



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 09:46 AM UTC

PDB ID : 6YFD / pdb_00006yfd
Title : Virus-like particle of Beihai levi-like virus 14
Authors : Rumnieks, J.; Kalnins, G.; Sisovs, M.; Lieknina, I.; Tars, K.
Deposited on : 2020-03-26
Resolution : 3.30 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

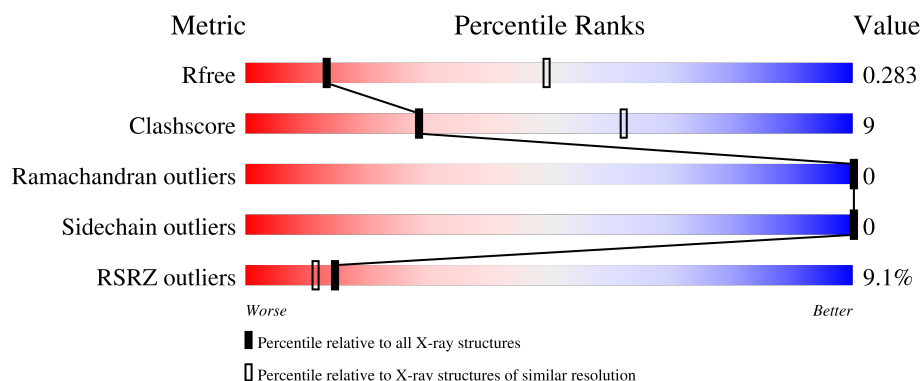
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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.



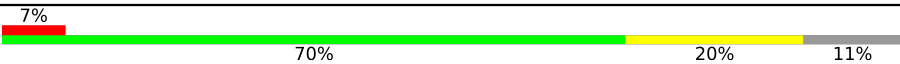
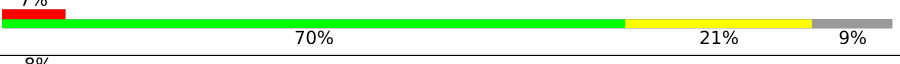
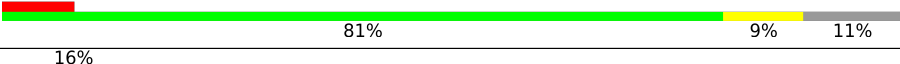
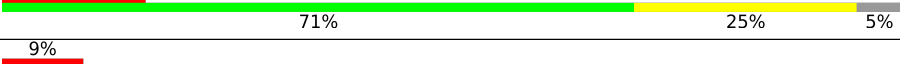
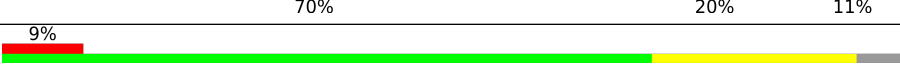
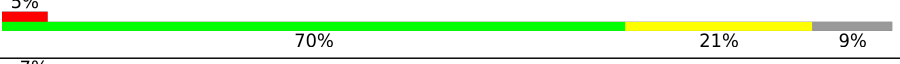
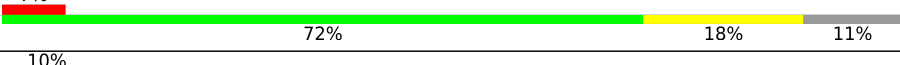
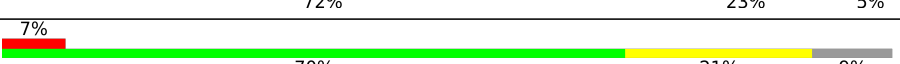
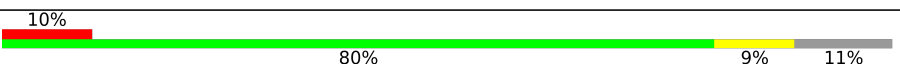
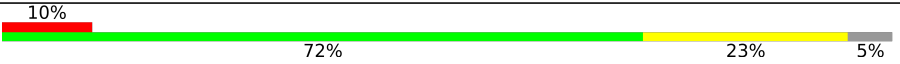
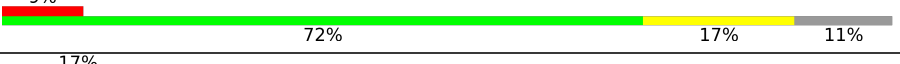
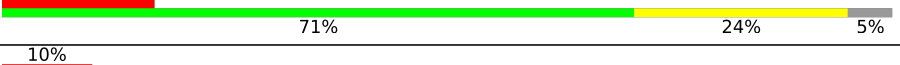
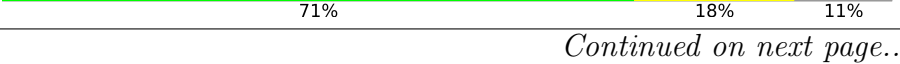
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	208	13% 70% 25% 5%
1	AB	208	12% 69% 22% 9%
1	AC	208	10% 73% 17% 11%
1	AD	208	9% 69% 26% 5%
1	AE	208	9% 66% 25% 9%

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Mol	Chain	Length	Quality of chain
1	AF	208	
1	AG	208	
1	AH	208	
1	AI	208	
1	AJ	208	
1	AK	208	
1	AL	208	
1	AM	208	
1	AN	208	
1	AO	208	
1	AP	208	
1	AQ	208	
1	AR	208	
1	AS	208	
1	AT	208	
1	AU	208	
1	AV	208	
1	AW	208	
1	AX	208	
1	AY	208	
1	AZ	208	
1	BA	208	
1	BB	208	
1	BC	208	
1	BD	208	

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Mol	Chain	Length	Quality of chain
1	BE	208	
1	BF	208	
1	BG	208	
1	BH	208	
1	BI	208	
1	BJ	208	
1	BK	208	
1	BL	208	
1	BM	208	
1	BN	208	
1	BO	208	
1	BP	208	
1	BQ	208	
1	BR	208	
1	BS	208	
1	BT	208	
1	BU	208	
1	BV	208	
1	BW	208	
1	BX	208	
1	BY	208	
1	BZ	208	
1	CA	208	
1	CB	208	
1	CC	208	

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Mol	Chain	Length	Quality of chain
1	CD	208	
1	CE	208	
1	CF	208	
1	CG	208	
1	CH	208	
1	CI	208	
1	CJ	208	
1	CK	208	
1	CL	208	
1	CM	208	
1	CN	208	
1	CO	208	
1	CP	208	
1	CQ	208	
1	CR	208	
1	CS	208	
1	CT	208	
1	CU	208	
1	CV	208	
1	CW	208	
1	CX	208	
1	CY	208	
1	CZ	208	
1	DA	208	
1	DB	208	

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Mol	Chain	Length	Quality of chain
1	DC	208	
1	DD	208	
1	DE	208	
1	DF	208	
1	DG	208	
1	DH	208	
1	DI	208	
1	DJ	208	
1	DK	208	
1	DL	208	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 126960 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	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	AB	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	AC	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	AD	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	AE	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	AF	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	AG	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	AH	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	AI	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	AJ	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	AK	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	AL	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	AM	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	AN	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	AO	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	AP	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AQ	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	AR	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	AS	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	AT	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	AU	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	AV	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	AW	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	AX	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	AY	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	AZ	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	BA	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	BB	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	BC	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	BD	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	BE	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	BF	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	BG	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	BH	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	BI	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	BJ	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	BK	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BL	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	BM	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	BN	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	BO	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	BP	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	BQ	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	BR	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	BS	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	BT	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	BU	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	BV	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	BW	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	BX	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	BY	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	BZ	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	CA	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	CB	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	CC	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	CD	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	CE	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	CF	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	CG	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	CH	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	CI	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	CJ	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	CK	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	CL	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	CM	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	CN	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	CO	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	CP	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	CQ	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	CR	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	CS	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	CT	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	CU	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	CV	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	CW	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	CX	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	CY	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	CZ	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	DA	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			

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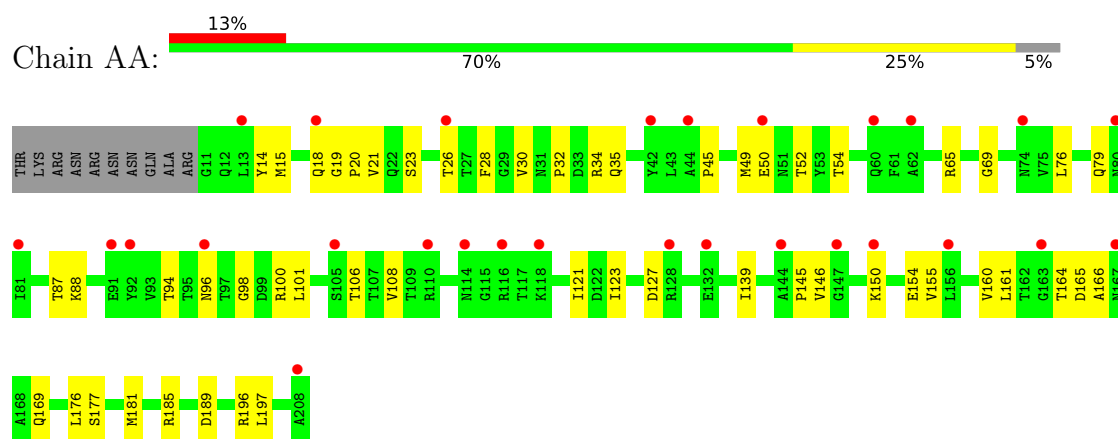
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	DB	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	DC	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	DD	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	DE	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	DF	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	DG	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	DH	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	DI	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	DJ	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	DK	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	DL	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			

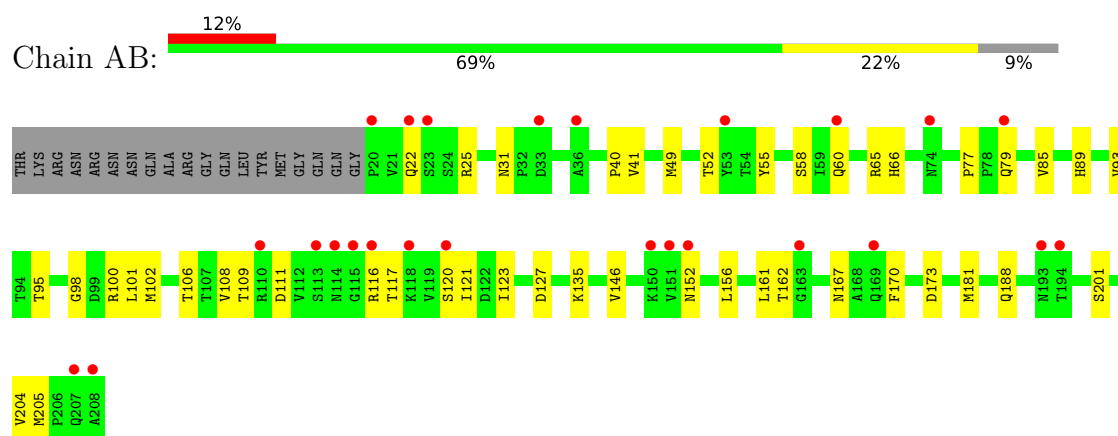
3 Residue-property plots [i](#)

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

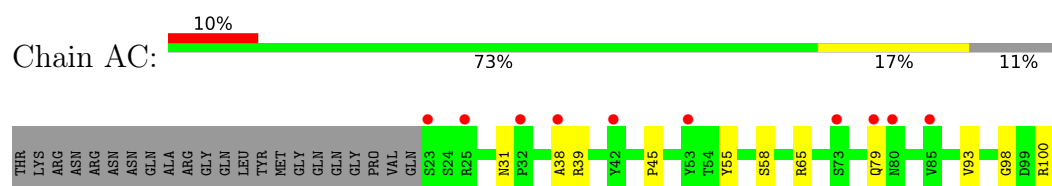
- Molecule 1: coat protein

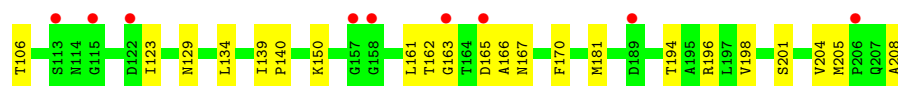


- Molecule 1: coat protein

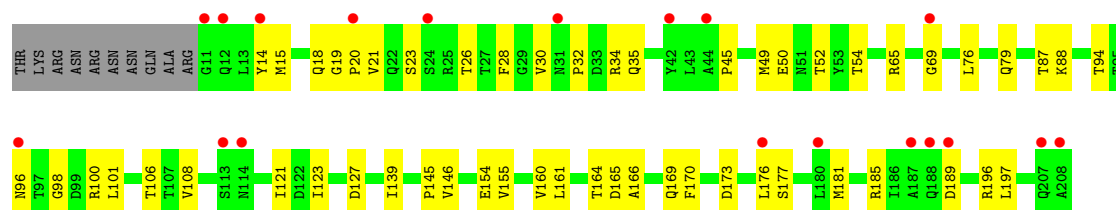
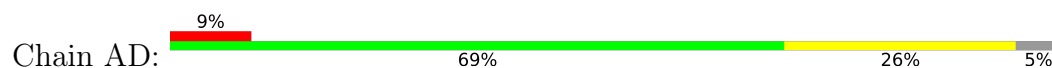


- Molecule 1: coat protein

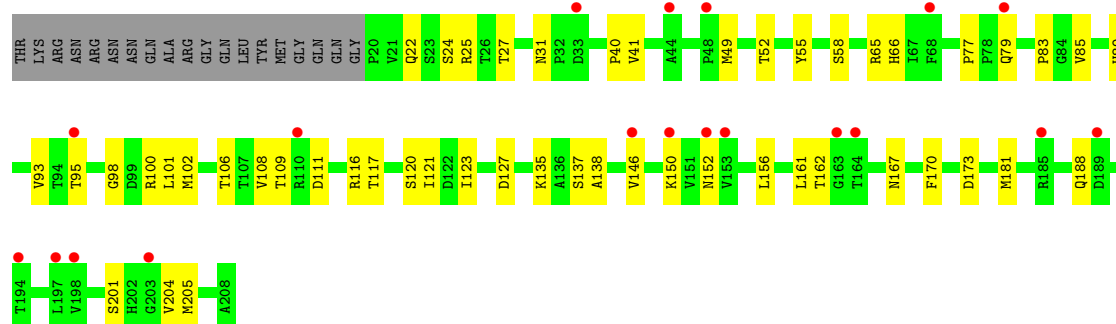




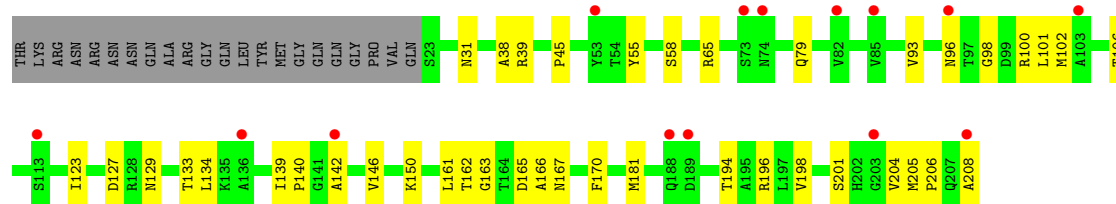
- Molecule 1: coat protein



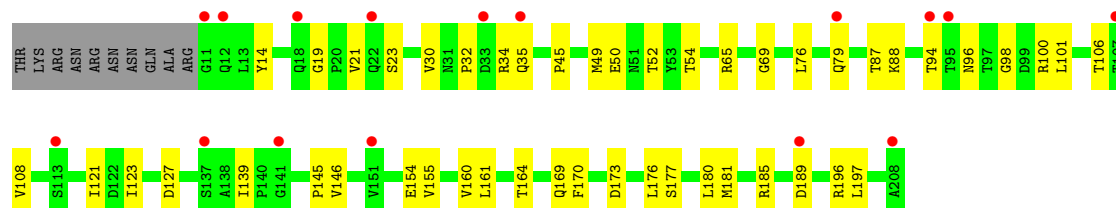
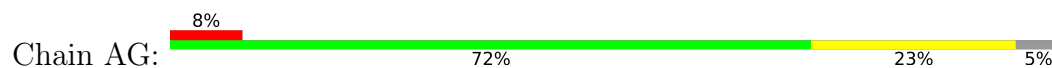
- Molecule 1: coat protein



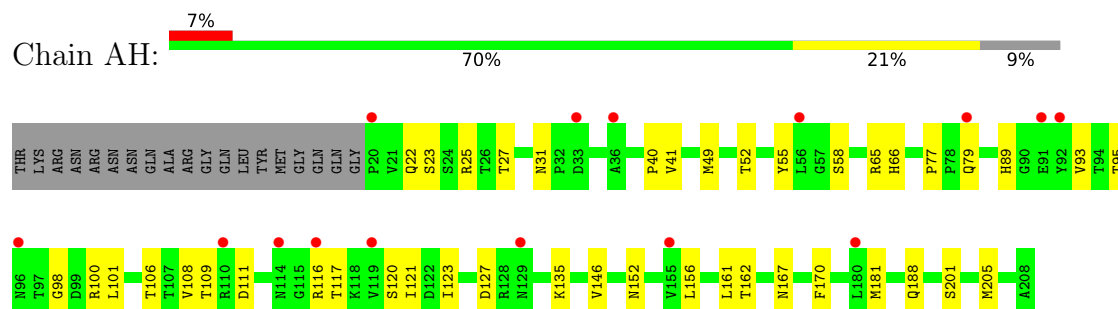
- Molecule 1: coat protein



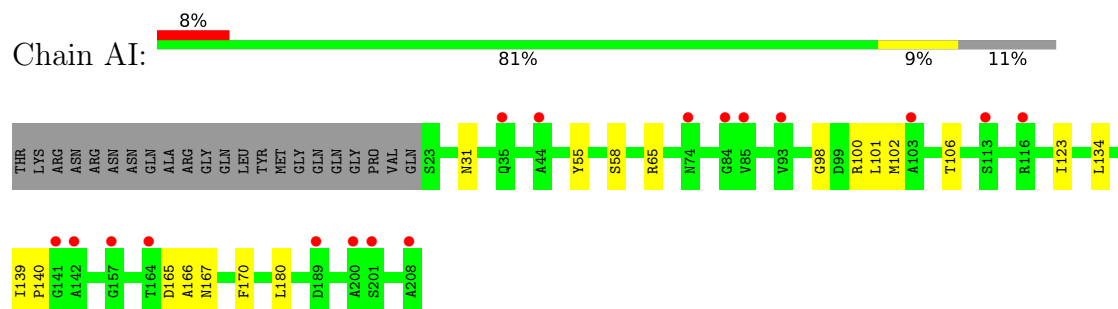
- Molecule 1: coat protein



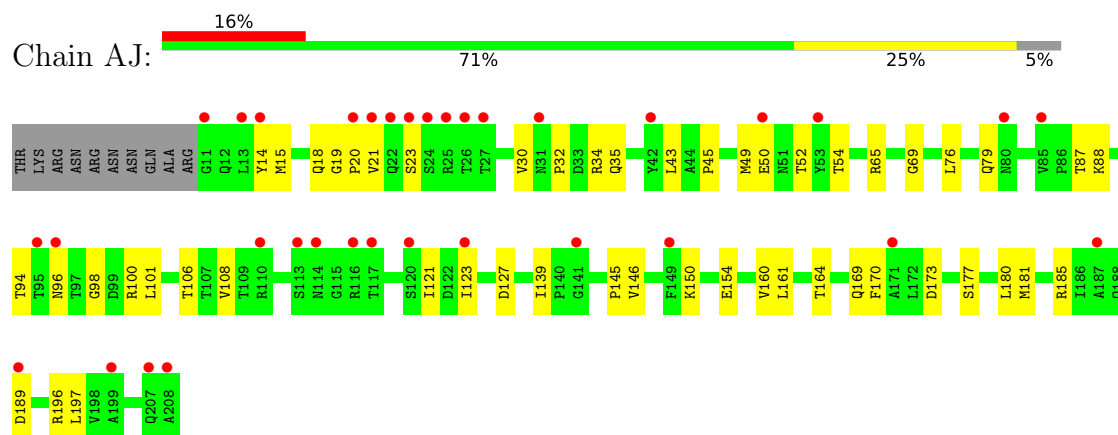
- Molecule 1: coat protein



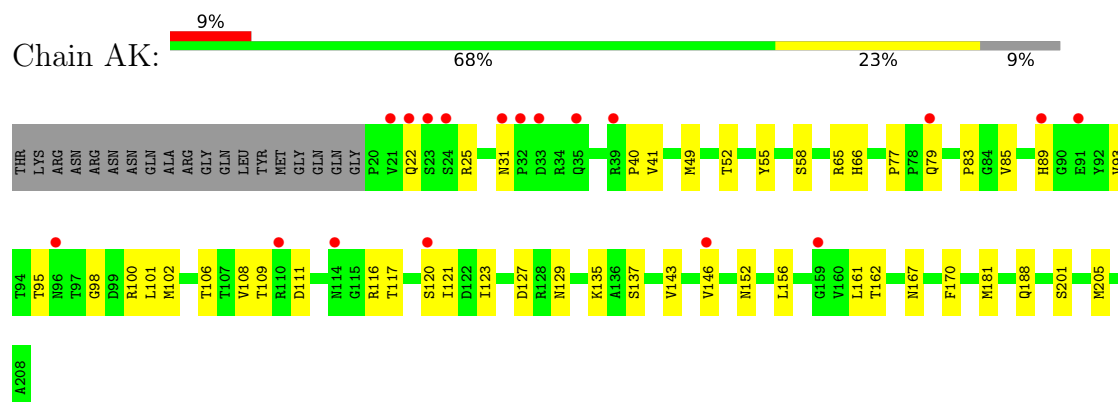
- Molecule 1: coat protein



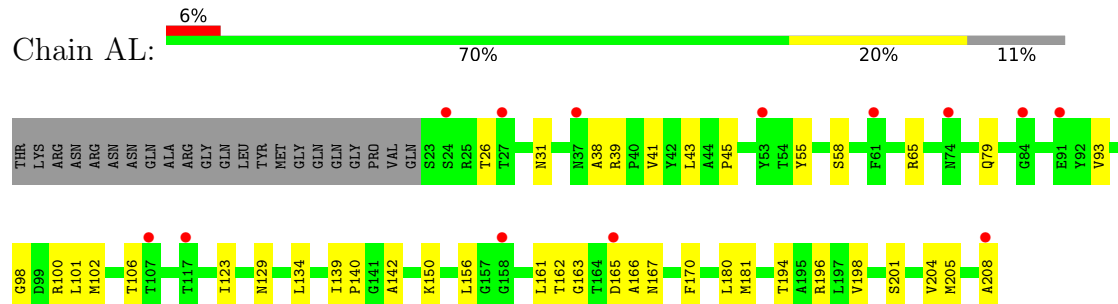
- Molecule 1: coat protein



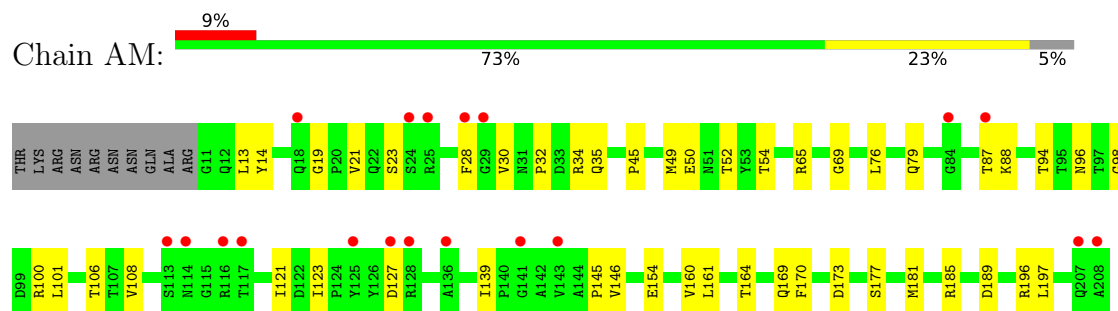
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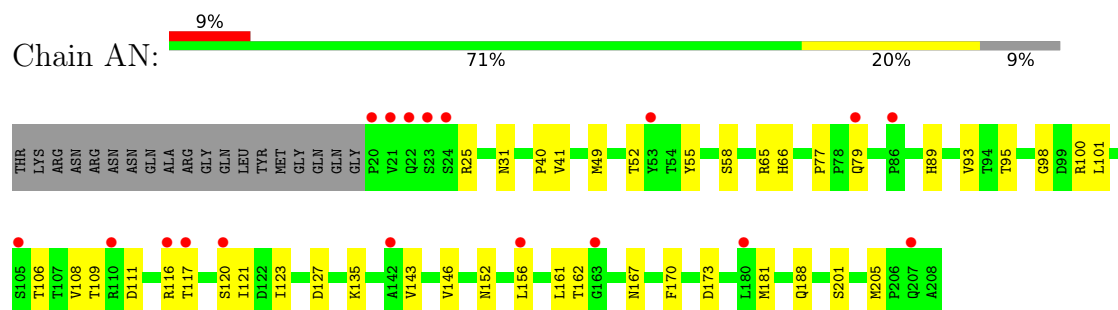
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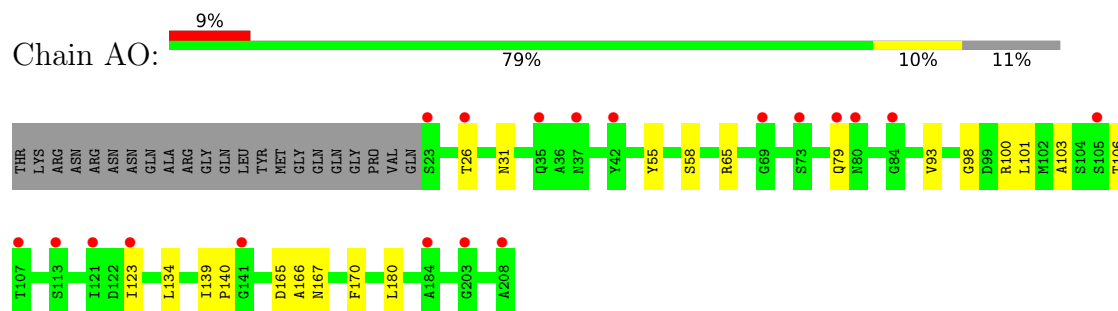
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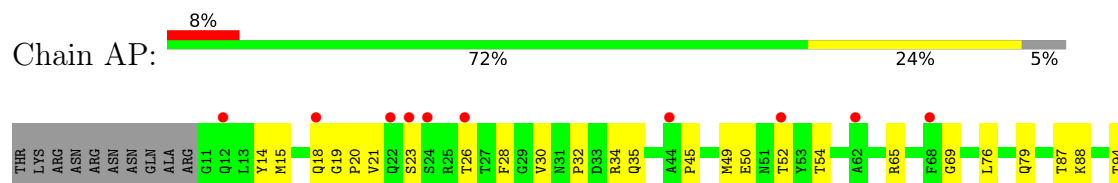
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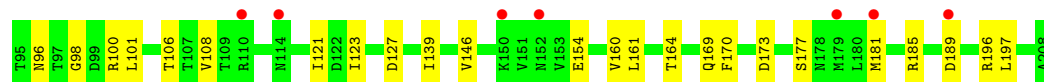


- Molecule 1: coat protein

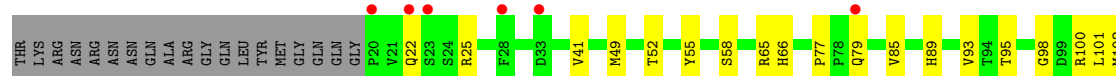
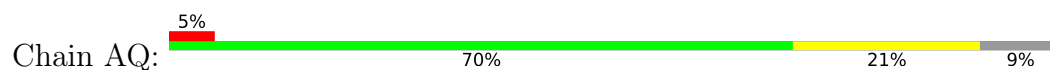


- Molecule 1: coat protein

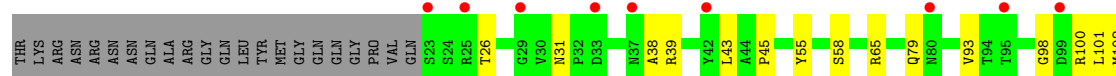
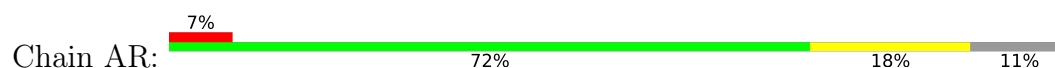




- Molecule 1: coat protein



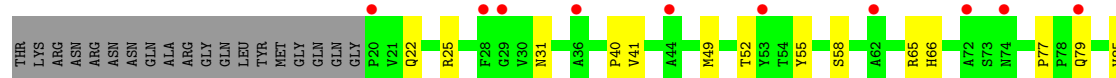
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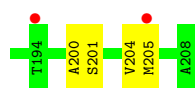


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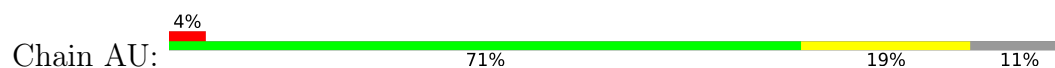


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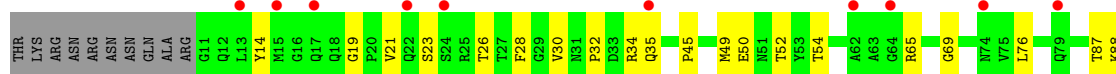
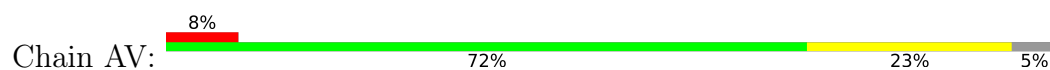




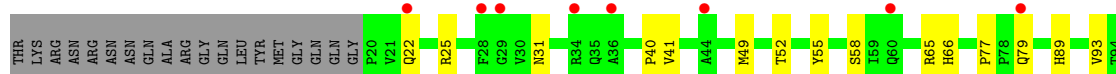
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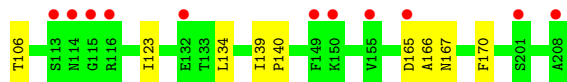
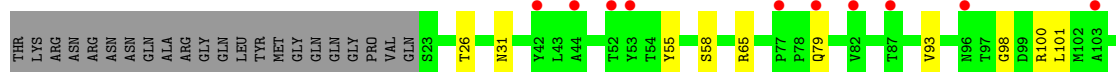
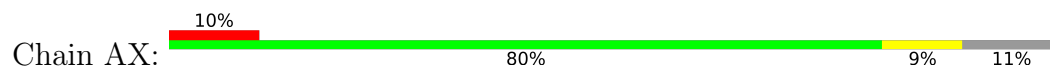
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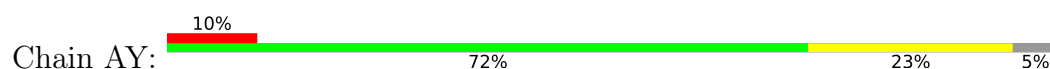
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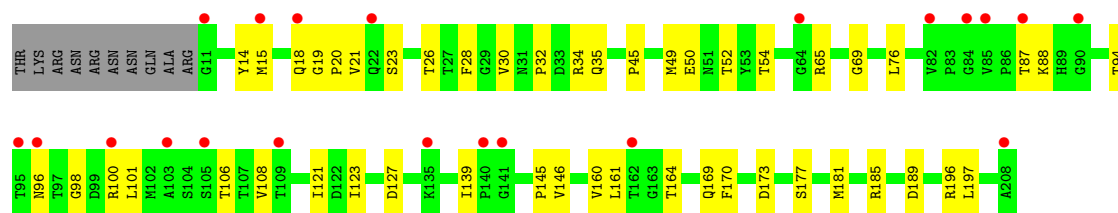


- Molecule 1: coat protein

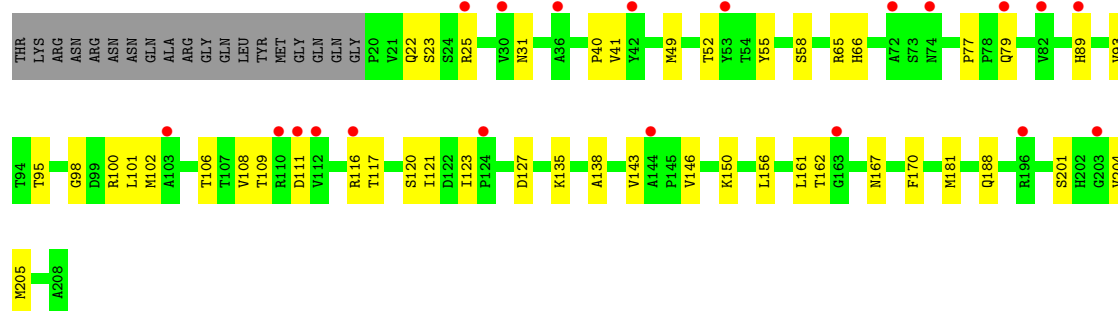


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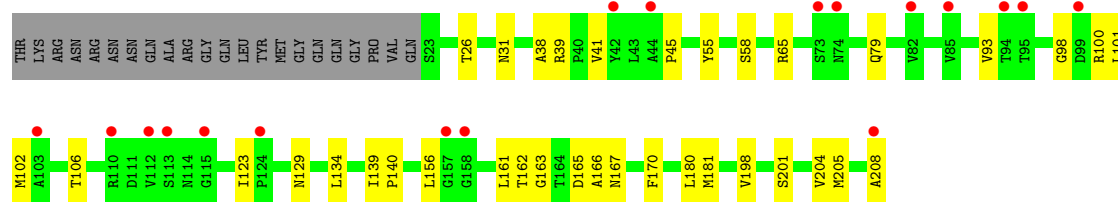
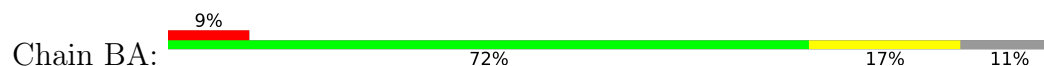




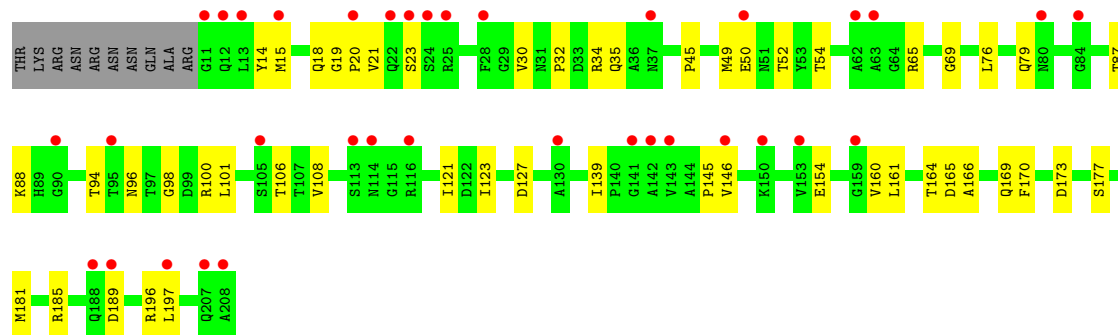
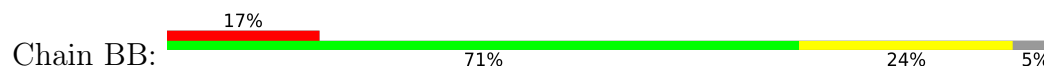
● Molecule 1: coat protein



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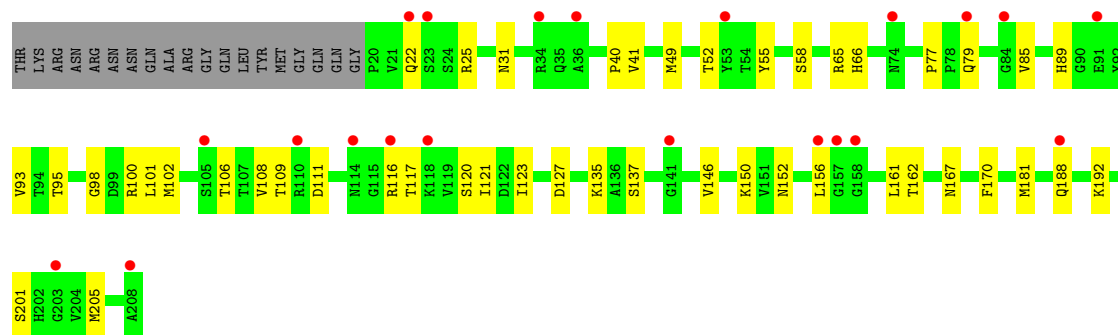


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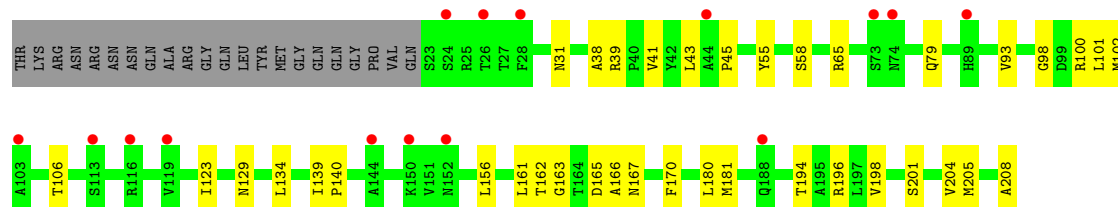
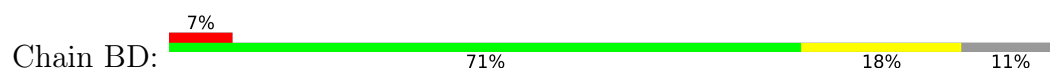


● Molecule 1: coat protein

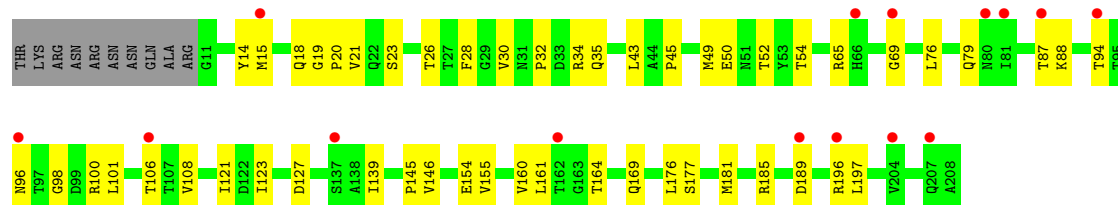
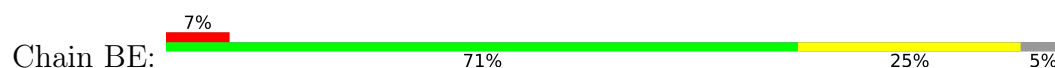




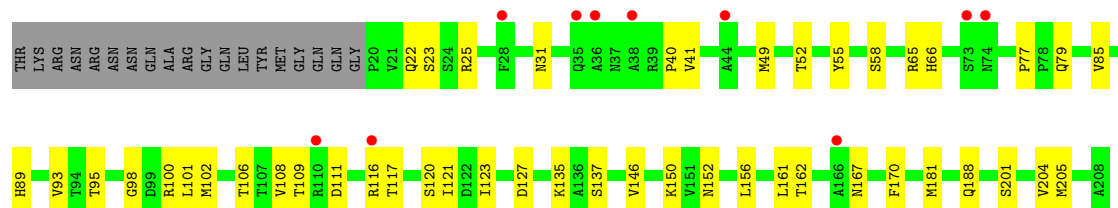
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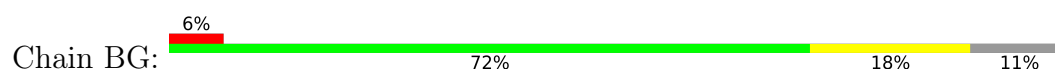
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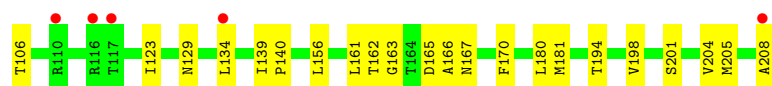


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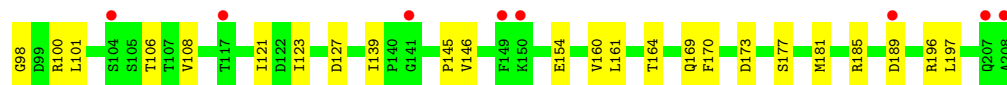
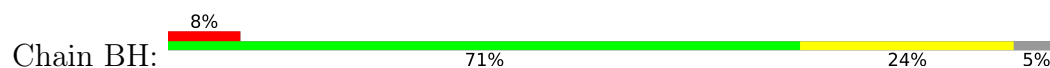


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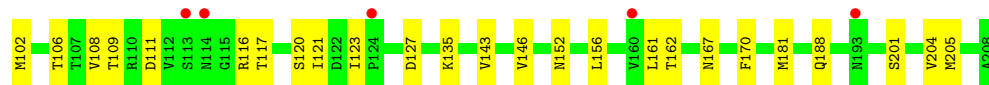
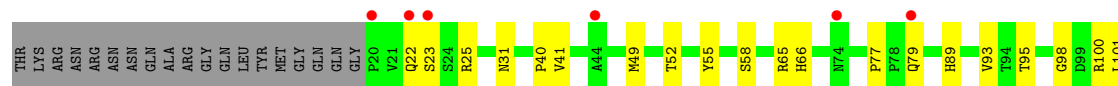




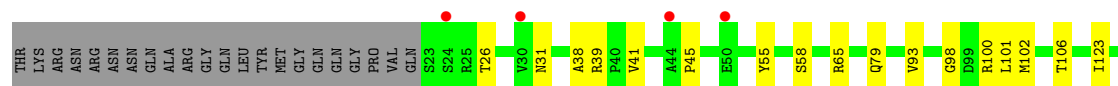
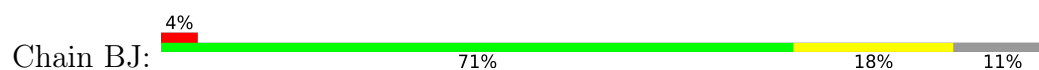
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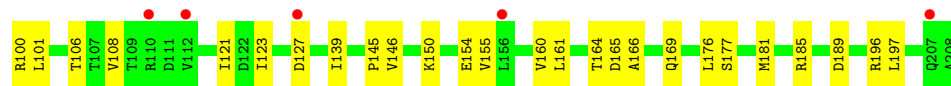
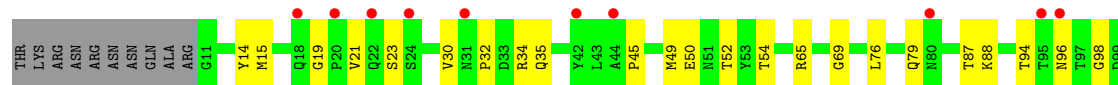
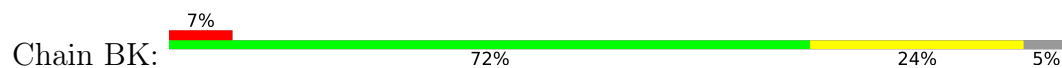
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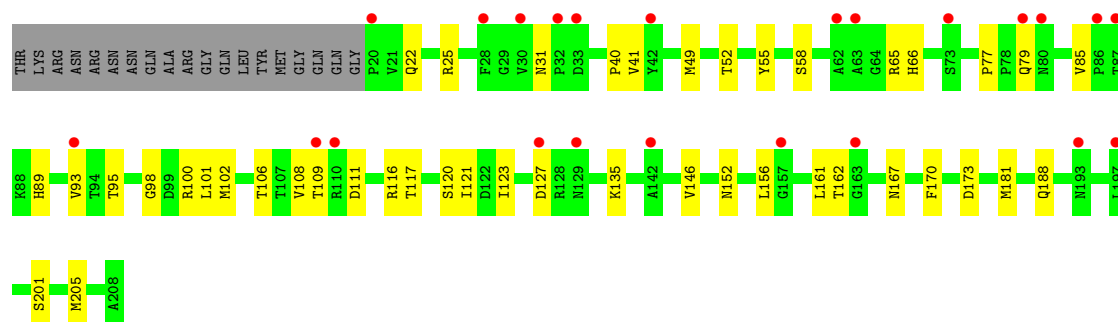


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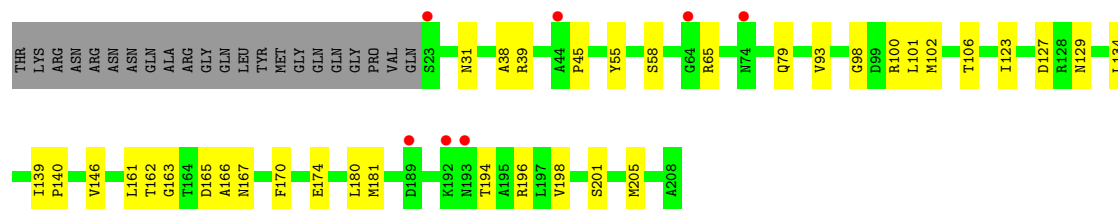
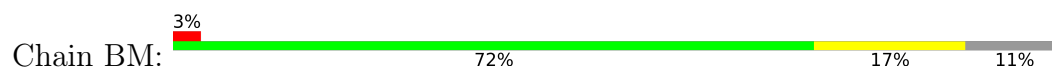


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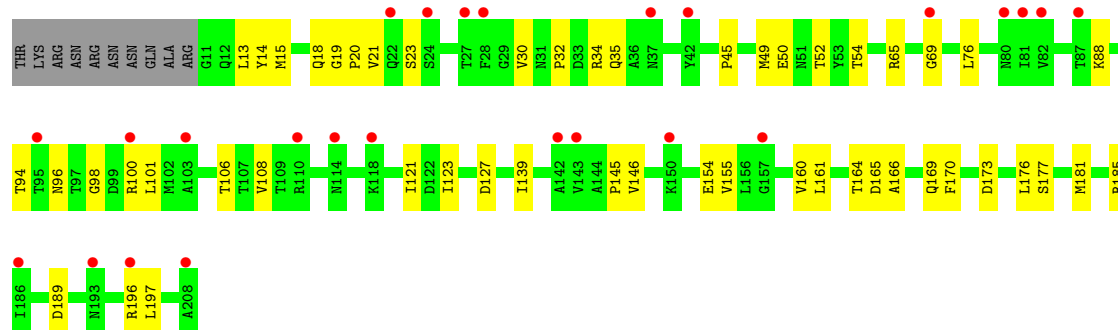
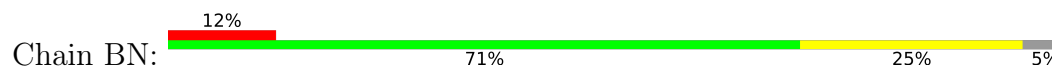




