



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:48 PM GMT

PDB ID : 1H2I  
Title : HUMAN RAD52 PROTEIN, N-TERMINAL DOMAIN  
Authors : Singleton, M.R.; Wentzell, L.M.; Liu, Y.; West, S.C.; Wigley, D.B.  
Deposited on : 2002-08-09  
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

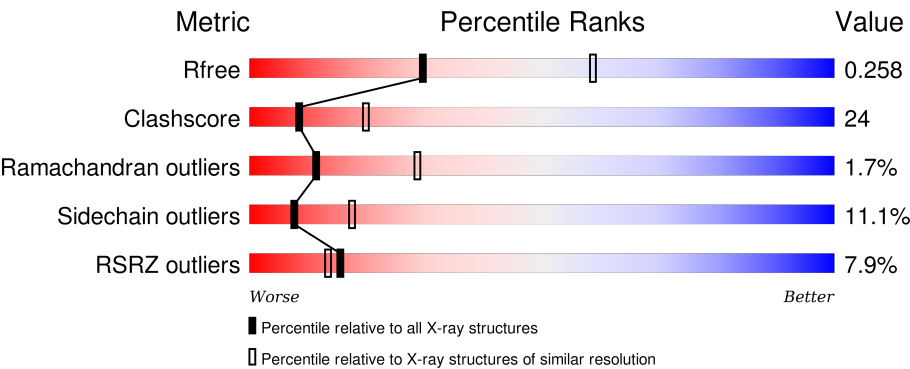
MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R <sub>free</sub>	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	A	209	<div><div>3%</div><div><div></div><div></div><div></div><div></div></div><div>55%28%5% • 11%</div></div>
1	B	209	<div><div>6%</div><div><div></div><div></div><div></div><div></div></div><div>58%22%7% • 11%</div></div>
1	C	209	<div><div>5%</div><div><div></div><div></div><div></div><div></div></div><div>59%23%5% • 11%</div></div>
1	D	209	<div><div>7%</div><div><div></div><div></div><div></div><div></div></div><div>56%26%5% • 11%</div></div>
1	E	209	<div><div>6%</div><div><div></div><div></div><div></div><div></div></div><div>53%27%6% • 11%</div></div>

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Mol	Chain	Length	Quality of chain
1	F	209	
1	G	209	
1	H	209	
1	I	209	
1	J	209	
1	K	209	
1	L	209	
1	M	209	
1	N	209	
1	O	209	
1	P	209	
1	Q	209	
1	R	209	
1	S	209	
1	T	209	
1	U	209	
1	V	209	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 32802 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 DNA REPAIR PROTEIN RAD52 HOMOLOG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	B	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	C	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	D	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	E	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	F	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	G	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	H	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	I	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	J	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	K	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	L	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	M	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	N	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	O	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			
1	P	186	Total	C	N	O	S	0	0	0
			1469	919	266	276	8			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	186	Total 1469	C 919	N 266	O 276	S 8	0	0	0
1	R	186	Total 1469	C 919	N 266	O 276	S 8	0	0	0
1	S	186	Total 1469	C 919	N 266	O 276	S 8	0	0	0
1	T	186	Total 1469	C 919	N 266	O 276	S 8	0	0	0
1	U	186	Total 1469	C 919	N 266	O 276	S 8	0	0	0
1	V	186	Total 1469	C 919	N 266	O 276	S 8	0	0	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	23	Total 23	O 23	0	0
2	B	22	Total 22	O 22	0	0
2	C	21	Total 21	O 21	0	0
2	D	24	Total 24	O 24	0	0
2	E	22	Total 22	O 22	0	0
2	F	25	Total 25	O 25	0	0
2	G	18	Total 18	O 18	0	0
2	H	22	Total 22	O 22	0	0
2	I	22	Total 22	O 22	0	0
2	J	20	Total 20	O 20	0	0
2	K	23	Total 23	O 23	0	0
2	L	21	Total 21	O 21	0	0
2	M	23	Total 23	O 23	0	0

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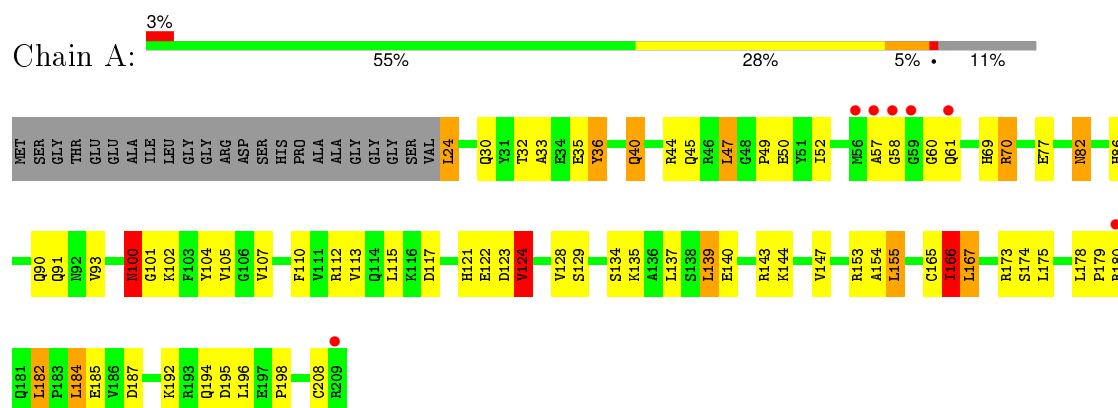
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	N	26	Total 26	O 26	0	0
2	O	17	Total 17	O 17	0	0
2	P	24	Total 24	O 24	0	0
2	Q	21	Total 21	O 21	0	0
2	R	22	Total 22	O 22	0	0
2	S	22	Total 22	O 22	0	0
2	T	22	Total 22	O 22	0	0
2	U	23	Total 23	O 23	0	0
2	V	21	Total 21	O 21	0	0

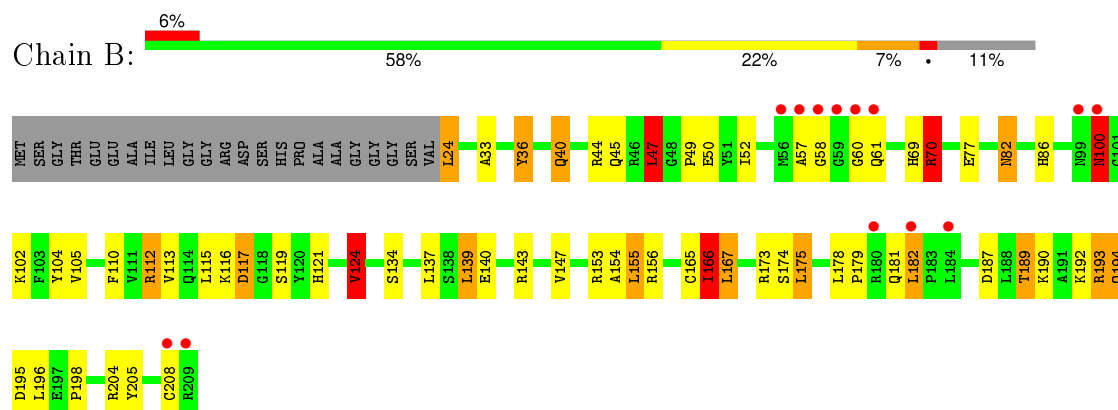
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

