	2.00	0.43
1:CS:237:VAL:HG23	1:CS:279:PHE:CD2	2.53	0.43
1:AA:8:ILE:HG22	1:AA:10:ILE:CD1	2.49	0.43
1:AB:454:ASN:HD21	1:AB:456:ALA:HB3	1.82	0.43
1:AC:232:THR:HB	1:AC:334:VAL:CG2	2.49	0.43
1:AC:252:VAL:HG22	1:AC:253:SER:N	2.33	0.43
1:AF:423:LYS:HE2	1:AF:449:GLU:O	2.18	0.43
1:AG:38:GLU:HB2	1:CF:35:VAL:CG2	2.49	0.43
1:AG:209:MET:HE2	1:AG:209:MET:HB3	1.94	0.43
1:AH:55:ARG:NH1	1:AK:272:TYR:CD2	2.86	0.43
1:AH:272:TYR:N	1:AH:272:TYR:HD1	2.16	0.43
1:AJ:207:VAL:HA	1:AJ:208:PRO:HD3	1.80	0.43
1:AK:252:VAL:HG22	1:AK:253:SER:N	2.33	0.43
1:AN:300:GLN:HE21	1:AN:300:GLN:HB2	1.60	0.43
1:AN:324:LEU:HD23	1:AN:324:LEU:C	2.43	0.43
1:AO:250:TRP:CZ3	1:AO:272:TYR:CD1	3.07	0.43
1:AO:263:ASN:O	1:AO:267:LYS:HG3	2.17	0.43
1:AO:272:TYR:CD2	1:AR:55:ARG:CZ	3.01	0.43
1:AO:401:ASP:O	1:AO:488:CYS:HA	2.19	0.43
1:AP:318:SER:HA	1:AP:319:GLY:HA2	1.76	0.43
1:AQ:275:GLU:O	1:AQ:276:ASP:C	2.61	0.43
1:AR:252:VAL:HG22	1:AR:253:SER:N	2.33	0.43
1:AS:74:ASN:ND2	1:AS:77:THR:OG1	2.52	0.43
1:AT:30:SER:O	1:AT:33:LYS:HB2	2.19	0.43
1:BC:324:LEU:HD23	1:BC:324:LEU:C	2.44	0.43
1:BD:423:LYS:HE2	1:BD:449:GLU:O	2.17	0.43
1:BD:454:ASN:HD21	1:BD:456:ALA:HB3	1.82	0.43
1:BD:454:ASN:ND2	1:BD:456:ALA:H	2.14	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:11:PRO:HG2	1:BI:18:ARG:HD2	2.00	0.43
1:BJ:10:ILE:CD1	1:BJ:20:LEU:HD13	2.49	0.43
1:BO:61:PHE:CD2	1:BO:243:ILE:HD11	2.53	0.43
1:BT:314:PRO:HB3	1:BT:324:LEU:HD13	2.01	0.43
1:BT:318:SER:HA	1:BT:319:GLY:HA2	1.81	0.43
1:BT:371:ASP:OD1	1:BT:381:MET:HG2	2.19	0.43
1:CB:381:MET:HE2	1:CB:381:MET:HB2	1.72	0.43
1:CE:371:ASP:OD1	1:CE:381:MET:HG2	2.18	0.43
1:CE:423:LYS:HE2	1:CE:449:GLU:O	2.17	0.43
1:CG:232:THR:HB	1:CG:334:VAL:CG2	2.48	0.43
1:CH:170:PHE:HD1	1:CH:389:MET:CE	2.27	0.43
1:CO:207:VAL:HA	1:CO:208:PRO:HD3	1.83	0.43
1:CP:25:ILE:HG23	1:CP:152:LEU:HD11	2.01	0.43
1:CP:256:ASN:HD22	1:CP:302:ASP:HA	1.84	0.43
1:AA:55:ARG:CZ	1:CC:272:TYR:CD2	3.02	0.43
1:AA:454:ASN:HD21	1:AA:456:ALA:HB3	1.84	0.43
1:AB:371:ASP:OD1	1:AB:381:MET:HG2	2.19	0.43
1:AC:300:GLN:HE21	1:AC:300:GLN:HB2	1.53	0.43
1:AF:55:ARG:CZ	1:BH:272:TYR:CE2	3.01	0.43
1:AF:404:LEU:HD22	1:AF:486:VAL:HG22	2.00	0.43
1:AK:232:THR:HB	1:AK:334:VAL:CG2	2.49	0.43
1:AK:237:VAL:HG23	1:AK:279:PHE:CD2	2.54	0.43
1:AL:55:ARG:HD3	1:CQ:272:TYR:HD2	1.80	0.43
1:AL:182:LEU:C	1:AL:182:LEU:HD12	2.43	0.43
1:AM:275:GLU:O	1:AM:276:ASP:C	2.61	0.43
1:AQ:226:VAL:HG13	1:AQ:228:GLY:H	1.83	0.43
1:AR:440:ALA:CB	1:AS:444:LEU:HD13	2.49	0.43
1:BB:203:THR:HB	1:BB:300:GLN:HG3	2.00	0.43
1:BB:238:HIS:HE1	1:BB:329:GLN:OE1	2.02	0.43
1:BC:18:ARG:HG2	1:BC:20:LEU:HD23	2.01	0.43
1:BG:189:PHE:HD2	1:BG:247:ILE:CD1	2.31	0.43
1:BG:404:LEU:HD23	1:BG:404:LEU:N	2.32	0.43
1:BI:189:PHE:CE2	1:BI:249:LEU:HD21	2.45	0.43
1:BL:226:VAL:HG13	1:BL:228:GLY:H	1.82	0.43
1:BO:61:PHE:CE2	1:BO:243:ILE:HD11	2.53	0.43
1:BP:55:ARG:CZ	1:CM:272:TYR:CE2	3.01	0.43
1:BP:79:ARG:HG3	1:BP:79:ARG:NH1	2.26	0.43
1:CD:239:ILE:HD12	1:CD:275:GLU:HA	1.99	0.43
1:CH:232:THR:HB	1:CH:334:VAL:CG2	2.49	0.43
1:CJ:25:ILE:HG23	1:CJ:152:LEU:HD11	2.01	0.43
1:CJ:47:MET:HE2	1:CJ:117:ALA:N	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:189:PHE:HD2	1:CJ:247:ILE:HD11	1.83	0.43
1:CL:272:TYR:N	1:CL:272:TYR:HD1	2.16	0.43
1:CO:250:TRP:CE3	1:CO:272:TYR:CD1	3.07	0.43
1:CO:404:LEU:N	1:CO:404:LEU:HD23	2.32	0.43
1:CP:226:VAL:HG13	1:CP:228:GLY:H	1.82	0.43
1:AB:43:ALA:HB1	1:AB:158:GLU:HA	2.01	0.43
1:AB:404:LEU:HD22	1:AB:486:VAL:HG22	2.00	0.43
1:AC:226:VAL:HG13	1:AC:228:GLY:H	1.83	0.43
1:AC:234:ARG:HG2	1:AC:280:GLU:HG2	2.00	0.43
1:AE:55:ARG:NH1	1:CP:272:TYR:CD2	2.86	0.43
1:AG:254:GLU:OE1	1:AG:259:THR:CG2	2.67	0.43
1:AK:10:ILE:HA	1:AK:11:PRO:HD3	1.88	0.43
1:AK:61:PHE:CD2	1:AK:243:ILE:HD11	2.54	0.43
1:AM:189:PHE:HD2	1:AM:247:ILE:HD11	1.83	0.43
1:AM:237:VAL:HG23	1:AM:279:PHE:CD2	2.54	0.43
1:AO:189:PHE:CE2	1:AO:249:LEU:HD21	2.53	0.43
1:AO:423:LYS:HE2	1:AO:449:GLU:O	2.18	0.43
1:AQ:234:ARG:CG	1:AQ:280:GLU:HG2	2.49	0.43
1:BC:423:LYS:HE2	1:BC:449:GLU:O	2.19	0.43
1:BD:272:TYR:CE2	1:BS:55:ARG:CZ	3.01	0.43
1:BF:189:PHE:HD2	1:BF:247:ILE:HD11	1.82	0.43
1:BH:189:PHE:HD2	1:BH:247:ILE:HD11	1.83	0.43
1:BI:272:TYR:N	1:BI:272:TYR:HD1	2.16	0.43
1:BJ:201:GLY:HA3	1:BJ:300:GLN:HG2	2.00	0.43
1:BM:324:LEU:HD23	1:BM:324:LEU:C	2.43	0.43
1:BP:55:ARG:NE	1:CM:272:TYR:HE2	2.10	0.43
1:BP:182:LEU:HG	1:BP:330:ILE:HB	1.99	0.43
1:CA:318:SER:HA	1:CA:319:GLY:HA2	1.77	0.43
1:CB:226:VAL:HG13	1:CB:228:GLY:H	1.84	0.43
1:CG:252:VAL:HG22	1:CG:253:SER:N	2.34	0.43
1:CJ:250:TRP:HZ3	1:CJ:272:TYR:HE1	1.58	0.43
1:CL:58:ALA:HB2	1:CL:102:GLY:HA3	2.00	0.43
1:CR:14:CYS:H	1:CR:138:ASN:ND2	2.15	0.43
1:CT:239:ILE:HD12	1:CT:275:GLU:HA	2.01	0.43
1:AD:55:ARG:NE	1:AN:272:TYR:HE2	2.11	0.43
1:AE:255:TRP:CE3	1:AE:285:SER:HB2	2.53	0.43
1:AH:171:ASP:HA	1:AH:172:PRO:HD3	1.78	0.43
1:AI:239:ILE:HD12	1:AI:275:GLU:HA	2.01	0.43
1:AN:14:CYS:H	1:AN:138:ASN:ND2	2.17	0.43
1:AQ:237:VAL:HG23	1:AQ:279:PHE:CD2	2.54	0.43
1:AR:442:GLN:NE2	1:AS:412:PHE:HB2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:188:PHE:C	1:AT:189:PHE:HD1	2.27	0.43
1:BB:263:ASN:O	1:BB:267:LYS:HG3	2.18	0.43
1:BC:11:PRO:HG2	1:BC:18:ARG:HD2	2.00	0.43
1:BE:404:LEU:HD22	1:BE:486:VAL:HG22	2.00	0.43
1:BF:232:THR:HB	1:BF:334:VAL:HG23	2.00	0.43
1:BF:272:TYR:N	1:BF:272:TYR:CD1	2.84	0.43
1:BF:437:HIS:CE1	1:BG:405:GLN:NE2	2.87	0.43
1:BG:318:SER:HA	1:BG:319:GLY:HA2	1.81	0.43
1:BH:15:GLN:NE2	1:BH:15:GLN:CA	2.80	0.43
1:BK:234:ARG:HG2	1:BK:280:GLU:HG2	1.99	0.43
1:BK:440:ALA:CB	1:BL:444:LEU:HD13	2.48	0.43
1:BN:232:THR:HB	1:BN:334:VAL:HG23	2.00	0.43
1:BO:250:TRP:HE3	1:BO:272:TYR:CD1	2.36	0.43
1:BO:423:LYS:HE2	1:BO:449:GLU:O	2.19	0.43
1:BP:207:VAL:HA	1:BP:208:PRO:HD3	1.83	0.43
1:BT:226:VAL:HG13	1:BT:228:GLY:H	1.83	0.43
1:CA:79:ARG:HG3	1:CA:79:ARG:NH1	2.29	0.43
1:CD:234:ARG:HG2	1:CD:280:GLU:HG2	1.99	0.43
1:CE:25:ILE:HG23	1:CE:152:LEU:HD11	2.01	0.43
1:CE:43:ALA:HB1	1:CE:158:GLU:HA	2.00	0.43
1:CE:324:LEU:HA	1:CE:325:PRO:HD3	1.85	0.43
1:CK:47:MET:HE2	1:CK:117:ALA:N	2.34	0.43
1:CK:232:THR:HB	1:CK:334:VAL:CG2	2.49	0.43
1:CN:404:LEU:HD22	1:CN:486:VAL:HG22	2.00	0.43
1:CP:163:LEU:HD12	1:CP:163:LEU:HA	1.90	0.43
1:AA:423:LYS:HE2	1:AA:449:GLU:O	2.18	0.43
1:AE:272:TYR:CE2	1:AM:55:ARG:CZ	3.01	0.43
1:AK:440:ALA:CB	1:AL:444:LEU:HD13	2.49	0.43
1:AL:404:LEU:N	1:AL:404:LEU:HD23	2.34	0.43
1:AL:418:SER:HB3	1:AM:407:SER:CB	2.49	0.43
1:AR:55:ARG:HG2	1:AR:55:ARG:HH11	1.83	0.43
1:AR:440:ALA:HB3	1:AS:444:LEU:HD13	2.01	0.43
1:AT:207:VAL:HA	1:AT:208:PRO:HD3	1.85	0.43
1:AT:237:VAL:HG23	1:AT:279:PHE:CD2	2.54	0.43
1:AT:365:ILE:CD1	1:AT:471:MET:HE2	2.48	0.43
1:BG:423:LYS:HE2	1:BG:449:GLU:O	2.18	0.43
1:BI:55:ARG:CD	1:BR:272:TYR:CD2	2.98	0.43
1:BI:300:GLN:HE21	1:BI:300:GLN:HB2	1.61	0.43
1:BI:404:LEU:N	1:BI:404:LEU:HD23	2.33	0.43
1:BK:207:VAL:HA	1:BK:208:PRO:HD3	1.86	0.43
1:BL:234:ARG:HG2	1:BL:280:GLU:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:437:HIS:CE1	1:BM:405:GLN:NE2	2.86	0.43
1:BN:437:HIS:CE1	1:BO:405:GLN:NE2	2.86	0.43
1:BO:237:VAL:HG23	1:BO:279:PHE:CD2	2.53	0.43
1:BP:300:GLN:HE21	1:BP:300:GLN:HB2	1.58	0.43
1:BP:393:HIS:CG	1:BP:496:PHE:HB3	2.54	0.43
1:BT:365:ILE:CD1	1:BT:471:MET:HE2	2.48	0.43
1:CA:381:MET:HE2	1:CA:381:MET:HB2	1.71	0.43
1:CA:423:LYS:HE2	1:CA:449:GLU:O	2.19	0.43
1:CB:79:ARG:HG3	1:CB:79:ARG:NH1	2.30	0.43
1:CB:272:TYR:N	1:CB:272:TYR:HD1	2.16	0.43
1:CC:209:MET:HE2	1:CC:209:MET:HB3	1.94	0.43
1:CD:189:PHE:HE2	1:CD:249:LEU:CD2	2.31	0.43
1:CD:272:TYR:CD2	1:CS:55:ARG:CD	2.97	0.43
1:CH:79:ARG:NH1	1:CH:79:ARG:CG	2.77	0.43
1:CH:272:TYR:N	1:CH:272:TYR:HD1	2.17	0.43
1:CI:272:TYR:CE2	1:CO:55:ARG:CZ	3.01	0.43
1:CI:272:TYR:CE2	1:CO:55:ARG:HD3	2.52	0.43
1:CI:275:GLU:O	1:CI:276:ASP:C	2.62	0.43
1:CJ:182:LEU:C	1:CJ:182:LEU:HD12	2.43	0.43
1:CL:423:LYS:HE2	1:CL:449:GLU:O	2.18	0.43
1:AB:189:PHE:HD2	1:AB:247:ILE:HD11	1.83	0.43
1:AF:275:GLU:O	1:AF:276:ASP:C	2.62	0.43
1:AF:381:MET:HE2	1:AF:381:MET:HB2	1.63	0.43
1:AM:10:ILE:HA	1:AM:11:PRO:HD3	1.89	0.43
1:AO:182:LEU:C	1:AO:182:LEU:HD12	2.43	0.43
1:AQ:440:ALA:HB3	1:AR:444:LEU:HD13	2.00	0.43
1:AT:232:THR:HB	1:AT:334:VAL:CG2	2.48	0.43
1:BA:487:LEU:HD21	1:BE:436:SER:O	2.19	0.43
1:BC:18:ARG:NH1	1:BC:18:ARG:HB2	2.34	0.43
1:BE:189:PHE:HD2	1:BE:247:ILE:HD11	1.83	0.43
1:BF:239:ILE:HD12	1:BF:275:GLU:HA	1.99	0.43
1:BH:171:ASP:HA	1:BH:172:PRO:HD3	1.78	0.43
1:BK:226:VAL:HG13	1:BK:228:GLY:H	1.83	0.43
1:BM:404:LEU:HD22	1:BM:486:VAL:HG22	2.00	0.43
1:BP:201:GLY:HA3	1:BP:300:GLN:HG2	1.99	0.43
1:BP:381:MET:HE2	1:BP:381:MET:HB2	1.67	0.43
1:BQ:272:TYR:CE2	1:CL:55:ARG:CZ	3.02	0.43
1:BR:14:CYS:H	1:BR:138:ASN:HD21	1.65	0.43
1:BS:239:ILE:HD12	1:BS:275:GLU:HA	2.01	0.43
1:CA:263:ASN:O	1:CA:267:LYS:HG3	2.18	0.43
1:CD:162:PHE:CD2	1:CD:163:LEU:HD13	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CD:189:PHE:HD2	1:CD:247:ILE:HD11	1.83	0.43
1:CD:418:SER:HB3	1:CE:407:SER:CB	2.49	0.43
1:CF:22:THR:OG1	1:CF:131:HIS:CD2	2.63	0.43
1:CI:381:MET:HB2	1:CI:381:MET:HE2	1.72	0.43
1:CL:9:TYR:HE1	1:CL:147:GLN:NE2	2.12	0.43
1:CM:189:PHE:HD2	1:CM:247:ILE:HD11	1.84	0.43
1:CM:423:LYS:HE2	1:CM:449:GLU:O	2.19	0.43
1:CN:171:ASP:HA	1:CN:172:PRO:HD3	1.78	0.43
1:CO:232:THR:HB	1:CO:334:VAL:CG2	2.49	0.43
1:CP:318:SER:HA	1:CP:319:GLY:HA2	1.75	0.43
1:AA:365:ILE:CD1	1:AA:471:MET:HE2	2.48	0.43
1:AB:404:LEU:N	1:AB:404:LEU:HD23	2.34	0.43
1:AC:272:TYR:CD2	1:BA:55:ARG:HD3	2.54	0.43
1:AD:55:ARG:HD3	1:AN:272:TYR:HD2	1.83	0.43
1:AG:436:SER:O	1:AH:487:LEU:HD21	2.18	0.43
1:AH:47:MET:HE2	1:AH:117:ALA:N	2.33	0.43
1:AI:232:THR:HB	1:AI:334:VAL:CG2	2.48	0.43
1:AJ:263:ASN:O	1:AJ:267:LYS:HG3	2.18	0.43
1:AK:404:LEU:HD22	1:AK:486:VAL:HG22	2.00	0.43
1:AK:437:HIS:CE1	1:AL:405:GLN:NE2	2.87	0.43
1:AN:189:PHE:HE1	1:AN:198:ARG:HG2	1.78	0.43
1:AN:423:LYS:HE2	1:AN:449:GLU:O	2.19	0.43
1:AP:171:ASP:HA	1:AP:172:PRO:HD3	1.79	0.43
1:AQ:404:LEU:N	1:AQ:404:LEU:HD23	2.34	0.43
1:AR:365:ILE:CD1	1:AR:471:MET:HE2	2.49	0.43
1:BA:191:LEU:CD2	1:BA:191:LEU:N	2.77	0.43
1:BD:207:VAL:HA	1:BD:208:PRO:HD3	1.81	0.43
1:BD:275:GLU:O	1:BD:276:ASP:C	2.61	0.43
1:BE:272:TYR:N	1:BE:272:TYR:HD1	2.16	0.43
1:BH:209:MET:HE2	1:BH:209:MET:HB3	1.92	0.43
1:BJ:25:ILE:HG23	1:BJ:152:LEU:HD11	2.01	0.43
1:BK:252:VAL:HG22	1:BK:253:SER:N	2.33	0.43
1:BK:440:ALA:HB3	1:BL:444:LEU:HD13	2.01	0.43
1:BL:423:LYS:HE2	1:BL:449:GLU:O	2.18	0.43
1:BP:232:THR:HB	1:BP:334:VAL:HG23	2.01	0.43
1:BS:11:PRO:HG2	1:BS:18:ARG:HD2	2.01	0.43
1:BT:252:VAL:HG22	1:BT:253:SER:N	2.33	0.43
1:CC:18:ARG:HG2	1:CC:20:LEU:HD23	2.01	0.43
1:CD:25:ILE:HG23	1:CD:152:LEU:HD11	2.01	0.43
1:CD:404:LEU:HD22	1:CD:486:VAL:HG22	2.00	0.43
1:CE:252:VAL:HG22	1:CE:253:SER:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:256:ASN:HD22	1:CE:302:ASP:HA	1.84	0.43
1:CF:272:TYR:N	1:CF:272:TYR:HD1	2.16	0.43
1:CI:378:ARG:CD	1:CI:379:VAL:H	2.31	0.43
1:CN:189:PHE:CE2	1:CN:249:LEU:HD21	2.44	0.43
1:CO:58:ALA:HB2	1:CO:102:GLY:HA3	1.99	0.43
1:CP:170:PHE:HD1	1:CP:389:MET:CE	2.30	0.43
1:CP:454:ASN:HD21	1:CP:456:ALA:HB3	1.84	0.43
1:CQ:423:LYS:HE2	1:CQ:449:GLU:O	2.19	0.43
1:AB:232:THR:HB	1:AB:334:VAL:CG2	2.49	0.42
1:AD:10:ILE:CD1	1:AD:20:LEU:HD13	2.49	0.42
1:AD:11:PRO:HG2	1:AD:18:ARG:CD	2.48	0.42
1:AD:272:TYR:HD2	1:AS:55:ARG:HD3	1.81	0.42
1:AE:263:ASN:O	1:AE:267:LYS:HG3	2.19	0.42
1:AI:442:GLN:NE2	1:AJ:412:PHE:HB2	2.34	0.42
1:AL:9:TYR:CE1	1:AL:147:GLN:NE2	2.87	0.42
1:AP:163:LEU:HD12	1:AP:163:LEU:HA	1.90	0.42
1:AR:207:VAL:HA	1:AR:208:PRO:HD3	1.84	0.42
1:AT:191:LEU:HD23	1:AT:191:LEU:N	2.21	0.42
1:BF:189:PHE:CE2	1:BF:249:LEU:HD21	2.49	0.42
1:BF:226:VAL:HG13	1:BF:228:GLY:H	1.84	0.42
1:BH:252:VAL:HG22	1:BH:253:SER:N	2.33	0.42
1:BN:163:LEU:HD12	1:BN:163:LEU:HA	1.89	0.42
1:BO:454:ASN:ND2	1:BO:456:ALA:H	2.12	0.42
1:BS:209:MET:HE2	1:BS:209:MET:HB3	1.91	0.42
1:CC:454:ASN:HD21	1:CC:456:ALA:HB3	1.82	0.42
1:CD:14:CYS:H	1:CD:138:ASN:ND2	2.13	0.42
1:CH:25:ILE:HG23	1:CH:152:LEU:HD11	2.01	0.42
1:CI:25:ILE:HG23	1:CI:152:LEU:HD11	2.01	0.42
1:CK:209:MET:HE2	1:CK:209:MET:HB3	1.89	0.42
1:CL:318:SER:HA	1:CL:319:GLY:HA2	1.79	0.42
1:CM:189:PHE:HE1	1:CM:198:ARG:HG2	1.76	0.42
1:CO:243:ILE:HD13	1:CR:61:PHE:CZ	2.54	0.42
1:AB:324:LEU:HD23	1:AB:324:LEU:C	2.44	0.42
1:AC:18:ARG:HG3	1:AC:19:TYR:N	2.34	0.42
1:AC:404:LEU:N	1:AC:404:LEU:HD23	2.34	0.42
1:AE:61:PHE:CZ	1:CP:243:ILE:HD13	2.54	0.42
1:AF:55:ARG:CZ	1:BH:272:TYR:CD2	3.02	0.42
1:AG:234:ARG:CG	1:AG:280:GLU:HG2	2.49	0.42
1:AH:404:LEU:HD22	1:AH:486:VAL:HG22	2.00	0.42
1:AI:55:ARG:HD2	1:AR:272:TYR:HE2	1.81	0.42
1:AJ:272:TYR:CD2	1:AQ:55:ARG:CD	3.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:189:PHE:HE2	1:AK:249:LEU:HD21	1.84	0.42
1:AL:423:LYS:HE2	1:AL:449:GLU:O	2.19	0.42
1:AM:170:PHE:CD1	1:AM:389:MET:HE1	2.52	0.42
1:AM:209:MET:HE2	1:AM:209:MET:HB3	1.94	0.42
1:AP:234:ARG:HG2	1:AP:280:GLU:HG2	2.01	0.42
1:AP:423:LYS:HE2	1:AP:449:GLU:O	2.19	0.42
1:AQ:324:LEU:HD23	1:AQ:324:LEU:C	2.45	0.42
1:AT:25:ILE:HG23	1:AT:152:LEU:HD11	2.01	0.42
1:BA:226:VAL:HG13	1:BA:228:GLY:H	1.84	0.42
1:BC:381:MET:HE2	1:BC:381:MET:HB2	1.70	0.42
1:BG:11:PRO:HG2	1:BG:18:ARG:CD	2.49	0.42
1:BG:237:VAL:HG23	1:BG:279:PHE:CD2	2.54	0.42
1:BK:263:ASN:O	1:BK:267:LYS:HG3	2.20	0.42
1:BK:381:MET:HE2	1:BK:381:MET:HB2	1.68	0.42
1:BP:250:TRP:HZ3	1:BP:272:TYR:CE1	2.27	0.42
1:BR:79:ARG:CG	1:BR:79:ARG:NH1	2.77	0.42
1:BS:207:VAL:HA	1:BS:208:PRO:HD3	1.85	0.42
1:CB:189:PHE:HD2	1:CB:247:ILE:HD11	1.83	0.42
1:CC:232:THR:HB	1:CC:334:VAL:CG2	2.50	0.42
1:CF:25:ILE:HG23	1:CF:152:LEU:HD11	2.01	0.42
1:CF:300:GLN:HE21	1:CF:300:GLN:HB2	1.57	0.42
1:CG:47:MET:HE2	1:CG:117:ALA:N	2.34	0.42
1:CH:393:HIS:CG	1:CH:496:PHE:HB3	2.53	0.42
1:CI:263:ASN:O	1:CI:267:LYS:HG3	2.18	0.42
1:CL:189:PHE:CE2	1:CL:249:LEU:HD21	2.54	0.42
1:CM:207:VAL:HA	1:CM:208:PRO:HD3	1.85	0.42
1:CN:191:LEU:CD2	1:CN:191:LEU:N	2.75	0.42
1:CP:454:ASN:ND2	1:CP:456:ALA:H	2.13	0.42
1:CR:418:SER:HB3	1:CS:407:SER:HB3	2.01	0.42
1:AA:232:THR:HB	1:AA:334:VAL:HG23	2.01	0.42
1:AC:272:TYR:CE2	1:BA:55:ARG:CZ	3.03	0.42
1:AE:55:ARG:CD	1:CP:272:TYR:CD2	2.98	0.42
1:AG:170:PHE:HD1	1:AG:389:MET:CE	2.29	0.42
1:AJ:285:SER:HA	1:AJ:286:PRO:HD3	1.91	0.42
1:AJ:318:SER:HA	1:AJ:319:GLY:HA2	1.80	0.42
1:AL:272:TYR:N	1:AL:272:TYR:CD1	2.86	0.42
1:AL:395:LEU:HB2	1:AL:497:TYR:HB2	2.01	0.42
1:AR:74:ASN:ND2	1:AR:77:THR:OG1	2.52	0.42
1:BD:263:ASN:O	1:BD:267:LYS:HG3	2.19	0.42
1:BF:75:ARG:NH2	1:BF:391:ALA:O	2.50	0.42
1:BF:191:LEU:HD23	1:BF:191:LEU:N	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:15:GLN:HA	1:BG:15:GLN:NE2	2.30	0.42
1:BH:33:LYS:O	1:BH:33:LYS:CG	2.62	0.42
1:BI:234:ARG:CG	1:BI:280:GLU:HG2	2.49	0.42
1:BI:381:MET:HE2	1:BI:381:MET:HB2	1.64	0.42
1:BJ:182:LEU:C	1:BJ:182:LEU:HD12	2.44	0.42
1:BK:25:ILE:HG23	1:BK:152:LEU:HD11	2.01	0.42
1:BM:203:THR:CB	1:BM:300:GLN:HG3	2.49	0.42
1:BO:11:PRO:HG2	1:BO:18:ARG:HD2	2.01	0.42
1:BS:324:LEU:C	1:BS:324:LEU:HD23	2.44	0.42
1:CE:22:THR:OG1	1:CE:131:HIS:CD2	2.58	0.42
1:CI:170:PHE:HD1	1:CI:389:MET:CE	2.29	0.42
1:CN:272:TYR:CD1	1:CN:272:TYR:N	2.87	0.42
1:CO:209:MET:HE2	1:CO:209:MET:HB3	1.92	0.42
1:CO:234:ARG:CG	1:CO:280:GLU:HG2	2.50	0.42
1:CP:170:PHE:CD1	1:CP:389:MET:HE1	2.49	0.42
1:AA:404:LEU:HD22	1:AA:486:VAL:HG22	2.00	0.42
1:AC:440:ALA:HB3	1:AD:444:LEU:HD13	2.02	0.42
1:AF:347:TYR:O	1:AJ:435:PRO:HB3	2.18	0.42
1:AH:14:CYS:H	1:AH:138:ASN:ND2	2.16	0.42
1:AI:404:LEU:N	1:AI:404:LEU:HD23	2.34	0.42
1:AN:252:VAL:HG22	1:AN:253:SER:N	2.34	0.42
1:AQ:272:TYR:N	1:AQ:272:TYR:CD1	2.85	0.42
1:AS:202:LEU:HD23	1:AS:202:LEU:HA	1.92	0.42
1:BA:73:TYR:CE2	1:BA:394:GLY:HA3	2.54	0.42
1:BA:189:PHE:HD2	1:BA:247:ILE:CD1	2.33	0.42
1:BA:423:LYS:HE2	1:BA:449:GLU:O	2.19	0.42
1:BD:300:GLN:HE21	1:BD:300:GLN:HB2	1.51	0.42
1:BF:79:ARG:CG	1:BF:79:ARG:NH1	2.80	0.42
1:BF:272:TYR:N	1:BF:272:TYR:HD1	2.17	0.42
1:BJ:324:LEU:HA	1:BJ:325:PRO:HD3	1.84	0.42
1:BJ:423:LYS:HE2	1:BJ:449:GLU:O	2.18	0.42
1:BL:7:VAL:HG12	1:BL:9:TYR:CE2	2.55	0.42
1:BL:324:LEU:HD23	1:BL:324:LEU:C	2.44	0.42
1:BO:175:PHE:CD2	1:BO:175:PHE:O	2.72	0.42
1:BP:25:ILE:HG23	1:BP:152:LEU:HD11	2.01	0.42
1:BS:239:ILE:HG23	1:BS:324:LEU:HD21	2.02	0.42
1:CD:43:ALA:HB1	1:CD:158:GLU:HA	2.00	0.42
1:CE:237:VAL:HG23	1:CE:279:PHE:CD2	2.54	0.42
1:CJ:171:ASP:HA	1:CJ:172:PRO:HD3	1.78	0.42
1:CJ:252:VAL:HG22	1:CJ:253:SER:N	2.35	0.42
1:CJ:404:LEU:HD22	1:CJ:486:VAL:HG22	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:324:LEU:HA	1:CM:325:PRO:HD3	1.89	0.42
1:CN:404:LEU:N	1:CN:404:LEU:HD23	2.35	0.42
1:CO:189:PHE:CE2	1:CO:249:LEU:HD21	2.53	0.42
1:CP:171:ASP:HA	1:CP:172:PRO:HD3	1.76	0.42
1:CP:234:ARG:HG2	1:CP:280:GLU:HG2	1.99	0.42
1:CQ:170:PHE:HD1	1:CQ:389:MET:CE	2.26	0.42
1:CT:234:ARG:HG2	1:CT:280:GLU:HG2	2.01	0.42
1:AA:300:GLN:HE21	1:AA:300:GLN:HB2	1.61	0.42
1:AE:12:LYS:HB3	1:AE:144:ALA:C	2.45	0.42
1:AI:454:ASN:ND2	1:AI:456:ALA:H	2.12	0.42
1:AJ:163:LEU:HD12	1:AJ:163:LEU:HA	1.88	0.42
1:AK:182:LEU:C	1:AK:182:LEU:HD12	2.44	0.42
1:AK:340:LEU:HD23	1:AK:340:LEU:HA	1.89	0.42
1:AN:209:MET:HE2	1:AN:209:MET:HB3	1.93	0.42
1:AO:229:MET:O	1:AO:290:THR:HG22	2.19	0.42
1:AP:189:PHE:HD2	1:AP:247:ILE:HD11	1.83	0.42
1:AQ:423:LYS:HE2	1:AQ:449:GLU:O	2.20	0.42
1:AR:170:PHE:HD1	1:AR:389:MET:CE	2.29	0.42
1:AR:226:VAL:HG13	1:AR:228:GLY:H	1.85	0.42
1:BK:423:LYS:HE2	1:BK:449:GLU:O	2.19	0.42
1:BM:171:ASP:HA	1:BM:172:PRO:HD3	1.79	0.42
1:BP:404:LEU:HD22	1:BP:486:VAL:HG22	2.01	0.42
1:BR:182:LEU:HG	1:BR:330:ILE:HB	2.01	0.42
1:BS:272:TYR:N	1:BS:272:TYR:CD1	2.88	0.42
1:CA:19:TYR:CZ	1:CA:81:THR:HG22	2.55	0.42
1:CA:36:GLN:HE22	1:CA:156:LEU:H	1.64	0.42
1:CC:263:ASN:O	1:CC:267:LYS:HG3	2.19	0.42
1:CH:14:CYS:H	1:CH:138:ASN:ND2	2.18	0.42
1:CJ:22:THR:OG1	1:CJ:131:HIS:CD2	2.60	0.42
1:CL:191:LEU:HD23	1:CL:191:LEU:N	2.19	0.42
1:CL:209:MET:HE2	1:CL:209:MET:HB3	1.97	0.42
1:CM:252:VAL:HG22	1:CM:253:SER:N	2.35	0.42
1:CQ:209:MET:HE2	1:CQ:209:MET:HB3	1.91	0.42
1:AA:239:ILE:HG23	1:AA:324:LEU:HD21	2.01	0.42
1:AB:423:LYS:HE2	1:AB:449:GLU:O	2.20	0.42
1:AC:74:ASN:ND2	1:AC:77:THR:OG1	2.53	0.42
1:AD:239:ILE:HD12	1:AD:275:GLU:HA	2.01	0.42
1:AE:74:ASN:ND2	1:AE:77:THR:OG1	2.53	0.42
1:AF:74:ASN:ND2	1:AF:77:THR:OG1	2.53	0.42
1:AF:241:ALA:HB1	1:AF:242:PRO:HD2	2.02	0.42
1:AF:371:ASP:OD1	1:AF:381:MET:HG2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:418:SER:HB3	1:AH:407:SER:HB3	2.02	0.42
1:AJ:263:ASN:HD22	1:AQ:5:ARG:HD3	1.84	0.42
1:AJ:324:LEU:HD23	1:AJ:324:LEU:C	2.44	0.42
1:AJ:423:LYS:HE2	1:AJ:449:GLU:O	2.20	0.42
1:AK:14:CYS:HB3	1:AK:64:LEU:HD21	2.01	0.42
1:AK:61:PHE:CE2	1:AK:243:ILE:HD11	2.55	0.42
1:AL:232:THR:HB	1:AL:334:VAL:HG23	2.01	0.42
1:AL:239:ILE:HG12	1:AL:326:ILE:CD1	2.50	0.42
1:AQ:79:ARG:HG3	1:AQ:79:ARG:NH1	2.32	0.42
1:AQ:272:TYR:N	1:AQ:272:TYR:HD1	2.18	0.42
1:AQ:340:LEU:HA	1:AQ:340:LEU:HD23	1.86	0.42
1:AT:55:ARG:CZ	1:BA:272:TYR:CE2	3.03	0.42
1:BC:171:ASP:HA	1:BC:172:PRO:HD3	1.78	0.42
1:BF:418:SER:HB3	1:BG:407:SER:HB3	2.01	0.42
1:BO:25:ILE:HD12	1:BO:128:PRO:HB2	2.01	0.42
1:BR:404:LEU:HD22	1:BR:486:VAL:HG22	2.01	0.42
1:BS:47:MET:HE2	1:BS:117:ALA:N	2.34	0.42
1:BS:275:GLU:O	1:BS:276:ASP:C	2.61	0.42
1:BS:300:GLN:HE21	1:BS:300:GLN:HB2	1.57	0.42
1:CF:284:ARG:CG	1:CF:284:ARG:NH1	2.74	0.42
1:CJ:300:GLN:HE21	1:CJ:300:GLN:HB2	1.59	0.42
1:CL:162:PHE:CD1	1:CM:287:TYR:HA	2.54	0.42
1:CM:108:ILE:HG23	1:CM:113:LEU:HD12	2.02	0.42
1:CN:47:MET:HE2	1:CN:117:ALA:N	2.35	0.42
1:CN:237:VAL:HG23	1:CN:279:PHE:CD2	2.54	0.42
1:CO:263:ASN:O	1:CO:267:LYS:HG3	2.19	0.42
1:CP:250:TRP:CE3	1:CP:272:TYR:CD1	3.08	0.42
1:CR:79:ARG:NH1	1:CR:79:ARG:HG3	2.15	0.42
1:AA:10:ILE:HG21	1:AA:146:TRP:CZ2	2.54	0.42
1:AF:191:LEU:CD2	1:AF:191:LEU:N	2.78	0.42
1:AF:232:THR:HB	1:AF:334:VAL:HG23	2.01	0.42
1:AF:318:SER:HA	1:AF:319:GLY:HA2	1.82	0.42
1:AI:55:ARG:NE	1:AR:272:TYR:CD2	2.87	0.42
1:AK:285:SER:HA	1:AK:286:PRO:HD3	1.93	0.42
1:AL:454:ASN:HD21	1:AL:456:ALA:HB3	1.84	0.42
1:AM:10:ILE:HG21	1:AM:146:TRP:CZ2	2.54	0.42
1:AM:381:MET:HE2	1:AM:381:MET:HB2	1.73	0.42
1:AN:55:ARG:CD	1:AS:272:TYR:CD2	3.00	0.42
1:AP:255:TRP:CE3	1:AP:285:SER:HB2	2.55	0.42
1:BA:182:LEU:C	1:BA:182:LEU:HD12	2.45	0.42
1:BG:454:ASN:HD22	1:BG:454:ASN:C	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:237:VAL:HG23	1:BI:279:PHE:CD2	2.54	0.42
1:BN:25:ILE:HG23	1:BN:152:LEU:HD11	2.01	0.42
1:CC:182:LEU:C	1:CC:182:LEU:HD12	2.44	0.42
1:CD:250:TRP:CE3	1:CD:272:TYR:CD1	3.07	0.42
1:CD:423:LYS:HE2	1:CD:449:GLU:O	2.20	0.42
1:CE:20:LEU:HB2	1:CE:132:PHE:O	2.19	0.42
1:CG:22:THR:OG1	1:CG:131:HIS:CD2	2.61	0.42
1:CH:324:LEU:HD23	1:CH:324:LEU:C	2.45	0.42
1:CK:318:SER:HA	1:CK:319:GLY:HA2	1.77	0.42
1:CM:237:VAL:HG23	1:CM:279:PHE:CD2	2.55	0.42
1:CR:83:SER:OG	1:CR:84:ALA:N	2.50	0.42
1:CS:252:VAL:HG22	1:CS:253:SER:N	2.35	0.42
1:AA:36:GLN:HE22	1:AA:156:LEU:H	1.68	0.42
1:AA:234:ARG:HG2	1:AA:280:GLU:HG2	2.01	0.42
1:AA:272:TYR:CD2	1:CT:55:ARG:CZ	3.03	0.42
1:AB:185:PRO:HA	1:AB:186:PRO:HD3	1.92	0.42
1:AD:191:LEU:HD23	1:AD:191:LEU:N	2.18	0.42
1:AD:232:THR:HB	1:AD:334:VAL:CG2	2.49	0.42
1:AH:272:TYR:HD2	1:CF:55:ARG:HD3	1.79	0.42
1:AJ:272:TYR:N	1:AJ:272:TYR:CD1	2.86	0.42
1:AN:79:ARG:CG	1:AN:79:ARG:NH1	2.74	0.42
1:AP:189:PHE:HE2	1:AP:249:LEU:CD2	2.33	0.42
1:AQ:108:ILE:HG23	1:AQ:113:LEU:HD12	2.00	0.42
1:BC:318:SER:HA	1:BC:319:GLY:HA2	1.78	0.42
1:BD:185:PRO:HA	1:BD:186:PRO:HD3	1.91	0.42
1:BG:182:LEU:C	1:BG:182:LEU:HD12	2.45	0.42
1:BL:188:PHE:C	1:BL:189:PHE:HD1	2.28	0.42
1:BL:207:VAL:HA	1:BL:208:PRO:HD3	1.87	0.42
1:BN:423:LYS:HE2	1:BN:449:GLU:O	2.20	0.42
1:BR:28:MET:CE	1:BR:152:LEU:HG	2.50	0.42
1:BT:14:CYS:H	1:BT:138:ASN:ND2	2.14	0.42
1:CA:234:ARG:CG	1:CA:280:GLU:HG2	2.49	0.42
1:CB:418:SER:HB3	1:CC:407:SER:HB3	2.01	0.42
1:CC:226:VAL:HG13	1:CC:228:GLY:H	1.85	0.42
1:CE:189:PHE:CE1	1:CE:198:ARG:HG2	2.53	0.42
1:CE:234:ARG:CG	1:CE:280:GLU:HG2	2.50	0.42
1:CF:20:LEU:HB2	1:CF:132:PHE:O	2.19	0.42
1:CG:209:MET:HE2	1:CG:209:MET:HB3	1.91	0.42
1:CG:395:LEU:HB2	1:CG:497:TYR:HB2	2.02	0.42
1:CH:207:VAL:HA	1:CH:208:PRO:HD3	1.84	0.42
1:CI:324:LEU:HA	1:CI:325:PRO:HD3	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CI:373:THR:CG2	1:CI:374:SER:N	2.83	0.42
1:CL:239:ILE:HD12	1:CL:275:GLU:HA	2.01	0.42
1:CM:201:GLY:HA3	1:CM:300:GLN:HG2	2.02	0.42
1:CN:162:PHE:CD2	1:CN:163:LEU:HD13	2.55	0.42
1:CO:108:ILE:HG23	1:CO:113:LEU:HD12	2.02	0.42
1:CO:237:VAL:HG23	1:CO:279:PHE:CD2	2.55	0.42
1:CO:381:MET:HB2	1:CO:381:MET:HE2	1.68	0.42
1:CQ:324:LEU:HD23	1:CQ:324:LEU:C	2.44	0.42
1:CR:47:MET:HE2	1:CR:117:ALA:N	2.35	0.42
1:CR:232:THR:HB	1:CR:334:VAL:CG2	2.49	0.42
1:AA:285:SER:HA	1:AA:286:PRO:HD3	1.92	0.42
1:AD:47:MET:HE2	1:AD:117:ALA:N	2.35	0.42
1:AH:58:ALA:HB2	1:AH:102:GLY:HA3	2.02	0.42
1:AI:79:ARG:NH1	1:AI:79:ARG:CG	2.79	0.42
1:AI:423:LYS:HE2	1:AI:449:GLU:O	2.19	0.42
1:AN:442:GLN:HE21	1:AO:412:PHE:HB2	1.85	0.42
1:AQ:77:THR:O	1:AQ:81:THR:HG23	2.20	0.42
1:AQ:263:ASN:O	1:AQ:267:LYS:HG3	2.19	0.42
1:AR:47:MET:HE2	1:AR:117:ALA:N	2.35	0.42
1:AT:324:LEU:HA	1:AT:325:PRO:HD3	1.87	0.42
1:BB:252:VAL:HG22	1:BB:253:SER:N	2.35	0.42
1:BB:300:GLN:HE21	1:BB:300:GLN:HB2	1.67	0.42
1:BC:232:THR:HB	1:BC:334:VAL:HG23	2.02	0.42
1:BD:47:MET:HE2	1:BD:117:ALA:N	2.35	0.42
1:BD:375:ASN:OD1	1:BD:376:THR:HG23	2.19	0.42
1:BF:14:CYS:H	1:BF:138:ASN:ND2	2.14	0.42
1:BG:175:PHE:CD2	1:BG:175:PHE:O	2.73	0.42
1:BH:318:SER:HA	1:BH:319:GLY:HA2	1.78	0.42
1:BI:285:SER:HA	1:BI:286:PRO:HD3	1.89	0.42
1:BK:237:VAL:HG23	1:BK:279:PHE:CD2	2.55	0.42
1:BK:272:TYR:N	1:BK:272:TYR:HD1	2.17	0.42
1:BN:55:ARG:CZ	1:BS:272:TYR:CE2	3.03	0.42
1:BS:108:ILE:HG23	1:BS:113:LEU:HD12	2.02	0.42
1:CC:237:VAL:HG23	1:CC:279:PHE:CD2	2.54	0.42
1:CE:185:PRO:HA	1:CE:186:PRO:HD3	1.92	0.42
1:CE:381:MET:HB2	1:CE:381:MET:HE2	1.59	0.42
1:CF:43:ALA:HB1	1:CF:158:GLU:HA	2.01	0.42
1:CF:379:VAL:CG1	1:CF:381:MET:CE	2.98	0.42
1:CI:285:SER:HA	1:CI:286:PRO:HD3	1.92	0.42
1:CJ:185:PRO:HA	1:CJ:186:PRO:HD3	1.88	0.42
1:CJ:404:LEU:N	1:CJ:404:LEU:HD23	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CQ:175:PHE:CD2	1:CQ:175:PHE:O	2.73	0.42
1:CS:232:THR:HB	1:CS:334:VAL:HG23	2.02	0.42
1:AA:182:LEU:HG	1:AA:330:ILE:HB	2.02	0.42
1:AB:207:VAL:HA	1:AB:208:PRO:HD3	1.83	0.42
1:AB:237:VAL:HG23	1:AB:279:PHE:CD2	2.55	0.42
1:AB:381:MET:HE2	1:AB:381:MET:HB2	1.68	0.42
1:AC:55:ARG:HD3	1:AT:272:TYR:HD2	1.82	0.42
1:AD:340:LEU:HD23	1:AD:340:LEU:HA	1.92	0.42
1:AE:252:VAL:HG22	1:AE:253:SER:N	2.35	0.42
1:AG:191:LEU:O	1:BG:144:ALA:HB3	2.20	0.42
1:AL:232:THR:HB	1:AL:334:VAL:CG2	2.50	0.42
1:AM:191:LEU:HD23	1:AM:191:LEU:N	2.16	0.42
1:AP:237:VAL:HG23	1:AP:279:PHE:CD2	2.55	0.42
1:AT:16:ALA:O	1:AT:17:ASN:HB2	2.20	0.42
1:BA:252:VAL:HG22	1:BA:253:SER:N	2.34	0.42
1:BA:412:PHE:HB2	1:BE:442:GLN:HE21	1.85	0.42
1:BB:232:THR:HB	1:BB:334:VAL:HG23	2.01	0.42
1:BD:239:ILE:HD12	1:BD:275:GLU:HA	2.02	0.42
1:BD:371:ASP:OD1	1:BD:381:MET:HG2	2.20	0.42
1:BJ:202:LEU:HD23	1:BJ:202:LEU:HA	1.87	0.42
1:BK:209:MET:HE2	1:BK:209:MET:HB3	1.90	0.42
1:BL:33:LYS:HB2	1:BL:33:LYS:HE2	1.96	0.42
1:BP:22:THR:HG1	1:BP:131:HIS:HD2	1.66	0.42
1:BQ:189:PHE:CE2	1:BQ:249:LEU:HD21	2.52	0.42
1:BR:171:ASP:HA	1:BR:172:PRO:HD3	1.78	0.42
1:BR:371:ASP:OD1	1:BR:381:MET:HG2	2.20	0.42
1:CJ:324:LEU:HA	1:CJ:325:PRO:HD3	1.88	0.42
1:CK:108:ILE:HG23	1:CK:113:LEU:HD12	2.01	0.42
1:CL:207:VAL:HA	1:CL:208:PRO:HD3	1.85	0.42
1:CM:232:THR:HB	1:CM:334:VAL:HG23	2.00	0.42
1:CN:234:ARG:HG2	1:CN:280:GLU:HG2	2.01	0.42
1:CO:239:ILE:HG23	1:CO:324:LEU:HD21	2.01	0.42
1:CO:403:LYS:C	1:CO:404:LEU:HD23	2.45	0.42
1:CP:252:VAL:HG22	1:CP:253:SER:N	2.35	0.42
1:CP:423:LYS:HE2	1:CP:449:GLU:O	2.20	0.42
1:CR:436:SER:O	1:CS:487:LEU:HD21	2.19	0.42
1:CT:182:LEU:HG	1:CT:330:ILE:HB	2.02	0.42
1:AE:209:MET:HE2	1:AE:209:MET:HB3	1.96	0.41
1:AF:182:LEU:HG	1:AF:330:ILE:HB	2.02	0.41
1:AH:32:PHE:CZ	1:AK:267:LYS:HG2	2.55	0.41
1:AI:189:PHE:HD2	1:AI:247:ILE:HD11	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:48:PRO:HG2	1:AJ:50:PHE:CZ	2.55	0.41
1:AL:203:THR:HB	1:AL:300:GLN:CD	2.45	0.41
1:AM:263:ASN:O	1:AM:267:LYS:HG3	2.20	0.41
1:AR:43:ALA:HB1	1:AR:158:GLU:HA	2.02	0.41
1:AT:252:VAL:HG22	1:AT:253:SER:N	2.35	0.41
1:BA:73:TYR:CZ	1:BA:394:GLY:HA3	2.55	0.41
1:BA:163:LEU:HD21	1:BA:458:ALA:HB2	2.01	0.41
1:BC:22:THR:OG1	1:BC:131:HIS:CD2	2.59	0.41
1:BD:285:SER:HA	1:BD:286:PRO:HD3	1.90	0.41
1:BE:175:PHE:CD2	1:BE:175:PHE:O	2.73	0.41
1:BF:15:GLN:HA	1:BF:15:GLN:HE21	1.84	0.41