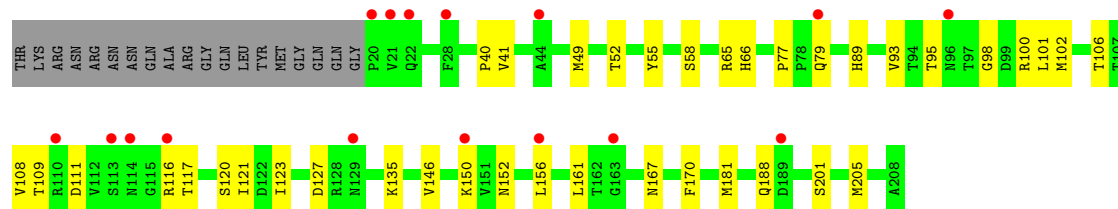
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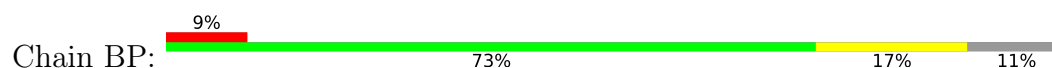
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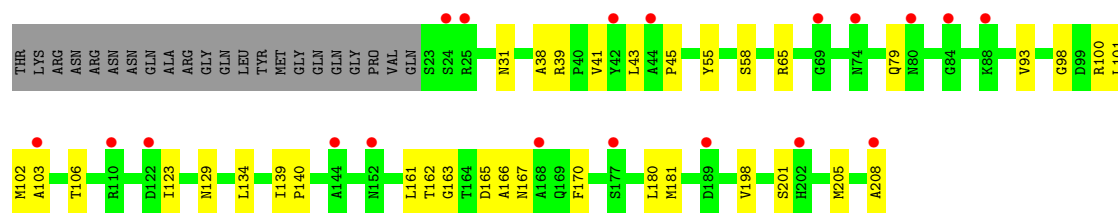


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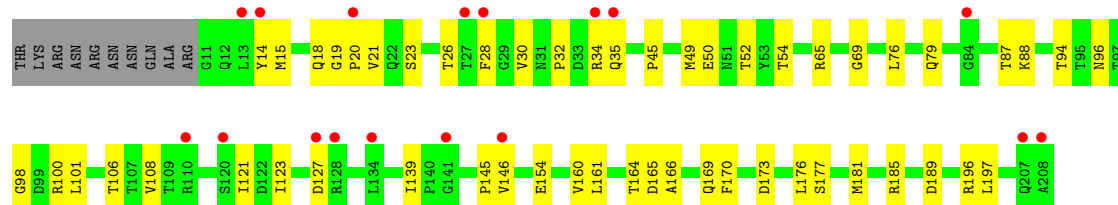
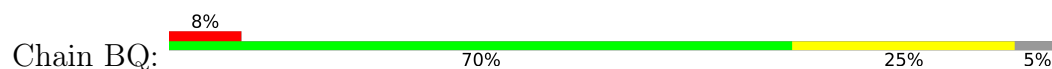


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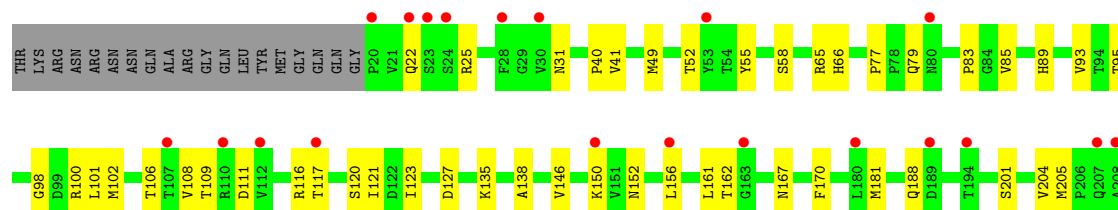




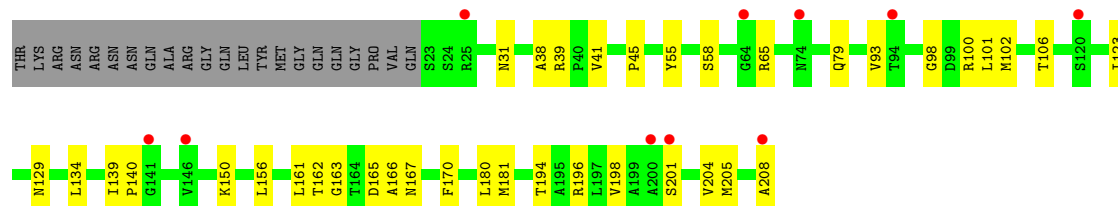
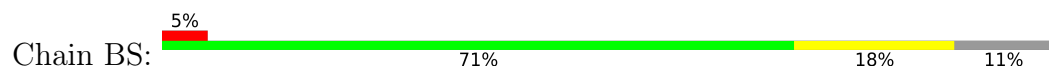
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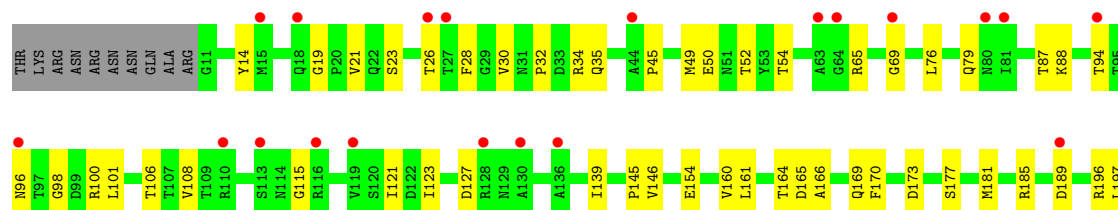
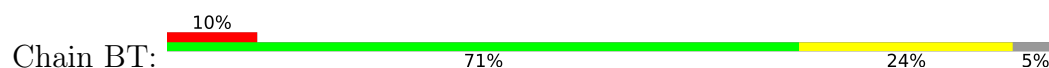
• Molecule 1: coat protein



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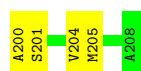
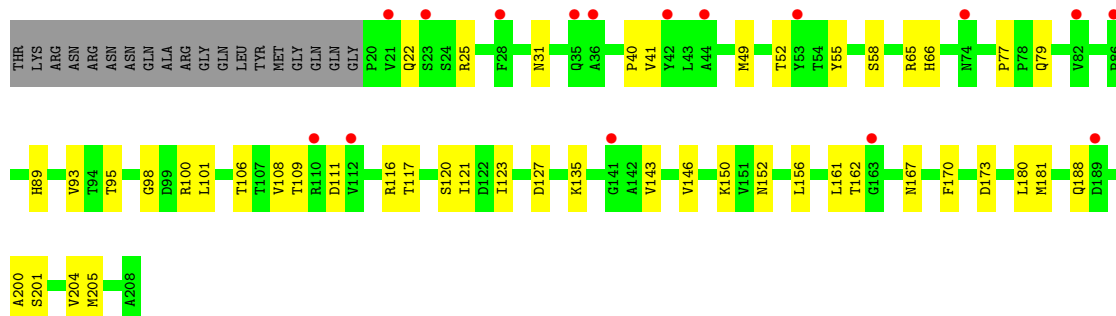


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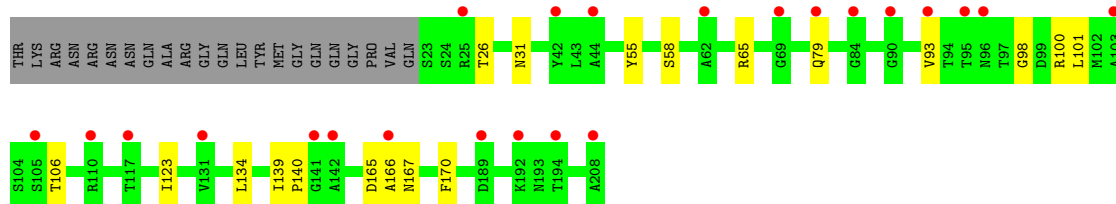
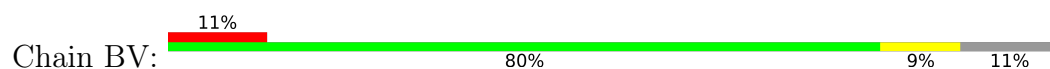




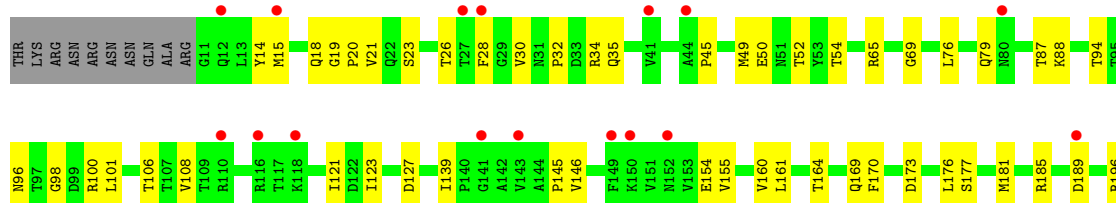
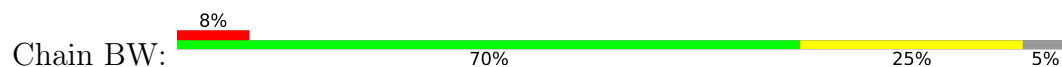
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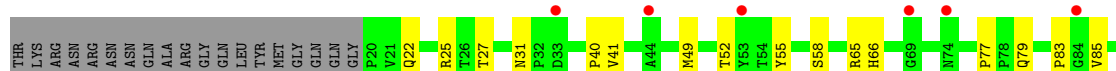
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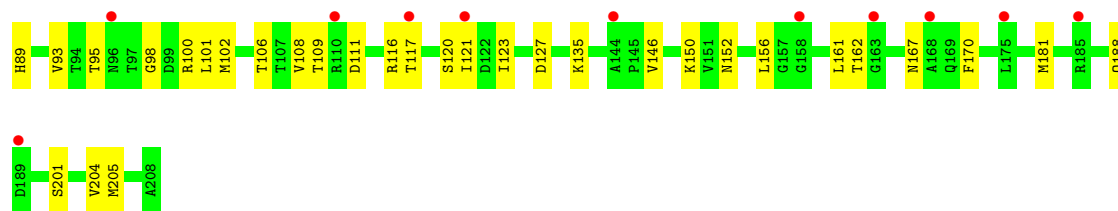


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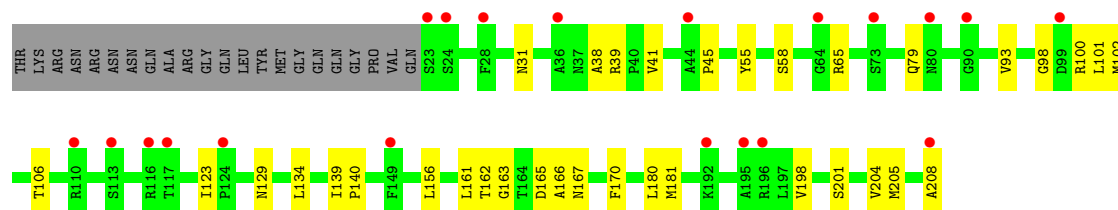
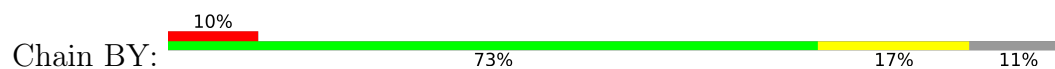


- Molecule 1: coat protein

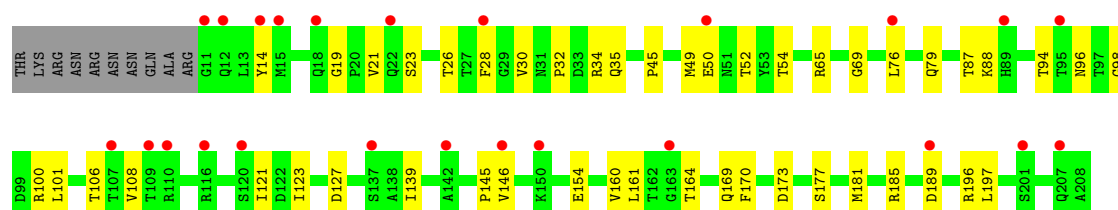
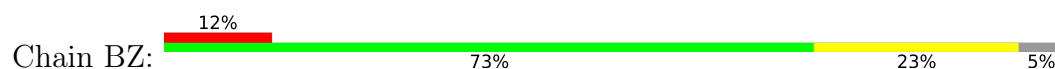




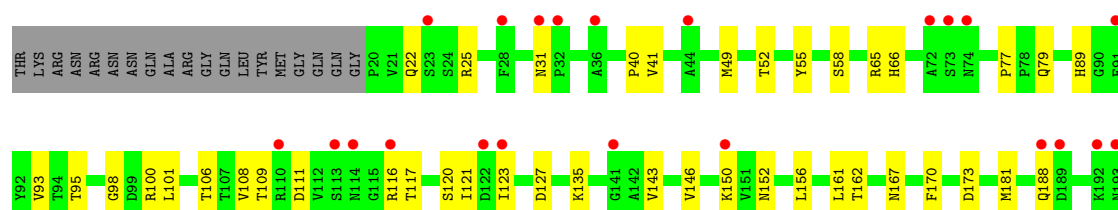
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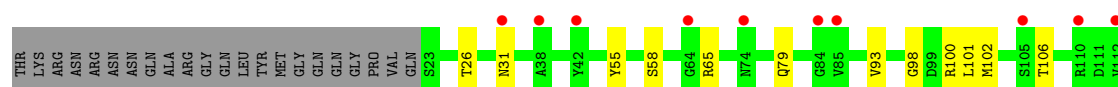
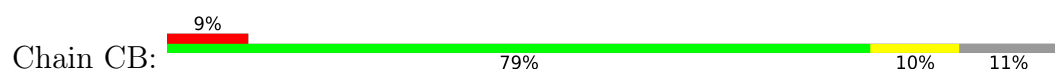
- Molecule 1: coat protein

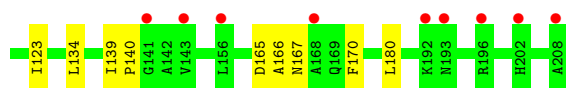


- Molecule 1: coat protein

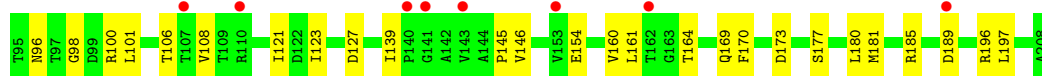
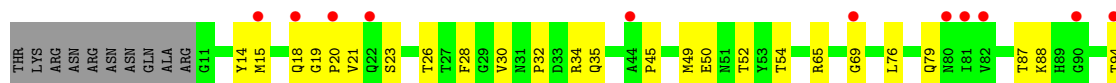
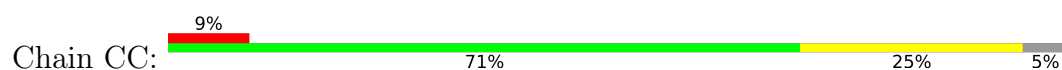


- Molecule 1: coat protein

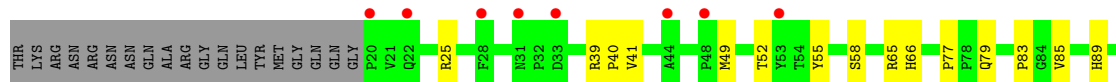
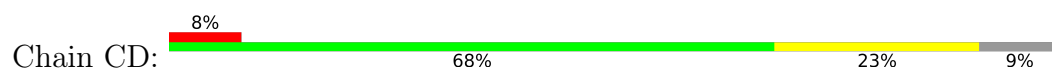




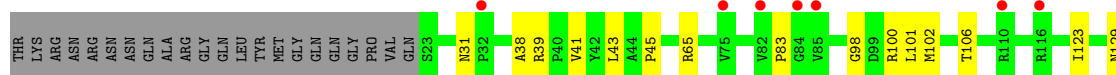
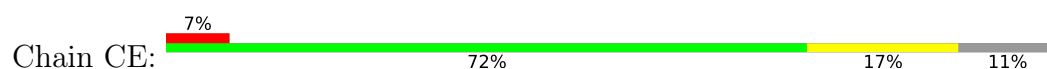
- Molecule 1: coat protein



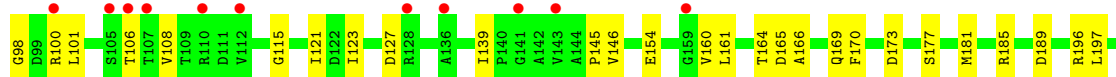
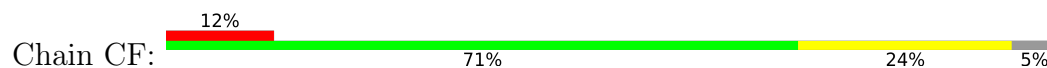
- Molecule 1: coat protein



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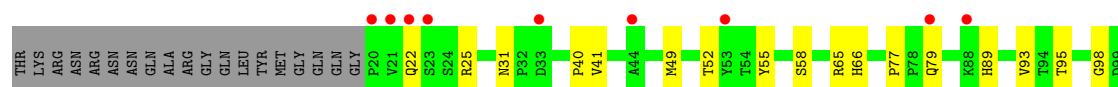
- Molecule 1: coat protein



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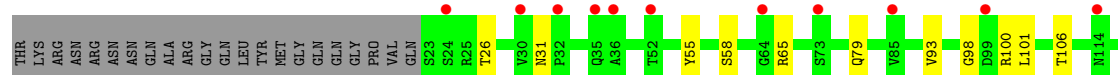
- Molecule 1: coat protein

Chain CG: 



- Molecule 1: coat protein

Chain CH: 



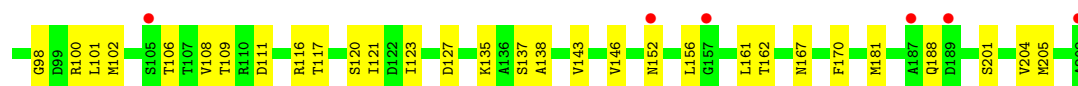
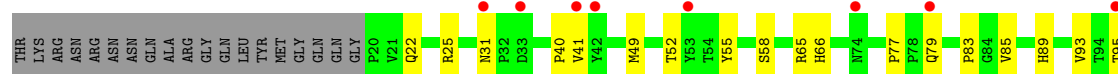
- Molecule 1: coat protein

Chain CI: 



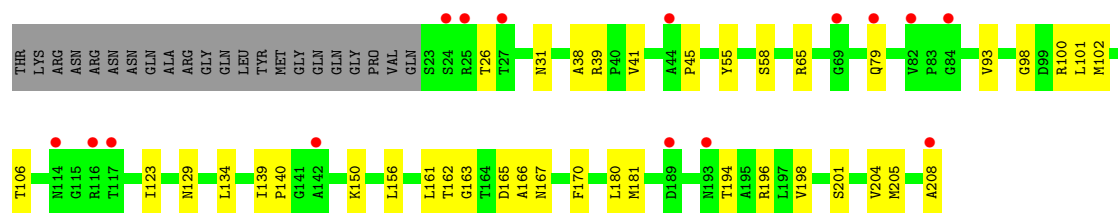
- Molecule 1: coat protein

Chain CJ: 

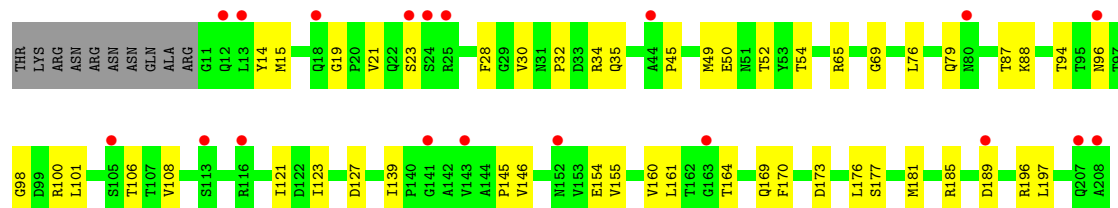
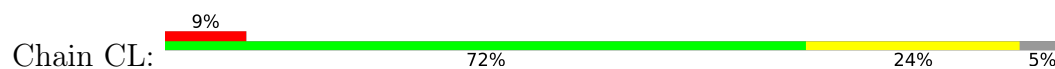


- Molecule 1: coat protein

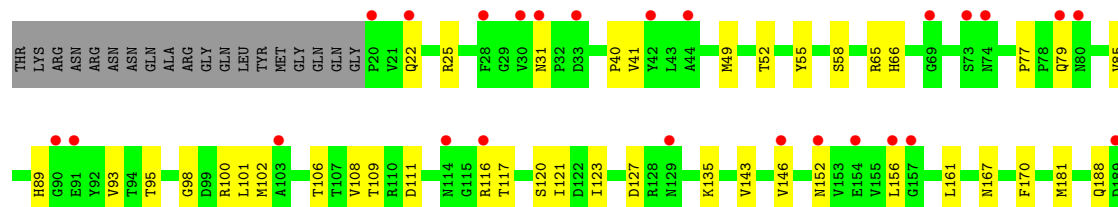
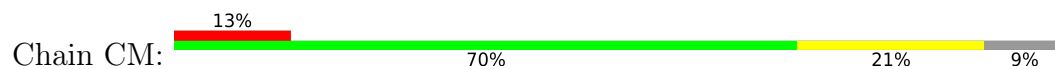
Chain CK: 



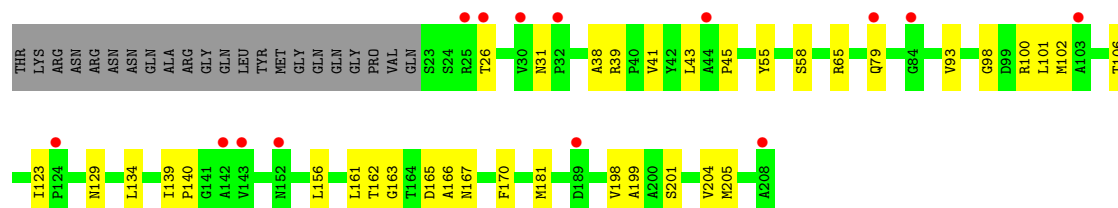
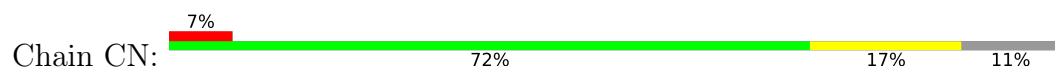
- Molecule 1: coat protein



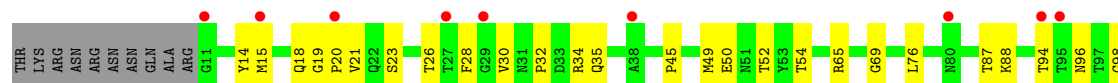
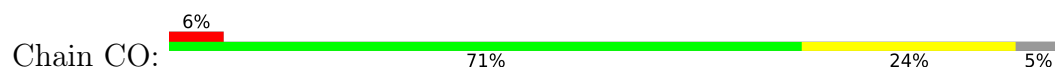
- Molecule 1: coat protein



- Molecule 1: coat protein

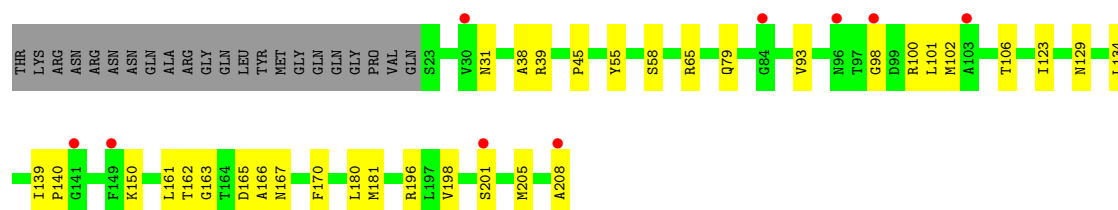
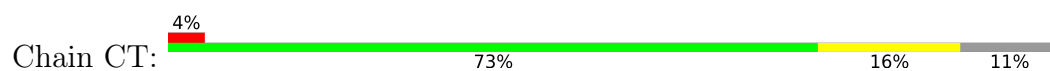


- Molecule 1: coat protein

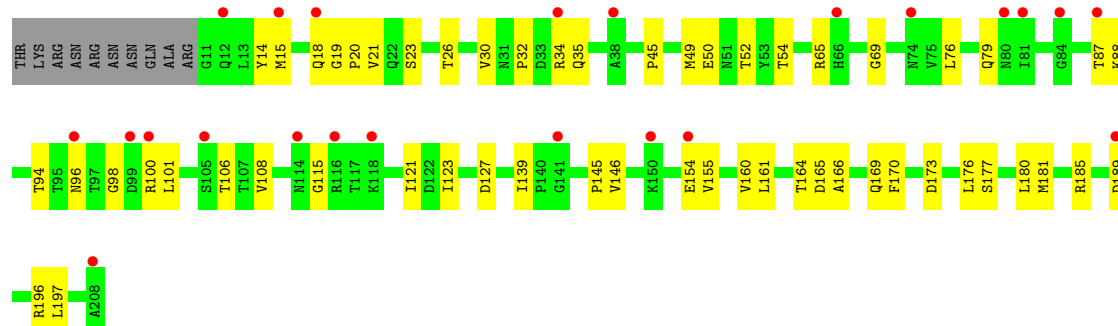




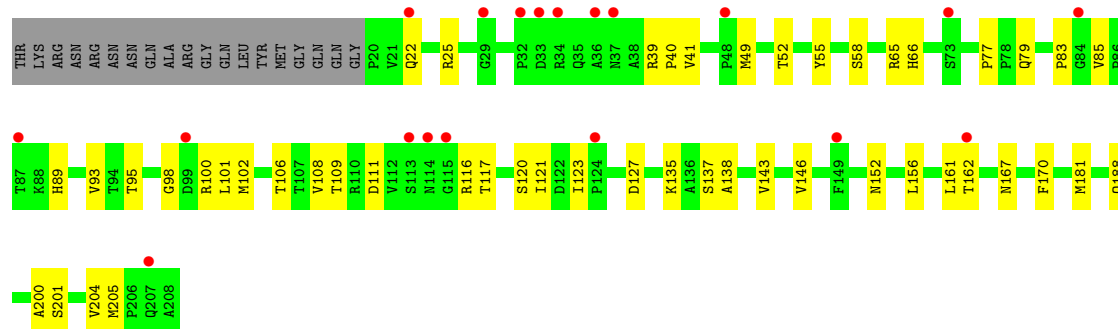
- Molecule 1: coat protein



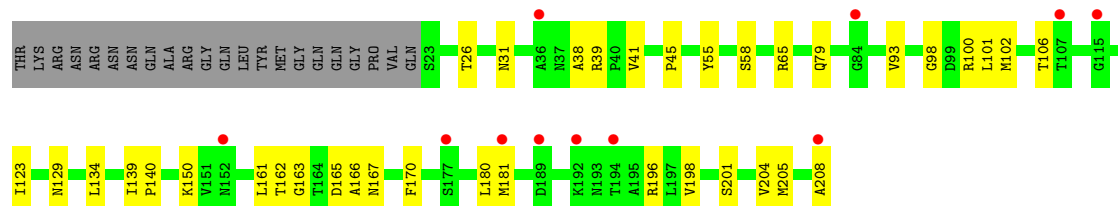
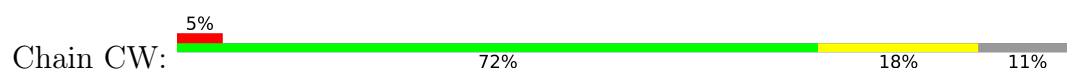
- Molecule 1: coat protein



- Molecule 1: coat protein

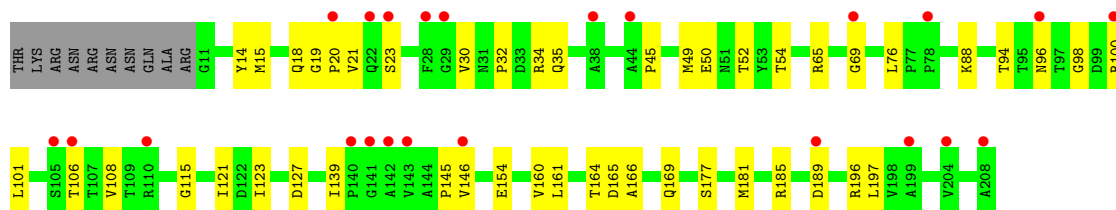


- Molecule 1: coat protein



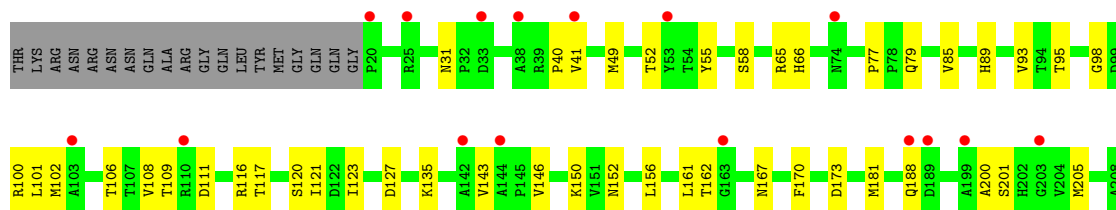
• Molecule 1: coat protein

Chain CX: 11% 73% 23% 5%



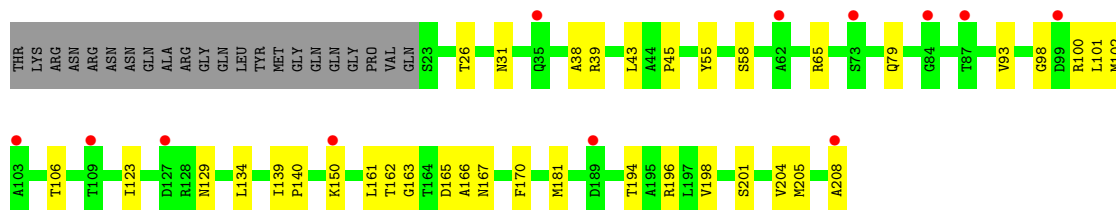
• Molecule 1: coat protein

Chain CY: 8% 69% 22% 9%



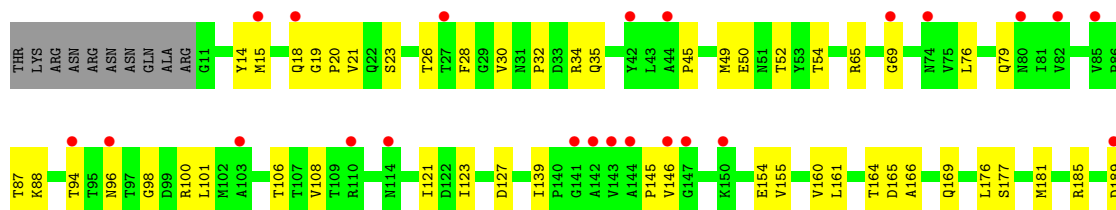
• Molecule 1: coat protein

Chain CZ: 6% 72% 18% 11%



• Molecule 1: coat protein

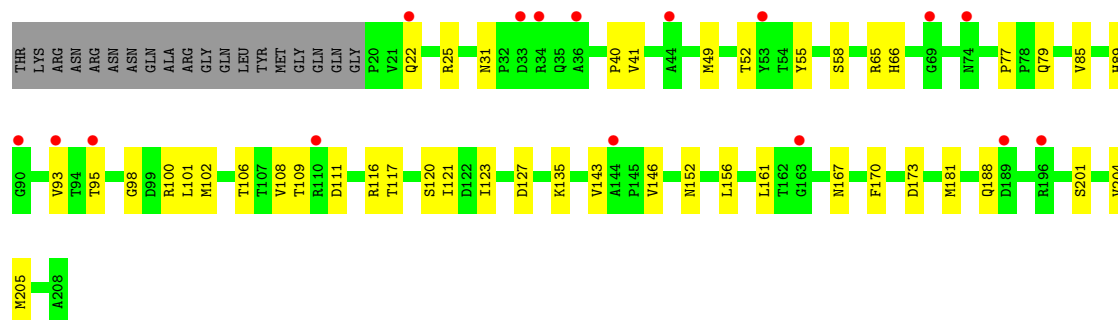
Chain DA: 12% 70% 25% 5%



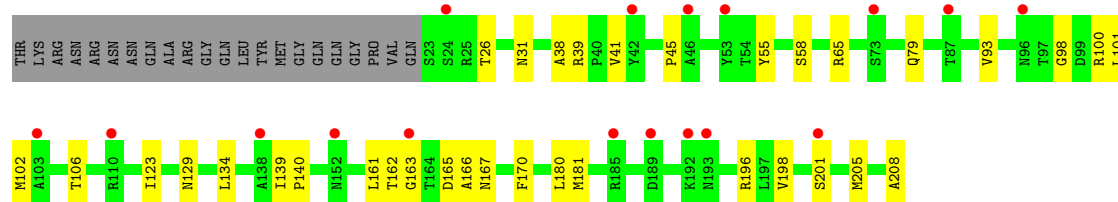
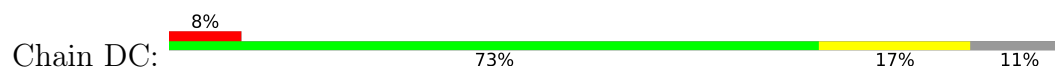
• Molecule 1: coat protein

Chain DB: 8% 69% 22% 9%

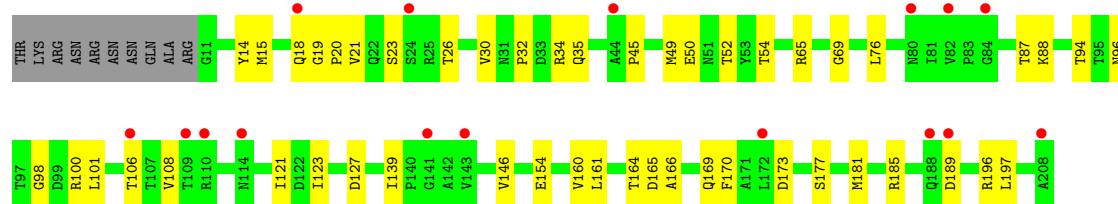
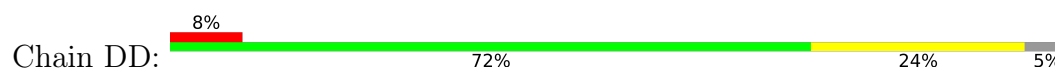




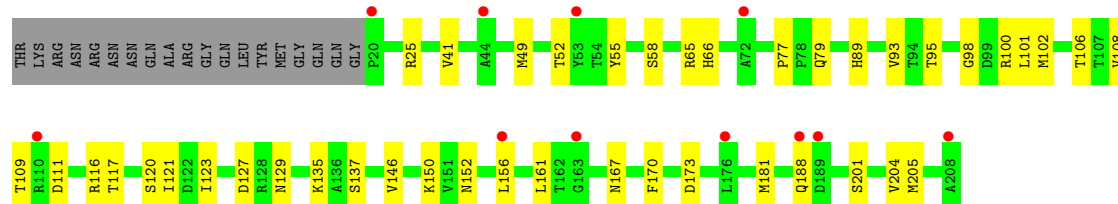
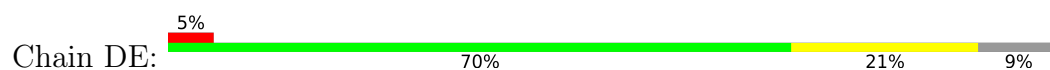
- Molecule 1: coat protein



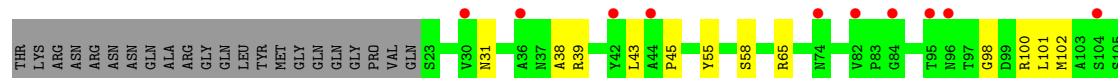
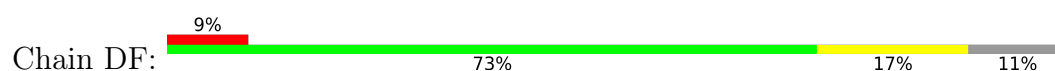
- Molecule 1: coat protein



- Molecule 1: coat protein

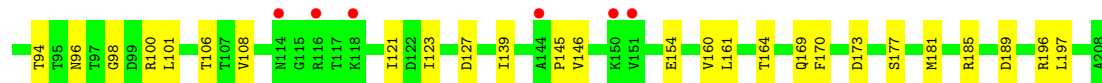
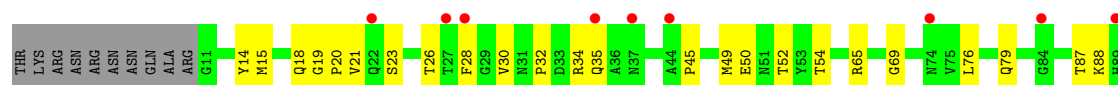
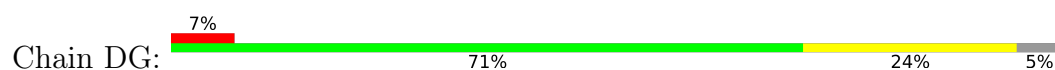


- Molecule 1: coat protein

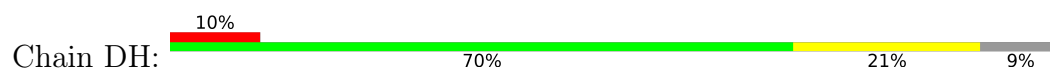




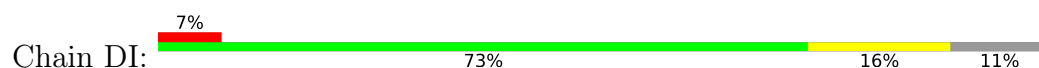
- Molecule 1: coat protein



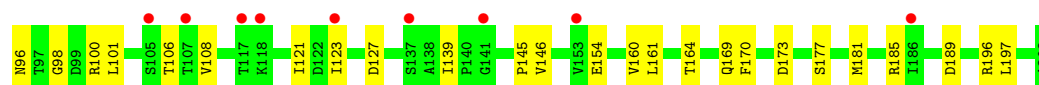
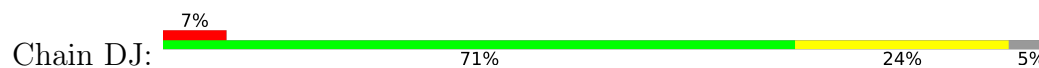
- Molecule 1: coat protein



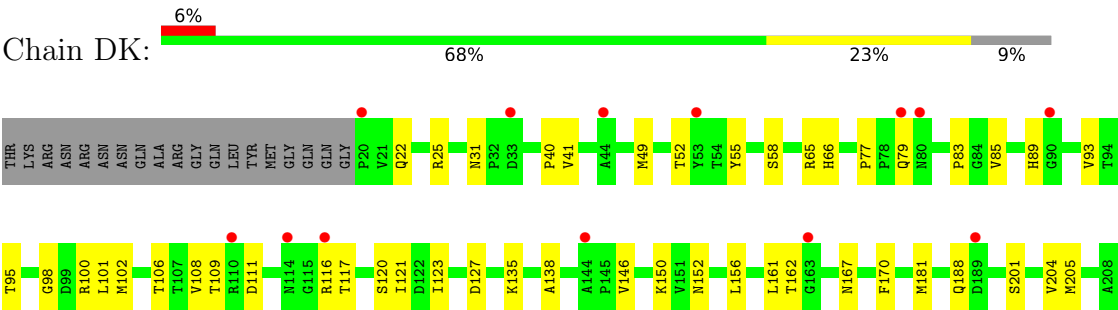
- Molecule 1: coat protein



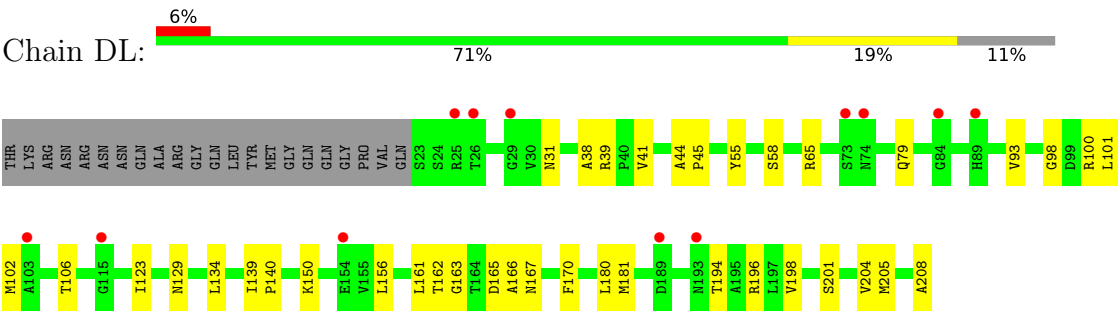
- Molecule 1: coat protein



● Molecule 1: coat protein



● Molecule 1: coat protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	328.67Å 373.71Å 310.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.33 – 3.30 49.33 – 3.30	Depositor EDS
% Data completeness (in resolution range)	92.6 (49.33-3.30) 94.4 (49.33-3.30)	Depositor EDS
R_{merge}	0.65	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.265 , 0.267 0.281 , 0.283	Depositor DCC
R_{free} test set	10027 reflections (1.87%)	wwPDB-VP
Wilson B-factor (Å ²)	97.5	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 65.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	126960	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.55% 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 [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.27	0/1492	0.52	0/2035
1	AB	0.28	0/1424	0.56	0/1944
1	AC	0.30	0/1400	0.54	0/1911
1	AD	0.27	0/1492	0.52	0/2035
1	AE	0.28	0/1424	0.56	0/1944
1	AF	0.30	0/1400	0.53	0/1911
1	AG	0.27	0/1492	0.53	0/2035
1	AH	0.28	0/1424	0.56	0/1944
1	AI	0.30	0/1400	0.54	0/1911
1	AJ	0.27	0/1492	0.52	0/2035
1	AK	0.29	0/1424	0.56	0/1944
1	AL	0.30	0/1400	0.54	0/1911
1	AM	0.27	0/1492	0.52	0/2035
1	AN	0.28	0/1424	0.56	0/1944
1	AO	0.30	0/1400	0.53	0/1911
1	AP	0.27	0/1492	0.52	0/2035
1	AQ	0.29	0/1424	0.56	0/1944
1	AR	0.30	0/1400	0.54	0/1911
1	AS	0.27	0/1492	0.53	0/2035
1	AT	0.29	0/1424	0.56	0/1944
1	AU	0.30	0/1400	0.53	0/1911
1	AV	0.27	0/1492	0.53	0/2035
1	AW	0.28	0/1424	0.56	0/1944
1	AX	0.30	0/1400	0.54	0/1911
1	AY	0.27	0/1492	0.52	0/2035
1	AZ	0.29	0/1424	0.56	0/1944
1	BA	0.30	0/1400	0.54	0/1911
1	BB	0.27	0/1492	0.52	0/2035
1	BC	0.28	0/1424	0.56	0/1944
1	BD	0.30	0/1400	0.54	0/1911
1	BE	0.27	0/1492	0.52	0/2035
1	BF	0.29	0/1424	0.56	0/1944
1	BG	0.30	0/1400	0.54	0/1911
1	BH	0.27	0/1492	0.52	0/2035

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BI	0.29	0/1424	0.56	0/1944
1	BJ	0.30	0/1400	0.54	0/1911
1	BK	0.27	0/1492	0.52	0/2035
1	BL	0.28	0/1424	0.56	0/1944
1	BM	0.30	0/1400	0.54	0/1911
1	BN	0.27	0/1492	0.52	0/2035
1	BO	0.28	0/1424	0.56	0/1944
1	BP	0.30	0/1400	0.54	0/1911
1	BQ	0.27	0/1492	0.53	0/2035
1	BR	0.29	0/1424	0.56	0/1944
1	BS	0.30	0/1400	0.54	0/1911
1	BT	0.27	0/1492	0.52	0/2035
1	BU	0.29	0/1424	0.56	0/1944
1	BV	0.30	0/1400	0.53	0/1911
1	BW	0.27	0/1492	0.52	0/2035
1	BX	0.29	0/1424	0.56	0/1944
1	BY	0.30	0/1400	0.54	0/1911
1	BZ	0.27	0/1492	0.52	0/2035
1	CA	0.28	0/1424	0.56	0/1944
1	CB	0.30	0/1400	0.54	0/1911
1	CC	0.27	0/1492	0.52	0/2035
1	CD	0.28	0/1424	0.56	0/1944
1	CE	0.30	0/1400	0.54	0/1911
1	CF	0.27	0/1492	0.52	0/2035
1	CG	0.29	0/1424	0.56	0/1944
1	CH	0.30	0/1400	0.54	0/1911
1	CI	0.27	0/1492	0.52	0/2035
1	CJ	0.28	0/1424	0.56	0/1944
1	CK	0.30	0/1400	0.54	0/1911
1	CL	0.27	0/1492	0.53	0/2035
1	CM	0.29	0/1424	0.56	0/1944
1	CN	0.30	0/1400	0.54	0/1911
1	CO	0.27	0/1492	0.52	0/2035
1	CP	0.28	0/1424	0.56	0/1944
1	CQ	0.30	0/1400	0.54	0/1911
1	CR	0.27	0/1492	0.52	0/2035
1	CS	0.29	0/1424	0.56	0/1944
1	CT	0.30	0/1400	0.53	0/1911
1	CU	0.27	0/1492	0.53	0/2035
1	CV	0.28	0/1424	0.56	0/1944
1	CW	0.30	0/1400	0.54	0/1911
1	CX	0.27	0/1492	0.53	0/2035
1	CY	0.29	0/1424	0.56	0/1944

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CZ	0.30	0/1400	0.54	0/1911
1	DA	0.27	0/1492	0.53	0/2035
1	DB	0.28	0/1424	0.56	0/1944
1	DC	0.30	0/1400	0.54	0/1911
1	DD	0.27	0/1492	0.52	0/2035
1	DE	0.29	0/1424	0.56	0/1944
1	DF	0.30	0/1400	0.54	0/1911
1	DG	0.27	0/1492	0.52	0/2035
1	DH	0.29	0/1424	0.56	0/1944
1	DI	0.30	0/1400	0.54	0/1911
1	DJ	0.27	0/1492	0.52	0/2035
1	DK	0.28	0/1424	0.56	0/1944
1	DL	0.30	0/1400	0.54	0/1911
All	All	0.28	0/129480	0.54	0/176700

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	1463	0	1446	39	0
1	AB	1396	0	1385	35	1
1	AC	1373	0	1360	35	0
1	AD	1463	0	1446	39	0
1	AE	1396	0	1385	42	0
1	AF	1373	0	1360	47	0
1	AG	1463	0	1446	32	0
1	AH	1396	0	1385	31	0
1	AI	1373	0	1360	11	2
1	AJ	1463	0	1446	37	0
1	AK	1396	0	1385	37	0
1	AL	1373	0	1360	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AM	1463	0	1446	33	0
1	AN	1396	0	1385	31	0
1	AO	1373	0	1360	14	1
1	AP	1463	0	1446	36	0
1	AQ	1396	0	1385	32	0
1	AR	1373	0	1360	37	0
1	AS	1463	0	1446	37	0
1	AT	1396	0	1385	38	0
1	AU	1373	0	1360	43	0
1	AV	1463	0	1446	35	0
1	AW	1396	0	1385	33	0
1	AX	1373	0	1360	12	2
1	AY	1463	0	1446	35	0
1	AZ	1396	0	1385	37	0
1	BA	1373	0	1360	36	0
1	BB	1463	0	1446	36	0
1	BC	1396	0	1385	36	1
1	BD	1373	0	1360	42	0
1	BE	1463	0	1446	39	0
1	BF	1396	0	1385	37	0
1	BG	1373	0	1360	38	0
1	BH	1463	0	1446	38	0
1	BI	1396	0	1385	37	0
1	BJ	1373	0	1360	39	0
1	BK	1463	0	1446	35	0
1	BL	1396	0	1385	35	0
1	BM	1373	0	1360	36	0
1	BN	1463	0	1446	35	0
1	BO	1396	0	1385	28	0
1	BP	1373	0	1360	34	0
1	BQ	1463	0	1446	38	0
1	BR	1396	0	1385	39	0
1	BS	1373	0	1360	44	0
1	BT	1463	0	1446	35	0
1	BU	1396	0	1385	37	0
1	BV	1373	0	1360	11	1
1	BW	1463	0	1446	38	0
1	BX	1396	0	1385	36	0
1	BY	1373	0	1360	35	0
1	BZ	1463	0	1446	33	0
1	CA	1396	0	1385	35	0
1	CB	1373	0	1360	13	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CC	1463	0	1446	39	0
1	CD	1396	0	1385	38	0
1	CE	1373	0	1360	44	0
1	CF	1463	0	1446	35	0
1	CG	1396	0	1385	34	0
1	CH	1373	0	1360	12	2
1	CI	1463	0	1446	38	0
1	CJ	1396	0	1385	41	0
1	CK	1373	0	1360	45	0
1	CL	1463	0	1446	35	0
1	CM	1396	0	1385	34	0
1	CN	1373	0	1360	36	0
1	CO	1463	0	1446	37	0
1	CP	1396	0	1385	43	0
1	CQ	1373	0	1360	40	0
1	CR	1463	0	1446	36	0
1	CS	1396	0	1385	35	0
1	CT	1373	0	1360	36	0
1	CU	1463	0	1446	40	0
1	CV	1396	0	1385	41	0
1	CW	1373	0	1360	38	0
1	CX	1463	0	1446	33	0
1	CY	1396	0	1385	34	0
1	CZ	1373	0	1360	40	0
1	DA	1463	0	1446	39	0
1	DB	1396	0	1385	34	0
1	DC	1373	0	1360	37	0
1	DD	1463	0	1446	35	0
1	DE	1396	0	1385	32	0
1	DF	1373	0	1360	36	0
1	DG	1463	0	1446	38	0
1	DH	1396	0	1385	34	0
1	DI	1373	0	1360	34	0
1	DJ	1463	0	1446	37	0
1	DK	1396	0	1385	38	0
1	DL	1373	0	1360	45	0
All	All	126960	0	125730	2230	7

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 9.