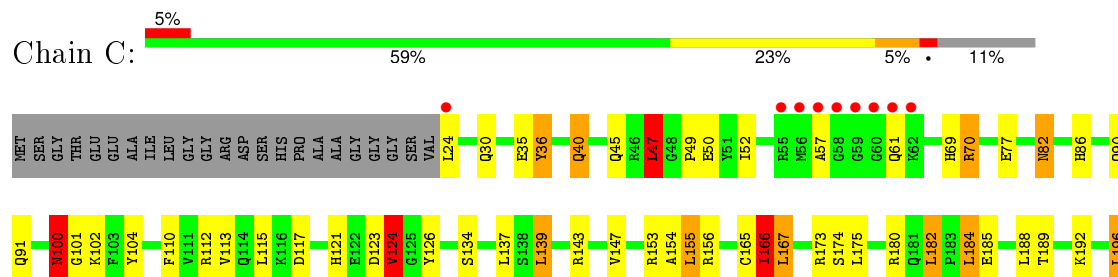
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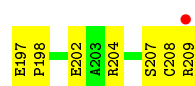


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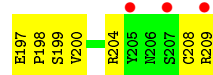
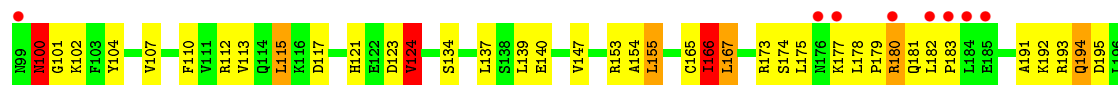


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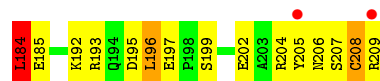




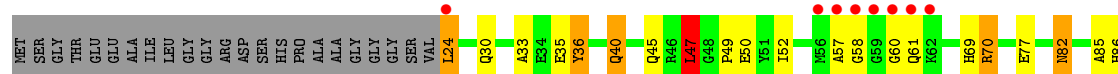
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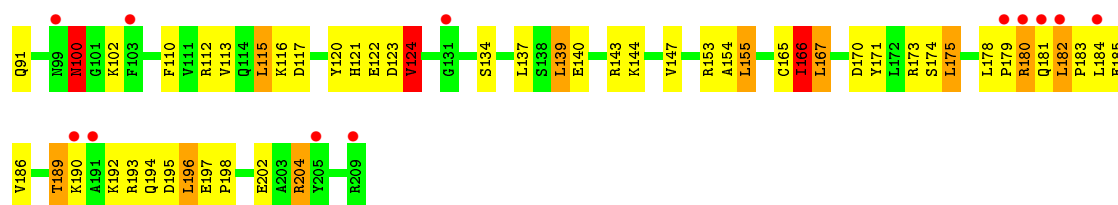
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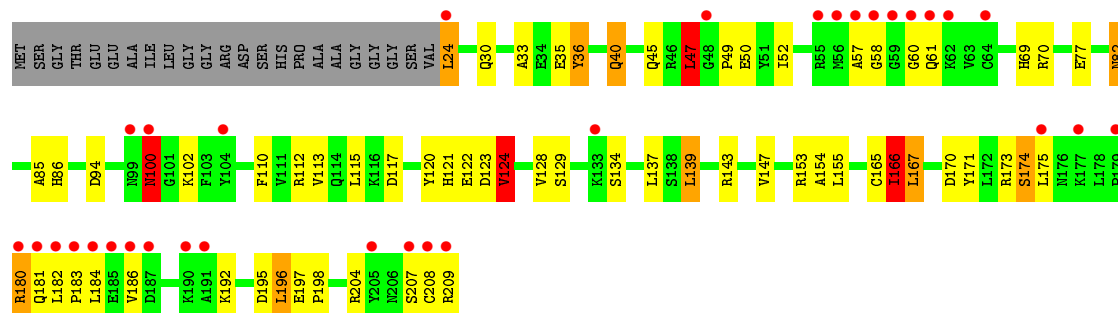
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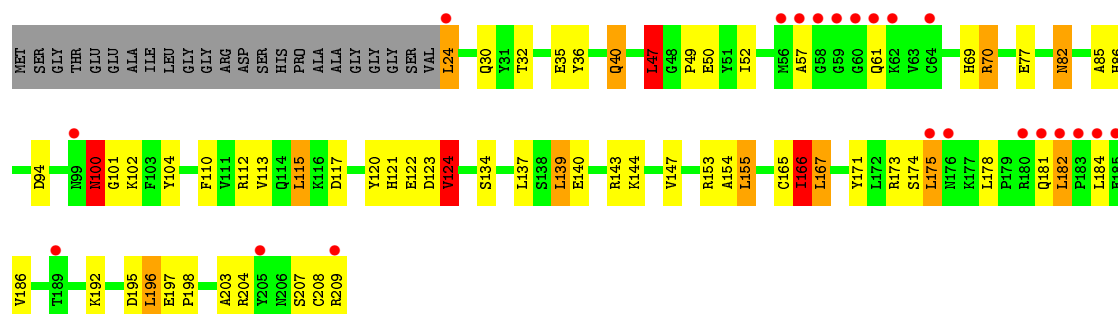




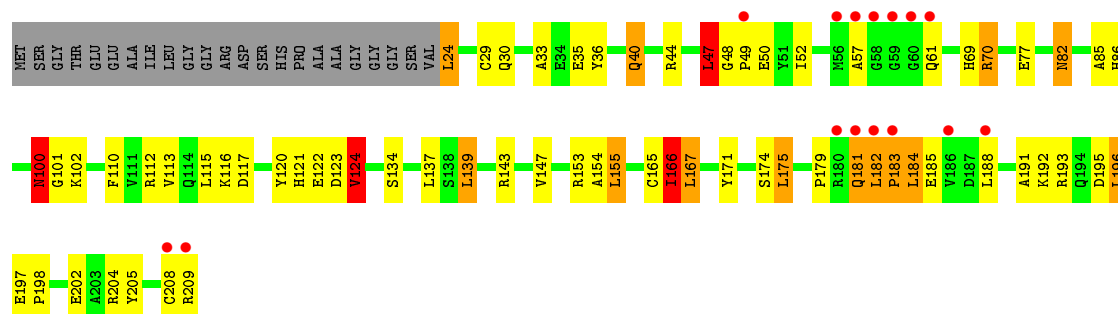
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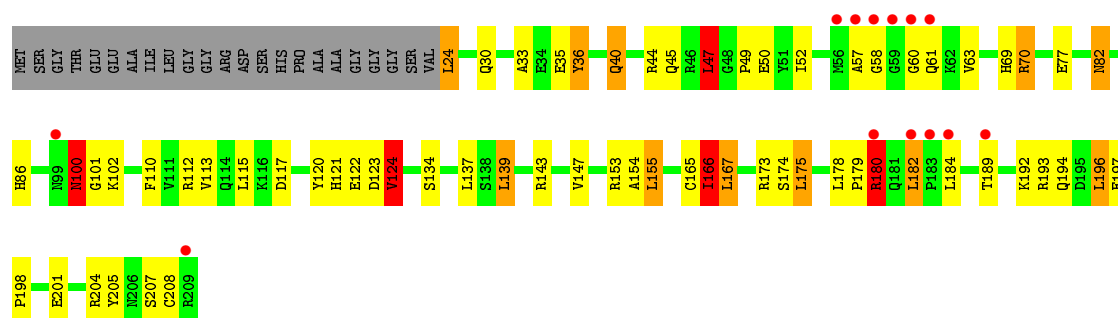


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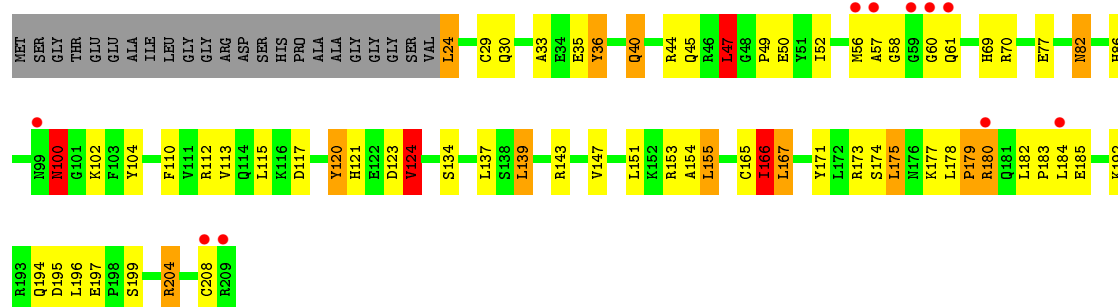