1:BF:232:THR:HB	1:BF:334:VAL:CG2	2.50	0.41
1:BI:55:ARG:HD3	1:BR:272:TYR:HD2	1.79	0.41
1:BN:404:LEU:HD22	1:BN:486:VAL:HG22	2.01	0.41
1:BQ:371:ASP:OD1	1:BQ:381:MET:HG2	2.20	0.41
1:BT:234:ARG:CG	1:BT:280:GLU:HG2	2.49	0.41
1:CA:440:ALA:CB	1:CB:444:LEU:HD13	2.49	0.41
1:CB:256:ASN:HD22	1:CB:302:ASP:HA	1.85	0.41
1:CF:189:PHE:CE2	1:CF:249:LEU:HD21	2.47	0.41
1:CI:232:THR:HB	1:CI:334:VAL:CG2	2.50	0.41
1:CJ:275:GLU:O	1:CJ:276:ASP:C	2.63	0.41
1:CK:189:PHE:CE2	1:CK:249:LEU:HD21	2.55	0.41
1:CL:232:THR:HB	1:CL:334:VAL:CG2	2.51	0.41
1:CN:393:HIS:CG	1:CN:496:PHE:HB3	2.54	0.41
1:CP:47:MET:HE2	1:CP:117:ALA:N	2.35	0.41
1:CS:203:THR:CB	1:CS:300:GLN:HG3	2.49	0.41
1:CS:318:SER:HA	1:CS:319:GLY:HA2	1.81	0.41
1:CS:381:MET:HB2	1:CS:381:MET:HE2	1.69	0.41
1:AB:259:THR:O	1:AB:259:THR:HG22	2.15	0.41
1:AD:188:PHE:C	1:AD:189:PHE:HD1	2.28	0.41
1:AF:43:ALA:HB1	1:AF:158:GLU:HA	2.02	0.41
1:AH:234:ARG:CG	1:AH:280:GLU:HG2	2.50	0.41
1:AK:52:ILE:HD11	1:AK:108:ILE:HD12	2.03	0.41
1:AK:207:VAL:HA	1:AK:208:PRO:HD3	1.82	0.41
1:AK:324:LEU:HA	1:AK:325:PRO:HD3	1.89	0.41
1:AM:454:ASN:ND2	1:AM:454:ASN:C	2.78	0.41
1:AN:182:LEU:HD12	1:AN:182:LEU:C	2.45	0.41
1:BD:182:LEU:C	1:BD:182:LEU:HD12	2.45	0.41
1:BE:16:ALA:O	1:BE:17:ASN:CB	2.64	0.41
1:BF:47:MET:HE2	1:BF:117:ALA:N	2.35	0.41
1:BF:182:LEU:HG	1:BF:330:ILE:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:33:LYS:O	1:BG:33:LYS:CG	2.62	0.41
1:BJ:162:PHE:CD2	1:BJ:163:LEU:HD13	2.55	0.41
1:BL:318:SER:HA	1:BL:319:GLY:HA2	1.77	0.41
1:BM:255:TRP:CE3	1:BM:285:SER:HB2	2.55	0.41
1:BP:170:PHE:CD1	1:BP:389:MET:HE1	2.48	0.41
1:BR:234:ARG:HG2	1:BR:280:GLU:HG2	2.01	0.41
1:BT:324:LEU:HD23	1:BT:324:LEU:C	2.45	0.41
1:CA:272:TYR:N	1:CA:272:TYR:HD1	2.17	0.41
1:CD:55:ARG:CD	1:CN:272:TYR:CD2	2.97	0.41
1:CF:423:LYS:HE2	1:CF:449:GLU:O	2.19	0.41
1:CG:175:PHE:CD2	1:CG:175:PHE:O	2.74	0.41
1:CH:442:GLN:NE2	1:CI:412:PHE:HB2	2.35	0.41
1:CI:239:ILE:HD12	1:CI:275:GLU:HA	2.00	0.41
1:CP:381:MET:HE2	1:CP:381:MET:HB2	1.65	0.41
1:CR:10:ILE:HA	1:CR:11:PRO:HD3	1.88	0.41
1:CS:324:LEU:HA	1:CS:325:PRO:HD3	1.85	0.41
1:AB:170:PHE:CD1	1:AB:389:MET:HE1	2.50	0.41
1:AC:163:LEU:HD12	1:AC:163:LEU:HA	1.90	0.41
1:AD:171:ASP:HA	1:AD:172:PRO:HD3	1.78	0.41
1:AD:371:ASP:OD1	1:AD:381:MET:HG2	2.20	0.41
1:AD:423:LYS:HE2	1:AD:449:GLU:O	2.19	0.41
1:AE:163:LEU:HD12	1:AE:163:LEU:HA	1.88	0.41
1:AE:423:LYS:HE2	1:AE:449:GLU:O	2.21	0.41
1:AF:170:PHE:HD1	1:AF:389:MET:CE	2.30	0.41
1:AJ:61:PHE:CD2	1:AJ:243:ILE:HD11	2.55	0.41
1:AJ:365:ILE:CD1	1:AJ:471:MET:HE2	2.49	0.41
1:AN:418:SER:HB3	1:AO:407:SER:HB3	2.01	0.41
1:AO:299:SER:C	1:AO:301:ARG:H	2.27	0.41
1:AP:250:TRP:HZ3	1:AP:272:TYR:CE1	2.33	0.41
1:AP:365:ILE:CD1	1:AP:471:MET:HE2	2.49	0.41
1:BI:20:LEU:HB2	1:BI:132:PHE:O	2.20	0.41
1:BL:239:ILE:HG23	1:BL:324:LEU:HD21	2.01	0.41
1:BO:73:TYR:CE2	1:BO:394:GLY:HA3	2.56	0.41
1:BO:272:TYR:CD2	1:BR:55:ARG:NH1	2.87	0.41
1:BP:272:TYR:HD2	1:CE:55:ARG:HD3	1.77	0.41
1:BP:324:LEU:HA	1:BP:325:PRO:HD3	1.84	0.41
1:BR:239:ILE:HG12	1:BR:326:ILE:CD1	2.50	0.41
1:BR:272:TYR:N	1:BR:272:TYR:HD1	2.18	0.41
1:BR:395:LEU:HB2	1:BR:497:TYR:HB2	2.01	0.41
1:BS:381:MET:HE2	1:BS:381:MET:HB2	1.63	0.41
1:CD:48:PRO:HG2	1:CD:50:PHE:CZ	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:437:HIS:CE1	1:CI:405:GLN:NE2	2.88	0.41
1:CJ:191:LEU:CD2	1:CJ:191:LEU:N	2.78	0.41
1:CL:403:LYS:C	1:CL:404:LEU:HD23	2.44	0.41
1:CL:440:ALA:CB	1:CM:444:LEU:HD13	2.50	0.41
1:CN:14:CYS:HB3	1:CN:64:LEU:HD21	2.01	0.41
1:CP:28:MET:CE	1:CP:152:LEU:HG	2.51	0.41
1:CP:444:LEU:HD13	1:CT:440:ALA:CB	2.50	0.41
1:CQ:162:PHE:CD1	1:CR:287:TYR:HA	2.56	0.41
1:CQ:395:LEU:HB2	1:CQ:497:TYR:HB2	2.01	0.41
1:CR:272:TYR:N	1:CR:272:TYR:HD1	2.18	0.41
1:AC:25:ILE:HG23	1:AC:152:LEU:HD11	2.01	0.41
1:AC:171:ASP:HA	1:AC:172:PRO:HD3	1.81	0.41
1:AG:182:LEU:HG	1:AG:330:ILE:HB	2.03	0.41
1:AH:15:GLN:HE21	1:AH:15:GLN:CA	2.24	0.41
1:AI:267:LYS:HG2	1:AO:32:PHE:CZ	2.55	0.41
1:AI:318:SER:HA	1:AI:319:GLY:HA2	1.78	0.41
1:AJ:234:ARG:CG	1:AJ:280:GLU:HG2	2.50	0.41
1:AL:442:GLN:NE2	1:AM:412:PHE:HB2	2.34	0.41
1:AM:163:LEU:HD12	1:AM:163:LEU:HA	1.82	0.41
1:AN:77:THR:O	1:AN:81:THR:HG23	2.20	0.41
1:AO:202:LEU:HB2	1:AO:304:SER:O	2.21	0.41
1:AO:294:LEU:CD1	1:AO:299:SER:HA	2.49	0.41
1:AP:222:LEU:O	1:AP:225:CYS:HB2	2.21	0.41
1:AR:182:LEU:HG	1:AR:330:ILE:HB	2.02	0.41
1:BA:18:ARG:HG3	1:BA:19:TYR:N	2.34	0.41
1:BD:38:GLU:HB3	1:BM:35:VAL:HG23	2.02	0.41
1:BD:55:ARG:HD3	1:BN:272:TYR:HD2	1.78	0.41
1:BG:232:THR:HB	1:BG:334:VAL:HG23	2.00	0.41
1:BG:381:MET:HB2	1:BG:381:MET:HE2	1.65	0.41
1:BG:454:ASN:HD21	1:BG:456:ALA:HB3	1.84	0.41
1:BI:25:ILE:HD12	1:BI:128:PRO:HB2	2.02	0.41
1:BI:238:HIS:HE1	1:BI:329:GLN:OE1	2.04	0.41
1:BN:202:LEU:HD23	1:BN:202:LEU:HA	1.93	0.41
1:BN:226:VAL:HG13	1:BN:228:GLY:H	1.86	0.41
1:BO:25:ILE:HG23	1:BO:152:LEU:HD11	2.02	0.41
1:BS:252:VAL:HG22	1:BS:253:SER:N	2.36	0.41
1:CB:423:LYS:HE2	1:CB:449:GLU:O	2.20	0.41
1:CD:232:THR:HB	1:CD:334:VAL:HG23	2.02	0.41
1:CD:371:ASP:OD1	1:CD:381:MET:HG2	2.20	0.41
1:CF:14:CYS:H	1:CF:138:ASN:ND2	2.18	0.41
1:CF:475:LEU:HB3	1:CF:478:ALA:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:285:SER:HA	1:CH:286:PRO:HD3	1.93	0.41
1:CP:255:TRP:CG	1:CP:286:PRO:HD3	2.56	0.41
1:CQ:45:LEU:HD23	1:CQ:45:LEU:HA	1.88	0.41
1:CQ:234:ARG:HG2	1:CQ:280:GLU:HG2	2.03	0.41
1:CS:79:ARG:HH11	1:CS:79:ARG:CG	2.33	0.41
1:AD:43:ALA:HB1	1:AD:158:GLU:HA	2.02	0.41
1:AE:22:THR:OG1	1:AE:131:HIS:CD2	2.60	0.41
1:AH:207:VAL:HA	1:AH:208:PRO:HD3	1.83	0.41
1:AK:33:LYS:HB2	1:AK:33:LYS:HE2	1.97	0.41
1:AM:272:TYR:CE2	1:CP:55:ARG:CZ	3.04	0.41
1:AM:272:TYR:N	1:AM:272:TYR:HD1	2.18	0.41
1:AN:47:MET:HE2	1:AN:117:ALA:N	2.35	0.41
1:AN:226:VAL:HG13	1:AN:228:GLY:H	1.85	0.41
1:AO:298:GLN:HE21	1:AO:303:MET:HE1	1.84	0.41
1:AQ:58:ALA:HB2	1:AQ:102:GLY:HA3	2.02	0.41
1:AS:182:LEU:HG	1:AS:330:ILE:HB	2.03	0.41
1:BA:11:PRO:HG2	1:BA:18:ARG:CD	2.51	0.41
1:BA:22:THR:OG1	1:BA:131:HIS:CD2	2.61	0.41
1:BD:189:PHE:HE1	1:BD:198:ARG:CG	2.27	0.41
1:BE:252:VAL:HG22	1:BE:253:SER:N	2.36	0.41
1:BG:238:HIS:HE1	1:BG:329:GLN:OE1	2.03	0.41
1:BG:300:GLN:HE21	1:BG:300:GLN:HB2	1.60	0.41
1:BJ:170:PHE:HD1	1:BJ:389:MET:CE	2.25	0.41
1:BJ:234:ARG:HG2	1:BJ:280:GLU:HG2	2.02	0.41
1:BK:239:ILE:HG23	1:BK:324:LEU:HD21	2.02	0.41
1:BQ:454:ASN:HD21	1:BQ:456:ALA:HB3	1.85	0.41
1:CC:189:PHE:HE2	1:CC:249:LEU:HD21	1.85	0.41
1:CD:22:THR:OG1	1:CD:131:HIS:CD2	2.58	0.41
1:CF:226:VAL:HG13	1:CF:228:GLY:H	1.85	0.41
1:CF:239:ILE:HG23	1:CF:324:LEU:HD21	2.02	0.41
1:CH:10:ILE:HA	1:CH:11:PRO:HD3	1.86	0.41
1:CJ:423:LYS:HE2	1:CJ:449:GLU:O	2.20	0.41
1:CK:232:THR:HB	1:CK:334:VAL:HG23	2.02	0.41
1:CL:232:THR:HB	1:CL:334:VAL:HG23	2.01	0.41
1:CO:232:THR:HB	1:CO:334:VAL:HG23	2.02	0.41
1:CP:182:LEU:C	1:CP:182:LEU:HD12	2.45	0.41
1:CP:444:LEU:HD13	1:CT:440:ALA:HB3	2.02	0.41
1:CR:77:THR:HA	1:CR:80:ILE:HD11	2.03	0.41
1:AB:171:ASP:HA	1:AB:172:PRO:HD3	1.79	0.41
1:AC:263:ASN:O	1:AC:267:LYS:HG3	2.20	0.41
1:AC:443:LYS:HD3	1:AC:443:LYS:HA	1.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:381:MET:HE2	1:AD:381:MET:HB2	1.64	0.41
1:AG:25:ILE:HG23	1:AG:152:LEU:HD11	2.03	0.41
1:AG:232:THR:HB	1:AG:334:VAL:HG23	2.01	0.41
1:AG:285:SER:HA	1:AG:286:PRO:HD3	1.94	0.41
1:AO:79:ARG:NH1	1:AO:79:ARG:CG	2.84	0.41
1:AP:182:LEU:C	1:AP:182:LEU:HD12	2.45	0.41
1:AQ:163:LEU:HD12	1:AQ:163:LEU:HA	1.87	0.41
1:AQ:241:ALA:HB1	1:AQ:242:PRO:HD2	2.03	0.41
1:AR:318:SER:HA	1:AR:319:GLY:HA2	1.75	0.41
1:AS:22:THR:OG1	1:AS:131:HIS:CD2	2.63	0.41
1:AS:239:ILE:HD12	1:AS:275:GLU:HA	2.02	0.41
1:AT:55:ARG:CZ	1:BA:272:TYR:CD2	3.04	0.41
1:BA:188:PHE:C	1:BA:189:PHE:HD1	2.29	0.41
1:BG:25:ILE:HD12	1:BG:128:PRO:HB2	2.03	0.41
1:BI:263:ASN:O	1:BI:267:LYS:HG3	2.20	0.41
1:BJ:371:ASP:OD1	1:BJ:381:MET:HG2	2.19	0.41
1:BJ:381:MET:HB2	1:BJ:381:MET:HE2	1.70	0.41
1:BN:340:LEU:HA	1:BN:340:LEU:HD23	1.87	0.41
1:BO:234:ARG:CG	1:BO:280:GLU:HG2	2.50	0.41
1:BS:423:LYS:HE2	1:BS:449:GLU:O	2.20	0.41
1:BT:263:ASN:O	1:BT:267:LYS:HG3	2.20	0.41
1:BT:300:GLN:HE21	1:BT:300:GLN:HB2	1.57	0.41
1:CC:239:ILE:HD12	1:CC:275:GLU:HA	2.01	0.41
1:CI:20:LEU:HB2	1:CI:132:PHE:O	2.21	0.41
1:CN:226:VAL:HG13	1:CN:228:GLY:H	1.85	0.41
1:CO:10:ILE:HA	1:CO:11:PRO:HD3	1.82	0.41
1:CP:22:THR:OG1	1:CP:131:HIS:CD2	2.64	0.41
1:CS:170:PHE:CD1	1:CS:389:MET:HE1	2.47	0.41
1:CS:234:ARG:CG	1:CS:280:GLU:HG2	2.51	0.41
1:AA:108:ILE:HG23	1:AA:113:LEU:HD12	2.02	0.41
1:AA:203:THR:HB	1:AA:300:GLN:HG3	2.02	0.41
1:AB:18:ARG:NH1	1:AB:18:ARG:HB2	2.36	0.41
1:AB:79:ARG:CG	1:AB:79:ARG:NH1	2.82	0.41
1:AB:257:GLY:O	1:AB:258:THR:HG22	2.20	0.41
1:AE:300:GLN:HE21	1:AE:300:GLN:HB2	1.72	0.41
1:AF:163:LEU:HD12	1:AF:163:LEU:HA	1.90	0.41
1:AK:189:PHE:CE2	1:AK:249:LEU:HD21	2.55	0.41
1:AN:170:PHE:HD1	1:AN:389:MET:CE	2.30	0.41
1:AN:414:LYS:HA	1:AO:411:GLU:HB3	2.02	0.41
1:AP:232:THR:HB	1:AP:334:VAL:CG2	2.51	0.41
1:AQ:318:SER:HA	1:AQ:319:GLY:HA2	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:234:ARG:CG	1:AS:280:GLU:HG2	2.51	0.41
1:BB:35:VAL:HG22	1:CA:38:GLU:HB2	2.03	0.41
1:BB:202:LEU:HD23	1:BB:202:LEU:HA	1.95	0.41
1:BH:237:VAL:HG23	1:BH:279:PHE:CD2	2.54	0.41
1:BI:52:ILE:HG12	1:BI:152:LEU:CD2	2.51	0.41
1:BJ:79:ARG:NH1	1:BJ:79:ARG:CG	2.73	0.41
1:BL:272:TYR:N	1:BL:272:TYR:HD1	2.19	0.41
1:BM:300:GLN:HE21	1:BM:300:GLN:HB2	1.66	0.41
1:BR:423:LYS:HE2	1:BR:449:GLU:O	2.21	0.41
1:BT:11:PRO:HG2	1:BT:18:ARG:HD2	2.03	0.41
1:CC:16:ALA:O	1:CC:17:ASN:HB2	2.20	0.41
1:CE:47:MET:HE2	1:CE:117:ALA:N	2.35	0.41
1:CE:454:ASN:ND2	1:CE:456:ALA:HB3	2.36	0.41
1:CG:404:LEU:HD22	1:CG:486:VAL:HG22	2.02	0.41
1:CI:232:THR:HB	1:CI:334:VAL:HG23	2.03	0.41
1:CI:234:ARG:CG	1:CI:280:GLU:HG2	2.51	0.41
1:CL:191:LEU:CD2	1:CL:191:LEU:N	2.75	0.41
1:CM:20:LEU:HB2	1:CM:132:PHE:O	2.21	0.41
1:CM:381:MET:HB2	1:CM:381:MET:HE2	1.71	0.41
1:CS:401:ASP:O	1:CS:488:CYS:HA	2.21	0.41
1:AA:232:THR:HB	1:AA:334:VAL:CG2	2.50	0.41
1:AB:182:LEU:C	1:AB:182:LEU:HD12	2.46	0.41
1:AE:371:ASP:OD1	1:AE:381:MET:HG2	2.20	0.41
1:AG:170:PHE:CD1	1:AG:389:MET:HE1	2.48	0.41
1:AH:256:ASN:HD22	1:AH:302:ASP:HA	1.86	0.41
1:AK:202:LEU:HB2	1:AK:304:SER:O	2.21	0.41
1:AM:436:SER:O	1:AN:487:LEU:HD21	2.21	0.41
1:AN:241:ALA:HB1	1:AN:242:PRO:HD2	2.03	0.41
1:AQ:285:SER:HA	1:AQ:286:PRO:HD3	1.93	0.41
1:AQ:324:LEU:HA	1:AQ:325:PRO:HD3	1.84	0.41
1:AR:239:ILE:HD12	1:AR:275:GLU:HA	2.02	0.41
1:AS:252:VAL:HG22	1:AS:253:SER:N	2.35	0.41
1:AS:454:ASN:ND2	1:AS:456:ALA:H	2.09	0.41
1:AT:55:ARG:NE	1:BA:272:TYR:HE2	2.10	0.41
1:AT:182:LEU:C	1:AT:182:LEU:HD12	2.46	0.41
1:BA:407:SER:HB3	1:BE:418:SER:HB3	2.01	0.41
1:BE:371:ASP:OD1	1:BE:381:MET:HG2	2.21	0.41
1:BF:285:SER:HA	1:BF:286:PRO:HD3	1.92	0.41
1:BH:335:ARG:N	1:BH:336:PRO:HD3	2.36	0.41
1:BI:209:MET:HE2	1:BI:209:MET:HB3	1.89	0.41
1:BI:232:THR:HB	1:BI:334:VAL:CG2	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:79:ARG:CG	1:BL:79:ARG:NH1	2.83	0.41
1:BL:191:LEU:HD23	1:BL:191:LEU:N	2.22	0.41
1:BO:182:LEU:HG	1:BO:330:ILE:HB	2.02	0.41
1:BO:209:MET:HE2	1:BO:209:MET:HB3	1.93	0.41
1:BT:241:ALA:HB1	1:BT:242:PRO:HD2	2.03	0.41
1:CD:250:TRP:CZ3	1:CD:272:TYR:CD1	3.08	0.41
1:CG:371:ASP:OD1	1:CG:381:MET:HG2	2.21	0.41
1:CH:162:PHE:CD1	1:CI:287:TYR:HA	2.56	0.41
1:CI:255:TRP:CE3	1:CI:285:SER:HB2	2.56	0.41
1:CJ:202:LEU:HB2	1:CJ:304:SER:O	2.21	0.41
1:CP:404:LEU:N	1:CP:404:LEU:HD23	2.36	0.41
1:CR:14:CYS:HB3	1:CR:64:LEU:HD21	2.01	0.41
1:AA:238:HIS:HE1	1:AA:329:GLN:OE1	2.04	0.41
1:AA:275:GLU:O	1:AA:276:ASP:C	2.64	0.41
1:AA:404:LEU:N	1:AA:404:LEU:HD23	2.36	0.41
1:AB:58:ALA:HB2	1:AB:102:GLY:CA	2.50	0.41
1:AC:14:CYS:H	1:AC:138:ASN:HD21	1.67	0.41
1:AC:256:ASN:HD22	1:AC:302:ASP:HA	1.85	0.41
1:AD:108:ILE:HG23	1:AD:113:LEU:HD12	2.03	0.41
1:AE:272:TYR:CD2	1:AM:55:ARG:CZ	3.04	0.41
1:AF:203:THR:HB	1:AF:300:GLN:CG	2.51	0.41
1:AF:287:TYR:HA	1:AJ:162:PHE:CD1	2.55	0.41
1:AG:38:GLU:CB	1:CF:35:VAL:CG2	2.99	0.41
1:AG:43:ALA:HB1	1:AG:158:GLU:HA	2.03	0.41
1:AG:207:VAL:HA	1:AG:208:PRO:HD3	1.81	0.41
1:AG:239:ILE:HG12	1:AG:326:ILE:CD1	2.50	0.41
1:AH:365:ILE:CD1	1:AH:471:MET:HE2	2.50	0.41
1:AI:47:MET:HE2	1:AI:117:ALA:N	2.36	0.41
1:AI:61:PHE:CD2	1:AI:243:ILE:HD11	2.55	0.41
1:AI:252:VAL:HG22	1:AI:253:SER:N	2.36	0.41
1:AI:379:VAL:CG1	1:AI:381:MET:CE	2.99	0.41
1:AJ:171:ASP:HA	1:AJ:172:PRO:HD3	1.78	0.41
1:AJ:175:PHE:CD2	1:AJ:175:PHE:O	2.74	0.41
1:AK:381:MET:HB2	1:AK:381:MET:HE2	1.70	0.41
1:AL:300:GLN:HE21	1:AL:300:GLN:HB2	1.67	0.41
1:AL:381:MET:HE2	1:AL:381:MET:HB2	1.65	0.41
1:AM:162:PHE:CD1	1:AN:287:TYR:HA	2.56	0.41
1:AN:202:LEU:HD23	1:AN:202:LEU:HA	1.90	0.41
1:AN:289:ARG:NH1	1:AN:337:ASP:OD1	2.54	0.41
1:AO:58:ALA:HB2	1:AO:102:GLY:HA3	2.01	0.41
1:AQ:170:PHE:HB2	1:AQ:496:PHE:HE1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AR:371:ASP:OD1	1:AR:381:MET:HG2	2.21	0.41
1:AS:77:THR:O	1:AS:81:THR:HG23	2.21	0.41
1:AT:28:MET:CE	1:AT:152:LEU:HG	2.51	0.41
1:AT:371:ASP:OD1	1:AT:381:MET:HG2	2.21	0.41
1:BA:275:GLU:O	1:BA:276:ASP:C	2.62	0.41
1:BC:209:MET:HE2	1:BC:209:MET:HB3	1.90	0.41
1:BC:275:GLU:O	1:BC:276:ASP:C	2.62	0.41
1:BC:365:ILE:CD1	1:BC:471:MET:HE2	2.51	0.41
1:BD:11:PRO:HG2	1:BD:18:ARG:HD2	2.02	0.41
1:BE:201:GLY:HA3	1:BE:300:GLN:HG2	2.02	0.41
1:BE:403:LYS:C	1:BE:404:LEU:HD23	2.46	0.41
1:BF:108:ILE:HG23	1:BF:113:LEU:HD12	2.02	0.41
1:BL:7:VAL:CG1	1:BL:9:TYR:CE2	3.04	0.41
1:BL:168:LEU:HD21	1:BL:389:MET:HE3	2.03	0.41
1:BL:170:PHE:HD1	1:BL:389:MET:CE	2.33	0.41
1:BN:55:ARG:CZ	1:BS:272:TYR:CD2	3.04	0.41
1:BN:207:VAL:HA	1:BN:208:PRO:HD3	1.83	0.41
1:BN:442:GLN:NE2	1:BO:412:PHE:HB2	2.34	0.41
1:BO:232:THR:HB	1:BO:334:VAL:HG23	2.03	0.41
1:BQ:170:PHE:HD1	1:BQ:389:MET:CE	2.30	0.41
1:BQ:191:LEU:HD23	1:BQ:191:LEU:N	2.20	0.41
1:BQ:340:LEU:HD23	1:BQ:340:LEU:HA	1.88	0.41
1:BR:189:PHE:CE1	1:BR:198:ARG:HG2	2.56	0.41
1:BR:318:SER:HA	1:BR:319:GLY:HA2	1.76	0.41
1:BS:37:TYR:O	1:BS:40:TRP:HB3	2.21	0.41
1:BT:20:LEU:HB2	1:BT:132:PHE:O	2.21	0.41
1:BT:20:LEU:HD11	1:BT:66:TRP:CD1	2.56	0.41
1:BT:324:LEU:HA	1:BT:325:PRO:HD3	1.88	0.41
1:CA:202:LEU:HD23	1:CA:202:LEU:HA	1.94	0.41
1:CC:189:PHE:HE1	1:CC:198:ARG:CG	2.30	0.41
1:CD:10:ILE:HA	1:CD:11:PRO:HD3	1.89	0.41
1:CD:55:ARG:CZ	1:CN:272:TYR:CD2	3.04	0.41
1:CG:239:ILE:HG23	1:CG:324:LEU:HD21	2.02	0.41
1:CH:47:MET:HE2	1:CH:117:ALA:N	2.35	0.41
1:CH:209:MET:HE2	1:CH:209:MET:HB3	1.90	0.41
1:CI:75:ARG:NH2	1:CI:391:ALA:O	2.53	0.41
1:CJ:182:LEU:HG	1:CJ:330:ILE:HB	2.03	0.41
1:CK:202:LEU:HD23	1:CK:202:LEU:HA	1.87	0.41
1:CK:371:ASP:OD1	1:CK:381:MET:HG2	2.21	0.41
1:CK:412:PHE:HB2	1:CO:442:GLN:HE21	1.86	0.41
1:CL:43:ALA:HB1	1:CL:158:GLU:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:14:CYS:H	1:CM:138:ASN:ND2	2.18	0.41
1:CM:47:MET:HE2	1:CM:117:ALA:N	2.35	0.41
1:CM:58:ALA:HB2	1:CM:102:GLY:HA3	2.02	0.41
1:CM:239:ILE:HG23	1:CM:324:LEU:HD21	2.02	0.41
1:CN:272:TYR:N	1:CN:272:TYR:HD1	2.18	0.41
1:CN:403:LYS:C	1:CN:404:LEU:HD23	2.45	0.41
1:CP:263:ASN:O	1:CP:267:LYS:HG3	2.20	0.41
1:CQ:170:PHE:HB2	1:CQ:496:PHE:HE1	1.85	0.41
1:CQ:182:LEU:HG	1:CQ:330:ILE:HB	2.02	0.41
1:CQ:207:VAL:HA	1:CQ:208:PRO:HD3	1.83	0.41
1:CR:162:PHE:CD1	1:CS:287:TYR:HA	2.56	0.41
1:CR:189:PHE:HD2	1:CR:247:ILE:HD11	1.86	0.41
1:CR:285:SER:HA	1:CR:286:PRO:HD3	1.91	0.41
1:CS:232:THR:HB	1:CS:334:VAL:CG2	2.51	0.41
1:CT:25:ILE:HG23	1:CT:152:LEU:HD11	2.03	0.41
1:CT:47:MET:HE2	1:CT:117:ALA:N	2.35	0.41
1:AA:182:LEU:HD12	1:AA:182:LEU:C	2.46	0.41
1:AB:202:LEU:HD23	1:AB:202:LEU:HA	1.88	0.41
1:AC:454:ASN:ND2	1:AC:456:ALA:HB3	2.36	0.41
1:AD:234:ARG:CG	1:AD:280:GLU:HG2	2.51	0.41
1:AE:197:LEU:HD21	1:AE:258:THR:HG21	2.02	0.41
1:AJ:381:MET:HE2	1:AJ:381:MET:HB2	1.61	0.41
1:AL:340:LEU:HD23	1:AL:340:LEU:HA	1.94	0.41
1:AM:272:TYR:CD2	1:CP:55:ARG:CZ	3.04	0.41
1:AP:252:VAL:HG22	1:AP:253:SER:N	2.36	0.41
1:AS:11:PRO:HG2	1:AS:18:ARG:CD	2.51	0.41
1:AS:170:PHE:CD1	1:AS:389:MET:HE1	2.45	0.41
1:BB:191:LEU:CD2	1:BB:191:LEU:N	2.73	0.41
1:BD:175:PHE:O	1:BD:175:PHE:CD2	2.74	0.41
1:BE:423:LYS:HE2	1:BE:449:GLU:O	2.20	0.41
1:BF:48:PRO:HG2	1:BF:50:PHE:CZ	2.56	0.41
1:BF:263:ASN:O	1:BF:267:LYS:HG3	2.21	0.41
1:BH:18:ARG:HG2	1:BH:20:LEU:HD23	2.03	0.41
1:BH:182:LEU:C	1:BH:182:LEU:HD12	2.46	0.41
1:BJ:234:ARG:CG	1:BJ:280:GLU:HG2	2.51	0.41
1:BK:188:PHE:C	1:BK:189:PHE:HD1	2.29	0.41
1:BP:250:TRP:HE3	1:BP:272:TYR:CD1	2.39	0.41
1:BQ:226:VAL:HG13	1:BQ:228:GLY:H	1.86	0.41
1:BR:47:MET:HE2	1:BR:117:ALA:N	2.36	0.41
1:BR:252:VAL:HG22	1:BR:253:SER:N	2.36	0.41
1:BS:285:SER:HA	1:BS:286:PRO:HD3	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:185:PRO:HA	1:BT:186:PRO:HD3	1.94	0.41
1:BT:285:SER:HA	1:BT:286:PRO:HD3	1.92	0.41
1:CD:252:VAL:HG22	1:CD:253:SER:N	2.35	0.41
1:CE:61:PHE:CE2	1:CE:243:ILE:HD11	2.56	0.41
1:CF:48:PRO:HG2	1:CF:50:PHE:CZ	2.56	0.41
1:CF:252:VAL:HG22	1:CF:253:SER:N	2.36	0.41
1:CG:74:ASN:ND2	1:CG:77:THR:OG1	2.54	0.41
1:CI:22:THR:OG1	1:CI:131:HIS:CD2	2.62	0.41
1:CL:234:ARG:CG	1:CL:280:GLU:HG2	2.51	0.41
1:CL:275:GLU:O	1:CL:276:ASP:C	2.64	0.41
1:CR:108:ILE:HG23	1:CR:113:LEU:HD12	2.03	0.41
1:CS:202:LEU:HD23	1:CS:202:LEU:HA	1.90	0.41
1:CS:275:GLU:O	1:CS:276:ASP:C	2.63	0.41
1:AA:11:PRO:HG2	1:AA:18:ARG:CD	2.51	0.40
1:AB:170:PHE:HD1	1:AB:389:MET:CE	2.33	0.40
1:AB:263:ASN:ND2	1:CB:32:PHE:HA	2.34	0.40
1:AC:189:PHE:CE2	1:AC:249:LEU:HD21	2.56	0.40
1:AC:202:LEU:HD23	1:AC:202:LEU:HA	1.91	0.40
1:AF:189:PHE:CE1	1:AF:198:ARG:HG2	2.55	0.40
1:AI:202:LEU:HA	1:AI:202:LEU:HD23	1.87	0.40
1:AI:418:SER:HB3	1:AJ:407:SER:CB	2.50	0.40
1:AI:440:ALA:CB	1:AJ:444:LEU:HD13	2.50	0.40
1:AJ:55:ARG:CZ	1:BL:272:TYR:CD2	3.04	0.40
1:AK:12:LYS:HB3	1:AK:144:ALA:C	2.46	0.40
1:AL:28:MET:CE	1:AL:152:LEU:HG	2.51	0.40
1:AL:250:TRP:HZ3	1:AL:272:TYR:HE1	1.64	0.40
1:AL:252:VAL:HG22	1:AL:253:SER:N	2.36	0.40
1:AM:203:THR:CB	1:AM:300:GLN:HG3	2.51	0.40
1:AP:275:GLU:O	1:AP:276:ASP:C	2.64	0.40
1:AQ:379:VAL:CG1	1:AQ:381:MET:CE	2.99	0.40
1:AQ:414:LYS:HA	1:AR:411:GLU:HB3	2.03	0.40
1:AT:18:ARG:HG3	1:AT:19:TYR:N	2.35	0.40
1:BC:201:GLY:HA3	1:BC:300:GLN:HG2	2.03	0.40
1:BE:272:TYR:CD2	1:BM:55:ARG:CZ	3.03	0.40
1:BG:48:PRO:HG2	1:BG:50:PHE:CZ	2.56	0.40
1:BL:340:LEU:HD23	1:BL:340:LEU:HA	1.92	0.40
1:BN:189:PHE:CE2	1:BN:249:LEU:HD21	2.48	0.40
1:BO:226:VAL:HG13	1:BO:228:GLY:H	1.85	0.40
1:BO:371:ASP:OD1	1:BO:381:MET:HG2	2.21	0.40
1:BP:239:ILE:HG12	1:BP:326:ILE:CD1	2.51	0.40
1:CB:14:CYS:H	1:CB:138:ASN:ND2	2.18	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:189:PHE:CE2	1:CC:249:LEU:HD21	2.56	0.40
1:CD:182:LEU:HG	1:CD:330:ILE:HB	2.03	0.40
1:CH:182:LEU:HG	1:CH:330:ILE:HB	2.02	0.40
1:CK:10:ILE:HG21	1:CK:146:TRP:CZ2	2.55	0.40
1:CM:182:LEU:HG	1:CM:330:ILE:HB	2.03	0.40
1:CO:9:TYR:HE1	1:CO:147:GLN:HE21	1.69	0.40
1:CO:175:PHE:CD2	1:CO:175:PHE:O	2.75	0.40
1:CP:79:ARG:CG	1:CP:79:ARG:NH1	2.78	0.40
1:CR:80:ILE:O	1:CR:81:THR:C	2.61	0.40
1:CR:170:PHE:HD1	1:CR:389:MET:CE	2.25	0.40
1:CS:226:VAL:HG13	1:CS:228:GLY:H	1.85	0.40
1:CT:12:LYS:HB3	1:CT:144:ALA:C	2.47	0.40
1:CT:252:VAL:HG22	1:CT:253:SER:N	2.35	0.40
1:AA:47:MET:HE2	1:AA:117:ALA:N	2.36	0.40
1:AB:175:PHE:CD2	1:AB:175:PHE:O	2.75	0.40
1:AD:236:ARG:HA	1:AD:278:SER:HA	2.03	0.40
1:AE:381:MET:HB2	1:AE:381:MET:HE2	1.71	0.40
1:AF:47:MET:HE2	1:AF:117:ALA:N	2.36	0.40
1:AG:287:TYR:C	1:AG:289:ARG:H	2.29	0.40
1:AH:434:GLY:O	1:AI:349:VAL:HG23	2.21	0.40
1:AI:203:THR:HB	1:AI:300:GLN:HG3	2.02	0.40
1:AK:47:MET:HG2	1:AK:117:ALA:HB2	2.03	0.40
1:AM:393:HIS:CG	1:AM:496:PHE:HB3	2.57	0.40
1:AS:163:LEU:HD12	1:AS:163:LEU:HA	1.90	0.40
1:AT:234:ARG:CG	1:AT:280:GLU:HG2	2.51	0.40
1:BA:365:ILE:CD1	1:BA:471:MET:HE2	2.50	0.40
1:BA:401:ASP:O	1:BA:488:CYS:HA	2.21	0.40
1:BD:25:ILE:HG23	1:BD:152:LEU:HD11	2.02	0.40
1:BE:238:HIS:HE1	1:BE:329:GLN:OE1	2.04	0.40
1:BF:272:TYR:HD2	1:CK:55:ARG:HD3	1.80	0.40
1:BF:381:MET:HB2	1:BF:381:MET:HE2	1.65	0.40
1:BG:272:TYR:CD2	1:CG:55:ARG:NH1	2.89	0.40
1:BH:35:VAL:O	1:BH:39:LYS:HG3	2.21	0.40
1:BI:170:PHE:CD1	1:BI:389:MET:HE1	2.48	0.40
1:BJ:185:PRO:HA	1:BJ:186:PRO:HD3	1.95	0.40
1:BL:263:ASN:O	1:BL:267:LYS:HG3	2.21	0.40
1:BM:22:THR:OG1	1:BM:131:HIS:CD2	2.65	0.40
1:BN:272:TYR:N	1:BN:272:TYR:HD1	2.18	0.40
1:BP:73:TYR:CE2	1:BP:394:GLY:HA3	2.56	0.40
1:BP:209:MET:HE2	1:BP:209:MET:HB3	1.93	0.40
1:BP:275:GLU:O	1:BP:276:ASP:C	2.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:437:HIS:CE1	1:BQ:405:GLN:NE2	2.89	0.40
1:BQ:36:GLN:HE22	1:BQ:156:LEU:H	1.63	0.40
1:BR:12:LYS:HB3	1:BR:144:ALA:C	2.46	0.40
1:BS:171:ASP:HA	1:BS:172:PRO:HD3	1.80	0.40
1:CA:444:LEU:HD13	1:CE:440:ALA:HB3	2.03	0.40
1:CB:300:GLN:HE21	1:CB:300:GLN:HB2	1.69	0.40
1:CD:175:PHE:O	1:CD:175:PHE:CD2	2.74	0.40
1:CE:11:PRO:HG2	1:CE:18:ARG:HD2	2.03	0.40
1:CE:197:LEU:HD13	1:CE:309:TYR:CE1	2.56	0.40
1:CH:28:MET:CE	1:CH:152:LEU:HG	2.51	0.40
1:CQ:203:THR:HB	1:CQ:300:GLN:HG3	2.03	0.40
1:CQ:335:ARG:N	1:CQ:336:PRO:HD3	2.36	0.40
1:CR:171:ASP:HA	1:CR:172:PRO:HD3	1.78	0.40
1:AB:12:LYS:HB3	1:AB:144:ALA:C	2.46	0.40
1:AC:318:SER:HA	1:AC:319:GLY:HA2	1.81	0.40
1:AD:25:ILE:HD12	1:AD:128:PRO:HB2	2.04	0.40
1:AF:285:SER:HA	1:AF:286:PRO:HD3	1.96	0.40
1:AJ:272:TYR:N	1:AJ:272:TYR:HD1	2.20	0.40
1:AL:443:LYS:HE2	1:AM:444:LEU:HB2	2.03	0.40
1:AN:175:PHE:CD2	1:AN:175:PHE:O	2.74	0.40
1:AP:285:SER:HA	1:AP:286:PRO:HD3	1.91	0.40
1:AR:379:VAL:CG1	1:AR:381:MET:CE	2.99	0.40
1:AS:326:ILE:HD13	1:AS:326:ILE:HA	1.94	0.40
1:BA:163:LEU:HD12	1:BA:163:LEU:HA	1.91	0.40
1:BD:232:THR:HB	1:BD:334:VAL:CG2	2.51	0.40
1:BE:340:LEU:HA	1:BE:340:LEU:HD23	1.90	0.40
1:BF:475:LEU:HB3	1:BF:478:ALA:HB2	2.03	0.40
1:BO:47:MET:HG2	1:BO:117:ALA:HB2	2.03	0.40
1:CE:191:LEU:HD23	1:CE:191:LEU:N	2.18	0.40
1:CF:429:ALA:HB3	1:CG:296:ALA:HB2	2.03	0.40
1:CH:381:MET:HE2	1:CH:381:MET:HB2	1.70	0.40
1:CK:395:LEU:HB2	1:CK:497:TYR:HB2	2.03	0.40
1:CK:440:ALA:CB	1:CL:444:LEU:HD13	2.52	0.40
1:CL:182:LEU:HD12	1:CL:182:LEU:C	2.45	0.40
1:CM:25:ILE:HG23	1:CM:152:LEU:HD11	2.03	0.40
1:CO:241:ALA:HB1	1:CO:242:PRO:HD2	2.03	0.40
1:CR:434:GLY:O	1:CS:349:VAL:HG23	2.22	0.40
1:AA:318:SER:HA	1:AA:319:GLY:HA2	1.82	0.40
1:AB:45:LEU:HD23	1:AB:45:LEU:HA	1.93	0.40
1:AF:418:SER:HB3	1:AG:407:SER:HB3	2.03	0.40
1:AG:272:TYR:CE2	1:BG:55:ARG:HD3	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:395:LEU:HB2	1:AH:497:TYR:HB2	2.04	0.40
1:AI:170:PHE:HB2	1:AI:496:PHE:HE1	1.86	0.40
1:AJ:324:LEU:HA	1:AJ:325:PRO:HD3	1.86	0.40
1:AN:20:LEU:HB2	1:AN:132:PHE:O	2.21	0.40
1:AN:308:PHE:CZ	1:AN:328:VAL:HG21	2.56	0.40
1:AP:61:PHE:CE2	1:AP:243:ILE:HD11	2.57	0.40
1:AQ:10:ILE:HA	1:AQ:11:PRO:HD3	1.84	0.40
1:BA:20:LEU:HB2	1:BA:132:PHE:O	2.21	0.40
1:BA:404:LEU:N	1:BA:404:LEU:HD23	2.37	0.40
1:BE:404:LEU:HD23	1:BE:404:LEU:N	2.36	0.40
1:BF:30:SER:HA	1:BF:37:TYR:CD1	2.57	0.40
1:BF:182:LEU:HD12	1:BF:182:LEU:C	2.46	0.40
1:BF:324:LEU:HA	1:BF:325:PRO:HD3	1.83	0.40
1:BF:379:VAL:CG1	1:BF:381:MET:CE	2.99	0.40
1:BF:395:LEU:HB2	1:BF:497:TYR:HB2	2.03	0.40
1:BJ:250:TRP:HE3	1:BJ:272:TYR:CD1	2.39	0.40
1:BL:189:PHE:HE2	1:BL:249:LEU:HD21	1.86	0.40
1:BL:275:GLU:O	1:BL:276:ASP:C	2.65	0.40
1:BM:318:SER:HA	1:BM:319:GLY:HA2	1.78	0.40
1:BP:365:ILE:CD1	1:BP:471:MET:HE2	2.50	0.40
1:BQ:108:ILE:HG23	1:BQ:113:LEU:HD12	2.03	0.40
1:BT:55:ARG:NH1	1:CA:272:TYR:CD2	2.90	0.40
1:CA:252:VAL:HG22	1:CA:253:SER:N	2.36	0.40
1:CA:440:ALA:HB3	1:CB:444:LEU:HD13	2.04	0.40
1:CC:163:LEU:HD12	1:CC:163:LEU:HA	1.88	0.40
1:CD:263:ASN:O	1:CD:267:LYS:HG3	2.21	0.40
1:CE:404:LEU:HD22	1:CE:486:VAL:HG22	2.02	0.40
1:CF:33:LYS:HB2	1:CF:33:LYS:HE2	1.96	0.40
1:CI:163:LEU:HA	1:CI:163:LEU:HD12	1.85	0.40
1:CI:189:PHE:CE1	1:CI:198:ARG:HG2	2.55	0.40
1:CJ:189:PHE:CE2	1:CJ:249:LEU:HD21	2.46	0.40
1:CK:175:PHE:CD2	1:CK:175:PHE:O	2.74	0.40
1:CK:404:LEU:HD22	1:CK:486:VAL:HG22	2.02	0.40
1:CP:207:VAL:HA	1:CP:208:PRO:HD3	1.86	0.40
1:CQ:340:LEU:HA	1:CQ:340:LEU:HD23	1.93	0.40
1:CQ:404:LEU:HD22	1:CQ:486:VAL:HG22	2.03	0.40
1:CR:75:ARG:NH2	1:CR:391:ALA:O	2.54	0.40
1:CR:203:THR:HB	1:CR:300:GLN:CD	2.47	0.40
1:CR:252:VAL:HG22	1:CR:253:SER:N	2.36	0.40
1:CR:423:LYS:HE2	1:CR:449:GLU:O	2.21	0.40
1:CT:189:PHE:HD2	1:CT:247:ILE:CD1	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:61:PHE:CD2	1:AA:243:ILE:HD11	2.56	0.40
1:AA:454:ASN:HD22	1:AA:454:ASN:C	2.29	0.40
1:AC:170:PHE:CD1	1:AC:389:MET:HE1	2.49	0.40
1:AF:22:THR:OG1	1:AF:131:HIS:CD2	2.60	0.40
1:AF:185:PRO:HA	1:AF:186:PRO:HD3	1.90	0.40
1:AM:418:SER:HB3	1:AN:407:SER:HB3	2.04	0.40
1:AN:108:ILE:HG23	1:AN:113:LEU:HD12	2.03	0.40
1:AN:275:GLU:O	1:AN:276:ASP:C	2.65	0.40
1:AO:234:ARG:CG	1:AO:280:GLU:HG2	2.52	0.40
1:AP:395:LEU:HB2	1:AP:497:TYR:HB2	2.03	0.40
1:AQ:22:THR:OG1	1:AQ:131:HIS:CD2	2.63	0.40
1:AQ:48:PRO:HG2	1:AQ:50:PHE:CZ	2.57	0.40
1:AR:42:THR:OG1	1:AS:267:LYS:O	2.29	0.40
1:AR:275:GLU:O	1:AR:276:ASP:C	2.65	0.40
1:AT:10:ILE:HG21	1:AT:146:TRP:CZ2	2.57	0.40
1:BA:207:VAL:HA	1:BA:208:PRO:HD3	1.86	0.40
1:BC:232:THR:HB	1:BC:334:VAL:CG2	2.52	0.40
1:BC:238:HIS:HE1	1:BC:329:GLN:OE1	2.05	0.40
1:BD:314:PRO:HB3	1:BD:324:LEU:HD13	2.04	0.40
1:BE:203:THR:HB	1:BE:300:GLN:CD	2.45	0.40
1:BG:163:LEU:HD12	1:BG:163:LEU:HA	1.93	0.40
1:BG:203:THR:HB	1:BG:300:GLN:HG3	2.04	0.40
1:BH:22:THR:OG1	1:BH:131:HIS:CD2	2.64	0.40
1:BI:35:VAL:HG23	1:BQ:38:GLU:HB3	2.04	0.40
1:BN:189:PHE:HD2	1:BN:247:ILE:HD11	1.86	0.40
1:BQ:171:ASP:HA	1:BQ:172:PRO:HD3	1.80	0.40
1:BR:255:TRP:CE3	1:BR:285:SER:HB2	2.56	0.40
1:CB:170:PHE:HB2	1:CB:496:PHE:HE1	1.86	0.40
1:CC:22:THR:OG1	1:CC:131:HIS:CD2	2.66	0.40
1:CC:61:PHE:CD2	1:CC:243:ILE:HD11	2.57	0.40
1:CC:340:LEU:HD23	1:CC:340:LEU:HA	1.92	0.40
1:CD:126:GLU:HG3	1:CD:127:SER:H	1.85	0.40
1:CG:48:PRO:HG2	1:CG:50:PHE:CZ	2.56	0.40
1:CG:440:ALA:HB3	1:CH:444:LEU:HD13	2.03	0.40
1:CH:175:PHE:CD2	1:CH:175:PHE:O	2.75	0.40
1:CH:241:ALA:HB1	1:CH:242:PRO:HD2	2.03	0.40
1:CH:314:PRO:HB3	1:CH:324:LEU:HD13	2.04	0.40
1:CH:434:GLY:O	1:CI:349:VAL:HG23	2.22	0.40
1:CI:354:SER:H	1:CI:378:ARG:HB3	1.86	0.40
1:CI:423:LYS:HE2	1:CI:449:GLU:O	2.21	0.40
1:CJ:163:LEU:HA	1:CJ:163:LEU:HD12	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:250:TRP:CZ3	1:CJ:272:TYR:CD1	3.08	0.40
1:CL:255:TRP:CG	1:CL:286:PRO:HD3	2.57	0.40
1:CM:404:LEU:HD22	1:CM:486:VAL:HG22	2.04	0.40
1:CN:12:LYS:HB3	1:CN:144:ALA:C	2.46	0.40
1:CN:182:LEU:HG	1:CN:330:ILE:HB	2.04	0.40
1:CN:275:GLU:O	1:CN:276:ASP:C	2.65	0.40
1:CN:381:MET:HE2	1:CN:381:MET:HB2	1.64	0.40
1:CO:326:ILE:HD13	1:CO:326:ILE:HA	1.90	0.40
1:CO:423:LYS:HE2	1:CO:449:GLU:O	2.21	0.40
1:CQ:47:MET:HE2	1:CQ:117:ALA:N	2.37	0.40