All (2230) 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:BM:31:ASN:O	1:DF:65:ARG:NH1	2.04	0.90
1:BG:31:ASN:O	1:CZ:65:ARG:NH1	2.04	0.90
1:AL:31:ASN:O	1:CK:65:ARG:NH1	2.05	0.89
1:AL:65:ARG:NH1	1:CK:31:ASN:O	2.09	0.85
1:BP:31:ASN:O	1:DI:65:ARG:NH1	2.09	0.85
1:BP:65:ARG:NH1	1:DI:31:ASN:O	2.09	0.85
1:AF:65:ARG:NH1	1:CE:31:ASN:O	2.10	0.85
1:BJ:65:ARG:NH1	1:DC:31:ASN:O	2.10	0.84
1:BJ:31:ASN:O	1:DC:65:ARG:NH1	2.10	0.83
1:BM:65:ARG:NH1	1:DF:31:ASN:O	2.10	0.83
1:BD:31:ASN:O	1:CW:65:ARG:NH1	2.11	0.83
1:AR:65:ARG:NH1	1:CN:31:ASN:O	2.12	0.82
1:BS:65:ARG:NH1	1:DL:31:ASN:O	2.13	0.82
1:AR:45:PRO:HA	1:CN:205:MET:HE2	1.62	0.82
1:BA:31:ASN:O	1:CT:65:ARG:NH1	2.13	0.81
1:BG:65:ARG:NH1	1:CZ:31:ASN:O	2.12	0.81
1:BD:65:ARG:NH1	1:CW:31:ASN:O	2.14	0.81
1:BS:31:ASN:O	1:DL:65:ARG:NH1	2.13	0.81
1:BA:65:ARG:NH1	1:CT:31:ASN:O	2.13	0.81
1:AU:31:ASN:O	1:CQ:65:ARG:NH1	2.13	0.80
1:AC:65:ARG:NH1	1:BY:31:ASN:O	2.15	0.79
1:AC:31:ASN:O	1:BY:65:ARG:NH1	2.16	0.79
1:AU:65:ARG:NH1	1:CQ:31:ASN:O	2.16	0.79
1:AW:40:PRO:HG3	1:BB:87:THR:HG22	1.65	0.78
1:BG:205:MET:HE2	1:CZ:45:PRO:HA	1.64	0.78
1:AR:31:ASN:O	1:CN:65:ARG:NH1	2.17	0.78
1:AV:87:THR:HG22	1:DH:40:PRO:HG3	1.64	0.78
1:BS:45:PRO:HA	1:DL:205:MET:HE2	1.66	0.77
1:BL:40:PRO:HG3	1:DA:87:THR:HG22	1.64	0.77
1:AF:31:ASN:O	1:CE:65:ARG:NH1	2.17	0.77
1:AF:45:PRO:HA	1:CE:205:MET:HE2	1.65	0.77
1:AR:205:MET:HE2	1:CN:45:PRO:HA	1.68	0.76
1:AP:87:THR:HG22	1:CD:40:PRO:HG3	1.67	0.76
1:AZ:25:ARG:NH2	1:DA:145:PRO:O	2.18	0.76
1:BA:205:MET:HE2	1:CT:45:PRO:HA	1.67	0.76
1:AG:87:THR:HG22	1:CG:40:PRO:HG3	1.68	0.76
1:BH:87:THR:HG22	1:BR:40:PRO:HG3	1.66	0.76
1:BS:205:MET:HE2	1:DL:45:PRO:HA	1.67	0.76
1:BO:40:PRO:HG3	1:DD:87:THR:HG22	1.68	0.75
1:BI:40:PRO:HG3	1:DG:87:THR:HG22	1.68	0.75
1:BK:87:THR:HG22	1:BU:40:PRO:HG3	1.68	0.75
1:AC:45:PRO:HA	1:BY:205:MET:HE2	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:205:MET:HE2	1:CQ:45:PRO:HA	1.67	0.74
1:BM:205:MET:HE2	1:DF:45:PRO:HA	1.68	0.74
1:AM:87:THR:HG22	1:CA:40:PRO:HG3	1.69	0.74
1:BF:40:PRO:HG3	1:BT:87:THR:HG22	1.69	0.74
1:BJ:205:MET:HE2	1:DC:45:PRO:HA	1.68	0.74
1:AG:127:ASP:HB2	1:AG:146:VAL:HG21	1.70	0.74
1:AW:25:ARG:NH2	1:DG:145:PRO:O	2.20	0.74
1:BI:25:ARG:NH2	1:BQ:145:PRO:O	2.21	0.74
1:BP:205:MET:HE2	1:DI:45:PRO:HA	1.67	0.74
1:CC:127:ASP:HB2	1:CC:146:VAL:HG21	1.70	0.74
1:AK:25:ARG:NH2	1:AM:145:PRO:O	2.21	0.73
1:CI:127:ASP:HB2	1:CI:146:VAL:HG21	1.70	0.73
1:CO:127:ASP:HB2	1:CO:146:VAL:HG21	1.70	0.73
1:AA:127:ASP:HB2	1:AA:146:VAL:HG21	1.70	0.73
1:AC:205:MET:HE2	1:BY:45:PRO:HA	1.70	0.73
1:BD:205:MET:HE2	1:CW:45:PRO:HA	1.69	0.73
1:BH:127:ASP:HB2	1:BH:146:VAL:HG21	1.70	0.73
1:BW:127:ASP:HB2	1:BW:146:VAL:HG21	1.70	0.73
1:CR:127:ASP:HB2	1:CR:146:VAL:HG21	1.70	0.73
1:AJ:87:THR:HG22	1:AN:40:PRO:HG3	1.70	0.73
1:AU:45:PRO:HA	1:CQ:205:MET:HE2	1.68	0.73
1:BP:45:PRO:HA	1:DI:205:MET:HE2	1.70	0.73
1:AM:127:ASP:HB2	1:AM:146:VAL:HG21	1.70	0.73
1:AA:87:THR:HG22	1:AK:40:PRO:HG3	1.71	0.73
1:AD:127:ASP:HB2	1:AD:146:VAL:HG21	1.70	0.73
1:BK:127:ASP:HB2	1:BK:146:VAL:HG21	1.70	0.73
1:AY:127:ASP:HB2	1:AY:146:VAL:HG21	1.70	0.73
1:DJ:127:ASP:HB2	1:DJ:146:VAL:HG21	1.70	0.73
1:AL:205:MET:HE2	1:CK:45:PRO:HA	1.71	0.72
1:BT:127:ASP:HB2	1:BT:146:VAL:HG21	1.70	0.72
1:BB:127:ASP:HB2	1:BB:146:VAL:HG21	1.70	0.72
1:BE:127:ASP:HB2	1:BE:146:VAL:HG21	1.70	0.72
1:BN:127:ASP:HB2	1:BN:146:VAL:HG21	1.70	0.72
1:AP:127:ASP:HB2	1:AP:146:VAL:HG21	1.70	0.72
1:AJ:127:ASP:HB2	1:AJ:146:VAL:HG21	1.70	0.72
1:BW:87:THR:HG22	1:DK:40:PRO:HG3	1.71	0.72
1:AZ:40:PRO:HG3	1:BE:87:THR:HG22	1.72	0.72
1:CM:40:PRO:HG3	1:CO:87:THR:HG22	1.71	0.72
1:AV:127:ASP:HB2	1:AV:146:VAL:HG21	1.70	0.72
1:BJ:45:PRO:HA	1:DC:205:MET:HE2	1.72	0.71
1:BK:145:PRO:O	1:DB:25:ARG:NH2	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BZ:87:THR:HG22	1:CV:40:PRO:HG3	1.71	0.71
1:CL:127:ASP:HB2	1:CL:146:VAL:HG21	1.70	0.71
1:AS:87:THR:HG22	1:BX:40:PRO:HG3	1.72	0.71
1:AS:127:ASP:HB2	1:AS:146:VAL:HG21	1.70	0.71
1:BM:45:PRO:HA	1:DF:205:MET:HE2	1.71	0.71
1:DG:127:ASP:HB2	1:DG:146:VAL:HG21	1.70	0.71
1:AV:145:PRO:O	1:BC:25:ARG:NH2	2.23	0.71
1:BQ:127:ASP:HB2	1:BQ:146:VAL:HG21	1.70	0.71
1:CL:145:PRO:O	1:CP:25:ARG:NH2	2.24	0.71
1:DA:127:ASP:HB2	1:DA:146:VAL:HG21	1.70	0.71
1:CS:40:PRO:HG3	1:DJ:87:THR:HG22	1.72	0.71
1:AE:25:ARG:NH2	1:AS:145:PRO:O	2.24	0.71
1:BX:25:ARG:NH2	1:DJ:145:PRO:O	2.23	0.71
1:DD:127:ASP:HB2	1:DD:146:VAL:HG21	1.70	0.71
1:BD:45:PRO:HA	1:CW:205:MET:HE2	1.72	0.70
1:BZ:127:ASP:HB2	1:BZ:146:VAL:HG21	1.70	0.70
1:CF:127:ASP:HB2	1:CF:146:VAL:HG21	1.70	0.70
1:CU:127:ASP:HB2	1:CU:146:VAL:HG21	1.70	0.70
1:CF:87:THR:HG22	1:CJ:40:PRO:HG3	1.73	0.70
1:AE:40:PRO:HG3	1:CR:87:THR:HG22	1.73	0.70
1:BA:45:PRO:HA	1:CT:205:MET:HE2	1.73	0.70
1:CX:127:ASP:HB2	1:CX:146:VAL:HG21	1.70	0.70
1:BC:40:PRO:HG3	1:BQ:87:THR:HG22	1.74	0.70
1:DG:49:MET:HE2	1:DG:52:THR:HG21	1.74	0.70
1:AA:145:PRO:O	1:CV:25:ARG:NH2	2.25	0.70
1:BE:145:PRO:O	1:BU:25:ARG:NH2	2.25	0.70
1:BQ:49:MET:HE2	1:BQ:52:THR:HG21	1.74	0.70
1:CI:87:THR:HG22	1:CP:40:PRO:HG3	1.72	0.70
1:AL:45:PRO:HA	1:CK:205:MET:HE2	1.73	0.70
1:CC:87:THR:HG22	1:CY:40:PRO:HG3	1.73	0.70
1:CR:49:MET:HE2	1:CR:52:THR:HG21	1.74	0.70
1:CR:145:PRO:O	1:DK:25:ARG:NH2	2.25	0.70
1:AH:25:ARG:NH2	1:CF:145:PRO:O	2.24	0.70
1:AS:49:MET:HE2	1:AS:52:THR:HG21	1.74	0.70
1:AY:49:MET:HE2	1:AY:52:THR:HG21	1.74	0.70
1:BZ:49:MET:HE2	1:BZ:52:THR:HG21	1.74	0.70
1:DA:49:MET:HE2	1:DA:52:THR:HG21	1.74	0.70
1:AA:49:MET:HE2	1:AA:52:THR:HG21	1.74	0.70
1:AP:49:MET:HE2	1:AP:52:THR:HG21	1.74	0.70
1:BB:145:PRO:O	1:BR:25:ARG:NH2	2.25	0.70
1:BN:145:PRO:O	1:DE:25:ARG:NH2	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DJ:49:MET:HE2	1:DJ:52:THR:HG21	1.74	0.70
1:AG:49:MET:HE2	1:AG:52:THR:HG21	1.74	0.69
1:CC:49:MET:HE2	1:CC:52:THR:HG21	1.74	0.69
1:AD:49:MET:HE2	1:AD:52:THR:HG21	1.74	0.69
1:BN:49:MET:HE2	1:BN:52:THR:HG21	1.74	0.69
1:CO:49:MET:HE2	1:CO:52:THR:HG21	1.74	0.69
1:CU:49:MET:HE2	1:CU:52:THR:HG21	1.74	0.69
1:AL:181:MET:HE1	1:CK:181:MET:HE1	1.73	0.69
1:BB:49:MET:HE2	1:BB:52:THR:HG21	1.74	0.69
1:BE:49:MET:HE2	1:BE:52:THR:HG21	1.74	0.69
1:BG:45:PRO:HA	1:CZ:205:MET:HE2	1.74	0.69
1:BH:49:MET:HE2	1:BH:52:THR:HG21	1.74	0.69
1:BW:49:MET:HE2	1:BW:52:THR:HG21	1.74	0.69
1:AH:40:PRO:HG3	1:CL:87:THR:HG22	1.74	0.69
1:AV:49:MET:HE2	1:AV:52:THR:HG21	1.74	0.69
1:AJ:49:MET:HE2	1:AJ:52:THR:HG21	1.74	0.69
1:AY:87:THR:HG22	1:DB:40:PRO:HG3	1.74	0.69
1:CL:49:MET:HE2	1:CL:52:THR:HG21	1.74	0.69
1:AB:40:PRO:HG3	1:CU:87:THR:HG22	1.74	0.69
1:CF:49:MET:HE2	1:CF:52:THR:HG21	1.74	0.69
1:CJ:25:ARG:NH2	1:CO:145:PRO:O	2.25	0.69
1:BK:49:MET:HE2	1:BK:52:THR:HG21	1.74	0.69
1:CU:45:PRO:HB3	1:CV:205:MET:HE3	1.75	0.69
1:DA:45:PRO:HB3	1:DB:205:MET:HE3	1.75	0.69
1:DD:49:MET:HE2	1:DD:52:THR:HG21	1.74	0.69
1:AD:45:PRO:HB3	1:AE:205:MET:HE3	1.75	0.68
1:AM:45:PRO:HB3	1:AN:205:MET:HE3	1.75	0.68
1:AM:49:MET:HE2	1:AM:52:THR:HG21	1.74	0.68
1:BZ:45:PRO:HB3	1:CA:205:MET:HE3	1.76	0.68
1:BE:45:PRO:HB3	1:BF:205:MET:HE3	1.75	0.68
1:BW:45:PRO:HB3	1:BX:205:MET:HE3	1.75	0.68
1:CC:45:PRO:HB3	1:CD:205:MET:HE3	1.75	0.68
1:CF:45:PRO:HB3	1:CG:205:MET:HE3	1.75	0.68
1:CX:45:PRO:HB3	1:CY:205:MET:HE3	1.75	0.68
1:DJ:45:PRO:HB3	1:DK:205:MET:HE3	1.75	0.68
1:BB:45:PRO:HB3	1:BC:205:MET:HE3	1.75	0.68
1:AG:45:PRO:HB3	1:AH:205:MET:HE3	1.75	0.68
1:AS:45:PRO:HB3	1:AT:205:MET:HE3	1.75	0.68
1:BN:45:PRO:HB3	1:BO:205:MET:HE3	1.75	0.68
1:BT:49:MET:HE2	1:BT:52:THR:HG21	1.74	0.68
1:CX:49:MET:HE2	1:CX:52:THR:HG21	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:45:PRO:HB3	1:AB:205:MET:HE3	1.75	0.68
1:BQ:45:PRO:HB3	1:BR:205:MET:HE3	1.75	0.68
1:BS:181:MET:HE1	1:DL:181:MET:HE1	1.76	0.68
1:DG:45:PRO:HB3	1:DH:205:MET:HE3	1.75	0.68
1:AD:87:THR:HG22	1:AT:40:PRO:HG3	1.74	0.67
1:BL:25:ARG:NH2	1:BT:145:PRO:O	2.27	0.67
1:BT:45:PRO:HB3	1:BU:205:MET:HE3	1.75	0.67
1:CI:49:MET:HE2	1:CI:52:THR:HG21	1.74	0.67
1:DD:45:PRO:HB3	1:DE:205:MET:HE3	1.75	0.67
1:AQ:25:ARG:NH2	1:CC:145:PRO:O	2.27	0.67
1:AY:45:PRO:HB3	1:AZ:205:MET:HE3	1.75	0.67
1:CL:45:PRO:HB3	1:CM:205:MET:HE3	1.75	0.67
1:AP:45:PRO:HB3	1:AQ:205:MET:HE3	1.76	0.67
1:BG:181:MET:HE1	1:CZ:181:MET:HE1	1.76	0.67
1:AY:145:PRO:O	1:BF:25:ARG:NH2	2.28	0.67
1:AJ:45:PRO:HB3	1:AK:205:MET:HE3	1.75	0.67
1:AV:45:PRO:HB3	1:AW:205:MET:HE3	1.75	0.67
1:CO:45:PRO:HB3	1:CP:205:MET:HE3	1.75	0.67
1:AF:205:MET:HE2	1:CE:45:PRO:HA	1.75	0.67
1:BH:45:PRO:HB3	1:BI:205:MET:HE3	1.75	0.67
1:AG:145:PRO:O	1:CM:25:ARG:NH2	2.28	0.67
1:CR:45:PRO:HB3	1:CS:205:MET:HE3	1.75	0.67
1:CI:45:PRO:HB3	1:CJ:205:MET:HE3	1.75	0.66
1:BJ:181:MET:HE1	1:DC:181:MET:HE1	1.78	0.66
1:AF:102:MET:HE2	1:CC:15:MET:HB2	1.78	0.66
1:BE:15:MET:HB2	1:CZ:102:MET:HE2	1.76	0.66
1:BD:181:MET:HE1	1:CW:181:MET:HE1	1.77	0.66
1:AF:181:MET:HE1	1:CE:181:MET:HE1	1.75	0.66
1:AT:25:ARG:NH2	1:BW:145:PRO:O	2.28	0.66
1:BK:45:PRO:HB3	1:BL:205:MET:HE3	1.75	0.66
1:CG:25:ARG:NH2	1:CI:145:PRO:O	2.28	0.66
1:AL:129:ASN:HD21	1:CJ:102:MET:HA	1.61	0.65
1:BS:102:MET:HE2	1:DJ:15:MET:HB2	1.78	0.65
1:CA:25:ARG:NH2	1:CU:145:PRO:O	2.29	0.65
1:AI:98:GLY:HA3	1:AI:101:LEU:HD12	1.79	0.65
1:AR:98:GLY:HA3	1:AR:101:LEU:HD12	1.79	0.65
1:BD:98:GLY:HA3	1:BD:101:LEU:HD12	1.79	0.65
1:BQ:15:MET:HB2	1:DL:102:MET:HE2	1.79	0.65
1:BS:98:GLY:HA3	1:BS:101:LEU:HD12	1.79	0.65
1:AD:145:PRO:O	1:CS:25:ARG:NH2	2.30	0.65
1:BJ:98:GLY:HA3	1:BJ:101:LEU:HD12	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:98:GLY:HA3	1:CE:101:LEU:HD12	1.79	0.65
1:CK:98:GLY:HA3	1:CK:101:LEU:HD12	1.79	0.65
1:CN:98:GLY:HA3	1:CN:101:LEU:HD12	1.79	0.65
1:DI:98:GLY:HA3	1:DI:101:LEU:HD12	1.79	0.65
1:AF:129:ASN:HD21	1:CD:102:MET:HA	1.61	0.65
1:AL:102:MET:HE2	1:CI:15:MET:HB2	1.78	0.65
1:BA:98:GLY:HA3	1:BA:101:LEU:HD12	1.79	0.65
1:BH:15:MET:HB2	1:DC:102:MET:HE2	1.79	0.64
1:AF:98:GLY:HA3	1:AF:101:LEU:HD12	1.79	0.64
1:BH:145:PRO:O	1:DH:25:ARG:NH2	2.29	0.64
1:BG:98:GLY:HA3	1:BG:101:LEU:HD12	1.79	0.64
1:BM:102:MET:HE2	1:DD:15:MET:HB2	1.78	0.64
1:CD:25:ARG:NH2	1:CX:145:PRO:O	2.30	0.64
1:CW:98:GLY:HA3	1:CW:101:LEU:HD12	1.79	0.64
1:AB:25:ARG:NH2	1:AJ:145:PRO:O	2.30	0.64
1:AC:98:GLY:HA3	1:AC:101:LEU:HD12	1.79	0.64
1:BY:98:GLY:HA3	1:BY:101:LEU:HD12	1.79	0.64
1:CQ:98:GLY:HA3	1:CQ:101:LEU:HD12	1.79	0.64
1:CT:98:GLY:HA3	1:CT:101:LEU:HD12	1.79	0.64
1:DC:98:GLY:HA3	1:DC:101:LEU:HD12	1.79	0.64
1:BK:15:MET:HB2	1:DF:102:MET:HE2	1.80	0.64
1:BP:98:GLY:HA3	1:BP:101:LEU:HD12	1.79	0.64
1:AH:98:GLY:HA3	1:AH:101:LEU:HD12	1.80	0.64
1:AX:98:GLY:HA3	1:AX:101:LEU:HD12	1.79	0.64
1:DF:98:GLY:HA3	1:DF:101:LEU:HD12	1.79	0.64
1:BM:181:MET:HE1	1:DF:181:MET:HE1	1.79	0.64
1:BX:98:GLY:HA3	1:BX:101:LEU:HD12	1.80	0.64
1:CB:98:GLY:HA3	1:CB:101:LEU:HD12	1.79	0.64
1:DE:98:GLY:HA3	1:DE:101:LEU:HD12	1.80	0.64
1:DL:98:GLY:HA3	1:DL:101:LEU:HD12	1.79	0.64
1:AK:98:GLY:HA3	1:AK:101:LEU:HD12	1.80	0.64
1:BM:98:GLY:HA3	1:BM:101:LEU:HD12	1.79	0.64
1:BU:98:GLY:HA3	1:BU:101:LEU:HD12	1.80	0.64
1:CD:98:GLY:HA3	1:CD:101:LEU:HD12	1.80	0.64
1:CG:98:GLY:HA3	1:CG:101:LEU:HD12	1.80	0.64
1:BO:98:GLY:HA3	1:BO:101:LEU:HD12	1.80	0.64
1:CY:98:GLY:HA3	1:CY:101:LEU:HD12	1.80	0.64
1:AO:98:GLY:HA3	1:AO:101:LEU:HD12	1.79	0.63
1:AU:98:GLY:HA3	1:AU:101:LEU:HD12	1.79	0.63
1:BV:98:GLY:HA3	1:BV:101:LEU:HD12	1.79	0.63
1:BL:98:GLY:HA3	1:BL:101:LEU:HD12	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:15:MET:HB2	1:CK:102:MET:HE2	1.79	0.63
1:AN:25:ARG:NH2	1:BZ:145:PRO:O	2.32	0.63
1:BG:102:MET:HE2	1:CX:15:MET:HB2	1.80	0.63
1:BR:98:GLY:HA3	1:BR:101:LEU:HD12	1.80	0.63
1:AB:98:GLY:HA3	1:AB:101:LEU:HD12	1.80	0.63
1:BB:15:MET:HB2	1:CW:102:MET:HE2	1.80	0.63
1:CA:98:GLY:HA3	1:CA:101:LEU:HD12	1.80	0.63
1:BF:98:GLY:HA3	1:BF:101:LEU:HD12	1.80	0.63
1:BM:102:MET:CE	1:DD:15:MET:HB2	2.28	0.63
1:BS:129:ASN:HD21	1:DK:102:MET:HA	1.64	0.63
1:CH:98:GLY:HA3	1:CH:101:LEU:HD12	1.79	0.63
1:CJ:98:GLY:HA3	1:CJ:101:LEU:HD12	1.80	0.63
1:AN:98:GLY:HA3	1:AN:101:LEU:HD12	1.80	0.63
1:CS:98:GLY:HA3	1:CS:101:LEU:HD12	1.80	0.63
1:CZ:98:GLY:HA3	1:CZ:101:LEU:HD12	1.79	0.63
1:BK:15:MET:HB2	1:DF:102:MET:CE	2.29	0.63
1:DH:98:GLY:HA3	1:DH:101:LEU:HD12	1.80	0.63
1:CP:98:GLY:HA3	1:CP:101:LEU:HD12	1.80	0.62
1:AY:15:MET:HB2	1:CT:102:MET:HE2	1.81	0.62
1:AL:98:GLY:HA3	1:AL:101:LEU:HD12	1.79	0.62
1:AT:98:GLY:HA3	1:AT:101:LEU:HD12	1.80	0.62
1:AU:181:MET:HE1	1:CQ:181:MET:HE1	1.79	0.62
1:AZ:98:GLY:HA3	1:AZ:101:LEU:HD12	1.80	0.62
1:CM:98:GLY:HA3	1:CM:101:LEU:HD12	1.80	0.62
1:DK:98:GLY:HA3	1:DK:101:LEU:HD12	1.80	0.62
1:AE:98:GLY:HA3	1:AE:101:LEU:HD12	1.80	0.62
1:BC:98:GLY:HA3	1:BC:101:LEU:HD12	1.80	0.62
1:AC:181:MET:HE1	1:BY:181:MET:HE1	1.81	0.62
1:AR:102:MET:HE2	1:CL:15:MET:HB2	1.80	0.62
1:AS:15:MET:HB2	1:CQ:102:MET:HE2	1.82	0.62
1:CV:98:GLY:HA3	1:CV:101:LEU:HD12	1.80	0.62
1:AC:102:MET:HE2	1:BW:15:MET:HB2	1.82	0.62
1:CD:65:ARG:NH1	1:CD:127:ASP:OD1	2.33	0.62
1:CM:65:ARG:NH1	1:CM:127:ASP:OD1	2.33	0.62
1:DB:98:GLY:HA3	1:DB:101:LEU:HD12	1.80	0.62
1:DE:65:ARG:NH1	1:DE:127:ASP:OD1	2.33	0.62
1:AN:65:ARG:NH1	1:AN:127:ASP:OD1	2.33	0.61
1:BC:65:ARG:NH1	1:BC:127:ASP:OD1	2.33	0.61
1:BL:65:ARG:NH1	1:BL:127:ASP:OD1	2.33	0.61
1:DB:65:ARG:NH1	1:DB:127:ASP:OD1	2.33	0.61
1:AB:65:ARG:NH1	1:AB:127:ASP:OD1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:102:MET:HE2	1:CU:15:MET:HB2	1.81	0.61
1:BI:65:ARG:NH1	1:BI:127:ASP:OD1	2.33	0.61
1:BU:65:ARG:NH1	1:BU:127:ASP:OD1	2.33	0.61
1:AK:65:ARG:NH1	1:AK:127:ASP:OD1	2.33	0.61
1:AU:102:MET:HE2	1:CO:15:MET:HB2	1.81	0.61
1:AZ:65:ARG:NH1	1:AZ:127:ASP:OD1	2.33	0.61
1:BA:181:MET:HE1	1:CT:181:MET:HE1	1.81	0.61
1:CG:65:ARG:NH1	1:CG:127:ASP:OD1	2.33	0.61
1:CY:65:ARG:NH1	1:CY:127:ASP:OD1	2.33	0.61
1:AW:98:GLY:HA3	1:AW:101:LEU:HD12	1.80	0.61
1:BI:98:GLY:HA3	1:BI:101:LEU:HD12	1.80	0.61
1:DK:65:ARG:NH1	1:DK:127:ASP:OD1	2.33	0.61
1:AQ:98:GLY:HA3	1:AQ:101:LEU:HD12	1.80	0.61
1:DH:65:ARG:NH1	1:DH:127:ASP:OD1	2.33	0.61
1:AE:102:MET:HA	1:CE:129:ASN:HD21	1.66	0.61
1:BE:15:MET:HB2	1:CZ:102:MET:CE	2.30	0.61
1:AH:65:ARG:NH1	1:AH:127:ASP:OD1	2.33	0.61
1:AR:181:MET:HE1	1:CN:181:MET:HE1	1.81	0.61
1:BO:65:ARG:NH1	1:BO:127:ASP:OD1	2.33	0.61
1:CA:65:ARG:NH1	1:CA:127:ASP:OD1	2.33	0.61
1:BJ:102:MET:HE2	1:DA:15:MET:HB2	1.81	0.61
1:AE:65:ARG:NH1	1:AE:127:ASP:OD1	2.33	0.60
1:CJ:65:ARG:NH1	1:CJ:127:ASP:OD1	2.33	0.60
1:CP:65:ARG:NH1	1:CP:127:ASP:OD1	2.33	0.60
1:CV:65:ARG:NH1	1:CV:127:ASP:OD1	2.33	0.60
1:BG:102:MET:CE	1:CX:15:MET:HB2	2.31	0.60
1:BR:65:ARG:NH1	1:BR:127:ASP:OD1	2.33	0.60
1:BR:102:MET:HA	1:DL:129:ASN:HD21	1.66	0.60
1:AK:102:MET:HA	1:CK:129:ASN:HD21	1.66	0.60
1:BP:181:MET:HE1	1:DI:181:MET:HE1	1.82	0.60
1:BX:65:ARG:NH1	1:BX:127:ASP:OD1	2.33	0.60
1:CS:65:ARG:NH1	1:CS:127:ASP:OD1	2.33	0.60
1:AT:65:ARG:NH1	1:AT:127:ASP:OD1	2.33	0.60
1:BN:15:MET:HB2	1:DI:102:MET:HE2	1.82	0.60
1:CJ:106:THR:OG1	1:CJ:123:ILE:HG22	2.02	0.60
1:AQ:65:ARG:NH1	1:AQ:127:ASP:OD1	2.33	0.60
1:BH:15:MET:HB2	1:DC:102:MET:CE	2.31	0.60
1:BI:106:THR:OG1	1:BI:123:ILE:HG22	2.02	0.60
1:AZ:102:MET:HA	1:CT:129:ASN:HD21	1.67	0.60
1:BC:106:THR:OG1	1:BC:123:ILE:HG22	2.02	0.60
1:BX:106:THR:OG1	1:BX:123:ILE:HG22	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:106:THR:OG1	1:AN:123:ILE:HG22	2.02	0.60
1:AF:65:ARG:HD3	1:CE:163:GLY:H	1.67	0.60
1:BF:65:ARG:NH1	1:BF:127:ASP:OD1	2.33	0.60
1:AD:15:MET:HB2	1:CE:102:MET:HE2	1.82	0.60
1:AW:65:ARG:NH1	1:AW:127:ASP:OD1	2.33	0.60
1:CS:106:THR:OG1	1:CS:123:ILE:HG22	2.02	0.60
1:CV:106:THR:OG1	1:CV:123:ILE:HG22	2.02	0.60
1:CY:106:THR:OG1	1:CY:123:ILE:HG22	2.02	0.60
1:DK:106:THR:OG1	1:DK:123:ILE:HG22	2.02	0.60
1:AP:15:MET:HB2	1:CN:102:MET:HE2	1.83	0.59
1:AQ:106:THR:OG1	1:AQ:123:ILE:HG22	2.02	0.59
1:DB:106:THR:OG1	1:DB:123:ILE:HG22	2.02	0.59
1:AK:106:THR:OG1	1:AK:123:ILE:HG22	2.02	0.59
1:AZ:106:THR:OG1	1:AZ:123:ILE:HG22	2.02	0.59
1:BP:102:MET:HE2	1:DG:15:MET:HB2	1.84	0.59
1:CA:106:THR:OG1	1:CA:123:ILE:HG22	2.02	0.59
1:AH:106:THR:OG1	1:AH:123:ILE:HG22	2.02	0.59
1:AT:106:THR:OG1	1:AT:123:ILE:HG22	2.02	0.59
1:AA:15:MET:HB2	1:BY:102:MET:HE2	1.84	0.59
1:AE:106:THR:OG1	1:AE:123:ILE:HG22	2.02	0.59
1:AL:65:ARG:HD3	1:CK:163:GLY:H	1.67	0.59
1:CM:106:THR:OG1	1:CM:123:ILE:HG22	2.02	0.59
1:BJ:102:MET:CE	1:DA:15:MET:HB2	2.32	0.59
1:BR:106:THR:OG1	1:BR:123:ILE:HG22	2.02	0.59
1:BO:106:THR:OG1	1:BO:123:ILE:HG22	2.02	0.59
1:CD:106:THR:OG1	1:CD:123:ILE:HG22	2.02	0.59
1:BS:102:MET:CE	1:DJ:15:MET:HB2	2.33	0.59
1:AU:129:ASN:HD21	1:CP:102:MET:HA	1.68	0.59
1:BD:129:ASN:HD21	1:CV:102:MET:HA	1.67	0.59
1:BA:163:GLY:H	1:CT:65:ARG:HD3	1.68	0.58
1:BL:106:THR:OG1	1:BL:123:ILE:HG22	2.02	0.58
1:BU:106:THR:OG1	1:BU:123:ILE:HG22	2.02	0.58
1:CP:106:THR:OG1	1:CP:123:ILE:HG22	2.02	0.58
1:DE:106:THR:OG1	1:DE:123:ILE:HG22	2.02	0.58
1:DH:106:THR:OG1	1:DH:123:ILE:HG22	2.02	0.58
1:AL:102:MET:CE	1:CI:15:MET:HB2	2.33	0.58
1:BB:15:MET:HB2	1:CW:102:MET:CE	2.33	0.58
1:BF:106:THR:OG1	1:BF:123:ILE:HG22	2.02	0.58
1:BM:38:ALA:HA	1:DF:201:SER:HB2	1.84	0.58
1:AC:102:MET:CE	1:BW:15:MET:HB2	2.34	0.58
1:AL:38:ALA:HA	1:CK:201:SER:HB2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:106:THR:OG1	1:AW:123:ILE:HG22	2.02	0.58
1:BX:167:ASN:HA	1:BX:170:PHE:HD2	1.69	0.58
1:AB:106:THR:OG1	1:AB:123:ILE:HG22	2.02	0.58
1:AK:167:ASN:HA	1:AK:170:PHE:HD2	1.69	0.58
1:BQ:15:MET:HB2	1:DL:102:MET:CE	2.33	0.58
1:BR:167:ASN:HA	1:BR:170:PHE:HD2	1.69	0.58
1:CG:106:THR:OG1	1:CG:123:ILE:HG22	2.02	0.58
1:AQ:167:ASN:HA	1:AQ:170:PHE:HD2	1.69	0.58
1:AT:167:ASN:HA	1:AT:170:PHE:HD2	1.69	0.58
1:AZ:167:ASN:HA	1:AZ:170:PHE:HD2	1.69	0.58
1:BG:38:ALA:HA	1:CZ:201:SER:HB2	1.84	0.58
1:AF:102:MET:CE	1:CC:15:MET:HB2	2.33	0.58
1:BF:167:ASN:HA	1:BF:170:PHE:HD2	1.69	0.58
1:CY:167:ASN:HA	1:CY:170:PHE:HD2	1.69	0.58
1:AW:167:ASN:HA	1:AW:170:PHE:HD2	1.69	0.58
1:BC:102:MET:HA	1:CW:129:ASN:HD21	1.68	0.58
1:AF:65:ARG:NH2	1:CE:162:THR:HB	2.18	0.58
1:AL:65:ARG:NH2	1:CK:162:THR:HB	2.19	0.58
1:CG:167:ASN:HA	1:CG:170:PHE:HD2	1.69	0.58
1:CS:167:ASN:HA	1:CS:170:PHE:HD2	1.69	0.58
1:AB:167:ASN:HA	1:AB:170:PHE:HD2	1.69	0.58
1:AU:65:ARG:HD3	1:CQ:163:GLY:H	1.69	0.58
1:BD:102:MET:CE	1:CU:15:MET:HB2	2.33	0.58
1:BI:102:MET:HA	1:DC:129:ASN:HD21	1.68	0.58
1:AE:167:ASN:HA	1:AE:170:PHE:HD2	1.69	0.57
1:AF:162:THR:HB	1:CE:65:ARG:NH2	2.19	0.57
1:BF:102:MET:HA	1:CZ:129:ASN:HD21	1.68	0.57
1:BI:167:ASN:HA	1:BI:170:PHE:HD2	1.69	0.57
1:AF:163:GLY:H	1:CE:65:ARG:HD3	1.68	0.57
1:AJ:15:MET:HB2	1:CK:102:MET:CE	2.33	0.57
1:BC:167:ASN:HA	1:BC:170:PHE:HD2	1.69	0.57
1:BS:65:ARG:NH2	1:DL:162:THR:HB	2.19	0.57
1:BU:167:ASN:HA	1:BU:170:PHE:HD2	1.69	0.57
1:CJ:167:ASN:HA	1:CJ:170:PHE:HD2	1.69	0.57
1:BA:102:MET:HE2	1:CR:15:MET:HB2	1.86	0.57
1:BS:65:ARG:HD3	1:DL:163:GLY:H	1.69	0.57
1:AS:15:MET:HB2	1:CQ:102:MET:CE	2.34	0.57
1:AS:106:THR:OG1	1:AS:123:ILE:HG22	2.05	0.57
1:BD:38:ALA:HA	1:CW:201:SER:HB2	1.86	0.57
1:BT:106:THR:OG1	1:BT:123:ILE:HG22	2.05	0.57
1:CV:167:ASN:HA	1:CV:170:PHE:HD2	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CX:106:THR:OG1	1:CX:123:ILE:HG22	2.05	0.57
1:DB:167:ASN:HA	1:DB:170:PHE:HD2	1.69	0.57
1:AV:106:THR:OG1	1:AV:123:ILE:HG22	2.05	0.57
1:AY:106:THR:OG1	1:AY:123:ILE:HG22	2.05	0.57
1:BS:163:GLY:H	1:DL:65:ARG:HD3	1.70	0.57
1:CF:106:THR:OG1	1:CF:123:ILE:HG22	2.05	0.57
1:DH:167:ASN:HA	1:DH:170:PHE:HD2	1.69	0.57
1:AP:106:THR:OG1	1:AP:123:ILE:HG22	2.05	0.57
1:BE:106:THR:OG1	1:BE:123:ILE:HG22	2.05	0.57
1:BO:167:ASN:HA	1:BO:170:PHE:HD2	1.69	0.57
1:DI:100:ARG:HH11	1:DI:134:LEU:HB3	1.70	0.57
1:DJ:106:THR:OG1	1:DJ:123:ILE:HG22	2.05	0.57
1:DL:100:ARG:HH11	1:DL:134:LEU:HB3	1.70	0.57
1:AA:15:MET:HB2	1:BY:102:MET:CE	2.34	0.57
1:AJ:106:THR:OG1	1:AJ:123:ILE:HG22	2.05	0.57
1:BS:100:ARG:HH11	1:BS:134:LEU:HB3	1.70	0.57
1:CP:167:ASN:HA	1:CP:170:PHE:HD2	1.69	0.57
1:AF:201:SER:HB2	1:CE:38:ALA:HA	1.85	0.57
1:AO:100:ARG:HH11	1:AO:134:LEU:HB3	1.70	0.57
1:AR:102:MET:CE	1:CL:15:MET:HB2	2.34	0.57
1:BW:106:THR:OG1	1:BW:123:ILE:HG22	2.05	0.57
1:CM:167:ASN:HA	1:CM:170:PHE:HD2	1.69	0.57
1:CZ:100:ARG:HH11	1:CZ:134:LEU:HB3	1.70	0.57
1:AG:106:THR:OG1	1:AG:123:ILE:HG22	2.05	0.56
1:AL:100:ARG:HH11	1:AL:134:LEU:HB3	1.70	0.56
1:AM:106:THR:OG1	1:AM:123:ILE:HG22	2.05	0.56
1:AU:100:ARG:HH11	1:AU:134:LEU:HB3	1.70	0.56
1:BB:106:THR:OG1	1:BB:123:ILE:HG22	2.05	0.56
1:BD:100:ARG:HH11	1:BD:134:LEU:HB3	1.70	0.56
1:BV:100:ARG:HH11	1:BV:134:LEU:HB3	1.70	0.56
1:BZ:106:THR:OG1	1:BZ:123:ILE:HG22	2.05	0.56
1:CB:100:ARG:HH11	1:CB:134:LEU:HB3	1.70	0.56
1:CH:100:ARG:HH11	1:CH:134:LEU:HB3	1.70	0.56
1:CR:106:THR:OG1	1:CR:123:ILE:HG22	2.05	0.56
1:DK:167:ASN:HA	1:DK:170:PHE:HD2	1.69	0.56
1:BN:15:MET:HB2	1:DI:102:MET:CE	2.34	0.56
1:BP:100:ARG:HH11	1:BP:134:LEU:HB3	1.70	0.56
1:CT:100:ARG:HH11	1:CT:134:LEU:HB3	1.70	0.56
1:DD:106:THR:OG1	1:DD:123:ILE:HG22	2.05	0.56
1:AD:15:MET:HB2	1:CE:102:MET:CE	2.35	0.56
1:AD:106:THR:OG1	1:AD:123:ILE:HG22	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:167:ASN:HA	1:AN:170:PHE:HD2	1.69	0.56
1:AT:102:MET:HA	1:CQ:129:ASN:HD21	1.70	0.56
1:AX:100:ARG:HH11	1:AX:134:LEU:HB3	1.70	0.56
1:BA:102:MET:CE	1:CR:15:MET:HB2	2.36	0.56
1:BA:162:THR:HB	1:CT:65:ARG:NH2	2.21	0.56
1:BK:106:THR:OG1	1:BK:123:ILE:HG22	2.05	0.56
1:BN:106:THR:OG1	1:BN:123:ILE:HG22	2.05	0.56
1:BP:102:MET:CE	1:DG:15:MET:HB2	2.34	0.56
1:BS:162:THR:HB	1:DL:65:ARG:NH2	2.20	0.56
1:CU:106:THR:OG1	1:CU:123:ILE:HG22	2.05	0.56
1:DE:167:ASN:HA	1:DE:170:PHE:HD2	1.69	0.56
1:AC:100:ARG:HH11	1:AC:134:LEU:HB3	1.70	0.56
1:BJ:201:SER:HB2	1:DC:38:ALA:HA	1.87	0.56
1:BY:100:ARG:HH11	1:BY:134:LEU:HB3	1.70	0.56
1:CI:106:THR:OG1	1:CI:123:ILE:HG22	2.05	0.56
1:DA:106:THR:OG1	1:DA:123:ILE:HG22	2.05	0.56
1:AF:167:ASN:HA	1:AF:170:PHE:HD2	1.71	0.56
1:AP:15:MET:HB2	1:CN:102:MET:CE	2.35	0.56
1:AR:129:ASN:HD21	1:CM:102:MET:HA	1.70	0.56
1:BJ:100:ARG:HH11	1:BJ:134:LEU:HB3	1.70	0.56
1:BL:167:ASN:HA	1:BL:170:PHE:HD2	1.69	0.56
1:CQ:167:ASN:HA	1:CQ:170:PHE:HD2	1.71	0.56
1:DC:100:ARG:HH11	1:DC:134:LEU:HB3	1.70	0.56
1:DG:106:THR:OG1	1:DG:123:ILE:HG22	2.05	0.56
1:AR:167:ASN:HA	1:AR:170:PHE:HD2	1.71	0.56
1:AU:102:MET:CE	1:CO:15:MET:HB2	2.34	0.56
1:AY:15:MET:HB2	1:CT:102:MET:CE	2.34	0.56
1:BG:129:ASN:HD21	1:CY:102:MET:HA	1.70	0.56
1:BG:167:ASN:HA	1:BG:170:PHE:HD2	1.71	0.56
1:BP:167:ASN:HA	1:BP:170:PHE:HD2	1.71	0.56
1:BY:167:ASN:HA	1:BY:170:PHE:HD2	1.71	0.56
1:CA:167:ASN:HA	1:CA:170:PHE:HD2	1.69	0.56
1:CE:167:ASN:HA	1:CE:170:PHE:HD2	1.71	0.56
1:DF:100:ARG:HH11	1:DF:134:LEU:HB3	1.70	0.56
1:AA:106:THR:OG1	1:AA:123:ILE:HG22	2.05	0.56
1:AR:100:ARG:HH11	1:AR:134:LEU:HB3	1.70	0.56
1:AU:65:ARG:NH2	1:CQ:162:THR:HB	2.20	0.56
1:AX:167:ASN:HA	1:AX:170:PHE:HD2	1.71	0.56
1:BD:167:ASN:HA	1:BD:170:PHE:HD2	1.71	0.56
1:BQ:106:THR:OG1	1:BQ:123:ILE:HG22	2.05	0.56
1:CL:106:THR:OG1	1:CL:123:ILE:HG22	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:26:THR:HG21	1:CO:20:PRO:HG3	1.86	0.56
1:AE:89:HIS:ND1	1:AE:111:ASP:OD1	2.35	0.56
1:BD:65:ARG:HD3	1:CW:163:GLY:H	1.70	0.56
1:BM:100:ARG:HH11	1:BM:134:LEU:HB3	1.70	0.56
1:CO:106:THR:OG1	1:CO:123:ILE:HG22	2.05	0.56
1:AO:167:ASN:HA	1:AO:170:PHE:HD2	1.71	0.56
1:CC:106:THR:OG1	1:CC:123:ILE:HG22	2.05	0.56
1:CN:167:ASN:HA	1:CN:170:PHE:HD2	1.71	0.56
1:DL:167:ASN:HA	1:DL:170:PHE:HD2	1.71	0.56
1:AL:167:ASN:HA	1:AL:170:PHE:HD2	1.71	0.56
1:CQ:100:ARG:HH11	1:CQ:134:LEU:HB3	1.70	0.56
1:AU:167:ASN:HA	1:AU:170:PHE:HD2	1.71	0.55
1:BH:106:THR:OG1	1:BH:123:ILE:HG22	2.05	0.55
1:BI:89:HIS:ND1	1:BI:111:ASP:OD1	2.35	0.55
1:BM:201:SER:HB2	1:DF:38:ALA:HA	1.88	0.55
1:BV:167:ASN:HA	1:BV:170:PHE:HD2	1.71	0.55
1:DF:167:ASN:HA	1:DF:170:PHE:HD2	1.71	0.55
1:AF:100:ARG:HH11	1:AF:134:LEU:HB3	1.70	0.55
1:BJ:38:ALA:HA	1:DC:201:SER:HB2	1.87	0.55
1:BS:201:SER:HB2	1:DL:38:ALA:HA	1.88	0.55
1:CH:167:ASN:HA	1:CH:170:PHE:HD2	1.71	0.55
1:CN:100:ARG:HH11	1:CN:134:LEU:HB3	1.70	0.55
1:AI:100:ARG:HH11	1:AI:134:LEU:HB3	1.70	0.55
1:BD:65:ARG:NH2	1:CW:162:THR:HB	2.21	0.55
1:CE:100:ARG:HH11	1:CE:134:LEU:HB3	1.70	0.55
1:BS:38:ALA:HA	1:DL:201:SER:HB2	1.88	0.55
1:BS:167:ASN:HA	1:BS:170:PHE:HD2	1.71	0.55
1:CZ:167:ASN:HA	1:CZ:170:PHE:HD2	1.71	0.55
1:AQ:95:THR:HB	1:AR:165:ASP:HB3	1.89	0.55
1:BD:163:GLY:H	1:CW:65:ARG:HD3	1.71	0.55
1:BG:100:ARG:HH11	1:BG:134:LEU:HB3	1.70	0.55
1:BG:201:SER:HB2	1:CZ:38:ALA:HA	1.89	0.55
1:BI:95:THR:HB	1:BJ:165:ASP:HB3	1.89	0.55
1:BJ:167:ASN:HA	1:BJ:170:PHE:HD2	1.71	0.55
1:BR:89:HIS:ND1	1:BR:111:ASP:OD1	2.35	0.55
1:BX:95:THR:HB	1:BY:165:ASP:HB3	1.89	0.55
1:CW:100:ARG:HH11	1:CW:134:LEU:HB3	1.70	0.55
1:CW:167:ASN:HA	1:CW:170:PHE:HD2	1.71	0.55
1:DC:167:ASN:HA	1:DC:170:PHE:HD2	1.71	0.55
1:AH:167:ASN:HA	1:AH:170:PHE:HD2	1.69	0.55
1:AI:167:ASN:HA	1:AI:170:PHE:HD2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:201:SER:HB2	1:CK:38:ALA:HA	1.88	0.55
1:AZ:89:HIS:ND1	1:AZ:111:ASP:OD1	2.35	0.55
1:BL:95:THR:HB	1:BM:165:ASP:HB3	1.89	0.55
1:BM:167:ASN:HA	1:BM:170:PHE:HD2	1.71	0.55
1:BO:102:MET:HA	1:DI:129:ASN:HD21	1.72	0.55
1:DE:89:HIS:ND1	1:DE:111:ASP:OD1	2.35	0.55
1:DI:167:ASN:HA	1:DI:170:PHE:HD2	1.71	0.55
1:AC:65:ARG:HD3	1:BY:163:GLY:H	1.72	0.55
1:AE:95:THR:HB	1:AF:165:ASP:HB3	1.89	0.55
1:BC:95:THR:HB	1:BD:165:ASP:HB3	1.89	0.55
1:CD:167:ASN:HA	1:CD:170:PHE:HD2	1.69	0.55
1:CM:95:THR:HB	1:CN:165:ASP:HB3	1.89	0.55
1:CP:95:THR:HB	1:CQ:165:ASP:HB3	1.89	0.55
1:DE:95:THR:HB	1:DF:165:ASP:HB3	1.89	0.55
1:AC:167:ASN:HA	1:AC:170:PHE:HD2	1.71	0.55
1:AU:38:ALA:HA	1:CQ:201:SER:HB2	1.88	0.55
1:BA:100:ARG:HH11	1:BA:134:LEU:HB3	1.70	0.55
1:BK:76:LEU:HG	1:BK:94:THR:HG23	1.89	0.55
1:CO:76:LEU:HG	1:CO:94:THR:HG23	1.89	0.55
1:DB:95:THR:HB	1:DC:165:ASP:HB3	1.89	0.55
1:AA:76:LEU:HG	1:AA:94:THR:HG23	1.89	0.55
1:AC:129:ASN:HD21	1:BX:102:MET:HA	1.72	0.55
1:BF:95:THR:HB	1:BG:165:ASP:HB3	1.89	0.55
1:CA:95:THR:HB	1:CB:165:ASP:HB3	1.89	0.55
1:CC:18:GLN:OE1	1:CR:21:VAL:HG21	2.07	0.55
1:CT:167:ASN:HA	1:CT:170:PHE:HD2	1.71	0.55
1:AD:76:LEU:HG	1:AD:94:THR:HG23	1.89	0.55
1:BF:89:HIS:ND1	1:BF:111:ASP:OD1	2.35	0.55
1:BQ:76:LEU:HG	1:BQ:94:THR:HG23	1.89	0.55
1:BR:95:THR:HB	1:BS:165:ASP:HB3	1.89	0.55
1:CB:167:ASN:HA	1:CB:170:PHE:HD2	1.71	0.55
1:DJ:76:LEU:HG	1:DJ:94:THR:HG23	1.89	0.55
1:AR:163:GLY:H	1:CN:65:ARG:HD3	1.72	0.54
1:AY:76:LEU:HG	1:AY:94:THR:HG23	1.89	0.54
1:BU:95:THR:HB	1:BV:165:ASP:HB3	1.89	0.54
1:BZ:76:LEU:HG	1:BZ:94:THR:HG23	1.89	0.54
1:CK:100:ARG:HH11	1:CK:134:LEU:HB3	1.70	0.54
1:AM:76:LEU:HG	1:AM:94:THR:HG23	1.89	0.54
1:BO:89:HIS:ND1	1:BO:111:ASP:OD1	2.35	0.54
1:CD:95:THR:HB	1:CE:165:ASP:HB3	1.89	0.54
1:CK:167:ASN:HA	1:CK:170:PHE:HD2	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DA:76:LEU:HG	1:DA:94:THR:HG23	1.89	0.54
1:AK:95:THR:HB	1:AL:165:ASP:HB3	1.89	0.54
1:AL:163:GLY:H	1:CK:65:ARG:HD3	1.72	0.54
1:AR:39:ARG:NH2	1:CN:198:VAL:O	2.41	0.54
1:AR:65:ARG:HD3	1:CN:163:GLY:H	1.71	0.54
1:BW:76:LEU:HG	1:BW:94:THR:HG23	1.89	0.54
1:CX:76:LEU:HG	1:CX:94:THR:HG23	1.89	0.54
1:DH:95:THR:HB	1:DI:165:ASP:HB3	1.89	0.54
1:AF:38:ALA:HA	1:CE:201:SER:HB2	1.89	0.54
1:AH:95:THR:HB	1:AI:165:ASP:HB3	1.89	0.54
1:BH:26:THR:HG21	1:DJ:20:PRO:HG3	1.89	0.54
1:CJ:95:THR:HB	1:CK:165:ASP:HB3	1.89	0.54
1:CU:76:LEU:HG	1:CU:94:THR:HG23	1.89	0.54
1:DD:76:LEU:HG	1:DD:94:THR:HG23	1.89	0.54
1:AK:89:HIS:ND1	1:AK:111:ASP:OD1	2.35	0.54
1:CF:76:LEU:HG	1:CF:94:THR:HG23	1.89	0.54
1:AQ:102:MET:HA	1:CN:129:ASN:HD21	1.72	0.54
1:CL:76:LEU:HG	1:CL:94:THR:HG23	1.89	0.54
1:AJ:76:LEU:HG	1:AJ:94:THR:HG23	1.89	0.54
1:AN:95:THR:HB	1:AO:165:ASP:HB3	1.89	0.54
1:AV:76:LEU:HG	1:AV:94:THR:HG23	1.89	0.54
1:BD:201:SER:HB2	1:CW:38:ALA:HA	1.88	0.54
1:AA:18:GLN:OE1	1:AS:21:VAL:HG21	2.08	0.54
1:AF:39:ARG:NH2	1:CE:198:VAL:O	2.40	0.54
1:AU:163:GLY:H	1:CQ:65:ARG:HD3	1.72	0.54
1:BB:76:LEU:HG	1:BB:94:THR:HG23	1.89	0.54
1:BE:21:VAL:HG21	1:CR:18:GLN:OE1	2.08	0.54
1:DG:76:LEU:HG	1:DG:94:THR:HG23	1.89	0.54
1:DK:95:THR:HB	1:DL:165:ASP:HB3	1.89	0.54
1:CR:76:LEU:HG	1:CR:94:THR:HG23	1.89	0.54
1:AN:89:HIS:ND1	1:AN:111:ASP:OD1	2.35	0.54
1:BT:76:LEU:HG	1:BT:94:THR:HG23	1.89	0.54
1:CV:95:THR:HB	1:CW:165:ASP:HB3	1.89	0.54
1:AB:95:THR:HB	1:AC:165:ASP:HB3	1.89	0.53
1:AU:201:SER:HB2	1:CQ:38:ALA:HA	1.90	0.53
1:BA:167:ASN:HA	1:BA:170:PHE:HD2	1.71	0.53
1:BN:76:LEU:HG	1:BN:94:THR:HG23	1.89	0.53
1:CG:95:THR:HB	1:CH:165:ASP:HB3	1.89	0.53
1:CM:89:HIS:ND1	1:CM:111:ASP:OD1	2.35	0.53
1:BC:31:ASN:HD21	1:BI:22:GLN:HA	1.72	0.53
1:CF:28:PHE:CE2	1:CK:102:MET:HE1	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CS:95:THR:HB	1:CT:165:ASP:HB3	1.89	0.53
1:CY:95:THR:HB	1:CZ:165:ASP:HB3	1.89	0.53
1:AR:65:ARG:NH2	1:CN:162:THR:HB	2.23	0.53
1:AR:162:THR:HB	1:CN:65:ARG:NH2	2.23	0.53
1:AW:89:HIS:ND1	1:AW:111:ASP:OD1	2.35	0.53
1:BD:162:THR:HB	1:CW:65:ARG:NH2	2.23	0.53
1:BJ:129:ASN:HD21	1:DB:102:MET:HA	1.73	0.53
1:BP:163:GLY:H	1:DI:65:ARG:HD3	1.73	0.53
1:AT:95:THR:HB	1:AU:165:ASP:HB3	1.89	0.53
1:BA:201:SER:HB2	1:CT:38:ALA:HA	1.89	0.53
1:CI:76:LEU:HG	1:CI:94:THR:HG23	1.89	0.53
1:CJ:89:HIS:ND1	1:CJ:111:ASP:OD1	2.35	0.53
1:AJ:196:ARG:HA	1:AK:41:VAL:HB	1.91	0.53
1:AP:76:LEU:HG	1:AP:94:THR:HG23	1.89	0.53
1:AW:95:THR:HB	1:AX:165:ASP:HB3	1.89	0.53
1:BJ:163:GLY:H	1:DC:65:ARG:HD3	1.72	0.53
1:BP:38:ALA:HA	1:DI:201:SER:HB2	1.91	0.53
1:DD:196:ARG:HA	1:DE:41:VAL:HB	1.91	0.53
1:AC:65:ARG:NH2	1:BY:162:THR:HB	2.23	0.53
1:AG:76:LEU:HG	1:AG:94:THR:HG23	1.89	0.53
1:BE:20:PRO:HG3	1:CC:26:THR:HG21	1.91	0.53
1:CX:196:ARG:HA	1:CY:41:VAL:HB	1.91	0.53
1:AD:196:ARG:HA	1:AE:41:VAL:HB	1.91	0.53
1:AP:196:ARG:HA	1:AQ:41:VAL:HB	1.91	0.53
1:AY:28:PHE:CE2	1:DC:102:MET:HE1	2.44	0.53
1:AZ:95:THR:HB	1:BA:165:ASP:HB3	1.89	0.53
1:BN:196:ARG:HA	1:BO:41:VAL:HB	1.91	0.53
1:BQ:196:ARG:HA	1:BR:41:VAL:HB	1.91	0.53
1:CL:196:ARG:HA	1:CM:41:VAL:HB	1.91	0.53
1:CO:196:ARG:HA	1:CP:41:VAL:HB	1.91	0.53
1:CP:89:HIS:ND1	1:CP:111:ASP:OD1	2.35	0.53
1:AC:201:SER:HB2	1:BY:38:ALA:HA	1.89	0.53
1:BA:38:ALA:HA	1:CT:201:SER:HB2	1.90	0.53
1:BB:196:ARG:HA	1:BC:41:VAL:HB	1.91	0.53
1:BM:129:ASN:HD21	1:DE:102:MET:HA	1.74	0.53
1:BO:95:THR:HB	1:BP:165:ASP:HB3	1.89	0.53
1:CC:76:LEU:HG	1:CC:94:THR:HG23	1.89	0.53
1:CF:196:ARG:HA	1:CG:41:VAL:HB	1.91	0.53
1:CU:196:ARG:HA	1:CV:41:VAL:HB	1.91	0.53
1:AC:38:ALA:HA	1:BY:201:SER:HB2	1.90	0.53
1:AC:162:THR:HB	1:BY:65:ARG:NH2	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:196:ARG:HA	1:BI:41:VAL:HB	1.91	0.53
1:CV:89:HIS:ND1	1:CV:111:ASP:OD1	2.35	0.53
1:DA:196:ARG:HA	1:DB:41:VAL:HB	1.91	0.53
1:DK:89:HIS:ND1	1:DK:111:ASP:OD1	2.35	0.53
1:AS:76:LEU:HG	1:AS:94:THR:HG23	1.89	0.53
1:BE:76:LEU:HG	1:BE:94:THR:HG23	1.89	0.53
1:CG:89:HIS:ND1	1:CG:111:ASP:OD1	2.35	0.53
1:AB:102:MET:HA	1:BY:129:ASN:HD21	1.73	0.52
1:AG:196:ARG:HA	1:AH:41:VAL:HB	1.91	0.52
1:BH:76:LEU:HG	1:BH:94:THR:HG23	1.89	0.52
1:BW:20:PRO:HG3	1:CU:26:THR:HG21	1.91	0.52
1:BW:196:ARG:HA	1:BX:41:VAL:HB	1.91	0.52
1:DG:196:ARG:HA	1:DH:41:VAL:HB	1.91	0.52
1:AH:89:HIS:ND1	1:AH:111:ASP:OD1	2.35	0.52
1:AR:201:SER:HB2	1:CN:38:ALA:HA	1.89	0.52
1:BE:196:ARG:HA	1:BF:41:VAL:HB	1.91	0.52
1:BQ:20:PRO:HG3	1:BW:26:THR:HG21	1.91	0.52
1:CC:196:ARG:HA	1:CD:41:VAL:HB	1.91	0.52
1:CD:89:HIS:ND1	1:CD:111:ASP:OD1	2.35	0.52
1:CS:89:HIS:ND1	1:CS:111:ASP:OD1	2.35	0.52
1:BU:89:HIS:ND1	1:BU:111:ASP:OD1	2.35	0.52
1:CH:139:ILE:HG23	1:CH:140:PRO:HD2	1.92	0.52
1:DA:21:VAL:HG21	1:DD:18:GLN:OE1	2.09	0.52
1:DL:139:ILE:HG23	1:DL:140:PRO:HD2	1.92	0.52
1:AD:18:GLN:OE1	1:AP:21:VAL:HG21	2.10	0.52
1:AD:98:GLY:HA3	1:AD:101:LEU:HD12	1.92	0.52
1:AV:196:ARG:HA	1:AW:41:VAL:HB	1.91	0.52
1:BJ:162:THR:HB	1:DC:65:ARG:NH2	2.24	0.52
1:CI:196:ARG:HA	1:CJ:41:VAL:HB	1.91	0.52
1:AU:162:THR:HB	1:CQ:65:ARG:NH2	2.23	0.52
1:AX:139:ILE:HG23	1:AX:140:PRO:HD2	1.92	0.52
1:BV:139:ILE:HG23	1:BV:140:PRO:HD2	1.92	0.52
1:CR:196:ARG:HA	1:CS:41:VAL:HB	1.91	0.52
1:AL:129:ASN:ND2	1:CJ:102:MET:SD	2.82	0.52
1:AL:162:THR:HB	1:CK:65:ARG:NH2	2.24	0.52
1:AP:20:PRO:HG3	1:CO:26:THR:HG21	1.90	0.52
1:BA:65:ARG:HD3	1:CT:163:GLY:H	1.75	0.52
1:BP:139:ILE:HG23	1:BP:140:PRO:HD2	1.92	0.52
1:BS:208:ALA:HB2	1:BX:204:VAL:HG21	1.92	0.52
1:BT:196:ARG:HA	1:BU:41:VAL:HB	1.91	0.52
1:CR:98:GLY:HA3	1:CR:101:LEU:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CU:98:GLY:HA3	1:CU:101:LEU:HD12	1.92	0.52
1:CZ:139:ILE:HG23	1:CZ:140:PRO:HD2	1.92	0.52
1:AJ:18:GLN:OE1	1:CF:21:VAL:HG21	2.09	0.52
1:AM:196:ARG:HA	1:AN:41:VAL:HB	1.91	0.52
1:BD:139:ILE:HG23	1:BD:140:PRO:HD2	1.92	0.52
1:BM:139:ILE:HG23	1:BM:140:PRO:HD2	1.92	0.52
1:BT:21:VAL:HG21	1:CX:18:GLN:OE1	2.09	0.52
1:AR:139:ILE:HG23	1:AR:140:PRO:HD2	1.92	0.52
1:BN:98:GLY:HA3	1:BN:101:LEU:HD12	1.92	0.52
1:BP:201:SER:HB2	1:DI:38:ALA:HA	1.91	0.52
1:BW:28:PHE:CE2	1:DL:102:MET:HE1	2.45	0.52
1:BZ:98:GLY:HA3	1:BZ:101:LEU:HD12	1.92	0.52
1:CA:89:HIS:ND1	1:CA:111:ASP:OD1	2.35	0.52
1:AA:196:ARG:HA	1:AB:41:VAL:HB	1.91	0.52
1:AC:163:GLY:H	1:BY:65:ARG:HD3	1.73	0.52
1:AF:139:ILE:HG23	1:AF:140:PRO:HD2	1.92	0.52
1:BA:129:ASN:HD21	1:CS:102:MET:HA	1.75	0.52
1:BG:65:ARG:HD3	1:CZ:163:GLY:H	1.74	0.52
1:BT:98:GLY:HA3	1:BT:101:LEU:HD12	1.92	0.52
1:CC:98:GLY:HA3	1:CC:101:LEU:HD12	1.91	0.52
1:DJ:196:ARG:HA	1:DK:41:VAL:HB	1.91	0.52
1:AF:102:MET:HE1	1:CR:28:PHE:CE2	2.45	0.52
1:AG:98:GLY:HA3	1:AG:101:LEU:HD12	1.92	0.52
1:AO:139:ILE:HG23	1:AO:140:PRO:HD2	1.92	0.52
1:AQ:89:HIS:ND1	1:AQ:111:ASP:OD1	2.35	0.52
1:AS:196:ARG:HA	1:AT:41:VAL:HB	1.91	0.52
1:AU:139:ILE:HG23	1:AU:140:PRO:HD2	1.92	0.52
1:DA:98:GLY:HA3	1:DA:101:LEU:HD12	1.92	0.52
1:AL:139:ILE:HG23	1:AL:140:PRO:HD2	1.92	0.51
1:BA:139:ILE:HG23	1:BA:140:PRO:HD2	1.92	0.51
1:BB:18:GLN:OE1	1:BZ:21:VAL:HG21	2.09	0.51
1:BI:204:VAL:HG21	1:DL:208:ALA:HB2	1.92	0.51
1:BS:139:ILE:HG23	1:BS:140:PRO:HD2	1.92	0.51
1:CK:139:ILE:HG23	1:CK:140:PRO:HD2	1.92	0.51
1:CW:139:ILE:HG23	1:CW:140:PRO:HD2	1.92	0.51
1:DI:139:ILE:HG23	1:DI:140:PRO:HD2	1.92	0.51
1:DJ:98:GLY:HA3	1:DJ:101:LEU:HD12	1.92	0.51
1:AC:139:ILE:HG23	1:AC:140:PRO:HD2	1.92	0.51
1:AM:98:GLY:HA3	1:AM:101:LEU:HD12	1.92	0.51
1:BB:98:GLY:HA3	1:BB:101:LEU:HD12	1.92	0.51
1:BG:65:ARG:NH2	1:CZ:162:THR:HB	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:98:GLY:HA3	1:BQ:101:LEU:HD12	1.91	0.51
1:CE:139:ILE:HG23	1:CE:140:PRO:HD2	1.92	0.51