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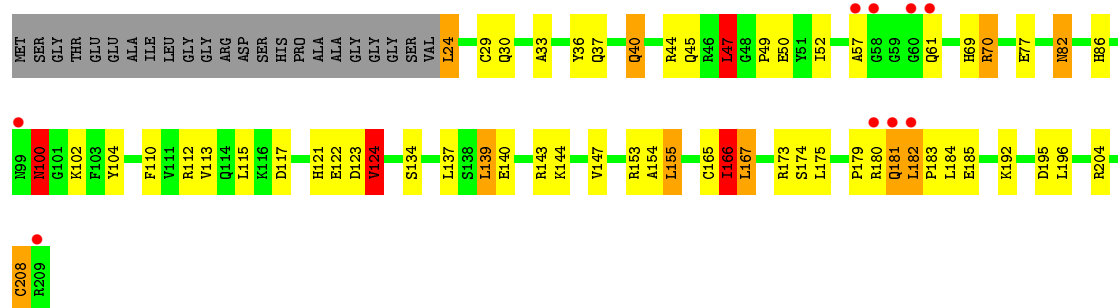




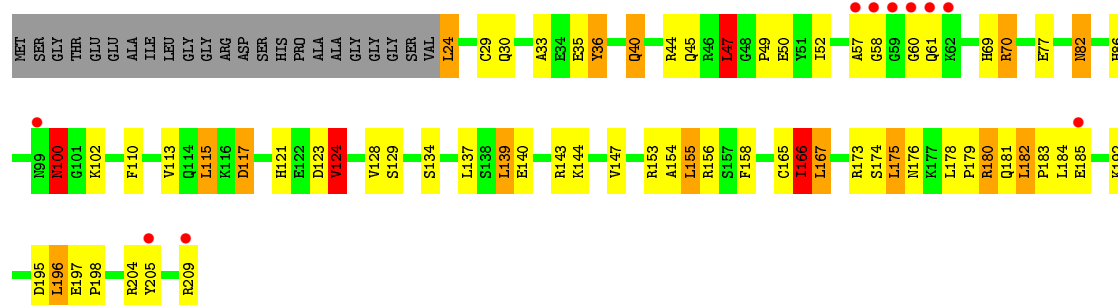
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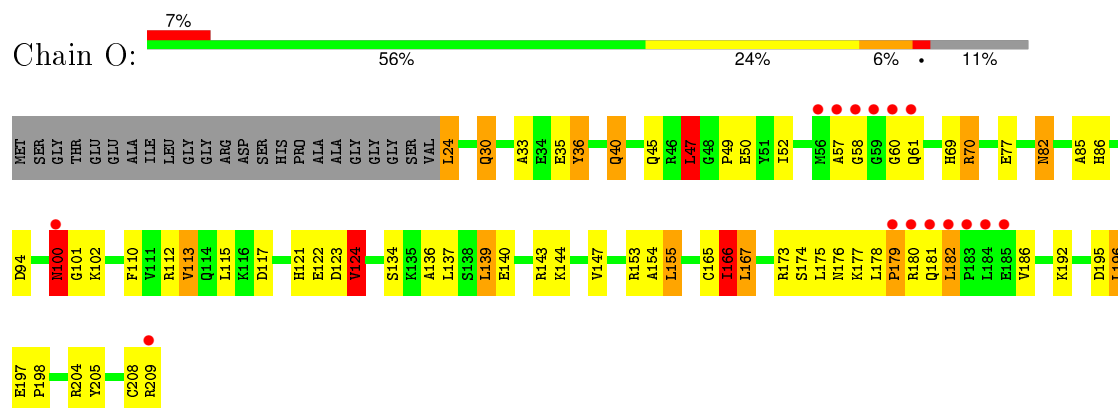
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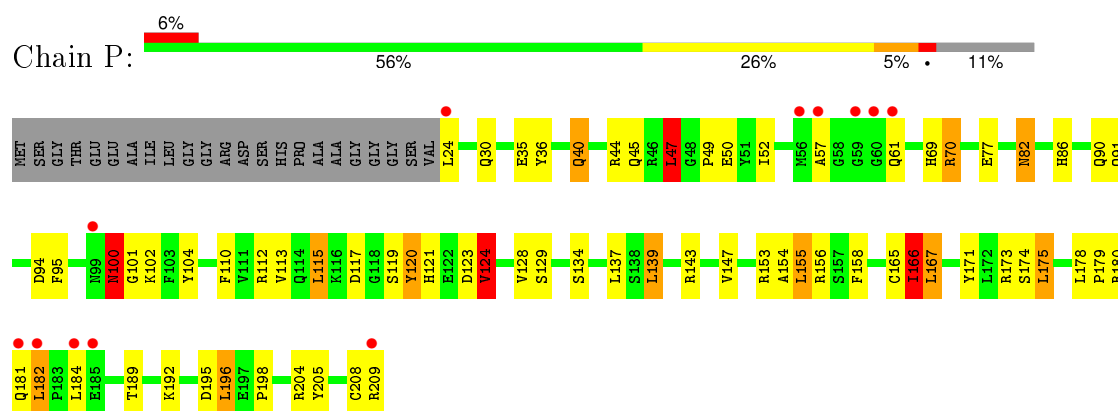
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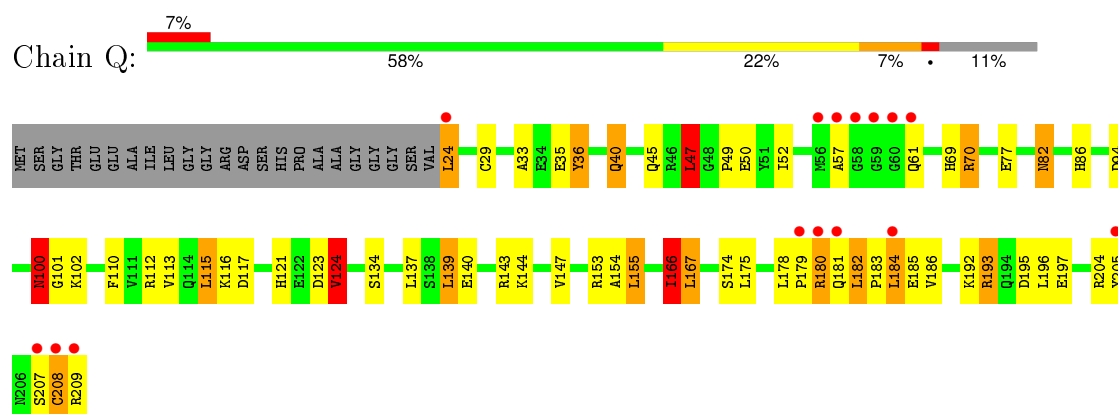
• Molecule 1: DNA REPAIR PROTEIN RAD52 HOMOLOG



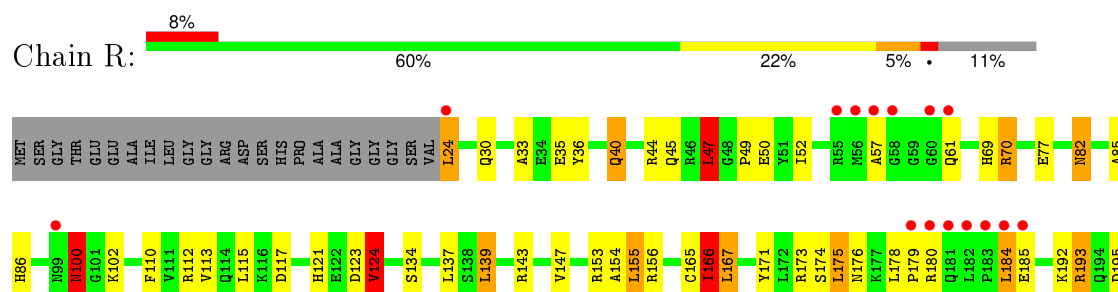
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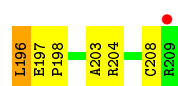