All (12) 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:BG:18:ARG:NH2	1:CJ:297:GLY:CA[2_646]	1.46	0.74
1:BD:463:ARG:NH2	1:CB:145:ASP:OD2[2_545]	1.54	0.66
1:AI:463:ARG:NH2	1:AM:360:LYS:CE[2_546]	1.57	0.63
1:AJ:301:ARG:NH2	1:AN:411:GLU:OE2[2_546]	1.59	0.61
1:AG:15:GLN:OE1	1:CI:81:THR:OG1[2_646]	1.80	0.40
1:AI:129:ARG:NH1	1:AM:355:GLU:OE1[2_546]	1.85	0.35
1:AI:375:ASN:ND2	1:AM:429:ALA:CB[2_546]	1.92	0.28
1:BD:463:ARG:NH2	1:CB:145:ASP:CG[2_545]	1.98	0.22
1:AI:126:GLU:OE2	1:AM:357:THR:CG2[2_546]	2.01	0.19
1:BE:212:THR:OG1	1:CB:212:THR:OG1[2_545]	2.05	0.15
1:AI:126:GLU:CD	1:AM:357:THR:CG2[2_546]	2.09	0.11
1:BG:18:ARG:NH2	1:CJ:297:GLY:N[2_646]	2.12	0.08