1:AD:20:PRO:HG3	1:AP:26:THR:HG21	1.92	0.51
1:AI:139:ILE:HG23	1:AI:140:PRO:HD2	1.92	0.51
1:AJ:20:PRO:HG3	1:CF:26:THR:HG21	1.93	0.51
1:AY:21:VAL:HG21	1:BH:18:GLN:OE1	2.10	0.51
1:BH:98:GLY:HA3	1:BH:101:LEU:HD12	1.92	0.51
1:BK:98:GLY:HA3	1:BK:101:LEU:HD12	1.92	0.51
1:CL:98:GLY:HA3	1:CL:101:LEU:HD12	1.92	0.51
1:CN:139:ILE:HG23	1:CN:140:PRO:HD2	1.92	0.51
1:AJ:98:GLY:HA3	1:AJ:101:LEU:HD12	1.92	0.51
1:AK:102:MET:SD	1:CK:129:ASN:ND2	2.84	0.51
1:AR:208:ALA:HB2	1:CP:204:VAL:HG21	1.93	0.51
1:AS:20:PRO:HG3	1:CI:26:THR:HG21	1.93	0.51
1:AZ:22:GLN:HA	1:BL:31:ASN:HD21	1.76	0.51
1:BK:196:ARG:HA	1:BL:41:VAL:HB	1.91	0.51
1:CO:98:GLY:HA3	1:CO:101:LEU:HD12	1.92	0.51
1:CT:139:ILE:HG23	1:CT:140:PRO:HD2	1.92	0.51
1:DD:98:GLY:HA3	1:DD:101:LEU:HD12	1.92	0.51
1:AA:98:GLY:HA3	1:AA:101:LEU:HD12	1.92	0.51
1:AF:129:ASN:ND2	1:CD:102:MET:SD	2.83	0.51
1:AP:98:GLY:HA3	1:AP:101:LEU:HD12	1.92	0.51
1:BP:65:ARG:NH1	1:DI:161:LEU:HD22	2.26	0.51
1:CQ:139:ILE:HG23	1:CQ:140:PRO:HD2	1.92	0.51
1:AE:22:GLN:HA	1:BX:31:ASN:HD21	1.75	0.51
1:AK:79:GLN:HB2	1:AK:93:VAL:HG12	1.93	0.51
1:AR:38:ALA:HA	1:CN:201:SER:HB2	1.92	0.51
1:AY:20:PRO:HG3	1:DJ:26:THR:HG21	1.92	0.51
1:AY:98:GLY:HA3	1:AY:101:LEU:HD12	1.91	0.51
1:BW:98:GLY:HA3	1:BW:101:LEU:HD12	1.92	0.51
1:CI:98:GLY:HA3	1:CI:101:LEU:HD12	1.91	0.51
1:DG:98:GLY:HA3	1:DG:101:LEU:HD12	1.92	0.51
1:BJ:139:ILE:HG23	1:BJ:140:PRO:HD2	1.92	0.51
1:BP:129:ASN:HD21	1:DH:102:MET:HA	1.76	0.51
1:CF:98:GLY:HA3	1:CF:101:LEU:HD12	1.91	0.51
1:DA:18:GLN:OE1	1:DG:21:VAL:HG21	2.11	0.51
1:AV:98:GLY:HA3	1:AV:101:LEU:HD12	1.92	0.51
1:AY:196:ARG:HA	1:AZ:41:VAL:HB	1.91	0.51
1:BD:198:VAL:O	1:CW:39:ARG:NH2	2.44	0.51
1:BG:208:ALA:HB2	1:CD:204:VAL:HG21	1.93	0.51
1:BQ:197:LEU:HD22	1:BR:117:THR:HG21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:139:ILE:HG23	1:CB:140:PRO:HD2	1.92	0.51
1:AA:197:LEU:HD22	1:AB:117:THR:HG21	1.93	0.51
1:AD:197:LEU:HD22	1:AE:117:THR:HG21	1.93	0.51
1:AL:208:ALA:HB2	1:CG:204:VAL:HG21	1.93	0.51
1:AS:98:GLY:HA3	1:AS:101:LEU:HD12	1.92	0.51
1:AU:39:ARG:NH2	1:CQ:198:VAL:O	2.44	0.51
1:AY:18:GLN:OE1	1:DJ:21:VAL:HG21	2.11	0.51
1:AY:197:LEU:HD22	1:AZ:117:THR:HG21	1.93	0.51
1:BQ:18:GLN:OE1	1:BW:21:VAL:HG21	2.11	0.51
1:BY:139:ILE:HG23	1:BY:140:PRO:HD2	1.92	0.51
1:BZ:196:ARG:HA	1:CA:41:VAL:HB	1.91	0.51
1:CX:98:GLY:HA3	1:CX:101:LEU:HD12	1.92	0.51
1:AQ:79:GLN:HB2	1:AQ:93:VAL:HG12	1.93	0.51
1:AS:197:LEU:HD22	1:AT:117:THR:HG21	1.93	0.51
1:AT:79:GLN:HB2	1:AT:93:VAL:HG12	1.93	0.51
1:BB:197:LEU:HD22	1:BC:117:THR:HG21	1.93	0.51
1:BG:163:GLY:H	1:CZ:65:ARG:HD3	1.75	0.51
1:AM:197:LEU:HD22	1:AN:117:THR:HG21	1.93	0.50
1:AU:208:ALA:HB2	1:CJ:204:VAL:HG21	1.93	0.50
1:CL:197:LEU:HD22	1:CM:117:THR:HG21	1.93	0.50
1:CX:197:LEU:HD22	1:CY:117:THR:HG21	1.93	0.50
1:DC:139:ILE:HG23	1:DC:140:PRO:HD2	1.92	0.50
1:BE:98:GLY:HA3	1:BE:101:LEU:HD12	1.92	0.50
1:BQ:21:VAL:HG21	1:CU:18:GLN:OE1	2.11	0.50
1:AC:39:ARG:NH2	1:BY:198:VAL:O	2.43	0.50
1:AJ:197:LEU:HD22	1:AK:117:THR:HG21	1.93	0.50
1:AP:197:LEU:HD22	1:AQ:117:THR:HG21	1.93	0.50
1:AV:21:VAL:HG21	1:BN:18:GLN:OE1	2.11	0.50
1:BC:89:HIS:ND1	1:BC:111:ASP:OD1	2.35	0.50
1:BF:79:GLN:HB2	1:BF:93:VAL:HG12	1.93	0.50
1:BJ:129:ASN:O	1:BJ:133:THR:OG1	2.23	0.50
1:BK:197:LEU:HD22	1:BL:117:THR:HG21	1.93	0.50
1:BS:39:ARG:NH2	1:DL:198:VAL:O	2.43	0.50
1:CF:197:LEU:HD22	1:CG:117:THR:HG21	1.93	0.50
1:CM:79:GLN:HB2	1:CM:93:VAL:HG12	1.93	0.50
1:BP:161:LEU:HD22	1:DI:65:ARG:NH1	2.26	0.50
1:CC:197:LEU:HD22	1:CD:117:THR:HG21	1.93	0.50
1:DD:197:LEU:HD22	1:DE:117:THR:HG21	1.93	0.50
1:DF:139:ILE:HG23	1:DF:140:PRO:HD2	1.92	0.50
1:AE:204:VAL:HG21	1:CQ:208:ALA:HB2	1.93	0.50
1:BF:22:GLN:HA	1:DB:31:ASN:HD21	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:139:ILE:HG23	1:BG:140:PRO:HD2	1.92	0.50
1:BL:79:GLN:HB2	1:BL:93:VAL:HG12	1.93	0.50
1:BP:162:THR:HB	1:DI:65:ARG:NH2	2.26	0.50
1:AE:162:THR:O	1:CR:79:GLN:NE2	2.44	0.50
1:BR:79:GLN:HB2	1:BR:93:VAL:HG12	1.93	0.50
1:CP:79:GLN:HB2	1:CP:93:VAL:HG12	1.93	0.50
1:DG:197:LEU:HD22	1:DH:117:THR:HG21	1.93	0.50
1:AG:197:LEU:HD22	1:AH:117:THR:HG21	1.93	0.50
1:AH:22:GLN:HA	1:CJ:31:ASN:HD21	1.76	0.50
1:AN:79:GLN:HB2	1:AN:93:VAL:HG12	1.93	0.50
1:AT:89:HIS:ND1	1:AT:111:ASP:OD1	2.35	0.50
1:BS:198:VAL:O	1:DL:39:ARG:NH2	2.45	0.50
1:CS:79:GLN:HB2	1:CS:93:VAL:HG12	1.93	0.50
1:AE:31:ASN:HD21	1:DK:22:GLN:HA	1.77	0.50
1:BG:162:THR:HB	1:CZ:65:ARG:NH2	2.26	0.50
1:BU:79:GLN:HB2	1:BU:93:VAL:HG12	1.93	0.50
1:CY:79:GLN:HB2	1:CY:93:VAL:HG12	1.93	0.50
1:DJ:197:LEU:HD22	1:DK:117:THR:HG21	1.93	0.50
1:AR:161:LEU:HD22	1:CN:65:ARG:NH1	2.27	0.50
1:AZ:79:GLN:HB2	1:AZ:93:VAL:HG12	1.93	0.50
1:BI:79:GLN:HB2	1:BI:93:VAL:HG12	1.93	0.50
1:BJ:65:ARG:NH2	1:DC:162:THR:HB	2.27	0.50
1:BJ:65:ARG:HD3	1:DC:163:GLY:H	1.75	0.50
1:BP:65:ARG:HD3	1:DI:163:GLY:H	1.76	0.50
1:BW:197:LEU:HD22	1:BX:117:THR:HG21	1.93	0.50
1:CI:197:LEU:HD22	1:CJ:117:THR:HG21	1.93	0.50
1:AB:79:GLN:HB2	1:AB:93:VAL:HG12	1.93	0.49
1:AC:198:VAL:O	1:BY:39:ARG:NH2	2.45	0.49
1:CY:89:HIS:ND1	1:CY:111:ASP:OD1	2.35	0.49
1:AH:31:ASN:HD21	1:CP:22:GLN:HA	1.77	0.49
1:BH:197:LEU:HD22	1:BI:117:THR:HG21	1.93	0.49
1:BX:79:GLN:HB2	1:BX:93:VAL:HG12	1.93	0.49
1:CG:79:GLN:HB2	1:CG:93:VAL:HG12	1.93	0.49
1:AH:79:GLN:HB2	1:AH:93:VAL:HG12	1.93	0.49
1:AV:197:LEU:HD22	1:AW:117:THR:HG21	1.93	0.49
1:BA:65:ARG:NH2	1:CT:162:THR:HB	2.27	0.49
1:BB:20:PRO:HG3	1:BZ:26:THR:HG21	1.93	0.49
1:BT:197:LEU:HD22	1:BU:117:THR:HG21	1.93	0.49
1:AB:89:HIS:ND1	1:AB:111:ASP:OD1	2.35	0.49
1:AE:79:GLN:HB2	1:AE:93:VAL:HG12	1.93	0.49
1:AU:198:VAL:O	1:CQ:39:ARG:NH2	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:65:ARG:NH1	1:CT:161:LEU:HD22	2.27	0.49
1:DA:197:LEU:HD22	1:DB:117:THR:HG21	1.93	0.49
1:DE:79:GLN:HB2	1:DE:93:VAL:HG12	1.93	0.49
1:DH:79:GLN:HB2	1:DH:93:VAL:HG12	1.93	0.49
1:BC:79:GLN:HB2	1:BC:93:VAL:HG12	1.93	0.49
1:BE:197:LEU:HD22	1:BF:117:THR:HG21	1.93	0.49
1:BO:79:GLN:HB2	1:BO:93:VAL:HG12	1.93	0.49
1:CU:197:LEU:HD22	1:CV:117:THR:HG21	1.93	0.49
1:DD:21:VAL:HG21	1:DG:18:GLN:OE1	2.12	0.49
1:DK:79:GLN:HB2	1:DK:93:VAL:HG12	1.93	0.49
1:AF:129:ASN:ND2	1:CD:102:MET:HA	2.28	0.49
1:AK:31:ASN:HD21	1:CV:22:GLN:HA	1.77	0.49
1:AR:198:VAL:O	1:CN:39:ARG:NH2	2.46	0.49
1:AT:127:ASP:HB2	1:AT:146:VAL:HG21	1.95	0.49
1:BH:69:GLY:HA3	1:BH:96:ASN:HB3	1.95	0.49
1:BT:69:GLY:HA3	1:BT:96:ASN:HB3	1.95	0.49
1:BW:69:GLY:HA3	1:BW:96:ASN:HB3	1.95	0.49
1:CO:69:GLY:HA3	1:CO:96:ASN:HB3	1.95	0.49
1:CV:79:GLN:HB2	1:CV:93:VAL:HG12	1.93	0.49
1:AF:196:ARG:HA	1:CE:41:VAL:HB	1.94	0.49
1:AF:208:ALA:HB2	1:AQ:204:VAL:HG21	1.95	0.49
1:AP:69:GLY:HA3	1:AP:96:ASN:HB3	1.95	0.49
1:BA:161:LEU:HD22	1:CT:65:ARG:NH1	2.27	0.49
1:BG:198:VAL:O	1:CZ:39:ARG:NH2	2.43	0.49
1:CD:79:GLN:HB2	1:CD:93:VAL:HG12	1.93	0.49
1:DB:79:GLN:HB2	1:DB:93:VAL:HG12	1.93	0.49
1:AD:69:GLY:HA3	1:AD:96:ASN:HB3	1.95	0.49
1:AH:127:ASP:HB2	1:AH:146:VAL:HG21	1.95	0.49
1:AW:79:GLN:HB2	1:AW:93:VAL:HG12	1.93	0.49
1:BN:197:LEU:HD22	1:BO:117:THR:HG21	1.93	0.49
1:BZ:197:LEU:HD22	1:CA:117:THR:HG21	1.93	0.49
1:CA:79:GLN:HB2	1:CA:93:VAL:HG12	1.93	0.49
1:CC:20:PRO:HG3	1:CR:26:THR:HG21	1.94	0.49
1:CR:197:LEU:HD22	1:CS:117:THR:HG21	1.93	0.49
1:AA:26:THR:HG21	1:CI:20:PRO:HG3	1.93	0.49
1:AB:127:ASP:HB2	1:AB:146:VAL:HG21	1.95	0.49
1:AC:65:ARG:NH1	1:BY:161:LEU:HD22	2.28	0.49
1:AM:79:GLN:NE2	1:CA:162:THR:O	2.46	0.49
1:AN:127:ASP:HB2	1:AN:146:VAL:HG21	1.95	0.49
1:BD:208:ALA:HB2	1:CA:204:VAL:HG21	1.94	0.49
1:BL:127:ASP:HB2	1:BL:146:VAL:HG21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BU:127:ASP:HB2	1:BU:146:VAL:HG21	1.95	0.49
1:CD:127:ASP:HB2	1:CD:146:VAL:HG21	1.95	0.49
1:CO:197:LEU:HD22	1:CP:117:THR:HG21	1.93	0.49
1:DA:69:GLY:HA3	1:DA:96:ASN:HB3	1.95	0.49
1:DG:69:GLY:HA3	1:DG:96:ASN:HB3	1.95	0.49
1:AJ:69:GLY:HA3	1:AJ:96:ASN:HB3	1.95	0.49
1:AQ:127:ASP:HB2	1:AQ:146:VAL:HG21	1.95	0.49
1:BJ:198:VAL:O	1:DC:39:ARG:NH2	2.45	0.49
1:CL:69:GLY:HA3	1:CL:96:ASN:HB3	1.95	0.49
1:CM:127:ASP:HB2	1:CM:146:VAL:HG21	1.95	0.49
1:CX:69:GLY:HA3	1:CX:96:ASN:HB3	1.95	0.49
1:DE:127:ASP:HB2	1:DE:146:VAL:HG21	1.95	0.49
1:AC:161:LEU:HD22	1:BY:65:ARG:NH1	2.28	0.48
1:BB:69:GLY:HA3	1:BB:96:ASN:HB3	1.95	0.48
1:CC:69:GLY:HA3	1:CC:96:ASN:HB3	1.95	0.48
1:AK:127:ASP:HB2	1:AK:146:VAL:HG21	1.95	0.48
1:AM:69:GLY:HA3	1:AM:96:ASN:HB3	1.95	0.48
1:AR:65:ARG:NH1	1:CN:161:LEU:HD22	2.28	0.48
1:DD:108:VAL:HG22	1:DD:121:ILE:HG12	1.96	0.48
1:AA:21:VAL:HG21	1:CI:18:GLN:OE1	2.14	0.48
1:AC:208:ALA:HB2	1:AT:204:VAL:HG21	1.95	0.48
1:CI:69:GLY:HA3	1:CI:96:ASN:HB3	1.95	0.48
1:CJ:79:GLN:HB2	1:CJ:93:VAL:HG12	1.93	0.48
1:CU:108:VAL:HG22	1:CU:121:ILE:HG12	1.96	0.48
1:DB:89:HIS:ND1	1:DB:111:ASP:OD1	2.35	0.48
1:DE:204:VAL:HG21	1:DI:208:ALA:HB2	1.95	0.48
1:AB:204:VAL:HG21	1:CK:208:ALA:HB2	1.96	0.48
1:AD:21:VAL:HG21	1:CO:18:GLN:OE1	2.13	0.48
1:BB:108:VAL:HG22	1:BB:121:ILE:HG12	1.96	0.48
1:BF:102:MET:SD	1:CZ:129:ASN:ND2	2.86	0.48
1:BP:106:THR:HG23	1:BP:123:ILE:HG22	1.96	0.48
1:BW:18:GLN:OE1	1:CU:21:VAL:HG21	2.13	0.48
1:CF:69:GLY:HA3	1:CF:96:ASN:HB3	1.95	0.48
1:CR:108:VAL:HG22	1:CR:121:ILE:HG12	1.96	0.48
1:CS:127:ASP:HB2	1:CS:146:VAL:HG21	1.95	0.48
1:AC:106:THR:HG23	1:AC:123:ILE:HG22	1.96	0.48
1:BA:198:VAL:O	1:CT:39:ARG:NH2	2.44	0.48
1:BL:102:MET:HA	1:DF:129:ASN:HD21	1.79	0.48
1:BM:106:THR:HG23	1:BM:123:ILE:HG22	1.96	0.48
1:CZ:106:THR:HG23	1:CZ:123:ILE:HG22	1.96	0.48
1:DI:106:THR:HG23	1:DI:123:ILE:HG22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:28:PHE:CE2	1:AL:102:MET:HE1	2.48	0.48
1:BS:106:THR:HG23	1:BS:123:ILE:HG22	1.96	0.48
1:BX:127:ASP:HB2	1:BX:146:VAL:HG21	1.95	0.48
1:BZ:108:VAL:HG22	1:BZ:121:ILE:HG12	1.96	0.48
1:CI:108:VAL:HG22	1:CI:121:ILE:HG12	1.96	0.48
1:CK:106:THR:HG23	1:CK:123:ILE:HG22	1.96	0.48
1:CR:69:GLY:HA3	1:CR:96:ASN:HB3	1.95	0.48
1:CV:127:ASP:HB2	1:CV:146:VAL:HG21	1.95	0.48
1:AK:100:ARG:HD2	1:AK:135:LYS:HG3	1.96	0.48
1:AL:106:THR:HG23	1:AL:123:ILE:HG22	1.96	0.48
1:AL:129:ASN:ND2	1:CJ:102:MET:HA	2.28	0.48
1:AU:65:ARG:NH1	1:CQ:161:LEU:HD22	2.29	0.48
1:BC:100:ARG:HD2	1:BC:135:LYS:HG3	1.96	0.48
1:BD:106:THR:HG23	1:BD:123:ILE:HG22	1.96	0.48
1:BG:102:MET:HE1	1:BT:28:PHE:CE2	2.49	0.48
1:BG:106:THR:HG23	1:BG:123:ILE:HG22	1.96	0.48
1:BI:127:ASP:HB2	1:BI:146:VAL:HG21	1.95	0.48
1:CA:127:ASP:HB2	1:CA:146:VAL:HG21	1.95	0.48
1:CH:106:THR:HG23	1:CH:123:ILE:HG22	1.96	0.48
1:DB:100:ARG:HD2	1:DB:135:LYS:HG3	1.96	0.48
1:DB:127:ASP:HB2	1:DB:146:VAL:HG21	1.95	0.48
1:AA:20:PRO:HG3	1:AS:26:THR:HG21	1.96	0.48
1:AG:69:GLY:HA3	1:AG:96:ASN:HB3	1.95	0.48
1:AO:106:THR:HG23	1:AO:123:ILE:HG22	1.96	0.48
1:AQ:100:ARG:HD2	1:AQ:135:LYS:HG3	1.96	0.48
1:AT:100:ARG:HD2	1:AT:135:LYS:HG3	1.96	0.48
1:BE:108:VAL:HG22	1:BE:121:ILE:HG12	1.96	0.48
1:BN:69:GLY:HA3	1:BN:96:ASN:HB3	1.95	0.48
1:BO:100:ARG:HD2	1:BO:135:LYS:HG3	1.96	0.48
1:CG:100:ARG:HD2	1:CG:135:LYS:HG3	1.96	0.48
1:CM:100:ARG:HD2	1:CM:135:LYS:HG3	1.96	0.48
1:CW:106:THR:HG23	1:CW:123:ILE:HG22	1.96	0.48
1:CY:100:ARG:HD2	1:CY:135:LYS:HG3	1.96	0.48
1:DA:108:VAL:HG22	1:DA:121:ILE:HG12	1.96	0.48
1:DH:89:HIS:ND1	1:DH:111:ASP:OD1	2.35	0.48
1:AM:108:VAL:HG22	1:AM:121:ILE:HG12	1.96	0.48
1:AU:161:LEU:HD22	1:CQ:65:ARG:NH1	2.29	0.48
1:AW:127:ASP:HB2	1:AW:146:VAL:HG21	1.95	0.48
1:AY:108:VAL:HG22	1:AY:121:ILE:HG12	1.96	0.48
1:BM:65:ARG:NH2	1:DF:162:THR:HB	2.29	0.48
1:BM:65:ARG:HD3	1:DF:163:GLY:H	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:127:ASP:HB2	1:BR:146:VAL:HG21	1.95	0.48
1:CA:100:ARG:HD2	1:CA:135:LYS:HG3	1.96	0.48
1:CV:100:ARG:HD2	1:CV:135:LYS:HG3	1.96	0.48
1:AQ:22:GLN:HA	1:CY:31:ASN:HD21	1.79	0.48
1:AS:108:VAL:HG22	1:AS:121:ILE:HG12	1.96	0.48
1:AY:26:THR:HG21	1:BH:20:PRO:HG3	1.95	0.48
1:AZ:100:ARG:HD2	1:AZ:135:LYS:HG3	1.96	0.48
1:BE:69:GLY:HA3	1:BE:96:ASN:HB3	1.95	0.48
1:BR:100:ARG:HD2	1:BR:135:LYS:HG3	1.96	0.48
1:BT:26:THR:HG21	1:CX:20:PRO:HG3	1.96	0.48
1:DH:127:ASP:HB2	1:DH:146:VAL:HG21	1.95	0.48
1:DK:100:ARG:HD2	1:DK:135:LYS:HG3	1.96	0.48
1:BK:69:GLY:HA3	1:BK:96:ASN:HB3	1.95	0.47
1:BK:108:VAL:HG22	1:BK:121:ILE:HG12	1.96	0.47
1:BN:108:VAL:HG22	1:BN:121:ILE:HG12	1.96	0.47
1:DD:69:GLY:HA3	1:DD:96:ASN:HB3	1.95	0.47
1:DE:100:ARG:HD2	1:DE:135:LYS:HG3	1.96	0.47
1:AG:108:VAL:HG22	1:AG:121:ILE:HG12	1.96	0.47
1:AV:108:VAL:HG22	1:AV:121:ILE:HG12	1.96	0.47
1:BZ:28:PHE:CE2	1:CW:102:MET:HE1	2.49	0.47
1:BZ:69:GLY:HA3	1:BZ:96:ASN:HB3	1.95	0.47
1:CJ:22:GLN:HA	1:CM:31:ASN:HD21	1.79	0.47
1:CJ:100:ARG:HD2	1:CJ:135:LYS:HG3	1.96	0.47
1:DL:106:THR:HG23	1:DL:123:ILE:HG22	1.96	0.47
1:AA:69:GLY:HA3	1:AA:96:ASN:HB3	1.95	0.47
1:AE:85:VAL:HG11	1:CE:204:VAL:HG11	1.96	0.47
1:AJ:108:VAL:HG22	1:AJ:121:ILE:HG12	1.96	0.47
1:AS:18:GLN:OE1	1:CI:21:VAL:HG21	2.15	0.47
1:AU:106:THR:HG23	1:AU:123:ILE:HG22	1.96	0.47
1:AW:31:ASN:HD21	1:BR:22:GLN:HA	1.79	0.47
1:BF:127:ASP:HB2	1:BF:146:VAL:HG21	1.95	0.47
1:BI:100:ARG:HD2	1:BI:135:LYS:HG3	1.96	0.47
1:BL:100:ARG:HD2	1:BL:135:LYS:HG3	1.96	0.47
1:BS:129:ASN:ND2	1:DK:102:MET:SD	2.88	0.47
1:BU:100:ARG:HD2	1:BU:135:LYS:HG3	1.96	0.47
1:BW:108:VAL:HG22	1:BW:121:ILE:HG12	1.96	0.47
1:CJ:127:ASP:HB2	1:CJ:146:VAL:HG21	1.95	0.47
1:CR:35:GLN:HB3	1:CR:160:VAL:HG23	1.97	0.47
1:CS:100:ARG:HD2	1:CS:135:LYS:HG3	1.96	0.47
1:CU:69:GLY:HA3	1:CU:96:ASN:HB3	1.95	0.47
1:DG:108:VAL:HG22	1:DG:121:ILE:HG12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DH:100:ARG:HD2	1:DH:135:LYS:HG3	1.96	0.47
1:DJ:69:GLY:HA3	1:DJ:96:ASN:HB3	1.95	0.47
1:DJ:108:VAL:HG22	1:DJ:121:ILE:HG12	1.96	0.47
1:DK:127:ASP:HB2	1:DK:146:VAL:HG21	1.95	0.47
1:BC:127:ASP:HB2	1:BC:146:VAL:HG21	1.95	0.47
1:BF:100:ARG:HD2	1:BF:135:LYS:HG3	1.96	0.47
1:BQ:35:GLN:HB3	1:BQ:160:VAL:HG23	1.97	0.47
1:BR:85:VAL:HG11	1:DL:204:VAL:HG11	1.97	0.47
1:CG:127:ASP:HB2	1:CG:146:VAL:HG21	1.95	0.47
1:CN:106:THR:HG23	1:CN:123:ILE:HG22	1.96	0.47
1:CO:35:GLN:HB3	1:CO:160:VAL:HG23	1.97	0.47
1:CP:100:ARG:HD2	1:CP:135:LYS:HG3	1.96	0.47
1:CP:127:ASP:HB2	1:CP:146:VAL:HG21	1.95	0.47
1:CX:108:VAL:HG22	1:CX:121:ILE:HG12	1.96	0.47
1:AZ:204:VAL:HG21	1:BJ:208:ALA:HB2	1.96	0.47
1:BJ:106:THR:HG23	1:BJ:123:ILE:HG22	1.96	0.47
1:BQ:108:VAL:HG22	1:BQ:121:ILE:HG12	1.96	0.47
1:CE:208:ALA:HB2	1:CS:204:VAL:HG21	1.94	0.47
1:CF:108:VAL:HG22	1:CF:121:ILE:HG12	1.96	0.47
1:CY:127:ASP:HB2	1:CY:146:VAL:HG21	1.95	0.47
1:AD:35:GLN:HB3	1:AD:160:VAL:HG23	1.97	0.47
1:AD:108:VAL:HG22	1:AD:121:ILE:HG12	1.96	0.47
1:AN:100:ARG:HD2	1:AN:135:LYS:HG3	1.96	0.47
1:BD:161:LEU:HD22	1:CW:65:ARG:NH1	2.30	0.47
1:BH:35:GLN:HB3	1:BH:160:VAL:HG23	1.97	0.47
1:BS:129:ASN:ND2	1:DK:102:MET:HA	2.30	0.47
1:CD:100:ARG:HD2	1:CD:135:LYS:HG3	1.96	0.47
1:CF:35:GLN:HB3	1:CF:160:VAL:HG23	1.97	0.47
1:CL:35:GLN:HB3	1:CL:160:VAL:HG23	1.97	0.47
1:CQ:106:THR:HG23	1:CQ:123:ILE:HG22	1.96	0.47
1:CU:35:GLN:HB3	1:CU:160:VAL:HG23	1.97	0.47
1:DD:26:THR:HG21	1:DG:20:PRO:HG3	1.96	0.47
1:AE:127:ASP:HB2	1:AE:146:VAL:HG21	1.95	0.47
1:AF:106:THR:HG23	1:AF:123:ILE:HG22	1.96	0.47
1:AF:161:LEU:HD22	1:CE:65:ARG:NH1	2.30	0.47
1:AH:162:THR:O	1:CL:79:GLN:NE2	2.48	0.47
1:AJ:35:GLN:HB3	1:AJ:160:VAL:HG23	1.97	0.47
1:AP:35:GLN:HB3	1:AP:160:VAL:HG23	1.97	0.47
1:AR:106:THR:HG23	1:AR:123:ILE:HG22	1.96	0.47
1:AW:204:VAL:HG21	1:BP:208:ALA:HB2	1.96	0.47
1:AY:69:GLY:HA3	1:AY:96:ASN:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:39:ARG:NH2	1:CW:198:VAL:O	2.47	0.47
1:BH:108:VAL:HG22	1:BH:121:ILE:HG12	1.96	0.47
1:BJ:65:ARG:NH1	1:DC:161:LEU:HD22	2.29	0.47
1:BJ:161:LEU:HD22	1:DC:65:ARG:NH1	2.30	0.47
1:BL:89:HIS:ND1	1:BL:111:ASP:OD1	2.35	0.47
1:BO:127:ASP:HB2	1:BO:146:VAL:HG21	1.95	0.47
1:BT:35:GLN:HB3	1:BT:160:VAL:HG23	1.97	0.47
1:BT:108:VAL:HG22	1:BT:121:ILE:HG12	1.96	0.47
1:BV:106:THR:HG23	1:BV:123:ILE:HG22	1.96	0.47
1:CB:106:THR:HG23	1:CB:123:ILE:HG22	1.96	0.47
1:CE:106:THR:HG23	1:CE:123:ILE:HG22	1.96	0.47
1:CX:35:GLN:HB3	1:CX:160:VAL:HG23	1.97	0.47
1:DA:35:GLN:HB3	1:DA:160:VAL:HG23	1.97	0.47
1:AF:100:ARG:NH1	1:AF:134:LEU:HB3	2.30	0.47
1:AI:102:MET:HE1	1:CL:28:PHE:CE2	2.49	0.47
1:AP:108:VAL:HG22	1:AP:121:ILE:HG12	1.96	0.47
1:AV:26:THR:HG21	1:BN:20:PRO:HG3	1.97	0.47
1:AX:106:THR:HG23	1:AX:123:ILE:HG22	1.96	0.47
1:AZ:127:ASP:HB2	1:AZ:146:VAL:HG21	1.95	0.47
1:BE:35:GLN:HB3	1:BE:160:VAL:HG23	1.97	0.47
1:BM:100:ARG:NH1	1:BM:134:LEU:HB3	2.30	0.47
1:BQ:69:GLY:HA3	1:BQ:96:ASN:HB3	1.95	0.47
1:CC:108:VAL:HG22	1:CC:121:ILE:HG12	1.96	0.47
1:CT:106:THR:HG23	1:CT:123:ILE:HG22	1.96	0.47
1:CZ:100:ARG:NH1	1:CZ:134:LEU:HB3	2.30	0.47
1:DF:106:THR:HG23	1:DF:123:ILE:HG22	1.96	0.47
1:DI:100:ARG:NH1	1:DI:134:LEU:HB3	2.30	0.47
1:DJ:35:GLN:HB3	1:DJ:160:VAL:HG23	1.97	0.47
1:AB:100:ARG:HD2	1:AB:135:LYS:HG3	1.96	0.47
1:AI:106:THR:HG23	1:AI:123:ILE:HG22	1.96	0.47
1:AL:41:VAL:HB	1:CK:196:ARG:HA	1.97	0.47
1:BN:35:GLN:HB3	1:BN:160:VAL:HG23	1.97	0.47
1:BP:65:ARG:NH2	1:DI:162:THR:HB	2.29	0.47
1:BX:89:HIS:ND1	1:BX:111:ASP:OD1	2.35	0.47
1:BY:106:THR:HG23	1:BY:123:ILE:HG22	1.96	0.47
1:CH:100:ARG:NH1	1:CH:134:LEU:HB3	2.30	0.47
1:CK:100:ARG:NH1	1:CK:134:LEU:HB3	2.30	0.47
1:AR:100:ARG:NH1	1:AR:134:LEU:HB3	2.30	0.47
1:AS:69:GLY:HA3	1:AS:96:ASN:HB3	1.95	0.47
1:AV:69:GLY:HA3	1:AV:96:ASN:HB3	1.95	0.47
1:BA:106:THR:HG23	1:BA:123:ILE:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:35:GLN:HB3	1:BK:160:VAL:HG23	1.97	0.47
1:BY:100:ARG:NH1	1:BY:134:LEU:HB3	2.30	0.47
1:BY:208:ALA:HB2	1:CV:204:VAL:HG21	1.97	0.47
1:CI:35:GLN:HB3	1:CI:160:VAL:HG23	1.97	0.47
1:CO:108:VAL:HG22	1:CO:121:ILE:HG12	1.96	0.47
1:AG:35:GLN:HB3	1:AG:160:VAL:HG23	1.97	0.46
1:AH:100:ARG:HD2	1:AH:135:LYS:HG3	1.96	0.46
1:AL:161:LEU:HD22	1:CK:65:ARG:NH1	2.30	0.46
1:AP:18:GLN:OE1	1:CO:21:VAL:HG21	2.15	0.46
1:AV:35:GLN:HB3	1:AV:160:VAL:HG23	1.97	0.46
1:AW:100:ARG:HD2	1:AW:135:LYS:HG3	1.96	0.46
1:BB:35:GLN:HB3	1:BB:160:VAL:HG23	1.97	0.46
1:BN:32:PRO:O	1:BN:34:ARG:NH1	2.49	0.46
1:CC:35:GLN:HB3	1:CC:160:VAL:HG23	1.97	0.46
1:CU:32:PRO:O	1:CU:34:ARG:NH1	2.49	0.46
1:AA:108:VAL:HG22	1:AA:121:ILE:HG12	1.96	0.46
1:AM:35:GLN:HB3	1:AM:160:VAL:HG23	1.97	0.46
1:AV:32:PRO:O	1:AV:34:ARG:NH1	2.49	0.46
1:BC:162:THR:O	1:BQ:79:GLN:NE2	2.49	0.46
1:BD:65:ARG:NH1	1:CW:161:LEU:HD22	2.29	0.46
1:BJ:100:ARG:NH1	1:BJ:134:LEU:HB3	2.30	0.46
1:BM:65:ARG:NH1	1:DF:161:LEU:HD22	2.31	0.46
1:CC:181:MET:HE1	1:CD:181:MET:HE1	1.98	0.46
1:CR:32:PRO:O	1:CR:34:ARG:NH1	2.49	0.46
1:CT:102:MET:HE1	1:DJ:28:PHE:CE2	2.50	0.46
1:DC:208:ALA:HB2	1:DH:204:VAL:HG21	1.98	0.46
1:AO:180:LEU:HD23	1:AO:180:LEU:HA	1.77	0.46
1:AP:79:GLN:NE2	1:CD:162:THR:O	2.48	0.46
1:AY:35:GLN:HB3	1:AY:160:VAL:HG23	1.97	0.46
1:BD:100:ARG:NH1	1:BD:134:LEU:HB3	2.30	0.46
1:BF:31:ASN:HD21	1:BL:22:GLN:HA	1.80	0.46
1:BG:41:VAL:HB	1:CZ:196:ARG:HA	1.97	0.46
1:BK:32:PRO:O	1:BK:34:ARG:NH1	2.49	0.46
1:BK:181:MET:HE1	1:BL:181:MET:HE1	1.98	0.46
1:BM:198:VAL:O	1:DF:39:ARG:NH2	2.47	0.46
1:BQ:26:THR:HG21	1:CU:20:PRO:HG3	1.96	0.46
1:BS:161:LEU:HD22	1:DL:65:ARG:NH1	2.30	0.46
1:BX:100:ARG:HD2	1:BX:135:LYS:HG3	1.96	0.46
1:BZ:35:GLN:HB3	1:BZ:160:VAL:HG23	1.97	0.46
1:CU:181:MET:HE1	1:CV:181:MET:HE1	1.98	0.46
1:CX:181:MET:HE1	1:CY:181:MET:HE1	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:35:GLN:HB3	1:AA:160:VAL:HG23	1.97	0.46
1:AB:77:PRO:HG2	1:AC:166:ALA:HB3	1.98	0.46
1:AL:100:ARG:NH1	1:AL:134:LEU:HB3	2.30	0.46
1:AX:100:ARG:NH1	1:AX:134:LEU:HB3	2.30	0.46
1:BQ:181:MET:HE1	1:BR:181:MET:HE1	1.98	0.46
1:BV:100:ARG:NH1	1:BV:134:LEU:HB3	2.30	0.46
1:BW:35:GLN:HB3	1:BW:160:VAL:HG23	1.97	0.46
1:CF:181:MET:HE1	1:CG:181:MET:HE1	1.98	0.46
1:CI:32:PRO:O	1:CI:34:ARG:NH1	2.49	0.46
1:CN:100:ARG:NH1	1:CN:134:LEU:HB3	2.30	0.46
1:DD:35:GLN:HB3	1:DD:160:VAL:HG23	1.97	0.46
1:DL:100:ARG:NH1	1:DL:134:LEU:HB3	2.30	0.46
1:AE:100:ARG:HD2	1:AE:135:LYS:HG3	1.96	0.46
1:AI:100:ARG:NH1	1:AI:134:LEU:HB3	2.30	0.46
1:AO:100:ARG:NH1	1:AO:134:LEU:HB3	2.30	0.46
1:AS:181:MET:HE1	1:AT:181:MET:HE1	1.98	0.46
1:AT:77:PRO:HG2	1:AU:166:ALA:HB3	1.98	0.46
1:AW:77:PRO:HG2	1:AX:166:ALA:HB3	1.98	0.46
1:BF:77:PRO:HG2	1:BG:166:ALA:HB3	1.98	0.46
1:DA:20:PRO:HG3	1:DG:26:THR:HG21	1.98	0.46
1:DG:32:PRO:O	1:DG:34:ARG:NH1	2.49	0.46
1:AE:102:MET:HA	1:CE:129:ASN:ND2	2.31	0.46
1:AL:65:ARG:NH1	1:CK:161:LEU:HD22	2.30	0.46
1:AS:35:GLN:HB3	1:AS:160:VAL:HG23	1.97	0.46
1:BS:65:ARG:NH1	1:DL:161:LEU:HD22	2.31	0.46
1:BU:204:VAL:HG21	1:CZ:208:ALA:HB2	1.98	0.46
1:CP:77:PRO:HG2	1:CQ:166:ALA:HB3	1.98	0.46
1:CT:100:ARG:NH1	1:CT:134:LEU:HB3	2.30	0.46
1:DA:181:MET:HE1	1:DB:181:MET:HE1	1.98	0.46
1:DF:100:ARG:NH1	1:DF:134:LEU:HB3	2.30	0.46
1:AA:79:GLN:NE2	1:AK:162:THR:O	2.48	0.46
1:AB:162:THR:O	1:CU:79:GLN:NE2	2.49	0.46
1:AD:181:MET:HE1	1:AE:181:MET:HE1	1.98	0.46
1:AG:181:MET:HE1	1:AH:181:MET:HE1	1.98	0.46
1:AY:32:PRO:O	1:AY:34:ARG:NH1	2.49	0.46
1:AZ:162:THR:O	1:BE:79:GLN:NE2	2.49	0.46
1:BA:208:ALA:HB2	1:DK:204:VAL:HG21	1.97	0.46
1:BH:181:MET:HE1	1:BI:181:MET:HE1	1.98	0.46
1:BP:198:VAL:O	1:DI:39:ARG:NH2	2.47	0.46
1:DC:106:THR:HG23	1:DC:123:ILE:HG22	1.96	0.46
1:DD:181:MET:HE1	1:DE:181:MET:HE1	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DE:77:PRO:HG2	1:DF:166:ALA:HB3	1.98	0.46
1:AA:181:MET:HE1	1:AB:181:MET:HE1	1.98	0.46
1:AJ:30:VAL:O	1:AJ:32:PRO:HD3	2.16	0.46
1:AV:181:MET:HE1	1:AW:181:MET:HE1	1.98	0.46
1:AZ:77:PRO:HG2	1:BA:166:ALA:HB3	1.98	0.46
1:BA:100:ARG:NH1	1:BA:134:LEU:HB3	2.30	0.46
1:BG:65:ARG:NH1	1:CZ:161:LEU:HD22	2.30	0.46
1:BJ:39:ARG:NH2	1:DC:198:VAL:O	2.48	0.46
1:BL:77:PRO:HG2	1:BM:166:ALA:HB3	1.98	0.46
1:BW:181:MET:HE1	1:BX:181:MET:HE1	1.98	0.46
1:BZ:30:VAL:O	1:BZ:32:PRO:HD3	2.16	0.46
1:BZ:32:PRO:O	1:BZ:34:ARG:NH1	2.49	0.46
1:BZ:181:MET:HE1	1:CA:181:MET:HE1	1.98	0.46
1:CS:77:PRO:HG2	1:CT:166:ALA:HB3	1.98	0.46
1:DD:30:VAL:O	1:DD:32:PRO:HD3	2.16	0.46
1:DG:181:MET:HE1	1:DH:181:MET:HE1	1.98	0.46
1:DK:77:PRO:HG2	1:DL:166:ALA:HB3	1.98	0.46
1:AF:150:LYS:HB2	1:CE:156:LEU:HD12	1.98	0.46
1:BA:41:VAL:HB	1:CT:196:ARG:HA	1.98	0.46
1:BB:181:MET:HE1	1:BC:181:MET:HE1	1.98	0.46
1:BD:102:MET:HE1	1:BQ:28:PHE:CE2	2.50	0.46
1:BN:181:MET:HE1	1:BO:181:MET:HE1	1.98	0.46
1:BP:100:ARG:NH1	1:BP:134:LEU:HB3	2.30	0.46
1:BT:181:MET:HE1	1:BU:181:MET:HE1	1.98	0.46
1:CE:100:ARG:NH1	1:CE:134:LEU:HB3	2.30	0.46
1:CJ:77:PRO:HG2	1:CK:166:ALA:HB3	1.98	0.46
1:CL:108:VAL:HG22	1:CL:121:ILE:HG12	1.96	0.46
1:CM:77:PRO:HG2	1:CN:166:ALA:HB3	1.98	0.46
1:CY:77:PRO:HG2	1:CZ:166:ALA:HB3	1.98	0.46
1:DD:32:PRO:O	1:DD:34:ARG:NH1	2.49	0.46
1:DG:30:VAL:O	1:DG:32:PRO:HD3	2.16	0.46
1:DG:35:GLN:HB3	1:DG:160:VAL:HG23	1.97	0.46
1:DI:180:LEU:HA	1:DI:180:LEU:HD23	1.77	0.46
1:DJ:32:PRO:O	1:DJ:34:ARG:NH1	2.49	0.46
1:AP:32:PRO:O	1:AP:34:ARG:NH1	2.49	0.46
1:BB:32:PRO:O	1:BB:34:ARG:NH1	2.49	0.46
1:BE:30:VAL:O	1:BE:32:PRO:HD3	2.16	0.46
1:BK:79:GLN:NE2	1:BU:162:THR:O	2.49	0.46
1:BN:30:VAL:O	1:BN:32:PRO:HD3	2.16	0.46
1:BR:77:PRO:HG2	1:BS:166:ALA:HB3	1.98	0.46
1:BU:77:PRO:HG2	1:BV:166:ALA:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:77:PRO:HG2	1:BY:166:ALA:HB3	1.98	0.46
1:AA:32:PRO:O	1:AA:34:ARG:NH1	2.49	0.45
1:AJ:32:PRO:O	1:AJ:34:ARG:NH1	2.49	0.45
1:AK:22:GLN:HA	1:CA:31:ASN:HD21	1.81	0.45
1:AL:196:ARG:HA	1:CK:41:VAL:HB	1.97	0.45
1:AQ:77:PRO:HG2	1:AR:166:ALA:HB3	1.98	0.45
1:AS:30:VAL:O	1:AS:32:PRO:HD3	2.16	0.45
1:AV:30:VAL:O	1:AV:32:PRO:HD3	2.16	0.45
1:BA:39:ARG:NH2	1:CT:198:VAL:O	2.48	0.45
1:BC:77:PRO:HG2	1:BD:166:ALA:HB3	1.98	0.45
1:BH:30:VAL:O	1:BH:32:PRO:HD3	2.16	0.45
1:BW:30:VAL:O	1:BW:32:PRO:HD3	2.16	0.45
1:CF:30:VAL:O	1:CF:32:PRO:HD3	2.16	0.45
1:CO:181:MET:HE1	1:CP:181:MET:HE1	1.98	0.45
1:CQ:100:ARG:NH1	1:CQ:134:LEU:HB3	2.30	0.45
1:DB:77:PRO:HG2	1:DC:166:ALA:HB3	1.98	0.45
1:AE:83:PRO:HG2	1:CE:194:THR:HG21	1.98	0.45
1:AP:181:MET:HE1	1:AQ:181:MET:HE1	1.98	0.45
1:AS:32:PRO:O	1:AS:34:ARG:NH1	2.49	0.45
1:AZ:31:ASN:HD21	1:BU:22:GLN:HA	1.81	0.45
1:BG:100:ARG:NH1	1:BG:134:LEU:HB3	2.30	0.45
1:BO:77:PRO:HG2	1:BP:166:ALA:HB3	1.98	0.45
1:CO:30:VAL:O	1:CO:32:PRO:HD3	2.16	0.45
1:CR:30:VAL:O	1:CR:32:PRO:HD3	2.16	0.45
1:CR:181:MET:HE1	1:CS:181:MET:HE1	1.98	0.45
1:DA:30:VAL:O	1:DA:32:PRO:HD3	2.16	0.45
1:AH:77:PRO:HG2	1:AI:166:ALA:HB3	1.98	0.45
1:AM:181:MET:HE1	1:AN:181:MET:HE1	1.98	0.45
1:AU:100:ARG:NH1	1:AU:134:LEU:HB3	2.30	0.45
1:BM:180:LEU:HD23	1:BM:180:LEU:HA	1.77	0.45
1:BR:204:VAL:HG21	1:CW:208:ALA:HB2	1.97	0.45
1:BS:100:ARG:NH1	1:BS:134:LEU:HB3	2.30	0.45
1:BT:30:VAL:O	1:BT:32:PRO:HD3	2.16	0.45
1:BT:32:PRO:O	1:BT:34:ARG:NH1	2.49	0.45
1:CC:30:VAL:O	1:CC:32:PRO:HD3	2.16	0.45
1:DJ:181:MET:HE1	1:DK:181:MET:HE1	1.98	0.45
1:AM:30:VAL:O	1:AM:32:PRO:HD3	2.16	0.45
1:AY:30:VAL:O	1:AY:32:PRO:HD3	2.16	0.45
1:AZ:102:MET:SD	1:CT:129:ASN:ND2	2.90	0.45
1:BC:22:GLN:HA	1:DH:31:ASN:HD21	1.81	0.45
1:CG:77:PRO:HG2	1:CH:166:ALA:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:30:VAL:O	1:CL:32:PRO:HD3	2.16	0.45
1:CL:181:MET:HE1	1:CM:181:MET:HE1	1.98	0.45
1:CO:32:PRO:O	1:CO:34:ARG:NH1	2.49	0.45
1:CU:30:VAL:O	1:CU:32:PRO:HD3	2.16	0.45
1:AD:32:PRO:O	1:AD:34:ARG:NH1	2.49	0.45
1:AW:22:GLN:HA	1:BI:31:ASN:HD21	1.81	0.45
1:BF:49:MET:HE3	1:BF:52:THR:HG21	1.99	0.45
1:BG:204:VAL:HG11	1:CY:85:VAL:HG11	1.99	0.45
1:BH:32:PRO:O	1:BH:34:ARG:NH1	2.49	0.45
1:BK:30:VAL:O	1:BK:32:PRO:HD3	2.16	0.45
1:AE:77:PRO:HG2	1:AF:166:ALA:HB3	1.98	0.45
1:AF:65:ARG:NH1	1:CE:161:LEU:HD22	2.31	0.45
1:AG:30:VAL:O	1:AG:32:PRO:HD3	2.16	0.45
1:AY:181:MET:HE1	1:AZ:181:MET:HE1	1.98	0.45
1:BB:30:VAL:O	1:BB:32:PRO:HD3	2.16	0.45
1:BR:49:MET:HE3	1:BR:52:THR:HG21	1.99	0.45
1:CA:77:PRO:HG2	1:CB:166:ALA:HB3	1.98	0.45
1:CY:49:MET:HE3	1:CY:52:THR:HG21	1.99	0.45
1:AK:77:PRO:HG2	1:AL:166:ALA:HB3	1.98	0.45
1:AM:32:PRO:O	1:AM:34:ARG:NH1	2.49	0.45
1:AQ:49:MET:HE3	1:AQ:52:THR:HG21	1.99	0.45
1:BH:21:VAL:HG21	1:DJ:18:GLN:OE1	2.16	0.45
1:BI:49:MET:HE3	1:BI:52:THR:HG21	1.99	0.45
1:BL:49:MET:HE3	1:BL:52:THR:HG21	1.99	0.45
1:BL:162:THR:O	1:DA:79:GLN:NE2	2.50	0.45
1:BQ:32:PRO:O	1:BQ:34:ARG:NH1	2.49	0.45
1:CM:49:MET:HE3	1:CM:52:THR:HG21	1.99	0.45
1:CV:49:MET:HE3	1:CV:52:THR:HG21	1.99	0.45
1:CW:100:ARG:NH1	1:CW:134:LEU:HB3	2.30	0.45
1:AC:100:ARG:NH1	1:AC:134:LEU:HB3	2.30	0.45
1:AC:140:PRO:HA	1:CV:137:SER:O	2.17	0.45
1:AD:28:PHE:CE2	1:AU:102:MET:HE1	2.52	0.45
1:AF:129:ASN:O	1:AF:133:THR:OG1	2.23	0.45
1:BC:102:MET:SD	1:CW:129:ASN:ND2	2.90	0.45
1:BI:162:THR:O	1:DG:79:GLN:NE2	2.49	0.45
1:BM:161:LEU:HD22	1:DF:65:ARG:NH1	2.31	0.45
1:BR:102:MET:SD	1:DL:129:ASN:ND2	2.90	0.45
1:CB:100:ARG:NH1	1:CB:134:LEU:HB3	2.30	0.45
1:CG:49:MET:HE3	1:CG:52:THR:HG21	1.99	0.45
1:CI:30:VAL:O	1:CI:32:PRO:HD3	2.16	0.45
1:CX:30:VAL:O	1:CX:32:PRO:HD3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:49:MET:HE3	1:AK:52:THR:HG21	1.99	0.45
1:AN:49:MET:HE3	1:AN:52:THR:HG21	1.99	0.45
1:AQ:85:VAL:HG11	1:CN:204:VAL:HG11	1.99	0.45
1:BC:49:MET:HE3	1:BC:52:THR:HG21	1.99	0.45
1:BG:161:LEU:HD22	1:CZ:65:ARG:NH1	2.32	0.45
1:BH:79:GLN:NE2	1:BR:162:THR:O	2.50	0.45
1:BI:77:PRO:HG2	1:BJ:166:ALA:HB3	1.98	0.45
1:CD:77:PRO:HG2	1:CE:166:ALA:HB3	1.98	0.45
1:AD:30:VAL:O	1:AD:32:PRO:HD3	2.16	0.45
1:AN:77:PRO:HG2	1:AO:166:ALA:HB3	1.98	0.45
1:AV:28:PHE:CE2	1:DI:102:MET:HE1	2.52	0.45
1:AW:49:MET:HE3	1:AW:52:THR:HG21	1.99	0.45
1:CJ:49:MET:HE3	1:CJ:52:THR:HG21	1.99	0.45
1:CS:162:THR:O	1:DJ:79:GLN:NE2	2.50	0.45
1:CV:77:PRO:HG2	1:CW:166:ALA:HB3	1.98	0.45
1:DH:49:MET:HE3	1:DH:52:THR:HG21	1.99	0.45
1:AG:32:PRO:O	1:AG:34:ARG:NH1	2.49	0.44
1:AJ:181:MET:HE1	1:AK:181:MET:HE1	1.98	0.44
1:BE:32:PRO:O	1:BE:34:ARG:NH1	2.49	0.44
1:BE:181:MET:HE1	1:BF:181:MET:HE1	1.98	0.44
1:BP:140:PRO:HA	1:DE:137:SER:O	2.16	0.44
1:DC:100:ARG:NH1	1:DC:134:LEU:HB3	2.30	0.44
1:AP:30:VAL:O	1:AP:32:PRO:HD3	2.16	0.44
1:BD:41:VAL:HB	1:CW:196:ARG:HA	1.99	0.44
1:BK:164:THR:HG22	1:BK:169:GLN:HG2	2.00	0.44
1:CC:32:PRO:O	1:CC:34:ARG:NH1	2.49	0.44
1:CI:79:GLN:NE2	1:CP:162:THR:O	2.50	0.44
1:DA:32:PRO:O	1:DA:34:ARG:NH1	2.49	0.44
1:DH:77:PRO:HG2	1:DI:166:ALA:HB3	1.98	0.44
1:AA:30:VAL:O	1:AA:32:PRO:HD3	2.16	0.44
1:AS:161:LEU:HG	1:AT:66:HIS:CE1	2.53	0.44
1:AV:164:THR:HG22	1:AV:169:GLN:HG2	2.00	0.44
1:CF:32:PRO:O	1:CF:34:ARG:NH1	2.49	0.44
1:CI:181:MET:HE1	1:CJ:181:MET:HE1	1.98	0.44
1:CL:32:PRO:O	1:CL:34:ARG:NH1	2.49	0.44
1:DD:161:LEU:HG	1:DE:66:HIS:CE1	2.53	0.44
1:DK:49:MET:HE3	1:DK:52:THR:HG21	1.99	0.44
1:AG:79:GLN:NE2	1:CG:162:THR:O	2.51	0.44
1:AL:198:VAL:O	1:CK:39:ARG:NH2	2.49	0.44
1:BF:204:VAL:HG21	1:CT:208:ALA:HB2	1.99	0.44
1:BJ:204:VAL:HG11	1:DB:85:VAL:HG11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:22:GLN:HA	1:CS:31:ASN:HD21	1.81	0.44
1:DG:164:THR:HG22	1:DG:169:GLN:HG2	2.00	0.44
1:DJ:164:THR:HG22	1:DJ:169:GLN:HG2	2.00	0.44
1:AV:161:LEU:HG	1:AW:66:HIS:CE1	2.53	0.44
1:BB:164:THR:HG22	1:BB:169:GLN:HG2	2.00	0.44
1:BQ:30:VAL:O	1:BQ:32:PRO:HD3	2.16	0.44
1:BS:204:VAL:HG11	1:DK:85:VAL:HG11	1.98	0.44
1:BT:161:LEU:HG	1:BU:66:HIS:CE1	2.53	0.44
1:CC:28:PHE:CE2	1:CZ:102:MET:HE1	2.53	0.44
1:CF:161:LEU:HG	1:CG:66:HIS:CE1	2.53	0.44
1:CX:161:LEU:HG	1:CY:66:HIS:CE1	2.53	0.44
1:CX:164:THR:HG22	1:CX:169:GLN:HG2	2.00	0.44
1:DJ:30:VAL:O	1:DJ:32:PRO:HD3	2.16	0.44
1:AB:49:MET:HE3	1:AB:52:THR:HG21	1.99	0.44
1:AD:161:LEU:HG	1:AE:66:HIS:CE1	2.53	0.44
1:BE:161:LEU:HG	1:BF:66:HIS:CE1	2.53	0.44
1:BI:102:MET:SD	1:DC:129:ASN:ND2	2.90	0.44
1:BZ:79:GLN:NE2	1:CV:162:THR:O	2.50	0.44
1:CI:161:LEU:HG	1:CJ:66:HIS:CE1	2.53	0.44
1:CM:55:TYR:O	1:CM:58:SER:HB3	2.18	0.44
1:CW:180:LEU:HD23	1:CW:180:LEU:HA	1.78	0.44
1:DG:161:LEU:HG	1:DH:66:HIS:CE1	2.53	0.44
1:DJ:161:LEU:HG	1:DK:66:HIS:CE1	2.53	0.44
1:AA:161:LEU:HG	1:AB:66:HIS:CE1	2.53	0.44
1:AE:137:SER:O	1:AU:140:PRO:HA	2.18	0.44
1:AF:194:THR:HG21	1:CD:83:PRO:CG	2.47	0.44
1:AM:161:LEU:HG	1:AN:66:HIS:CE1	2.53	0.44
1:AS:79:GLN:NE2	1:BX:162:THR:O	2.51	0.44
1:AS:164:THR:HG22	1:AS:169:GLN:HG2	2.00	0.44
1:AY:19:GLY:O	1:AY:21:VAL:HG23	2.18	0.44
1:BD:180:LEU:HD23	1:BD:180:LEU:HA	1.78	0.44
1:BH:161:LEU:HG	1:BI:66:HIS:CE1	2.53	0.44
1:BM:170:PHE:HE1	1:DF:194:THR:C	2.26	0.44
1:BW:32:PRO:O	1:BW:34:ARG:NH1	2.49	0.44
1:CR:161:LEU:HG	1:CS:66:HIS:CE1	2.53	0.44
1:DE:49:MET:HE3	1:DE:52:THR:HG21	1.99	0.44
1:AG:19:GLY:O	1:AG:21:VAL:HG23	2.18	0.44
1:AK:137:SER:O	1:AO:140:PRO:HA	2.18	0.44
1:AL:39:ARG:NH2	1:CK:198:VAL:O	2.50	0.44
1:AL:208:ALA:CB	1:CG:204:VAL:HG21	2.47	0.44
1:BT:164:THR:HG22	1:BT:169:GLN:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BW:19:GLY:O	1:BW:21:VAL:HG23	2.18	0.44
1:CO:161:LEU:HG	1:CP:66:HIS:CE1	2.53	0.44
1:CR:164:THR:HG22	1:CR:169:GLN:HG2	2.00	0.44
1:AG:161:LEU:HG	1:AH:66:HIS:CE1	2.53	0.44
1:AH:49:MET:HE3	1:AH:52:THR:HG21	1.99	0.44
1:AP:164:THR:HG22	1:AP:169:GLN:HG2	2.00	0.44
1:AT:85:VAL:HG11	1:CQ:204:VAL:HG11	1.99	0.44
1:AV:19:GLY:O	1:AV:21:VAL:HG23	2.18	0.44
1:BE:19:GLY:O	1:BE:21:VAL:HG23	2.18	0.44
1:BH:164:THR:HG22	1:BH:169:GLN:HG2	2.00	0.44
1:BI:55:TYR:O	1:BI:58:SER:HB3	2.18	0.44
1:BN:164:THR:HG22	1:BN:169:GLN:HG2	2.00	0.44
1:BQ:161:LEU:HG	1:BR:66:HIS:CE1	2.53	0.44
1:BU:31:ASN:HD21	1:DB:22:GLN:HA	1.82	0.44
1:BW:161:LEU:HG	1:BX:66:HIS:CE1	2.53	0.44
1:BZ:161:LEU:HG	1:CA:66:HIS:CE1	2.53	0.44
1:CA:55:TYR:O	1:CA:58:SER:HB3	2.18	0.44
1:CC:19:GLY:O	1:CC:21:VAL:HG23	2.18	0.44
1:CD:49:MET:HE3	1:CD:52:THR:HG21	1.99	0.44
1:CE:180:LEU:HD23	1:CE:180:LEU:HA	1.78	0.44
1:CI:164:THR:HG22	1:CI:169:GLN:HG2	2.00	0.44
1:CL:19:GLY:O	1:CL:21:VAL:HG23	2.18	0.44
1:CS:49:MET:HE3	1:CS:52:THR:HG21	1.99	0.44
1:DB:49:MET:HE3	1:DB:52:THR:HG21	1.99	0.44
1:DK:55:TYR:O	1:DK:58:SER:HB3	2.18	0.44
1:AE:83:PRO:CG	1:CE:194:THR:HG21	2.47	0.43
1:AM:19:GLY:O	1:AM:21:VAL:HG23	2.18	0.43
1:AM:164:THR:HG22	1:AM:169:GLN:HG2	2.00	0.43
1:AQ:55:TYR:O	1:AQ:58:SER:HB3	2.18	0.43
1:AR:180:LEU:HD23	1:AR:180:LEU:HA	1.77	0.43
1:AS:19:GLY:O	1:AS:21:VAL:HG23	2.18	0.43
1:AY:161:LEU:HG	1:AZ:66:HIS:CE1	2.53	0.43
1:BB:161:LEU:HG	1:BC:66:HIS:CE1	2.53	0.43
1:BC:55:TYR:O	1:BC:58:SER:HB3	2.18	0.43
1:BG:180:LEU:HD23	1:BG:180:LEU:HA	1.78	0.43
1:BM:39:ARG:NH2	1:DF:198:VAL:O	2.50	0.43
1:CA:49:MET:HE3	1:CA:52:THR:HG21	1.99	0.43
1:CF:164:THR:HG22	1:CF:169:GLN:HG2	2.00	0.43
1:CP:49:MET:HE3	1:CP:52:THR:HG21	1.99	0.43
1:CV:55:TYR:O	1:CV:58:SER:HB3	2.18	0.43
1:DB:55:TYR:O	1:DB:58:SER:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DF:180:LEU:HA	1:DF:180:LEU:HD23	1.77	0.43
1:DG:19:GLY:O	1:DG:21:VAL:HG23	2.18	0.43
1:AL:194:THR:HG21	1:CJ:83:PRO:CG	2.48	0.43
1:AN:55:TYR:O	1:AN:58:SER:HB3	2.18	0.43
1:AT:49:MET:HE3	1:AT:52:THR:HG21	1.99	0.43
1:AU:204:VAL:HG11	1:CP:85:VAL:HG11	2.00	0.43
1:BA:204:VAL:HG11	1:CS:85:VAL:HG11	2.00	0.43
1:BQ:164:THR:HG22	1:BQ:169:GLN:HG2	2.00	0.43
1:BR:55:TYR:O	1:BR:58:SER:HB3	2.18	0.43
1:BZ:19:GLY:O	1:BZ:21:VAL:HG23	2.18	0.43
1:CG:22:GLN:HA	1:CP:31:ASN:HD21	1.82	0.43
1:CJ:55:TYR:O	1:CJ:58:SER:HB3	2.18	0.43
1:CO:19:GLY:O	1:CO:21:VAL:HG23	2.18	0.43
1:CU:161:LEU:HG	1:CV:66:HIS:CE1	2.53	0.43
1:AB:108:VAL:HG22	1:AB:121:ILE:HG12	2.01	0.43
1:AJ:19:GLY:O	1:AJ:21:VAL:HG23	2.18	0.43
1:AP:161:LEU:HG	1:AQ:66:HIS:CE1	2.53	0.43
1:AW:55:TYR:O	1:AW:58:SER:HB3	2.18	0.43
1:BJ:41:VAL:HB	1:DC:196:ARG:HA	2.00	0.43
1:BK:19:GLY:O	1:BK:21:VAL:HG23	2.18	0.43
1:BO:49:MET:HE3	1:BO:52:THR:HG21	1.99	0.43
1:BU:49:MET:HE3	1:BU:52:THR:HG21	1.99	0.43
1:BU:108:VAL:HG22	1:BU:121:ILE:HG12	2.01	0.43
1:CC:79:GLN:NE2	1:CY:162:THR:O	2.52	0.43
1:CC:161:LEU:HG	1:CD:66:HIS:CE1	2.53	0.43
1:CG:55:TYR:O	1:CG:58:SER:HB3	2.18	0.43
1:CL:161:LEU:HG	1:CM:66:HIS:CE1	2.53	0.43
1:CR:19:GLY:O	1:CR:21:VAL:HG23	2.18	0.43
1:DJ:19:GLY:O	1:DJ:21:VAL:HG23	2.18	0.43
1:AB:55:TYR:O	1:AB:58:SER:HB3	2.18	0.43
1:AJ:161:LEU:HG	1:AK:66:HIS:CE1	2.53	0.43
1:AZ:49:MET:HE3	1:AZ:52:THR:HG21	1.99	0.43
1:BA:102:MET:HE1	1:BE:28:PHE:CE2	2.54	0.43
1:BD:204:VAL:HG11	1:CV:85:VAL:HG11	2.00	0.43
1:BK:161:LEU:HG	1:BL:66:HIS:CE1	2.53	0.43
1:BO:102:MET:SD	1:DI:129:ASN:ND2	2.91	0.43
1:CL:164:THR:HG22	1:CL:169:GLN:HG2	2.00	0.43
1:CU:164:THR:HG22	1:CU:169:GLN:HG2	2.00	0.43
1:DH:55:TYR:O	1:DH:58:SER:HB3	2.18	0.43
1:AA:19:GLY:O	1:AA:21:VAL:HG23	2.18	0.43
1:AD:19:GLY:O	1:AD:21:VAL:HG23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:27:THR:O	1:CS:25:ARG:HA	2.17	0.43
1:AG:50:GLU:O	1:AG:54:THR:HG23	2.19	0.43
1:AH:55:TYR:O	1:AH:58:SER:HB3	2.18	0.43
