



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:21 PM UTC

PDB ID : 6YFF / pdb_00006yff
Title : Virus-like particle of Beihai levi-like virus 21
Authors : Rumnieks, J.; Kalnins, G.; Sisovs, M.; Lieknina, I.; Tars, K.
Deposited on : 2020-03-26
Resolution : 3.09 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

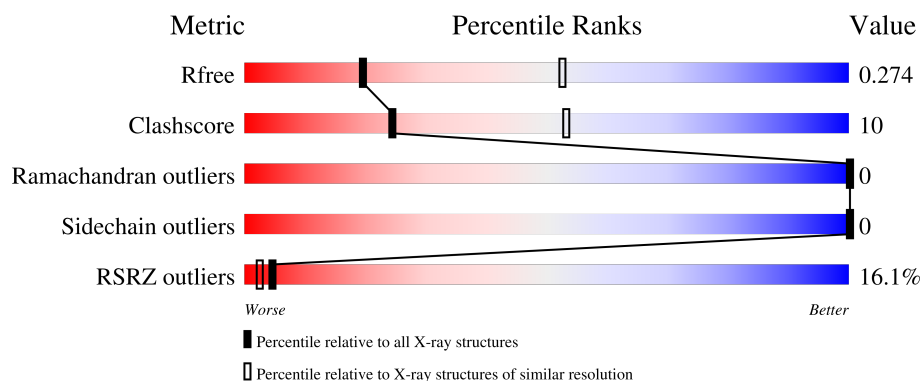
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.09 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	2010 (3.10-3.06)
Clashscore	190562	2102 (3.10-3.06)
Ramachandran outliers	187476	1982 (3.10-3.06)
Sidechain outliers	187428	1981 (3.10-3.06)
RSRZ outliers	180081	2010 (3.10-3.06)

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	126	8% 79% 21%
1	AB	126	3% 87% 13%
1	AC	126	11% 82% 18%
1	AD	126	6% 78% 22%
1	AE	126	6% 85% 15%

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Mol	Chain	Length	Quality of chain
1	AF	126	
1	AG	126	
1	AH	126	
1	AI	126	
1	AJ	126	
1	AK	126	
1	AL	126	
1	AM	126	
1	AN	126	
1	AO	126	
1	AP	126	
1	AQ	126	
1	AR	126	
1	AS	126	
1	AT	126	
1	AU	126	
1	AV	126	
1	AW	126	
1	AX	126	
1	AY	126	
1	AZ	126	
1	BA	126	
1	BB	126	
1	BC	126	
1	BD	126	

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Mol	Chain	Length	Quality of chain
1	BE	126	
1	BF	126	
1	BG	126	
1	BH	126	
1	BI	126	
1	BJ	126	
1	BK	126	
1	BL	126	
1	BM	126	
1	BN	126	
1	BO	126	
1	BP	126	
1	BQ	126	
1	BR	126	
1	BS	126	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 43650 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	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AB	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AC	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AD	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AE	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AF	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AG	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AH	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AI	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AJ	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AK	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AL	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AM	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AN	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AO	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	AP	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AQ	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	AR	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	AS	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	AT	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	AU	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	AV	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	AW	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	AX	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	AY	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	AZ	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	BA	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	BB	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	BC	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	BD	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	BE	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	BF	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	BG	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	BH	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	BI	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	BJ	126	Total 970	C 605	N 176	O 187	S 2	0	0	0
1	BK	126	Total 970	C 605	N 176	O 187	S 2	0	0	0

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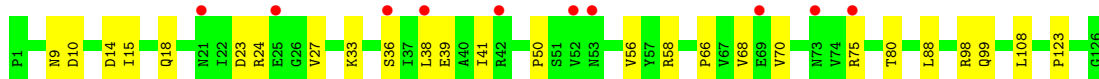
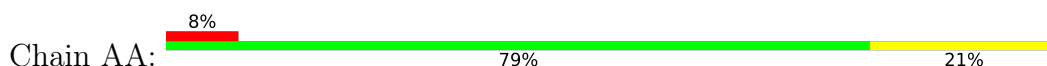
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BL	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	BM	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	BN	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	BO	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	BP	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	BQ	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	BR	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			
1	BS	126	Total	C	N	O	S	0	0	0
			970	605	176	187	2			

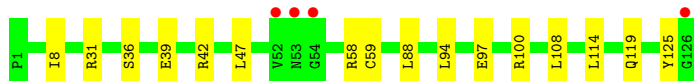
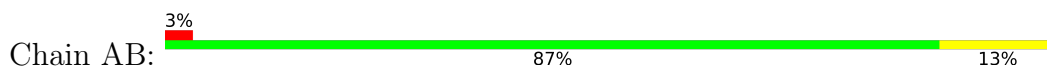
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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.

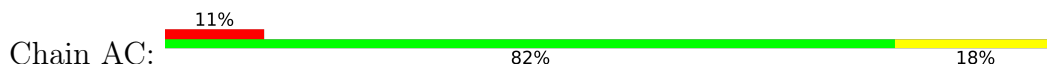
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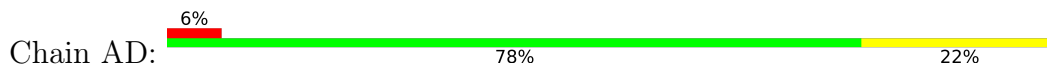
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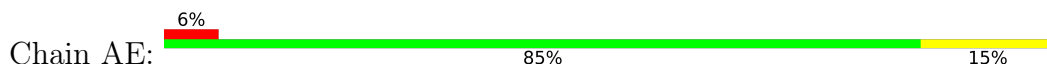
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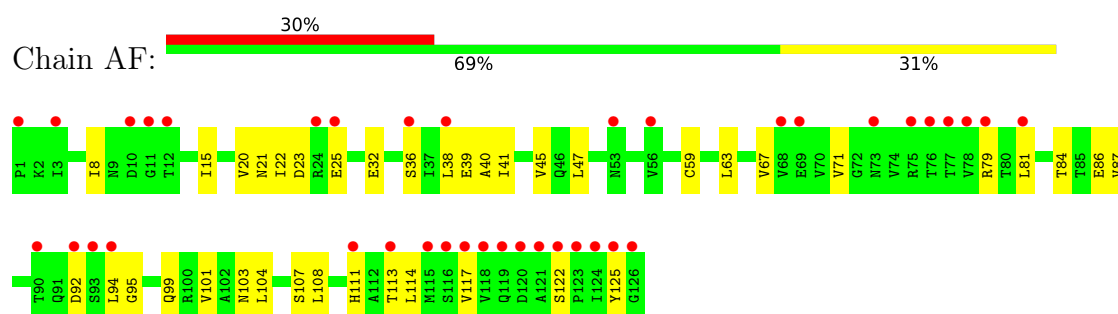
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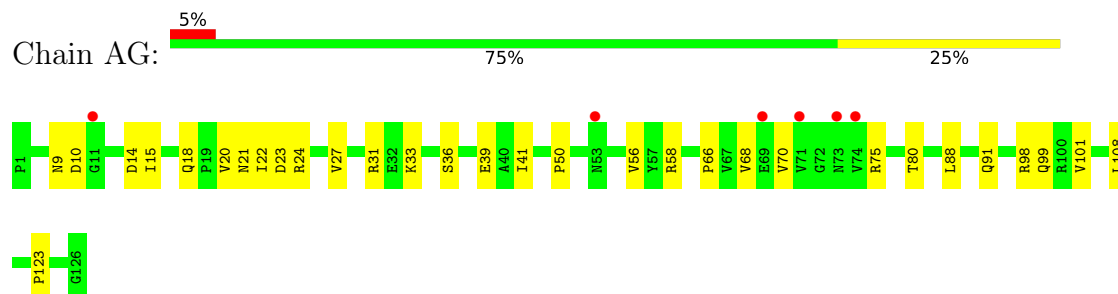
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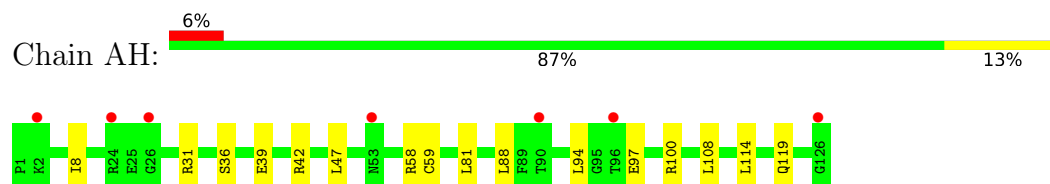
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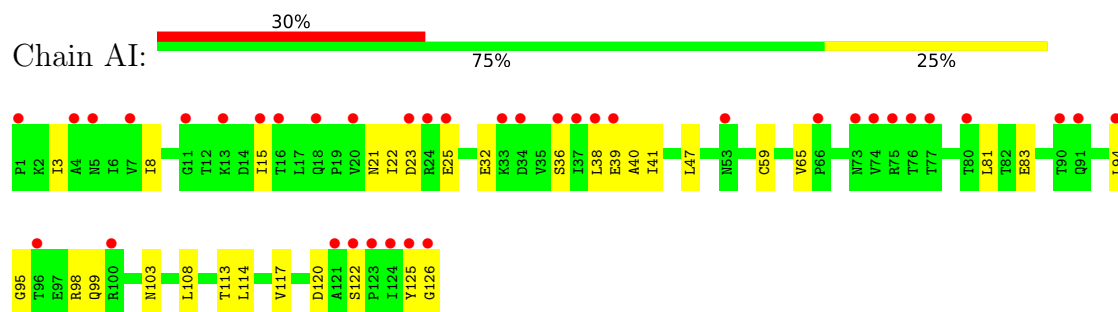
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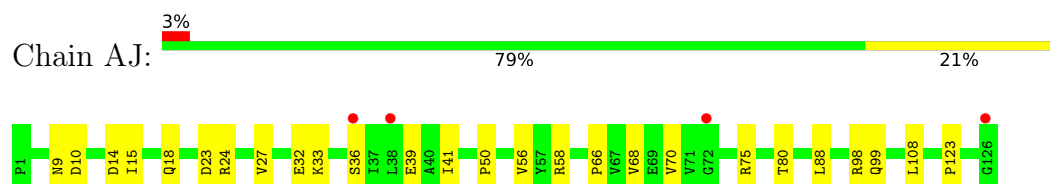
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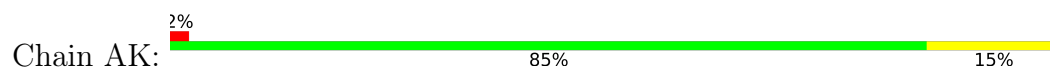
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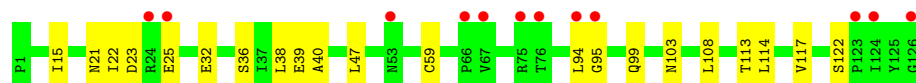
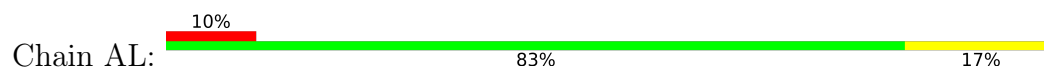


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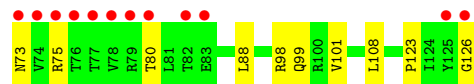
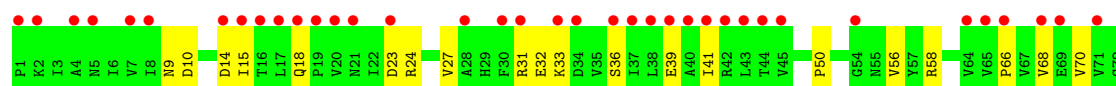
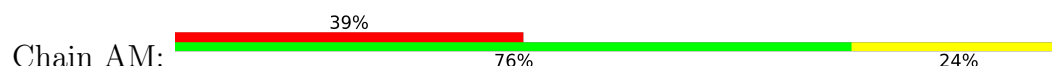




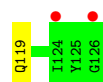
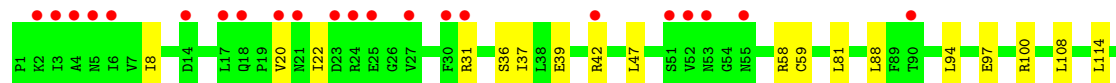
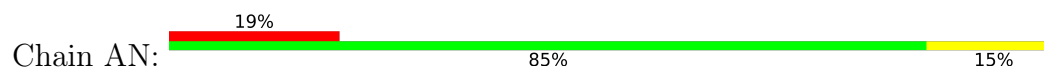
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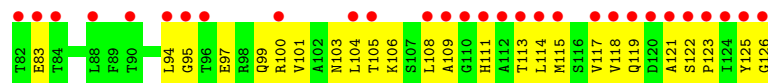
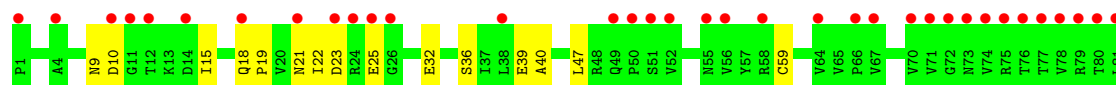
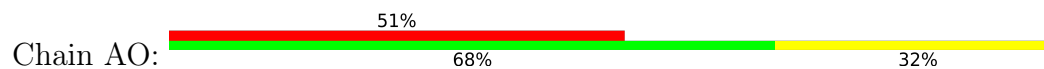
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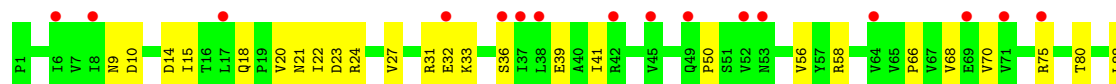
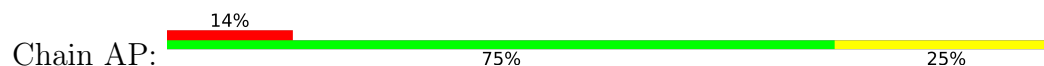
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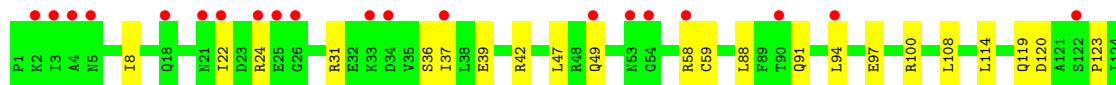
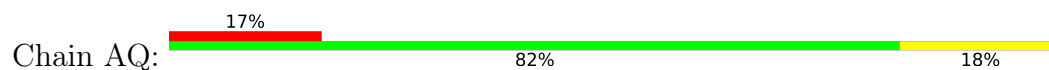


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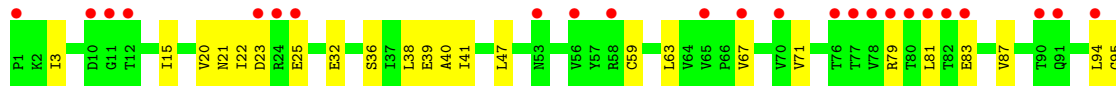
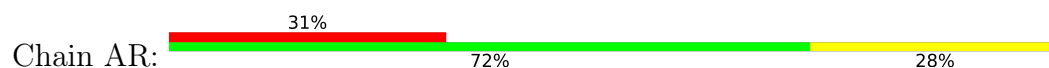




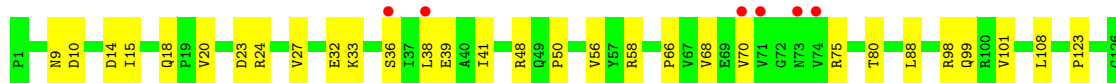
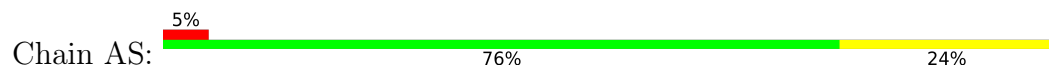
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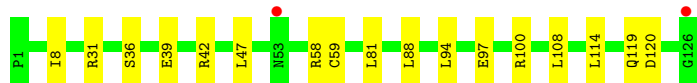
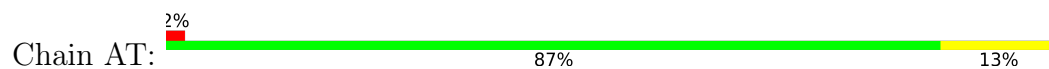
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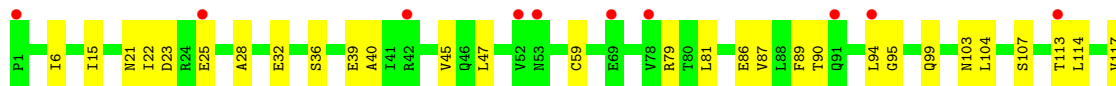
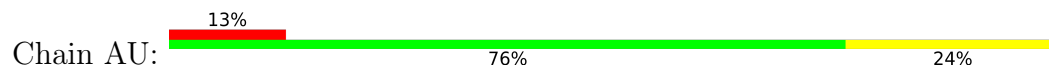
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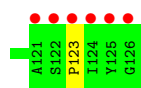


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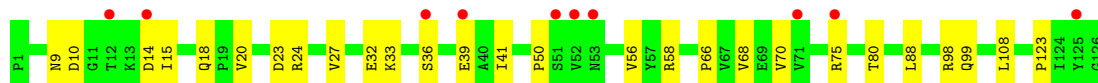
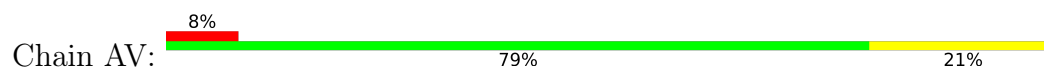


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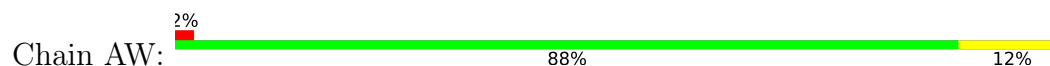