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	502/504 (100%)	478 (95%)	23 (5%)	1 (0%)	43	72
1	AB	502/504 (100%)	483 (96%)	18 (4%)	1 (0%)	43	72
1	AC	502/504 (100%)	480 (96%)	20 (4%)	2 (0%)	30	60
1	AD	502/504 (100%)	482 (96%)	20 (4%)	0	100	100
1	AE	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	43	72
1	AF	502/504 (100%)	482 (96%)	20 (4%)	0	100	100
1	AG	502/504 (100%)	480 (96%)	18 (4%)	4 (1%)	16	48
1	AH	502/504 (100%)	481 (96%)	19 (4%)	2 (0%)	30	60
1	AI	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	43	72
1	AJ	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	43	72
1	AK	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	43	72
1	AL	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	43	72
1	AM	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	43	72
1	AN	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	43	72
1	AO	502/504 (100%)	483 (96%)	18 (4%)	1 (0%)	43	72
1	AP	502/504 (100%)	483 (96%)	19 (4%)	0	100	100
1	AQ	502/504 (100%)	483 (96%)	18 (4%)	1 (0%)	43	72
1	AR	502/504 (100%)	483 (96%)	18 (4%)	1 (0%)	43	72
1	AS	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	43	72
1	AT	502/504 (100%)	484 (96%)	17 (3%)	1 (0%)	43	72
1	BA	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	43	72
1	BB	502/504 (100%)	481 (96%)	19 (4%)	2 (0%)	30	60
1	BC	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	43	72
1	BD	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	43	72
1	BE	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	43	72
1	BF	502/504 (100%)	481 (96%)	19 (4%)	2 (0%)	30	60
1	BG	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	43	72
1	BH	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	43	72
1	BI	502/504 (100%)	479 (95%)	23 (5%)	0	100	100
1	BJ	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	43	72
1	BK	502/504 (100%)	483 (96%)	18 (4%)	1 (0%)	43	72
1	BL	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	43	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BM	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	43	72
1	BN	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	43	72
1	BO	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	43	72
1	BP	502/504 (100%)	479 (95%)	21 (4%)	2 (0%)	30	60
1	BQ	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	43	72
1	BR	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	43	72
1	BS	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	43	72
1	BT	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	43	72
1	CA	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	43	72
1	CB	502/504 (100%)	483 (96%)	18 (4%)	1 (0%)	43	72
1	CC	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	43	72
1	CD	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	43	72
1	CE	502/504 (100%)	483 (96%)	18 (4%)	1 (0%)	43	72
1	CF	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	43	72
1	CG	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	43	72
1	CH	502/504 (100%)	481 (96%)	21 (4%)	0	100	100
1	CI	502/504 (100%)	481 (96%)	19 (4%)	2 (0%)	30	60
1	CJ	502/504 (100%)	484 (96%)	17 (3%)	1 (0%)	43	72
1	CK	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	43	72
1	CL	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	43	72
1	CM	502/504 (100%)	480 (96%)	20 (4%)	2 (0%)	30	60
1	CN	502/504 (100%)	482 (96%)	20 (4%)	0	100	100
1	CO	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	43	72
1	CP	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	43	72
1	CQ	502/504 (100%)	482 (96%)	18 (4%)	2 (0%)	30	60
1	CR	502/504 (100%)	479 (95%)	21 (4%)	2 (0%)	30	60
1	CS	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	43	72
1	CT	502/504 (100%)	479 (95%)	22 (4%)	1 (0%)	43	72
All	All	30120/30240 (100%)	28873 (96%)	1181 (4%)	66 (0%)	43	72