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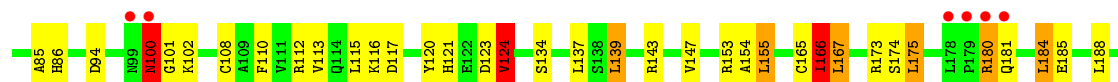


• Molecule 1: DNA REPAIR PROTEIN RAD52 HOMOLOG

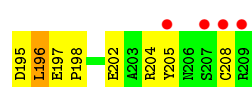
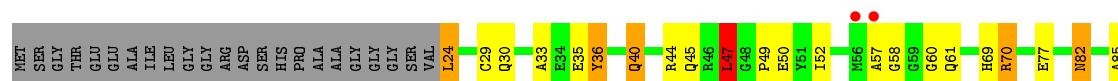




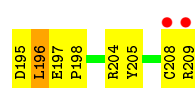
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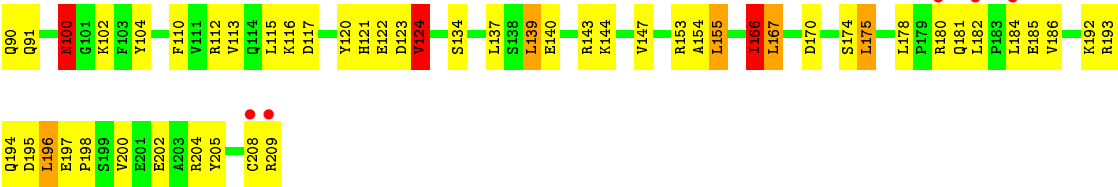


• Molecule 1: DNA REPAIR PROTEIN RAD52 HOMOLOG



• Molecule 1: DNA REPAIR PROTEIN RAD52 HOMOLOG





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	117.26Å 127.32Å 191.23Å 90.00° 90.29° 90.00°	Depositor
Resolution (Å)	30.00 – 2.70 29.86 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.9 (30.00-2.70) 97.0 (29.86-2.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.48 (at 2.68Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.225 , 0.262 0.225 , 0.258	Depositor DCC
$R_{free}$ test set	7511 reflections (5.03%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.4	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 54.9	EDS
Estimated twinning fraction	0.015 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 149457 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	32802	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	A	0.77	0/1493	0.89	2/2006 (0.1%)
1	B	0.84	1/1493 (0.1%)	0.97	7/2006 (0.3%)
1	C	0.77	0/1493	0.94	5/2006 (0.2%)
1	D	0.69	0/1493	0.84	2/2006 (0.1%)
1	E	0.62	0/1493	0.83	3/2006 (0.1%)
1	F	0.58	0/1493	0.78	2/2006 (0.1%)
1	G	0.54	0/1493	0.79	2/2006 (0.1%)
1	H	0.54	0/1493	0.79	2/2006 (0.1%)
1	I	0.57	0/1493	0.80	2/2006 (0.1%)
1	J	0.61	1/1493 (0.1%)	0.81	3/2006 (0.1%)
1	K	0.70	1/1493 (0.1%)	0.83	2/2006 (0.1%)
1	L	0.79	1/1493 (0.1%)	0.92	3/2006 (0.1%)
1	M	0.77	1/1493 (0.1%)	0.90	2/2006 (0.1%)
1	N	0.81	2/1493 (0.1%)	0.93	5/2006 (0.2%)
1	O	0.74	1/1493 (0.1%)	0.89	4/2006 (0.2%)
1	P	0.71	0/1493	0.88	3/2006 (0.1%)
1	Q	0.71	1/1493 (0.1%)	0.86	3/2006 (0.1%)
1	R	0.71	0/1493	0.89	5/2006 (0.2%)
1	S	0.77	2/1493 (0.1%)	0.88	4/2006 (0.2%)
1	T	0.73	1/1493 (0.1%)	0.87	3/2006 (0.1%)
1	U	0.71	1/1493 (0.1%)	0.87	3/2006 (0.1%)
1	V	0.74	0/1493	0.86	3/2006 (0.1%)
All	All	0.71	13/32846 (0.0%)	0.87	70/44132 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	2
1	E	0	2
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	K	0	1
1	L	0	3
1	M	0	1
1	N	0	1
1	O	0	1
1	P	0	2
1	Q	0	1
1	T	0	2
1	U	0	1
1	V	0	1
All	All	0	28

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S	29	CYS	CB-SG	-7.25	1.70	1.82
1	J	29	CYS	CB-SG	-6.87	1.70	1.82
1	N	29	CYS	CB-SG	-6.86	1.70	1.82
1	L	29	CYS	CB-SG	-6.64	1.71	1.82
1	M	29	CYS	CB-SG	-6.22	1.71	1.82
1	B	117	ASP	CB-CG	-6.15	1.38	1.51
1	Q	29	CYS	CB-SG	-5.58	1.72	1.81
1	N	117	ASP	CB-CG	-5.47	1.40	1.51
1	T	29	CYS	CB-SG	-5.41	1.73	1.81
1	S	108	CYS	CB-SG	-5.32	1.73	1.81
1	U	29	CYS	CB-SG	-5.24	1.73	1.81
1	O	113	VAL	CB-CG1	-5.08	1.42	1.52
1	K	201	GLU	CG-CD	5.04	1.59	1.51