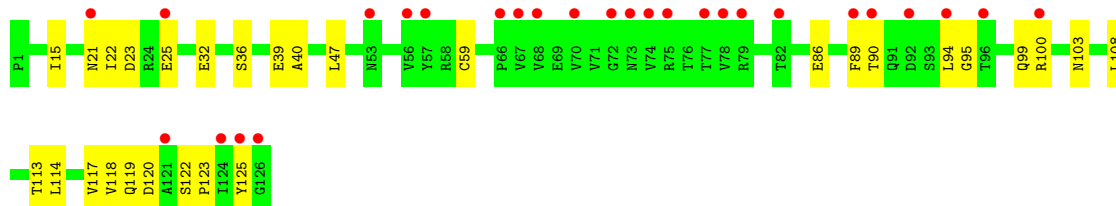
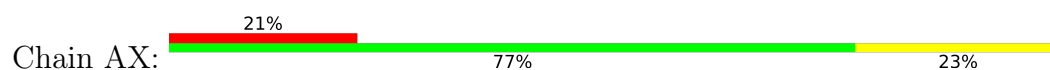
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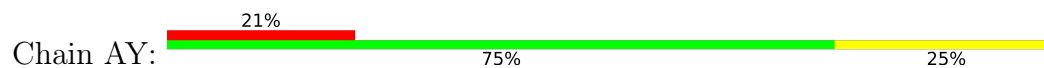
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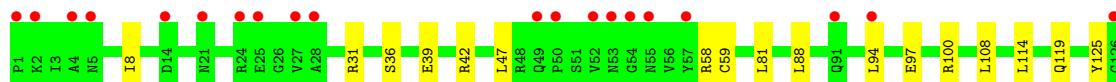
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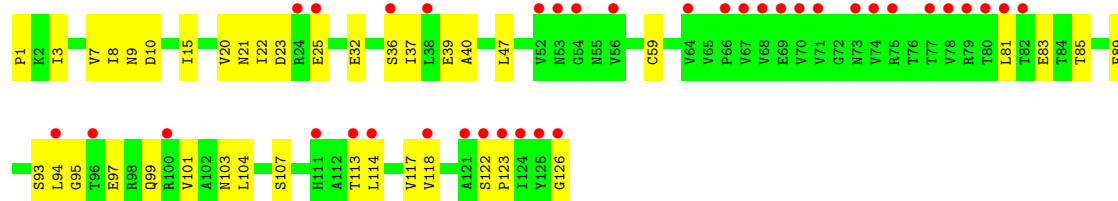
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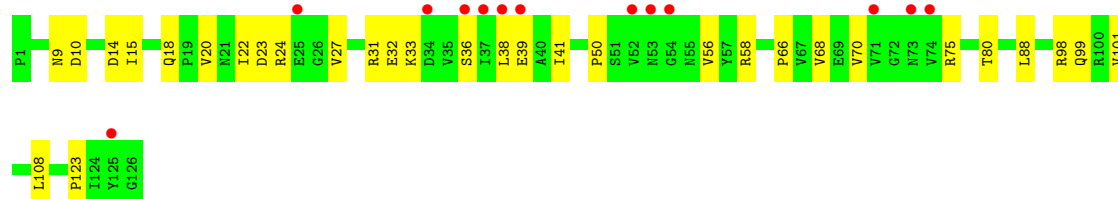
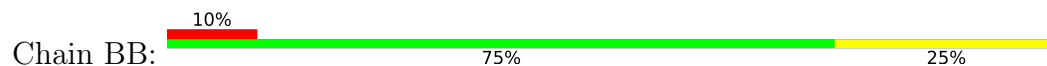
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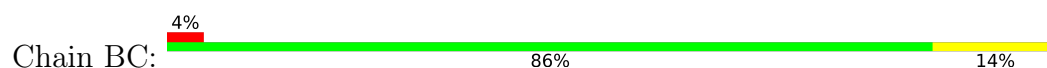
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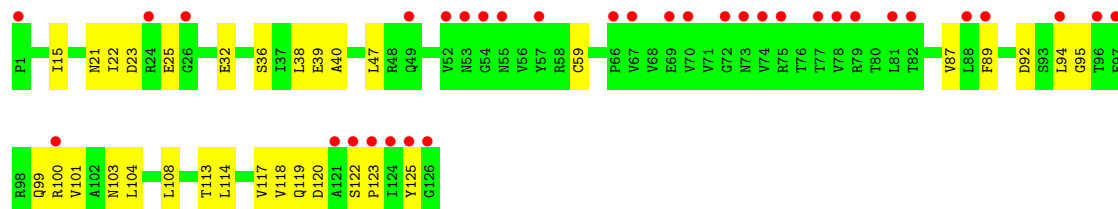
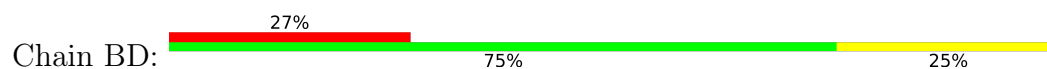
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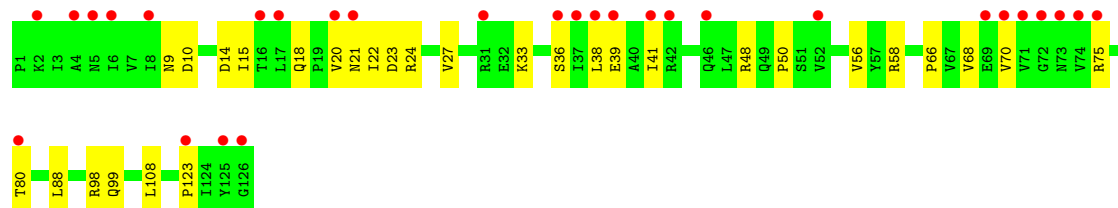
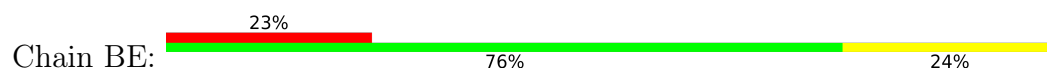
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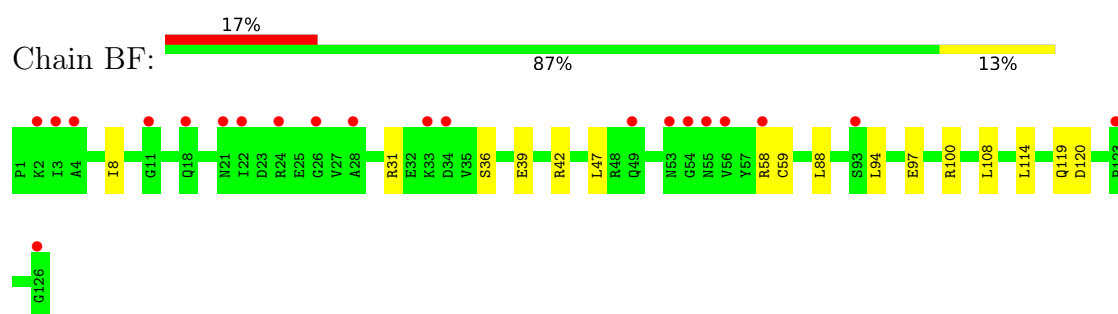
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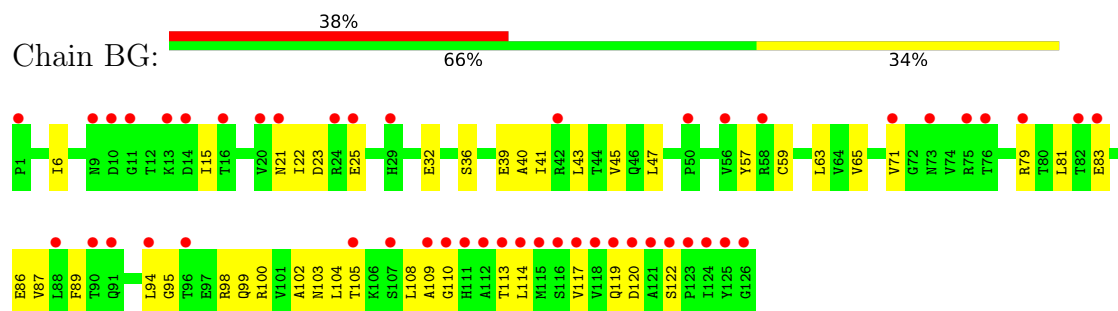
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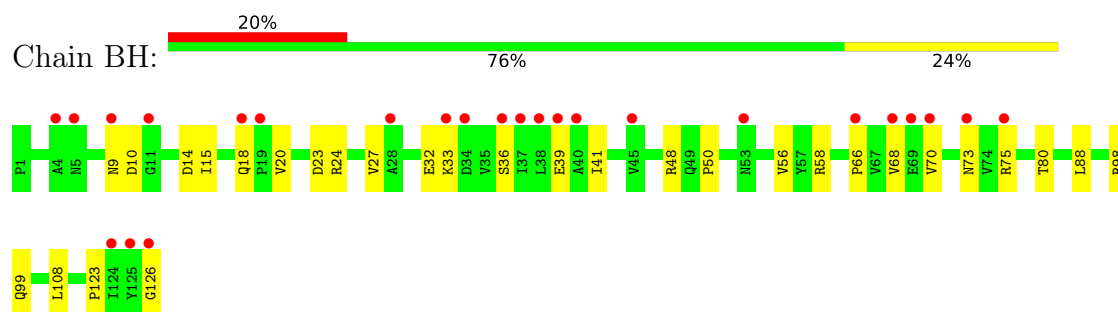
- Molecule 1: coat protein



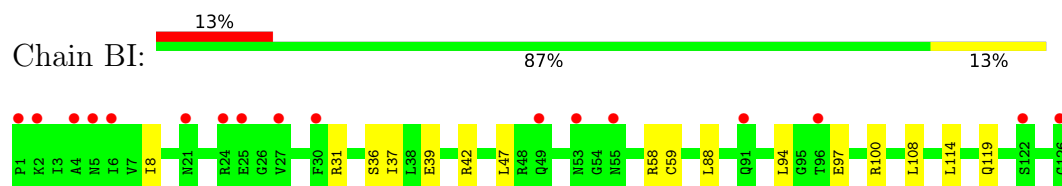
- Molecule 1: coat protein



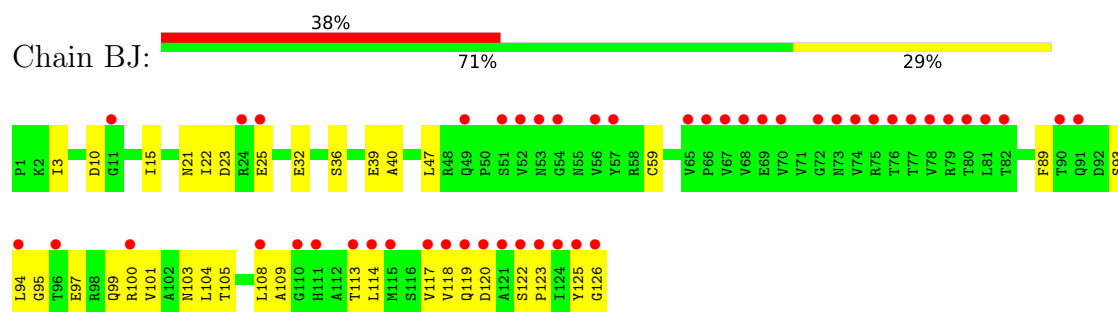
- Molecule 1: coat protein



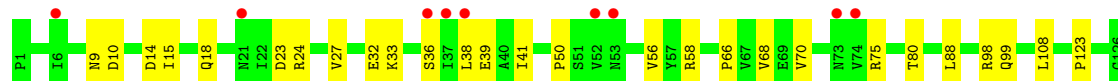
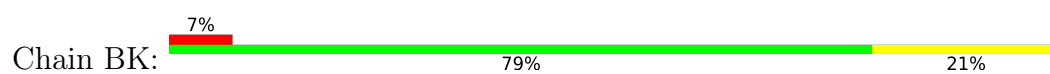
- Molecule 1: coat protein



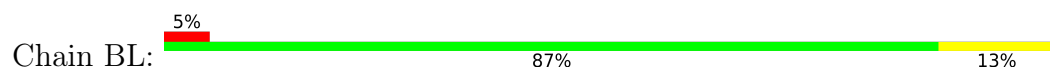
- Molecule 1: coat protein



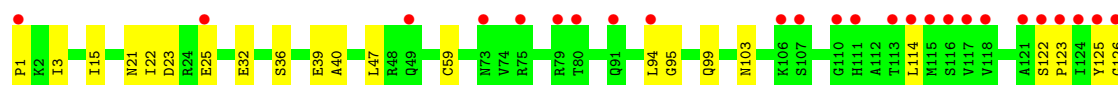
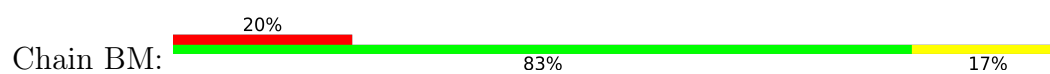
- Molecule 1: coat protein



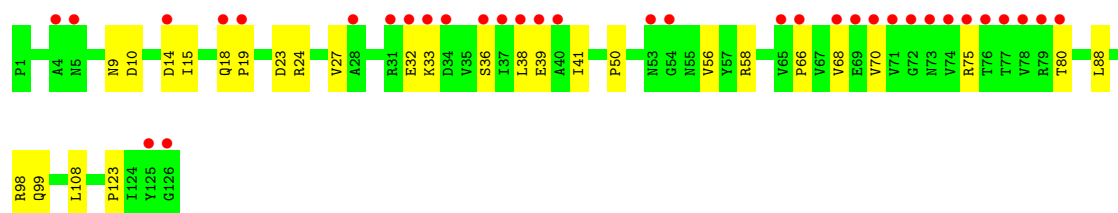
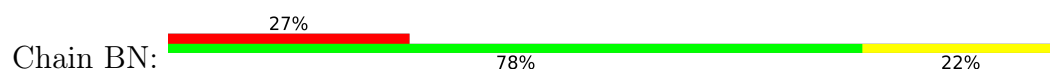
- Molecule 1: coat protein



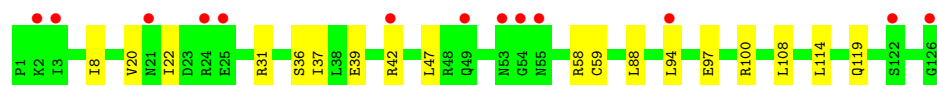
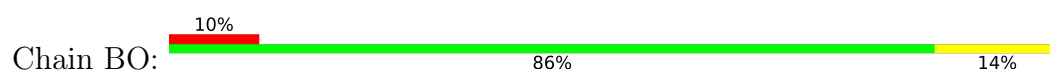
- Molecule 1: coat protein



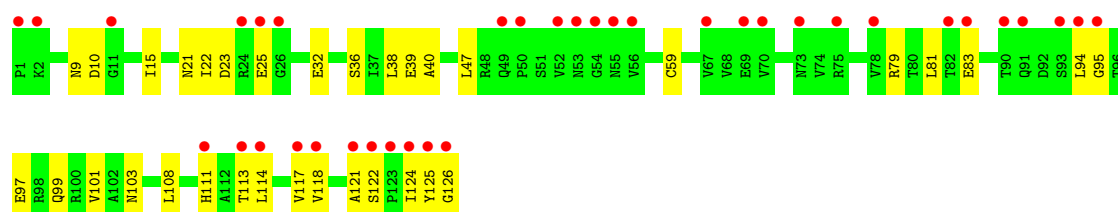
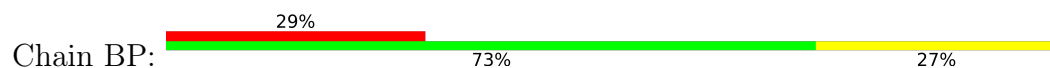
- Molecule 1: coat protein



- Molecule 1: coat protein

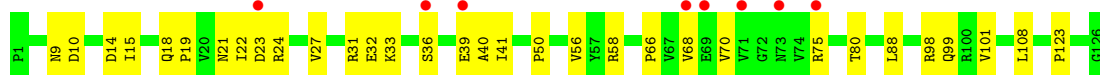


- Molecule 1: coat protein



- Molecule 1: coat protein

Chain BQ:  6% 75% 25%



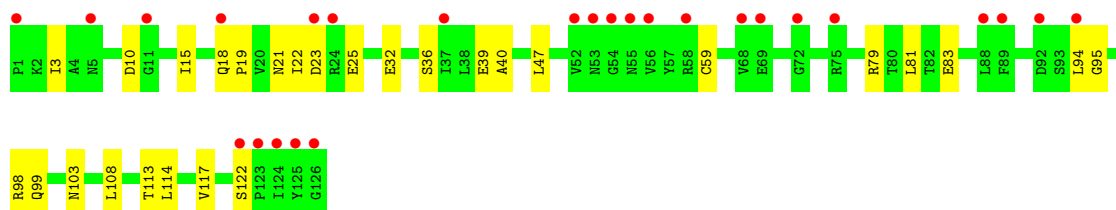
- Molecule 1: coat protein

Chain BR:  87% 13%



- Molecule 1: coat protein

Chain BS:  21% 78% 22%



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	296.94Å 306.88Å 322.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.94 – 3.09 48.94 – 3.09	Depositor EDS
% Data completeness (in resolution range)	98.7 (48.94-3.09) 99.1 (48.94-3.09)	Depositor EDS
R_{merge}	0.36	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 3.07Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.266 , 0.271 0.268 , 0.274	Depositor DCC
R_{free} test set	9989 reflections (3.77%)	wwPDB-VP
Wilson B-factor (Å ²)	91.6	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 83.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.000 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	43650	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.06% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.26	0/980	0.54	0/1331
1	AB	0.24	0/980	0.48	0/1331
1	AC	0.26	0/980	0.49	0/1331
1	AD	0.27	0/980	0.54	0/1331
1	AE	0.24	0/980	0.48	0/1331
1	AF	0.26	0/980	0.49	0/1331
1	AG	0.27	0/980	0.54	0/1331
1	AH	0.24	0/980	0.48	0/1331
1	AI	0.26	0/980	0.49	0/1331
1	AJ	0.27	0/980	0.54	0/1331
1	AK	0.24	0/980	0.48	0/1331
1	AL	0.27	0/980	0.49	0/1331
1	AM	0.27	0/980	0.54	0/1331
1	AN	0.24	0/980	0.48	0/1331
1	AO	0.26	0/980	0.49	0/1331
1	AP	0.27	0/980	0.54	0/1331
1	AQ	0.24	0/980	0.48	0/1331
1	AR	0.27	0/980	0.49	0/1331
1	AS	0.27	0/980	0.54	0/1331
1	AT	0.24	0/980	0.48	0/1331
1	AU	0.26	0/980	0.49	0/1331
1	AV	0.27	0/980	0.54	0/1331
1	AW	0.24	0/980	0.48	0/1331
1	AX	0.27	0/980	0.49	0/1331
1	AY	0.26	0/980	0.54	0/1331
1	AZ	0.24	0/980	0.48	0/1331
1	BA	0.27	0/980	0.49	0/1331
1	BB	0.27	0/980	0.54	0/1331
1	BC	0.24	0/980	0.48	0/1331
1	BD	0.27	0/980	0.49	0/1331
1	BE	0.27	0/980	0.54	0/1331
1	BF	0.24	0/980	0.48	0/1331
1	BG	0.26	0/980	0.49	0/1331
1	BH	0.27	0/980	0.54	0/1331

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BI	0.24	0/980	0.48	0/1331
1	BJ	0.27	0/980	0.49	0/1331
1	BK	0.26	0/980	0.54	0/1331
1	BL	0.24	0/980	0.48	0/1331
1	BM	0.27	0/980	0.49	0/1331
1	BN	0.27	0/980	0.54	0/1331
1	BO	0.24	0/980	0.48	0/1331
1	BP	0.27	0/980	0.49	0/1331
1	BQ	0.27	0/980	0.54	0/1331
1	BR	0.24	0/980	0.48	0/1331
1	BS	0.26	0/980	0.49	0/1331
All	All	0.26	0/44100	0.51	0/59895

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	970	0	1014	18	0
1	AB	970	0	1014	15	1
1	AC	970	0	1014	13	1
1	AD	970	0	1014	22	0
1	AE	970	0	1014	18	0
1	AF	970	0	1014	52	0
1	AG	970	0	1014	30	0
1	AH	970	0	1014	16	0
1	AI	970	0	1014	30	0
1	AJ	970	0	1014	18	0
1	AK	970	0	1014	18	0
1	AL	970	0	1014	13	0
1	AM	970	0	1014	23	0
1	AN	970	0	1014	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AO	970	0	1014	80	0
1	AP	970	0	1014	37	0
1	AQ	970	0	1014	37	0
1	AR	970	0	1014	46	0
1	AS	970	0	1014	24	0
1	AT	970	0	1014	17	0
1	AU	970	0	1014	35	0
1	AV	970	0	1014	19	0
1	AW	970	0	1014	16	0
1	AX	970	0	1014	27	0
1	AY	970	0	1014	31	0
1	AZ	970	0	1014	20	0
1	BA	970	0	1014	55	0
1	BB	970	0	1014	24	0
1	BC	970	0	1014	18	0
1	BD	970	0	1014	37	0
1	BE	970	0	1014	32	0
1	BF	970	0	1014	15	0
1	BG	970	0	1014	67	0
1	BH	970	0	1014	24	0
1	BI	970	0	1014	17	0
1	BJ	970	0	1014	56	0
1	BK	970	0	1014	19	0
1	BL	970	0	1014	15	1
1	BM	970	0	1014	10	3
1	BN	970	0	1014	22	0
1	BO	970	0	1014	18	0
1	BP	970	0	1014	41	0
1	BQ	970	0	1014	24	0
1	BR	970	0	1014	17	0
1	BS	970	0	1014	28	0
All	All	43650	0	45630	883	4

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 10.