All (66) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BP	82	ALA
1	CR	87	VAL
1	AG	273	VAL
1	CI	377	CYS
1	BM	17	ASN
1	AC	78	SER
1	BB	17	ASN
1	BD	17	ASN
1	BF	78	SER
1	CM	17	ASN
1	AG	269	PRO
1	AH	17	ASN
1	BA	498	GLY
1	AG	17	ASN
1	AN	498	GLY
1	AT	498	GLY
1	BG	498	GLY
1	BP	498	GLY
1	BT	498	GLY
1	CF	498	GLY
1	CG	498	GLY
1	CI	78	SER
1	CQ	17	ASN
1	CT	498	GLY
1	AE	498	GLY
1	AQ	498	GLY
1	BF	498	GLY
1	BK	498	GLY
1	BL	498	GLY
1	CK	498	GLY
1	CL	498	GLY
1	CM	498	GLY
1	CO	498	GLY
1	CR	498	GLY
1	AA	498	GLY
1	AG	498	GLY
1	AK	498	GLY
1	AM	498	GLY
1	BC	498	GLY
1	BE	498	GLY
1	BJ	498	GLY
1	BN	498	GLY
1	BO	498	GLY

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Mol	Chain	Res	Type
1	CD	498	GLY
1	AJ	498	GLY
1	AS	498	GLY
1	BH	498	GLY
1	BR	498	GLY
1	BS	498	GLY
1	CB	498	GLY
1	CP	498	GLY
1	CS	498	GLY
1	AH	498	GLY
1	AI	498	GLY
1	AO	498	GLY
1	AR	498	GLY
1	BB	498	GLY
1	CA	498	GLY
1	CE	498	GLY
1	CJ	498	GLY
1	CQ	498	GLY
1	AB	498	GLY
1	AC	498	GLY
1	AL	498	GLY
1	BQ	498	GLY
1	CC	498	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	430/430 (100%)	407 (95%)	23 (5%)	20	46
1	AB	430/430 (100%)	399 (93%)	31 (7%)	13	40
1	AC	430/430 (100%)	402 (94%)	28 (6%)	15	43
1	AD	430/430 (100%)	405 (94%)	25 (6%)	18	45
1	AE	430/430 (100%)	407 (95%)	23 (5%)	20	46
1	AF	430/430 (100%)	405 (94%)	25 (6%)	18	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AG	430/430 (100%)	402 (94%)	28 (6%)	15	43
1	AH	430/430 (100%)	401 (93%)	29 (7%)	15	42
1	AI	430/430 (100%)	403 (94%)	27 (6%)	16	43
1	AJ	430/430 (100%)	408 (95%)	22 (5%)	21	47
1	AK	430/430 (100%)	407 (95%)	23 (5%)	20	46
1	AL	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	AM	430/430 (100%)	406 (94%)	24 (6%)	19	46
1	AN	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	AO	430/430 (100%)	403 (94%)	27 (6%)	16	43
1	AP	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	AQ	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	AR	430/430 (100%)	405 (94%)	25 (6%)	18	45
1	AS	430/430 (100%)	405 (94%)	25 (6%)	18	45
1	AT	430/430 (100%)	405 (94%)	25 (6%)	18	45
1	BA	430/430 (100%)	405 (94%)	25 (6%)	18	45
1	BB	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	BC	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	BD	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	BE	430/430 (100%)	405 (94%)	25 (6%)	18	45
1	BF	430/430 (100%)	402 (94%)	28 (6%)	15	43
1	BG	430/430 (100%)	406 (94%)	24 (6%)	19	46
1	BH	430/430 (100%)	403 (94%)	27 (6%)	16	43
1	BI	430/430 (100%)	407 (95%)	23 (5%)	20	46
1	BJ	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	BK	430/430 (100%)	403 (94%)	27 (6%)	16	43
1	BL	430/430 (100%)	402 (94%)	28 (6%)	15	43
1	BM	430/430 (100%)	403 (94%)	27 (6%)	16	43
1	BN	430/430 (100%)	405 (94%)	25 (6%)	18	45
1	BO	430/430 (100%)	405 (94%)	25 (6%)	18	45
1	BP	430/430 (100%)	406 (94%)	24 (6%)	19	46
1	BQ	430/430 (100%)	404 (94%)	26 (6%)	17	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BR	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	BS	430/430 (100%)	405 (94%)	25 (6%)	18	45
1	BT	430/430 (100%)	406 (94%)	24 (6%)	19	46
1	CA	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	CB	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	CC	430/430 (100%)	405 (94%)	25 (6%)	18	45
1	CD	430/430 (100%)	406 (94%)	24 (6%)	19	46
1	CE	430/430 (100%)	403 (94%)	27 (6%)	16	43
1	CF	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	CG	430/430 (100%)	406 (94%)	24 (6%)	19	46
1	CH	430/430 (100%)	403 (94%)	27 (6%)	16	43
1	CI	430/430 (100%)	402 (94%)	28 (6%)	15	43
1	CJ	430/430 (100%)	405 (94%)	25 (6%)	18	45
1	CK	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	CL	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	CM	430/430 (100%)	402 (94%)	28 (6%)	15	43
1	CN	430/430 (100%)	407 (95%)	23 (5%)	20	46
1	CO	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	CP	430/430 (100%)	403 (94%)	27 (6%)	16	43
1	CQ	430/430 (100%)	404 (94%)	26 (6%)	17	44
1	CR	430/430 (100%)	403 (94%)	27 (6%)	16	43
1	CS	430/430 (100%)	406 (94%)	24 (6%)	19	46
1	CT	430/430 (100%)	406 (94%)	24 (6%)	19	46
All	All	25800/25800 (100%)	24258 (94%)	1542 (6%)	17	44

All (1542) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AA	105	SER
1	AA	129	ARG
1	AA	160	THR
1	AA	161	SER
1	AA	163	LEU
1	AA	167	THR

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Mol	Chain	Res	Type
1	AA	182	LEU
1	AA	191	LEU
1	AA	199	SER
1	AA	226	VAL
1	AA	234	ARG
1	AA	243	ILE
1	AA	260	MET
1	AA	272	TYR
1	AA	284	ARG
1	AA	289	ARG
1	AA	301	ARG
1	AA	384	ASN
1	AA	404	LEU
1	AA	449	GLU
1	AA	454	ASN
1	AA	475	LEU
1	AA	504	VAL
1	AB	18	ARG
1	AB	79	ARG
1	AB	105	SER
1	AB	129	ARG
1	AB	160	THR
1	AB	161	SER
1	AB	163	LEU
1	AB	167	THR
1	AB	182	LEU
1	AB	191	LEU
1	AB	199	SER
1	AB	226	VAL
1	AB	234	ARG
1	AB	243	ILE
1	AB	258	THR
1	AB	261	ASP
1	AB	265	LEU
1	AB	272	TYR
1	AB	274	GLU
1	AB	284	ARG
1	AB	289	ARG
1	AB	299	SER
1	AB	300	GLN
1	AB	301	ARG
1	AB	360	LYS

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Mol	Chain	Res	Type
1	AB	384	ASN
1	AB	404	LEU
1	AB	449	GLU
1	AB	454	ASN
1	AB	475	LEU
1	AB	504	VAL
1	AC	10	ILE
1	AC	56	LEU
1	AC	105	SER
1	AC	129	ARG
1	AC	160	THR
1	AC	161	SER
1	AC	163	LEU
1	AC	167	THR
1	AC	182	LEU
1	AC	191	LEU
1	AC	199	SER
1	AC	226	VAL
1	AC	234	ARG
1	AC	243	ILE
1	AC	260	MET
1	AC	272	TYR
1	AC	274	GLU
1	AC	284	ARG
1	AC	289	ARG
1	AC	300	GLN
1	AC	301	ARG
1	AC	360	LYS
1	AC	384	ASN
1	AC	404	LEU
1	AC	449	GLU
1	AC	454	ASN
1	AC	475	LEU
1	AC	504	VAL
1	AD	15	GLN
1	AD	79	ARG
1	AD	105	SER
1	AD	129	ARG
1	AD	160	THR
1	AD	163	LEU
1	AD	167	THR
1	AD	182	LEU

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Mol	Chain	Res	Type
1	AD	191	LEU
1	AD	199	SER
1	AD	226	VAL
1	AD	234	ARG
1	AD	243	ILE
1	AD	260	MET
1	AD	272	TYR
1	AD	274	GLU
1	AD	284	ARG
1	AD	289	ARG
1	AD	301	ARG
1	AD	384	ASN
1	AD	404	LEU
1	AD	449	GLU
1	AD	454	ASN
1	AD	475	LEU
1	AD	504	VAL
1	AE	10	ILE
1	AE	105	SER
1	AE	160	THR
1	AE	163	LEU
1	AE	167	THR
1	AE	182	LEU
1	AE	191	LEU
1	AE	199	SER
1	AE	226	VAL
1	AE	234	ARG
1	AE	243	ILE
1	AE	260	MET
1	AE	272	TYR
1	AE	284	ARG
1	AE	289	ARG
1	AE	301	ARG
1	AE	360	LYS
1	AE	384	ASN
1	AE	404	LEU
1	AE	449	GLU
1	AE	454	ASN
1	AE	475	LEU
1	AE	504	VAL
1	AF	79	ARG
1	AF	105	SER

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Mol	Chain	Res	Type
1	AF	129	ARG
1	AF	160	THR
1	AF	161	SER
1	AF	163	LEU
1	AF	167	THR
1	AF	182	LEU
1	AF	191	LEU
1	AF	199	SER
1	AF	226	VAL
1	AF	234	ARG
1	AF	243	ILE
1	AF	260	MET
1	AF	272	TYR
1	AF	284	ARG
1	AF	289	ARG
1	AF	301	ARG
1	AF	360	LYS
1	AF	384	ASN
1	AF	404	LEU
1	AF	449	GLU
1	AF	454	ASN
1	AF	475	LEU
1	AF	504	VAL
1	AG	10	ILE
1	AG	79	ARG
1	AG	105	SER
1	AG	129	ARG
1	AG	160	THR
1	AG	161	SER
1	AG	163	LEU
1	AG	167	THR
1	AG	182	LEU
1	AG	191	LEU
1	AG	226	VAL
1	AG	234	ARG
1	AG	243	ILE
1	AG	258	THR
1	AG	259	THR
1	AG	269	PRO
1	AG	275	GLU
1	AG	276	ASP
1	AG	284	ARG

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Mol	Chain	Res	Type
1	AG	289	ARG
1	AG	300	GLN
1	AG	301	ARG
1	AG	384	ASN
1	AG	404	LEU
1	AG	449	GLU
1	AG	454	ASN
1	AG	475	LEU
1	AG	504	VAL
1	AH	10	ILE
1	AH	15	GLN
1	AH	18	ARG
1	AH	56	LEU
1	AH	105	SER
1	AH	129	ARG
1	AH	160	THR
1	AH	161	SER
1	AH	163	LEU
1	AH	167	THR
1	AH	182	LEU
1	AH	191	LEU
1	AH	199	SER
1	AH	226	VAL
1	AH	234	ARG
1	AH	243	ILE
1	AH	260	MET
1	AH	272	TYR
1	AH	274	GLU
1	AH	284	ARG
1	AH	289	ARG
1	AH	300	GLN
1	AH	360	LYS
1	AH	384	ASN
1	AH	404	LEU
1	AH	449	GLU
1	AH	454	ASN
1	AH	475	LEU
1	AH	504	VAL
1	AI	18	ARG
1	AI	79	ARG
1	AI	105	SER
1	AI	129	ARG

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Mol	Chain	Res	Type
1	AI	160	THR
1	AI	161	SER
1	AI	163	LEU
1	AI	167	THR
1	AI	182	LEU
1	AI	191	LEU
1	AI	199	SER
1	AI	226	VAL
1	AI	234	ARG
1	AI	243	ILE
1	AI	260	MET
1	AI	272	TYR
1	AI	274	GLU
1	AI	284	ARG
1	AI	289	ARG
1	AI	300	GLN
1	AI	301	ARG
1	AI	384	ASN
1	AI	404	LEU
1	AI	449	GLU
1	AI	454	ASN
1	AI	475	LEU
1	AI	504	VAL
1	AJ	105	SER
1	AJ	129	ARG
1	AJ	160	THR
1	AJ	161	SER
1	AJ	163	LEU
1	AJ	167	THR
1	AJ	182	LEU
1	AJ	191	LEU
1	AJ	199	SER
1	AJ	226	VAL
1	AJ	234	ARG
1	AJ	243	ILE
1	AJ	272	TYR
1	AJ	284	ARG
1	AJ	289	ARG
1	AJ	301	ARG
1	AJ	384	ASN
1	AJ	404	LEU
1	AJ	449	GLU

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Mol	Chain	Res	Type
1	AJ	454	ASN
1	AJ	475	LEU
1	AJ	504	VAL
1	AK	105	SER
1	AK	129	ARG
1	AK	160	THR
1	AK	161	SER
1	AK	163	LEU
1	AK	167	THR
1	AK	182	LEU
1	AK	191	LEU
1	AK	199	SER
1	AK	226	VAL
1	AK	234	ARG
1	AK	243	ILE
1	AK	260	MET
1	AK	272	TYR
1	AK	284	ARG
1	AK	289	ARG
1	AK	301	ARG
1	AK	384	ASN
1	AK	404	LEU
1	AK	449	GLU
1	AK	454	ASN
1	AK	475	LEU
1	AK	504	VAL
1	AL	10	ILE
1	AL	79	ARG
1	AL	105	SER
1	AL	129	ARG
1	AL	160	THR
1	AL	161	SER
1	AL	163	LEU
1	AL	167	THR
1	AL	182	LEU
1	AL	191	LEU
1	AL	199	SER
1	AL	226	VAL
1	AL	234	ARG
1	AL	243	ILE
1	AL	260	MET
1	AL	272	TYR

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Mol	Chain	Res	Type
1	AL	284	ARG
1	AL	289	ARG
1	AL	299	SER
1	AL	301	ARG
1	AL	384	ASN
1	AL	404	LEU
1	AL	449	GLU
1	AL	454	ASN
1	AL	475	LEU
1	AL	504	VAL
1	AM	105	SER
1	AM	129	ARG
1	AM	160	THR
1	AM	161	SER
1	AM	163	LEU
1	AM	167	THR
1	AM	182	LEU
1	AM	191	LEU
1	AM	199	SER
1	AM	226	VAL
1	AM	234	ARG
1	AM	243	ILE
1	AM	260	MET
1	AM	272	TYR
1	AM	274	GLU
1	AM	284	ARG
1	AM	289	ARG
1	AM	301	ARG
1	AM	384	ASN
1	AM	404	LEU
1	AM	449	GLU
1	AM	454	ASN
1	AM	475	LEU
1	AM	504	VAL
1	AN	10	ILE
1	AN	79	ARG
1	AN	105	SER
1	AN	129	ARG
1	AN	160	THR
1	AN	161	SER
1	AN	163	LEU
1	AN	167	THR

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Mol	Chain	Res	Type
1	AN	182	LEU
1	AN	191	LEU
1	AN	199	SER
1	AN	226	VAL
1	AN	234	ARG
1	AN	243	ILE
1	AN	260	MET
1	AN	272	TYR
1	AN	284	ARG
1	AN	289	ARG
1	AN	301	ARG
1	AN	360	LYS
1	AN	384	ASN
1	AN	404	LEU
1	AN	449	GLU
1	AN	454	ASN
1	AN	475	LEU
1	AN	504	VAL
1	AO	10	ILE
1	AO	105	SER
1	AO	129	ARG
1	AO	160	THR
1	AO	161	SER
1	AO	163	LEU
1	AO	167	THR
1	AO	182	LEU
1	AO	191	LEU
1	AO	199	SER
1	AO	226	VAL
1	AO	234	ARG
1	AO	243	ILE
1	AO	260	MET
1	AO	272	TYR
1	AO	284	ARG
1	AO	290	THR
1	AO	294	LEU
1	AO	300	GLN
1	AO	301	ARG
1	AO	360	LYS
1	AO	384	ASN
1	AO	404	LEU
1	AO	449	GLU

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Mol	Chain	Res	Type
1	AO	454	ASN
1	AO	475	LEU
1	AO	504	VAL
1	AP	79	ARG
1	AP	105	SER
1	AP	129	ARG
1	AP	160	THR
1	AP	161	SER
1	AP	163	LEU
1	AP	167	THR
1	AP	182	LEU
1	AP	191	LEU
1	AP	199	SER
1	AP	226	VAL
1	AP	234	ARG
1	AP	243	ILE
1	AP	260	MET
1	AP	272	TYR
1	AP	274	GLU
1	AP	284	ARG
1	AP	289	ARG
1	AP	301	ARG
1	AP	360	LYS
1	AP	384	ASN
1	AP	404	LEU
1	AP	449	GLU
1	AP	454	ASN
1	AP	475	LEU
1	AP	504	VAL
1	AQ	10	ILE
1	AQ	105	SER
1	AQ	129	ARG
1	AQ	160	THR
1	AQ	161	SER
1	AQ	163	LEU
1	AQ	167	THR
1	AQ	182	LEU
1	AQ	191	LEU
1	AQ	199	SER
1	AQ	226	VAL
1	AQ	234	ARG
1	AQ	243	ILE

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Mol	Chain	Res	Type
1	AQ	260	MET
1	AQ	272	TYR
1	AQ	274	GLU
1	AQ	284	ARG
1	AQ	289	ARG
1	AQ	301	ARG
1	AQ	360	LYS
1	AQ	384	ASN
1	AQ	404	LEU
1	AQ	449	GLU
1	AQ	454	ASN
1	AQ	475	LEU
1	AQ	504	VAL
1	AR	75	ARG
1	AR	105	SER
1	AR	129	ARG
1	AR	160	THR
1	AR	161	SER
1	AR	163	LEU
1	AR	167	THR
1	AR	182	LEU
1	AR	191	LEU
1	AR	199	SER
1	AR	226	VAL
1	AR	234	ARG
1	AR	243	ILE
1	AR	260	MET
1	AR	272	TYR
1	AR	284	ARG
1	AR	289	ARG
1	AR	300	GLN
1	AR	301	ARG
1	AR	384	ASN
1	AR	404	LEU
1	AR	449	GLU
1	AR	454	ASN
1	AR	475	LEU
1	AR	504	VAL
1	AS	10	ILE
1	AS	105	SER
1	AS	129	ARG
1	AS	160	THR