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	124	VAL	CB-CA-C	-6.89	98.31	111.40
1	P	124	VAL	CB-CA-C	-6.87	98.36	111.40
1	B	156	ARG	NE-CZ-NH2	-6.63	116.98	120.30
1	D	124	VAL	CB-CA-C	-6.56	98.93	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	124	VAL	CB-CA-C	-6.54	98.97	111.40
1	B	124	VAL	CB-CA-C	-6.46	99.13	111.40
1	B	117	ASP	CB-CG-OD2	-6.42	112.52	118.30
1	L	124	VAL	CB-CA-C	-6.37	99.30	111.40
1	U	124	VAL	CB-CA-C	-6.37	99.31	111.40
1	M	124	VAL	CB-CA-C	-6.35	99.34	111.40
1	R	124	VAL	CB-CA-C	-6.34	99.35	111.40
1	A	124	VAL	CB-CA-C	-6.34	99.35	111.40
1	E	124	VAL	CB-CA-C	-6.29	99.44	111.40
1	V	124	VAL	CB-CA-C	-6.23	99.56	111.40
1	O	124	VAL	CB-CA-C	-6.20	99.63	111.40
1	F	124	VAL	CB-CA-C	-6.19	99.64	111.40
1	R	156	ARG	NE-CZ-NH2	-6.09	117.25	120.30
1	B	70	ARG	NE-CZ-NH1	-6.07	117.27	120.30
1	K	124	VAL	CB-CA-C	-6.03	99.94	111.40
1	O	47	LEU	CA-CB-CG	5.96	129.01	115.30
1	H	124	VAL	CB-CA-C	-5.96	100.08	111.40
1	P	47	LEU	CA-CB-CG	5.89	128.84	115.30
1	E	47	LEU	CA-CB-CG	5.88	128.82	115.30
1	J	47	LEU	CA-CB-CG	5.83	128.70	115.30
1	T	124	VAL	CB-CA-C	-5.79	100.39	111.40
1	Q	47	LEU	CA-CB-CG	5.78	128.59	115.30
1	N	47	LEU	CA-CB-CG	5.77	128.57	115.30
1	U	100	ASN	N-CA-C	-5.75	95.46	111.00
1	C	47	LEU	CA-CB-CG	5.73	128.49	115.30
1	V	47	LEU	CA-CB-CG	5.73	128.47	115.30
1	C	156	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	N	117	ASP	CB-CG-OD2	-5.70	113.17	118.30
1	S	124	VAL	CB-CA-C	-5.61	100.74	111.40
1	T	47	LEU	CA-CB-CG	5.60	128.18	115.30
1	G	124	VAL	CB-CA-C	-5.59	100.78	111.40
1	Q	124	VAL	CB-CA-C	-5.58	100.80	111.40
1	N	156	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	L	47	LEU	CA-CB-CG	5.57	128.11	115.30
1	H	47	LEU	CA-CB-CG	5.56	128.08	115.30
1	M	47	LEU	CA-CB-CG	5.55	128.07	115.30
1	G	47	LEU	CA-CB-CG	5.54	128.05	115.30
1	S	47	LEU	CA-CB-CG	5.53	128.02	115.30
1	N	156	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	V	100	ASN	N-CA-C	-5.50	96.16	111.00
1	I	47	LEU	CA-CB-CG	5.39	127.70	115.30
1	F	47	LEU	CA-CB-CG	5.38	127.67	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	100	ASN	N-CA-C	-5.38	96.48	111.00
1	O	100	ASN	N-CA-C	-5.33	96.61	111.00
1	L	100	ASN	N-CA-C	-5.33	96.61	111.00
1	B	47	LEU	CA-CB-CG	5.31	127.51	115.30
1	B	100	ASN	N-CA-C	-5.28	96.75	111.00
1	U	47	LEU	CA-CB-CG	5.28	127.43	115.30
1	A	100	ASN	N-CA-C	-5.27	96.77	111.00
1	Q	100	ASN	N-CA-C	-5.25	96.81	111.00
1	B	112	ARG	NE-CZ-NH2	-5.25	117.67	120.30
1	E	100	ASN	N-CA-C	-5.20	96.97	111.00
1	R	100	ASN	N-CA-C	-5.19	96.99	111.00
1	J	124	VAL	CB-CA-C	-5.16	101.59	111.40
1	R	112	ARG	NE-CZ-NH2	-5.15	117.72	120.30
1	S	30	GLN	N-CA-C	-5.14	97.12	111.00
1	K	47	LEU	CA-CB-CG	5.11	127.06	115.30
1	S	25	CYS	CA-CB-SG	-5.10	104.82	114.00
1	J	100	ASN	N-CA-C	-5.10	97.24	111.00
1	O	30	GLN	N-CA-C	-5.10	97.24	111.00
1	C	156	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	T	181	GLN	N-CA-C	-5.06	97.35	111.00
1	R	47	LEU	CA-CB-CG	5.03	126.87	115.30
1	P	156	ARG	NE-CZ-NH1	5.03	122.81	120.30
1	D	100	ASN	N-CA-C	-5.02	97.45	111.00
1	I	124	VAL	CB-CA-C	-5.01	101.88	111.40

There are no chirality outliers.

All (28) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	104	TYR	Sidechain
1	A	36	TYR	Sidechain
1	B	104	TYR	Sidechain
1	B	36	TYR	Sidechain
1	C	104	TYR	Sidechain
1	C	36	TYR	Sidechain
1	D	104	TYR	Sidechain
1	D	36	TYR	Sidechain
1	E	104	TYR	Sidechain
1	E	36	TYR	Sidechain
1	F	36	TYR	Sidechain
1	G	36	TYR	Sidechain
1	H	36	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	I	104	TYR	Sidechain
1	K	36	TYR	Sidechain
1	L	104	TYR	Sidechain
1	L	120	TYR	Sidechain
1	L	36	TYR	Sidechain
1	M	104	TYR	Sidechain
1	N	36	TYR	Sidechain
1	O	36	TYR	Sidechain
1	P	104	TYR	Sidechain
1	P	120	TYR	Sidechain
1	Q	36	TYR	Sidechain
1	T	104	TYR	Sidechain
1	T	36	TYR	Sidechain
1	U	104	TYR	Sidechain
1	V	104	TYR	Sidechain

## 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	A	1469	0	1457	87	0
1	B	1469	0	1457	93	0
1	C	1469	0	1457	78	0
1	D	1469	0	1457	85	0
1	E	1469	0	1457	88	0
1	F	1469	0	1457	77	0
1	G	1469	0	1457	106	0
1	H	1469	0	1457	89	0
1	I	1469	0	1457	82	0
1	J	1469	0	1457	82	0
1	K	1469	0	1457	99	0
1	L	1469	0	1457	104	0
1	M	1469	0	1457	70	0
1	N	1469	0	1457	85	0
1	O	1469	0	1457	83	0
1	P	1469	0	1457	85	0
1	Q	1469	0	1457	89	0
1	R	1469	0	1457	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S	1469	0	1457	89	0
1	T	1469	0	1457	87	0
1	U	1469	0	1457	86	0
1	V	1469	0	1457	92	0
2	A	23	0	0	1	0
2	B	22	0	0	2	0
2	C	21	0	0	1	0
2	D	24	0	0	1	0
2	E	22	0	0	0	0
2	F	25	0	0	1	0
2	G	18	0	0	1	0
2	H	22	0	0	0	0
2	I	22	0	0	1	0
2	J	20	0	0	1	0
2	K	23	0	0	1	0
2	L	21	0	0	0	0
2	M	23	0	0	0	0
2	N	26	0	0	0	0
2	O	17	0	0	0	0
2	P	24	0	0	1	0
2	Q	21	0	0	1	0
2	R	22	0	0	0	0
2	S	22	0	0	1	0
2	T	22	0	0	1	0
2	U	23	0	0	2	0
2	V	21	0	0	1	0
All	All	32802	0	32054	1544	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 24.