All (883) 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:AO:105:THR:OG1	1:BG:83:GLU:HG3	1.49	1.12
1:AQ:24:ARG:HD3	1:AY:24:ARG:O	1.53	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:126:GLY:C	1:BE:24:ARG:HH22	1.61	1.07
1:AS:24:ARG:NH2	1:BP:126:GLY:OXT	1.87	1.05
1:AQ:24:ARG:HA	1:AY:24:ARG:HH21	1.23	1.01
1:AI:122:SER:HB2	1:BB:20:VAL:O	1.61	1.01
1:AO:126:GLY:OXT	1:BE:24:ARG:NH2	1.94	1.00
1:AP:21:ASN:HA	1:BJ:125:TYR:CD2	1.99	0.97
1:AO:104:LEU:HB3	1:BG:63:LEU:CD2	2.00	0.90
1:AO:125:TYR:CD2	1:BE:21:ASN:HA	2.07	0.88
1:AO:119:GLN:O	1:BG:98:ARG:NE	2.07	0.88
1:AG:21:ASN:HA	1:BD:125:TYR:CD2	2.09	0.87
1:AO:104:LEU:HD13	1:BG:63:LEU:HD21	1.58	0.84
1:AR:71:VAL:HG22	1:BH:73:ASN:HD22	1.41	0.84
1:AQ:22:ILE:HB	1:AZ:125:TYR:OH	1.78	0.84
1:AG:31:ARG:NH2	1:BD:120:ASP:O	2.12	0.82
1:AO:10:ASP:HA	1:BG:104:LEU:HG	1.61	0.82
1:BS:36:SER:HB2	1:BS:39:GLU:HG2	1.62	0.82
1:AR:36:SER:HB2	1:AR:39:GLU:HG2	1.62	0.82
1:BD:36:SER:HB2	1:BD:39:GLU:HG2	1.62	0.82
1:AL:36:SER:HB2	1:AL:39:GLU:HG2	1.62	0.82
1:AF:36:SER:HB2	1:AF:39:GLU:HG2	1.62	0.81
1:AO:36:SER:HB2	1:AO:39:GLU:HG2	1.62	0.81
1:BM:36:SER:HB2	1:BM:39:GLU:HG2	1.62	0.81
1:AI:36:SER:HB2	1:AI:39:GLU:HG2	1.62	0.81
1:BG:36:SER:HB2	1:BG:39:GLU:HG2	1.62	0.81
1:AG:22:ILE:H	1:BD:125:TYR:CB	1.94	0.81
1:AX:36:SER:HB2	1:AX:39:GLU:HG2	1.62	0.81
1:AC:36:SER:HB2	1:AC:39:GLU:HG2	1.62	0.81
1:BA:36:SER:HB2	1:BA:39:GLU:HG2	1.62	0.81
1:AU:36:SER:HB2	1:AU:39:GLU:HG2	1.62	0.80
1:AG:22:ILE:H	1:BD:125:TYR:HB2	1.45	0.80
1:BJ:36:SER:HB2	1:BJ:39:GLU:HG2	1.62	0.80
1:BP:36:SER:HB2	1:BP:39:GLU:HG2	1.62	0.80
1:AO:121:ALA:HB1	1:BG:57:TYR:CE2	2.20	0.77
1:AO:125:TYR:CE2	1:BE:21:ASN:HA	2.20	0.77
1:AO:109:ALA:HB1	1:BG:105:THR:HG22	1.67	0.77
1:AD:123:PRO:HB3	1:AE:47:LEU:HB3	1.67	0.77
1:AG:123:PRO:HB3	1:AH:47:LEU:HB3	1.67	0.77
1:AV:20:VAL:O	1:BS:122:SER:HB2	1.84	0.76
1:BK:123:PRO:HB3	1:BL:47:LEU:HB3	1.68	0.76
1:AR:41:ILE:HD11	1:BJ:100:ARG:HH21	1.50	0.76
1:BB:98:ARG:NH1	1:BC:119:GLN:O	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:125:TYR:CD1	1:BE:22:ILE:HB	2.20	0.76
1:BB:123:PRO:HB3	1:BC:47:LEU:HB3	1.68	0.76
1:AJ:123:PRO:HB3	1:AK:47:LEU:HB3	1.67	0.76
1:AV:98:ARG:NH1	1:AW:119:GLN:O	2.19	0.76
1:AY:98:ARG:NH1	1:AZ:119:GLN:O	2.19	0.76
1:BH:123:PRO:HB3	1:BI:47:LEU:HB3	1.67	0.76
1:BK:98:ARG:NH1	1:BL:119:GLN:O	2.19	0.76
1:AP:123:PRO:HB3	1:AQ:47:LEU:HB3	1.67	0.76
1:AS:98:ARG:NH1	1:AT:119:GLN:O	2.19	0.76
1:BH:98:ARG:NH1	1:BI:119:GLN:O	2.19	0.76
1:AF:81:LEU:HB2	1:BA:101:VAL:HG21	1.67	0.76
1:BN:123:PRO:HB3	1:BO:47:LEU:HB3	1.67	0.76
1:BQ:123:PRO:HB3	1:BR:47:LEU:HB3	1.67	0.76
1:AO:126:GLY:C	1:BE:24:ARG:NH2	2.41	0.76
1:AV:123:PRO:HB3	1:AW:47:LEU:HB3	1.67	0.76
1:BE:98:ARG:NH1	1:BF:119:GLN:O	2.19	0.76
1:BE:123:PRO:HB3	1:BF:47:LEU:HB3	1.67	0.76
1:AJ:98:ARG:NH1	1:AK:119:GLN:O	2.19	0.76
1:AM:98:ARG:NH1	1:AN:119:GLN:O	2.19	0.76
1:AQ:24:ARG:HB2	1:AY:24:ARG:HE	1.51	0.76
1:BQ:98:ARG:NH1	1:BR:119:GLN:O	2.19	0.76
1:AY:123:PRO:HB3	1:AZ:47:LEU:HB3	1.67	0.75
1:BN:98:ARG:NH1	1:BO:119:GLN:O	2.19	0.75
1:AA:98:ARG:NH1	1:AB:119:GLN:O	2.19	0.75
1:AA:123:PRO:HB3	1:AB:47:LEU:HB3	1.67	0.75
1:AD:98:ARG:NH1	1:AE:119:GLN:O	2.19	0.75
1:AG:98:ARG:NH1	1:AH:119:GLN:O	2.19	0.75
1:AP:98:ARG:NH1	1:AQ:119:GLN:O	2.19	0.75
1:AO:104:LEU:HB3	1:BG:63:LEU:HD21	1.68	0.75
1:AQ:22:ILE:HB	1:AZ:125:TYR:HH	1.51	0.74
1:AS:123:PRO:HB3	1:AT:47:LEU:HB3	1.67	0.74
1:AO:101:VAL:HG21	1:BG:81:LEU:CB	2.17	0.74
1:AM:123:PRO:HB3	1:AN:47:LEU:HB3	1.67	0.74
1:AX:123:PRO:HB3	1:BS:47:LEU:HB3	1.68	0.73
1:AO:123:PRO:HA	1:BG:47:LEU:HB3	1.70	0.73
1:AX:119:GLN:HG2	1:BS:99:GLN:HA	1.71	0.73
1:AR:81:LEU:HB2	1:BJ:101:VAL:HG21	1.69	0.72
1:AO:100:ARG:HH21	1:BG:41:ILE:HD11	1.53	0.72
1:AR:41:ILE:HD11	1:BJ:100:ARG:NH2	2.05	0.72
1:AO:10:ASP:O	1:BG:100:ARG:HA	1.90	0.72
1:AO:125:TYR:HD1	1:BE:22:ILE:HB	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AR:83:GLU:HG3	1:BJ:105:THR:OG1	1.90	0.71
1:AM:73:ASN:HD22	1:BG:71:VAL:HG22	1.56	0.71
1:AY:126:GLY:HA3	1:BS:3:ILE:HG23	1.74	0.69
1:AF:104:LEU:HD21	1:BA:10:ASP:HB3	1.73	0.69
1:AR:63:LEU:CD2	1:BJ:104:LEU:HB3	2.22	0.69
1:AF:81:LEU:CB	1:BA:101:VAL:HG21	2.22	0.69
1:AF:107:SER:CB	1:BA:9:ASN:H	2.05	0.69
1:AP:22:ILE:H	1:BJ:125:TYR:CB	2.05	0.69
1:AX:119:GLN:NE2	1:BS:99:GLN:HG3	2.08	0.68
1:AO:97:GLU:CD	1:BG:79:ARG:HE	2.02	0.68
1:AD:24:ARG:NH2	1:BA:126:GLY:OXT	2.24	0.68
1:AI:99:GLN:HG3	1:BD:119:GLN:HE21	1.60	0.67
1:AR:67:VAL:HG11	1:BJ:97:GLU:OE1	1.95	0.67
1:AR:63:LEU:HD21	1:BJ:104:LEU:HB3	1.76	0.67
1:AO:97:GLU:HB3	1:BG:81:LEU:HD11	1.77	0.67
1:AQ:22:ILE:HB	1:AZ:125:TYR:CZ	2.30	0.66
1:AO:101:VAL:HG21	1:BG:81:LEU:HB3	1.75	0.66
1:AO:105:THR:HG1	1:BG:83:GLU:HG3	1.60	0.66
1:AU:87:VAL:HG11	1:BP:118:VAL:HG11	1.77	0.66
1:AR:71:VAL:CG2	1:BH:73:ASN:HD22	2.09	0.65
1:AK:94:LEU:HB2	1:AK:97:GLU:HG3	1.79	0.65
1:AZ:94:LEU:HB2	1:AZ:97:GLU:HG3	1.79	0.65
1:AE:94:LEU:HB2	1:AE:97:GLU:HG3	1.79	0.65
1:AR:63:LEU:HD21	1:BJ:104:LEU:HD13	1.78	0.65
1:AO:100:ARG:NH2	1:BG:41:ILE:HD11	2.12	0.64
1:AT:94:LEU:HB2	1:AT:97:GLU:HG3	1.79	0.64
1:AO:105:THR:HG23	1:BG:83:GLU:OE2	1.96	0.64
1:BR:94:LEU:HB2	1:BR:97:GLU:HG3	1.79	0.64
1:AB:94:LEU:HB2	1:AB:97:GLU:HG3	1.79	0.64
1:BI:94:LEU:HB2	1:BI:97:GLU:HG3	1.79	0.64
1:AH:94:LEU:HB2	1:AH:97:GLU:HG3	1.79	0.64
1:AQ:91:GLN:O	1:BA:37:ILE:HB	1.97	0.64
1:AR:98:ARG:NE	1:BJ:119:GLN:O	2.30	0.64
1:AI:47:LEU:HB3	1:BD:123:PRO:HB3	1.80	0.64
1:BF:94:LEU:HB2	1:BF:97:GLU:HG3	1.79	0.64
1:AR:81:LEU:CB	1:BJ:101:VAL:HG21	2.28	0.63
1:BC:94:LEU:HB2	1:BC:97:GLU:HG3	1.79	0.63
1:BO:94:LEU:HB2	1:BO:97:GLU:HG3	1.79	0.63
1:AN:94:LEU:HB2	1:AN:97:GLU:HG3	1.79	0.63
1:AQ:94:LEU:HB2	1:AQ:97:GLU:HG3	1.79	0.63
1:BL:94:LEU:HB2	1:BL:97:GLU:HG3	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:87:VAL:HG11	1:BA:118:VAL:HG11	1.81	0.63
1:AQ:24:ARG:HA	1:AY:24:ARG:NH2	2.05	0.63
1:AI:3:ILE:HG23	1:BH:126:GLY:HA3	1.81	0.62
1:AW:94:LEU:HB2	1:AW:97:GLU:HG3	1.79	0.62
1:AU:81:LEU:HD12	1:BP:101:VAL:CG2	2.30	0.62
1:AO:97:GLU:CB	1:BG:81:LEU:HD11	2.29	0.62
1:AO:10:ASP:OD2	1:BG:100:ARG:NE	2.33	0.62
1:AP:22:ILE:N	1:BJ:125:TYR:CG	2.67	0.61
1:AP:24:ARG:HH22	1:BJ:126:GLY:C	2.08	0.61
1:AU:45:VAL:HB	1:BP:124:ILE:HD12	1.82	0.61
1:AO:101:VAL:HG21	1:BG:81:LEU:HB2	1.80	0.61
1:AO:123:PRO:CA	1:BG:47:LEU:HB3	2.30	0.61
1:AD:24:ARG:HH22	1:BA:126:GLY:C	2.09	0.61
1:AO:125:TYR:HB2	1:BE:22:ILE:O	2.01	0.60
1:BI:31:ARG:HD3	1:BI:42:ARG:HH12	1.66	0.60
1:AG:20:VAL:HG13	1:BD:122:SER:HB2	1.84	0.60
1:AH:31:ARG:HD3	1:AH:42:ARG:HH12	1.66	0.60
1:AO:104:LEU:HB3	1:BG:63:LEU:HD22	1.83	0.60
1:AQ:31:ARG:HD3	1:AQ:42:ARG:HH12	1.66	0.60
1:AX:119:GLN:HE21	1:BS:99:GLN:HG3	1.66	0.60
1:AZ:31:ARG:HD3	1:AZ:42:ARG:HH12	1.66	0.60
1:BR:31:ARG:HD3	1:BR:42:ARG:HH12	1.67	0.60
1:AE:31:ARG:HD3	1:AE:42:ARG:HH12	1.67	0.60
1:AB:31:ARG:HD3	1:AB:42:ARG:HH12	1.66	0.60
1:BF:31:ARG:HD3	1:BF:42:ARG:HH12	1.66	0.60
1:BL:31:ARG:HD3	1:BL:42:ARG:HH12	1.67	0.60
1:AR:98:ARG:HD2	1:BJ:118:VAL:O	2.02	0.60
1:AK:31:ARG:HD3	1:AK:42:ARG:HH12	1.66	0.59
1:AI:99:GLN:HG3	1:BD:119:GLN:NE2	2.17	0.59
1:AN:31:ARG:HD3	1:AN:42:ARG:HH12	1.67	0.59
1:AW:31:ARG:HD3	1:AW:42:ARG:HH12	1.66	0.59
1:BC:31:ARG:HD3	1:BC:42:ARG:HH12	1.67	0.59
1:AQ:49:GLN:CD	1:BA:20:VAL:CG1	2.76	0.59
1:AF:67:VAL:HG11	1:BA:97:GLU:OE1	2.03	0.58
1:AS:24:ARG:HH22	1:BP:126:GLY:C	2.06	0.58
1:BO:31:ARG:HD3	1:BO:42:ARG:HH12	1.66	0.58
1:AF:107:SER:OG	1:BA:9:ASN:HB3	2.03	0.58
1:AU:81:LEU:HD12	1:BP:101:VAL:HG21	1.85	0.58
1:AI:8:ILE:CD1	1:BD:104:LEU:HD22	2.33	0.58
1:AF:63:LEU:HD21	1:BA:104:LEU:HB3	1.84	0.58
1:AT:31:ARG:HD3	1:AT:42:ARG:HH12	1.66	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:72:GLY:HA3	1:BC:69:GLU:OE2	2.04	0.58
1:AO:104:LEU:CD1	1:BG:63:LEU:HD21	2.33	0.58
1:AI:98:ARG:HD2	1:BD:118:VAL:O	2.04	0.58
1:AO:118:VAL:O	1:BG:98:ARG:HD2	2.04	0.58
1:AF:81:LEU:HD12	1:BA:101:VAL:CG2	2.34	0.58
1:AX:90:THR:OG1	1:BS:79:ARG:HD2	2.04	0.57
1:AI:126:GLY:OXT	1:BB:24:ARG:NH2	2.34	0.57
1:AO:105:THR:OG1	1:BG:83:GLU:CG	2.39	0.57
1:AO:122:SER:C	1:BG:47:LEU:HD23	2.30	0.57
1:AI:8:ILE:HD12	1:BD:104:LEU:HD22	1.87	0.57
1:AS:20:VAL:O	1:BP:122:SER:HB2	2.05	0.56
1:AI:41:ILE:HD11	1:BD:100:ARG:NH2	2.20	0.56
1:AI:83:GLU:CG	1:BD:87:VAL:HG22	2.36	0.55
1:AN:37:ILE:HG22	1:AP:91:GLN:HG3	1.88	0.55
1:AO:125:TYR:CG	1:BE:22:ILE:N	2.68	0.55
1:AO:115:MET:HE3	1:BG:102:ALA:HB1	1.89	0.55
1:AF:86:GLU:O	1:BA:83:GLU:HA	2.07	0.55
1:AS:9:ASN:ND2	1:AS:14:ASP:OD2	2.38	0.55
1:AP:22:ILE:H	1:BJ:125:TYR:HB2	1.70	0.55
1:AR:67:VAL:HG21	1:BJ:97:GLU:CD	2.31	0.55
1:AS:23:ASP:HB3	1:AS:27:VAL:H	1.72	0.55
1:AF:107:SER:HB3	1:BA:9:ASN:H	1.70	0.55
1:AY:23:ASP:HB3	1:AY:27:VAL:H	1.72	0.55
1:AM:23:ASP:HB3	1:AM:27:VAL:H	1.72	0.55
1:AD:23:ASP:HB3	1:AD:27:VAL:H	1.72	0.55
1:BE:23:ASP:HB3	1:BE:27:VAL:H	1.72	0.55
1:AV:23:ASP:HB3	1:AV:27:VAL:H	1.72	0.54
1:AD:58:ARG:HG2	1:AD:88:LEU:HD22	1.90	0.54
1:AJ:15:ILE:HD13	1:AJ:41:ILE:HD12	1.90	0.54
1:AP:15:ILE:HD13	1:AP:41:ILE:HD12	1.90	0.54
1:AY:15:ILE:HD13	1:AY:41:ILE:HD12	1.90	0.54
1:BB:58:ARG:HG2	1:BB:88:LEU:HD22	1.90	0.54
1:AJ:23:ASP:HB3	1:AJ:27:VAL:H	1.72	0.54
1:AM:31:ARG:NH2	1:BG:120:ASP:O	2.40	0.54
1:AO:125:TYR:CE1	1:BE:22:ILE:HG13	2.42	0.54
1:AP:58:ARG:HG2	1:AP:88:LEU:HD22	1.90	0.54
1:BB:23:ASP:HB3	1:BB:27:VAL:H	1.72	0.54
1:BE:15:ILE:HD13	1:BE:41:ILE:HD12	1.90	0.54
1:BK:15:ILE:HD13	1:BK:41:ILE:HD12	1.90	0.54
1:AN:31:ARG:NH2	1:AQ:120:ASP:O	2.41	0.54
1:AO:125:TYR:CD1	1:BE:22:ILE:N	2.75	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:23:ASP:HB3	1:AG:27:VAL:H	1.72	0.54
1:AU:89:PHE:HA	1:BP:81:LEU:HD22	1.90	0.54
1:BK:23:ASP:HB3	1:BK:27:VAL:H	1.72	0.54
1:BH:23:ASP:HB3	1:BH:27:VAL:H	1.72	0.54
1:AG:15:ILE:HD13	1:AG:41:ILE:HD12	1.90	0.54
1:AP:23:ASP:HB3	1:AP:27:VAL:H	1.72	0.54
1:BQ:23:ASP:HB3	1:BQ:27:VAL:H	1.72	0.54
1:AA:23:ASP:HB3	1:AA:27:VAL:H	1.72	0.54
1:AO:104:LEU:CB	1:BG:63:LEU:HD21	2.36	0.54
1:BQ:15:ILE:HD13	1:BQ:41:ILE:HD12	1.90	0.54
1:BN:23:ASP:HB3	1:BN:27:VAL:H	1.72	0.53
1:AF:81:LEU:HD12	1:BA:101:VAL:HG21	1.90	0.53
1:AF:101:VAL:HG21	1:BA:81:LEU:HD12	1.89	0.53
1:AS:58:ARG:HG2	1:AS:88:LEU:HD22	1.90	0.53
1:AY:58:ARG:HG2	1:AY:88:LEU:HD22	1.90	0.53
1:AD:9:ASN:ND2	1:AD:14:ASP:OD2	2.38	0.53
1:AQ:49:GLN:CD	1:BA:20:VAL:HG13	2.34	0.53
1:AQ:49:GLN:CG	1:BA:21:ASN:HB2	2.38	0.53
1:BE:58:ARG:HG2	1:BE:88:LEU:HD22	1.90	0.53
1:BH:9:ASN:ND2	1:BH:14:ASP:OD2	2.38	0.53
1:BH:15:ILE:HD13	1:BH:41:ILE:HD12	1.90	0.53
1:BQ:58:ARG:HG2	1:BQ:88:LEU:HD22	1.90	0.53
1:AA:58:ARG:HG2	1:AA:88:LEU:HD22	1.90	0.53
1:AG:58:ARG:HG2	1:AG:88:LEU:HD22	1.90	0.53
1:AO:9:ASN:C	1:BG:104:LEU:HD23	2.34	0.53
1:AO:118:VAL:HG13	1:BG:89:PHE:CE2	2.43	0.53
1:AV:15:ILE:HD13	1:AV:41:ILE:HD12	1.90	0.53
1:BH:58:ARG:HG2	1:BH:88:LEU:HD22	1.90	0.53
1:BN:58:ARG:HG2	1:BN:88:LEU:HD22	1.90	0.53
1:AO:118:VAL:HG11	1:BG:87:VAL:HG11	1.90	0.53
1:BN:15:ILE:HD13	1:BN:41:ILE:HD12	1.90	0.53
1:AD:15:ILE:HD13	1:AD:41:ILE:HD12	1.90	0.53
1:AO:106:LYS:HA	1:BG:109:ALA:HB1	1.91	0.53
1:AO:118:VAL:HG13	1:BG:89:PHE:CD2	2.43	0.53
1:BK:58:ARG:HG2	1:BK:88:LEU:HD22	1.90	0.53
1:AA:15:ILE:HD13	1:AA:41:ILE:HD12	1.90	0.53
1:AL:99:GLN:O	1:AL:103:ASN:ND2	2.41	0.53
1:AV:9:ASN:ND2	1:AV:14:ASP:OD2	2.38	0.53
1:AJ:58:ARG:HG2	1:AJ:88:LEU:HD22	1.90	0.53
1:AM:15:ILE:HD13	1:AM:41:ILE:HD12	1.90	0.53
1:AO:101:VAL:CG2	1:BG:81:LEU:HB2	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:15:ILE:HD13	1:AS:41:ILE:HD12	1.90	0.53
1:AV:58:ARG:HG2	1:AV:88:LEU:HD22	1.90	0.53
1:AY:9:ASN:ND2	1:AY:14:ASP:OD2	2.38	0.52
1:BA:99:GLN:O	1:BA:103:ASN:ND2	2.41	0.52
1:BM:99:GLN:O	1:BM:103:ASN:ND2	2.41	0.52
1:AH:58:ARG:HG2	1:AH:88:LEU:HD22	1.92	0.52
1:AQ:24:ARG:CA	1:AY:24:ARG:HH21	2.10	0.52
1:AQ:58:ARG:HG2	1:AQ:88:LEU:HD22	1.92	0.52
1:BE:9:ASN:ND2	1:BE:14:ASP:OD2	2.38	0.52
1:AG:22:ILE:HG13	1:BD:125:TYR:CD1	2.44	0.52
1:BF:58:ARG:HG2	1:BF:88:LEU:HD22	1.92	0.52
1:BN:36:SER:HB2	1:BN:39:GLU:HG2	1.92	0.52
1:AB:58:ARG:HG2	1:AB:88:LEU:HD22	1.92	0.52
1:AG:36:SER:HB2	1:AG:39:GLU:HG2	1.92	0.52
1:AM:126:GLY:HA3	1:AR:3:ILE:HG23	1.91	0.52
1:AN:22:ILE:HD12	1:AQ:125:TYR:OH	2.10	0.52
1:AX:89:PHE:HA	1:BS:81:LEU:HD22	1.91	0.52
1:BH:36:SER:HB2	1:BH:39:GLU:HG2	1.92	0.52
1:BS:99:GLN:O	1:BS:103:ASN:ND2	2.41	0.52
1:AE:108:LEU:HD22	1:AE:114:LEU:HD11	1.92	0.52
1:AG:9:ASN:ND2	1:AG:14:ASP:OD2	2.38	0.52
1:AO:104:LEU:CB	1:BG:63:LEU:CD2	2.82	0.52
1:AU:123:PRO:HB3	1:BP:47:LEU:HB3	1.91	0.52
1:BE:36:SER:HB2	1:BE:39:GLU:HG2	1.92	0.52
1:AF:79:ARG:NE	1:BA:97:GLU:OE2	2.28	0.52
1:AU:86:GLU:O	1:BP:83:GLU:HA	2.10	0.52
1:BB:15:ILE:HD13	1:BB:41:ILE:HD12	1.90	0.52
1:BI:58:ARG:HG2	1:BI:88:LEU:HD22	1.92	0.52
1:BK:36:SER:HB2	1:BK:39:GLU:HG2	1.92	0.52
1:BO:108:LEU:HD22	1:BO:114:LEU:HD11	1.92	0.52
1:AF:99:GLN:O	1:AF:103:ASN:ND2	2.41	0.52
1:AW:58:ARG:HG2	1:AW:88:LEU:HD22	1.92	0.52
1:AW:108:LEU:HD22	1:AW:114:LEU:HD11	1.92	0.52
1:BB:36:SER:HB2	1:BB:39:GLU:HG2	1.92	0.52
1:BR:58:ARG:HG2	1:BR:88:LEU:HD22	1.92	0.52
1:AM:58:ARG:HG2	1:AM:88:LEU:HD22	1.90	0.52
1:AE:58:ARG:HG2	1:AE:88:LEU:HD22	1.92	0.51
1:AN:37:ILE:CG2	1:AP:91:GLN:HG3	2.40	0.51
1:AO:122:SER:HB2	1:BE:20:VAL:O	2.09	0.51
1:AV:36:SER:HB2	1:AV:39:GLU:HG2	1.92	0.51
1:BL:58:ARG:HG2	1:BL:88:LEU:HD22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BO:58:ARG:HG2	1:BO:88:LEU:HD22	1.92	0.51
1:AO:114:LEU:HD21	1:BG:45:VAL:CG1	2.40	0.51
1:AZ:31:ARG:HD3	1:AZ:42:ARG:NH1	2.25	0.51
1:BI:108:LEU:HD22	1:BI:114:LEU:HD11	1.92	0.51
1:AH:108:LEU:HD22	1:AH:114:LEU:HD11	1.92	0.51
1:AN:31:ARG:HD3	1:AN:42:ARG:NH1	2.25	0.51
1:AN:58:ARG:HG2	1:AN:88:LEU:HD22	1.92	0.51
1:AP:36:SER:HB2	1:AP:39:GLU:HG2	1.92	0.51
1:AS:36:SER:HB2	1:AS:39:GLU:HG2	1.92	0.51
1:AT:108:LEU:HD22	1:AT:114:LEU:HD11	1.92	0.51
1:AZ:108:LEU:HD22	1:AZ:114:LEU:HD11	1.92	0.51
1:BF:108:LEU:HD22	1:BF:114:LEU:HD11	1.92	0.51
1:AA:36:SER:HB2	1:AA:39:GLU:HG2	1.92	0.51
1:AD:36:SER:HB2	1:AD:39:GLU:HG2	1.92	0.51
1:AU:47:LEU:HD21	1:BP:121:ALA:HA	1.91	0.51
1:BC:108:LEU:HD22	1:BC:114:LEU:HD11	1.92	0.51
1:BQ:36:SER:HB2	1:BQ:39:GLU:HG2	1.92	0.51
1:AF:111:HIS:CD2	1:BA:7:VAL:O	2.63	0.51
1:AG:22:ILE:N	1:BD:125:TYR:CG	2.79	0.51
1:AK:58:ARG:HG2	1:AK:88:LEU:HD22	1.92	0.51
1:AX:99:GLN:O	1:AX:103:ASN:ND2	2.41	0.51
1:BI:31:ARG:HD3	1:BI:42:ARG:NH1	2.25	0.51
1:BO:31:ARG:HD3	1:BO:42:ARG:NH1	2.25	0.51
1:AE:125:TYR:OH	1:BO:22:ILE:HD12	2.10	0.51
1:AH:31:ARG:HD3	1:AH:42:ARG:NH1	2.25	0.51
1:AJ:36:SER:HB2	1:AJ:39:GLU:HG2	1.92	0.51
1:AQ:31:ARG:HD3	1:AQ:42:ARG:NH1	2.25	0.51
1:AO:9:ASN:O	1:BG:104:LEU:HD23	2.11	0.51
1:BF:31:ARG:HD3	1:BF:42:ARG:NH1	2.25	0.51
1:BJ:99:GLN:O	1:BJ:103:ASN:ND2	2.41	0.51
1:AA:9:ASN:ND2	1:AA:14:ASP:OD2	2.38	0.51
1:AK:108:LEU:HD22	1:AK:114:LEU:HD11	1.92	0.51
1:AO:125:TYR:CD1	1:BE:22:ILE:CB	2.92	0.51
1:AR:47:LEU:HB3	1:BJ:123:PRO:HB3	1.92	0.51
1:AT:31:ARG:HD3	1:AT:42:ARG:NH1	2.25	0.51
1:AZ:58:ARG:HG2	1:AZ:88:LEU:HD22	1.92	0.51
1:BL:31:ARG:HD3	1:BL:42:ARG:NH1	2.25	0.51
1:BR:31:ARG:HD3	1:BR:42:ARG:NH1	2.25	0.51
1:BR:108:LEU:HD22	1:BR:114:LEU:HD11	1.92	0.51
1:AB:31:ARG:HD3	1:AB:42:ARG:NH1	2.25	0.51
1:AC:99:GLN:O	1:AC:103:ASN:ND2	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:9:ASN:ND2	1:AM:14:ASP:OD2	2.38	0.51
1:BC:58:ARG:HG2	1:BC:88:LEU:HD22	1.92	0.51
1:BG:99:GLN:O	1:BG:103:ASN:ND2	2.41	0.51
1:BP:99:GLN:O	1:BP:103:ASN:ND2	2.41	0.51
1:AT:58:ARG:HG2	1:AT:88:LEU:HD22	1.92	0.50
1:BC:31:ARG:HD3	1:BC:42:ARG:NH1	2.25	0.50
1:BN:23:ASP:HB2	1:BN:27:VAL:HB	1.94	0.50
1:AP:23:ASP:HB2	1:AP:27:VAL:HB	1.94	0.50
1:AR:81:LEU:HD22	1:BJ:89:PHE:HB2	1.94	0.50
1:AW:31:ARG:HD3	1:AW:42:ARG:NH1	2.25	0.50
1:AX:86:GLU:O	1:BS:83:GLU:HA	2.11	0.50
1:AY:36:SER:HB2	1:AY:39:GLU:HG2	1.92	0.50
1:BL:108:LEU:HD22	1:BL:114:LEU:HD11	1.92	0.50
1:AN:108:LEU:HD22	1:AN:114:LEU:HD11	1.92	0.50
1:AQ:108:LEU:HD22	1:AQ:114:LEU:HD11	1.92	0.50
1:AR:79:ARG:HD2	1:BJ:93:SER:HA	1.94	0.50
1:AR:79:ARG:CD	1:BJ:93:SER:HA	2.42	0.50
1:BH:23:ASP:HB2	1:BH:27:VAL:HB	1.94	0.50
1:AB:108:LEU:HD22	1:AB:114:LEU:HD11	1.92	0.50
1:AD:23:ASP:HB2	1:AD:27:VAL:HB	1.93	0.50
1:AI:99:GLN:O	1:AI:103:ASN:ND2	2.41	0.50
1:AR:99:GLN:O	1:AR:103:ASN:ND2	2.41	0.50
1:AK:31:ARG:HD3	1:AK:42:ARG:NH1	2.25	0.50
1:AU:47:LEU:HD23	1:BP:122:SER:N	2.26	0.50
1:AF:20:VAL:O	1:BN:123:PRO:HG3	2.12	0.50
1:AG:23:ASP:HB2	1:AG:27:VAL:HB	1.93	0.50
1:AM:23:ASP:HB2	1:AM:27:VAL:HB	1.93	0.50
1:AY:39:GLU:HB3	1:AY:68:VAL:HG21	1.94	0.50
1:BK:23:ASP:HB2	1:BK:27:VAL:HB	1.93	0.50
1:BK:39:GLU:HB3	1:BK:68:VAL:HG21	1.94	0.50
1:AF:84:THR:O	1:BA:85:THR:HA	2.11	0.50
1:AM:36:SER:HB2	1:AM:39:GLU:HG2	1.92	0.50
1:BH:39:GLU:HB3	1:BH:68:VAL:HG21	1.94	0.50
1:BN:39:GLU:HB3	1:BN:68:VAL:HG21	1.94	0.50
1:AA:23:ASP:HB2	1:AA:27:VAL:HB	1.93	0.49
1:AI:83:GLU:HG3	1:BD:87:VAL:HG22	1.94	0.49
1:AS:23:ASP:HB2	1:AS:27:VAL:HB	1.93	0.49
1:AX:47:LEU:HD13	1:AX:59:CYS:HB2	1.94	0.49
1:BE:39:GLU:HB3	1:BE:68:VAL:HG21	1.94	0.49
1:AO:9:ASN:O	1:BG:104:LEU:HA	2.12	0.49
1:BE:66:PRO:HA	1:BE:80:THR:HG22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:23:ASP:HB2	1:BQ:27:VAL:HB	1.94	0.49
1:AE:31:ARG:HD3	1:AE:42:ARG:NH1	2.25	0.49
1:AF:47:LEU:HD13	1:AF:59:CYS:HB2	1.94	0.49
1:BK:9:ASN:ND2	1:BK:14:ASP:OD2	2.38	0.49
1:BN:9:ASN:ND2	1:BN:14:ASP:OD2	2.38	0.49
1:BN:66:PRO:HA	1:BN:80:THR:HG22	1.95	0.49
1:BP:47:LEU:HD13	1:BP:59:CYS:HB2	1.94	0.49
1:AA:66:PRO:HA	1:AA:80:THR:HG22	1.95	0.49
1:AJ:23:ASP:HB2	1:AJ:27:VAL:HB	1.93	0.49
1:AS:39:GLU:HB3	1:AS:68:VAL:HG21	1.94	0.49
1:BB:39:GLU:HB3	1:BB:68:VAL:HG21	1.94	0.49
1:AA:39:GLU:HB3	1:AA:68:VAL:HG21	1.94	0.49
1:AI:125:TYR:CD1	1:BB:22:ILE:HB	2.47	0.49
1:AU:81:LEU:CD1	1:BP:101:VAL:HG21	2.42	0.49
1:AV:39:GLU:HB3	1:AV:68:VAL:HG21	1.94	0.49
1:AC:47:LEU:HD13	1:AC:59:CYS:HB2	1.94	0.49
1:AJ:66:PRO:HA	1:AJ:80:THR:HG22	1.95	0.49
1:AP:20:VAL:O	1:BJ:125:TYR:CE2	2.66	0.49
1:AP:21:ASN:HA	1:BJ:125:TYR:CE2	2.45	0.49
1:AV:66:PRO:HA	1:AV:80:THR:HG22	1.95	0.49
1:AP:21:ASN:OD1	1:BJ:125:TYR:HB3	2.11	0.49
1:AU:79:ARG:NH2	1:BP:97:GLU:OE1	2.42	0.49
1:BD:47:LEU:HD13	1:BD:59:CYS:HB2	1.95	0.49
1:BD:99:GLN:O	1:BD:103:ASN:ND2	2.41	0.49
1:BE:23:ASP:HB2	1:BE:27:VAL:HB	1.93	0.49
1:BQ:66:PRO:HA	1:BQ:80:THR:HG22	1.95	0.49
1:AD:39:GLU:HB3	1:AD:68:VAL:HG21	1.94	0.49
1:AL:47:LEU:HD13	1:AL:59:CYS:HB2	1.94	0.49
1:AM:39:GLU:HB3	1:AM:68:VAL:HG21	1.94	0.49
1:AN:20:VAL:HG13	1:AQ:123:PRO:HD2	1.94	0.49
1:BK:66:PRO:HA	1:BK:80:THR:HG22	1.94	0.49
1:AF:81:LEU:HD22	1:BA:89:PHE:HB2	1.94	0.49
1:AP:39:GLU:HB3	1:AP:68:VAL:HG21	1.94	0.49
1:AU:47:LEU:HD13	1:AU:59:CYS:HB2	1.94	0.49
1:AY:66:PRO:HA	1:AY:80:THR:HG22	1.95	0.49
1:BA:47:LEU:HD13	1:BA:59:CYS:HB2	1.94	0.49
1:AF:104:LEU:CD2	1:BA:10:ASP:HB3	2.41	0.48
1:AV:23:ASP:HB2	1:AV:27:VAL:HB	1.94	0.48
1:BG:47:LEU:HD13	1:BG:59:CYS:HB2	1.94	0.48
1:AF:125:TYR:O	1:BA:3:ILE:HG22	2.13	0.48
1:AM:66:PRO:HA	1:AM:80:THR:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:99:GLN:O	1:AO:103:ASN:ND2	2.41	0.48
1:BQ:39:GLU:HB3	1:BQ:68:VAL:HG21	1.94	0.48
1:AF:81:LEU:HD22	1:BA:89:PHE:CB	2.42	0.48
1:BB:23:ASP:HB2	1:BB:27:VAL:HB	1.93	0.48
1:BH:66:PRO:HA	1:BH:80:THR:HG22	1.95	0.48
1:AG:39:GLU:HB3	1:AG:68:VAL:HG21	1.94	0.48
1:AO:108:LEU:HD11	1:BG:43:LEU:HD13	1.94	0.48
1:BJ:47:LEU:HD13	1:BJ:59:CYS:HB2	1.95	0.48
1:AD:66:PRO:HA	1:AD:80:THR:HG22	1.95	0.48
1:AF:79:ARG:NE	1:BA:93:SER:HA	2.28	0.48
1:AR:47:LEU:HD13	1:AR:59:CYS:HB2	1.94	0.48
1:AY:23:ASP:HB2	1:AY:27:VAL:HB	1.93	0.48
1:AG:66:PRO:HA	1:AG:80:THR:HG22	1.95	0.48
1:AO:105:THR:HG23	1:BG:83:GLU:CD	2.38	0.48
1:BM:47:LEU:HD13	1:BM:59:CYS:HB2	1.94	0.48
1:AG:22:ILE:N	1:BD:125:TYR:HB2	2.24	0.48
1:AO:114:LEU:HD23	1:AO:114:LEU:HA	1.67	0.48
1:AP:22:ILE:HB	1:BJ:125:TYR:HD1	1.79	0.48
1:AP:31:ARG:NH2	1:BJ:120:ASP:O	2.46	0.48
1:AR:63:LEU:HD21	1:BJ:104:LEU:CB	2.42	0.48
1:AG:91:GLN:HG3	1:BI:37:ILE:HG22	1.95	0.48
1:AI:47:LEU:HD13	1:AI:59:CYS:HB2	1.94	0.48
1:AJ:39:GLU:HB3	1:AJ:68:VAL:HG21	1.94	0.48
1:AP:20:VAL:HG13	1:BJ:122:SER:HB2	1.96	0.48
1:BB:66:PRO:HA	1:BB:80:THR:HG22	1.95	0.48
1:AO:47:LEU:HD13	1:AO:59:CYS:HB2	1.95	0.48
1:AR:41:ILE:HD13	1:BJ:104:LEU:HD11	1.96	0.48
1:BB:9:ASN:ND2	1:BB:14:ASP:OD2	2.38	0.48
1:BS:47:LEU:HD13	1:BS:59:CYS:HB2	1.94	0.48
1:AU:99:GLN:O	1:AU:103:ASN:ND2	2.41	0.47
1:AS:66:PRO:HA	1:AS:80:THR:HG22	1.95	0.47