1:AP:19:GLY:O	1:AP:21:VAL:HG23	2.18	0.43
1:AU:180:LEU:HD23	1:AU:180:LEU:HA	1.77	0.43
1:BN:19:GLY:O	1:BN:21:VAL:HG23	2.18	0.43
1:BN:161:LEU:HG	1:BO:66:HIS:CE1	2.53	0.43
1:BU:55:TYR:O	1:BU:58:SER:HB3	2.18	0.43
1:CF:50:GLU:O	1:CF:54:THR:HG23	2.19	0.43
1:CO:164:THR:HG22	1:CO:169:GLN:HG2	2.00	0.43
1:CX:32:PRO:O	1:CX:34:ARG:NH1	2.49	0.43
1:DE:55:TYR:O	1:DE:58:SER:HB3	2.18	0.43
1:AA:50:GLU:O	1:AA:54:THR:HG23	2.19	0.43
1:AK:55:TYR:O	1:AK:58:SER:HB3	2.18	0.43
1:BC:31:ASN:H	1:BI:23:SER:HB3	1.82	0.43
1:BG:194:THR:C	1:CZ:170:PHE:HE1	2.26	0.43
1:BP:103:ALA:HB2	1:DE:129:ASN:HB3	1.99	0.43
1:CJ:108:VAL:HG22	1:CJ:121:ILE:HG12	2.01	0.43
1:CU:19:GLY:O	1:CU:21:VAL:HG23	2.18	0.43
1:CX:50:GLU:O	1:CX:54:THR:HG23	2.19	0.43
1:CY:55:TYR:O	1:CY:58:SER:HB3	2.18	0.43
1:DG:50:GLU:O	1:DG:54:THR:HG23	2.19	0.43
1:DH:108:VAL:HG22	1:DH:121:ILE:HG12	2.01	0.43
1:AA:164:THR:HG22	1:AA:169:GLN:HG2	2.00	0.43
1:AB:31:ASN:HD21	1:CA:22:GLN:HA	1.83	0.43
1:AE:55:TYR:O	1:AE:58:SER:HB3	2.18	0.43
1:AF:194:THR:HG21	1:CD:83:PRO:HG2	2.01	0.43
1:AM:50:GLU:O	1:AM:54:THR:HG23	2.19	0.43
1:AT:55:TYR:O	1:AT:58:SER:HB3	2.18	0.43
1:BH:19:GLY:O	1:BH:21:VAL:HG23	2.18	0.43
1:BH:87:THR:HG22	1:BR:40:PRO:CG	2.43	0.43
1:BL:55:TYR:O	1:BL:58:SER:HB3	2.18	0.43
1:BS:196:ARG:HA	1:DL:41:VAL:HB	2.01	0.43
1:BS:208:ALA:CB	1:BX:204:VAL:HG21	2.49	0.43
1:CP:108:VAL:HG22	1:CP:121:ILE:HG12	2.01	0.43
1:DA:161:LEU:HG	1:DB:66:HIS:CE1	2.53	0.43
1:AE:49:MET:HE3	1:AE:52:THR:HG21	1.99	0.43
1:AE:138:ALA:O	1:CE:139:ILE:HD11	2.19	0.43
1:AF:204:VAL:HG11	1:CD:85:VAL:HG11	2.01	0.43
1:AJ:164:THR:HG22	1:AJ:169:GLN:HG2	2.00	0.43
1:AL:139:ILE:HD11	1:CJ:138:ALA:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:22:GLN:HA	1:DK:31:ASN:HD21	1.81	0.43
1:AV:50:GLU:O	1:AV:54:THR:HG23	2.19	0.43
1:BF:108:VAL:HG22	1:BF:121:ILE:HG12	2.01	0.43
1:BG:39:ARG:NH2	1:CZ:198:VAL:O	2.52	0.43
1:BI:108:VAL:HG22	1:BI:121:ILE:HG12	2.01	0.43
1:BN:50:GLU:O	1:BN:54:THR:HG23	2.19	0.43
1:BP:41:VAL:HB	1:DI:196:ARG:HA	2.01	0.43
1:BQ:50:GLU:O	1:BQ:54:THR:HG23	2.19	0.43
1:BR:108:VAL:HG22	1:BR:121:ILE:HG12	2.01	0.43
1:BT:88:LYS:HE2	1:BU:201:SER:O	2.19	0.43
1:BW:50:GLU:O	1:BW:54:THR:HG23	2.19	0.43
1:BX:108:VAL:HG22	1:BX:121:ILE:HG12	2.01	0.43
1:CC:50:GLU:O	1:CC:54:THR:HG23	2.19	0.43
1:CD:55:TYR:O	1:CD:58:SER:HB3	2.18	0.43
1:CM:108:VAL:HG22	1:CM:121:ILE:HG12	2.01	0.43
1:CN:140:PRO:HA	1:CP:137:SER:O	2.19	0.43
1:CO:50:GLU:O	1:CO:54:THR:HG23	2.19	0.43
1:CS:55:TYR:O	1:CS:58:SER:HB3	2.18	0.43
1:CU:88:LYS:HE2	1:CV:201:SER:O	2.19	0.43
1:CY:108:VAL:HG22	1:CY:121:ILE:HG12	2.01	0.43
1:DD:88:LYS:HE2	1:DE:201:SER:O	2.19	0.43
1:DD:164:THR:HG22	1:DD:169:GLN:HG2	2.00	0.43
1:DK:108:VAL:HG22	1:DK:121:ILE:HG12	2.01	0.43
1:AD:164:THR:HG22	1:AD:169:GLN:HG2	2.00	0.43
1:AJ:88:LYS:HE2	1:AK:201:SER:O	2.19	0.43
1:AL:156:LEU:HD12	1:CK:150:LYS:HB2	2.01	0.43
1:AL:180:LEU:HA	1:AL:180:LEU:HD23	1.77	0.43
1:AM:14:TYR:HE2	1:AM:23:SER:HA	1.84	0.43
1:AT:108:VAL:HG22	1:AT:121:ILE:HG12	2.01	0.43
1:AW:162:THR:O	1:BB:79:GLN:NE2	2.51	0.43
1:AZ:55:TYR:O	1:AZ:58:SER:HB3	2.18	0.43
1:BA:156:LEU:HD12	1:CT:150:LYS:HB2	2.01	0.43
1:BC:85:VAL:HG11	1:CW:204:VAL:HG11	2.01	0.43
1:BK:50:GLU:O	1:BK:54:THR:HG23	2.19	0.43
1:BP:39:ARG:NH2	1:DI:198:VAL:O	2.49	0.43
1:BX:49:MET:HE3	1:BX:52:THR:HG21	1.99	0.43
1:BZ:164:THR:HG22	1:BZ:169:GLN:HG2	2.00	0.43
1:CC:164:THR:HG22	1:CC:169:GLN:HG2	2.00	0.43
1:CD:137:SER:O	1:CZ:140:PRO:HA	2.18	0.43
1:CU:50:GLU:O	1:CU:54:THR:HG23	2.19	0.43
1:AD:88:LYS:HE2	1:AE:201:SER:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:108:VAL:HG22	1:AE:121:ILE:HG12	2.01	0.43
1:AQ:108:VAL:HG22	1:AQ:121:ILE:HG12	2.01	0.43
1:AS:14:TYR:HE2	1:AS:23:SER:HA	1.84	0.43
1:AS:88:LYS:HE2	1:AT:201:SER:O	2.19	0.43
1:BD:196:ARG:HA	1:CW:41:VAL:HB	2.01	0.43
1:BI:102:MET:HA	1:DC:129:ASN:ND2	2.34	0.43
1:CG:31:ASN:HD21	1:CM:22:GLN:HA	1.84	0.43
1:CN:102:MET:HE1	1:CO:28:PHE:CE2	2.54	0.43
1:CP:55:TYR:O	1:CP:58:SER:HB3	2.18	0.43
1:CX:14:TYR:HE2	1:CX:23:SER:HA	1.84	0.43
1:CX:19:GLY:O	1:CX:21:VAL:HG23	2.18	0.43
1:AJ:50:GLU:O	1:AJ:54:THR:HG23	2.19	0.42
1:AN:108:VAL:HG22	1:AN:121:ILE:HG12	2.01	0.42
1:AT:137:SER:O	1:BY:140:PRO:HA	2.19	0.42
1:BE:88:LYS:HE2	1:BF:201:SER:O	2.19	0.42
1:BF:162:THR:O	1:BT:79:GLN:NE2	2.52	0.42
1:BG:43:LEU:HD12	1:BG:43:LEU:HA	1.90	0.42
1:BN:88:LYS:HE2	1:BO:201:SER:O	2.19	0.42
1:BX:55:TYR:O	1:BX:58:SER:HB3	2.18	0.42
1:CG:108:VAL:HG22	1:CG:121:ILE:HG12	2.01	0.42
1:CI:50:GLU:O	1:CI:54:THR:HG23	2.19	0.42
1:CV:108:VAL:HG22	1:CV:121:ILE:HG12	2.01	0.42
1:DE:108:VAL:HG22	1:DE:121:ILE:HG12	2.01	0.42
1:AG:164:THR:HG22	1:AG:169:GLN:HG2	2.00	0.42
1:AK:109:THR:HB	1:AK:120:SER:OG	2.20	0.42
1:AM:28:PHE:CE2	1:CB:102:MET:HE1	2.54	0.42
1:AP:14:TYR:HE2	1:AP:23:SER:HA	1.84	0.42
1:AR:129:ASN:ND2	1:CM:102:MET:SD	2.92	0.42
1:AR:204:VAL:HG11	1:CM:85:VAL:HG11	2.01	0.42
1:AV:88:LYS:HE2	1:AW:201:SER:O	2.19	0.42
1:AY:50:GLU:O	1:AY:54:THR:HG23	2.19	0.42
1:BD:129:ASN:ND2	1:CV:102:MET:SD	2.92	0.42
1:BH:88:LYS:HE2	1:BI:201:SER:O	2.19	0.42
1:BS:139:ILE:HD11	1:DK:138:ALA:O	2.19	0.42
1:BT:19:GLY:O	1:BT:21:VAL:HG23	2.18	0.42
1:CD:108:VAL:HG22	1:CD:121:ILE:HG12	2.01	0.42
1:CF:19:GLY:O	1:CF:21:VAL:HG23	2.18	0.42
1:CI:19:GLY:O	1:CI:21:VAL:HG23	2.18	0.42
1:DA:19:GLY:O	1:DA:21:VAL:HG23	2.18	0.42
1:DA:50:GLU:O	1:DA:54:THR:HG23	2.19	0.42
1:DA:164:THR:HG22	1:DA:169:GLN:HG2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DB:108:VAL:HG22	1:DB:121:ILE:HG12	2.01	0.42
1:DD:19:GLY:O	1:DD:21:VAL:HG23	2.18	0.42
1:DD:50:GLU:O	1:DD:54:THR:HG23	2.19	0.42
1:AE:109:THR:HB	1:AE:120:SER:OG	2.20	0.42
1:AL:170:PHE:HE1	1:CK:194:THR:C	2.27	0.42
1:BB:50:GLU:O	1:BB:54:THR:HG23	2.19	0.42
1:BL:40:PRO:CG	1:DA:87:THR:HG22	2.41	0.42
1:BM:163:GLY:H	1:DF:65:ARG:HD3	1.82	0.42
1:BU:109:THR:HB	1:BU:120:SER:OG	2.20	0.42
1:CA:109:THR:HB	1:CA:120:SER:OG	2.20	0.42
1:CJ:109:THR:HB	1:CJ:120:SER:OG	2.20	0.42
1:CL:50:GLU:O	1:CL:54:THR:HG23	2.19	0.42
1:CM:109:THR:HB	1:CM:120:SER:HG	1.83	0.42
1:DA:88:LYS:HE2	1:DB:201:SER:O	2.19	0.42
1:AA:14:TYR:HE2	1:AA:23:SER:HA	1.84	0.42
1:AF:198:VAL:O	1:CE:39:ARG:NH2	2.49	0.42
1:AK:108:VAL:HG22	1:AK:121:ILE:HG12	2.01	0.42
1:AM:88:LYS:HE2	1:AN:201:SER:O	2.19	0.42
1:AP:50:GLU:O	1:AP:54:THR:HG23	2.19	0.42
1:AR:196:ARG:HA	1:CN:41:VAL:HB	2.02	0.42
1:AW:108:VAL:HG22	1:AW:121:ILE:HG12	2.01	0.42
1:BB:88:LYS:HE2	1:BC:201:SER:O	2.19	0.42
1:BE:50:GLU:O	1:BE:54:THR:HG23	2.19	0.42
1:BH:14:TYR:HE2	1:BH:23:SER:HA	1.84	0.42
1:BO:109:THR:HB	1:BO:120:SER:OG	2.20	0.42
1:BQ:14:TYR:HE2	1:BQ:23:SER:HA	1.84	0.42
1:BS:170:PHE:HE1	1:DL:194:THR:C	2.27	0.42
1:BU:180:LEU:HD23	1:BU:180:LEU:HA	1.90	0.42
1:BW:88:LYS:HE2	1:BX:201:SER:O	2.19	0.42
1:CF:14:TYR:HE2	1:CF:23:SER:HA	1.84	0.42
1:CR:50:GLU:O	1:CR:54:THR:HG23	2.19	0.42
1:CZ:43:LEU:HD12	1:CZ:43:LEU:HA	1.90	0.42
1:DA:26:THR:HG21	1:DD:20:PRO:HG3	2.00	0.42
1:DB:109:THR:HB	1:DB:120:SER:OG	2.20	0.42
1:DG:14:TYR:HE2	1:DG:23:SER:HA	1.84	0.42
1:DG:88:LYS:HE2	1:DH:201:SER:O	2.19	0.42
1:DJ:14:TYR:HE2	1:DJ:23:SER:HA	1.84	0.42
1:DJ:88:LYS:HE2	1:DK:201:SER:O	2.19	0.42
1:AH:109:THR:HB	1:AH:120:SER:OG	2.20	0.42
1:AI:180:LEU:HD23	1:AI:180:LEU:HA	1.78	0.42
1:AU:41:VAL:HB	1:CQ:196:ARG:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:14:TYR:HE2	1:AV:23:SER:HA	1.84	0.42
1:AV:185:ARG:O	1:AV:189:ASP:HB2	2.20	0.42
1:AY:164:THR:HG22	1:AY:169:GLN:HG2	2.00	0.42
1:BG:170:PHE:HE1	1:CZ:194:THR:C	2.28	0.42
1:BK:88:LYS:HE2	1:BL:201:SER:O	2.19	0.42
1:BO:55:TYR:O	1:BO:58:SER:HB3	2.18	0.42
1:BR:102:MET:HA	1:DL:129:ASN:ND2	2.32	0.42
1:BW:164:THR:HG22	1:BW:169:GLN:HG2	2.00	0.42
1:CC:14:TYR:HE2	1:CC:23:SER:HA	1.84	0.42
1:CF:88:LYS:HE2	1:CG:201:SER:O	2.19	0.42
1:CL:88:LYS:HE2	1:CM:201:SER:O	2.19	0.42
1:CQ:180:LEU:HA	1:CQ:180:LEU:HD23	1.78	0.42
1:CS:109:THR:HB	1:CS:120:SER:OG	2.20	0.42
1:DA:14:TYR:HE2	1:DA:23:SER:HA	1.84	0.42
1:AA:154:GLU:HB3	1:AB:152:ASN:HB2	2.02	0.42
1:AB:109:THR:HB	1:AB:120:SER:OG	2.20	0.42
1:AD:100:ARG:NH1	1:AD:139:ILE:O	2.53	0.42
1:AF:39:ARG:HB3	1:CE:199:ALA:O	2.19	0.42
1:AG:14:TYR:HE2	1:AG:23:SER:HA	1.84	0.42
1:AM:154:GLU:HB3	1:AN:152:ASN:HB2	2.02	0.42
1:AM:185:ARG:O	1:AM:189:ASP:HB2	2.20	0.42
1:AS:28:PHE:CE2	1:BY:102:MET:HE1	2.55	0.42
1:AS:185:ARG:O	1:AS:189:ASP:HB2	2.20	0.42
1:BB:19:GLY:O	1:BB:21:VAL:HG23	2.18	0.42
1:BE:154:GLU:HB3	1:BF:152:ASN:HB2	2.02	0.42
1:BE:164:THR:HG22	1:BE:169:GLN:HG2	2.00	0.42
1:BE:185:ARG:O	1:BE:189:ASP:HB2	2.20	0.42
1:BF:102:MET:HA	1:CZ:129:ASN:ND2	2.35	0.42
1:BH:50:GLU:O	1:BH:54:THR:HG23	2.19	0.42
1:BH:65:ARG:HD3	1:BI:161:LEU:HB3	2.02	0.42
1:BJ:194:THR:C	1:DC:170:PHE:HE1	2.28	0.42
1:BL:108:VAL:HG22	1:BL:121:ILE:HG12	2.01	0.42
1:BN:65:ARG:HD3	1:BO:161:LEU:HB3	2.02	0.42
1:BN:185:ARG:O	1:BN:189:ASP:HB2	2.20	0.42
1:BO:108:VAL:HG22	1:BO:121:ILE:HG12	2.01	0.42
1:BP:43:LEU:HD12	1:BP:43:LEU:HA	1.90	0.42
1:BR:109:THR:HB	1:BR:120:SER:OG	2.20	0.42
1:CA:108:VAL:HG22	1:CA:121:ILE:HG12	2.01	0.42
1:CF:65:ARG:HD3	1:CG:161:LEU:HB3	2.02	0.42
1:CI:65:ARG:HD3	1:CJ:161:LEU:HB3	2.02	0.42
1:CI:100:ARG:NH1	1:CI:139:ILE:O	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:137:SER:O	1:CQ:140:PRO:HA	2.19	0.42
1:CO:88:LYS:HE2	1:CP:201:SER:O	2.19	0.42
1:CV:109:THR:HB	1:CV:120:SER:OG	2.20	0.42
1:CX:65:ARG:HD3	1:CY:161:LEU:HB3	2.02	0.42
1:AA:88:LYS:HE2	1:AB:201:SER:O	2.19	0.42
1:AB:22:GLN:HA	1:AN:31:ASN:HD21	1.83	0.42
1:AB:85:VAL:HG11	1:BY:204:VAL:HG11	2.01	0.42
1:AD:154:GLU:HB3	1:AE:152:ASN:HB2	2.02	0.42
1:AF:142:ALA:O	1:CC:14:TYR:HB2	2.19	0.42
1:AJ:154:GLU:HB3	1:AK:152:ASN:HB2	2.02	0.42
1:AK:85:VAL:HG11	1:CK:204:VAL:HG11	2.00	0.42
1:AQ:116:ARG:HG3	1:AQ:156:LEU:HD23	2.02	0.42
1:AS:154:GLU:HB3	1:AT:152:ASN:HB2	2.02	0.42
1:AV:87:THR:HG22	1:DH:40:PRO:CG	2.42	0.42
1:AV:100:ARG:NH1	1:AV:139:ILE:O	2.53	0.42
1:AY:88:LYS:HE2	1:AZ:201:SER:O	2.19	0.42
1:AZ:108:VAL:HG22	1:AZ:121:ILE:HG12	2.01	0.42
1:BE:34:ARG:HD3	1:BE:161:LEU:HD23	2.02	0.42
1:BF:55:TYR:O	1:BF:58:SER:HB3	2.18	0.42
1:BK:185:ARG:O	1:BK:189:ASP:HB2	2.20	0.42
1:BL:109:THR:HB	1:BL:120:SER:OG	2.20	0.42
1:BN:14:TYR:HE2	1:BN:23:SER:HA	1.84	0.42
1:BN:100:ARG:NH1	1:BN:139:ILE:O	2.53	0.42
1:BQ:100:ARG:NH1	1:BQ:139:ILE:O	2.53	0.42
1:BT:65:ARG:HD3	1:BU:161:LEU:HB3	2.02	0.42
1:BW:65:ARG:HD3	1:BX:161:LEU:HB3	2.02	0.42
1:BW:185:ARG:O	1:BW:189:ASP:HB2	2.20	0.42
1:CE:129:ASN:O	1:CE:133:THR:OG1	2.23	0.42
1:CI:88:LYS:HE2	1:CJ:201:SER:O	2.19	0.42
1:CL:100:ARG:NH1	1:CL:139:ILE:O	2.53	0.42
1:CO:65:ARG:HD3	1:CP:161:LEU:HB3	2.02	0.42
1:CR:185:ARG:O	1:CR:189:ASP:HB2	2.20	0.42
1:CX:88:LYS:HE2	1:CY:201:SER:O	2.19	0.42
1:DA:177:SER:HB2	1:DB:188:GLN:OE1	2.20	0.42
1:DG:65:ARG:HD3	1:DH:161:LEU:HB3	2.02	0.42
1:DJ:50:GLU:O	1:DJ:54:THR:HG23	2.19	0.42
1:DJ:100:ARG:NH1	1:DJ:139:ILE:O	2.53	0.42
1:DJ:185:ARG:O	1:DJ:189:ASP:HB2	2.20	0.42
1:AC:204:VAL:HG11	1:BX:85:VAL:HG11	2.02	0.42
1:AE:102:MET:SD	1:CE:129:ASN:ND2	2.92	0.42
1:AF:139:ILE:HD11	1:CD:138:ALA:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:88:LYS:HE2	1:AH:201:SER:O	2.19	0.42
1:AJ:79:GLN:NE2	1:AN:162:THR:O	2.53	0.42
1:AJ:185:ARG:O	1:AJ:189:ASP:HB2	2.20	0.42
1:AM:34:ARG:HD3	1:AM:161:LEU:HD23	2.02	0.42
1:AP:65:ARG:HD3	1:AQ:161:LEU:HB3	2.02	0.42
1:AP:88:LYS:HE2	1:AQ:201:SER:O	2.19	0.42
1:BB:100:ARG:NH1	1:BB:139:ILE:O	2.53	0.42
1:BC:108:VAL:HG22	1:BC:121:ILE:HG12	2.01	0.42
1:BC:109:THR:HB	1:BC:120:SER:OG	2.20	0.42
1:BI:109:THR:HB	1:BI:120:SER:OG	2.19	0.42
1:BK:14:TYR:HE2	1:BK:23:SER:HA	1.84	0.42
1:BO:116:ARG:HG3	1:BO:156:LEU:HD23	2.02	0.42
1:BQ:88:LYS:HE2	1:BR:201:SER:O	2.19	0.42
1:BT:14:TYR:HE2	1:BT:23:SER:HA	1.84	0.42
1:BT:50:GLU:O	1:BT:54:THR:HG23	2.19	0.42
1:BW:14:TYR:HE2	1:BW:23:SER:HA	1.84	0.42
1:BZ:100:ARG:NH1	1:BZ:139:ILE:O	2.53	0.42
1:CB:55:TYR:O	1:CB:58:SER:HB3	2.20	0.42
1:CO:177:SER:HB2	1:CP:188:GLN:OE1	2.20	0.42
1:CR:88:LYS:HE2	1:CS:201:SER:O	2.19	0.42
1:CS:108:VAL:HG22	1:CS:121:ILE:HG12	2.01	0.42
1:CU:177:SER:HB2	1:CV:188:GLN:OE1	2.20	0.42
1:DA:100:ARG:NH1	1:DA:139:ILE:O	2.53	0.42
1:DJ:154:GLU:HB3	1:DK:152:ASN:HB2	2.02	0.42
1:AF:79:GLN:HB2	1:AF:93:VAL:HG12	2.02	0.42
1:AH:108:VAL:HG22	1:AH:121:ILE:HG12	2.01	0.42
1:AM:65:ARG:HD3	1:AN:161:LEU:HB3	2.02	0.42
1:AP:100:ARG:NH1	1:AP:139:ILE:O	2.53	0.42
1:AP:154:GLU:HB3	1:AQ:152:ASN:HB2	2.02	0.42
1:AQ:109:THR:HB	1:AQ:120:SER:OG	2.20	0.42
1:AS:50:GLU:O	1:AS:54:THR:HG23	2.19	0.42
1:AT:109:THR:HB	1:AT:120:SER:OG	2.20	0.42
1:AW:40:PRO:CG	1:BB:87:THR:HG22	2.43	0.42
1:AW:109:THR:HB	1:AW:120:SER:OG	2.20	0.42
1:BA:180:LEU:HA	1:BA:180:LEU:HD23	1.77	0.42
1:BB:14:TYR:HE2	1:BB:23:SER:HA	1.84	0.42
1:BK:87:THR:HG22	1:BU:40:PRO:CG	2.45	0.42
1:BK:100:ARG:NH1	1:BK:139:ILE:O	2.53	0.42
1:BK:154:GLU:HB3	1:BL:152:ASN:HB2	2.02	0.42
1:BN:177:SER:HB2	1:BO:188:GLN:OE1	2.20	0.42
1:BS:55:TYR:O	1:BS:58:SER:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BZ:34:ARG:HD3	1:BZ:161:LEU:HD23	2.02	0.42
1:BZ:177:SER:HB2	1:CA:188:GLN:OE1	2.20	0.42
1:CC:88:LYS:HE2	1:CD:201:SER:O	2.19	0.42
1:CC:185:ARG:O	1:CC:189:ASP:HB2	2.20	0.42
1:CI:34:ARG:HD3	1:CI:161:LEU:HD23	2.02	0.42
1:CL:154:GLU:HB3	1:CM:152:ASN:HB2	2.02	0.42
1:CO:100:ARG:NH1	1:CO:139:ILE:O	2.53	0.42
1:CT:79:GLN:HB2	1:CT:93:VAL:HG12	2.02	0.42
1:CX:100:ARG:NH1	1:CX:139:ILE:O	2.53	0.42
1:CX:177:SER:HB2	1:CY:188:GLN:OE1	2.20	0.42
1:CY:116:ARG:HG3	1:CY:156:LEU:HD23	2.02	0.42
1:DD:65:ARG:HD3	1:DE:161:LEU:HB3	2.02	0.42
1:DF:55:TYR:O	1:DF:58:SER:HB3	2.20	0.42
1:DG:177:SER:HB2	1:DH:188:GLN:OE1	2.20	0.42
1:DL:55:TYR:O	1:DL:58:SER:HB3	2.20	0.42
1:AA:34:ARG:HD3	1:AA:161:LEU:HD23	2.02	0.42
1:AA:177:SER:HB2	1:AB:188:GLN:OE1	2.20	0.42
1:AD:50:GLU:O	1:AD:54:THR:HG23	2.19	0.42
1:AD:185:ARG:O	1:AD:189:ASP:HB2	2.20	0.42
1:AF:170:PHE:HE1	1:CE:194:THR:C	2.28	0.42
1:AG:100:ARG:NH1	1:AG:139:ILE:O	2.53	0.42
1:AJ:100:ARG:NH1	1:AJ:139:ILE:O	2.53	0.42
1:AR:150:LYS:HB2	1:CN:156:LEU:HD12	2.01	0.42
1:AS:65:ARG:HD3	1:AT:161:LEU:HB3	2.02	0.42
1:AW:116:ARG:HG3	1:AW:156:LEU:HD23	2.02	0.42
1:BB:185:ARG:O	1:BB:189:ASP:HB2	2.20	0.42
1:BC:116:ARG:HG3	1:BC:156:LEU:HD23	2.02	0.42
1:BD:79:GLN:HB2	1:BD:93:VAL:HG12	2.02	0.42
1:BD:129:ASN:ND2	1:CV:102:MET:HA	2.33	0.42
1:BF:116:ARG:HG3	1:BF:156:LEU:HD23	2.02	0.42
1:BH:34:ARG:HD3	1:BH:161:LEU:HD23	2.02	0.42
1:BH:154:GLU:HB3	1:BI:152:ASN:HB2	2.02	0.42
1:BI:116:ARG:HG3	1:BI:156:LEU:HD23	2.02	0.42
1:BK:34:ARG:HD3	1:BK:161:LEU:HD23	2.02	0.42
1:BM:79:GLN:HB2	1:BM:93:VAL:HG12	2.02	0.42
1:BM:194:THR:C	1:DF:170:PHE:HE1	2.28	0.42
1:BQ:177:SER:HB2	1:BR:188:GLN:OE1	2.20	0.42
1:BR:116:ARG:HG3	1:BR:156:LEU:HD23	2.02	0.42
1:BT:185:ARG:O	1:BT:189:ASP:HB2	2.20	0.42
1:BU:109:THR:HB	1:BU:120:SER:HG	1.84	0.42
1:BW:177:SER:HB2	1:BX:188:GLN:OE1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:55:TYR:O	1:BY:58:SER:HB3	2.20	0.42
1:CC:100:ARG:NH1	1:CC:139:ILE:O	2.53	0.42
1:CD:116:ARG:HG3	1:CD:156:LEU:HD23	2.02	0.42
1:CG:116:ARG:HG3	1:CG:156:LEU:HD23	2.02	0.42
1:CH:55:TYR:O	1:CH:58:SER:HB3	2.20	0.42
1:CO:34:ARG:HD3	1:CO:161:LEU:HD23	2.02	0.42
1:CO:154:GLU:HB3	1:CP:152:ASN:HB2	2.02	0.42
1:CR:154:GLU:HB3	1:CS:152:ASN:HB2	2.02	0.42
1:CR:177:SER:HB2	1:CS:188:GLN:OE1	2.20	0.42
1:CW:55:TYR:O	1:CW:58:SER:HB3	2.20	0.42
1:DK:109:THR:HB	1:DK:120:SER:OG	2.20	0.42
1:DK:116:ARG:HG3	1:DK:156:LEU:HD23	2.02	0.42
1:AG:185:ARG:O	1:AG:189:ASP:HB2	2.20	0.41
1:AJ:65:ARG:HD3	1:AK:161:LEU:HB3	2.02	0.41
1:AJ:177:SER:HB2	1:AK:188:GLN:OE1	2.20	0.41
1:AL:79:GLN:HB2	1:AL:93:VAL:HG12	2.02	0.41
1:AM:177:SER:HB2	1:AN:188:GLN:OE1	2.20	0.41
1:AT:102:MET:HA	1:CQ:129:ASN:ND2	2.35	0.41
1:AT:102:MET:SD	1:CQ:129:ASN:ND2	2.93	0.41
1:AU:55:TYR:O	1:AU:58:SER:HB3	2.20	0.41
1:AU:129:ASN:ND2	1:CP:102:MET:SD	2.93	0.41
1:AX:79:GLN:HB2	1:AX:93:VAL:HG12	2.02	0.41
1:BB:34:ARG:HD3	1:BB:161:LEU:HD23	2.02	0.41
1:BF:85:VAL:HG11	1:CZ:204:VAL:HG11	2.02	0.41
1:BH:185:ARG:O	1:BH:189:ASP:HB2	2.20	0.41
1:BI:40:PRO:CG	1:DG:87:THR:HG22	2.46	0.41
1:BQ:19:GLY:O	1:BQ:21:VAL:HG23	2.18	0.41
1:BS:194:THR:C	1:DL:170:PHE:HE1	2.28	0.41
1:BT:100:ARG:NH1	1:BT:139:ILE:O	2.53	0.41
1:BU:116:ARG:HG3	1:BU:156:LEU:HD23	2.02	0.41
1:BW:79:GLN:NE2	1:DK:162:THR:O	2.53	0.41
1:BZ:14:TYR:HE2	1:BZ:23:SER:HA	1.84	0.41
1:BZ:50:GLU:O	1:BZ:54:THR:HG23	2.19	0.41
1:BZ:185:ARG:O	1:BZ:189:ASP:HB2	2.20	0.41
1:CF:185:ARG:O	1:CF:189:ASP:HB2	2.20	0.41
1:CJ:116:ARG:HG3	1:CJ:156:LEU:HD23	2.02	0.41
1:CK:180:LEU:HD23	1:CK:180:LEU:HA	1.77	0.41
1:CL:65:ARG:HD3	1:CM:161:LEU:HB3	2.02	0.41
1:CM:116:ARG:HG3	1:CM:156:LEU:HD23	2.02	0.41
1:CO:185:ARG:O	1:CO:189:ASP:HB2	2.20	0.41
1:CT:55:TYR:O	1:CT:58:SER:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:116:ARG:HG3	1:CV:156:LEU:HD23	2.02	0.41
1:DD:185:ARG:O	1:DD:189:ASP:HB2	2.20	0.41
1:AA:65:ARG:HD3	1:AB:161:LEU:HB3	2.02	0.41
1:AA:185:ARG:O	1:AA:189:ASP:HB2	2.20	0.41
1:AC:55:TYR:O	1:AC:58:SER:HB3	2.20	0.41
1:AF:55:TYR:O	1:AF:58:SER:HB3	2.20	0.41
1:AM:100:ARG:NH1	1:AM:139:ILE:O	2.53	0.41
1:AP:177:SER:HB2	1:AQ:188:GLN:OE1	2.20	0.41
1:AU:196:ARG:HA	1:CQ:41:VAL:HB	2.02	0.41
1:AV:65:ARG:HD3	1:AW:161:LEU:HB3	2.02	0.41
1:AV:197:LEU:HD23	1:AV:197:LEU:HA	1.89	0.41
1:BG:55:TYR:O	1:BG:58:SER:HB3	2.20	0.41
1:BQ:185:ARG:O	1:BQ:189:ASP:HB2	2.20	0.41
1:BX:109:THR:HB	1:BX:120:SER:OG	2.20	0.41
1:BX:116:ARG:HG3	1:BX:156:LEU:HD23	2.02	0.41
1:CK:55:TYR:O	1:CK:58:SER:HB3	2.20	0.41
1:CL:177:SER:HB2	1:CM:188:GLN:OE1	2.20	0.41
1:CR:14:TYR:HE2	1:CR:23:SER:HA	1.84	0.41
1:CU:14:TYR:HE2	1:CU:23:SER:HA	1.84	0.41
1:DJ:65:ARG:HD3	1:DK:161:LEU:HB3	2.02	0.41
1:DJ:177:SER:HB2	1:DK:188:GLN:OE1	2.20	0.41
1:AH:116:ARG:HG3	1:AH:156:LEU:HD23	2.02	0.41
1:AO:55:TYR:O	1:AO:58:SER:HB3	2.20	0.41
1:AU:139:ILE:HD11	1:CP:138:ALA:O	2.20	0.41
1:AU:156:LEU:HD12	1:CQ:150:LYS:HB2	2.03	0.41
1:AY:34:ARG:HD3	1:AY:161:LEU:HD23	2.02	0.41
1:AY:177:SER:HB2	1:AZ:188:GLN:OE1	2.20	0.41
1:AZ:109:THR:HB	1:AZ:120:SER:OG	2.20	0.41
1:BE:100:ARG:NH1	1:BE:139:ILE:O	2.53	0.41
1:BJ:180:LEU:HA	1:BJ:180:LEU:HD23	1.77	0.41
1:BK:65:ARG:HD3	1:BL:161:LEU:HB3	2.02	0.41
1:BP:55:TYR:O	1:BP:58:SER:HB3	2.20	0.41
1:BP:79:GLN:HB2	1:BP:93:VAL:HG12	2.02	0.41
1:BS:150:LYS:HB2	1:DL:156:LEU:HD12	2.01	0.41
1:BT:115:GLY:N	1:BU:200:ALA:O	2.53	0.41
1:BZ:88:LYS:HE2	1:CA:201:SER:O	2.19	0.41
1:CC:177:SER:HB2	1:CD:188:GLN:OE1	2.20	0.41
1:CF:100:ARG:NH1	1:CF:139:ILE:O	2.53	0.41
1:CF:177:SER:HB2	1:CG:188:GLN:OE1	2.20	0.41
1:CI:177:SER:HB2	1:CJ:188:GLN:OE1	2.20	0.41
1:CO:14:TYR:HE2	1:CO:23:SER:HA	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:100:ARG:NH1	1:CR:139:ILE:O	2.53	0.41
1:CU:115:GLY:N	1:CV:200:ALA:O	2.53	0.41
1:DE:109:THR:HB	1:DE:120:SER:OG	2.20	0.41
1:DG:154:GLU:HB3	1:DH:152:ASN:HB2	2.02	0.41
1:DG:185:ARG:O	1:DG:189:ASP:HB2	2.20	0.41
1:AD:65:ARG:HD3	1:AE:161:LEU:HB3	2.02	0.41
1:AF:65:ARG:HB2	1:CE:163:GLY:HA3	2.02	0.41
1:AK:116:ARG:HG3	1:AK:156:LEU:HD23	2.02	0.41
1:AL:55:TYR:O	1:AL:58:SER:HB3	2.20	0.41
1:AL:142:ALA:O	1:CI:14:TYR:HB2	2.20	0.41
1:AL:150:LYS:HB2	1:CK:156:LEU:HD12	2.01	0.41
1:AL:194:THR:HG21	1:CJ:83:PRO:HG2	2.02	0.41
1:AR:55:TYR:O	1:AR:58:SER:HB3	2.20	0.41
1:AY:100:ARG:NH1	1:AY:139:ILE:O	2.53	0.41
1:BD:43:LEU:HD12	1:BD:43:LEU:HA	1.90	0.41
1:BD:55:TYR:O	1:BD:58:SER:HB3	2.20	0.41
1:BE:65:ARG:HD3	1:BF:161:LEU:HB3	2.02	0.41
1:BH:100:ARG:NH1	1:BH:139:ILE:O	2.53	0.41
1:BM:162:THR:HB	1:DF:65:ARG:NH2	2.35	0.41
1:BW:100:ARG:NH1	1:BW:139:ILE:O	2.53	0.41
1:BZ:65:ARG:HD3	1:CA:161:LEU:HB3	2.02	0.41
1:CL:14:TYR:HE2	1:CL:23:SER:HA	1.84	0.41
1:CM:109:THR:HB	1:CM:120:SER:OG	2.20	0.41
1:CX:115:GLY:N	1:CY:200:ALA:O	2.53	0.41
1:CX:185:ARG:O	1:CX:189:ASP:HB2	2.20	0.41
1:DD:34:ARG:HD3	1:DD:161:LEU:HD23	2.02	0.41
1:DD:177:SER:HB2	1:DE:188:GLN:OE1	2.20	0.41
1:AB:116:ARG:HG3	1:AB:156:LEU:HD23	2.02	0.41
1:AJ:43:LEU:HD12	1:AJ:43:LEU:HA	1.93	0.41
1:AP:185:ARG:O	1:AP:189:ASP:HB2	2.20	0.41
1:AS:177:SER:HB2	1:AT:188:GLN:OE1	2.20	0.41
1:AU:194:THR:HG21	1:CP:83:PRO:HG2	2.02	0.41
1:AV:177:SER:HB2	1:AW:188:GLN:OE1	2.20	0.41
1:AZ:138:ALA:O	1:CT:139:ILE:HD11	2.21	0.41
1:BB:154:GLU:HB3	1:BC:152:ASN:HB2	2.02	0.41
1:BD:139:ILE:HD11	1:CV:138:ALA:O	2.21	0.41
1:BE:14:TYR:HE2	1:BE:23:SER:HA	1.84	0.41
1:BL:85:VAL:HG11	1:DF:204:VAL:HG11	2.01	0.41
1:BL:109:THR:HB	1:BL:120:SER:HG	1.85	0.41
1:BR:83:PRO:HG2	1:DL:194:THR:HG21	2.03	0.41
1:BS:41:VAL:HB	1:DL:196:ARG:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:180:LEU:HA	1:BS:180:LEU:HD23	1.78	0.41
1:BT:154:GLU:HB3	1:BU:152:ASN:HB2	2.02	0.41
1:BY:180:LEU:HA	1:BY:180:LEU:HD23	1.77	0.41
1:BZ:154:GLU:HB3	1:CA:152:ASN:HB2	2.02	0.41
1:CK:79:GLN:HB2	1:CK:93:VAL:HG12	2.02	0.41
1:CN:55:TYR:O	1:CN:58:SER:HB3	2.20	0.41
1:DA:185:ARG:O	1:DA:189:ASP:HB2	2.20	0.41
1:DC:55:TYR:O	1:DC:58:SER:HB3	2.20	0.41
1:DD:14:TYR:HE2	1:DD:23:SER:HA	1.84	0.41
1:DG:100:ARG:NH1	1:DG:139:ILE:O	2.53	0.41
1:DL:180:LEU:HD23	1:DL:180:LEU:HA	1.77	0.41
1:AG:177:SER:HB2	1:AH:188:GLN:OE1	2.20	0.41
1:AK:102:MET:HA	1:CK:129:ASN:ND2	2.33	0.41
1:AN:116:ARG:HG3	1:AN:156:LEU:HD23	2.02	0.41
1:AV:34:ARG:HD3	1:AV:161:LEU:HD23	2.02	0.41
1:AY:14:TYR:HE2	1:AY:23:SER:HA	1.84	0.41
1:BC:102:MET:HA	1:CW:129:ASN:ND2	2.34	0.41
1:BG:129:ASN:ND2	1:CY:102:MET:SD	2.94	0.41
1:BG:156:LEU:HD12	1:CZ:150:LYS:HB2	2.02	0.41
1:BJ:55:TYR:O	1:BJ:58:SER:HB3	2.20	0.41
1:BK:177:SER:HB2	1:BL:188:GLN:OE1	2.20	0.41
1:BM:170:PHE:HE1	1:DF:194:THR:CA	2.33	0.41
1:BR:31:ASN:HD21	1:DH:22:GLN:HA	1.86	0.41
1:BS:194:THR:HG21	1:DK:83:PRO:CG	2.51	0.41
1:CD:109:THR:HB	1:CD:120:SER:OG	2.20	0.41
1:CI:154:GLU:HB3	1:CJ:152:ASN:HB2	2.02	0.41
1:CI:185:ARG:O	1:CI:189:ASP:HB2	2.20	0.41
1:CN:79:GLN:HB2	1:CN:93:VAL:HG12	2.02	0.41
1:CP:109:THR:HB	1:CP:120:SER:OG	2.20	0.41
1:DC:79:GLN:HB2	1:DC:93:VAL:HG12	2.02	0.41
1:DI:55:TYR:O	1:DI:58:SER:HB3	2.20	0.41
1:AK:83:PRO:CG	1:CK:194:THR:HG21	2.50	0.41
1:AN:109:THR:HB	1:AN:120:SER:OG	2.20	0.41
1:AS:115:GLY:N	1:AT:200:ALA:O	2.53	0.41
1:BA:55:TYR:O	1:BA:58:SER:HB3	2.20	0.41
1:BB:177:SER:HB2	1:BC:188:GLN:OE1	2.20	0.41
1:BD:156:LEU:HD12	1:CW:150:LYS:HB2	2.02	0.41
1:BD:194:THR:HG21	1:CV:83:PRO:HG2	2.01	0.41
1:BE:18:GLN:OE1	1:CC:21:VAL:HG21	2.20	0.41
1:BE:26:THR:HG21	1:CR:20:PRO:HG3	2.02	0.41
1:BE:177:SER:HB2	1:BF:188:GLN:OE1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:109:THR:HB	1:BF:120:SER:OG	2.20	0.41
1:BH:177:SER:HB2	1:BI:188:GLN:OE1	2.20	0.41
1:BI:204:VAL:HG21	1:DL:208:ALA:CB	2.51	0.41
1:BJ:102:MET:HE1	1:DG:28:PHE:CE2	2.55	0.41
1:BW:34:ARG:HD3	1:BW:161:LEU:HD23	2.02	0.41
1:BY:79:GLN:HB2	1:BY:93:VAL:HG12	2.02	0.41
1:CC:34:ARG:HD3	1:CC:161:LEU:HD23	2.02	0.41
1:CE:43:LEU:HD12	1:CE:43:LEU:HA	1.90	0.41
1:CF:34:ARG:HD3	1:CF:161:LEU:HD23	2.02	0.41
1:CI:14:TYR:HE2	1:CI:23:SER:HA	1.84	0.41
1:CP:143:VAL:HA	1:CQ:26:THR:HG22	2.03	0.41
1:CW:79:GLN:HB2	1:CW:93:VAL:HG12	2.02	0.41
1:DA:154:GLU:HB3	1:DB:152:ASN:HB2	2.02	0.41
1:DC:180:LEU:HD23	1:DC:180:LEU:HA	1.78	0.41
1:AB:161:LEU:HD23	1:AB:161:LEU:HA	1.93	0.41
1:AC:79:GLN:HB2	1:AC:93:VAL:HG12	2.02	0.41
1:AC:196:ARG:HA	1:BY:41:VAL:HB	2.02	0.41
1:AD:14:TYR:HE2	1:AD:23:SER:HA	1.84	0.41
1:AD:79:GLN:NE2	1:AT:162:THR:O	2.54	0.41
1:AG:34:ARG:HD3	1:AG:161:LEU:HD23	2.02	0.41
1:AJ:170:PHE:O	1:AJ:173:ASP:HB2	2.21	0.41
1:AU:79:GLN:HB2	1:AU:93:VAL:HG12	2.02	0.41
1:BF:23:SER:HB3	1:DB:31:ASN:H	1.85	0.41
1:BH:170:PHE:O	1:BH:173:ASP:HB2	2.21	0.41
1:BJ:79:GLN:HB2	1:BJ:93:VAL:HG12	2.02	0.41
1:BL:116:ARG:HG3	1:BL:156:LEU:HD23	2.02	0.41
1:BQ:154:GLU:HB3	1:BR:152:ASN:HB2	2.02	0.41
1:BR:83:PRO:CG	1:DL:194:THR:HG21	2.51	0.41
1:BV:55:TYR:O	1:BV:58:SER:HB3	2.20	0.41
1:CA:116:ARG:HG3	1:CA:156:LEU:HD23	2.02	0.41
1:CL:185:ARG:O	1:CL:189:ASP:HB2	2.20	0.41
1:CQ:55:TYR:O	1:CQ:58:SER:HB3	2.20	0.41
1:CU:154:GLU:HB3	1:CV:152:ASN:HB2	2.02	0.41
1:CZ:55:TYR:O	1:CZ:58:SER:HB3	2.20	0.41
1:DB:143:VAL:HA	1:DC:26:THR:HG22	2.03	0.41
1:DD:154:GLU:HB3	1:DE:152:ASN:HB2	2.02	0.41
1:AC:140:PRO:O	1:CV:137:SER:HB3	2.21	0.41
1:AD:34:ARG:HD3	1:AD:161:LEU:HD23	2.02	0.41
1:AH:23:SER:HB3	1:CJ:31:ASN:H	1.86	0.41
1:AH:27:THR:O	1:CM:25:ARG:HA	2.21	0.41
1:AJ:34:ARG:HD3	1:AJ:161:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:180:LEU:HD23	1:AJ:180:LEU:HA	1.91	0.41
1:AL:43:LEU:HD12	1:AL:43:LEU:HA	1.90	0.41
1:AL:204:VAL:HG11	1:CJ:85:VAL:HG11	2.03	0.41
1:AN:170:PHE:O	1:AN:173:ASP:HB2	2.21	0.41
1:AO:79:GLN:HB2	1:AO:93:VAL:HG12	2.02	0.41
1:AV:154:GLU:HB3	1:AW:152:ASN:HB2	2.02	0.41
1:AW:143:VAL:HA	1:AX:26:THR:HG22	2.03	0.41
1:AX:55:TYR:O	1:AX:58:SER:HB3	2.20	0.41
1:AZ:143:VAL:HA	1:BA:26:THR:HG22	2.03	0.41
1:BC:121:ILE:O	1:BC:150:LYS:HA	2.21	0.41
1:BF:121:ILE:O	1:BF:150:LYS:HA	2.21	0.41
1:BJ:140:PRO:HA	1:DH:137:SER:O	2.21	0.41
1:BM:102:MET:HE1	1:DA:28:PHE:CE2	2.56	0.41
1:BN:34:ARG:HD3	1:BN:161:LEU:HD23	2.02	0.41
1:BN:154:GLU:HB3	1:BO:152:ASN:HB2	2.02	0.41
1:BO:121:ILE:O	1:BO:150:LYS:HA	2.21	0.41
1:BS:194:THR:HG21	1:DK:83:PRO:HG2	2.02	0.41
1:BT:170:PHE:O	1:BT:173:ASP:HB2	2.21	0.41
1:BV:79:GLN:HB2	1:BV:93:VAL:HG12	2.02	0.41
1:BW:170:PHE:O	1:BW:173:ASP:HB2	2.21	0.41
1:CA:143:VAL:HA	1:CB:26:THR:HG22	2.03	0.41
1:CC:154:GLU:HB3	1:CD:152:ASN:HB2	2.02	0.41
1:CE:208:ALA:CB	1:CS:204:VAL:HG21	2.51	0.41
1:CF:79:GLN:NE2	1:CJ:162:THR:O	2.53	0.41
1:CF:115:GLY:N	1:CG:200:ALA:O	2.53	0.41
1:CF:154:GLU:HB3	1:CG:152:ASN:HB2	2.02	0.41
1:CG:143:VAL:HA	1:CH:26:THR:HG22	2.03	0.41
1:CU:34:ARG:HD3	1:CU:161:LEU:HD23	2.02	0.41
1:CU:65:ARG:HD3	1:CV:161:LEU:HB3	2.02	0.41
1:CU:100:ARG:NH1	1:CU:139:ILE:O	2.53	0.41
1:CU:185:ARG:O	1:CU:189:ASP:HB2	2.20	0.41
1:CX:34:ARG:HD3	1:CX:161:LEU:HD23	2.02	0.41
1:DE:109:THR:HB	1:DE:120:SER:HG	1.85	0.41
1:DE:116:ARG:HG3	1:DE:156:LEU:HD23	2.02	0.41
1:DF:43:LEU:HD12	1:DF:43:LEU:HA	1.90	0.41
1:DG:170:PHE:O	1:DG:173:ASP:HB2	2.21	0.41
1:DH:109:THR:HB	1:DH:120:SER:OG	2.20	0.41
1:DH:170:PHE:O	1:DH:173:ASP:HB2	2.21	0.41
1:AA:100:ARG:NH1	1:AA:139:ILE:O	2.53	0.41
1:AB:170:PHE:O	1:AB:173:ASP:HB2	2.21	0.41
1:AE:24:SER:HA	1:CS:22:GLN:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:65:ARG:HD3	1:AH:161:LEU:HB3	2.02	0.41
1:AJ:14:TYR:HE2	1:AJ:23:SER:HA	1.84	0.41
1:AK:129:ASN:HB3	1:AO:103:ALA:HB2	2.03	0.41
1:AM:87:THR:HG22	1:CA:40:PRO:CG	2.46	0.41
1:AS:100:ARG:NH1	1:AS:139:ILE:O	2.53	0.41
1:AT:116:ARG:HG3	1:AT:156:LEU:HD23	2.02	0.41
1:AT:121:ILE:O	1:AT:150:LYS:HA	2.21	0.41
1:AU:43:LEU:HD12	1:AU:43:LEU:HA	1.90	0.41
1:AY:170:PHE:O	1:AY:173:ASP:HB2	2.21	0.41
1:AZ:102:MET:HA	1:CT:129:ASN:ND2	2.33	0.41
1:BA:79:GLN:HB2	1:BA:93:VAL:HG12	2.02	0.41
1:BA:140:PRO:HA	1:BF:137:SER:O	2.21	0.41
1:BB:65:ARG:HD3	1:BC:161:LEU:HB3	2.02	0.41
1:BD:194:THR:HG21	1:CV:83:PRO:CG	2.50	0.41
1:BD:208:ALA:CB	1:CA:204:VAL:HG21	2.51	0.41
1:BE:43:LEU:HD12	1:BE:43:LEU:HA	1.93	0.41
1:BE:176:LEU:HD23	1:BE:176:LEU:HA	1.93	0.41
1:BM:55:TYR:O	1:BM:58:SER:HB3	2.20	0.41
1:BP:180:LEU:HA	1:BP:180:LEU:HD23	1.78	0.41
1:BQ:176:LEU:HD23	1:BQ:176:LEU:HA	1.93	0.41
1:BW:154:GLU:HB3	1:BX:152:ASN:HB2	2.02	0.41
1:CA:170:PHE:O	1:CA:173:ASP:HB2	2.21	0.41
1:CC:180:LEU:HD23	1:CC:180:LEU:HA	1.91	0.41
1:CG:170:PHE:O	1:CG:173:ASP:HB2	2.21	0.41
1:CI:170:PHE:O	1:CI:173:ASP:HB2	2.21	0.41
1:CJ:143:VAL:HA	1:CK:26:THR:HG22	2.03	0.41
1:CO:115:GLY:N	1:CP:200:ALA:O	2.53	0.41
1:CR:34:ARG:HD3	1:CR:161:LEU:HD23	2.02	0.41
1:CR:65:ARG:HD3	1:CS:161:LEU:HB3	2.02	0.41
1:DE:121:ILE:O	1:DE:150:LYS:HA	2.21	0.41
1:DG:34:ARG:HD3	1:DG:161:LEU:HD23	2.02	0.41
1:AD:165:ASP:OD1	1:AD:166:ALA:N	2.55	0.40
1:AE:116:ARG:HG3	1:AE:156:LEU:HD23	2.02	0.40
1:AE:170:PHE:O	1:AE:173:ASP:HB2	2.21	0.40
1:AF:206:PRO:O	1:CE:83:PRO:HB3	2.20	0.40
1:AG:154:GLU:HB3	1:AH:152:ASN:HB2	2.02	0.40
1:AI:55:TYR:O	1:AI:58:SER:HB3	2.20	0.40
1:AL:65:ARG:HB2	1:CK:163:GLY:HA3	2.02	0.40
1:AQ:143:VAL:HA	1:AR:26:THR:HG22	2.03	0.40
1:AR:79:GLN:HB2	1:AR:93:VAL:HG12	2.02	0.40
1:AU:150:LYS:HB2	1:CQ:156:LEU:HD12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:121:ILE:O	1:AW:150:LYS:HA	2.21	0.40
1:AY:65:ARG:HD3	1:AZ:161:LEU:HB3	2.02	0.40
1:AZ:23:SER:HB3	1:BL:31:ASN:H	1.86	0.40
1:AZ:116:ARG:HG3	1:AZ:156:LEU:HD23	2.02	0.40
1:BB:165:ASP:OD1	1:BB:166:ALA:N	2.55	0.40
1:BG:79:GLN:HB2	1:BG:93:VAL:HG12	2.02	0.40
1:BJ:196:ARG:HA	1:DC:41:VAL:HB	2.03	0.40
1:BK:155:VAL:CG1	1:BK:176:LEU:HD13	2.52	0.40
1:BT:34:ARG:HD3	1:BT:161:LEU:HD23	2.02	0.40
1:BT:177:SER:HB2	1:BU:188:GLN:OE1	2.20	0.40
1:CB:79:GLN:HB2	1:CB:93:VAL:HG12	2.02	0.40
1:CC:65:ARG:HD3	1:CD:161:LEU:HB3	2.02	0.40
1:CF:165:ASP:OD1	1:CF:166:ALA:N	2.55	0.40
1:CH:79:GLN:HB2	1:CH:93:VAL:HG12	2.02	0.40
1:CL:170:PHE:O	1:CL:173:ASP:HB2	2.21	0.40
1:CS:170:PHE:O	1:CS:173:ASP:HB2	2.21	0.40
1:CX:154:GLU:HB3	1:CY:152:ASN:HB2	2.02	0.40
1:CY:109:THR:HB	1:CY:120:SER:OG	2.20	0.40
1:CY:143:VAL:HA	1:CZ:26:THR:HG22	2.03	0.40
1:DB:116:ARG:HG3	1:DB:156:LEU:HD23	2.02	0.40
1:DB:170:PHE:O	1:DB:173:ASP:HB2	2.21	0.40
1:DD:100:ARG:NH1	1:DD:139:ILE:O	2.53	0.40
1:DI:79:GLN:HB2	1:DI:93:VAL:HG12	2.02	0.40
1:AG:180:LEU:HD23	1:AG:180:LEU:HA	1.91	0.40
1:AM:170:PHE:O	1:AM:173:ASP:HB2	2.21	0.40
1:AN:161:LEU:HD23	1:AN:161:LEU:HA	1.93	0.40
1:AP:28:PHE:CE2	1:CE:102:MET:HE1	2.56	0.40
1:AR:39:ARG:HB3	1:CN:199:ALA:O	2.21	0.40
1:AR:43:LEU:HD12	1:AR:43:LEU:HA	1.90	0.40
1:AS:165:ASP:OD1	1:AS:166:ALA:N	2.54	0.40
1:AU:194:THR:HG21	1:CP:83:PRO:CG	2.51	0.40
1:AZ:121:ILE:O	1:AZ:150:LYS:HA	2.21	0.40
1:BH:28:PHE:CE2	1:BS:102:MET:HE1	2.56	0.40
1:BK:165:ASP:OD1	1:BK:166:ALA:N	2.55	0.40
1:BQ:165:ASP:OD1	1:BQ:166:ALA:N	2.55	0.40
1:BR:138:ALA:O	1:DL:139:ILE:HD11	2.21	0.40
1:BS:79:GLN:HB2	1:BS:93:VAL:HG12	2.02	0.40
1:BT:165:ASP:OD1	1:BT:166:ALA:N	2.55	0.40
1:BU:143:VAL:HA	1:BV:26:THR:HG22	2.03	0.40
1:BX:121:ILE:O	1:BX:150:LYS:HA	2.21	0.40
1:CF:170:PHE:O	1:CF:173:ASP:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:137:SER:O	1:CK:140:PRO:HA	2.21	0.40
1:CJ:25:ARG:HA	1:CP:27:THR:O	2.22	0.40
1:CL:176:LEU:HD23	1:CL:176:LEU:HA	1.93	0.40
1:CV:39:ARG:HH11	1:CV:39:ARG:HD3	1.76	0.40
1:CV:143:VAL:HA	1:CW:26:THR:HG22	2.03	0.40
1:CY:170:PHE:O	1:CY:173:ASP:HB2	2.21	0.40
1:DA:34:ARG:HD3	1:DA:161:LEU:HD23	2.02	0.40
1:DA:65:ARG:HD3	1:DB:161:LEU:HB3	2.02	0.40
1:DA:165:ASP:OD1	1:DA:166:ALA:N	2.55	0.40
1:DD:170:PHE:O	1:DD:173:ASP:HB2	2.21	0.40
1:DJ:34:ARG:HD3	1:DJ:161:LEU:HD23	2.02	0.40
1:DL:44:ALA:HA	1:DL:45:PRO:HD3	1.98	0.40
1:AA:155:VAL:CG1	1:AA:176:LEU:HD13	2.52	0.40
1:AA:165:ASP:OD1	1:AA:166:ALA:N	2.55	0.40
1:AD:155:VAL:CG1	1:AD:176:LEU:HD13	2.52	0.40
1:AD:177:SER:HB2	1:AE:188:GLN:OE1	2.20	0.40
1:AF:96:ASN:HD21	1:AF:106:THR:HG1	1.68	0.40
1:AN:143:VAL:HA	1:AO:26:THR:HG22	2.03	0.40
1:AT:25:ARG:HA	1:BX:27:THR:O	2.22	0.40
1:AT:31:ASN:HD21	1:CS:22:GLN:HA	1.85	0.40
1:AV:165:ASP:OD1	1:AV:166:ALA:N	2.55	0.40
1:AY:185:ARG:O	1:AY:189:ASP:HB2	2.20	0.40
1:BL:170:PHE:O	1:BL:173:ASP:HB2	2.21	0.40
1:BM:196:ARG:NH2	1:DF:174:GLU:OE1	2.55	0.40
1:BN:13:LEU:HD12	1:BN:13:LEU:HA	1.95	0.40
1:BN:170:PHE:O	1:BN:173:ASP:HB2	2.21	0.40
1:BS:156:LEU:HD12	1:DL:150:LYS:HB2	2.02	0.40
1:CC:170:PHE:O	1:CC:173:ASP:HB2	2.21	0.40
1:CI:155:VAL:CG1	1:CI:176:LEU:HD13	2.52	0.40
1:CM:143:VAL:HA	1:CN:26:THR:HG22	2.03	0.40
1:CN:43:LEU:HD12	1:CN:43:LEU:HA	1.89	0.40
1:CU:180:LEU:HD23	1:CU:180:LEU:HA	1.91	0.40
1:CZ:79:GLN:HB2	1:CZ:93:VAL:HG12	2.02	0.40
1:DH:121:ILE:O	1:DH:150:LYS:HA	2.21	0.40
1:DJ:170:PHE:O	1:DJ:173:ASP:HB2	2.21	0.40
1:AB:204:VAL:HG21	1:CK:208:ALA:CB	2.52	0.40
1:AC:150:LYS:HB2	1:BY:156:LEU:HD12	2.04	0.40
1:AE:121:ILE:O	1:AE:150:LYS:HA	2.21	0.40
1:AF:127:ASP:HB2	1:AF:146:VAL:HG21	2.04	0.40
1:AK:143:VAL:HA	1:AL:26:THR:HG22	2.03	0.40
1:AL:194:THR:C	1:CK:170:PHE:HE1	2.30	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:34:ARG:HD3	1:AP:161:LEU:HD23	2.02	0.40
1:AP:170:PHE:O	1:AP:173:ASP:HB2	2.21	0.40
1:AZ:204:VAL:HG21	1:BJ:208:ALA:CB	2.52	0.40
1:BB:170:PHE:O	1:BB:173:ASP:HB2	2.21	0.40
1:BE:155:VAL:CG1	1:BE:176:LEU:HD13	2.52	0.40
1:BQ:65:ARG:HD3	1:BR:161:LEU:HB3	2.02	0.40
1:BQ:170:PHE:O	1:BQ:173:ASP:HB2	2.21	0.40
1:BU:121:ILE:O	1:BU:150:LYS:HA	2.21	0.40
1:BU:170:PHE:O	1:BU:173:ASP:HB2	2.21	0.40
1:BW:155:VAL:CG1	1:BW:176:LEU:HD13	2.52	0.40
1:CA:121:ILE:O	1:CA:150:LYS:HA	2.21	0.40
1:CD:39:ARG:HH11	1:CD:39:ARG:HD3	1.76	0.40
1:CL:34:ARG:HD3	1:CL:161:LEU:HD23	2.02	0.40
1:CL:155:VAL:CG1	1:CL:176:LEU:HD13	2.52	0.40
1:CO:165:ASP:OD1	1:CO:166:ALA:N	2.55	0.40
1:CQ:79:GLN:HB2	1:CQ:93:VAL:HG12	2.02	0.40
1:CU:155:VAL:CG1	1:CU:176:LEU:HD13	2.52	0.40
1:CU:165:ASP:OD1	1:CU:166:ALA:N	2.55	0.40
1:CU:170:PHE:O	1:CU:173:ASP:HB2	2.21	0.40
1:CX:165:ASP:OD1	1:CX:166:ALA:N	2.55	0.40
1:CY:121:ILE:O	1:CY:150:LYS:HA	2.21	0.40
1:DA:155:VAL:CG1	1:DA:176:LEU:HD13	2.52	0.40
1:DD:165:ASP:OD1	1:DD:166:ALA:N	2.55	0.40
1:DE:170:PHE:O	1:DE:173:ASP:HB2	2.21	0.40
1:DH:143:VAL:HA	1:DI:26:THR:HG22	2.03	0.40
1:DK:121:ILE:O	1:DK:150:LYS:HA	2.21	0.40
1:DL:79:GLN:HB2	1:DL:93:VAL:HG12	2.02	0.40
1:AA:121:ILE:O	1:AA:150:LYS:HA	2.22	0.40
1:AC:194:THR:HG21	1:BX:83:PRO:HG2	2.04	0.40
1:AD:170:PHE:O	1:AD:173:ASP:HB2	2.21	0.40
1:AF:208:ALA:CB	1:AQ:204:VAL:HG21	2.51	0.40
1:AG:155:VAL:CG1	1:AG:176:LEU:HD13	2.52	0.40
1:AG:170:PHE:O	1:AG:173:ASP:HB2	2.21	0.40
1:AJ:121:ILE:O	1:AJ:150:LYS:HA	2.22	0.40
1:AM:13:LEU:HD12	1:AM:13:LEU:HA	1.95	0.40
1:AQ:170:PHE:O	1:AQ:173:ASP:HB2	2.21	0.40
1:AU:129:ASN:ND2	1:CP:102:MET:HA	2.33	0.40
1:AV:170:PHE:O	1:AV:173:ASP:HB2	2.21	0.40
1:AX:140:PRO:HA	1:BC:137:SER:O	2.22	0.40
1:BI:143:VAL:HA	1:BJ:26:THR:HG22	2.03	0.40
1:BK:121:ILE:O	1:BK:150:LYS:HA	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:127:ASP:HB2	1:BM:146:VAL:HG21	2.04	0.40
1:BM:174:GLU:OE1	1:DF:196:ARG:NH2	2.55	0.40
1:BN:155:VAL:CG1	1:BN:176:LEU:HD13	2.52	0.40
1:BN:165:ASP:OD1	1:BN:166:ALA:N	2.55	0.40
1:BR:121:ILE:O	1:BR:150:LYS:HA	2.21	0.40
1:BZ:170:PHE:O	1:BZ:173:ASP:HB2	2.21	0.40
1:CB:180:LEU:HD23	1:CB:180:LEU:HA	1.78	0.40
1:CD:121:ILE:O	1:CD:150:LYS:HA	2.21	0.40
1:CH:127:ASP:HB2	1:CH:146:VAL:HG21	2.04	0.40
1:CP:116:ARG:HG3	1:CP:156:LEU:HD23	2.02	0.40
1:CP:121:ILE:O	1:CP:150:LYS:HA	2.21	0.40
1:CP:170:PHE:O	1:CP:173:ASP:HB2	2.21	0.40
1:CQ:127:ASP:HB2	1:CQ:146:VAL:HG21	2.04	0.40
1:CT:180:LEU:HA	1:CT:180:LEU:HD23	1.78	0.40
1:DB:204:VAL:HG21	1:DF:208:ALA:HB2	2.03	0.40