All (1544) 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:K:193:ARG:HB3	1:L:180:ARG:NH2	1.55	1.21
1:C:182:LEU:HD23	1:C:182:LEU:H	1.01	1.17
1:B:193:ARG:HG2	1:B:193:ARG:HH11	0.98	1.14
1:K:193:ARG:HB3	1:L:180:ARG:HH21	1.02	1.07
1:C:182:LEU:H	1:C:182:LEU:CD2	1.66	1.04
1:K:193:ARG:CB	1:L:180:ARG:HH21	1.70	1.03
1:Q:182:LEU:H	1:Q:182:LEU:HD23	1.20	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:50:GLU:HA	1:I:181:GLN:HE22	1.25	1.01
1:B:189:THR:HG22	1:B:190:LYS:HG3	1.43	1.00
1:N:182:LEU:HD22	1:N:182:LEU:H	1.21	0.99
1:M:182:LEU:H	1:M:182:LEU:HD23	1.25	0.99
1:Q:182:LEU:H	1:Q:182:LEU:CD2	1.77	0.97
1:F:204:ARG:HG3	1:F:204:ARG:HH21	1.28	0.95
1:L:208:CYS:HB2	1:N:33:ALA:HB2	1.47	0.93
1:K:193:ARG:HB3	1:L:180:ARG:CZ	1.98	0.92
1:B:193:ARG:CG	1:B:193:ARG:HH11	1.79	0.92
1:G:182:LEU:HD23	1:G:182:LEU:H	1.34	0.92
1:N:182:LEU:CD2	1:N:182:LEU:H	1.83	0.91
1:N:192:LYS:HE2	1:N:197:GLU:OE2	1.71	0.90
1:U:40:GLN:HE21	1:U:40:GLN:HA	1.36	0.90
1:A:167:LEU:HD13	1:A:167:LEU:H	1.35	0.90
1:C:182:LEU:HD23	1:C:182:LEU:N	1.86	0.90
1:D:167:LEU:H	1:D:167:LEU:HD13	1.36	0.90
1:Q:40:GLN:HE21	1:Q:40:GLN:HA	1.38	0.89
1:C:167:LEU:HD13	1:C:167:LEU:H	1.36	0.89
1:P:182:LEU:H	1:P:182:LEU:HD23	1.35	0.89
1:V:40:GLN:HE21	1:V:40:GLN:HA	1.37	0.89
1:J:50:GLU:HA	1:J:181:GLN:NE2	1.88	0.88
1:I:40:GLN:HA	1:I:40:GLN:HE21	1.39	0.88
1:J:167:LEU:H	1:J:167:LEU:HD13	1.37	0.88
1:K:167:LEU:HD13	1:K:167:LEU:H	1.39	0.88
1:V:180:ARG:HG2	1:V:181:GLN:N	1.88	0.88
1:J:40:GLN:HA	1:J:40:GLN:HE21	1.38	0.88
1:A:40:GLN:HA	1:A:40:GLN:HE21	1.38	0.87
1:O:167:LEU:HD13	1:O:167:LEU:H	1.38	0.87
1:R:184:LEU:HD22	1:R:185:GLU:H	1.39	0.87
1:D:182:LEU:H	1:D:182:LEU:HD23	1.39	0.87
1:M:40:GLN:HE21	1:M:40:GLN:HA	1.40	0.87
1:L:110:PHE:CE2	1:L:124:VAL:HG13	2.09	0.87
1:T:167:LEU:H	1:T:167:LEU:HD13	1.40	0.86
1:K:40:GLN:HA	1:K:40:GLN:HE21	1.40	0.86
1:V:100:ASN:ND2	1:V:102:LYS:HB2	1.90	0.86
1:L:192:LYS:HB2	1:M:45:GLN:HE21	1.41	0.86
1:T:40:GLN:HE21	1:T:40:GLN:HA	1.40	0.86
1:B:40:GLN:HE21	1:B:40:GLN:HA	1.40	0.86
1:N:40:GLN:HE21	1:N:40:GLN:HA	1.40	0.86
1:A:100:ASN:ND2	1:A:102:LYS:HB2	1.91	0.86
1:E:167:LEU:HD13	1:E:167:LEU:H	1.39	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:167:LEU:H	1:F:167:LEU:HD13	1.39	0.86
1:V:180:ARG:HG2	1:V:181:GLN:H	1.41	0.86
1:B:167:LEU:HD13	1:B:167:LEU:H	1.38	0.86
1:Q:192:LYS:HE2	1:Q:197:GLU:OE2	1.76	0.85
1:R:167:LEU:H	1:R:167:LEU:HD13	1.39	0.85
1:O:40:GLN:HA	1:O:40:GLN:HE21	1.42	0.85
1:L:167:LEU:HD13	1:L:167:LEU:H	1.39	0.85
1:H:167:LEU:HD13	1:H:167:LEU:H	1.41	0.85
1:O:100:ASN:ND2	1:O:102:LYS:HB2	1.92	0.85
1:B:193:ARG:NH1	1:B:193:ARG:HG2	1.79	0.84
1:Q:184:LEU:CD2	1:Q:185:GLU:H	1.89	0.84
1:C:40:GLN:HA	1:C:40:GLN:HE21	1.42	0.84
1:L:192:LYS:HE2	1:L:197:GLU:OE2	1.77	0.84
1:L:40:GLN:HA	1:L:40:GLN:HE21	1.40	0.84
1:O:182:LEU:H	1:O:182:LEU:HD23	1.41	0.84
1:D:40:GLN:HE21	1:D:40:GLN:HA	1.43	0.84
1:P:182:LEU:H	1:P:182:LEU:CD2	1.91	0.84
1:M:167:LEU:H	1:M:167:LEU:HD13	1.42	0.84
1:G:184:LEU:HD23	1:G:185:GLU:N	1.92	0.84
1:U:167:LEU:H	1:U:167:LEU:HD13	1.40	0.84
1:M:100:ASN:ND2	1:M:102:LYS:HB2	1.93	0.83
1:P:147:VAL:HG21	1:Q:124:VAL:HG22	1.61	0.83
1:R:40:GLN:HA	1:R:40:GLN:HE21	1.43	0.83
1:S:40:GLN:HE21	1:S:40:GLN:HA	1.42	0.82
1:Q:167:LEU:HD13	1:Q:167:LEU:H	1.44	0.82
1:E:100:ASN:ND2	1:E:102:LYS:HB2	1.95	0.82
1:G:40:GLN:HA	1:G:40:GLN:HE21	1.44	0.82
1:E:40:GLN:HE21	1:E:40:GLN:HA	1.44	0.82
1:J:100:ASN:ND2	1:J:102:LYS:HB2	1.95	0.82
1:V:167:LEU:H	1:V:167:LEU:HD13	1.42	0.82
1:R:147:VAL:HG21	1:S:124:VAL:HG22	1.61	0.81
1:P:100:ASN:ND2	1:P:102:LYS:HB2	1.95	0.81
1:G:167:LEU:H	1:G:167:LEU:HD13	1.45	0.81
1:A:182:LEU:HD23	1:A:182:LEU:H	1.45	0.81
1:A:184:LEU:HD23	1:A:185:GLU:H	1.43	0.81
1:H:40:GLN:HE21	1:H:40:GLN:HA	1.45	0.81
1:A:184:LEU:CD2	1:A:185:GLU:H	1.94	0.80
1:S:100:ASN:ND2	1:S:102:LYS:HB2	1.95	0.80
1:I:167:LEU:H	1:I:167:LEU:HD13	1.46	0.80
1:Q:100:ASN:ND2	1:Q:102:LYS:HB2	1.96	0.80
1:P:40:GLN:HE21	1:P:40:GLN:HA	1.46	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:208:CYS:HB2	1:T:33:ALA:HB2	1.64	0.80
1:S:167:LEU:H	1:S:167:LEU:HD13	1.47	0.80
1:B:182:LEU:H	1:B:182:LEU:HD23	1.47	0.80
1:S:184:LEU:HD23	1:S:185:GLU:H	1.45	0.79
1:F:147:VAL:HG21	1:G:124:VAL:HG22	1.62	0.79
1:P:204:ARG:HG3	1:Q:35:GLU:OE1	1.82	0.79
1:L:100:ASN:ND2	1:L:102:LYS:HB2	1.97	0.79