1:AU:47:LEU:CD2	1:BP:121:ALA:C	2.87	0.47
1:BC:31:ARG:NH2	1:BF:120:ASP:O	2.47	0.47
1:BQ:9:ASN:ND2	1:BQ:14:ASP:OD2	2.38	0.47
1:AP:9:ASN:ND2	1:AP:14:ASP:OD2	2.38	0.47
1:AR:122:SER:HB2	1:BH:20:VAL:O	2.15	0.47
1:AO:108:LEU:HD11	1:BG:43:LEU:CD1	2.44	0.47
1:AU:6:ILE:HG23	1:BP:111:HIS:CE1	2.50	0.47
1:AX:114:LEU:HA	1:AX:114:LEU:HD23	1.67	0.47
1:AG:99:GLN:HG3	1:AH:119:GLN:NE2	2.30	0.47
1:AP:66:PRO:HA	1:AP:80:THR:HG22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:99:GLN:HG3	1:BL:119:GLN:NE2	2.30	0.47
1:BN:99:GLN:HG3	1:BO:119:GLN:NE2	2.30	0.47
1:AJ:99:GLN:HG3	1:AK:119:GLN:NE2	2.30	0.47
1:AM:99:GLN:HG3	1:AN:119:GLN:NE2	2.30	0.47
1:AP:50:PRO:HB3	1:AP:56:VAL:N	2.30	0.47
1:AY:99:GLN:HG3	1:AZ:119:GLN:NE2	2.30	0.47
1:BN:50:PRO:HB3	1:BN:56:VAL:N	2.30	0.47
1:AJ:9:ASN:ND2	1:AJ:14:ASP:OD2	2.38	0.47
1:AS:99:GLN:HG3	1:AT:119:GLN:NE2	2.30	0.47
1:BB:50:PRO:HB3	1:BB:56:VAL:N	2.30	0.47
1:BH:99:GLN:HG3	1:BI:119:GLN:NE2	2.30	0.47
1:BK:50:PRO:HB3	1:BK:56:VAL:N	2.30	0.47
1:BE:50:PRO:HB3	1:BE:56:VAL:N	2.30	0.47
1:AF:111:HIS:HD2	1:BA:7:VAL:O	1.98	0.47
1:AP:22:ILE:N	1:BJ:125:TYR:CD1	2.83	0.47
1:AV:50:PRO:HB3	1:AV:56:VAL:N	2.30	0.47
1:AC:122:SER:O	1:AC:122:SER:OG	2.33	0.46
1:AF:20:VAL:O	1:BN:123:PRO:CG	2.63	0.46
1:AQ:49:GLN:HG3	1:BA:21:ASN:HB2	1.96	0.46
1:AS:50:PRO:HB3	1:AS:56:VAL:N	2.30	0.46
1:BQ:99:GLN:HG3	1:BR:119:GLN:NE2	2.30	0.46
1:BG:122:SER:O	1:BG:122:SER:OG	2.33	0.46
1:BQ:50:PRO:HB3	1:BQ:56:VAL:N	2.30	0.46
1:AP:99:GLN:HG3	1:AQ:119:GLN:NE2	2.30	0.46
1:AR:47:LEU:HB3	1:BJ:123:PRO:HA	1.97	0.46
1:AR:104:LEU:HG	1:BJ:10:ASP:HA	1.96	0.46
1:AX:125:TYR:CD2	1:BQ:21:ASN:HA	2.50	0.46
1:AB:47:LEU:HD13	1:AB:59:CYS:HB2	1.98	0.46
1:AM:50:PRO:HB3	1:AM:56:VAL:N	2.30	0.46
1:AD:50:PRO:HB3	1:AD:56:VAL:N	2.30	0.46
1:BE:99:GLN:HG3	1:BF:119:GLN:NE2	2.30	0.46
1:BI:47:LEU:HD13	1:BI:59:CYS:HB2	1.98	0.46
1:AD:99:GLN:HG3	1:AE:119:GLN:NE2	2.30	0.46
1:AE:47:LEU:HD13	1:AE:59:CYS:HB2	1.98	0.46
1:AJ:50:PRO:HB3	1:AJ:56:VAL:N	2.30	0.46
1:BC:47:LEU:HD13	1:BC:59:CYS:HB2	1.98	0.46
1:BF:47:LEU:HD13	1:BF:59:CYS:HB2	1.98	0.46
1:AE:123:PRO:HD2	1:BO:20:VAL:HG13	1.96	0.46
1:AF:79:ARG:NH2	1:BA:97:GLU:OE1	2.49	0.46
1:AG:91:GLN:HG3	1:BI:37:ILE:CG2	2.46	0.46
1:AI:81:LEU:HD22	1:BD:89:PHE:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:122:SER:O	1:AO:122:SER:OG	2.33	0.46
1:AW:47:LEU:HD13	1:AW:59:CYS:HB2	1.98	0.46
1:BH:50:PRO:HB3	1:BH:56:VAL:N	2.30	0.46
1:BO:47:LEU:HD13	1:BO:59:CYS:HB2	1.98	0.46
1:AA:99:GLN:HG3	1:AB:119:GLN:NE2	2.30	0.46
1:AF:41:ILE:HD13	1:BA:104:LEU:HD11	1.98	0.46
1:AG:50:PRO:HB3	1:AG:56:VAL:N	2.30	0.46
1:AL:38:LEU:HD23	1:AL:38:LEU:HA	1.81	0.46
1:AQ:47:LEU:HD13	1:AQ:59:CYS:HB2	1.98	0.46
1:BR:47:LEU:HD13	1:BR:59:CYS:HB2	1.98	0.46
1:AA:50:PRO:HB3	1:AA:56:VAL:N	2.30	0.46
1:AV:99:GLN:HG3	1:AW:119:GLN:NE2	2.30	0.46
1:BB:99:GLN:HG3	1:BC:119:GLN:NE2	2.30	0.46
1:AO:99:GLN:HG3	1:BG:119:GLN:HE21	1.81	0.46
1:AQ:22:ILE:O	1:AZ:125:TYR:CE1	2.69	0.46
1:AT:47:LEU:HD13	1:AT:59:CYS:HB2	1.98	0.46
1:BM:114:LEU:HD23	1:BM:114:LEU:HA	1.67	0.46
1:AO:83:GLU:HG2	1:BG:86:GLU:O	2.16	0.45
1:AY:50:PRO:HB3	1:AY:56:VAL:N	2.30	0.45
1:AO:118:VAL:HG21	1:BG:87:VAL:HB	1.97	0.45
1:AR:104:LEU:HD21	1:BJ:10:ASP:HB3	1.98	0.45
1:AZ:47:LEU:HD13	1:AZ:59:CYS:HB2	1.98	0.45
1:BL:47:LEU:HD13	1:BL:59:CYS:HB2	1.98	0.45
1:BM:23:ASP:HB3	1:BM:25:GLU:H	1.82	0.45
1:AU:23:ASP:HB3	1:AU:25:GLU:H	1.82	0.45
1:AU:114:LEU:HD23	1:AU:114:LEU:HA	1.67	0.45
1:AH:47:LEU:HD13	1:AH:59:CYS:HB2	1.98	0.45
1:AO:106:LYS:HD2	1:BG:110:GLY:HA2	1.98	0.45
1:AY:126:GLY:CA	1:BS:3:ILE:HG23	2.45	0.45
1:BP:23:ASP:HB3	1:BP:25:GLU:H	1.82	0.45
1:AK:47:LEU:HD13	1:AK:59:CYS:HB2	1.98	0.45
1:AN:47:LEU:HD13	1:AN:59:CYS:HB2	1.98	0.45
1:BS:122:SER:O	1:BS:122:SER:OG	2.33	0.45
1:AL:114:LEU:HA	1:AL:114:LEU:HD23	1.67	0.45
1:AO:97:GLU:OE1	1:BG:79:ARG:NH2	2.50	0.45
1:AB:108:LEU:HD22	1:AB:114:LEU:CD1	2.47	0.45
1:AF:108:LEU:HD12	1:BA:8:ILE:HG21	1.99	0.45
1:AU:81:LEU:HD12	1:BP:101:VAL:HG23	1.99	0.45
1:AW:114:LEU:HD23	1:AW:114:LEU:HA	1.81	0.45
1:AX:118:VAL:O	1:BS:98:ARG:HD2	2.17	0.45
1:BJ:23:ASP:HB3	1:BJ:25:GLU:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:23:ASP:HB3	1:BS:25:GLU:H	1.82	0.45
1:AI:98:ARG:HB2	1:BD:118:VAL:HG12	1.97	0.45
1:AF:8:ILE:HB	1:BA:107:SER:CB	2.46	0.45
1:AI:23:ASP:HB3	1:AI:25:GLU:H	1.82	0.45
1:AK:108:LEU:HD22	1:AK:114:LEU:CD1	2.47	0.45
1:AL:122:SER:O	1:AL:122:SER:OG	2.33	0.45
1:AP:22:ILE:HB	1:BJ:125:TYR:CD1	2.51	0.45
1:AX:89:PHE:CB	1:BS:81:LEU:HD22	2.47	0.45
1:AX:122:SER:O	1:AX:122:SER:OG	2.33	0.45
1:AZ:108:LEU:HD22	1:AZ:114:LEU:CD1	2.47	0.45
1:BL:108:LEU:HD22	1:BL:114:LEU:CD1	2.47	0.45
1:AT:108:LEU:HD22	1:AT:114:LEU:CD1	2.47	0.44
1:AW:108:LEU:HD22	1:AW:114:LEU:CD1	2.47	0.44
1:BK:38:LEU:HD23	1:BK:38:LEU:HA	1.86	0.44
1:BL:114:LEU:HD23	1:BL:114:LEU:HA	1.81	0.44
1:AQ:108:LEU:HD22	1:AQ:114:LEU:CD1	2.47	0.44
1:AX:23:ASP:HB3	1:AX:25:GLU:H	1.82	0.44
1:BC:108:LEU:HD22	1:BC:114:LEU:CD1	2.47	0.44
1:BO:108:LEU:HD22	1:BO:114:LEU:CD1	2.47	0.44
1:AK:73:ASN:O	1:BC:78:VAL:HG11	2.18	0.44
1:AL:23:ASP:HB3	1:AL:25:GLU:H	1.82	0.44
1:AP:18:GLN:HG3	1:AP:33:LYS:HB2	2.00	0.44
1:AR:23:ASP:HB3	1:AR:25:GLU:H	1.82	0.44
1:BQ:18:GLN:HG3	1:BQ:33:LYS:HB2	2.00	0.44
1:BR:108:LEU:HD22	1:BR:114:LEU:CD1	2.47	0.44
1:AU:104:LEU:HG	1:BP:10:ASP:HA	2.00	0.44
1:AX:125:TYR:HB2	1:BQ:22:ILE:H	1.82	0.44
1:BI:114:LEU:HD23	1:BI:114:LEU:HA	1.81	0.44
1:AE:108:LEU:HD22	1:AE:114:LEU:CD1	2.47	0.44
1:BJ:114:LEU:HA	1:BJ:114:LEU:HD23	1.67	0.44
1:BH:23:ASP:OD1	1:BH:24:ARG:N	2.51	0.44
1:BN:23:ASP:OD1	1:BN:24:ARG:N	2.51	0.44
1:AH:108:LEU:HD22	1:AH:114:LEU:CD1	2.47	0.44
1:AI:120:ASP:O	1:BB:31:ARG:NH2	2.48	0.44
1:AN:108:LEU:HD22	1:AN:114:LEU:CD1	2.47	0.44
1:AP:22:ILE:HG13	1:BJ:125:TYR:CE1	2.53	0.44
1:BD:114:LEU:HD23	1:BD:114:LEU:HA	1.67	0.44
1:BE:18:GLN:HG3	1:BE:33:LYS:HB2	2.00	0.44
1:BI:108:LEU:HD22	1:BI:114:LEU:CD1	2.47	0.44
1:BN:18:GLN:HG3	1:BN:33:LYS:HB2	2.00	0.44
1:AC:23:ASP:HB3	1:AC:25:GLU:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:18:GLN:HG3	1:AJ:33:LYS:HB2	2.00	0.44
1:AU:45:VAL:CG2	1:BP:114:LEU:HD21	2.47	0.44
1:BS:114:LEU:HA	1:BS:114:LEU:HD23	1.67	0.44
1:AF:47:LEU:HB3	1:BA:123:PRO:HB3	2.00	0.44
1:AM:123:PRO:CG	1:AR:20:VAL:O	2.66	0.44
1:AV:23:ASP:OD1	1:AV:24:ARG:N	2.51	0.44
1:AD:18:GLN:HG3	1:AD:33:LYS:HB2	2.00	0.43
1:AD:91:GLN:HG3	1:BO:37:ILE:HG22	2.00	0.43
1:AF:122:SER:O	1:AF:122:SER:OG	2.33	0.43
1:AG:23:ASP:OD1	1:AG:24:ARG:N	2.51	0.43
1:AR:87:VAL:HG11	1:BJ:118:VAL:HG11	2.00	0.43
1:AS:23:ASP:OD1	1:AS:24:ARG:N	2.51	0.43
1:AY:18:GLN:HG3	1:AY:33:LYS:HB2	2.00	0.43
1:AZ:114:LEU:HD23	1:AZ:114:LEU:HA	1.81	0.43
1:BE:23:ASP:OD1	1:BE:24:ARG:N	2.51	0.43
1:BF:108:LEU:HD22	1:BF:114:LEU:CD1	2.47	0.43
1:BK:23:ASP:OD1	1:BK:24:ARG:N	2.51	0.43
1:AD:23:ASP:OD1	1:AD:24:ARG:N	2.51	0.43
1:AF:23:ASP:HB3	1:AF:25:GLU:H	1.82	0.43
1:AG:70:VAL:HG22	1:AG:75:ARG:HG2	2.00	0.43
1:AO:23:ASP:HB3	1:AO:25:GLU:H	1.82	0.43
1:AP:22:ILE:HG13	1:BJ:125:TYR:CD1	2.54	0.43
1:AR:114:LEU:HA	1:AR:114:LEU:HD23	1.67	0.43
1:AT:120:ASP:O	1:AW:31:ARG:NH2	2.51	0.43
1:AY:23:ASP:OD1	1:AY:24:ARG:N	2.51	0.43
1:BD:23:ASP:HB3	1:BD:25:GLU:H	1.82	0.43
1:AA:18:GLN:HG3	1:AA:33:LYS:HB2	2.00	0.43
1:AE:120:ASP:O	1:BO:31:ARG:NH2	2.51	0.43
1:AG:108:LEU:HD13	1:AH:8:ILE:HD13	2.00	0.43
1:BA:23:ASP:HB3	1:BA:25:GLU:H	1.82	0.43
1:BB:18:GLN:HG3	1:BB:33:LYS:HB2	2.00	0.43
1:BD:38:LEU:HD23	1:BD:38:LEU:HA	1.81	0.43
1:AA:108:LEU:HD13	1:AB:8:ILE:HD13	2.01	0.43
1:AD:108:LEU:HD13	1:AE:8:ILE:HD13	2.01	0.43
1:AR:99:GLN:HA	1:BJ:119:GLN:HG2	2.00	0.43
1:BG:23:ASP:HB3	1:BG:25:GLU:H	1.82	0.43
1:BH:108:LEU:HD13	1:BI:8:ILE:HD13	2.01	0.43
1:AG:20:VAL:O	1:BD:125:TYR:CE2	2.71	0.43
1:AO:97:GLU:OE2	1:BG:79:ARG:NE	2.38	0.43
1:AV:108:LEU:HD13	1:AW:8:ILE:HD13	2.01	0.43
1:BA:32:GLU:HB3	1:BA:40:ALA:HB1	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:38:LEU:HD23	1:BB:38:LEU:HA	1.86	0.43
1:AA:70:VAL:HG22	1:AA:75:ARG:HG2	2.01	0.43
1:AO:117:VAL:O	1:BG:47:LEU:HD22	2.19	0.43
1:AO:117:VAL:CG1	1:BG:47:LEU:HB2	2.49	0.43
1:AP:108:LEU:HD13	1:AQ:8:ILE:HD13	2.01	0.43
1:AU:47:LEU:CD2	1:BP:122:SER:N	2.82	0.43
1:AY:70:VAL:HG22	1:AY:75:ARG:HG2	2.00	0.43
1:BH:70:VAL:HG22	1:BH:75:ARG:HG2	2.00	0.43
1:BJ:15:ILE:HG23	1:BJ:32:GLU:HG3	2.01	0.43
1:BK:108:LEU:HD13	1:BL:8:ILE:HD13	2.01	0.43
1:AD:20:VAL:O	1:BA:122:SER:HB2	2.18	0.43
1:AF:32:GLU:HB3	1:AF:40:ALA:HB1	2.01	0.43
1:AF:38:LEU:HD23	1:AF:38:LEU:HA	1.81	0.43
1:AM:70:VAL:HG22	1:AM:75:ARG:HG2	2.00	0.43
1:AQ:49:GLN:NE2	1:BA:20:VAL:HG13	2.34	0.43
1:AY:108:LEU:HD13	1:AZ:8:ILE:HD13	2.01	0.43
1:BA:15:ILE:HG23	1:BA:32:GLU:HG3	2.01	0.43
1:BB:23:ASP:OD1	1:BB:24:ARG:N	2.51	0.43
1:BD:15:ILE:HG23	1:BD:32:GLU:HG3	2.01	0.43
1:BH:18:GLN:HG3	1:BH:33:LYS:HB2	2.00	0.43
1:BJ:32:GLU:HB3	1:BJ:40:ALA:HB1	2.01	0.43
1:BO:36:SER:HB3	1:BO:39:GLU:HG2	2.01	0.43
1:BQ:23:ASP:OD1	1:BQ:24:ARG:N	2.51	0.43
1:AC:15:ILE:HG23	1:AC:32:GLU:HG3	2.01	0.43
1:AF:122:SER:OG	1:BA:1:PRO:N	2.49	0.43
1:AL:15:ILE:HG23	1:AL:32:GLU:HG3	2.01	0.43
1:AM:18:GLN:HG3	1:AM:33:LYS:HB2	2.00	0.43
1:AM:23:ASP:OD1	1:AM:24:ARG:N	2.51	0.43
1:AN:114:LEU:HD23	1:AN:114:LEU:HA	1.81	0.43
1:AQ:36:SER:HB3	1:AQ:39:GLU:HG2	2.01	0.43
1:AS:70:VAL:HG22	1:AS:75:ARG:HG2	2.00	0.43
1:AS:108:LEU:HD13	1:AT:8:ILE:HD13	2.01	0.43
1:AU:15:ILE:HG23	1:AU:32:GLU:HG3	2.01	0.43
1:BG:15:ILE:HG23	1:BG:32:GLU:HG3	2.01	0.43
1:BK:70:VAL:HG22	1:BK:75:ARG:HG2	2.00	0.43
1:AL:32:GLU:HB3	1:AL:40:ALA:HB1	2.01	0.43
1:AR:15:ILE:HG23	1:AR:32:GLU:HG3	2.01	0.43
1:AV:18:GLN:HG3	1:AV:33:LYS:HB2	2.00	0.43
1:AZ:36:SER:HB3	1:AZ:39:GLU:CG	2.49	0.43
1:BB:108:LEU:HD13	1:BC:8:ILE:HD13	2.01	0.43
1:BI:36:SER:HB3	1:BI:39:GLU:CG	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:32:GLU:HB3	1:BM:40:ALA:HB1	2.01	0.43
1:AC:114:LEU:HD23	1:AC:114:LEU:HA	1.67	0.43
1:AE:36:SER:HB3	1:AE:39:GLU:CG	2.49	0.43
1:AF:81:LEU:HD12	1:BA:101:VAL:HG23	2.01	0.43
1:AH:114:LEU:HD23	1:AH:114:LEU:HA	1.81	0.43
1:AJ:23:ASP:OD1	1:AJ:24:ARG:N	2.51	0.43
1:AO:15:ILE:HG23	1:AO:32:GLU:HG3	2.01	0.43
1:AR:32:GLU:HB3	1:AR:40:ALA:HB1	2.01	0.43
1:AU:107:SER:CB	1:BP:9:ASN:H	2.32	0.43
1:AV:70:VAL:HG22	1:AV:75:ARG:HG2	2.00	0.43
1:BA:94:LEU:HD12	1:BA:95:GLY:H	1.84	0.43
1:BI:36:SER:HB3	1:BI:39:GLU:HG2	2.01	0.43
1:AD:70:VAL:HG22	1:AD:75:ARG:HG2	2.00	0.42
1:AE:36:SER:HB3	1:AE:39:GLU:HG2	2.01	0.42
1:AH:36:SER:HB3	1:AH:39:GLU:CG	2.49	0.42
1:AN:36:SER:HB3	1:AN:39:GLU:HG2	2.01	0.42
1:AP:70:VAL:HG22	1:AP:75:ARG:HG2	2.01	0.42
1:AX:15:ILE:HG23	1:AX:32:GLU:HG3	2.01	0.42
1:BE:38:LEU:HD23	1:BE:38:LEU:HA	1.86	0.42
1:BJ:122:SER:O	1:BJ:122:SER:OG	2.33	0.42
1:BP:15:ILE:HG23	1:BP:32:GLU:HG3	2.01	0.42
1:BP:122:SER:O	1:BP:122:SER:OG	2.33	0.42
1:AG:18:GLN:HG3	1:AG:33:LYS:HB2	2.00	0.42
1:AJ:70:VAL:HG22	1:AJ:75:ARG:HG2	2.00	0.42
1:AO:32:GLU:HB3	1:AO:40:ALA:HB1	2.01	0.42
1:AS:18:GLN:HG3	1:AS:33:LYS:HB2	2.00	0.42
1:AY:38:LEU:HD23	1:AY:38:LEU:HA	1.86	0.42
1:BM:15:ILE:HG23	1:BM:32:GLU:HG3	2.01	0.42
1:BP:32:GLU:HB3	1:BP:40:ALA:HB1	2.01	0.42
1:AB:36:SER:HB3	1:AB:39:GLU:CG	2.49	0.42
1:AH:36:SER:HB3	1:AH:39:GLU:HG2	2.01	0.42
1:AL:21:ASN:OD1	1:AL:22:ILE:N	2.53	0.42
1:AW:36:SER:HB3	1:AW:39:GLU:CG	2.49	0.42
1:BE:108:LEU:HD13	1:BF:8:ILE:HD13	2.01	0.42
1:BG:94:LEU:HD12	1:BG:95:GLY:H	1.84	0.42
1:BK:18:GLN:HG3	1:BK:33:LYS:HB2	2.00	0.42
1:BQ:70:VAL:HG22	1:BQ:75:ARG:HG2	2.00	0.42
1:BR:36:SER:HB3	1:BR:39:GLU:CG	2.49	0.42
1:AF:125:TYR:O	1:BA:3:ILE:CG2	2.67	0.42
1:AO:21:ASN:OD1	1:AO:22:ILE:N	2.53	0.42
1:AT:36:SER:HB3	1:AT:39:GLU:CG	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AX:120:ASP:O	1:BQ:31:ARG:NH2	2.51	0.42
1:BD:32:GLU:HB3	1:BD:40:ALA:HB1	2.01	0.42
1:BG:32:GLU:HB3	1:BG:40:ALA:HB1	2.01	0.42
1:BQ:108:LEU:HD13	1:BR:8:ILE:HD13	2.01	0.42
1:BR:114:LEU:HD23	1:BR:114:LEU:HA	1.81	0.42
1:AC:21:ASN:OD1	1:AC:22:ILE:N	2.53	0.42
1:AF:15:ILE:HG23	1:AF:32:GLU:HG3	2.01	0.42
1:AI:32:GLU:HB3	1:AI:40:ALA:HB1	2.01	0.42
1:AN:36:SER:HB3	1:AN:39:GLU:CG	2.49	0.42
1:AO:94:LEU:HD12	1:AO:95:GLY:H	1.84	0.42
1:AQ:36:SER:HB3	1:AQ:39:GLU:CG	2.49	0.42
1:AR:47:LEU:HB3	1:BJ:123:PRO:CA	2.50	0.42
1:AX:21:ASN:OD1	1:AX:22:ILE:N	2.53	0.42
1:BB:70:VAL:HG22	1:BB:75:ARG:HG2	2.00	0.42
1:BL:36:SER:HB3	1:BL:39:GLU:HG2	2.01	0.42
1:BM:21:ASN:OD1	1:BM:22:ILE:N	2.53	0.42
1:BO:36:SER:HB3	1:BO:39:GLU:CG	2.49	0.42
1:BR:36:SER:HB3	1:BR:39:GLU:HG2	2.01	0.42
1:AA:23:ASP:OD1	1:AA:24:ARG:N	2.51	0.42
1:AC:18:GLN:HA	1:AC:19:PRO:HD3	1.94	0.42
1:AF:79:ARG:HH21	1:BA:97:GLU:CD	2.28	0.42
1:AP:23:ASP:OD1	1:AP:24:ARG:N	2.51	0.42
1:AT:36:SER:HB3	1:AT:39:GLU:HG2	2.01	0.42
1:AU:94:LEU:HD12	1:AU:95:GLY:H	1.84	0.42
1:AC:94:LEU:HD12	1:AC:95:GLY:H	1.84	0.42
1:AF:21:ASN:OD1	1:AF:22:ILE:N	2.53	0.42
1:AF:63:LEU:CD2	1:BA:104:LEU:HB3	2.48	0.42
1:AI:8:ILE:HG13	1:BD:104:LEU:CD2	2.49	0.42
1:AI:15:ILE:HG23	1:AI:32:GLU:HG3	2.01	0.42
1:AI:21:ASN:OD1	1:AI:22:ILE:N	2.53	0.42
1:AR:21:ASN:OD1	1:AR:22:ILE:N	2.53	0.42
1:AR:71:VAL:HG22	1:BH:73:ASN:ND2	2.21	0.42
1:AU:81:LEU:CB	1:BP:101:VAL:HG21	2.49	0.42
1:BA:21:ASN:OD1	1:BA:22:ILE:N	2.53	0.42
1:BE:70:VAL:HG22	1:BE:75:ARG:HG2	2.00	0.42
1:BM:122:SER:O	1:BM:122:SER:OG	2.33	0.42
1:AB:36:SER:HB3	1:AB:39:GLU:HG2	2.01	0.42
1:AB:125:TYR:OH	1:BR:22:ILE:HB	2.20	0.42
1:AF:92:ASP:OD1	1:AF:92:ASP:N	2.53	0.42
1:AF:94:LEU:HD12	1:AF:95:GLY:H	1.84	0.42
1:AI:114:LEU:HA	1:AI:114:LEU:HD23	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:36:SER:HB3	1:AK:39:GLU:HG2	2.01	0.42
1:AP:24:ARG:NH2	1:BJ:126:GLY:OXT	2.52	0.42
1:AX:32:GLU:HB3	1:AX:40:ALA:HB1	2.01	0.42
1:BC:36:SER:HB3	1:BC:39:GLU:CG	2.49	0.42
1:BD:21:ASN:OD1	1:BD:22:ILE:N	2.53	0.42
1:BL:36:SER:HB3	1:BL:39:GLU:CG	2.49	0.42
1:BN:70:VAL:HG22	1:BN:75:ARG:HG2	2.00	0.42
1:BS:32:GLU:HB3	1:BS:40:ALA:HB1	2.01	0.42
1:AR:105:THR:HG22	1:BJ:109:ALA:HB1	2.02	0.42
1:AU:123:PRO:HD3	1:BP:47:LEU:HD23	2.01	0.42
1:BD:92:ASP:OD1	1:BD:92:ASP:N	2.53	0.42
1:BJ:94:LEU:HD12	1:BJ:95:GLY:H	1.84	0.42
1:BM:94:LEU:HD12	1:BM:95:GLY:H	1.85	0.42
1:BS:18:GLN:HA	1:BS:19:PRO:HD3	1.94	0.42
1:BS:94:LEU:HD12	1:BS:95:GLY:H	1.84	0.42
1:AC:32:GLU:HB3	1:AC:40:ALA:HB1	2.01	0.42
1:AK:36:SER:HB3	1:AK:39:GLU:CG	2.49	0.42
1:AL:94:LEU:HD12	1:AL:95:GLY:H	1.84	0.42
1:AM:108:LEU:HD13	1:AN:8:ILE:HD13	2.01	0.42
1:AU:21:ASN:OD1	1:AU:22:ILE:N	2.53	0.42
1:BF:36:SER:HB3	1:BF:39:GLU:CG	2.49	0.42
1:BG:21:ASN:OD1	1:BG:22:ILE:N	2.53	0.42
1:BN:18:GLN:HA	1:BN:19:PRO:HD3	1.96	0.42
1:AA:10:ASP:OD2	1:AB:100:ARG:HD2	2.20	0.41
1:AD:10:ASP:OD2	1:AE:100:ARG:HD2	2.20	0.41
1:AJ:10:ASP:OD2	1:AK:100:ARG:HD2	2.20	0.41
1:AO:114:LEU:HD21	1:BG:45:VAL:HG13	2.02	0.41
1:AR:94:LEU:HD12	1:AR:95:GLY:H	1.84	0.41
1:AS:15:ILE:HG23	1:AS:32:GLU:HG3	2.02	0.41
1:AU:22:ILE:HD13	1:BP:126:GLY:N	2.35	0.41
1:BN:15:ILE:HG23	1:BN:32:GLU:HG3	2.02	0.41
1:BN:108:LEU:HD13	1:BO:8:ILE:HD13	2.01	0.41
1:AF:122:SER:HB2	1:AY:20:VAL:O	2.20	0.41
1:AG:20:VAL:C	1:BD:125:TYR:CE2	2.98	0.41
1:AM:10:ASP:OD2	1:AN:100:ARG:HD2	2.20	0.41
1:AO:115:MET:CE	1:BG:102:ALA:HB1	2.50	0.41
1:AS:10:ASP:OD2	1:AT:100:ARG:HD2	2.20	0.41
1:AU:32:GLU:HB3	1:AU:40:ALA:HB1	2.01	0.41
1:BH:10:ASP:OD2	1:BI:100:ARG:HD2	2.20	0.41
1:AF:81:LEU:CD1	1:BA:101:VAL:HG21	2.50	0.41
1:AI:38:LEU:HD23	1:AI:38:LEU:HA	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:104:LEU:HD12	1:BG:65:VAL:HG21	2.00	0.41
1:AU:113:THR:O	1:AU:117:VAL:HG23	2.21	0.41
1:AX:89:PHE:HB2	1:BS:81:LEU:HD22	2.01	0.41
1:AY:15:ILE:HG23	1:AY:32:GLU:HG3	2.02	0.41
1:BA:113:THR:O	1:BA:117:VAL:HG23	2.21	0.41
1:BB:10:ASP:OD2	1:BC:100:ARG:HD2	2.20	0.41
1:BF:36:SER:HB3	1:BF:39:GLU:HG2	2.01	0.41
1:BQ:18:GLN:HA	1:BQ:19:PRO:HD3	1.96	0.41
1:AA:38:LEU:HD23	1:AA:38:LEU:HA	1.86	0.41
1:AG:10:ASP:OD2	1:AH:100:ARG:HD2	2.20	0.41
1:AI:94:LEU:HD12	1:AI:95:GLY:H	1.84	0.41
1:AJ:108:LEU:HD13	1:AK:8:ILE:HD13	2.01	0.41
1:AL:113:THR:O	1:AL:117:VAL:HG23	2.21	0.41
1:AO:113:THR:O	1:AO:117:VAL:HG23	2.21	0.41
1:AP:15:ILE:HG23	1:AP:32:GLU:HG3	2.02	0.41
1:AQ:24:ARG:HB2	1:AY:24:ARG:NE	2.29	0.41
1:BK:10:ASP:OD2	1:BL:100:ARG:HD2	2.20	0.41
1:BQ:15:ILE:HG23	1:BQ:32:GLU:HG3	2.02	0.41
1:BS:15:ILE:HG23	1:BS:32:GLU:HG3	2.01	0.41
1:BS:21:ASN:OD1	1:BS:22:ILE:N	2.53	0.41
1:AU:104:LEU:HD21	1:BP:10:ASP:HB3	2.01	0.41
1:AY:10:ASP:OD2	1:AZ:100:ARG:HD2	2.20	0.41
1:BD:122:SER:O	1:BD:122:SER:OG	2.33	0.41
1:BG:108:LEU:HG	1:BG:114:LEU:CD1	2.51	0.41
1:BJ:113:THR:O	1:BJ:117:VAL:HG23	2.21	0.41
1:AF:113:THR:O	1:AF:117:VAL:HG23	2.21	0.41
1:AF:114:LEU:HA	1:AF:114:LEU:HD23	1.67	0.41
1:AI:108:LEU:HG	1:AI:114:LEU:CD1	2.51	0.41
1:AK:114:LEU:HD23	1:AK:114:LEU:HA	1.81	0.41
1:AN:37:ILE:HG22	1:AP:91:GLN:CG	2.51	0.41
1:AX:89:PHE:CA	1:BS:81:LEU:HD22	2.50	0.41
1:AX:108:LEU:HG	1:AX:114:LEU:CD1	2.51	0.41
1:BE:10:ASP:OD2	1:BF:100:ARG:HD2	2.20	0.41
1:BG:113:THR:O	1:BG:117:VAL:HG23	2.21	0.41
1:BH:15:ILE:HG23	1:BH:32:GLU:HG3	2.02	0.41
1:BJ:21:ASN:OD1	1:BJ:22:ILE:N	2.53	0.41
1:BP:21:ASN:OD1	1:BP:22:ILE:N	2.53	0.41
1:BQ:101:VAL:HG21	1:BR:81:LEU:HB2	2.03	0.41
1:AJ:15:ILE:HG23	1:AJ:32:GLU:HG3	2.02	0.41
1:AR:113:THR:O	1:AR:117:VAL:HG23	2.21	0.41
1:AS:38:LEU:HD23	1:AS:38:LEU:HA	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AX:94:LEU:HD12	1:AX:95:GLY:H	1.85	0.41
1:BB:101:VAL:HG21	1:BC:81:LEU:HB2	2.03	0.41
1:BC:36:SER:HB3	1:BC:39:GLU:HG2	2.01	0.41
1:BN:10:ASP:OD2	1:BO:100:ARG:HD2	2.20	0.41
1:AI:113:THR:O	1:AI:117:VAL:HG23	2.21	0.41
1:AM:15:ILE:HG23	1:AM:32:GLU:HG3	2.03	0.41
1:AO:111:HIS:CD2	1:BG:6:ILE:HG23	2.55	0.41
1:AQ:49:GLN:HG2	1:BA:21:ASN:HB2	2.03	0.41
1:AR:63:LEU:HD21	1:BJ:104:LEU:CD1	2.49	0.41
1:AW:36:SER:HB3	1:AW:39:GLU:HG2	2.01	0.41
1:AC:113:THR:O	1:AC:117:VAL:HG23	2.21	0.41
1:AF:108:LEU:HG	1:AF:114:LEU:CD1	2.51	0.41
1:AG:101:VAL:HG21	1:AH:81:LEU:HB2	2.03	0.41
1:AO:18:GLN:HA	1:AO:19:PRO:HD3	1.94	0.41
1:AR:38:LEU:HD23	1:AR:38:LEU:HA	1.81	0.41
1:AR:79:ARG:NE	1:BJ:93:SER:HA	2.36	0.41
1:AU:90:THR:OG1	1:BP:79:ARG:HD2	2.21	0.41
1:AY:101:VAL:HG21	1:AZ:81:LEU:HB2	2.03	0.41
1:AZ:36:SER:HB3	1:AZ:39:GLU:HG2	2.01	0.41
1:BN:38:LEU:HD23	1:BN:38:LEU:HA	1.86	0.41
1:BP:38:LEU:HA	1:BP:38:LEU:HD23	1.81	0.41
1:BP:94:LEU:HD12	1:BP:95:GLY:H	1.84	0.41
1:BP:113:THR:O	1:BP:117:VAL:HG23	2.21	0.41
1:BP:114:LEU:HD23	1:BP:114:LEU:HA	1.67	0.41
1:AD:101:VAL:HG21	1:AE:81:LEU:HB2	2.03	0.41
1:AS:101:VAL:HG21	1:AT:81:LEU:HB2	2.03	0.41
1:AX:113:THR:O	1:AX:117:VAL:HG23	2.21	0.41
1:BD:113:THR:O	1:BD:117:VAL:HG23	2.21	0.41
1:BP:108:LEU:HG	1:BP:114:LEU:CD1	2.51	0.41
1:BQ:10:ASP:OD2	1:BR:100:ARG:HD2	2.20	0.41
1:AF:71:VAL:HG22	1:AY:73:ASN:HD22	1.86	0.40
1:AP:10:ASP:OD2	1:AQ:100:ARG:HD2	2.20	0.40
1:AQ:37:ILE:CD1	1:AY:98:ARG:NH2	2.84	0.40
1:BD:108:LEU:HG	1:BD:114:LEU:CD1	2.51	0.40
1:BS:108:LEU:HG	1:BS:114:LEU:CD1	2.51	0.40
1:AM:101:VAL:HG21	1:AN:81:LEU:HB2	2.03	0.40
1:AQ:91:GLN:HG3	1:BA:37:ILE:CG2	2.51	0.40
1:AU:28:ALA:HB2	1:BP:124:ILE:HB	2.03	0.40
1:AV:15:ILE:HG23	1:AV:32:GLU:HG3	2.03	0.40
1:BD:94:LEU:HD12	1:BD:95:GLY:H	1.84	0.40
1:AF:45:VAL:CG2	1:BA:114:LEU:HD21	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:65:VAL:HG21	1:BD:101:VAL:HG22	2.03	0.40
1:AO:108:LEU:HG	1:AO:114:LEU:CD1	2.51	0.40
1:AR:108:LEU:HG	1:AR:114:LEU:CD1	2.51	0.40
1:BB:15:ILE:HG23	1:BB:32:GLU:HG3	2.02	0.40
1:BS:113:THR:O	1:BS:117:VAL:HG23	2.21	0.40
1:AC:108:LEU:HG	1:AC:114:LEU:CD1	2.51	0.40
1:AQ:91:GLN:HG3	1:BA:37:ILE:HG21	2.03	0.40
1:AS:48:ARG:HD3	1:AS:58:ARG:HD2	2.04	0.40
1:AV:10:ASP:OD2	1:AW:100:ARG:HD2	2.20	0.40
1:AX:100:ARG:NE	1:BS:10:ASP:OD2	2.55	0.40
1:BE:48:ARG:HD3	1:BE:58:ARG:HD2	2.04	0.40
1:BH:48:ARG:HD3	1:BH:58:ARG:HD2	2.04	0.40
1:BJ:108:LEU:HG	1:BJ:114:LEU:CD1	2.51	0.40
1:AK:80:THR:O	1:AK:81:LEU:HD23	2.22	0.40
1:AL:108:LEU:HG	1:AL:114:LEU:CD1	2.51	0.40
1:AR:124:ILE:HG22	1:BJ:3:ILE:HB	2.04	0.40
1:AT:114:LEU:HD23	1:AT:114:LEU:HA	1.81	0.40
1:AU:22:ILE:HD13	1:BP:125:TYR:C	2.47	0.40
1:BK:15:ILE:HG23	1:BK:32:GLU:HG3	2.02	0.40
1:BQ:32:GLU:HB3	1:BQ:40:ALA:HB1	2.04	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:125:TYR:OH	1:BM:126:GLY:O[2_555]	1.74	0.46
1:AB:125:TYR:OH	1:AC:126:GLY:O[3_555]	2.00	0.20
1:BM:3:ILE:N	1:BM:125:TYR:O[2_555]	2.12	0.08
1:BM:1:PRO:N	1:BM:123:PRO:O[2_555]	2.16	0.04