All (7) 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:AB:60:GLN:OE1	1:BC:192:LYS:NZ[4_556]	1.89	0.31
1:AI:65:ARG:NH1	1:AX:31:ASN:O[2_555]	2.09	0.11
1:BV:31:ASN:O	1:BV:65:ARG:NH1[2_555]	2.13	0.07
1:AO:31:ASN:O	1:AO:65:ARG:NH1[2_555]	2.16	0.04
1:AI:31:ASN:O	1:AX:65:ARG:NH1[2_555]	2.17	0.03
1:CB:31:ASN:O	1:CH:65:ARG:NH1[2_555]	2.18	0.02
1:CB:65:ARG:NH1	1:CH:31:ASN:O[2_555]	2.18	0.02

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	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AB	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AC	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AD	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AE	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AF	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AG	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AH	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AI	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AJ	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AK	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AL	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AM	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AN	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AO	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AP	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AQ	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AR	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AS	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AT	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AU	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AV	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AW	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AX	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AY	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AZ	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BA	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BB	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BC	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BD	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BE	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BF	187/208 (90%)	183 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BG	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BH	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BI	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BJ	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BK	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BL	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BM	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BN	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BO	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BP	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BQ	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BR	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BS	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BT	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BU	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BV	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BW	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BX	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BY	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BZ	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CA	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CB	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CC	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CD	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CE	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CF	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CG	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CH	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CI	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CJ	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CK	184/208 (88%)	182 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CL	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CM	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CN	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CO	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CP	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CQ	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CR	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CS	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CT	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CU	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CV	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CW	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CX	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CY	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CZ	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	DA	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	DB	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	DC	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	DD	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	DE	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	DF	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	DG	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	DH	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	DI	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	DJ	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	DK	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	DL	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
All	All	17010/18720 (91%)	16680 (98%)	330 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	155/164 (94%)	155 (100%)	0	100	100
1	AB	149/164 (91%)	149 (100%)	0	100	100
1	AC	146/164 (89%)	146 (100%)	0	100	100
1	AD	155/164 (94%)	155 (100%)	0	100	100
1	AE	149/164 (91%)	149 (100%)	0	100	100
1	AF	146/164 (89%)	146 (100%)	0	100	100
1	AG	155/164 (94%)	155 (100%)	0	100	100
1	AH	149/164 (91%)	149 (100%)	0	100	100
1	AI	146/164 (89%)	146 (100%)	0	100	100
1	AJ	155/164 (94%)	155 (100%)	0	100	100
1	AK	149/164 (91%)	149 (100%)	0	100	100
1	AL	146/164 (89%)	146 (100%)	0	100	100
1	AM	155/164 (94%)	155 (100%)	0	100	100
1	AN	149/164 (91%)	149 (100%)	0	100	100
1	AO	146/164 (89%)	146 (100%)	0	100	100
1	AP	155/164 (94%)	155 (100%)	0	100	100
1	AQ	149/164 (91%)	149 (100%)	0	100	100
1	AR	146/164 (89%)	146 (100%)	0	100	100
1	AS	155/164 (94%)	155 (100%)	0	100	100
1	AT	149/164 (91%)	149 (100%)	0	100	100
1	AU	146/164 (89%)	146 (100%)	0	100	100
1	AV	155/164 (94%)	155 (100%)	0	100	100
1	AW	149/164 (91%)	149 (100%)	0	100	100
1	AX	146/164 (89%)	146 (100%)	0	100	100
1	AY	155/164 (94%)	155 (100%)	0	100	100
1	AZ	149/164 (91%)	149 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BA	146/164 (89%)	146 (100%)	0	100	100
1	BB	155/164 (94%)	155 (100%)	0	100	100
1	BC	149/164 (91%)	149 (100%)	0	100	100
1	BD	146/164 (89%)	146 (100%)	0	100	100
1	BE	155/164 (94%)	155 (100%)	0	100	100
1	BF	149/164 (91%)	149 (100%)	0	100	100
1	BG	146/164 (89%)	146 (100%)	0	100	100
1	BH	155/164 (94%)	155 (100%)	0	100	100
1	BI	149/164 (91%)	149 (100%)	0	100	100
1	BJ	146/164 (89%)	146 (100%)	0	100	100
1	BK	155/164 (94%)	155 (100%)	0	100	100
1	BL	149/164 (91%)	149 (100%)	0	100	100
1	BM	146/164 (89%)	146 (100%)	0	100	100
1	BN	155/164 (94%)	155 (100%)	0	100	100
1	BO	149/164 (91%)	149 (100%)	0	100	100
1	BP	146/164 (89%)	146 (100%)	0	100	100
1	BQ	155/164 (94%)	155 (100%)	0	100	100
1	BR	149/164 (91%)	149 (100%)	0	100	100
1	BS	146/164 (89%)	146 (100%)	0	100	100
1	BT	155/164 (94%)	155 (100%)	0	100	100
1	BU	149/164 (91%)	149 (100%)	0	100	100
1	BV	146/164 (89%)	146 (100%)	0	100	100
1	BW	155/164 (94%)	155 (100%)	0	100	100
1	BX	149/164 (91%)	149 (100%)	0	100	100
1	BY	146/164 (89%)	146 (100%)	0	100	100
1	BZ	155/164 (94%)	155 (100%)	0	100	100
1	CA	149/164 (91%)	149 (100%)	0	100	100
1	CB	146/164 (89%)	146 (100%)	0	100	100
1	CC	155/164 (94%)	155 (100%)	0	100	100
1	CD	149/164 (91%)	149 (100%)	0	100	100
1	CE	146/164 (89%)	146 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CF	155/164 (94%)	155 (100%)	0	100	100
1	CG	149/164 (91%)	149 (100%)	0	100	100
1	CH	146/164 (89%)	146 (100%)	0	100	100
1	CI	155/164 (94%)	155 (100%)	0	100	100
1	CJ	149/164 (91%)	149 (100%)	0	100	100
1	CK	146/164 (89%)	146 (100%)	0	100	100
1	CL	155/164 (94%)	155 (100%)	0	100	100
1	CM	149/164 (91%)	149 (100%)	0	100	100
1	CN	146/164 (89%)	146 (100%)	0	100	100
1	CO	155/164 (94%)	155 (100%)	0	100	100
1	CP	149/164 (91%)	149 (100%)	0	100	100
1	CQ	146/164 (89%)	146 (100%)	0	100	100
1	CR	155/164 (94%)	155 (100%)	0	100	100
1	CS	149/164 (91%)	149 (100%)	0	100	100
1	CT	146/164 (89%)	146 (100%)	0	100	100
1	CU	155/164 (94%)	155 (100%)	0	100	100
1	CV	149/164 (91%)	149 (100%)	0	100	100
1	CW	146/164 (89%)	146 (100%)	0	100	100
1	CX	155/164 (94%)	155 (100%)	0	100	100
1	CY	149/164 (91%)	149 (100%)	0	100	100
1	CZ	146/164 (89%)	146 (100%)	0	100	100
1	DA	155/164 (94%)	155 (100%)	0	100	100
1	DB	149/164 (91%)	149 (100%)	0	100	100
1	DC	146/164 (89%)	146 (100%)	0	100	100
1	DD	155/164 (94%)	155 (100%)	0	100	100
1	DE	149/164 (91%)	149 (100%)	0	100	100
1	DF	146/164 (89%)	146 (100%)	0	100	100
1	DG	155/164 (94%)	155 (100%)	0	100	100
1	DH	149/164 (91%)	149 (100%)	0	100	100
1	DI	146/164 (89%)	146 (100%)	0	100	100
1	DJ	155/164 (94%)	155 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	DK	149/164 (91%)	149 (100%)	0	100	100
1	DL	146/164 (89%)	146 (100%)	0	100	100
All	All	13500/14760 (92%)	13500 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (102) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	17	GLN
1	AA	96	ASN
1	AA	178	ASN
1	AB	22	GLN
1	AC	129	ASN
1	AC	207	GLN
1	AD	96	ASN
1	AE	31	ASN
1	AF	129	ASN
1	AF	207	GLN
1	AG	96	ASN
1	AH	31	ASN
1	AJ	96	ASN
1	AK	31	ASN
1	AL	129	ASN
1	AM	96	ASN
1	AP	17	GLN
1	AR	129	ASN
1	AR	207	GLN
1	AS	96	ASN
1	AU	79	GLN
1	AU	129	ASN
1	AU	207	GLN
1	AV	17	GLN
1	AV	79	GLN
1	AV	96	ASN
1	AW	31	ASN
1	AY	96	ASN
1	AY	178	ASN
1	AZ	31	ASN
1	BA	129	ASN
1	BA	207	GLN