1:U:192:LYS:HB2	1:V:45:GLN:NE2	1.97	0.79
1:D:100:ASN:ND2	1:D:102:LYS:HB2	1.98	0.78
1:K:100:ASN:ND2	1:K:102:LYS:HB2	1.98	0.78
1:C:100:ASN:ND2	1:C:102:LYS:HB2	1.96	0.78
1:F:100:ASN:ND2	1:F:102:LYS:HB2	1.99	0.78
1:U:100:ASN:ND2	1:U:102:LYS:HB2	1.99	0.78
1:F:40:GLN:HA	1:F:40:GLN:HE21	1.48	0.78
1:N:167:LEU:HD13	1:N:167:LEU:H	1.49	0.78
1:P:167:LEU:HD13	1:P:167:LEU:H	1.49	0.78
1:T:166:ILE:HG22	1:T:167:LEU:HD12	1.66	0.78
1:A:33:ALA:HB2	1:J:208:CYS:HB2	1.64	0.78
1:A:110:PHE:CE2	1:A:124:VAL:HG13	2.19	0.77
1:I:100:ASN:ND2	1:I:102:LYS:HB2	1.99	0.77
1:R:100:ASN:ND2	1:R:102:LYS:HB2	1.99	0.77
1:D:110:PHE:CE2	1:D:124:VAL:HG13	2.19	0.77
1:S:47:LEU:H	1:S:47:LEU:HD23	1.48	0.77
1:N:69:HIS:HB3	1:O:167:LEU:HD21	1.66	0.77
1:U:204:ARG:HG3	1:V:35:GLU:OE1	1.83	0.77
1:H:147:VAL:HG21	1:I:124:VAL:HG22	1.66	0.77
1:N:100:ASN:ND2	1:N:102:LYS:HB2	1.99	0.77
1:R:192:LYS:HE2	1:R:197:GLU:OE2	1.83	0.77
1:V:110:PHE:CE2	1:V:124:VAL:HG13	2.19	0.77
1:D:147:VAL:HG21	1:E:124:VAL:HG22	1.66	0.77
1:I:182:LEU:H	1:I:182:LEU:HD23	1.49	0.77
1:U:110:PHE:CE2	1:U:124:VAL:HG13	2.20	0.76
1:L:147:VAL:HG21	1:M:124:VAL:HG22	1.68	0.76
1:P:208:CYS:HB2	1:R:33:ALA:HB2	1.67	0.76
1:H:100:ASN:ND2	1:H:102:LYS:HB2	1.99	0.76
1:E:86:HIS:ND1	1:F:121:HIS:HD2	1.84	0.76
1:L:192:LYS:HB2	1:M:45:GLN:NE2	1.99	0.76
1:B:110:PHE:CE2	1:B:124:VAL:HG13	2.19	0.76
1:J:40:GLN:CA	1:J:40:GLN:HE21	1.99	0.76
1:U:147:VAL:HG21	1:V:124:VAL:HG22	1.68	0.76
1:M:208:CYS:HB3	1:O:33:ALA:HB2	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:193:ARG:HG2	1:Q:193:ARG:HH11	1.50	0.76
1:J:204:ARG:HG3	1:K:35:GLU:OE1	1.86	0.75
1:I:50:GLU:HA	1:I:181:GLN:NE2	2.00	0.75
1:S:110:PHE:CE2	1:S:124:VAL:HG13	2.21	0.75
1:F:196:LEU:HD11	1:F:198:PRO:HG3	1.69	0.75
1:K:193:ARG:HB3	1:L:180:ARG:NE	2.01	0.75
1:G:100:ASN:ND2	1:G:102:LYS:HB2	2.01	0.75
1:M:182:LEU:N	1:M:182:LEU:HD23	2.02	0.75
1:I:195:ASP:HB3	1:J:77:GLU:HG3	1.68	0.75
1:S:147:VAL:HG21	1:T:124:VAL:HG22	1.67	0.75
1:U:205:TYR:HE2	1:U:209:ARG:NH2	1.85	0.75
1:Q:205:TYR:CE1	1:S:37:GLN:HB2	2.22	0.74
1:J:147:VAL:HG21	1:K:124:VAL:HG22	1.69	0.74
1:F:166:ILE:HG22	1:F:167:LEU:HD12	1.69	0.74
1:G:204:ARG:HG3	1:G:204:ARG:HH21	1.50	0.74
1:K:110:PHE:CE2	1:K:124:VAL:HG13	2.21	0.74
1:L:134:SER:HB3	1:L:137:LEU:HB2	1.69	0.74
1:Q:184:LEU:HD23	1:Q:185:GLU:H	1.51	0.74
1:T:110:PHE:CE2	1:T:124:VAL:HG13	2.22	0.74
1:K:192:LYS:HE2	1:K:197:GLU:OE2	1.87	0.74
1:E:110:PHE:CE2	1:E:124:VAL:HG13	2.22	0.74
1:N:147:VAL:HG21	1:O:124:VAL:HG22	1.67	0.74
1:U:182:LEU:H	1:U:182:LEU:HD23	1.51	0.74
1:I:166:ILE:HG22	1:I:167:LEU:HD12	1.70	0.74
1:H:110:PHE:CE2	1:H:124:VAL:HG13	2.23	0.74
1:C:47:LEU:HD23	1:C:47:LEU:H	1.52	0.74
1:J:184:LEU:HD13	1:J:185:GLU:H	1.53	0.74
1:F:110:PHE:CE2	1:F:124:VAL:HG13	2.23	0.73
1:D:204:ARG:HG3	1:E:35:GLU:OE1	1.88	0.73
1:F:86:HIS:ND1	1:G:121:HIS:HD2	1.87	0.73
1:C:47:LEU:N	1:C:47:LEU:HD23	2.02	0.73
1:R:166:ILE:HG22	1:R:167:LEU:HD12	1.70	0.73
1:G:186:VAL:HG11	1:H:171:TYR:HA	1.70	0.73
1:I:50:GLU:CA	1:I:181:GLN:HE22	2.01	0.73
1:G:110:PHE:CE2	1:G:124:VAL:HG13	2.24	0.73
1:H:186:VAL:HG21	1:I:171:TYR:HA	1.71	0.72
1:Q:147:VAL:HG21	1:R:124:VAL:HG22	1.71	0.72
1:U:184:LEU:HD13	1:U:185:GLU:O	1.89	0.72
1:M:70:ARG:HH11	1:M:70:ARG:HG3	1.54	0.72
1:D:82:ASN:H	1:D:82:ASN:HD22	1.36	0.72
1:K:193:ARG:HE	1:L:180:ARG:NH2	1.87	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:40:GLN:CA	1:Q:40:GLN:HE21	2.02	0.72
1:D:47:LEU:N	1:D:47:LEU:HD23	2.04	0.72
1:D:47:LEU:HD23	1:D:47:LEU:H	1.54	0.72
1:B:100:ASN:ND2	1:B:102:LYS:HB2	2.03	0.72
1:B:192:LYS:HB2	1:C:45:GLN:HE21	1.55	0.72
1:O:110:PHE:CE2	1:O:124:VAL:HG13	2.24	0.72
1:A:166:ILE:HG22	1:A:167:LEU:HD12	1.70	0.72
1:P:192:LYS:HB2	1:Q:45:GLN:NE2	2.05	0.72
1:K:40:GLN:CA	1:K:40:GLN:HE21	2.01	0.72
1:M:110:PHE:CE2	1:M:124:VAL:HG13	2.25	0.72
1:A:82:ASN:H	1:A:82:ASN:HD22	1.36	0.72
1:J:181:GLN:O	1:J:181:GLN:HG3	1.90	0.71
1:I:147:VAL:HG21	1:J:124:VAL:HG22	1.71	0.71
1:P:192:LYS:HB2	1:Q:45:GLN:HE21	1.55	0.71
1:A:47:LEU:N	1:A:47:LEU:HD23	2.05	0.71
1:R:47:LEU:N	1:R:47:LEU:HD23	2.05	0.71
1:N:185:GLU:OE1	1:O:177:LYS:NZ	2.23	0.71
1:D:167:LEU:H	1:D:167:LEU:CD1	2.01	0.71
1:T:147:VAL:HG21	1:U:124:VAL:HG22	1.71	0.71
1:G:180:ARG:HG2	1:G:181:GLN:H	1.54	0.71
1:R:110:PHE:CE2	1:R:124:VAL:HG13	2.25	0.71
1:J:110:PHE:CE2	1:J:124:VAL:HG13	2.26	0.71