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	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AB	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	AC	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AD	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AE	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	AF	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AG	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AH	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	AI	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AJ	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AK	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	AL	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AM	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AN	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	AO	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AP	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AQ	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	AR	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AS	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AT	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	AU	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AV	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AW	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	AX	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AY	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	AZ	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	BA	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	BB	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	BC	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	BD	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	BE	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	BF	124/126 (98%)	121 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BG	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	BH	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	BI	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	BJ	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	BK	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	BL	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	BM	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	BN	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	BO	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	BP	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	BQ	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
1	BR	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
1	BS	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
All	All	5580/5670 (98%)	5475 (98%)	105 (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	111/111 (100%)	111 (100%)	0	100	100
1	AB	111/111 (100%)	111 (100%)	0	100	100
1	AC	111/111 (100%)	111 (100%)	0	100	100
1	AD	111/111 (100%)	111 (100%)	0	100	100
1	AE	111/111 (100%)	111 (100%)	0	100	100
1	AF	111/111 (100%)	111 (100%)	0	100	100
1	AG	111/111 (100%)	111 (100%)	0	100	100
1	AH	111/111 (100%)	111 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AI	111/111 (100%)	111 (100%)	0	100	100
1	AJ	111/111 (100%)	111 (100%)	0	100	100
1	AK	111/111 (100%)	111 (100%)	0	100	100
1	AL	111/111 (100%)	111 (100%)	0	100	100
1	AM	111/111 (100%)	111 (100%)	0	100	100
1	AN	111/111 (100%)	111 (100%)	0	100	100
1	AO	111/111 (100%)	111 (100%)	0	100	100
1	AP	111/111 (100%)	111 (100%)	0	100	100
1	AQ	111/111 (100%)	111 (100%)	0	100	100
1	AR	111/111 (100%)	111 (100%)	0	100	100
1	AS	111/111 (100%)	111 (100%)	0	100	100
1	AT	111/111 (100%)	111 (100%)	0	100	100
1	AU	111/111 (100%)	111 (100%)	0	100	100
1	AV	111/111 (100%)	111 (100%)	0	100	100
1	AW	111/111 (100%)	111 (100%)	0	100	100
1	AX	111/111 (100%)	111 (100%)	0	100	100
1	AY	111/111 (100%)	111 (100%)	0	100	100
1	AZ	111/111 (100%)	111 (100%)	0	100	100
1	BA	111/111 (100%)	111 (100%)	0	100	100
1	BB	111/111 (100%)	111 (100%)	0	100	100
1	BC	111/111 (100%)	111 (100%)	0	100	100
1	BD	111/111 (100%)	111 (100%)	0	100	100
1	BE	111/111 (100%)	111 (100%)	0	100	100
1	BF	111/111 (100%)	111 (100%)	0	100	100
1	BG	111/111 (100%)	111 (100%)	0	100	100
1	BH	111/111 (100%)	111 (100%)	0	100	100
1	BI	111/111 (100%)	111 (100%)	0	100	100
1	BJ	111/111 (100%)	111 (100%)	0	100	100
1	BK	111/111 (100%)	111 (100%)	0	100	100
1	BL	111/111 (100%)	111 (100%)	0	100	100
1	BM	111/111 (100%)	111 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BN	111/111 (100%)	111 (100%)	0	100	100
1	BO	111/111 (100%)	111 (100%)	0	100	100
1	BP	111/111 (100%)	111 (100%)	0	100	100
1	BQ	111/111 (100%)	111 (100%)	0	100	100
1	BR	111/111 (100%)	111 (100%)	0	100	100
1	BS	111/111 (100%)	111 (100%)	0	100	100
All	All	4995/4995 (100%)	4995 (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 (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	AB	49	GLN
1	AE	49	GLN
1	AM	73	ASN
1	AN	49	GLN
1	AP	29	HIS
1	AQ	49	GLN
1	AU	49	GLN
1	AW	49	GLN
1	AX	49	GLN
1	AX	119	GLN
1	AZ	49	GLN
1	BC	49	GLN
1	BD	119	GLN
1	BF	49	GLN
1	BG	49	GLN
1	BG	119	GLN
1	BH	73	ASN
1	BJ	49	GLN
1	BL	49	GLN
1	BM	49	GLN
1	BQ	29	HIS
1	BS	49	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	126/126 (100%)	0.59	10 (7%) 18 10	43, 70, 145, 230	0
1	AB	126/126 (100%)	0.22	4 (3%) 50 28	41, 65, 115, 171	0
1	AC	126/126 (100%)	0.93	14 (11%) 10 5	51, 83, 156, 194	0
1	AD	126/126 (100%)	0.54	7 (5%) 30 15	43, 70, 145, 230	0
1	AE	126/126 (100%)	0.36	7 (5%) 30 15	41, 65, 115, 171	0
1	AF	126/126 (100%)	1.71	38 (30%) 1 1	51, 83, 156, 194	0
1	AG	126/126 (100%)	0.42	6 (4%) 35 18	43, 70, 145, 230	0
1	AH	126/126 (100%)	0.39	7 (5%) 30 15	41, 65, 115, 171	0
1	AI	126/126 (100%)	1.59	38 (30%) 1 1	51, 83, 156, 194	0
1	AJ	126/126 (100%)	0.48	4 (3%) 50 28	43, 70, 145, 230	0
1	AK	126/126 (100%)	0.26	3 (2%) 59 37	41, 65, 115, 171	0
1	AL	126/126 (100%)	1.00	12 (9%) 14 7	51, 83, 156, 194	0
1	AM	126/126 (100%)	1.66	49 (38%) 1 0	43, 70, 145, 230	0
1	AN	126/126 (100%)	1.20	24 (19%) 3 2	41, 65, 115, 171	0
1	AO	126/126 (100%)	2.33	64 (50%) 0 0	51, 83, 156, 194	0
1	AP	126/126 (100%)	1.00	18 (14%) 6 4	43, 70, 145, 230	0
1	AQ	126/126 (100%)	0.94	21 (16%) 4 2	41, 65, 115, 171	0
1	AR	126/126 (100%)	1.45	39 (30%) 1 1	51, 83, 156, 194	0
1	AS	126/126 (100%)	0.37	6 (4%) 35 18	43, 70, 145, 230	0
1	AT	126/126 (100%)	0.13	2 (1%) 70 47	41, 65, 115, 171	0
1	AU	126/126 (100%)	0.94	16 (12%) 8 5	51, 83, 156, 194	0
1	AV	126/126 (100%)	0.48	10 (7%) 18 10	43, 70, 145, 230	0
1	AW	126/126 (100%)	0.18	3 (2%) 59 37	41, 65, 115, 171	0
1	AX	126/126 (100%)	1.37	27 (21%) 2 1	51, 83, 156, 194	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AY	126/126 (100%)	1.08	26 (20%) 2 1	43, 70, 145, 230	0
1	AZ	126/126 (100%)	0.85	20 (15%) 5 2	41, 65, 115, 171	0
1	BA	126/126 (100%)	1.57	37 (29%) 1 1	51, 83, 156, 194	0
1	BB	126/126 (100%)	0.57	13 (10%) 12 6	43, 70, 145, 230	0
1	BC	126/126 (100%)	0.32	5 (3%) 42 23	41, 65, 115, 171	0
1	BD	126/126 (100%)	1.47	34 (26%) 1 1	51, 83, 156, 194	0
1	BE	126/126 (100%)	1.21	29 (23%) 2 1	43, 70, 145, 230	0
1	BF	126/126 (100%)	0.92	21 (16%) 4 2	41, 65, 115, 171	0
1	BG	126/126 (100%)	1.96	48 (38%) 1 0	51, 83, 156, 194	0
1	BH	126/126 (100%)	1.23	25 (19%) 3 2	43, 70, 145, 230	0
1	BI	126/126 (100%)	0.87	17 (13%) 7 4	41, 65, 115, 171	0
1	BJ	126/126 (100%)	1.96	48 (38%) 1 0	51, 83, 156, 194	0
1	BK	126/126 (100%)	0.60	9 (7%) 22 11	43, 70, 145, 230	0
1	BL	126/126 (100%)	0.25	6 (4%) 35 18	41, 65, 115, 171	0
1	BM	126/126 (100%)	1.11	25 (19%) 3 2	51, 83, 156, 194	0
1	BN	126/126 (100%)	1.34	34 (26%) 1 1	43, 70, 145, 230	0
1	BO	126/126 (100%)	0.74	13 (10%) 12 6	41, 65, 115, 171	0
1	BP	126/126 (100%)	1.60	37 (29%) 1 1	51, 83, 156, 194	0
1	BQ	126/126 (100%)	0.48	8 (6%) 26 13	43, 70, 145, 230	0
1	BR	126/126 (100%)	0.17	1 (0%) 82 63	41, 65, 115, 171	0
1	BS	126/126 (100%)	1.29	26 (20%) 2 1	51, 83, 156, 194	0
All	All	5670/5670 (100%)	0.94	911 (16%) 4 2	41, 73, 146, 230	0