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Mol	Chain	Res	Type
1	BB	96	ASN
1	BC	31	ASN
1	BD	129	ASN
1	BD	207	GLN
1	BE	96	ASN
1	BF	31	ASN
1	BG	129	ASN
1	BG	207	GLN
1	BH	17	GLN
1	BH	96	ASN
1	BH	178	ASN
1	BJ	129	ASN
1	BK	96	ASN
1	BL	31	ASN
1	BM	129	ASN
1	BN	79	GLN
1	BN	96	ASN
1	BP	79	GLN
1	BP	129	ASN
1	BQ	96	ASN
1	BS	129	ASN
1	BS	207	GLN
1	BT	96	ASN
1	BW	96	ASN
1	BX	22	GLN
1	BX	31	ASN
1	BY	129	ASN
1	BY	207	GLN
1	BZ	17	GLN
1	BZ	96	ASN
1	CA	22	GLN
1	CC	96	ASN
1	CD	22	GLN
1	CE	129	ASN
1	CE	207	GLN
1	CF	17	GLN
1	CF	96	ASN
1	CI	96	ASN
1	CJ	31	ASN
1	CK	129	ASN
1	CL	96	ASN
1	CM	31	ASN

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Mol	Chain	Res	Type
1	CN	129	ASN
1	CO	96	ASN
1	CQ	129	ASN
1	CQ	207	GLN
1	CR	17	GLN
1	CR	202	HIS
1	CS	22	GLN
1	CT	129	ASN
1	CU	17	GLN
1	CU	96	ASN
1	CW	129	ASN
1	CX	79	GLN
1	CX	96	ASN
1	CX	178	ASN
1	CZ	129	ASN
1	DA	96	ASN
1	DB	31	ASN
1	DC	129	ASN
1	DD	17	GLN
1	DD	96	ASN
1	DF	79	GLN
1	DF	129	ASN
1	DG	96	ASN
1	DI	129	ASN
1	DJ	96	ASN
1	DK	31	ASN
1	DL	129	ASN
1	DL	207	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	198/208 (95%)	1.09	28 (14%) 6 5	67, 89, 121, 184	0
1	AB	189/208 (90%)	1.01	25 (13%) 7 6	60, 89, 124, 186	0
1	AC	186/208 (89%)	0.90	20 (10%) 11 9	65, 88, 115, 141	0
1	AD	198/208 (95%)	0.91	19 (9%) 13 11	67, 89, 121, 184	0
1	AE	189/208 (90%)	0.93	19 (10%) 12 10	60, 89, 124, 186	0
1	AF	186/208 (89%)	0.78	14 (7%) 20 15	65, 88, 115, 141	0
1	AG	198/208 (95%)	0.86	16 (8%) 18 13	67, 89, 121, 184	0
1	AH	189/208 (90%)	0.81	15 (7%) 18 14	60, 89, 124, 186	0
1	AI	186/208 (89%)	1.00	17 (9%) 15 11	65, 88, 115, 141	0
1	AJ	198/208 (95%)	1.10	34 (17%) 4 4	67, 89, 121, 184	0
1	AK	189/208 (90%)	0.96	18 (9%) 14 11	60, 89, 124, 186	0
1	AL	186/208 (89%)	0.97	13 (6%) 22 15	65, 88, 115, 141	0
1	AM	198/208 (95%)	0.88	19 (9%) 13 11	67, 89, 121, 184	0
1	AN	189/208 (90%)	1.03	18 (9%) 14 11	60, 89, 124, 186	0
1	AO	186/208 (89%)	1.01	19 (10%) 12 10	65, 88, 115, 141	0
1	AP	198/208 (95%)	0.89	17 (8%) 16 12	67, 89, 121, 184	0
1	AQ	189/208 (90%)	0.71	10 (5%) 32 22	60, 89, 124, 186	0
1	AR	186/208 (89%)	0.79	14 (7%) 20 15	65, 88, 115, 141	0
1	AS	198/208 (95%)	0.83	21 (10%) 11 9	67, 89, 121, 184	0
1	AT	189/208 (90%)	0.85	20 (10%) 11 9	60, 89, 124, 186	0
1	AU	186/208 (89%)	0.80	8 (4%) 40 25	65, 88, 115, 141	0
1	AV	198/208 (95%)	0.74	17 (8%) 16 12	67, 89, 121, 184	0
1	AW	189/208 (90%)	0.78	14 (7%) 20 15	60, 89, 124, 186	0
1	AX	186/208 (89%)	0.90	21 (11%) 10 8	65, 88, 115, 141	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AY	198/208 (95%)	0.89	21 (10%) 11 9	67, 89, 121, 184	0
1	AZ	189/208 (90%)	0.93	20 (10%) 11 9	60, 89, 124, 186	0
1	BA	186/208 (89%)	0.89	18 (9%) 13 11	65, 88, 115, 141	0
1	BB	198/208 (95%)	1.11	35 (17%) 4 3	67, 89, 121, 184	0
1	BC	189/208 (90%)	0.96	21 (11%) 10 9	60, 89, 124, 186	0
1	BD	186/208 (89%)	0.91	15 (8%) 18 13	65, 88, 115, 141	0
1	BE	198/208 (95%)	0.91	15 (7%) 20 14	67, 89, 121, 184	0
1	BF	189/208 (90%)	0.79	10 (5%) 32 22	60, 89, 124, 186	0
1	BG	186/208 (89%)	0.87	13 (6%) 22 15	65, 88, 115, 141	0
1	BH	198/208 (95%)	0.69	17 (8%) 16 12	67, 89, 121, 184	0
1	BI	189/208 (90%)	0.74	11 (5%) 29 19	60, 89, 124, 186	0
1	BJ	186/208 (89%)	0.73	9 (4%) 35 24	65, 88, 115, 141	0
1	BK	198/208 (95%)	0.88	15 (7%) 20 14	67, 89, 121, 184	0
1	BL	189/208 (90%)	0.93	23 (12%) 8 7	60, 89, 124, 186	0
1	BM	186/208 (89%)	0.76	7 (3%) 44 30	65, 88, 115, 141	0
1	BN	198/208 (95%)	0.93	25 (12%) 8 6	67, 89, 121, 184	0
1	BO	189/208 (90%)	0.74	16 (8%) 16 13	60, 89, 124, 186	0
1	BP	186/208 (89%)	0.85	19 (10%) 12 10	65, 88, 115, 141	0
1	BQ	198/208 (95%)	0.90	17 (8%) 16 12	67, 89, 121, 184	0
1	BR	189/208 (90%)	0.85	20 (10%) 11 9	60, 89, 124, 186	0
1	BS	186/208 (89%)	0.68	10 (5%) 31 21	65, 88, 115, 141	0
1	BT	198/208 (95%)	0.95	21 (10%) 11 9	67, 89, 121, 184	0
1	BU	189/208 (90%)	0.98	16 (8%) 16 13	60, 89, 124, 186	0
1	BV	186/208 (89%)	1.04	23 (12%) 8 6	65, 88, 115, 141	0
1	BW	198/208 (95%)	0.83	16 (8%) 18 13	67, 89, 121, 184	0
1	BX	189/208 (90%)	0.76	17 (8%) 15 11	60, 89, 124, 186	0
1	BY	186/208 (89%)	0.92	20 (10%) 11 9	65, 88, 115, 141	0
1	BZ	198/208 (95%)	0.97	24 (12%) 8 7	67, 89, 121, 184	0
1	CA	189/208 (90%)	0.96	24 (12%) 8 6	60, 89, 124, 186	0
1	CB	186/208 (89%)	0.98	19 (10%) 12 10	65, 88, 115, 141	0
1	CC	198/208 (95%)	0.84	19 (9%) 13 11	67, 89, 121, 184	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	CD	189/208 (90%)	0.78	17 (8%)	15 11	60, 89, 124, 186	0
1	CE	186/208 (89%)	0.81	14 (7%)	20 15	65, 88, 115, 141	0
1	CF	198/208 (95%)	1.02	24 (12%)	8 7	67, 89, 121, 184	0
1	CG	189/208 (90%)	0.82	16 (8%)	16 13	60, 89, 124, 186	0
1	CH	186/208 (89%)	1.05	21 (11%)	10 8	65, 88, 115, 141	0
1	CI	198/208 (95%)	0.70	16 (8%)	18 13	67, 89, 121, 184	0
1	CJ	189/208 (90%)	0.88	14 (7%)	20 15	60, 89, 124, 186	0
1	CK	186/208 (89%)	0.90	15 (8%)	18 13	65, 88, 115, 141	0
1	CL	198/208 (95%)	0.85	19 (9%)	13 11	67, 89, 121, 184	0
1	CM	189/208 (90%)	0.92	27 (14%)	6 5	60, 89, 124, 186	0
1	CN	186/208 (89%)	0.67	14 (7%)	20 15	65, 88, 115, 141	0
1	CO	198/208 (95%)	0.78	12 (6%)	27 18	67, 89, 121, 184	0
1	CP	189/208 (90%)	0.70	10 (5%)	32 22	60, 89, 124, 186	0
1	CQ	186/208 (89%)	0.84	19 (10%)	12 10	65, 88, 115, 141	0
1	CR	198/208 (95%)	0.83	15 (7%)	20 14	67, 89, 121, 184	0
1	CS	189/208 (90%)	0.78	12 (6%)	26 17	60, 89, 124, 186	0
1	CT	186/208 (89%)	0.67	9 (4%)	35 24	65, 88, 115, 141	0
1	CU	198/208 (95%)	0.90	23 (11%)	9 8	67, 89, 121, 184	0
1	CV	189/208 (90%)	0.78	19 (10%)	12 10	60, 89, 124, 186	0
1	CW	186/208 (89%)	0.87	11 (5%)	28 19	65, 88, 115, 141	0
1	CX	198/208 (95%)	0.95	23 (11%)	9 8	67, 89, 121, 184	0
1	CY	189/208 (90%)	0.85	16 (8%)	16 13	60, 89, 124, 186	0
1	CZ	186/208 (89%)	0.86	12 (6%)	25 17	65, 88, 115, 141	0
1	DA	198/208 (95%)	1.01	24 (12%)	8 7	67, 89, 121, 184	0
1	DB	189/208 (90%)	0.88	16 (8%)	16 13	60, 89, 124, 186	0
1	DC	186/208 (89%)	0.80	17 (9%)	15 11	65, 88, 115, 141	0
1	DD	198/208 (95%)	0.83	16 (8%)	18 13	67, 89, 121, 184	0
1	DE	189/208 (90%)	0.78	11 (5%)	29 19	60, 89, 124, 186	0
1	DF	186/208 (89%)	0.92	18 (9%)	13 11	65, 88, 115, 141	0
1	DG	198/208 (95%)	0.67	15 (7%)	20 14	67, 89, 121, 184	0
1	DH	189/208 (90%)	0.89	21 (11%)	10 9	60, 89, 124, 186	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	DI	186/208 (89%)	0.84	14 (7%)	20 15	65, 88, 115, 141	0
1	DJ	198/208 (95%)	0.80	14 (7%)	22 15	67, 89, 121, 184	0
1	DK	189/208 (90%)	0.72	13 (6%)	23 16	60, 89, 124, 186	0
1	DL	186/208 (89%)	0.77	12 (6%)	25 17	65, 88, 115, 141	0
All	All	17190/18720 (91%)	0.87	1561 (9%)	15 11	60, 89, 120, 186	0

All (1561) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AY	141	GLY	7.3
1	CQ	84	GLY	6.9
1	BB	208	ALA	6.2
1	DI	141	GLY	6.1
1	AK	23	SER	5.8
1	CF	22	GLN	5.7
1	AO	208	ALA	5.5
1	DA	142	ALA	5.5
1	BR	208	ALA	5.4
1	BN	208	ALA	5.4
1	BD	113	SER	5.3
1	CX	29	GLY	5.1
1	AS	136	ALA	5.1
1	BR	22	GLN	5.0
1	BZ	11	GLY	5.0
1	BO	20	PRO	4.9
1	BC	158	GLY	4.9
1	AN	23	SER	4.9
1	CM	114	ASN	4.9
1	AK	22	GLN	4.9
1	AD	208	ALA	4.8
1	AM	113	SER	4.8
1	CL	24	SER	4.8
1	AO	84	GLY	4.7
1	AF	85	VAL	4.7
1	BK	22	GLN	4.6
1	AA	13	LEU	4.5
1	CV	87	THR	4.5
1	AI	113	SER	4.5
1	AX	201	SER	4.5
1	BX	53	TYR	4.5
1	BB	141	GLY	4.4

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Mol	Chain	Res	Type	RSRZ
1	AL	158	GLY	4.4
1	AK	21	VAL	4.4
1	DH	189	ASP	4.4
1	CW	177	SER	4.4
1	BQ	141	GLY	4.4
1	DF	189	ASP	4.3
1	BB	114	ASN	4.3
1	CP	208	ALA	4.3
1	AY	90	GLY	4.3
1	AL	208	ALA	4.3
1	AJ	11	GLY	4.3
1	CN	208	ALA	4.3
1	CU	18	GLN	4.2
1	CE	82	VAL	4.2
1	AP	114	ASN	4.2
1	CM	116	ARG	4.2
1	CH	122	ASP	4.2
1	DF	74	ASN	4.2
1	AS	141	GLY	4.1
1	AG	208	ALA	4.1
1	AX	150	LYS	4.1
1	AZ	116	ARG	4.1
1	BO	116	ARG	4.1
1	AI	208	ALA	4.1
1	CW	208	ALA	4.1
1	CK	193	ASN	4.1
1	DA	147	GLY	4.1
1	CM	22	GLN	4.0
1	AE	44	ALA	4.0
1	AE	163	GLY	4.0
1	DH	114	ASN	4.0
1	BV	44	ALA	4.0
1	CJ	41	VAL	4.0
1	BP	44	ALA	4.0
1	DL	103	ALA	4.0
1	BC	156	LEU	4.0
1	AY	105	SER	4.0
1	CH	150	LYS	4.0
1	AV	22	GLN	3.9
1	AN	24	SER	3.9
1	BO	189	ASP	3.9
1	CK	84	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
1	AA	208	ALA	3.9
1	CD	113	SER	3.9
1	AJ	95	THR	3.9
1	CL	189	ASP	3.9
1	CR	148	SER	3.9
1	AI	142	ALA	3.9
1	CB	193	ASN	3.9
1	CX	28	PHE	3.9
1	AL	53	TYR	3.8
1	AW	60	GLN	3.8
1	BW	28	PHE	3.8
1	CQ	113	SER	3.8
1	AD	176	LEU	3.8
1	BX	110	ARG	3.8
1	BW	80	ASN	3.8
1	CI	24	SER	3.8
1	AD	44	ALA	3.8
1	DE	163	GLY	3.8
1	CH	201	SER	3.8
1	AB	53	TYR	3.8
1	AN	116	ARG	3.8
1	BJ	24	SER	3.8
1	AV	189	ASP	3.8
1	AI	141	GLY	3.8
1	BT	18	GLN	3.7
1	CQ	189	ASP	3.7
1	AX	149	PHE	3.7
1	CH	208	ALA	3.7
1	AN	79	GLN	3.7
1	CW	152	ASN	3.7
1	AE	33	ASP	3.7
1	BO	21	VAL	3.7
1	DI	193	ASN	3.7
1	BO	114	ASN	3.7
1	CT	96	ASN	3.7
1	BY	24	SER	3.7
1	CC	141	GLY	3.7
1	DK	90	GLY	3.7
1	CX	105	SER	3.6
1	AP	22	GLN	3.6
1	AF	203	GLY	3.6
1	BE	80	ASN	3.6

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Mol	Chain	Res	Type	RSRZ
1	CB	141	GLY	3.6
1	BV	42	TYR	3.6
1	CH	189	ASP	3.6
1	CL	12	GLN	3.6
1	DB	163	GLY	3.6
1	AH	20	PRO	3.6
1	DA	96	ASN	3.6
1	BA	44	ALA	3.6
1	CQ	42	TYR	3.6
1	AG	11	GLY	3.6
1	BC	116	ARG	3.6
1	BF	44	ALA	3.6
1	CX	23	SER	3.6
1	AB	116	ARG	3.6
1	CT	141	GLY	3.6
1	CH	24	SER	3.6
1	AE	203	GLY	3.5
1	BB	23	SER	3.5
1	CX	110	ARG	3.5
1	CX	20	PRO	3.5
1	AJ	13	LEU	3.5
1	CL	113	SER	3.5
1	AX	44	ALA	3.5
1	BA	103	ALA	3.5
1	BT	44	ALA	3.5
1	AA	116	ARG	3.5
1	AA	80	ASN	3.5
1	CA	114	ASN	3.5
1	CV	37	ASN	3.5
1	AM	24	SER	3.5
1	AN	163	GLY	3.5
1	BC	22	GLN	3.5
1	BL	79	GLN	3.5
1	AR	103	ALA	3.5
1	BB	20	PRO	3.5
1	DK	110	ARG	3.5
1	AA	26	THR	3.5
1	AD	69	GLY	3.5
1	CY	163	GLY	3.5
1	AJ	113	SER	3.5
1	BI	74	ASN	3.4
1	BP	152	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
1	AD	180	LEU	3.4
1	AK	114	ASN	3.4
1	BL	163	GLY	3.4
1	AL	27	THR	3.4
1	BN	80	ASN	3.4
1	CL	25	ARG	3.4
1	CY	203	GLY	3.4
1	AX	103	ALA	3.4
1	AA	167	ASN	3.4
1	BK	80	ASN	3.4
1	CF	12	GLN	3.4
1	AX	113	SER	3.4
1	AR	156	LEU	3.4
1	BA	158	GLY	3.4
1	BU	44	ALA	3.4
1	BV	142	ALA	3.4
1	CF	141	GLY	3.4
1	DC	103	ALA	3.4
1	AB	114	ASN	3.4
1	BV	96	ASN	3.4
1	CF	80	ASN	3.4
1	AC	165	ASP	3.4
1	DA	146	VAL	3.4
1	CF	84	GLY	3.4
1	CT	103	ALA	3.4
1	AW	22	GLN	3.4
1	CD	116	ARG	3.3
1	CE	189	ASP	3.3
1	CV	33	ASP	3.3
1	DA	189	ASP	3.3
1	AP	44	ALA	3.3
1	AQ	159	GLY	3.3
1	BK	44	ALA	3.3
1	CA	31	ASN	3.3
1	CM	30	VAL	3.3
1	BY	90	GLY	3.3
1	CN	84	GLY	3.3
1	DE	208	ALA	3.3
1	DH	159	GLY	3.3
1	DL	29	GLY	3.3
1	BE	207	GLN	3.3
1	BL	32	PRO	3.3

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Mol	Chain	Res	Type	RSRZ
1	DK	80	ASN	3.3
1	CB	168	ALA	3.3
1	CJ	105	SER	3.3
1	CQ	103	ALA	3.3
1	AR	189	ASP	3.3
1	BU	189	ASP	3.3
1	AO	79	GLN	3.3
1	BZ	109	THR	3.3
1	CI	17	GLN	3.3
1	CV	34	ARG	3.3
1	DH	28	PHE	3.3
1	AX	96	ASN	3.3
1	DC	192	LYS	3.3
1	BG	44	ALA	3.3
1	CZ	208	ALA	3.3
1	AS	111	ASP	3.3
1	CM	33	ASP	3.3
1	CS	33	ASP	3.3
1	DI	189	ASP	3.3
1	BB	22	GLN	3.3
1	CM	79	GLN	3.3
1	AB	74	ASN	3.3
1	CU	114	ASN	3.3
1	AM	208	ALA	3.3
1	AI	157	GLY	3.3
1	BC	157	GLY	3.3
1	AW	34	ARG	3.2
1	DD	189	ASP	3.2
1	AW	28	PHE	3.2
1	AR	95	THR	3.2
1	BH	117	THR	3.2
1	CG	21	VAL	3.2
1	AI	103	ALA	3.2
1	CN	25	ARG	3.2
1	AB	23	SER	3.2
1	BB	24	SER	3.2
1	BW	150	LYS	3.2
1	DA	150	LYS	3.2
1	BX	189	ASP	3.2
1	CC	82	VAL	3.2
1	BZ	95	THR	3.2
1	AB	193	ASN	3.2