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Mol	Chain	Res	Type
1	AS	161	SER
1	AS	163	LEU
1	AS	167	THR
1	AS	182	LEU
1	AS	191	LEU
1	AS	199	SER
1	AS	226	VAL
1	AS	234	ARG
1	AS	243	ILE
1	AS	260	MET
1	AS	272	TYR
1	AS	284	ARG
1	AS	289	ARG
1	AS	301	ARG
1	AS	305	SER
1	AS	384	ASN
1	AS	404	LEU
1	AS	449	GLU
1	AS	454	ASN
1	AS	475	LEU
1	AS	504	VAL
1	AT	105	SER
1	AT	129	ARG
1	AT	160	THR
1	AT	161	SER
1	AT	163	LEU
1	AT	167	THR
1	AT	182	LEU
1	AT	191	LEU
1	AT	199	SER
1	AT	226	VAL
1	AT	234	ARG
1	AT	243	ILE
1	AT	260	MET
1	AT	272	TYR
1	AT	274	GLU
1	AT	284	ARG
1	AT	289	ARG
1	AT	300	GLN
1	AT	301	ARG
1	AT	384	ASN
1	AT	404	LEU

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Mol	Chain	Res	Type
1	AT	449	GLU
1	AT	454	ASN
1	AT	475	LEU
1	AT	504	VAL
1	BA	10	ILE
1	BA	79	ARG
1	BA	105	SER
1	BA	129	ARG
1	BA	160	THR
1	BA	161	SER
1	BA	163	LEU
1	BA	167	THR
1	BA	182	LEU
1	BA	191	LEU
1	BA	199	SER
1	BA	226	VAL
1	BA	234	ARG
1	BA	243	ILE
1	BA	260	MET
1	BA	272	TYR
1	BA	284	ARG
1	BA	289	ARG
1	BA	301	ARG
1	BA	384	ASN
1	BA	404	LEU
1	BA	449	GLU
1	BA	454	ASN
1	BA	475	LEU
1	BA	504	VAL
1	BB	79	ARG
1	BB	105	SER
1	BB	129	ARG
1	BB	160	THR
1	BB	161	SER
1	BB	163	LEU
1	BB	167	THR
1	BB	182	LEU
1	BB	191	LEU
1	BB	199	SER
1	BB	226	VAL
1	BB	234	ARG
1	BB	243	ILE

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Mol	Chain	Res	Type
1	BB	260	MET
1	BB	272	TYR
1	BB	284	ARG
1	BB	289	ARG
1	BB	300	GLN
1	BB	301	ARG
1	BB	360	LYS
1	BB	384	ASN
1	BB	404	LEU
1	BB	449	GLU
1	BB	454	ASN
1	BB	475	LEU
1	BB	504	VAL
1	BC	18	ARG
1	BC	56	LEU
1	BC	105	SER
1	BC	129	ARG
1	BC	160	THR
1	BC	161	SER
1	BC	163	LEU
1	BC	167	THR
1	BC	182	LEU
1	BC	191	LEU
1	BC	199	SER
1	BC	226	VAL
1	BC	234	ARG
1	BC	243	ILE
1	BC	260	MET
1	BC	272	TYR
1	BC	284	ARG
1	BC	289	ARG
1	BC	301	ARG
1	BC	360	LYS
1	BC	384	ASN
1	BC	404	LEU
1	BC	449	GLU
1	BC	454	ASN
1	BC	475	LEU
1	BC	504	VAL
1	BD	15	GLN
1	BD	56	LEU
1	BD	105	SER

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Mol	Chain	Res	Type
1	BD	129	ARG
1	BD	160	THR
1	BD	161	SER
1	BD	163	LEU
1	BD	167	THR
1	BD	182	LEU
1	BD	191	LEU
1	BD	226	VAL
1	BD	234	ARG
1	BD	243	ILE
1	BD	260	MET
1	BD	272	TYR
1	BD	274	GLU
1	BD	284	ARG
1	BD	289	ARG
1	BD	300	GLN
1	BD	301	ARG
1	BD	384	ASN
1	BD	404	LEU
1	BD	449	GLU
1	BD	454	ASN
1	BD	475	LEU
1	BD	504	VAL
1	BE	105	SER
1	BE	129	ARG
1	BE	160	THR
1	BE	161	SER
1	BE	163	LEU
1	BE	167	THR
1	BE	182	LEU
1	BE	191	LEU
1	BE	199	SER
1	BE	226	VAL
1	BE	234	ARG
1	BE	243	ILE
1	BE	260	MET
1	BE	272	TYR
1	BE	274	GLU
1	BE	284	ARG
1	BE	289	ARG
1	BE	300	GLN
1	BE	301	ARG

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Mol	Chain	Res	Type
1	BE	384	ASN
1	BE	404	LEU
1	BE	449	GLU
1	BE	454	ASN
1	BE	475	LEU
1	BE	504	VAL
1	BF	10	ILE
1	BF	18	ARG
1	BF	79	ARG
1	BF	105	SER
1	BF	129	ARG
1	BF	160	THR
1	BF	161	SER
1	BF	163	LEU
1	BF	167	THR
1	BF	182	LEU
1	BF	191	LEU
1	BF	199	SER
1	BF	226	VAL
1	BF	234	ARG
1	BF	243	ILE
1	BF	260	MET
1	BF	272	TYR
1	BF	284	ARG
1	BF	289	ARG
1	BF	299	SER
1	BF	301	ARG
1	BF	360	LYS
1	BF	384	ASN
1	BF	404	LEU
1	BF	449	GLU
1	BF	454	ASN
1	BF	475	LEU
1	BF	504	VAL
1	BG	105	SER
1	BG	129	ARG
1	BG	160	THR
1	BG	161	SER
1	BG	163	LEU
1	BG	167	THR
1	BG	182	LEU
1	BG	191	LEU

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Mol	Chain	Res	Type
1	BG	199	SER
1	BG	226	VAL
1	BG	234	ARG
1	BG	243	ILE
1	BG	260	MET
1	BG	272	TYR
1	BG	274	GLU
1	BG	284	ARG
1	BG	289	ARG
1	BG	301	ARG
1	BG	384	ASN
1	BG	404	LEU
1	BG	449	GLU
1	BG	454	ASN
1	BG	475	LEU
1	BG	504	VAL
1	BH	15	GLN
1	BH	18	ARG
1	BH	105	SER
1	BH	129	ARG
1	BH	160	THR
1	BH	161	SER
1	BH	163	LEU
1	BH	167	THR
1	BH	182	LEU
1	BH	191	LEU
1	BH	199	SER
1	BH	226	VAL
1	BH	234	ARG
1	BH	243	ILE
1	BH	260	MET
1	BH	272	TYR
1	BH	284	ARG
1	BH	289	ARG
1	BH	301	ARG
1	BH	305	SER
1	BH	360	LYS
1	BH	384	ASN
1	BH	404	LEU
1	BH	449	GLU
1	BH	454	ASN
1	BH	475	LEU

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Mol	Chain	Res	Type
1	BH	504	VAL
1	BI	105	SER
1	BI	129	ARG
1	BI	160	THR
1	BI	161	SER
1	BI	163	LEU
1	BI	167	THR
1	BI	182	LEU
1	BI	191	LEU
1	BI	199	SER
1	BI	226	VAL
1	BI	234	ARG
1	BI	243	ILE
1	BI	260	MET
1	BI	272	TYR
1	BI	284	ARG
1	BI	289	ARG
1	BI	301	ARG
1	BI	384	ASN
1	BI	404	LEU
1	BI	449	GLU
1	BI	454	ASN
1	BI	475	LEU
1	BI	504	VAL
1	BJ	18	ARG
1	BJ	79	ARG
1	BJ	105	SER
1	BJ	129	ARG
1	BJ	160	THR
1	BJ	161	SER
1	BJ	163	LEU
1	BJ	167	THR
1	BJ	182	LEU
1	BJ	191	LEU
1	BJ	199	SER
1	BJ	226	VAL
1	BJ	234	ARG
1	BJ	243	ILE
1	BJ	260	MET
1	BJ	272	TYR
1	BJ	274	GLU
1	BJ	284	ARG

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Mol	Chain	Res	Type
1	BJ	289	ARG
1	BJ	301	ARG
1	BJ	384	ASN
1	BJ	404	LEU
1	BJ	449	GLU
1	BJ	454	ASN
1	BJ	475	LEU
1	BJ	504	VAL
1	BK	18	ARG
1	BK	105	SER
1	BK	129	ARG
1	BK	160	THR
1	BK	161	SER
1	BK	163	LEU
1	BK	167	THR
1	BK	182	LEU
1	BK	191	LEU
1	BK	199	SER
1	BK	226	VAL
1	BK	229	MET
1	BK	234	ARG
1	BK	243	ILE
1	BK	260	MET
1	BK	272	TYR
1	BK	284	ARG
1	BK	289	ARG
1	BK	299	SER
1	BK	300	GLN
1	BK	301	ARG
1	BK	384	ASN
1	BK	404	LEU
1	BK	449	GLU
1	BK	454	ASN
1	BK	475	LEU
1	BK	504	VAL
1	BL	79	ARG
1	BL	105	SER
1	BL	129	ARG
1	BL	160	THR
1	BL	161	SER
1	BL	163	LEU
1	BL	167	THR

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Mol	Chain	Res	Type
1	BL	182	LEU
1	BL	191	LEU
1	BL	199	SER
1	BL	226	VAL
1	BL	234	ARG
1	BL	243	ILE
1	BL	260	MET
1	BL	272	TYR
1	BL	274	GLU
1	BL	284	ARG
1	BL	289	ARG
1	BL	299	SER
1	BL	300	GLN
1	BL	301	ARG
1	BL	360	LYS
1	BL	384	ASN
1	BL	404	LEU
1	BL	449	GLU
1	BL	454	ASN
1	BL	475	LEU
1	BL	504	VAL
1	BM	18	ARG
1	BM	79	ARG
1	BM	105	SER
1	BM	129	ARG
1	BM	160	THR
1	BM	161	SER
1	BM	163	LEU
1	BM	167	THR
1	BM	182	LEU
1	BM	191	LEU
1	BM	199	SER
1	BM	226	VAL
1	BM	234	ARG
1	BM	243	ILE
1	BM	260	MET
1	BM	272	TYR
1	BM	274	GLU
1	BM	284	ARG
1	BM	289	ARG
1	BM	300	GLN
1	BM	301	ARG

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Mol	Chain	Res	Type
1	BM	384	ASN
1	BM	404	LEU
1	BM	449	GLU
1	BM	454	ASN
1	BM	475	LEU
1	BM	504	VAL
1	BN	18	ARG
1	BN	105	SER
1	BN	129	ARG
1	BN	160	THR
1	BN	161	SER
1	BN	163	LEU
1	BN	167	THR
1	BN	182	LEU
1	BN	191	LEU
1	BN	199	SER
1	BN	226	VAL
1	BN	234	ARG
1	BN	243	ILE
1	BN	260	MET
1	BN	272	TYR
1	BN	274	GLU
1	BN	284	ARG
1	BN	289	ARG
1	BN	301	ARG
1	BN	384	ASN
1	BN	404	LEU
1	BN	449	GLU
1	BN	454	ASN
1	BN	475	LEU
1	BN	504	VAL
1	BO	15	GLN
1	BO	105	SER
1	BO	129	ARG
1	BO	160	THR
1	BO	161	SER
1	BO	163	LEU
1	BO	167	THR
1	BO	182	LEU
1	BO	191	LEU
1	BO	199	SER
1	BO	226	VAL

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Mol	Chain	Res	Type
1	BO	234	ARG
1	BO	243	ILE
1	BO	260	MET
1	BO	272	TYR
1	BO	284	ARG
1	BO	289	ARG
1	BO	301	ARG
1	BO	360	LYS
1	BO	384	ASN
1	BO	404	LEU
1	BO	449	GLU
1	BO	454	ASN
1	BO	475	LEU
1	BO	504	VAL
1	BP	79	ARG
1	BP	105	SER
1	BP	160	THR
1	BP	161	SER
1	BP	163	LEU
1	BP	167	THR
1	BP	182	LEU
1	BP	191	LEU
1	BP	199	SER
1	BP	226	VAL
1	BP	234	ARG
1	BP	243	ILE
1	BP	260	MET
1	BP	272	TYR
1	BP	284	ARG
1	BP	289	ARG
1	BP	300	GLN
1	BP	301	ARG
1	BP	384	ASN
1	BP	404	LEU
1	BP	449	GLU
1	BP	454	ASN
1	BP	475	LEU
1	BP	504	VAL
1	BQ	56	LEU
1	BQ	105	SER
1	BQ	129	ARG
1	BQ	160	THR

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Mol	Chain	Res	Type
1	BQ	161	SER
1	BQ	163	LEU
1	BQ	167	THR
1	BQ	182	LEU
1	BQ	191	LEU
1	BQ	199	SER
1	BQ	226	VAL
1	BQ	234	ARG
1	BQ	243	ILE
1	BQ	260	MET
1	BQ	272	TYR
1	BQ	284	ARG
1	BQ	289	ARG
1	BQ	301	ARG
1	BQ	305	SER
1	BQ	360	LYS
1	BQ	384	ASN
1	BQ	404	LEU
1	BQ	449	GLU
1	BQ	454	ASN
1	BQ	475	LEU
1	BQ	504	VAL
1	BR	79	ARG
1	BR	105	SER
1	BR	129	ARG
1	BR	160	THR
1	BR	161	SER
1	BR	163	LEU
1	BR	167	THR
1	BR	182	LEU
1	BR	191	LEU
1	BR	199	SER
1	BR	226	VAL
1	BR	234	ARG
1	BR	243	ILE
1	BR	260	MET
1	BR	272	TYR
1	BR	274	GLU
1	BR	284	ARG
1	BR	289	ARG
1	BR	299	SER
1	BR	301	ARG

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Mol	Chain	Res	Type
1	BR	384	ASN
1	BR	404	LEU
1	BR	449	GLU
1	BR	454	ASN
1	BR	475	LEU
1	BR	504	VAL
1	BS	79	ARG
1	BS	105	SER
1	BS	129	ARG
1	BS	160	THR
1	BS	161	SER
1	BS	163	LEU
1	BS	167	THR
1	BS	182	LEU
1	BS	191	LEU
1	BS	199	SER
1	BS	226	VAL
1	BS	234	ARG
1	BS	243	ILE
1	BS	260	MET
1	BS	274	GLU
1	BS	284	ARG
1	BS	289	ARG
1	BS	299	SER
1	BS	301	ARG
1	BS	384	ASN
1	BS	404	LEU
1	BS	449	GLU
1	BS	454	ASN
1	BS	475	LEU
1	BS	504	VAL
1	BT	105	SER
1	BT	129	ARG
1	BT	160	THR
1	BT	161	SER
1	BT	163	LEU
1	BT	167	THR
1	BT	182	LEU
1	BT	191	LEU
1	BT	199	SER
1	BT	226	VAL
1	BT	234	ARG

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Mol	Chain	Res	Type
1	BT	243	ILE
1	BT	260	MET
1	BT	272	TYR
1	BT	284	ARG
1	BT	289	ARG
1	BT	299	SER
1	BT	300	GLN
1	BT	384	ASN
1	BT	404	LEU
1	BT	449	GLU
1	BT	454	ASN
1	BT	475	LEU
1	BT	504	VAL
1	CA	10	ILE
1	CA	18	ARG
1	CA	105	SER
1	CA	129	ARG
1	CA	160	THR
1	CA	161	SER
1	CA	163	LEU
1	CA	167	THR
1	CA	182	LEU
1	CA	191	LEU
1	CA	226	VAL
1	CA	234	ARG
1	CA	243	ILE
1	CA	260	MET
1	CA	272	TYR
1	CA	274	GLU
1	CA	284	ARG
1	CA	289	ARG
1	CA	301	ARG
1	CA	360	LYS
1	CA	384	ASN
1	CA	404	LEU
1	CA	449	GLU
1	CA	454	ASN
1	CA	475	LEU
1	CA	504	VAL
1	CB	15	GLN
1	CB	105	SER
1	CB	129	ARG

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Mol	Chain	Res	Type
1	CB	160	THR
1	CB	161	SER
1	CB	163	LEU
1	CB	167	THR
1	CB	182	LEU
1	CB	191	LEU
1	CB	199	SER
1	CB	226	VAL
1	CB	234	ARG
1	CB	243	ILE
1	CB	260	MET
1	CB	272	TYR
1	CB	284	ARG
1	CB	289	ARG
1	CB	300	GLN
1	CB	301	ARG
1	CB	360	LYS
1	CB	384	ASN
1	CB	404	LEU
1	CB	449	GLU
1	CB	454	ASN
1	CB	475	LEU
1	CB	504	VAL
1	CC	10	ILE
1	CC	105	SER
1	CC	129	ARG
1	CC	160	THR
1	CC	161	SER
1	CC	163	LEU
1	CC	167	THR
1	CC	182	LEU
1	CC	191	LEU
1	CC	199	SER
1	CC	226	VAL
1	CC	234	ARG
1	CC	243	ILE
1	CC	260	MET
1	CC	272	TYR
1	CC	284	ARG
1	CC	289	ARG
1	CC	301	ARG
1	CC	360	LYS

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Mol	Chain	Res	Type
1	CC	384	ASN
1	CC	404	LEU
1	CC	449	GLU
1	CC	454	ASN
1	CC	475	LEU
1	CC	504	VAL
1	CD	79	ARG
1	CD	105	SER
1	CD	129	ARG
1	CD	160	THR
1	CD	163	LEU
1	CD	167	THR
1	CD	182	LEU
1	CD	191	LEU
1	CD	199	SER
1	CD	226	VAL
1	CD	234	ARG
1	CD	243	ILE
1	CD	260	MET
1	CD	272	TYR
1	CD	274	GLU
1	CD	284	ARG
1	CD	289	ARG
1	CD	301	ARG
1	CD	384	ASN
1	CD	404	LEU
1	CD	449	GLU
1	CD	454	ASN
1	CD	475	LEU
1	CD	504	VAL
1	CE	56	LEU
1	CE	79	ARG
1	CE	105	SER
1	CE	129	ARG
1	CE	160	THR
1	CE	161	SER
1	CE	163	LEU
1	CE	167	THR
1	CE	182	LEU
1	CE	191	LEU
1	CE	199	SER
1	CE	226	VAL

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Mol	Chain	Res	Type
1	CE	234	ARG
1	CE	243	ILE
1	CE	260	MET
1	CE	272	TYR
1	CE	274	GLU
1	CE	284	ARG
1	CE	289	ARG
1	CE	300	GLN
1	CE	301	ARG
1	CE	384	ASN
1	CE	404	LEU
1	CE	449	GLU
1	CE	454	ASN
1	CE	475	LEU
1	CE	504	VAL
1	CF	18	ARG
1	CF	79	ARG
1	CF	105	SER
1	CF	129	ARG
1	CF	160	THR
1	CF	161	SER
1	CF	163	LEU
1	CF	167	THR
1	CF	182	LEU
1	CF	191	LEU
1	CF	226	VAL
1	CF	234	ARG
1	CF	243	ILE
1	CF	260	MET
1	CF	272	TYR
1	CF	274	GLU
1	CF	284	ARG
1	CF	289	ARG
1	CF	301	ARG
1	CF	360	LYS
1	CF	384	ASN
1	CF	404	LEU
1	CF	449	GLU
1	CF	454	ASN
1	CF	475	LEU
1	CF	504	VAL
1	CG	79	ARG

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Mol	Chain	Res	Type
1	CG	105	SER
1	CG	129	ARG
1	CG	160	THR
1	CG	161	SER
1	CG	163	LEU
1	CG	167	THR
1	CG	182	LEU
1	CG	191	LEU
1	CG	199	SER
1	CG	226	VAL
1	CG	234	ARG
1	CG	243	ILE
1	CG	260	MET
1	CG	272	TYR
1	CG	284	ARG
1	CG	289	ARG
1	CG	301	ARG
1	CG	384	ASN
1	CG	404	LEU
1	CG	449	GLU
1	CG	454	ASN
1	CG	475	LEU
1	CG	504	VAL
1	CH	10	ILE
1	CH	15	GLN
1	CH	105	SER
1	CH	129	ARG
1	CH	160	THR
1	CH	161	SER
1	CH	163	LEU
1	CH	167	THR
1	CH	182	LEU
1	CH	191	LEU
1	CH	199	SER
1	CH	226	VAL
1	CH	234	ARG
1	CH	243	ILE
1	CH	260	MET
1	CH	272	TYR
1	CH	274	GLU
1	CH	284	ARG
1	CH	289	ARG

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Mol	Chain	Res	Type
1	CH	301	ARG
1	CH	360	LYS
1	CH	384	ASN
1	CH	404	LEU
1	CH	449	GLU
1	CH	454	ASN
1	CH	475	LEU
1	CH	504	VAL
1	CI	105	SER
1	CI	129	ARG
1	CI	160	THR
1	CI	161	SER
1	CI	163	LEU
1	CI	167	THR
1	CI	182	LEU
1	CI	191	LEU
1	CI	199	SER
1	CI	226	VAL
1	CI	234	ARG
1	CI	243	ILE
1	CI	260	MET
1	CI	272	TYR
1	CI	274	GLU
1	CI	284	ARG
1	CI	289	ARG
1	CI	299	SER
1	CI	300	GLN
1	CI	301	ARG
1	CI	377	CYS
1	CI	379	VAL
1	CI	384	ASN
1	CI	404	LEU
1	CI	449	GLU
1	CI	454	ASN
1	CI	475	LEU
1	CI	504	VAL
1	CJ	18	ARG
1	CJ	105	SER
1	CJ	129	ARG
1	CJ	160	THR
1	CJ	161	SER
1	CJ	163	LEU

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Mol	Chain	Res	Type
1	CJ	167	THR
1	CJ	182	LEU
1	CJ	191	LEU
1	CJ	199	SER
1	CJ	226	VAL
1	CJ	234	ARG
1	CJ	243	ILE
1	CJ	260	MET
1	CJ	272	TYR
1	CJ	274	GLU
1	CJ	284	ARG
1	CJ	289	ARG
1	CJ	301	ARG
1	CJ	384	ASN
1	CJ	404	LEU
1	CJ	449	GLU
1	CJ	454	ASN
1	CJ	475	LEU
1	CJ	504	VAL
1	CK	15	GLN
1	CK	77	THR
1	CK	105	SER
1	CK	129	ARG
1	CK	160	THR
1	CK	161	SER
1	CK	163	LEU
1	CK	167	THR
1	CK	182	LEU
1	CK	191	LEU
1	CK	199	SER
1	CK	226	VAL
1	CK	234	ARG
1	CK	243	ILE
1	CK	260	MET
1	CK	272	TYR
1	CK	284	ARG
1	CK	289	ARG
1	CK	301	ARG
1	CK	360	LYS
1	CK	384	ASN
1	CK	404	LEU
1	CK	449	GLU

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Mol	Chain	Res	Type
1	CK	454	ASN
1	CK	475	LEU
1	CK	504	VAL
1	CL	105	SER
1	CL	129	ARG
1	CL	160	THR
1	CL	161	SER
1	CL	163	LEU
1	CL	167	THR
1	CL	182	LEU
1	CL	191	LEU
1	CL	199	SER
1	CL	226	VAL
1	CL	234	ARG
1	CL	243	ILE
1	CL	260	MET
1	CL	272	TYR
1	CL	274	GLU
1	CL	284	ARG
1	CL	289	ARG
1	CL	299	SER
1	CL	301	ARG
1	CL	360	LYS
1	CL	384	ASN
1	CL	404	LEU
1	CL	449	GLU
1	CL	454	ASN
1	CL	475	LEU
1	CL	504	VAL
1	CM	10	ILE
1	CM	56	LEU
1	CM	105	SER
1	CM	129	ARG
1	CM	160	THR
1	CM	161	SER
1	CM	163	LEU
1	CM	167	THR
1	CM	182	LEU
1	CM	191	LEU
1	CM	199	SER
1	CM	226	VAL
1	CM	234	ARG