All (911) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AO	121	ALA	10.5
1	BJ	121	ALA	10.3
1	BJ	126	GLY	9.3
1	AF	126	GLY	8.9
1	AO	123	PRO	8.1
1	BA	126	GLY	8.0
1	BP	126	GLY	7.9
1	BD	126	GLY	7.8
1	AO	122	SER	7.8

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Mol	Chain	Res	Type	RSRZ
1	AO	125	TYR	7.6
1	AO	114	LEU	7.3
1	BS	126	GLY	7.2
1	AO	124	ILE	6.9
1	BJ	125	TYR	6.8
1	BG	14	ASP	6.6
1	AF	125	TYR	6.6
1	AO	126	GLY	6.6
1	BJ	122	SER	6.4
1	BA	124	ILE	6.2
1	AO	111	HIS	6.1
1	AO	113	THR	6.0
1	BG	122	SER	6.0
1	BJ	118	VAL	6.0
1	BJ	124	ILE	5.8
1	AO	118	VAL	5.8
1	BP	124	ILE	5.8
1	BM	122	SER	5.7
1	BG	126	GLY	5.7
1	BG	112	ALA	5.7
1	BD	125	TYR	5.6
1	BP	122	SER	5.5
1	BA	125	TYR	5.4
1	BP	121	ALA	5.4
1	AM	18	GLN	5.3
1	BJ	123	PRO	5.3
1	BG	110	GLY	5.3
1	BG	113	THR	5.3
1	BP	125	TYR	5.3
1	AF	121	ALA	5.3
1	BG	124	ILE	5.3
1	BH	39	GLU	5.3
1	AX	73	ASN	5.2
1	BA	121	ALA	5.2
1	BD	78	VAL	5.1
1	BP	123	PRO	5.1
1	BD	94	LEU	5.1
1	BG	111	HIS	5.1
1	AM	39	GLU	5.1
1	BA	78	VAL	5.0
1	AF	11	GLY	5.0
1	BG	121	ALA	5.0