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Mol	Chain	Res	Type	RSRZ
1	BE	96	ASN	3.2
1	AA	92	TYR	3.2
1	BI	79	GLN	3.2
1	DG	22	GLN	3.2
1	BA	95	THR	3.2
1	AZ	203	GLY	3.2
1	BB	150	LYS	3.2
1	AJ	189	ASP	3.2
1	BZ	189	ASP	3.2
1	AT	72	ALA	3.2
1	DB	74	ASN	3.2
1	AB	22	GLN	3.2
1	DH	194	THR	3.2
1	CK	189	ASP	3.1
1	AJ	14	TYR	3.1
1	CA	188	GLN	3.1
1	BD	73	SER	3.1
1	CM	44	ALA	3.1
1	AJ	141	GLY	3.1
1	CL	163	GLY	3.1
1	CT	98	GLY	3.1
1	DH	64	GLY	3.1
1	AF	74	ASN	3.1
1	BC	74	ASN	3.1
1	BC	114	ASN	3.1
1	BR	53	TYR	3.1
1	AT	79	GLN	3.1
1	CF	208	ALA	3.1
1	CK	44	ALA	3.1
1	CZ	62	ALA	3.1
1	DF	208	ALA	3.1
1	AB	120	SER	3.1
1	AD	11	GLY	3.1
1	CB	84	GLY	3.1
1	CZ	84	GLY	3.1
1	BT	189	ASP	3.1
1	BR	28	PHE	3.1
1	BZ	28	PHE	3.1
1	DI	85	VAL	3.1
1	AY	140	PRO	3.1
1	BH	53	TYR	3.1
1	DJ	118	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	BL	63	ALA	3.1
1	BL	142	ALA	3.1
1	BZ	207	GLN	3.1
1	CE	208	ALA	3.1
1	CK	79	GLN	3.1
1	BL	157	GLY	3.1
1	BU	163	GLY	3.1
1	CF	29	GLY	3.1
1	BC	23	SER	3.1
1	BB	189	ASP	3.1
1	BA	74	ASN	3.1
1	CP	193	ASN	3.1
1	CU	74	ASN	3.1
1	AC	115	GLY	3.1
1	CF	52	THR	3.1
1	DD	109	THR	3.1
1	DL	115	GLY	3.1
1	BV	189	ASP	3.1
1	DC	189	ASP	3.1
1	BE	15	MET	3.1
1	BR	20	PRO	3.1
1	AJ	42	TYR	3.1
1	AA	74	ASN	3.0
1	AB	208	ALA	3.0
1	AD	114	ASN	3.0
1	AF	142	ALA	3.0
1	BP	208	ALA	3.0
1	CQ	44	ALA	3.0
1	CU	208	ALA	3.0
1	AW	79	GLN	3.0
1	CG	79	GLN	3.0
1	AS	84	GLY	3.0
1	CQ	185	ARG	3.0
1	AG	94	THR	3.0
1	BK	95	THR	3.0
1	BN	143	VAL	3.0
1	BA	113	SER	3.0
1	BJ	189	ASP	3.0
1	CP	53	TYR	3.0
1	AQ	208	ALA	3.0
1	BN	142	ALA	3.0
1	AR	37	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
1	AP	12	GLN	3.0
1	BA	110	ARG	3.0
1	BB	12	GLN	3.0
1	BZ	15	MET	3.0
1	CA	91	GLU	3.0
1	CI	113	SER	3.0
1	CD	33	ASP	3.0
1	CM	156	LEU	3.0
1	DB	36	ALA	3.0
1	CK	25	ARG	3.0
1	AF	188	GLN	3.0
1	AM	207	GLN	3.0
1	BF	74	ASN	3.0
1	CM	69	GLY	3.0
1	CR	69	GLY	3.0
1	CX	69	GLY	3.0
1	BN	82	VAL	3.0
1	AY	87	THR	3.0
1	CM	154	GLU	3.0
1	BV	110	ARG	3.0
1	DI	136	ALA	3.0
1	AR	99	ASP	3.0
1	CM	189	ASP	3.0
1	BW	143	VAL	3.0
1	DI	114	ASN	3.0
1	BR	107	THR	3.0
1	BT	26	THR	3.0
1	BV	194	THR	3.0
1	BV	105	SER	3.0
1	CA	44	ALA	3.0
1	BN	118	LYS	3.0
1	AG	33	ASP	3.0
1	AY	11	GLY	3.0
1	BQ	84	GLY	3.0
1	CV	84	GLY	3.0
1	CG	22	GLN	3.0
1	AL	74	ASN	3.0
1	AT	114	ASN	3.0
1	AN	117	THR	3.0
1	AK	91	GLU	2.9
1	AX	132	GLU	2.9
1	BQ	20	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	CE	116	ARG	2.9
1	AA	62	ALA	2.9
1	AF	103	ALA	2.9
1	BM	192	LYS	2.9
1	AB	113	SER	2.9
1	CG	53	TYR	2.9
1	AI	189	ASP	2.9
1	AE	152	ASN	2.9
1	BH	80	ASN	2.9
1	CA	193	ASN	2.9
1	CQ	74	ASN	2.9
1	BD	116	ARG	2.9
1	BV	103	ALA	2.9
1	AC	113	SER	2.9
1	AF	113	SER	2.9
1	AO	42	TYR	2.9
1	BD	119	VAL	2.9
1	AB	115	GLY	2.9
1	AR	29	GLY	2.9
1	CU	84	GLY	2.9
1	DF	157	GLY	2.9
1	DE	189	ASP	2.9
1	DH	79	GLN	2.9
1	AA	128	ARG	2.9
1	AR	193	ASN	2.9
1	BB	80	ASN	2.9
1	DG	150	LYS	2.9
1	DJ	107	THR	2.9
1	AJ	208	ALA	2.9
1	BB	63	ALA	2.9
1	CI	156	LEU	2.9
1	CU	15	MET	2.9
1	AI	164	THR	2.9
1	BT	27	THR	2.9
1	DL	26	THR	2.9
1	AI	200	ALA	2.9
1	BB	130	ALA	2.9
1	BS	200	ALA	2.9
1	BU	82	VAL	2.9
1	BW	41	VAL	2.9
1	CX	146	VAL	2.9
1	DB	69	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	BR	110	ARG	2.9
1	CI	110	ARG	2.9
1	AD	113	SER	2.9
1	BR	23	SER	2.9
1	DC	73	SER	2.9
1	CV	22	GLN	2.9
1	BF	38	ALA	2.9
1	BN	87	THR	2.9
1	BX	168	ALA	2.9
1	CX	208	ALA	2.9
1	BY	80	ASN	2.9
1	CO	114	ASN	2.9
1	AU	84	GLY	2.9
1	BA	115	GLY	2.9
1	BC	53	TYR	2.9
1	AP	179	MET	2.9
1	DH	188	GLN	2.8
1	AV	62	ALA	2.8
1	BB	62	ALA	2.8
1	CI	189	ASP	2.8
1	CX	44	ALA	2.8
1	DB	189	ASP	2.8
1	AG	107	THR	2.8
1	BR	117	THR	2.8
1	CO	95	THR	2.8
1	AH	114	ASN	2.8
1	AJ	80	ASN	2.8
1	AM	143	VAL	2.8
1	BR	30	VAL	2.8
1	CJ	74	ASN	2.8
1	CE	185	ARG	2.8
1	DK	116	ARG	2.8
1	BH	141	GLY	2.8
1	AA	42	TYR	2.8
1	CB	42	TYR	2.8
1	DK	53	TYR	2.8
1	AK	79	GLN	2.8
1	BB	207	GLN	2.8
1	BK	18	GLN	2.8
1	BZ	22	GLN	2.8
1	CH	73	SER	2.8
1	CI	22	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	CU	105	SER	2.8
1	BU	36	ALA	2.8
1	AE	146	VAL	2.8
1	AN	110	ARG	2.8
1	BB	50	GLU	2.8
1	BT	128	ARG	2.8
1	BU	110	ARG	2.8
1	AD	96	ASN	2.8
1	BH	96	ASN	2.8
1	AO	141	GLY	2.8
1	BE	69	GLY	2.8
1	CO	11	GLY	2.8
1	BO	44	ALA	2.8
1	BY	208	ALA	2.8
1	CY	103	ALA	2.8
1	CY	142	ALA	2.8
1	AZ	110	ARG	2.8
1	DI	48	PRO	2.8
1	BA	85	VAL	2.8
1	AK	33	ASP	2.8
1	BC	91	GLU	2.8
1	BE	189	ASP	2.8
1	CA	189	ASP	2.8
1	AZ	74	ASN	2.8
1	BO	129	ASN	2.8
1	BP	80	ASN	2.8
1	CE	84	GLY	2.8
1	CG	163	GLY	2.8
1	DK	114	ASN	2.8
1	BF	35	GLN	2.8
1	BI	44	ALA	2.8
1	DA	208	ALA	2.8
1	BQ	110	ARG	2.8
1	CL	116	ARG	2.8
1	BN	150	LYS	2.8
1	BR	112	VAL	2.8
1	CA	23	SER	2.8
1	BH	95	THR	2.8
1	CF	107	THR	2.8
1	BB	28	PHE	2.8
1	CY	33	ASP	2.8
1	BB	159	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	BM	193	ASN	2.8
1	CB	74	ASN	2.8
1	CO	80	ASN	2.8
1	CY	74	ASN	2.8
1	AF	53	TYR	2.8
1	AA	110	ARG	2.8
1	BC	79	GLN	2.8
1	BH	208	ALA	2.8
1	BT	130	ALA	2.8
1	BW	118	LYS	2.8
1	CP	22	GLN	2.8
1	AZ	30	VAL	2.8
1	CH	32	PRO	2.8
1	AJ	50	GLU	2.8
1	CO	27	THR	2.8
1	CW	107	THR	2.8
1	AD	189	ASP	2.7
1	AX	165	ASP	2.7
1	DB	90	GLY	2.7
1	DC	163	GLY	2.7
1	AF	96	ASN	2.7
1	AV	74	ASN	2.7
1	CF	96	ASN	2.7
1	CK	114	ASN	2.7
1	CJ	53	TYR	2.7
1	BH	150	LYS	2.7
1	BY	36	ALA	2.7
1	CF	44	ALA	2.7
1	DA	44	ALA	2.7
1	DH	63	ALA	2.7
1	AM	28	PHE	2.7
1	BS	141	GLY	2.7
1	CA	122	ASP	2.7
1	CJ	189	ASP	2.7
1	BG	110	ARG	2.7
1	BN	193	ASN	2.7
1	CP	51	ASN	2.7
1	AW	44	ALA	2.7
1	CS	191	PRO	2.7
1	DG	28	PHE	2.7
1	AP	26	THR	2.7
1	AS	27	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	BP	84	GLY	2.7
1	BS	94	THR	2.7
1	BV	95	THR	2.7
1	CS	163	GLY	2.7
1	CV	73	SER	2.7
1	AI	74	ASN	2.7
1	CN	103	ALA	2.7
1	CY	38	ALA	2.7
1	DG	114	ASN	2.7
1	BK	112	VAL	2.7
1	CH	85	VAL	2.7
1	AJ	116	ARG	2.7
1	BM	64	GLY	2.7
1	CL	141	GLY	2.7
1	AT	87	THR	2.7
1	BB	95	THR	2.7
1	CQ	95	THR	2.7
1	AT	53	TYR	2.7
1	BN	42	TYR	2.7
1	CJ	33	ASP	2.7
1	CO	38	ALA	2.7
1	BA	82	VAL	2.7
1	CX	143	VAL	2.7
1	AB	152	ASN	2.7
1	DG	74	ASN	2.7
1	BH	207	GLN	2.7
1	BL	20	PRO	2.7
1	CR	18	GLN	2.7
1	CX	22	GLN	2.7
1	CR	110	ARG	2.7
1	DB	34	ARG	2.7
1	AC	157	GLY	2.7
1	AZ	163	GLY	2.7
1	BD	150	LYS	2.7
1	BX	69	GLY	2.7
1	CM	91	GLU	2.7
1	BA	94	THR	2.7
1	CK	27	THR	2.7
1	DB	95	THR	2.7
1	BY	113	SER	2.7
1	CB	208	ALA	2.7
1	AC	53	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	AE	197	LEU	2.7
1	DD	143	VAL	2.7
1	AE	189	ASP	2.7
1	CN	189	ASP	2.7
1	BN	114	ASN	2.7
1	AE	79	GLN	2.6
1	AG	35	GLN	2.6
1	CU	116	ARG	2.6
1	BV	192	LYS	2.6
1	AG	137	SER	2.6
1	AP	23	SER	2.6
1	AT	166	ALA	2.6
1	AZ	36	ALA	2.6
1	BG	208	ALA	2.6
1	BK	24	SER	2.6
1	BT	204	VAL	2.6
1	CN	44	ALA	2.6
1	DB	44	ALA	2.6
1	DI	30	VAL	2.6
1	BZ	14	TYR	2.6
1	CY	53	TYR	2.6
1	AF	189	ASP	2.6
1	BH	189	ASP	2.6
1	AK	32	PRO	2.6
1	AV	114	ASN	2.6
1	BJ	150	LYS	2.6
1	CA	74	ASN	2.6
1	CB	192	LYS	2.6
1	CI	114	ASN	2.6
1	CJ	152	ASN	2.6
1	DH	31	ASN	2.6
1	DH	192	LYS	2.6
1	BB	11	GLY	2.6
1	BB	197	LEU	2.6
1	BD	103	ALA	2.6
1	CB	38	ALA	2.6
1	CO	208	ALA	2.6
1	DK	44	ALA	2.6
1	AC	73	SER	2.6
1	BS	201	SER	2.6
1	CG	23	SER	2.6
1	DJ	137	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	AC	25	ARG	2.6
1	CF	128	ARG	2.6
1	DA	110	ARG	2.6
1	BW	15	MET	2.6
1	CE	32	PRO	2.6
1	AG	22	GLN	2.6
1	AL	37	ASN	2.6
1	AM	18	GLN	2.6
1	AM	114	ASN	2.6
1	AQ	79	GLN	2.6
1	AS	80	ASN	2.6
1	BU	35	GLN	2.6
1	DA	114	ASN	2.6
1	BT	64	GLY	2.6
1	CC	69	GLY	2.6
1	CO	29	GLY	2.6
1	DB	196	ARG	2.6
1	BD	24	SER	2.6
1	BF	28	PHE	2.6
1	AC	189	ASP	2.6
1	CQ	188	GLN	2.6
1	CX	189	ASP	2.6
1	AY	96	ASN	2.6
1	CP	163	GLY	2.6
1	BU	21	VAL	2.6
1	BV	208	ALA	2.6
1	DA	143	VAL	2.6
1	DC	87	THR	2.6
1	BY	192	LYS	2.6
1	AD	24	SER	2.6
1	AZ	89	HIS	2.6
1	CM	28	PHE	2.6
1	BG	48	PRO	2.6
1	CO	20	PRO	2.6
1	CP	20	PRO	2.6
1	CT	201	SER	2.6
1	AG	18	GLN	2.6
1	BQ	207	GLN	2.6
1	DG	35	GLN	2.6
1	AA	114	ASN	2.6
1	AT	189	ASP	2.6
1	BR	163	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	BW	141	GLY	2.6
1	AH	180	LEU	2.6
1	AN	180	LEU	2.6
1	DE	156	LEU	2.6
1	AB	36	ALA	2.6
1	AX	116	ARG	2.6
1	BB	146	VAL	2.6
1	BI	160	VAL	2.6
1	BL	30	VAL	2.6
1	CB	85	VAL	2.6
1	CT	208	ALA	2.6
1	DF	44	ALA	2.6
1	DG	118	LYS	2.6
1	DI	196	ARG	2.6
1	AY	95	THR	2.6
1	BN	81	ILE	2.5
1	BN	186	ILE	2.5
1	BQ	28	PHE	2.5
1	AD	14	TYR	2.5
1	AS	89	HIS	2.5
1	AX	42	TYR	2.5
1	DB	53	TYR	2.5
1	AJ	20	PRO	2.5
1	CD	20	PRO	2.5
1	AK	24	SER	2.5
1	AS	113	SER	2.5
1	BB	105	SER	2.5
1	AC	79	GLN	2.5
1	AY	22	GLN	2.5
1	BR	207	GLN	2.5
1	BX	84	GLY	2.5
1	CR	11	GLY	2.5
1	CV	29	GLY	2.5
1	CW	115	GLY	2.5
1	BA	99	ASP	2.5
1	BB	143	VAL	2.5
1	BQ	34	ARG	2.5
1	BT	96	ASN	2.5
1	CC	189	ASP	2.5
1	CL	143	VAL	2.5
1	CV	99	ASP	2.5
1	CZ	99	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	DC	152	ASN	2.5
1	AH	36	ALA	2.5
1	BV	117	THR	2.5
1	AW	163	GLY	2.5
1	BB	113	SER	2.5
1	AO	35	GLN	2.5
1	BP	69	GLY	2.5
1	DC	201	SER	2.5
1	DF	177	SER	2.5
1	DH	113	SER	2.5
1	BQ	128	ARG	2.5
1	CF	110	ARG	2.5
1	AA	91	GLU	2.5
1	AQ	33	ASP	2.5
1	CL	152	ASN	2.5
1	CM	31	ASN	2.5
1	CX	38	ALA	2.5
1	CZ	103	ALA	2.5
1	CZ	189	ASP	2.5
1	DK	33	ASP	2.5
1	AJ	26	THR	2.5
1	AJ	27	THR	2.5
1	CC	94	THR	2.5
1	CC	140	PRO	2.5
1	DG	89	HIS	2.5
1	DH	86	PRO	2.5
1	AS	100	ARG	2.5
1	BT	110	ARG	2.5
1	DJ	141	GLY	2.5
1	AQ	23	SER	2.5
1	AS	24	SER	2.5
1	BZ	120	SER	2.5
1	DD	188	GLN	2.5
1	AH	119	VAL	2.5
1	AI	93	VAL	2.5
1	CR	198	VAL	2.5
1	AC	38	ALA	2.5
1	BB	142	ALA	2.5
1	BC	208	ALA	2.5
1	BF	36	ALA	2.5
1	BP	103	ALA	2.5
1	AA	132	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	AL	165	ASP	2.5
1	AT	74	ASN	2.5
1	BQ	127	ASP	2.5
1	BW	189	ASP	2.5
1	CI	20	PRO	2.5
1	CX	140	PRO	2.5
1	AE	150	LYS	2.5
1	BQ	134	LEU	2.5
1	CW	192	LYS	2.5
1	DL	89	HIS	2.5
1	AU	141	GLY	2.5
1	BB	84	GLY	2.5
1	BX	163	GLY	2.5
1	AN	207	GLN	2.5
1	BI	22	GLN	2.5
1	BV	79	GLN	2.5
1	CL	207	GLN	2.5
1	CN	30	VAL	2.5
1	BI	23	SER	2.5
1	CR	105	SER	2.5
1	DL	154	GLU	2.5
1	AE	68	PHE	2.5
1	AU	189	ASP	2.5
1	CA	28	PHE	2.5
1	CU	80	ASN	2.5
1	DC	96	ASN	2.5
1	AK	39	ARG	2.5
1	BB	116	ARG	2.5
1	BR	150	LYS	2.5
1	CC	110	ARG	2.5
1	CZ	150	LYS	2.5
1	BG	42	TYR	2.5
1	BK	42	TYR	2.5
1	BP	202	HIS	2.5
1	AT	29	GLY	2.5
1	BV	141	GLY	2.5
1	DA	141	GLY	2.5
1	BT	119	VAL	2.5
1	CE	85	VAL	2.5
1	CM	146	VAL	2.5
1	CR	143	VAL	2.5
1	DD	82	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	CL	18	GLN	2.5
1	BJ	44	ALA	2.4
1	AN	105	SER	2.4
1	AO	23	SER	2.4
1	AO	105	SER	2.4
1	BY	73	SER	2.4
1	AB	33	ASP	2.4
1	BI	193	ASN	2.4
1	CA	116	ARG	2.4
1	CM	193	ASN	2.4
1	CW	189	ASP	2.4
1	CY	189	ASP	2.4
1	DD	114	ASN	2.4
1	DG	116	ARG	2.4
1	BK	156	LEU	2.4
1	CF	87	THR	2.4
1	DD	172	LEU	2.4
1	AQ	20	PRO	2.4
1	CV	32	PRO	2.4
1	BH	14	TYR	2.4
1	AB	151	VAL	2.4
1	BU	112	VAL	2.4
1	BV	69	GLY	2.4
1	AH	79	GLN	2.4
1	AS	200	ALA	2.4
1	BP	144	ALA	2.4
1	BQ	208	ALA	2.4
1	BX	144	ALA	2.4
1	CL	208	ALA	2.4
1	CU	38	ALA	2.4
1	CV	36	ALA	2.4
1	CX	142	ALA	2.4
1	DG	44	ALA	2.4
1	BH	15	MET	2.4
1	AF	73	SER	2.4
1	AJ	24	SER	2.4
1	CA	73	SER	2.4
1	AA	150	LYS	2.4
1	AE	110	ARG	2.4
1	AU	110	ARG	2.4
1	BQ	13	LEU	2.4
1	AC	80	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	BD	152	ASN	2.4
1	BE	94	THR	2.4
1	BI	114	ASN	2.4
1	CD	31	ASN	2.4
1	BU	86	PRO	2.4
1	CY	20	PRO	2.4
1	AO	69	GLY	2.4
1	BS	146	VAL	2.4
1	BV	131	VAL	2.4
1	CM	42	TYR	2.4
1	DD	84	GLY	2.4
1	DH	141	GLY	2.4
1	BW	44	ALA	2.4
1	BZ	142	ALA	2.4
1	CX	199	ALA	2.4
1	DA	144	ALA	2.4
1	DI	103	ALA	2.4
1	AA	60	GLN	2.4
1	AD	207	GLN	2.4
1	AM	128	ARG	2.4
1	BL	110	ARG	2.4
1	BY	196	ARG	2.4
1	AS	120	SER	2.4
1	BC	105	SER	2.4
1	CF	105	SER	2.4
1	CG	113	SER	2.4
1	CK	24	SER	2.4
1	DH	120	SER	2.4
1	DI	201	SER	2.4
1	BJ	197	LEU	2.4
1	BL	197	LEU	2.4
1	CG	180	LEU	2.4
1	AA	96	ASN	2.4
1	AN	20	PRO	2.4
1	AT	86	PRO	2.4
1	AW	114	ASN	2.4
1	BI	20	PRO	2.4
1	BK	31	ASN	2.4
1	BY	117	THR	2.4
1	CD	117	THR	2.4
1	CM	152	ASN	2.4
1	CV	114	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	CW	194	THR	2.4
1	DH	74	ASN	2.4
1	BL	93	VAL	2.4
1	AK	159	GLY	2.4
1	AL	84	GLY	2.4
1	AN	53	TYR	2.4
1	AX	115	GLY	2.4
1	AY	64	GLY	2.4
1	CV	115	GLY	2.4
1	DC	53	TYR	2.4
1	BD	144	ALA	2.4
1	BM	44	ALA	2.4
1	CW	36	ALA	2.4
1	DA	103	ALA	2.4
1	DE	44	ALA	2.4
1	CC	18	GLN	2.4
1	AI	116	ARG	2.4
1	AJ	110	ARG	2.4
1	AM	116	ARG	2.4
1	AT	110	ARG	2.4
1	CF	100	ARG	2.4
1	BR	156	LEU	2.4
1	CM	73	SER	2.4
1	AE	153	VAL	2.4
1	AN	21	VAL	2.4
1	AY	82	VAL	2.4
1	BK	20	PRO	2.4
1	CV	48	PRO	2.4
1	DD	106	THR	2.4
1	AK	31	ASN	2.4
1	AK	96	ASN	2.4
1	BC	84	GLY	2.4
1	BS	74	ASN	2.4
1	BT	69	GLY	2.4
1	CG	115	GLY	2.4
1	CQ	147	GLY	2.4
1	CW	84	GLY	2.4
1	DJ	64	GLY	2.4
1	DL	74	ASN	2.4
1	AI	44	ALA	2.4
1	AO	123	ILE	2.4
1	AU	44	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	CD	44	ALA	2.4
1	CI	208	ALA	2.4
1	CN	142	ALA	2.4
1	BZ	150	LYS	2.4
1	BY	28	PHE	2.4
1	AF	82	VAL	2.4
1	CK	82	VAL	2.4
1	AP	52	THR	2.3
1	BB	90	GLY	2.3
1	BU	141	GLY	2.3
1	BV	90	GLY	2.3
1	CF	159	GLY	2.3
1	DF	190	GLY	2.3
1	AB	150	LYS	2.3
1	AR	114	ASN	2.3
1	AS	142	ALA	2.3
1	AV	196	ARG	2.3
1	AZ	144	ALA	2.3
1	CC	81	ILE	2.3
1	CE	152	ASN	2.3
1	DA	80	ASN	2.3
1	BF	116	ARG	2.3
1	BP	189	ASP	2.3
1	CK	116	ARG	2.3
1	DE	110	ARG	2.3
1	CQ	180	LEU	2.3
1	CZ	35	GLN	2.3
1	AU	50	GLU	2.3
1	DJ	153	VAL	2.3
1	AO	73	SER	2.3
1	AZ	124	PRO	2.3
1	BN	24	SER	2.3
1	CP	113	SER	2.3
1	DE	20	PRO	2.3
1	DJ	24	SER	2.3
1	DL	73	SER	2.3
1	AE	194	THR	2.3
1	AW	110	ARG	2.3
1	BG	116	ARG	2.3
1	BN	157	GLY	2.3
1	BO	163	GLY	2.3
1	BY	110	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	CC	90	GLY	2.3
1	CO	94	THR	2.3
1	CU	118	LYS	2.3
1	AJ	123	ILE	2.3
1	DF	95	THR	2.3
1	AT	36	ALA	2.3
1	CY	144	ALA	2.3
1	DJ	123	ILE	2.3
1	DK	144	ALA	2.3
1	AR	42	TYR	2.3
1	CJ	31	ASN	2.3
1	DA	15	MET	2.3
1	DA	42	TYR	2.3
1	BO	156	LEU	2.3
1	BB	188	GLN	2.3
1	BD	188	GLN	2.3
1	DK	79	GLN	2.3
1	BG	50	GLU	2.3
1	AE	198	VAL	2.3
1	BA	124	PRO	2.3
1	BN	196	ARG	2.3
1	CN	32	PRO	2.3
1	CS	32	PRO	2.3
1	AS	11	GLY	2.3
1	AT	141	GLY	2.3
1	BA	73	SER	2.3
1	BH	104	SER	2.3
1	BI	113	SER	2.3
1	BM	23	SER	2.3
1	BN	69	GLY	2.3
1	DH	158	GLY	2.3
1	BQ	27	THR	2.3
1	CO	142	ALA	2.3
1	DF	36	ALA	2.3
1	CM	205	MET	2.3
1	AT	28	PHE	2.3
1	AX	79	GLN	2.3
1	BN	22	GLN	2.3
1	BW	12	GLN	2.3
1	CV	207	GLN	2.3
1	DE	188	GLN	2.3
1	CF	112	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	CQ	192	LYS	2.3
1	CT	30	VAL	2.3
1	DG	151	VAL	2.3
1	CB	110	ARG	2.3
1	BI	124	PRO	2.3
1	CS	20	PRO	2.3
1	AI	84	GLY	2.3
1	CG	158	GLY	2.3
1	CQ	141	GLY	2.3
1	AF	136	ALA	2.3
1	AW	36	ALA	2.3
1	AZ	72	ALA	2.3
1	BD	44	ALA	2.3
1	CJ	208	ALA	2.3
1	AB	194	THR	2.3
1	AO	113	SER	2.3
1	BL	73	SER	2.3
1	BN	95	THR	2.3
1	BZ	201	SER	2.3
1	CF	106	THR	2.3
1	AH	56	LEU	2.3
1	AZ	42	TYR	2.3
1	BL	42	TYR	2.3
1	BP	42	TYR	2.3
1	BY	149	PHE	2.3
1	AH	96	ASN	2.3
1	AH	129	ASN	2.3
1	BM	74	ASN	2.3
1	BU	74	ASN	2.3
1	DF	96	ASN	2.3
1	AC	122	ASP	2.3
1	AG	12	GLN	2.3
1	AH	33	ASP	2.3
1	BP	122	ASP	2.3
1	BQ	35	GLN	2.3
1	BZ	12	GLN	2.3
1	CI	207	GLN	2.3
1	CN	79	GLN	2.3
1	CU	100	ARG	2.3
1	DF	82	VAL	2.3
1	AB	20	PRO	2.3
1	AD	20	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	BX	121	ILE	2.3
1	CM	20	PRO	2.3
1	AF	208	ALA	2.3
1	AJ	171	ALA	2.3
1	BH	69	GLY	2.3
1	AY	15	MET	2.3
1	BX	44	ALA	2.3
1	CG	44	ALA	2.3
1	CM	103	ALA	2.3
1	CS	44	ALA	2.3
1	DJ	44	ALA	2.3
1	BN	27	THR	2.3
1	CC	162	THR	2.3
1	CD	95	THR	2.3
1	CK	117	THR	2.3
1	CQ	87	THR	2.3
1	AM	125	TYR	2.3
1	AX	53	TYR	2.3
1	BA	42	TYR	2.3
1	BD	28	PHE	2.3
1	CA	113	SER	2.3
1	CZ	73	SER	2.3
1	DF	104	SER	2.3
1	BU	42	TYR	2.3
1	AU	114	ASN	2.3
1	AD	12	GLN	2.3
1	AQ	22	GLN	2.3
1	AY	135	LYS	2.3
1	BX	96	ASN	2.3
1	BB	25	ARG	2.3
1	BF	110	ARG	2.3
1	BK	110	ARG	2.3
1	DC	110	ARG	2.3
1	AZ	112	VAL	2.3
1	BE	204	VAL	2.3
1	BY	99	ASP	2.3
1	AA	44	ALA	2.2
1	BC	36	ALA	2.2
1	BC	203	GLY	2.2
1	BG	103	ALA	2.2
1	BL	62	ALA	2.2
1	BS	208	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	BT	63	ALA	2.2
1	BV	62	ALA	2.2
1	BY	195	ALA	2.2
1	CD	187	ALA	2.2
1	CJ	187	ALA	2.2
1	CO	15	MET	2.2
1	CQ	208	ALA	2.2
1	CU	141	GLY	2.2
1	CY	199	ALA	2.2
1	AN	156	LEU	2.2
1	BJ	134	LEU	2.2
1	CG	156	LEU	2.2
1	AE	95	THR	2.2
1	AG	95	THR	2.2
1	BX	117	THR	2.2
1	CS	194	THR	2.2
1	AJ	53	TYR	2.2
1	BY	23	SER	2.2
1	CH	192	LYS	2.2
1	AS	110	ARG	2.2
1	BN	100	ARG	2.2
1	BP	110	ARG	2.2
1	BW	110	ARG	2.2
1	DD	110	ARG	2.2
1	AB	79	GLN	2.2
1	AI	85	VAL	2.2
1	AS	96	ASN	2.2
1	AV	143	VAL	2.2
1	BB	37	ASN	2.2
1	BG	74	ASN	2.2
1	CH	114	ASN	2.2
1	DA	82	VAL	2.2
1	AQ	189	ASP	2.2
1	CD	127	ASP	2.2
1	CD	189	ASP	2.2
1	AC	32	PRO	2.2
1	AU	197	LEU	2.2
1	AW	208	ALA	2.2
1	BP	168	ALA	2.2
1	CH	197	LEU	2.2
1	CL	44	ALA	2.2
1	CR	141	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	DD	44	ALA	2.2
1	AJ	149	PHE	2.2
1	AQ	28	PHE	2.2
1	BU	28	PHE	2.2
1	BW	149	PHE	2.2
1	AE	164	THR	2.2
1	AL	117	THR	2.2
1	BE	106	THR	2.2
1	BL	109	THR	2.2
1	CX	106	THR	2.2
1	CZ	87	THR	2.2
1	AZ	53	TYR	2.2
1	BE	196	ARG	2.2
1	BO	110	ARG	2.2
1	CE	196	ARG	2.2
1	BF	73	SER	2.2
1	AH	155	VAL	2.2
1	BB	153	VAL	2.2
1	AB	207	GLN	2.2
1	AD	188	GLN	2.2
1	CJ	79	GLN	2.2
1	BH	74	ASN	2.2
1	BT	80	ASN	2.2
1	CA	123	ILE	2.2
1	CH	186	ILE	2.2
1	DJ	186	ILE	2.2
1	AA	144	ALA	2.2
1	AG	141	GLY	2.2
1	AS	208	ALA	2.2
1	AT	20	PRO	2.2
1	AV	15	MET	2.2
1	AZ	111	ASP	2.2
1	BL	33	ASP	2.2
1	AX	208	ALA	2.2
1	BA	157	GLY	2.2
1	BC	141	GLY	2.2
1	BF	166	ALA	2.2
1	BL	86	PRO	2.2
1	BR	180	LEU	2.2
1	BX	33	ASP	2.2
1	CP	189	ASP	2.2
1	BS	64	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	CK	208	ALA	2.2
1	CW	181	MET	2.2
1	DF	84	GLY	2.2
1	CF	88	LYS	2.2
1	BN	28	PHE	2.2
1	BX	185	ARG	2.2
1	DL	25	ARG	2.2
1	AL	107	THR	2.2
1	BT	94	THR	2.2
1	BW	27	THR	2.2
1	BZ	107	THR	2.2
1	CN	26	THR	2.2
1	CR	94	THR	2.2
1	CJ	42	TYR	2.2
1	DC	42	TYR	2.2
1	BQ	146	VAL	2.2
1	BZ	146	VAL	2.2
1	CX	204	VAL	2.2
1	DB	93	VAL	2.2
1	AJ	23	SER	2.2
1	CS	120	SER	2.2
1	AB	60	GLN	2.2
1	AV	35	GLN	2.2
1	BC	188	GLN	2.2
1	DD	18	GLN	2.2
1	DH	22	GLN	2.2
1	AO	37	ASN	2.2
1	AX	114	ASN	2.2
1	BL	80	ASN	2.2
1	BW	152	ASN	2.2
1	CB	31	ASN	2.2
1	DA	74	ASN	2.2
1	AA	163	GLY	2.2
1	AN	142	ALA	2.2
1	AY	103	ALA	2.2
1	BX	158	GLY	2.2
1	CH	64	GLY	2.2
1	CK	142	ALA	2.2
1	CV	124	PRO	2.2
1	DC	46	ALA	2.2
1	AR	33	ASP	2.2
1	BC	118	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	AP	110	ARG	2.2
1	AR	25	ARG	2.2
1	AY	100	ARG	2.2
1	BS	25	ARG	2.2
1	CV	149	PHE	2.2
1	AK	89	HIS	2.2
1	AO	26	THR	2.2
1	AX	52	THR	2.2
1	BG	117	THR	2.2
1	CZ	109	THR	2.2
1	AH	92	TYR	2.2
1	AX	155	VAL	2.2
1	BA	112	VAL	2.2
1	AA	81	ILE	2.2
1	AC	23	SER	2.2
1	AI	201	SER	2.2
1	BE	137	SER	2.2
1	BT	81	ILE	2.2
1	CC	22	GLN	2.2
1	DC	24	SER	2.2
1	CL	13	LEU	2.2
1	AA	147	GLY	2.2
1	AB	118	LYS	2.2
1	AJ	96	ASN	2.2
1	AC	163	GLY	2.2
1	AP	150	LYS	2.2
1	BJ	193	ASN	2.2
1	BX	74	ASN	2.2
1	CA	36	ALA	2.2
1	CD	152	ASN	2.2
1	BY	124	PRO	2.2
1	BZ	163	GLY	2.2
1	CA	141	GLY	2.2
1	CC	20	PRO	2.2
1	CI	150	LYS	2.2
1	DE	72	ALA	2.2
1	DG	144	ALA	2.2
1	AW	29	GLY	2.2
1	DL	84	GLY	2.2
1	CD	110	ARG	2.2
1	CY	25	ARG	2.2
1	AM	127	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	CT	149	PHE	2.2
1	BZ	89	HIS	2.2
1	AC	85	VAL	2.1
1	AM	117	THR	2.1
1	AV	95	THR	2.1
1	BH	21	VAL	2.1
1	BL	87	THR	2.1
1	CR	27	THR	2.1
1	DE	53	TYR	2.1
1	CU	81	ILE	2.1
1	AG	79	GLN	2.1
1	AN	22	GLN	2.1
1	AV	13	LEU	2.1
1	AZ	79	GLN	2.1
1	BO	79	GLN	2.1
1	BZ	76	LEU	2.1
1	CI	12	GLN	2.1
1	CU	12	GLN	2.1
1	CY	188	GLN	2.1
1	BV	166	ALA	2.1
1	CL	105	SER	2.1
1	CU	150	LYS	2.1
1	AP	62	ALA	2.1
1	DD	24	SER	2.1
1	DD	208	ALA	2.1
1	DI	113	SER	2.1
1	BP	25	ARG	2.1
1	BT	116	ARG	2.1
1	CA	110	ARG	2.1
1	CC	80	ASN	2.1
1	CH	145	PRO	2.1
1	CH	203	GLY	2.1
1	CM	90	GLY	2.1
1	BK	96	ASN	2.1
1	CM	80	ASN	2.1
1	CM	129	ASN	2.1
1	CU	96	ASN	2.1
1	DC	193	ASN	2.1
1	DD	80	ASN	2.1
1	DF	129	ASN	2.1
1	BL	28	PHE	2.1
1	CG	33	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	DB	33	ASP	2.1
1	AS	95	THR	2.1
1	AW	95	THR	2.1
1	AY	109	THR	2.1
1	BR	194	THR	2.1
1	CC	107	THR	2.1
1	AS	81	ILE	2.1
1	AT	88	LYS	2.1
1	BO	150	LYS	2.1
1	BP	88	LYS	2.1
1	AV	79	GLN	2.1
1	AJ	199	ALA	2.1
1	BN	103	ALA	2.1
1	CC	44	ALA	2.1
1	CE	110	ARG	2.1
1	CH	36	ALA	2.1
1	CX	100	ARG	2.1
1	DC	138	ALA	2.1
1	AG	113	SER	2.1
1	AL	24	SER	2.1
1	AV	64	GLY	2.1
1	BP	177	SER	2.1
1	BR	24	SER	2.1
1	BS	120	SER	2.1
1	BT	113	SER	2.1
1	CA	201	SER	2.1
1	CB	105	SER	2.1
1	CE	158	GLY	2.1
1	DA	69	GLY	2.1
1	DG	84	GLY	2.1
1	AD	31	ASN	2.1
1	AO	80	ASN	2.1
1	BO	28	PHE	2.1
1	CI	80	ASN	2.1
1	DG	37	ASN	2.1
1	AJ	21	VAL	2.1
1	AW	151	VAL	2.1
1	AY	85	VAL	2.1
1	BL	127	ASP	2.1
1	CB	143	VAL	2.1
1	CC	153	VAL	2.1
1	CE	75	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	CF	143	VAL	2.1
1	CH	99	ASP	2.1
1	CU	189	ASP	2.1
1	CY	41	VAL	2.1
1	DK	189	ASP	2.1
1	CU	66	HIS	2.1
1	BD	26	THR	2.1
1	BE	87	THR	2.1
1	CG	88	LYS	2.1
1	DJ	117	THR	2.1
1	AE	185	ARG	2.1
1	AP	181	MET	2.1
1	AZ	25	ARG	2.1
1	BB	15	MET	2.1
1	BN	110	ARG	2.1
1	BY	116	ARG	2.1
1	CQ	110	ARG	2.1
1	DB	110	ARG	2.1
1	DH	116	ARG	2.1
1	AA	18	GLN	2.1
1	AM	136	ALA	2.1
1	BZ	18	GLN	2.1
1	CA	200	ALA	2.1
1	CG	207	GLN	2.1
1	CP	79	GLN	2.1
1	DB	22	GLN	2.1
1	DF	142	ALA	2.1
1	DJ	38	ALA	2.1
1	AM	29	GLY	2.1
1	CB	64	GLY	2.1
1	DD	141	GLY	2.1
1	AL	61	PHE	2.1
1	AN	120	SER	2.1
1	BP	24	SER	2.1
1	CF	23	SER	2.1
1	AJ	114	ASN	2.1
1	BD	74	ASN	2.1
1	BO	96	ASN	2.1
1	BR	80	ASN	2.1
1	CN	152	ASN	2.1
1	CB	112	VAL	2.1
1	CN	143	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	CR	146	VAL	2.1
1	BD	89	HIS	2.1
1	BE	66	HIS	2.1
1	BR	189	ASP	2.1
1	CS	161	LEU	2.1
1	AJ	117	THR	2.1
1	AK	110	ARG	2.1
1	AT	194	THR	2.1
1	AX	87	THR	2.1
1	BZ	116	ARG	2.1
1	CH	52	THR	2.1
1	DA	94	THR	2.1
1	DF	42	TYR	2.1
1	DH	162	THR	2.1
1	BT	15	MET	2.1
1	AT	44	ALA	2.1
1	AT	62	ALA	2.1
1	AY	208	ALA	2.1
1	BT	136	ALA	2.1
1	AB	169	GLN	2.1
1	AI	35	GLN	2.1
1	AJ	22	GLN	2.1
1	AS	12	GLN	2.1
1	AB	163	GLY	2.1
1	AO	203	GLY	2.1
1	AH	91	GLU	2.1
1	AL	91	GLU	2.1
1	AX	77	PRO	2.1
1	BH	149	PHE	2.1
1	CU	154	GLU	2.1
1	CX	78	PRO	2.1
1	AP	24	SER	2.1
1	AR	23	SER	2.1
1	BZ	137	SER	2.1
1	AK	146	VAL	2.1
1	AX	82	VAL	2.1
1	BJ	30	VAL	2.1
1	BV	93	VAL	2.1
1	CI	151	VAL	2.1
1	DA	85	VAL	2.1
1	AA	118	LYS	2.1
1	AQ	114	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	AV	96	ASN	2.1
1	BN	37	ASN	2.1
1	CL	96	ASN	2.1
1	CR	150	LYS	2.1
1	AJ	25	ARG	2.1
1	BC	110	ARG	2.1
1	CY	110	ARG	2.1
1	DE	176	LEU	2.1
1	AP	189	ASP	2.1
1	DL	189	ASP	2.1
1	AC	42	TYR	2.1
1	BE	162	THR	2.1
1	CD	53	TYR	2.1
1	CF	95	THR	2.1
1	CU	87	THR	2.1
1	CV	162	THR	2.1
1	DA	27	THR	2.1
1	AD	187	ALA	2.1
1	AJ	187	ALA	2.1
1	BA	208	ALA	2.1
1	CF	136	ALA	2.1
1	CS	208	ALA	2.1
1	DB	144	ALA	2.1
1	DH	36	ALA	2.1
1	AC	158	GLY	2.1
1	BK	207	GLN	2.1
1	BO	22	GLN	2.1
1	BV	84	GLY	2.1
1	CJ	157	GLY	2.1
1	CT	84	GLY	2.1
1	DA	18	GLN	2.1
1	DK	163	GLY	2.1
1	AA	50	GLU	2.1
1	AC	206	PRO	2.1
1	CD	28	PHE	2.1
1	CR	149	PHE	2.1
1	CS	124	PRO	2.1
1	CC	143	VAL	2.0
1	DF	30	VAL	2.0
1	AC	105	SER	2.0
1	AV	24	SER	2.0
1	BQ	120	SER	2.0

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Mol	Chain	Res	Type	RSRZ
1	CV	113	SER	2.0
1	AB	110	ARG	2.0
1	AJ	31	ASN	2.0
1	AO	121	ILE	2.0
1	AP	152	ASN	2.0
1	BG	134	LEU	2.0
1	BP	74	ASN	2.0
1	BW	116	ARG	2.0
1	BZ	110	ARG	2.0
1	CQ	96	ASN	2.0
1	CX	96	ASN	2.0
1	DC	185	ARG	2.0
1	DL	193	ASN	2.0
1	CB	202	HIS	2.0
1	CC	15	MET	2.0
1	AD	42	TYR	2.0
1	AM	87	THR	2.0
1	AO	184	ALA	2.0
1	AY	162	THR	2.0
1	AZ	103	ALA	2.0
1	BM	189	ASP	2.0
1	BQ	14	TYR	2.0
1	CA	72	ALA	2.0
1	CJ	95	THR	2.0
1	CZ	127	ASP	2.0
1	DG	27	THR	2.0
1	AJ	207	GLN	2.0
1	AK	35	GLN	2.0
1	AM	141	GLY	2.0
1	AP	18	GLN	2.0
1	AE	48	PRO	2.0
1	AN	86	PRO	2.0
1	AP	68	PHE	2.0
1	AS	79	GLN	2.0
1	AV	17	GLN	2.0
1	AV	141	GLY	2.0
1	AY	18	GLN	2.0
1	AY	84	GLY	2.0
1	CD	22	GLN	2.0
1	CH	35	GLN	2.0
1	CR	79	GLN	2.0
1	CX	141	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	CD	48	PRO	2.0
1	CG	20	PRO	2.0
1	CN	124	PRO	2.0
1	CA	192	LYS	2.0
1	CE	150	LYS	2.0
1	AZ	82	VAL	2.0
1	BG	82	VAL	2.0
1	CH	30	VAL	2.0
1	CQ	30	VAL	2.0
1	AA	156	LEU	2.0
1	AH	110	ARG	2.0
1	AM	25	ARG	2.0
1	AZ	196	ARG	2.0
1	BB	13	LEU	2.0
1	BG	101	LEU	2.0
1	BX	175	LEU	2.0
1	CU	34	ARG	2.0
1	AA	105	SER	2.0
1	AJ	120	SER	2.0
1	AK	120	SER	2.0
1	BE	81	ILE	2.0
1	BO	113	SER	2.0
1	BU	23	SER	2.0
1	CL	23	SER	2.0
1	CS	121	ILE	2.0
1	DJ	105	SER	2.0
1	AR	80	ASN	2.0
1	AT	205	MET	2.0
1	BL	129	ASN	2.0
1	BL	193	ASN	2.0
1	CL	80	ASN	2.0
1	CM	74	ASN	2.0
1	DI	89	HIS	2.0
1	AO	107	THR	2.0
1	BY	44	ALA	2.0
1	CI	136	ALA	2.0
1	BU	53	TYR	2.0
1	AG	189	ASP	2.0
1	BK	127	ASP	2.0
1	CU	99	ASP	2.0
1	AM	84	GLY	2.0
1	BY	64	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	CK	69	GLY	2.0
1	CM	157	GLY	2.0
1	DI	29	GLY	2.0
1	CA	32	PRO	2.0
1	CA	150	LYS	2.0
1	DJ	35	GLN	2.0
1	DK	20	PRO	2.0
1	AG	151	VAL	2.0
1	AH	116	ARG	2.0
1	AJ	85	VAL	2.0
1	BJ	50	GLU	2.0
1	BZ	50	GLU	2.0
1	BC	34	ARG	2.0
1	BV	25	ARG	2.0
1	CB	196	ARG	2.0
1	CB	156	LEU	2.0
1	DF	176	LEU	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.