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Mol	Chain	Res	Type
1	CM	243	ILE
1	CM	260	MET
1	CM	272	TYR
1	CM	274	GLU
1	CM	284	ARG
1	CM	289	ARG
1	CM	299	SER
1	CM	301	ARG
1	CM	360	LYS
1	CM	384	ASN
1	CM	404	LEU
1	CM	449	GLU
1	CM	454	ASN
1	CM	475	LEU
1	CM	504	VAL
1	CN	105	SER
1	CN	160	THR
1	CN	161	SER
1	CN	163	LEU
1	CN	167	THR
1	CN	182	LEU
1	CN	191	LEU
1	CN	199	SER
1	CN	226	VAL
1	CN	234	ARG
1	CN	243	ILE
1	CN	260	MET
1	CN	272	TYR
1	CN	284	ARG
1	CN	289	ARG
1	CN	301	ARG
1	CN	360	LYS
1	CN	384	ASN
1	CN	404	LEU
1	CN	449	GLU
1	CN	454	ASN
1	CN	475	LEU
1	CN	504	VAL
1	CO	79	ARG
1	CO	105	SER
1	CO	129	ARG
1	CO	160	THR

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Mol	Chain	Res	Type
1	CO	161	SER
1	CO	163	LEU
1	CO	167	THR
1	CO	182	LEU
1	CO	191	LEU
1	CO	199	SER
1	CO	226	VAL
1	CO	234	ARG
1	CO	243	ILE
1	CO	260	MET
1	CO	272	TYR
1	CO	274	GLU
1	CO	284	ARG
1	CO	289	ARG
1	CO	301	ARG
1	CO	305	SER
1	CO	384	ASN
1	CO	404	LEU
1	CO	449	GLU
1	CO	454	ASN
1	CO	475	LEU
1	CO	504	VAL
1	CP	10	ILE
1	CP	79	ARG
1	CP	105	SER
1	CP	129	ARG
1	CP	160	THR
1	CP	161	SER
1	CP	163	LEU
1	CP	167	THR
1	CP	182	LEU
1	CP	191	LEU
1	CP	199	SER
1	CP	226	VAL
1	CP	234	ARG
1	CP	243	ILE
1	CP	260	MET
1	CP	272	TYR
1	CP	284	ARG
1	CP	289	ARG
1	CP	300	GLN
1	CP	301	ARG

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Mol	Chain	Res	Type
1	CP	360	LYS
1	CP	384	ASN
1	CP	404	LEU
1	CP	449	GLU
1	CP	454	ASN
1	CP	475	LEU
1	CP	504	VAL
1	CQ	105	SER
1	CQ	129	ARG
1	CQ	160	THR
1	CQ	161	SER
1	CQ	163	LEU
1	CQ	167	THR
1	CQ	182	LEU
1	CQ	191	LEU
1	CQ	199	SER
1	CQ	226	VAL
1	CQ	229	MET
1	CQ	234	ARG
1	CQ	243	ILE
1	CQ	260	MET
1	CQ	272	TYR
1	CQ	284	ARG
1	CQ	289	ARG
1	CQ	300	GLN
1	CQ	301	ARG
1	CQ	360	LYS
1	CQ	384	ASN
1	CQ	404	LEU
1	CQ	449	GLU
1	CQ	454	ASN
1	CQ	475	LEU
1	CQ	504	VAL
1	CR	12	LYS
1	CR	78	SER
1	CR	79	ARG
1	CR	85	ASP
1	CR	105	SER
1	CR	129	ARG
1	CR	160	THR
1	CR	161	SER
1	CR	163	LEU

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Mol	Chain	Res	Type
1	CR	167	THR
1	CR	182	LEU
1	CR	191	LEU
1	CR	199	SER
1	CR	226	VAL
1	CR	234	ARG
1	CR	243	ILE
1	CR	260	MET
1	CR	272	TYR
1	CR	284	ARG
1	CR	289	ARG
1	CR	299	SER
1	CR	301	ARG
1	CR	384	ASN
1	CR	404	LEU
1	CR	449	GLU
1	CR	475	LEU
1	CR	504	VAL
1	CS	105	SER
1	CS	129	ARG
1	CS	160	THR
1	CS	161	SER
1	CS	163	LEU
1	CS	167	THR
1	CS	182	LEU
1	CS	191	LEU
1	CS	199	SER
1	CS	226	VAL
1	CS	234	ARG
1	CS	243	ILE
1	CS	260	MET
1	CS	272	TYR
1	CS	284	ARG
1	CS	289	ARG
1	CS	301	ARG
1	CS	360	LYS
1	CS	384	ASN
1	CS	404	LEU
1	CS	449	GLU
1	CS	454	ASN
1	CS	475	LEU
1	CS	504	VAL

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Mol	Chain	Res	Type
1	CT	105	SER
1	CT	129	ARG
1	CT	160	THR
1	CT	161	SER
1	CT	163	LEU
1	CT	167	THR
1	CT	182	LEU
1	CT	191	LEU
1	CT	199	SER
1	CT	226	VAL
1	CT	234	ARG
1	CT	243	ILE
1	CT	260	MET
1	CT	272	TYR
1	CT	284	ARG
1	CT	289	ARG
1	CT	299	SER
1	CT	301	ARG
1	CT	384	ASN
1	CT	404	LEU
1	CT	449	GLU
1	CT	454	ASN
1	CT	475	LEU
1	CT	504	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (742) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	36	GLN
1	AA	74	ASN
1	AA	98	HIS
1	AA	131	HIS
1	AA	138	ASN
1	AA	238	HIS
1	AA	288	HIS
1	AA	300	GLN
1	AA	454	ASN
1	AB	24	ASN
1	AB	36	GLN
1	AB	74	ASN
1	AB	98	HIS
1	AB	131	HIS

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Mol	Chain	Res	Type
1	AB	138	ASN
1	AB	238	HIS
1	AB	256	ASN
1	AB	263	ASN
1	AB	288	HIS
1	AB	300	GLN
1	AB	396	HIS
1	AB	454	ASN
1	AC	24	ASN
1	AC	36	GLN
1	AC	74	ASN
1	AC	98	HIS
1	AC	131	HIS
1	AC	238	HIS
1	AC	256	ASN
1	AC	263	ASN
1	AC	288	HIS
1	AC	300	GLN
1	AC	396	HIS
1	AC	437	HIS
1	AC	454	ASN
1	AD	24	ASN
1	AD	36	GLN
1	AD	74	ASN
1	AD	98	HIS
1	AD	131	HIS
1	AD	138	ASN
1	AD	238	HIS
1	AD	256	ASN
1	AD	288	HIS
1	AD	300	GLN
1	AD	437	HIS
1	AD	454	ASN
1	AE	24	ASN
1	AE	36	GLN
1	AE	74	ASN
1	AE	98	HIS
1	AE	131	HIS
1	AE	138	ASN
1	AE	238	HIS
1	AE	256	ASN
1	AE	263	ASN

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Mol	Chain	Res	Type
1	AE	288	HIS
1	AE	300	GLN
1	AE	454	ASN
1	AF	15	GLN
1	AF	24	ASN
1	AF	36	GLN
1	AF	74	ASN
1	AF	98	HIS
1	AF	131	HIS
1	AF	138	ASN
1	AF	238	HIS
1	AF	256	ASN
1	AF	263	ASN
1	AF	288	HIS
1	AF	300	GLN
1	AF	437	HIS
1	AF	454	ASN
1	AG	24	ASN
1	AG	36	GLN
1	AG	74	ASN
1	AG	98	HIS
1	AG	131	HIS
1	AG	138	ASN
1	AG	238	HIS
1	AG	256	ASN
1	AG	288	HIS
1	AG	300	GLN
1	AG	437	HIS
1	AG	454	ASN
1	AH	15	GLN
1	AH	24	ASN
1	AH	36	GLN
1	AH	74	ASN
1	AH	98	HIS
1	AH	131	HIS
1	AH	138	ASN
1	AH	238	HIS
1	AH	256	ASN
1	AH	263	ASN
1	AH	288	HIS
1	AH	300	GLN
1	AH	454	ASN

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Mol	Chain	Res	Type
1	AI	24	ASN
1	AI	36	GLN
1	AI	74	ASN
1	AI	98	HIS
1	AI	131	HIS
1	AI	138	ASN
1	AI	238	HIS
1	AI	256	ASN
1	AI	288	HIS
1	AI	300	GLN
1	AI	437	HIS
1	AI	454	ASN
1	AJ	15	GLN
1	AJ	24	ASN
1	AJ	36	GLN
1	AJ	74	ASN
1	AJ	98	HIS
1	AJ	131	HIS
1	AJ	138	ASN
1	AJ	238	HIS
1	AJ	256	ASN
1	AJ	263	ASN
1	AJ	288	HIS
1	AJ	437	HIS
1	AJ	454	ASN
1	AK	24	ASN
1	AK	36	GLN
1	AK	74	ASN
1	AK	98	HIS
1	AK	131	HIS
1	AK	138	ASN
1	AK	238	HIS
1	AK	256	ASN
1	AK	288	HIS
1	AK	300	GLN
1	AK	437	HIS
1	AK	454	ASN
1	AL	24	ASN
1	AL	36	GLN
1	AL	74	ASN
1	AL	98	HIS
1	AL	131	HIS

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Mol	Chain	Res	Type
1	AL	138	ASN
1	AL	238	HIS
1	AL	256	ASN
1	AL	263	ASN
1	AL	288	HIS
1	AL	396	HIS
1	AL	454	ASN
1	AM	24	ASN
1	AM	36	GLN
1	AM	74	ASN
1	AM	98	HIS
1	AM	131	HIS
1	AM	238	HIS
1	AM	256	ASN
1	AM	263	ASN
1	AM	288	HIS
1	AM	437	HIS
1	AM	454	ASN
1	AN	24	ASN
1	AN	36	GLN
1	AN	74	ASN
1	AN	98	HIS
1	AN	131	HIS
1	AN	138	ASN
1	AN	238	HIS
1	AN	256	ASN
1	AN	263	ASN
1	AN	288	HIS
1	AN	300	GLN
1	AN	437	HIS
1	AN	454	ASN
1	AO	24	ASN
1	AO	36	GLN
1	AO	74	ASN
1	AO	98	HIS
1	AO	131	HIS
1	AO	138	ASN
1	AO	238	HIS
1	AO	256	ASN
1	AO	263	ASN
1	AO	288	HIS
1	AO	300	GLN

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Mol	Chain	Res	Type
1	AO	323	GLN
1	AO	437	HIS
1	AO	454	ASN
1	AP	24	ASN
1	AP	36	GLN
1	AP	74	ASN
1	AP	98	HIS
1	AP	131	HIS
1	AP	138	ASN
1	AP	147	GLN
1	AP	238	HIS
1	AP	256	ASN
1	AP	263	ASN
1	AP	288	HIS
1	AP	300	GLN
1	AP	437	HIS
1	AP	454	ASN
1	AQ	24	ASN
1	AQ	36	GLN
1	AQ	74	ASN
1	AQ	98	HIS
1	AQ	131	HIS
1	AQ	238	HIS
1	AQ	256	ASN
1	AQ	263	ASN
1	AQ	288	HIS
1	AQ	300	GLN
1	AQ	454	ASN
1	AR	24	ASN
1	AR	36	GLN
1	AR	74	ASN
1	AR	98	HIS
1	AR	131	HIS
1	AR	138	ASN
1	AR	147	GLN
1	AR	238	HIS
1	AR	256	ASN
1	AR	288	HIS
1	AR	300	GLN
1	AR	454	ASN
1	AS	15	GLN
1	AS	24	ASN

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Mol	Chain	Res	Type
1	AS	36	GLN
1	AS	74	ASN
1	AS	98	HIS
1	AS	131	HIS
1	AS	138	ASN
1	AS	238	HIS
1	AS	256	ASN
1	AS	263	ASN
1	AS	288	HIS
1	AS	300	GLN
1	AS	437	HIS
1	AS	454	ASN
1	AT	24	ASN
1	AT	36	GLN
1	AT	74	ASN
1	AT	98	HIS
1	AT	131	HIS
1	AT	138	ASN
1	AT	238	HIS
1	AT	256	ASN
1	AT	288	HIS
1	AT	300	GLN
1	AT	454	ASN
1	BA	36	GLN
1	BA	74	ASN
1	BA	98	HIS
1	BA	131	HIS
1	BA	138	ASN
1	BA	238	HIS
1	BA	256	ASN
1	BA	263	ASN
1	BA	288	HIS
1	BA	300	GLN
1	BA	437	HIS
1	BA	454	ASN
1	BB	24	ASN
1	BB	36	GLN
1	BB	74	ASN
1	BB	98	HIS
1	BB	131	HIS
1	BB	138	ASN
1	BB	238	HIS

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Mol	Chain	Res	Type
1	BB	256	ASN
1	BB	263	ASN
1	BB	288	HIS
1	BB	300	GLN
1	BB	454	ASN
1	BC	24	ASN
1	BC	36	GLN
1	BC	74	ASN
1	BC	98	HIS
1	BC	131	HIS
1	BC	138	ASN
1	BC	238	HIS
1	BC	256	ASN
1	BC	288	HIS
1	BC	300	GLN
1	BC	454	ASN
1	BD	24	ASN
1	BD	36	GLN
1	BD	74	ASN
1	BD	98	HIS
1	BD	131	HIS
1	BD	138	ASN
1	BD	238	HIS
1	BD	256	ASN
1	BD	263	ASN
1	BD	288	HIS
1	BD	300	GLN
1	BD	454	ASN
1	BE	24	ASN
1	BE	36	GLN
1	BE	74	ASN
1	BE	98	HIS
1	BE	131	HIS
1	BE	138	ASN
1	BE	147	GLN
1	BE	238	HIS
1	BE	256	ASN
1	BE	263	ASN
1	BE	288	HIS
1	BE	300	GLN
1	BE	437	HIS
1	BE	454	ASN

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Mol	Chain	Res	Type
1	BF	15	GLN
1	BF	24	ASN
1	BF	36	GLN
1	BF	74	ASN
1	BF	98	HIS
1	BF	131	HIS
1	BF	138	ASN
1	BF	147	GLN
1	BF	238	HIS
1	BF	288	HIS
1	BF	300	GLN
1	BF	396	HIS
1	BF	437	HIS
1	BF	454	ASN
1	BG	15	GLN
1	BG	24	ASN
1	BG	36	GLN
1	BG	74	ASN
1	BG	98	HIS
1	BG	131	HIS
1	BG	138	ASN
1	BG	238	HIS
1	BG	256	ASN
1	BG	263	ASN
1	BG	288	HIS
1	BG	300	GLN
1	BG	437	HIS
1	BG	454	ASN
1	BH	15	GLN
1	BH	24	ASN
1	BH	36	GLN
1	BH	74	ASN
1	BH	98	HIS
1	BH	131	HIS
1	BH	138	ASN
1	BH	238	HIS
1	BH	256	ASN
1	BH	263	ASN
1	BH	288	HIS
1	BH	437	HIS
1	BH	454	ASN
1	BI	36	GLN

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Mol	Chain	Res	Type
1	BI	74	ASN
1	BI	98	HIS
1	BI	131	HIS
1	BI	138	ASN
1	BI	238	HIS
1	BI	256	ASN
1	BI	263	ASN
1	BI	288	HIS
1	BI	300	GLN
1	BI	437	HIS
1	BI	454	ASN
1	BJ	24	ASN
1	BJ	36	GLN
1	BJ	74	ASN
1	BJ	98	HIS
1	BJ	131	HIS
1	BJ	138	ASN
1	BJ	238	HIS
1	BJ	256	ASN
1	BJ	263	ASN
1	BJ	288	HIS
1	BJ	300	GLN
1	BJ	454	ASN
1	BK	24	ASN
1	BK	36	GLN
1	BK	74	ASN
1	BK	98	HIS
1	BK	131	HIS
1	BK	138	ASN
1	BK	238	HIS
1	BK	256	ASN
1	BK	263	ASN
1	BK	288	HIS
1	BK	437	HIS
1	BK	454	ASN
1	BL	24	ASN
1	BL	36	GLN
1	BL	74	ASN
1	BL	98	HIS
1	BL	131	HIS
1	BL	138	ASN
1	BL	147	GLN

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Mol	Chain	Res	Type
1	BL	238	HIS
1	BL	263	ASN
1	BL	288	HIS
1	BL	300	GLN
1	BL	437	HIS
1	BL	454	ASN
1	BM	24	ASN
1	BM	36	GLN
1	BM	74	ASN
1	BM	98	HIS
1	BM	131	HIS
1	BM	138	ASN
1	BM	238	HIS
1	BM	256	ASN
1	BM	288	HIS
1	BM	300	GLN
1	BM	454	ASN
1	BN	24	ASN
1	BN	36	GLN
1	BN	74	ASN
1	BN	98	HIS
1	BN	131	HIS
1	BN	138	ASN
1	BN	238	HIS
1	BN	256	ASN
1	BN	263	ASN
1	BN	288	HIS
1	BN	437	HIS
1	BN	454	ASN
1	BO	15	GLN
1	BO	24	ASN
1	BO	36	GLN
1	BO	74	ASN
1	BO	98	HIS
1	BO	131	HIS
1	BO	138	ASN
1	BO	147	GLN
1	BO	238	HIS
1	BO	256	ASN
1	BO	288	HIS
1	BO	300	GLN
1	BO	454	ASN

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Mol	Chain	Res	Type
1	BP	24	ASN
1	BP	36	GLN
1	BP	74	ASN
1	BP	98	HIS
1	BP	131	HIS
1	BP	138	ASN
1	BP	238	HIS
1	BP	256	ASN
1	BP	263	ASN
1	BP	288	HIS
1	BP	300	GLN
1	BP	437	HIS
1	BP	454	ASN
1	BQ	24	ASN
1	BQ	36	GLN
1	BQ	74	ASN
1	BQ	98	HIS
1	BQ	131	HIS
1	BQ	138	ASN
1	BQ	238	HIS
1	BQ	256	ASN
1	BQ	263	ASN
1	BQ	288	HIS
1	BQ	300	GLN
1	BQ	437	HIS
1	BQ	454	ASN
1	BR	24	ASN
1	BR	36	GLN
1	BR	74	ASN
1	BR	98	HIS
1	BR	131	HIS
1	BR	238	HIS
1	BR	256	ASN
1	BR	263	ASN
1	BR	288	HIS
1	BR	300	GLN
1	BR	437	HIS
1	BR	454	ASN
1	BS	15	GLN
1	BS	24	ASN
1	BS	36	GLN
1	BS	74	ASN

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Mol	Chain	Res	Type
1	BS	98	HIS
1	BS	131	HIS
1	BS	138	ASN
1	BS	238	HIS
1	BS	256	ASN
1	BS	288	HIS
1	BS	300	GLN
1	BS	454	ASN
1	BT	24	ASN
1	BT	36	GLN
1	BT	74	ASN
1	BT	98	HIS
1	BT	131	HIS
1	BT	138	ASN
1	BT	238	HIS
1	BT	256	ASN
1	BT	263	ASN
1	BT	288	HIS
1	BT	300	GLN
1	BT	437	HIS
1	BT	454	ASN
1	CA	24	ASN
1	CA	36	GLN
1	CA	74	ASN
1	CA	98	HIS
1	CA	131	HIS
1	CA	138	ASN
1	CA	238	HIS
1	CA	256	ASN
1	CA	263	ASN
1	CA	288	HIS
1	CA	396	HIS
1	CA	454	ASN
1	CB	24	ASN
1	CB	36	GLN
1	CB	74	ASN
1	CB	98	HIS
1	CB	131	HIS
1	CB	138	ASN
1	CB	238	HIS
1	CB	256	ASN
1	CB	263	ASN

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Mol	Chain	Res	Type
1	CB	288	HIS
1	CB	300	GLN
1	CB	454	ASN
1	CC	24	ASN
1	CC	36	GLN
1	CC	74	ASN
1	CC	98	HIS
1	CC	131	HIS
1	CC	238	HIS
1	CC	288	HIS
1	CC	300	GLN
1	CC	437	HIS
1	CC	454	ASN
1	CD	24	ASN
1	CD	36	GLN
1	CD	74	ASN
1	CD	98	HIS
1	CD	131	HIS
1	CD	138	ASN
1	CD	238	HIS
1	CD	256	ASN
1	CD	263	ASN
1	CD	288	HIS
1	CD	454	ASN
1	CE	24	ASN
1	CE	36	GLN
1	CE	74	ASN
1	CE	98	HIS
1	CE	131	HIS
1	CE	138	ASN
1	CE	238	HIS
1	CE	256	ASN
1	CE	263	ASN
1	CE	288	HIS
1	CE	300	GLN
1	CE	437	HIS
1	CE	454	ASN
1	CF	24	ASN
1	CF	36	GLN
1	CF	74	ASN
1	CF	98	HIS
1	CF	131	HIS

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Mol	Chain	Res	Type
1	CF	138	ASN
1	CF	238	HIS
1	CF	256	ASN
1	CF	288	HIS
1	CF	300	GLN
1	CF	437	HIS
1	CF	454	ASN
1	CG	24	ASN
1	CG	36	GLN
1	CG	74	ASN
1	CG	98	HIS
1	CG	131	HIS
1	CG	138	ASN
1	CG	147	GLN
1	CG	238	HIS
1	CG	263	ASN
1	CG	288	HIS
1	CG	300	GLN
1	CG	454	ASN
1	CH	15	GLN
1	CH	24	ASN
1	CH	36	GLN
1	CH	74	ASN
1	CH	98	HIS
1	CH	131	HIS
1	CH	138	ASN
1	CH	238	HIS
1	CH	256	ASN
1	CH	288	HIS
1	CH	437	HIS
1	CH	454	ASN
1	CI	24	ASN
1	CI	36	GLN
1	CI	74	ASN
1	CI	98	HIS
1	CI	131	HIS
1	CI	138	ASN
1	CI	238	HIS
1	CI	256	ASN
1	CI	288	HIS
1	CI	300	GLN
1	CI	437	HIS

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Mol	Chain	Res	Type
1	CI	454	ASN
1	CJ	15	GLN
1	CJ	24	ASN
1	CJ	36	GLN
1	CJ	74	ASN
1	CJ	98	HIS
1	CJ	131	HIS
1	CJ	138	ASN
1	CJ	238	HIS
1	CJ	256	ASN
1	CJ	263	ASN
1	CJ	288	HIS
1	CJ	300	GLN
1	CJ	437	HIS
1	CJ	454	ASN
1	CK	24	ASN
1	CK	36	GLN
1	CK	74	ASN
1	CK	98	HIS
1	CK	131	HIS
1	CK	138	ASN
1	CK	147	GLN
1	CK	238	HIS
1	CK	256	ASN
1	CK	263	ASN
1	CK	288	HIS
1	CK	437	HIS
1	CK	454	ASN
1	CL	24	ASN
1	CL	36	GLN
1	CL	74	ASN
1	CL	98	HIS
1	CL	131	HIS
1	CL	138	ASN
1	CL	238	HIS
1	CL	256	ASN
1	CL	288	HIS
1	CL	396	HIS
1	CL	437	HIS
1	CL	454	ASN
1	CM	24	ASN
1	CM	36	GLN

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Mol	Chain	Res	Type
1	CM	74	ASN
1	CM	98	HIS
1	CM	131	HIS
1	CM	138	ASN
1	CM	238	HIS
1	CM	256	ASN
1	CM	288	HIS
1	CM	454	ASN
1	CN	24	ASN
1	CN	36	GLN
1	CN	74	ASN
1	CN	98	HIS
1	CN	131	HIS
1	CN	138	ASN
1	CN	238	HIS
1	CN	256	ASN
1	CN	288	HIS
1	CN	300	GLN
1	CN	437	HIS
1	CN	454	ASN
1	CO	24	ASN
1	CO	36	GLN
1	CO	74	ASN
1	CO	98	HIS
1	CO	131	HIS
1	CO	138	ASN
1	CO	147	GLN
1	CO	238	HIS
1	CO	256	ASN
1	CO	263	ASN
1	CO	288	HIS
1	CO	300	GLN
1	CO	454	ASN
1	CP	24	ASN
1	CP	36	GLN
1	CP	74	ASN
1	CP	98	HIS
1	CP	131	HIS
1	CP	138	ASN
1	CP	238	HIS
1	CP	256	ASN
1	CP	263	ASN

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Mol	Chain	Res	Type
1	CP	288	HIS
1	CP	300	GLN
1	CP	437	HIS
1	CP	454	ASN
1	CQ	24	ASN
1	CQ	36	GLN
1	CQ	74	ASN
1	CQ	98	HIS
1	CQ	131	HIS
1	CQ	138	ASN
1	CQ	147	GLN
1	CQ	238	HIS
1	CQ	288	HIS
1	CQ	300	GLN
1	CQ	323	GLN
1	CQ	437	HIS
1	CQ	454	ASN
1	CR	24	ASN
1	CR	36	GLN
1	CR	74	ASN
1	CR	98	HIS
1	CR	131	HIS
1	CR	138	ASN
1	CR	238	HIS
1	CR	256	ASN
1	CR	263	ASN
1	CR	288	HIS
1	CR	300	GLN
1	CR	437	HIS
1	CR	454	ASN
1	CS	15	GLN
1	CS	24	ASN
1	CS	36	GLN
1	CS	74	ASN
1	CS	98	HIS
1	CS	131	HIS
1	CS	138	ASN
1	CS	238	HIS
1	CS	256	ASN
1	CS	263	ASN
1	CS	288	HIS
1	CS	437	HIS