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Mol	Chain	Res	Type	RSRZ
1	AO	67	VAL	5.0
1	AM	33	LYS	5.0
1	BJ	114	LEU	4.9
1	AO	73	ASN	4.9
1	BM	126	GLY	4.9
1	AX	53	ASN	4.8
1	BM	125	TYR	4.8
1	AO	81	LEU	4.8
1	BD	124	ILE	4.8
1	AO	56	VAL	4.8
1	BG	118	VAL	4.8
1	BJ	67	VAL	4.8
1	BN	18	GLN	4.7
1	AR	121	ALA	4.7
1	BS	125	TYR	4.7
1	AF	12	THR	4.7
1	AI	125	TYR	4.7
1	BN	71	VAL	4.7
1	BI	53	ASN	4.7
1	BJ	81	LEU	4.6
1	AO	117	VAL	4.6
1	BH	126	GLY	4.6
1	AM	38	LEU	4.6
1	BA	122	SER	4.6
1	BJ	79	ARG	4.5
1	BI	21	ASN	4.5
1	AX	126	GLY	4.5
1	AF	120	ASP	4.5
1	AM	36	SER	4.5
1	AL	126	GLY	4.5
1	AR	125	TYR	4.5
1	AI	124	ILE	4.5
1	BG	123	PRO	4.5
1	AO	26	GLY	4.4
1	BG	107	SER	4.4
1	AX	78	VAL	4.4
1	BE	38	LEU	4.4
1	AI	1	PRO	4.4
1	BA	123	PRO	4.4
1	AM	34	ASP	4.4
1	AO	52	VAL	4.4
1	BG	125	TYR	4.4

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Mol	Chain	Res	Type	RSRZ
1	AF	118	VAL	4.4
1	BJ	78	VAL	4.3
1	BL	53	ASN	4.3
1	BN	39	GLU	4.3
1	AH	53	ASN	4.3
1	BE	21	ASN	4.3
1	AX	94	LEU	4.3
1	BG	114	LEU	4.2
1	AR	126	GLY	4.2
1	AP	53	ASN	4.2
1	BN	34	ASP	4.2
1	AM	126	GLY	4.2
1	AX	72	GLY	4.2
1	AM	42	ARG	4.2
1	AY	39	GLU	4.1
1	AF	94	LEU	4.1
1	AF	53	ASN	4.1
1	BQ	73	ASN	4.1
1	BS	53	ASN	4.1
1	BR	126	GLY	4.1
1	AR	81	LEU	4.1
1	AX	67	VAL	4.1
1	BP	94	LEU	4.1
1	AR	119	GLN	4.1
1	BJ	113	THR	4.0
1	AF	117	VAL	4.0
1	BQ	68	VAL	4.0
1	BH	125	TYR	4.0
1	BA	94	LEU	4.0
1	AO	78	VAL	4.0
1	AZ	53	ASN	4.0
1	AO	66	PRO	4.0
1	AM	66	PRO	3.9
1	AR	78	VAL	3.9
1	BJ	111	HIS	3.9
1	AY	36	SER	3.9
1	BN	36	SER	3.9
1	AF	24	ARG	3.9
1	AF	124	ILE	3.9
1	AO	94	LEU	3.9
1	AG	73	ASN	3.9
1	AQ	34	ASP	3.9

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Mol	Chain	Res	Type	RSRZ
1	BG	10	ASP	3.9
1	BP	2	LYS	3.9
1	AD	36	SER	3.9
1	AY	126	GLY	3.9
1	BN	73	ASN	3.9
1	BA	81	LEU	3.9
1	AR	11	GLY	3.8
1	AY	38	LEU	3.8
1	AC	125	TYR	3.8
1	AF	76	THR	3.8
1	BJ	57	TYR	3.8
1	BM	110	GLY	3.8
1	BP	53	ASN	3.8
1	BS	52	VAL	3.8
1	BP	24	ARG	3.8
1	AC	73	ASN	3.8
1	BD	121	ALA	3.8
1	BN	33	LYS	3.8
1	AM	74	VAL	3.7
1	BA	67	VAL	3.7
1	BJ	117	VAL	3.7
1	AI	25	GLU	3.7
1	AZ	25	GLU	3.7
1	BN	69	GLU	3.7
1	BD	96	THR	3.7
1	BO	53	ASN	3.7
1	AY	125	TYR	3.7
1	AX	96	THR	3.7
1	AO	79	ARG	3.7
1	AU	125	TYR	3.7
1	BJ	94	LEU	3.7
1	BB	53	ASN	3.7
1	AO	74	VAL	3.6
1	BP	117	VAL	3.6
1	BH	36	SER	3.6
1	AM	28	ALA	3.6
1	AY	68	VAL	3.6
1	BP	114	LEU	3.6
1	BE	73	ASN	3.6
1	BF	22	ILE	3.6
1	AM	71	VAL	3.6
1	BG	116	SER	3.6

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Mol	Chain	Res	Type	RSRZ
1	AR	65	VAL	3.5
1	AK	53	ASN	3.5
1	AM	37	ILE	3.5
1	BD	55	ASN	3.5
1	AU	42	ARG	3.5
1	BB	36	SER	3.5
1	BJ	77	THR	3.5
1	BF	54	GLY	3.5
1	BN	28	ALA	3.5
1	AF	113	THR	3.5
1	AM	54	GLY	3.5
1	BH	38	LEU	3.5
1	BK	21	ASN	3.5
1	BJ	80	THR	3.5
1	AC	122	SER	3.5
1	BE	126	GLY	3.5
1	BN	74	VAL	3.5
1	AM	4	ALA	3.5
1	AO	75	ARG	3.5
1	AN	5	ASN	3.5
1	BD	67	VAL	3.4
1	AO	80	THR	3.4
1	BM	124	ILE	3.4
1	AX	82	THR	3.4
1	BA	77	THR	3.4
1	BK	73	ASN	3.4
1	AM	43	LEU	3.4
1	AI	126	GLY	3.4
1	BF	28	ALA	3.4
1	AI	73	ASN	3.4
1	AO	82	THR	3.4
1	BD	73	ASN	3.4
1	BM	113	THR	3.4
1	AM	5	ASN	3.4
1	AZ	21	ASN	3.4
1	BG	73	ASN	3.4
1	AI	38	LEU	3.4
1	AR	118	VAL	3.4
1	AX	66	PRO	3.4
1	AN	21	ASN	3.3
1	BE	20	VAL	3.3
1	BH	68	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	BS	123	PRO	3.3
1	BN	5	ASN	3.3
1	AQ	24	ARG	3.3
1	AM	69	GLU	3.3
1	AR	111	HIS	3.3
1	BN	66	PRO	3.3
1	BN	77	THR	3.3
1	AQ	21	ASN	3.3
1	AJ	36	SER	3.3
1	AR	122	SER	3.3
1	BD	123	PRO	3.3
1	BH	18	GLN	3.3
1	BS	24	ARG	3.3
1	AO	71	VAL	3.3
1	BE	39	GLU	3.3
1	BI	126	GLY	3.3
1	AN	14	ASP	3.3
1	AF	119	GLN	3.3
1	BM	49	GLN	3.3
1	AF	25	GLU	3.3
1	AI	75	ARG	3.2
1	AO	24	ARG	3.2
1	AX	125	TYR	3.2
1	BQ	36	SER	3.2
1	BI	49	GLN	3.2
1	AI	24	ARG	3.2
1	BA	100	ARG	3.2
1	AM	31	ARG	3.2
1	AN	126	GLY	3.2
1	BG	83	GLU	3.2
1	BA	114	LEU	3.2
1	BJ	74	VAL	3.2
1	BN	40	ALA	3.2
1	BG	9	ASN	3.2
1	AX	56	VAL	3.2
1	AF	111	HIS	3.2
1	BS	122	SER	3.2
1	BN	80	THR	3.2
1	BP	113	THR	3.2
1	BN	4	ALA	3.2
1	BJ	73	ASN	3.2
1	AM	30	PHE	3.2

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Mol	Chain	Res	Type	RSRZ
1	BJ	68	VAL	3.2
1	BM	123	PRO	3.2
1	BN	19	PRO	3.2
1	BF	34	ASP	3.1
1	AC	110	GLY	3.1
1	AE	53	ASN	3.1
1	AU	123	PRO	3.1
1	AZ	91	GLN	3.1
1	AI	96	THR	3.1
1	BG	120	ASP	3.1
1	BS	88	LEU	3.1
1	AN	25	GLU	3.1
1	BN	68	VAL	3.1
1	BQ	71	VAL	3.1
1	BM	111	HIS	3.1
1	AZ	49	GLN	3.1
1	BC	49	GLN	3.1
1	AN	90	THR	3.1
1	AO	88	LEU	3.1
1	BD	122	SER	3.1
1	BE	17	LEU	3.1
1	BQ	69	GLU	3.1
1	BJ	70	VAL	3.1
1	BD	100	ARG	3.1
1	BQ	75	ARG	3.1
1	BN	125	TYR	3.1
1	AH	2	LYS	3.1
1	BG	119	GLN	3.1
1	AI	122	SER	3.1
1	AB	52	VAL	3.1
1	AM	68	VAL	3.1
1	AP	42	ARG	3.1
1	BA	52	VAL	3.1
1	BQ	39	GLU	3.1
1	BD	88	LEU	3.1
1	AI	90	THR	3.1
1	BS	72	GLY	3.1
1	AF	122	SER	3.1
1	AV	36	SER	3.1
1	BJ	52	VAL	3.1
1	BN	78	VAL	3.1
1	AO	115	MET	3.1

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Mol	Chain	Res	Type	RSRZ
1	AI	121	ALA	3.0
1	AM	40	ALA	3.0
1	AP	38	LEU	3.0
1	BA	111	HIS	3.0
1	AO	11	GLY	3.0
1	AO	77	THR	3.0
1	BA	70	VAL	3.0
1	BF	2	LYS	3.0
1	BP	93	SER	3.0
1	BD	66	PRO	3.0
1	BM	121	ALA	3.0
1	BN	31	ARG	3.0
1	AO	110	GLY	3.0
1	BI	2	LYS	3.0
1	AM	41	ILE	3.0
1	AR	1	PRO	3.0
1	BG	109	ALA	3.0
1	BJ	75	ARG	3.0
1	AD	53	ASN	3.0
1	AM	73	ASN	3.0
1	AY	18	GLN	3.0
1	BN	72	GLY	3.0
1	BD	52	VAL	3.0
1	BD	1	PRO	3.0
1	AM	17	LEU	3.0
1	BS	94	LEU	3.0
1	BE	125	TYR	3.0
1	AQ	53	ASN	3.0
1	BB	73	ASN	3.0
1	AF	90	THR	3.0
1	AM	82	THR	3.0
1	BM	94	LEU	3.0
1	BP	25	GLU	3.0
1	AO	50	PRO	3.0
1	BD	79	ARG	3.0
1	AO	95	GLY	3.0
1	BG	11	GLY	3.0
1	BG	117	VAL	3.0
1	AI	94	LEU	2.9
1	AU	122	SER	2.9
1	AR	67	VAL	2.9
1	BO	126	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	BP	78	VAL	2.9
1	BP	55	ASN	2.9
1	AA	75	ARG	2.9
1	AM	80	THR	2.9
1	AO	58	ARG	2.9
1	AY	75	ARG	2.9
1	AQ	2	LYS	2.9
1	AN	4	ALA	2.9
1	BJ	51	SER	2.9
1	AO	10	ASP	2.9
1	AR	79	ARG	2.9
1	AX	75	ARG	2.9
1	BK	38	LEU	2.9
1	AU	53	ASN	2.9
1	BA	73	ASN	2.9
1	BI	96	THR	2.9
1	BJ	69	GLU	2.9
1	AR	56	VAL	2.9
1	BM	118	VAL	2.9
1	AC	126	GLY	2.9
1	AO	119	GLN	2.9
1	AQ	33	LYS	2.9
1	AM	76	THR	2.9
1	AX	90	THR	2.9
1	BD	53	ASN	2.9
1	BA	71	VAL	2.9
1	BS	56	VAL	2.9
1	AZ	24	ARG	2.9
1	AZ	2	LYS	2.9
1	AF	92	ASP	2.9
1	BS	92	ASP	2.9
1	AC	121	ALA	2.9
1	AF	77	THR	2.9
1	AO	1	PRO	2.9
1	AR	12	THR	2.9
1	AU	121	ALA	2.9
1	AY	53	ASN	2.9
1	AV	52	VAL	2.9
1	AO	108	LEU	2.9
1	BM	106	LYS	2.9
1	AR	10	ASP	2.8
1	AZ	14	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	BP	50	PRO	2.8
1	AN	52	VAL	2.8
1	AS	71	VAL	2.8
1	BO	42	ARG	2.8
1	BE	6	ILE	2.8
1	BH	37	ILE	2.8
1	BJ	49	GLN	2.8
1	AM	19	PRO	2.8
1	BC	25	GLU	2.8
1	BG	96	THR	2.8
1	BP	82	THR	2.8
1	AD	73	ASN	2.8
1	AF	73	ASN	2.8
1	AR	124	ILE	2.8
1	BN	38	LEU	2.8
1	AC	118	VAL	2.8
1	AX	74	VAL	2.8
1	AI	33	LYS	2.8
1	AY	69	GLU	2.8
1	BD	82	THR	2.8
1	BJ	82	THR	2.8
1	AQ	26	GLY	2.8
1	AY	55	ASN	2.8
1	AO	109	ALA	2.8
1	AY	33	LYS	2.8
1	BA	66	PRO	2.8
1	AH	96	THR	2.8
1	AQ	22	ILE	2.8
1	BS	23	ASP	2.8
1	AO	55	ASN	2.8
1	BA	79	ARG	2.8
1	BH	28	ALA	2.8
1	AM	45	VAL	2.8
1	BE	74	VAL	2.8
1	BK	36	SER	2.8
1	AH	126	GLY	2.7
1	AR	120	ASP	2.7
1	AM	21	ASN	2.7
1	AN	18	GLN	2.7
1	BG	91	GLN	2.7
1	AF	123	PRO	2.7
1	AI	123	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
1	BJ	54	GLY	2.7
1	BF	24	ARG	2.7
1	AN	53	ASN	2.7
1	BA	53	ASN	2.7
1	BH	9	ASN	2.7
1	AV	71	VAL	2.7
1	AZ	94	LEU	2.7
1	AV	39	GLU	2.7
1	BI	25	GLU	2.7
1	BP	69	GLU	2.7
1	AF	79	ARG	2.7
1	BK	53	ASN	2.7
1	AP	52	VAL	2.7
1	AU	78	VAL	2.7
1	BG	1	PRO	2.7
1	AC	24	ARG	2.7
1	AO	72	GLY	2.7
1	AU	126	GLY	2.7
1	AR	80	THR	2.7
1	BD	24	ARG	2.7
1	AM	14	ASP	2.7
1	AO	112	ALA	2.7
1	AP	125	TYR	2.7
1	AU	52	VAL	2.7
1	AA	73	ASN	2.7
1	AI	53	ASN	2.7
1	BA	38	LEU	2.7
1	BG	94	LEU	2.7
1	AI	37	ILE	2.7
1	AP	37	ILE	2.7
1	BJ	66	PRO	2.7
1	BS	124	ILE	2.7
1	AV	75	ARG	2.7
1	BS	75	ARG	2.7
1	AQ	90	THR	2.7
1	AA	38	LEU	2.7
1	AV	14	ASP	2.7
1	BF	53	ASN	2.7
1	AL	123	PRO	2.6
1	AU	124	ILE	2.6
1	BF	49	GLN	2.6
1	BN	37	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	AB	54	GLY	2.6
1	AW	126	GLY	2.6
1	AZ	126	GLY	2.6
1	BN	32	GLU	2.6
1	AH	90	THR	2.6
1	AO	84	THR	2.6
1	AU	113	THR	2.6
1	AR	112	ALA	2.6
1	BK	52	VAL	2.6
1	AF	1	PRO	2.6
1	BG	115	MET	2.6
1	BH	66	PRO	2.6
1	AI	18	GLN	2.6
1	BS	89	PHE	2.6
1	AB	126	GLY	2.6
1	AI	11	GLY	2.6
1	BA	74	VAL	2.6
1	BJ	65	VAL	2.6
1	AI	36	SER	2.6
1	AX	124	ILE	2.6
1	BH	34	ASP	2.6
1	AA	53	ASN	2.6
1	AT	126	GLY	2.6
1	BF	126	GLY	2.6
1	BJ	11	GLY	2.6
1	AP	69	GLU	2.6
1	AL	94	LEU	2.6
1	AU	94	LEU	2.6
1	AX	70	VAL	2.6
1	BD	77	THR	2.6
1	BG	16	THR	2.6
1	BL	52	VAL	2.6
1	BP	70	VAL	2.6
1	AO	100	ARG	2.6
1	AF	36	SER	2.6
1	BB	125	TYR	2.6
1	BE	8	ILE	2.6
1	BE	37	ILE	2.6
1	BM	91	GLN	2.6
1	AE	72	GLY	2.6
1	AP	126	GLY	2.6
1	BF	21	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	AX	77	THR	2.6
1	BE	16	THR	2.6
1	BJ	96	THR	2.6
1	BP	90	THR	2.6
1	BF	3	ILE	2.6
1	AF	115	MET	2.6
1	BJ	119	GLN	2.6
1	BH	11	GLY	2.6
1	BP	26	GLY	2.6
1	AV	53	ASN	2.6
1	AU	69	GLU	2.6
1	BD	69	GLU	2.6
1	BO	24	ARG	2.6
1	BD	57	TYR	2.5
1	BP	111	HIS	2.5
1	AA	36	SER	2.5
1	AJ	126	GLY	2.5
1	AQ	126	GLY	2.5
1	BF	11	GLY	2.5
1	AC	25	GLU	2.5
1	AD	71	VAL	2.5
1	AI	74	VAL	2.5
1	AO	120	ASP	2.5
1	AS	73	ASN	2.5
1	BF	55	ASN	2.5
1	AX	25	GLU	2.5
1	AQ	3	ILE	2.5
1	AR	113	THR	2.5
1	AC	94	LEU	2.5
1	AD	126	GLY	2.5
1	AG	11	GLY	2.5
1	BD	72	GLY	2.5
1	AA	42	ARG	2.5
1	AF	75	ARG	2.5
1	AR	24	ARG	2.5
1	AI	7	VAL	2.5
1	BP	67	VAL	2.5
1	AI	4	ALA	2.5
1	AI	34	ASP	2.5
1	BD	97	GLU	2.5
1	BS	69	GLU	2.5
1	BH	124	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	AR	123	PRO	2.5
1	BG	88	LEU	2.5
1	AQ	54	GLY	2.5
1	BI	24	ARG	2.5
1	BJ	24	ARG	2.5
1	AG	74	VAL	2.5
1	BA	118	VAL	2.5
1	BP	118	VAL	2.5
1	AB	53	ASN	2.5
1	AI	5	ASN	2.5
1	AM	23	ASP	2.5
1	BH	53	ASN	2.5
1	BN	14	ASP	2.5
1	AO	90	THR	2.5
1	BJ	72	GLY	2.5
1	AG	71	VAL	2.5
1	AM	64	VAL	2.5
1	AN	124	ILE	2.5
1	AP	8	ILE	2.5
1	AF	10	ASP	2.5
1	BJ	120	ASP	2.5
1	BA	80	THR	2.5
1	AN	2	LYS	2.5
1	BG	13	LYS	2.5
1	AS	38	LEU	2.5
1	BG	42	ARG	2.5
1	AM	65	VAL	2.5
1	BE	71	VAL	2.5
1	BM	117	VAL	2.5
1	AL	25	GLU	2.4
1	AU	25	GLU	2.4
1	BE	69	GLU	2.4
1	BM	25	GLU	2.4
1	AO	104	LEU	2.4
1	AR	82	THR	2.4
1	BA	82	THR	2.4
1	BM	114	LEU	2.4
1	BM	1	PRO	2.4
1	BH	45	VAL	2.4
1	AZ	4	ALA	2.4
1	BD	49	GLN	2.4
1	BB	37	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	AF	93	SER	2.4
1	AM	16	THR	2.4
1	AO	21	ASN	2.4
1	AR	53	ASN	2.4
1	BA	96	THR	2.4
1	BE	5	ASN	2.4
1	BE	123	PRO	2.4
1	AE	126	GLY	2.4
1	AM	78	VAL	2.4
1	BL	126	GLY	2.4
1	BP	54	GLY	2.4
1	BH	40	ALA	2.4
1	AN	42	ARG	2.4
1	AO	25	GLU	2.4
1	AO	83	GLU	2.4
1	BS	58	ARG	2.4
1	BI	55	ASN	2.4
1	BD	70	VAL	2.4
1	BE	70	VAL	2.4
1	BG	20	VAL	2.4
1	BO	54	GLY	2.4
1	AR	115	MET	2.4
1	BO	49	GLN	2.4
1	AL	24	ARG	2.4
1	BN	75	ARG	2.4
1	BB	38	LEU	2.4
1	AE	96	THR	2.4
1	AI	76	THR	2.4
1	AO	12	THR	2.4
1	BB	71	VAL	2.4
1	BG	90	THR	2.4
1	BI	27	VAL	2.4
1	AE	73	ASN	2.4
1	AN	6	ILE	2.4
1	AX	57	TYR	2.4
1	BG	75	ARG	2.4
1	AJ	38	LEU	2.4
1	AE	25	GLU	2.4
1	AP	32	GLU	2.4
1	AF	78	VAL	2.4
1	AN	27	VAL	2.4
1	BN	70	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	BP	56	VAL	2.4
1	AJ	72	GLY	2.3
1	BD	26	GLY	2.3
1	BF	26	GLY	2.3
1	BJ	90	THR	2.3
1	BP	11	GLY	2.3
1	AM	8	ILE	2.3
1	AM	15	ILE	2.3
1	AY	73	ASN	2.3
1	BI	5	ASN	2.3
1	AI	23	ASP	2.3
1	AP	17	LEU	2.3
1	AQ	49	GLN	2.3
1	AG	69	GLU	2.3
1	BJ	25	GLU	2.3
1	BE	52	VAL	2.3
1	AF	116	SER	2.3
1	AZ	50	PRO	2.3
1	AO	96	THR	2.3
1	AR	77	THR	2.3
1	AY	12	THR	2.3
1	BJ	76	THR	2.3
1	BN	76	THR	2.3
1	AX	121	ALA	2.3
1	BH	4	ALA	2.3
1	AA	21	ASN	2.3
1	AV	125	TYR	2.3
1	BJ	53	ASN	2.3
1	BO	55	ASN	2.3
1	BP	73	ASN	2.3
1	BQ	23	ASP	2.3
1	AN	30	PHE	2.3
1	BJ	91	GLN	2.3
1	BS	18	GLN	2.3
1	BA	69	GLU	2.3
1	AR	70	VAL	2.3
1	AR	117	VAL	2.3
1	AX	68	VAL	2.3
1	BG	56	VAL	2.3
1	AI	13	LYS	2.3
1	BL	2	LYS	2.3
1	AW	24	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	AX	100	ARG	2.3
1	BA	75	ARG	2.3
1	AO	51	SER	2.3
1	AQ	37	ILE	2.3
1	AM	77	THR	2.3
1	BG	105	THR	2.3
1	AY	5	ASN	2.3
1	BD	81	LEU	2.3
1	BN	53	ASN	2.3
1	AQ	18	GLN	2.3
1	AM	7	VAL	2.3
1	AO	64	VAL	2.3
1	BH	33	LYS	2.3
1	AX	79	ARG	2.3
1	BC	24	ARG	2.3
1	BG	24	ARG	2.3
1	BG	79	ARG	2.3
1	AL	95	GLY	2.3
1	AZ	54	GLY	2.3
1	BK	6	ILE	2.3
1	AC	109	ALA	2.3
1	AF	81	LEU	2.3
1	AT	53	ASN	2.3
1	BG	21	ASN	2.3
1	AO	18	GLN	2.3
1	AR	91	GLN	2.3
1	BF	18	GLN	2.3
1	BI	91	GLN	2.3
1	AF	56	VAL	2.3
1	BD	75	ARG	2.3
1	BF	4	ALA	2.3
1	BJ	115	MET	2.3
1	AI	16	THR	2.3
1	AZ	55	ASN	2.3
1	AM	79	ARG	2.3
1	BP	75	ARG	2.3
1	AF	68	VAL	2.3
1	BA	68	VAL	2.3
1	BG	71	VAL	2.3
1	BA	25	GLU	2.2
1	AN	3	ILE	2.2
1	BH	19	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	AR	90	THR	2.2
1	BG	76	THR	2.2
1	BE	36	SER	2.2
1	BM	116	SER	2.2
1	BO	122	SER	2.2
1	AH	24	ARG	2.2
1	AP	71	VAL	2.2
1	AX	21	ASN	2.2
1	AZ	52	VAL	2.2
1	BC	53	ASN	2.2
1	BJ	56	VAL	2.2
1	AE	34	ASP	2.2
1	AR	25	GLU	2.2
1	AY	17	LEU	2.2
1	BE	4	ALA	2.2
1	BM	115	MET	2.2
1	AC	96	THR	2.2
1	AM	125	TYR	2.2
1	AQ	58	ARG	2.2
1	AR	58	ARG	2.2
1	AQ	122	SER	2.2
1	BA	36	SER	2.2
1	AS	74	VAL	2.2
1	AQ	5	ASN	2.2
1	AL	124	ILE	2.2
1	AU	1	PRO	2.2
1	BO	94	LEU	2.2
1	BE	75	ARG	2.2
1	AR	76	THR	2.2
1	AL	67	VAL	2.2
1	AS	70	VAL	2.2
1	BA	64	VAL	2.2
1	BP	91	GLN	2.2
1	AN	55	ASN	2.2
1	AQ	25	GLU	2.2
1	BO	25	GLU	2.2
1	BC	126	GLY	2.2
1	BF	123	PRO	2.2
1	BI	4	ALA	2.2
1	BP	1	PRO	2.2
1	BP	95	GLY	2.2
1	AM	2	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	BF	33	LYS	2.2
1	BG	29	HIS	2.2
1	BP	52	VAL	2.2
1	AI	91	GLN	2.2
1	AP	49	GLN	2.2
1	AU	91	GLN	2.2
1	BJ	108	LEU	2.2
1	AA	25	GLU	2.2
1	AY	28	ALA	2.2
1	AZ	28	ALA	2.2
1	BH	69	GLU	2.2
1	BM	73	ASN	2.2
1	BS	55	ASN	2.2
1	BD	54	GLY	2.2
1	BH	75	ARG	2.2
1	AN	23	ASP	2.2
1	AO	23	ASP	2.2
1	AC	70	VAL	2.1
1	AR	96	THR	2.1
1	AZ	57	TYR	2.1
1	AO	49	GLN	2.1
1	AI	100	ARG	2.1
1	AK	25	GLU	2.1
1	AQ	4	ALA	2.1
1	AM	75	ARG	2.1
1	AP	75	ARG	2.1
1	AY	54	GLY	2.1
1	BH	5	ASN	2.1
1	AR	23	ASP	2.1
1	AX	92	ASP	2.1
1	BB	52	VAL	2.1
1	AI	80	THR	2.1
1	AO	76	THR	2.1
1	BE	80	THR	2.1
1	BG	82	THR	2.1
1	AY	37	ILE	2.1
1	BS	37	ILE	2.1
1	BE	31	ARG	2.1
1	AH	26	GLY	2.1
1	AI	39	GLU	2.1
1	BI	1	PRO	2.1
1	BJ	110	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	BM	107	SER	2.1
1	BP	83	GLU	2.1
1	AM	20	VAL	2.1
1	AO	70	VAL	2.1
1	AZ	27	VAL	2.1
1	AL	76	THR	2.1
1	AM	44	THR	2.1
1	BO	2	LYS	2.1
1	AN	24	ARG	2.1
1	BJ	100	ARG	2.1
1	AL	66	PRO	2.1
1	AR	83	GLU	2.1
1	BG	25	GLU	2.1
1	BG	50	PRO	2.1
1	BS	11	GLY	2.1
1	BF	93	SER	2.1
1	BI	122	SER	2.1
1	AL	53	ASN	2.1
1	BH	73	ASN	2.1
1	AA	52	VAL	2.1
1	AY	52	VAL	2.1
1	BH	70	VAL	2.1
1	AF	38	LEU	2.1
1	AN	17	LEU	2.1
1	AO	14	ASP	2.1
1	AQ	94	LEU	2.1
1	AR	94	LEU	2.1
1	AY	6	ILE	2.1
1	AI	77	THR	2.1
1	BF	58	ARG	2.1
1	BB	54	GLY	2.1
1	AA	69	GLU	2.1
1	AC	69	GLU	2.1
1	AM	1	PRO	2.1
1	AS	36	SER	2.1
1	BB	74	VAL	2.1
1	AY	13	LYS	2.1
1	BE	2	LYS	2.1
1	BS	5	ASN	2.1
1	BA	24	ARG	2.1
1	BG	58	ARG	2.1
1	BM	79	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	AO	4	ALA	2.1
1	BA	54	GLY	2.1
1	BB	25	GLU	2.1
1	BD	89	PHE	2.1
1	BI	30	PHE	2.1
1	BS	1	PRO	2.1
1	AD	68	VAL	2.0
1	AP	64	VAL	2.0
1	BA	56	VAL	2.0
1	BF	56	VAL	2.0
1	BK	74	VAL	2.0
1	AN	51	SER	2.0
1	AP	36	SER	2.0
1	AV	51	SER	2.0
1	AY	124	ILE	2.0
1	BE	41	ILE	2.0
1	BE	42	ARG	2.0
1	BI	6	ILE	2.0
1	BM	75	ARG	2.0
1	AV	12	THR	2.0
1	AW	90	THR	2.0
1	AY	34	ASP	2.0
1	BA	113	THR	2.0
1	BB	34	ASP	2.0
1	AK	126	GLY	2.0
1	AI	66	PRO	2.0
1	AX	89	PHE	2.0
1	BE	46	GLN	2.0
1	BN	126	GLY	2.0
1	BP	49	GLN	2.0
1	AZ	1	PRO	2.0
1	AF	69	GLU	2.0
1	AM	83	GLU	2.0
1	AD	74	VAL	2.0
1	AI	20	VAL	2.0
1	BN	65	VAL	2.0
1	BS	68	VAL	2.0
1	AL	75	ARG	2.0
1	AN	31	ARG	2.0
1	AO	38	LEU	2.0
1	BN	79	ARG	2.0
1	AF	3	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	AI	15	ILE	2.0
1	BL	51	SER	2.0
1	BO	3	ILE	2.0
1	AG	53	ASN	2.0
1	AZ	5	ASN	2.0
1	BO	21	ASN	2.0
1	AO	105	THR	2.0
1	AY	40	ALA	2.0
1	AY	80	THR	2.0
1	BL	90	THR	2.0
1	BM	80	THR	2.0
1	BE	72	GLY	2.0
1	BN	54	GLY	2.0
1	BS	54	GLY	2.0
1	AN	20	VAL	2.0
1	AP	45	VAL	2.0
1	BB	39	GLU	2.0
1	BD	74	VAL	2.0
1	AP	6	ILE	2.0
1	BK	37	ILE	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.