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Mol	Chain	Res	Type
1	CS	454	ASN
1	CT	15	GLN
1	CT	24	ASN
1	CT	36	GLN
1	CT	74	ASN
1	CT	98	HIS
1	CT	131	HIS
1	CT	138	ASN
1	CT	238	HIS
1	CT	263	ASN
1	CT	288	HIS
1	CT	300	GLN
1	CT	437	HIS
1	CT	454	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	504/504 (100%)	0.05	4 (0%) 82 60	51, 87, 117, 148	0
1	AB	504/504 (100%)	0.15	7 (1%) 73 48	55, 90, 122, 148	0
1	AC	504/504 (100%)	-0.00	2 (0%) 88 72	42, 76, 104, 147	0
1	AD	504/504 (100%)	-0.11	0 100 100	33, 68, 99, 130	0
1	AE	504/504 (100%)	-0.08	0 100 100	46, 75, 105, 119	0
1	AF	504/504 (100%)	-0.02	1 (0%) 91 80	41, 80, 110, 166	0
1	AG	504/504 (100%)	0.06	2 (0%) 88 72	46, 83, 118, 165	0
1	AH	504/504 (100%)	-0.07	0 100 100	44, 74, 105, 131	0
1	AI	504/504 (100%)	-0.11	2 (0%) 88 72	29, 65, 98, 141	0
1	AJ	504/504 (100%)	-0.11	0 100 100	34, 67, 99, 137	0
1	AK	504/504 (100%)	-0.04	0 100 100	37, 72, 104, 142	0
1	AL	504/504 (100%)	-0.08	2 (0%) 88 72	31, 67, 94, 131	0
1	AM	504/504 (100%)	-0.11	1 (0%) 91 80	32, 65, 96, 117	0
1	AN	504/504 (100%)	-0.16	0 100 100	29, 64, 94, 128	0
1	AO	504/504 (100%)	-0.13	2 (0%) 88 72	34, 66, 93, 124	0
1	AP	504/504 (100%)	-0.09	0 100 100	34, 69, 96, 124	0
1	AQ	504/504 (100%)	-0.16	1 (0%) 91 80	28, 60, 88, 111	0
1	AR	504/504 (100%)	-0.19	1 (0%) 91 80	23, 57, 89, 120	0
1	AS	504/504 (100%)	-0.20	1 (0%) 91 80	30, 60, 92, 124	0
1	AT	504/504 (100%)	-0.13	0 100 100	35, 69, 100, 141	0
1	BA	504/504 (100%)	0.39	9 (1%) 67 42	47, 90, 125, 207	0
1	BB	504/504 (100%)	0.71	21 (4%) 40 25	67, 105, 138, 173	0
1	BC	504/504 (100%)	0.84	24 (4%) 35 23	71, 114, 149, 205	0
1	BD	504/504 (100%)	0.64	13 (2%) 57 35	62, 104, 133, 170	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	BE	504/504 (100%)	0.44	4 (0%) 82 60	48, 89, 122, 158	0
1	BF	504/504 (100%)	0.68	9 (1%) 67 42	63, 99, 131, 191	0
1	BG	504/504 (100%)	0.62	10 (1%) 65 41	59, 93, 125, 154	0
1	BH	504/504 (100%)	0.54	9 (1%) 67 42	48, 95, 130, 160	0
1	BI	504/504 (100%)	0.70	12 (2%) 59 37	65, 108, 143, 170	0
1	BJ	504/504 (100%)	0.76	14 (2%) 55 34	70, 109, 140, 195	0
1	BK	504/504 (100%)	0.30	2 (0%) 88 72	47, 85, 116, 178	0
1	BL	504/504 (100%)	0.10	2 (0%) 88 72	42, 75, 105, 152	0
1	BM	504/504 (100%)	0.42	11 (2%) 62 39	45, 84, 121, 181	0
1	BN	504/504 (100%)	0.55	6 (1%) 76 51	59, 98, 129, 176	0
1	BO	504/504 (100%)	0.49	7 (1%) 73 48	56, 98, 127, 161	0
1	BP	504/504 (100%)	0.94	43 (8%) 16 14	77, 124, 163, 199	0
1	BQ	504/504 (100%)	0.89	24 (4%) 35 23	78, 122, 162, 199	0
1	BR	504/504 (100%)	0.84	24 (4%) 35 23	76, 116, 149, 189	0
1	BS	504/504 (100%)	0.89	20 (3%) 42 27	72, 117, 152, 210	0
1	BT	504/504 (100%)	1.04	40 (7%) 18 15	87, 127, 161, 200	0
1	CA	504/504 (100%)	0.86	20 (3%) 42 27	76, 120, 153, 177	0
1	CB	504/504 (100%)	0.72	20 (3%) 42 27	68, 106, 141, 177	0
1	CC	504/504 (100%)	0.64	13 (2%) 57 35	55, 102, 137, 204	0
1	CD	504/504 (100%)	0.59	19 (3%) 44 28	68, 105, 141, 172	0
1	CE	504/504 (100%)	0.79	20 (3%) 42 27	72, 119, 149, 191	0
1	CF	504/504 (100%)	0.27	3 (0%) 85 66	41, 85, 115, 151	0
1	CG	504/504 (100%)	0.49	10 (1%) 65 41	57, 88, 121, 163	0
1	CH	504/504 (100%)	0.44	6 (1%) 76 51	58, 90, 124, 179	0
1	CI	504/504 (100%)	0.32	11 (2%) 62 39	44, 84, 121, 188	0
1	CJ	504/504 (100%)	0.12	0 100 100	44, 77, 110, 151	0
1	CK	504/504 (100%)	0.58	9 (1%) 67 42	61, 103, 133, 150	0
1	CL	504/504 (100%)	0.65	8 (1%) 70 45	68, 114, 148, 184	0
1	CM	504/504 (100%)	0.61	14 (2%) 55 34	64, 111, 141, 186	0
1	CN	504/504 (100%)	0.41	5 (0%) 79 55	62, 97, 127, 171	0
1	CO	504/504 (100%)	0.35	7 (1%) 73 48	59, 91, 126, 157	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	CP	504/504 (100%)	0.05	2 (0%)	88	72	41, 73, 105, 133	0
1	CQ	504/504 (100%)	0.17	4 (0%)	82	60	46, 76, 112, 171	0
1	CR	504/504 (100%)	0.23	4 (0%)	82	60	45, 84, 114, 172	0
1	CS	504/504 (100%)	0.24	3 (0%)	85	66	45, 86, 119, 153	0
1	CT	504/504 (100%)	0.26	2 (0%)	88	72	52, 82, 111, 136	0
All	All	30240/30240 (100%)	0.33	510 (1%)	69	43	23, 89, 135, 210	0

All (510) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BD	116	HIS	4.6
1	BG	383	GLU	4.1
1	BF	426	GLY	4.0
1	BI	143	ALA	3.9
1	BP	155	GLU	3.8
1	BQ	126	GLU	3.8
1	BD	72	ALA	3.8
1	BO	345	ASP	3.8
1	CI	116	HIS	3.7
1	BT	68	MET	3.7
1	CA	401	ASP	3.7
1	BQ	72	ALA	3.6
1	CN	417	GLY	3.6
1	CM	274	GLU	3.6
1	BP	123	THR	3.6
1	BS	274	GLU	3.5
1	CD	1	GLY	3.4
1	BD	6	GLY	3.4
1	BR	383	GLU	3.4
1	BH	345	ASP	3.3
1	CA	460	PRO	3.3
1	CO	72	ALA	3.3
1	BH	126	GLU	3.3
1	CB	383	GLU	3.3
1	CG	433	ASP	3.2
1	BM	417	GLY	3.2
1	BT	420	THR	3.2
1	BG	17	ASN	3.2
1	BR	191	LEU	3.2
1	CD	383	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
1	AI	126	GLU	3.2
1	BP	280	GLU	3.2
1	BF	313	GLY	3.1
1	CK	22	THR	3.1
1	CE	282	LYS	3.1
1	BM	124	THR	3.1
1	CG	160	THR	3.1
1	BP	504	VAL	3.1
1	CG	165	LYS	3.1
1	BJ	124	THR	3.1
1	BM	126	GLU	3.1
1	AL	1	GLY	3.1
1	BB	199	SER	3.0
1	CI	126	GLU	3.0
1	BM	115	GLY	3.0
1	AB	72	ALA	3.0
1	BC	72	ALA	3.0
1	CK	417	GLY	3.0
1	BP	124	THR	3.0
1	AO	157	GLU	3.0
1	CA	158	GLU	3.0
1	BQ	160	THR	3.0
1	BQ	107	GLU	3.0
1	BQ	186	PRO	3.0
1	BT	6	GLY	3.0
1	BF	116	HIS	2.9
1	CM	116	HIS	2.9
1	BP	9	TYR	2.9
1	BH	288	HIS	2.9
1	CA	461	ASN	2.9
1	BJ	205	GLY	2.9
1	BT	5	ARG	2.9
1	BC	345	ASP	2.9
1	BB	6	GLY	2.9
1	BJ	196	ALA	2.9
1	CA	196	ALA	2.9
1	CE	225	CYS	2.9
1	BP	492	PRO	2.8
1	BI	122	SER	2.8
1	BP	157	GLU	2.8
1	CD	433	ASP	2.8
1	BT	269	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	AB	155	GLU	2.8
1	BB	107	GLU	2.8
1	CK	280	GLU	2.8
1	CB	410	THR	2.8
1	AB	383	GLU	2.8
1	BF	383	GLU	2.8
1	BT	72	ALA	2.8
1	CM	121	LYS	2.8
1	CB	269	PRO	2.8
1	BG	270	GLY	2.8
1	BJ	206	GLN	2.8
1	CH	22	THR	2.8
1	CL	196	ALA	2.8
1	CA	317	PRO	2.8
1	AA	417	GLY	2.8
1	BC	123	THR	2.8
1	BD	160	THR	2.8
1	AC	383	GLU	2.7
1	BC	431	GLY	2.7
1	CE	280	GLU	2.7
1	CG	157	GLU	2.7
1	AI	375	ASN	2.7
1	CE	123	THR	2.7
1	CG	127	SER	2.7
1	BR	185	PRO	2.7
1	BT	467	TYR	2.7
1	CC	433	ASP	2.7
1	BA	426	GLY	2.7
1	CC	144	ALA	2.7
1	BN	127	SER	2.7
1	BP	436	SER	2.7
1	BC	164	GLY	2.7
1	CB	6	GLY	2.7
1	BP	184	CYS	2.7
1	CF	123	THR	2.7
1	BT	383	GLU	2.7
1	CA	449	GLU	2.7
1	CD	126	GLU	2.7
1	BO	417	GLY	2.6
1	CE	117	ALA	2.6
1	BQ	124	THR	2.6
1	BQ	414	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	BC	24	ASN	2.6
1	BJ	17	ASN	2.6
1	BO	498	GLY	2.6
1	CB	417	GLY	2.6
1	BC	126	GLU	2.6
1	CP	383	GLU	2.6
1	CT	313	GLY	2.6
1	BT	66	TRP	2.6
1	CM	158	GLU	2.6
1	BT	461	ASN	2.6
1	BR	357	THR	2.6
1	BS	410	THR	2.6
1	BT	345	ASP	2.6
1	CO	383	GLU	2.6
1	BT	124	THR	2.6
1	AQ	383	GLU	2.6
1	BH	190	ASP	2.6
1	CI	463	ARG	2.6
1	BJ	442	GLN	2.6
1	CL	310	ALA	2.6
1	BT	372	PHE	2.6
1	BT	396	HIS	2.5
1	BB	22	THR	2.5
1	BP	133	THR	2.5
1	BB	435	PRO	2.5
1	BI	426	GLY	2.5
1	BK	6	GLY	2.5
1	BJ	220	SER	2.5
1	BS	127	SER	2.5
1	BF	445	GLU	2.5
1	BP	215	VAL	2.5
1	BP	364	GLU	2.5
1	CC	157	GLU	2.5
1	CM	7	VAL	2.5
1	BB	433	ASP	2.5
1	BF	454	ASN	2.5
1	BG	417	GLY	2.5
1	CC	4	GLY	2.5
1	BK	123	THR	2.5
1	BT	123	THR	2.5
1	BS	234	ARG	2.5
1	CB	127	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	CM	275	GLU	2.5
1	CA	72	ALA	2.5
1	CC	405	GLN	2.5
1	CH	123	THR	2.5
1	BJ	116	HIS	2.5
1	CA	127	SER	2.5
1	BN	504	VAL	2.5
1	AA	157	GLU	2.5
1	BN	126	GLU	2.5
1	CE	383	GLU	2.5
1	CK	332	GLU	2.5
1	BE	296	ALA	2.5
1	BI	84	ALA	2.5
1	BT	196	ALA	2.5
1	CB	196	ALA	2.5
1	BA	269	PRO	2.5
1	BQ	269	PRO	2.5
1	BR	186	PRO	2.5
1	CN	433	ASP	2.5
1	BB	5	ARG	2.5
1	BR	258	THR	2.5
1	BP	287	TYR	2.5
1	BC	107	GLU	2.5
1	BM	411	GLU	2.5
1	BQ	39	LYS	2.5
1	BR	443	LYS	2.5
1	BB	13	ASP	2.5
1	CD	504	VAL	2.5
1	BQ	116	HIS	2.4
1	CL	502	PHE	2.4
1	BP	171	ASP	2.4
1	BP	345	ASP	2.4
1	CL	345	ASP	2.4
1	BE	437	HIS	2.4
1	BG	126	GLU	2.4
1	CF	107	GLU	2.4
1	CF	126	GLU	2.4
1	CO	362	GLU	2.4
1	BP	269	PRO	2.4
1	BT	498	GLY	2.4
1	BQ	433	ASP	2.4
1	BS	360	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	CC	482	LYS	2.4
1	CL	184	CYS	2.4
1	BA	383	GLU	2.4
1	BS	408	LEU	2.4
1	CA	98	HIS	2.4
1	CC	383	GLU	2.4
1	BI	144	ALA	2.4
1	CE	500	THR	2.4
1	AR	383	GLU	2.4
1	BC	383	GLU	2.4
1	CL	126	GLU	2.4
1	CL	5	ARG	2.4
1	BL	173	GLY	2.4
1	BM	426	GLY	2.4
1	BR	410	THR	2.4
1	BT	133	THR	2.4
1	CM	276	ASP	2.4
1	BB	280	GLU	2.4
1	BP	449	GLU	2.4
1	BM	116	HIS	2.4
1	BR	472	ALA	2.4
1	CE	14	CYS	2.4
1	BC	165	LYS	2.4
1	BT	105	SER	2.4
1	CE	465	SER	2.4
1	CI	465	SER	2.4
1	CR	465	SER	2.4
1	CA	491	ARG	2.4
1	CC	499	ARG	2.4
1	CD	401	ASP	2.4
1	AS	383	GLU	2.4
1	BB	112	GLU	2.4
1	BE	383	GLU	2.4
1	BN	157	GLU	2.4
1	CI	38	GLU	2.4
1	CO	165	LYS	2.4
1	CG	437	HIS	2.3
1	BA	173	GLY	2.3
1	BB	426	GLY	2.3
1	BJ	314	PRO	2.3
1	BP	70	PHE	2.3
1	BP	173	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	BT	417	GLY	2.3
1	CC	297	GLY	2.3
1	BA	7	VAL	2.3
1	BI	124	THR	2.3
1	BT	483	VAL	2.3
1	CQ	383	GLU	2.3
1	CA	116	HIS	2.3
1	BC	127	SER	2.3
1	BJ	465	SER	2.3
1	BT	270	GLY	2.3
1	CB	186	PRO	2.3
1	CE	313	GLY	2.3
1	BT	410	THR	2.3
1	CO	167	THR	2.3
1	CB	282	LYS	2.3
1	BP	196	ALA	2.3
1	BN	345	ASP	2.3
1	BD	191	LEU	2.3
1	BQ	6	GLY	2.3
1	BD	124	THR	2.3
1	BQ	225	CYS	2.3
1	AG	383	GLU	2.3
1	BG	173	GLY	2.3
1	BS	186	PRO	2.3
1	CP	313	GLY	2.3
1	BS	133	THR	2.3
1	CH	121	LYS	2.3
1	BQ	312	ALA	2.3
1	BR	369	PHE	2.3
1	CA	61	PHE	2.3
1	BH	383	GLU	2.3
1	CD	274	GLU	2.3
1	CL	112	GLU	2.3
1	BC	21	GLY	2.3
1	BC	173	GLY	2.3
1	CB	185	PRO	2.3
1	CC	269	PRO	2.3
1	BC	500	THR	2.3
1	BD	384	ASN	2.3
1	BR	437	HIS	2.3
1	BQ	406	TRP	2.3
1	BB	440	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	AA	300	GLN	2.3
1	BH	407	SER	2.3
1	BF	230	GLY	2.3
1	BR	313	GLY	2.3
1	BT	7	VAL	2.3
1	AB	190	ASP	2.3
1	BB	195	THR	2.2
1	BD	133	THR	2.2
1	BI	138	ASN	2.2
1	BP	117	ALA	2.2
1	BR	309	TYR	2.2
1	BQ	127	SER	2.2
1	AC	126	GLU	2.2
1	BG	483	VAL	2.2
1	BJ	208	PRO	2.2
1	BP	228	GLY	2.2
1	BT	111	GLY	2.2
1	CD	499	ARG	2.2
1	BP	408	LEU	2.2
1	CD	345	ASP	2.2
1	BC	244	PHE	2.2
1	BF	72	ALA	2.2
1	CG	322	ALA	2.2
1	BP	467	TYR	2.2
1	BS	37	TYR	2.2
1	BJ	126	GLU	2.2
1	BP	169	VAL	2.2
1	CE	364	GLU	2.2
1	CM	172	PRO	2.2
1	CM	225	CYS	2.2
1	BQ	410	THR	2.2
1	BD	375	ASN	2.2
1	AB	116	HIS	2.2
1	BA	116	HIS	2.2
1	CN	116	HIS	2.2
1	BH	72	ALA	2.2
1	BS	278	SER	2.2
1	CD	287	TYR	2.2
1	CD	465	SER	2.2
1	AA	504	VAL	2.2
1	BO	383	GLU	2.2
1	BQ	426	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	CE	344	GLU	2.2
1	CI	383	GLU	2.2
1	BQ	315	ILE	2.2
1	CI	125	PHE	2.2
1	CE	190	ASP	2.2
1	CC	116	HIS	2.2
1	CN	437	HIS	2.2
1	CQ	116	HIS	2.2
1	CA	456	ALA	2.2
1	CE	429	ALA	2.2
1	CS	429	ALA	2.2
1	BM	149	VAL	2.2
1	BS	394	GLY	2.2
1	CD	115	GLY	2.2
1	BF	124	THR	2.2
1	BT	195	THR	2.2
1	CI	165	LYS	2.2
1	BD	14	CYS	2.2
1	BM	14	CYS	2.2
1	BC	241	ALA	2.2
1	BP	154	ALA	2.2
1	BR	116	HIS	2.2
1	BS	196	ALA	2.2
1	CB	310	ALA	2.2
1	CD	276	ASP	2.2
1	CD	396	HIS	2.2
1	CE	499	ARG	2.2
1	BL	413	GLY	2.2
1	BT	125	PHE	2.2
1	BT	280	GLU	2.2
1	CQ	126	GLU	2.2
1	BC	410	THR	2.2
1	BD	310	ALA	2.1
1	BB	225	CYS	2.1
1	BP	116	HIS	2.1
1	CH	14	CYS	2.1
1	CM	499	ARG	2.1
1	BT	421	ILE	2.1
1	BP	125	PHE	2.1
1	BI	383	GLU	2.1
1	CO	282	LYS	2.1
1	BB	123	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	CA	410	THR	2.1
1	CB	160	THR	2.1
1	BP	389	MET	2.1
1	BR	408	LEU	2.1
1	BO	196	ALA	2.1
1	BP	139	ASN	2.1
1	BJ	436	SER	2.1
1	BT	94	HIS	2.1
1	BI	66	TRP	2.1
1	CD	403	LYS	2.1
1	BC	11	PRO	2.1
1	CM	173	GLY	2.1
1	BD	60	ALA	2.1
1	BI	499	ARG	2.1
1	BQ	17	ASN	2.1
1	BR	436	SER	2.1
1	BP	41	ILE	2.1
1	BS	116	HIS	2.1
1	CA	194	VAL	2.1
1	CM	165	LYS	2.1
1	BP	262	TRP	2.1
1	BQ	66	TRP	2.1
1	CH	245	TYR	2.1
1	BB	413	GLY	2.1
1	BC	4	GLY	2.1
1	BH	417	GLY	2.1
1	BT	4	GLY	2.1
1	CC	417	GLY	2.1
1	BR	358	LEU	2.1
1	BR	43	ALA	2.1
1	BB	243	ILE	2.1
1	BT	304	SER	2.1
1	CK	465	SER	2.1
1	BR	452	VAL	2.1
1	BA	437	HIS	2.1
1	BI	437	HIS	2.1
1	CE	116	HIS	2.1
1	CB	21	GLY	2.1
1	CD	467	TYR	2.1
1	CH	9	TYR	2.1
1	CO	173	GLY	2.1
1	CR	173	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	BP	48	PRO	2.1
1	BT	314	PRO	2.1
1	CB	47	MET	2.1
1	CB	172	PRO	2.1
1	BQ	383	GLU	2.1
1	BS	158	GLU	2.1
1	CB	112	GLU	2.1
1	CI	107	GLU	2.1
1	CR	344	GLU	2.1
1	BA	41	ILE	2.1
1	BB	360	LYS	2.1
1	BM	121	LYS	2.1
1	BS	214	LYS	2.1
1	CG	143	ALA	2.1
1	BS	415	SER	2.1
1	CQ	165	LYS	2.1
1	CS	69	SER	2.1
1	BB	176	ASN	2.1
1	CD	461	ASN	2.1
1	BR	194	VAL	2.1
1	BC	295	LEU	2.1
1	BP	85	ASP	2.1
1	BP	111	GLY	2.1
1	BQ	1	GLY	2.1
1	BS	382	GLY	2.1
1	CI	1	GLY	2.1
1	BN	124	THR	2.1
1	BP	377	CYS	2.1
1	BR	214	LYS	2.1
1	CA	474	LYS	2.1
1	CI	360	LYS	2.1
1	CB	391	ALA	2.1
1	BC	32	PHE	2.1
1	BP	147	GLN	2.1
1	BT	197	LEU	2.1
1	AL	313	GLY	2.0
1	AM	297	GLY	2.0
1	BE	116	HIS	2.0
1	BG	457	GLY	2.0
1	BT	73	TYR	2.0
1	BS	93	PRO	2.0
1	AB	126	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	CM	123	THR	2.0
1	AF	165	LYS	2.0
1	BO	158	GLU	2.0
1	BT	144	ALA	2.0
1	BP	386	PHE	2.0
1	BS	279	PHE	2.0
1	CE	464	PHE	2.0
1	BR	114	CYS	2.0
1	BT	14	CYS	2.0
1	BT	452	VAL	2.0
1	CB	206	GLN	2.0
1	AB	111	GLY	2.0
1	BP	257	GLY	2.0
1	BB	116	HIS	2.0
1	BC	245	TYR	2.0
1	BP	216	TYR	2.0
1	CG	269	PRO	2.0
1	CK	51	LYS	2.0
1	BD	123	THR	2.0
1	CR	167	THR	2.0
1	AO	383	GLU	2.0
1	BQ	359	ASP	2.0
1	CA	344	GLU	2.0
1	CD	275	GLU	2.0
1	BR	197	LEU	2.0
1	BT	407	SER	2.0
1	CA	244	PHE	2.0
1	CA	440	ALA	2.0
1	CB	436	SER	2.0
1	CD	127	SER	2.0
1	BR	226	VAL	2.0
1	BT	240	CYS	2.0
1	CS	106	CYS	2.0
1	BA	282	LYS	2.0
1	BC	51	LYS	2.0
1	CC	282	LYS	2.0
1	CG	417	GLY	2.0
1	CM	382	GLY	2.0
1	CB	187	ILE	2.0
1	AG	437	HIS	2.0
1	BB	437	HIS	2.0
1	BG	449	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	BS	250	TRP	2.0
1	CE	95	TRP	2.0
1	BH	424	LEU	2.0
1	BJ	449	GLU	2.0
1	BM	383	GLU	2.0
1	BP	383	GLU	2.0
1	BP	412	PHE	2.0
1	CE	107	GLU	2.0
1	CE	125	PHE	2.0
1	CK	383	GLU	2.0
1	CN	126	GLU	2.0
1	BG	415	SER	2.0
1	CK	345	ASP	2.0
1	CK	371	ASP	2.0
1	BC	504	VAL	2.0
1	BI	53	VAL	2.0
1	BO	504	VAL	2.0
1	CT	194	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.