1:R:86:HIS:ND1	1:S:121:HIS:HD2	1.88	0.71
1:T:100:ASN:ND2	1:T:102:LYS:HB2	2.05	0.71
1:E:166:ILE:HG22	1:E:167:LEU:HD12	1.72	0.71
1:E:147:VAL:HG21	1:F:124:VAL:HG22	1.70	0.71
1:C:184:LEU:HD12	1:C:185:GLU:O	1.89	0.71
1:A:124:VAL:HG22	1:K:147:VAL:HG21	1.72	0.71
1:G:147:VAL:HG21	1:H:124:VAL:HG22	1.72	0.71
1:O:147:VAL:HG21	1:P:124:VAL:HG22	1.73	0.71
1:M:184:LEU:HD23	1:M:185:GLU:H	1.55	0.71
1:A:182:LEU:H	1:A:182:LEU:CD2	2.04	0.71
1:O:69:HIS:HB3	1:P:167:LEU:HD21	1.71	0.71
1:A:47:LEU:H	1:A:47:LEU:HD23	1.56	0.71
1:U:40:GLN:CA	1:U:40:GLN:HE21	2.03	0.70
1:N:110:PHE:CE2	1:N:124:VAL:HG13	2.26	0.70
1:D:36:TYR:OH	1:D:40:GLN:HG3	1.91	0.70
1:R:134:SER:HB3	1:R:137:LEU:HB2	1.74	0.70
1:A:40:GLN:HE21	1:A:40:GLN:CA	2.05	0.70
1:L:40:GLN:HE21	1:L:40:GLN:CA	2.04	0.70
1:R:70:ARG:HG3	1:R:70:ARG:HH11	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:182:LEU:HD23	1:L:182:LEU:H	1.55	0.70
1:Q:182:LEU:N	1:Q:182:LEU:HD23	2.02	0.70
1:R:40:GLN:CA	1:R:40:GLN:HE21	2.05	0.70
1:G:166:ILE:HG22	1:G:167:LEU:HD12	1.73	0.70
1:J:50:GLU:HA	1:J:181:GLN:HE22	1.57	0.70
1:S:47:LEU:N	1:S:47:LEU:HD23	2.07	0.70
1:F:47:LEU:H	1:F:47:LEU:HD23	1.56	0.70
1:T:204:ARG:HG3	1:U:35:GLU:OE1	1.92	0.70
1:R:47:LEU:H	1:R:47:LEU:HD23	1.56	0.69
1:P:86:HIS:ND1	1:Q:121:HIS:HD2	1.89	0.69
1:O:47:LEU:N	1:O:47:LEU:HD23	2.07	0.69
1:B:167:LEU:CD1	1:B:167:LEU:H	2.04	0.69
1:M:147:VAL:HG21	1:N:124:VAL:HG22	1.73	0.69
1:F:47:LEU:HD23	1:F:47:LEU:N	2.07	0.69
1:U:196:LEU:HD12	1:U:198:PRO:HG3	1.74	0.69
1:V:40:GLN:HE21	1:V:40:GLN:CA	2.04	0.69
1:V:47:LEU:H	1:V:47:LEU:HD23	1.56	0.69
1:B:40:GLN:CA	1:B:40:GLN:HE21	2.06	0.69
1:Q:82:ASN:H	1:Q:82:ASN:HD22	1.38	0.69
1:L:124:VAL:HG22	1:V:147:VAL:HG21	1.74	0.69
1:V:47:LEU:N	1:V:47:LEU:HD23	2.07	0.69
1:Q:86:HIS:ND1	1:R:121:HIS:HD2	1.90	0.69
1:K:193:ARG:HH12	1:L:182:LEU:HD22	1.58	0.69
1:S:184:LEU:HD23	1:S:185:GLU:N	2.08	0.69
1:D:166:ILE:HG22	1:D:167:LEU:HD12	1.75	0.69
1:C:167:LEU:CD1	1:C:167:LEU:H	2.06	0.69
1:G:36:TYR:OH	1:G:40:GLN:HG3	1.91	0.69
1:V:166:ILE:HG22	1:V:167:LEU:HD12	1.75	0.69
1:U:196:LEU:CD1	1:U:198:PRO:HG3	2.23	0.69
1:K:182:LEU:HD23	1:K:182:LEU:H	1.57	0.69
1:U:86:HIS:ND1	1:V:121:HIS:HD2	1.91	0.69
1:T:208:CYS:HB3	1:V:33:ALA:HB2	1.75	0.69
1:O:192:LYS:HB2	1:P:45:GLN:NE2	2.08	0.69
1:O:134:SER:HB3	1:O:137:LEU:HB2	1.74	0.69
1:V:82:ASN:HD22	1:V:82:ASN:H	1.40	0.69
1:T:47:LEU:HD23	1:T:47:LEU:H	1.58	0.69
1:G:86:HIS:ND1	1:H:121:HIS:HD2	1.91	0.69
1:I:40:GLN:CA	1:I:40:GLN:HE21	2.04	0.69
1:P:47:LEU:HD23	1:P:47:LEU:N	2.08	0.68
1:T:186:VAL:HG21	1:U:171:TYR:HA	1.74	0.68
1:E:82:ASN:HD22	1:E:82:ASN:H	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:36:TYR:OH	1:Q:40:GLN:HG3	1.93	0.68
1:T:47:LEU:HD23	1:T:47:LEU:N	2.08	0.68
1:F:192:LYS:HB3	1:G:47:LEU:HA	1.76	0.68
1:L:86:HIS:ND1	1:M:121:HIS:HD2	1.92	0.68
1:C:110:PHE:CE2	1:C:124:VAL:HG13	2.28	0.68
1:L:82:ASN:H	1:L:82:ASN:HD22	1.41	0.68
1:I:86:HIS:ND1	1:J:121:HIS:HD2	1.91	0.68
1:F:204:ARG:HG3	1:F:204:ARG:NH2	2.04	0.68
1:C:184:LEU:HD13	1:C:185:GLU:N	2.09	0.68
1:U:205:TYR:CE2	1:U:209:ARG:NH2	2.62	0.68
1:A:167:LEU:H	1:A:167:LEU:CD1	2.07	0.67
1:N:82:ASN:HD22	1:N:82:ASN:H	1.42	0.67
1:C:166:ILE:HG22	1:C:167:LEU:HD12	1.76	0.67
1:G:186:VAL:HB	1:H:174:SER:HB3	1.76	0.67
1:B:147:VAL:HG21	1:C:124:VAL:HG22	1.76	0.67
1:N:179:PRO:O	1:N:180:ARG:O	2.11	0.67
1:A:121:HIS:HD2	1:K:86:HIS:ND1	1.91	0.67
1:L:166:ILE:HG22	1:L:167:LEU:HD12	1.75	0.67
1:H:166:ILE:HG22	1:H:167:LEU:HD12	1.75	0.67
1:G:180:ARG:HG2	1:G:181:GLN:N	2.08	0.67
1:L:184:LEU:HD23	1:L:185:GLU:N	2.09	0.67
1:R:113:VAL:HG12	1:R:154:ALA:HB1	1.77	0.67
1:U:166:ILE:HG22	1:U:167:LEU:HD12	1.76	0.67
1:C:147:VAL:HG21	1:D:124:VAL:HG22	1.77	0.67
1:T:86:HIS:ND1	1:U:121:HIS:HD2	1.92	0.67
1:T:50:GLU:HA	1:T:181:GLN:NE2	2.10	0.67
1:N:70:ARG:HH11	1:N:70:ARG:HG3	1.60	0.67
1:R:52:ILE:HG13	1:R:175:LEU:HD11	1.77	0.67
1:G:134:SER:HB3	1:G:137:LEU:HB2	1.77	0.67
1:G:182:LEU:CD2	1:G:182:LEU:H	2.06	0.67
1:K:47:LEU:HD23	1:K:47:LEU:N	2.09	0.67
1:C:40:GLN:CA	1:C:40:GLN:HE21	2.06	0.67
1:C:184:LEU:HD13	1:C:185:GLU:H	1.59	0.67
1:M:184:LEU:HD23	1:M:185:GLU:N	2.10	0.67
1:U:134:SER:HB3	1:U:137:LEU:HB2	1.75	0.67
1:H:69:HIS:HB3	1:I:167:LEU:HD21	1.77	0.66
1:N:166:ILE:HG22	1:N:167:LEU:HD12	1.77	0.66
1:U:47:LEU:HD23	1:U:47:LEU:N	2.10	0.66
1:O:192:LYS:HE2	1:O:197:GLU:OE2	1.95	0.66
1:T:181:GLN:O	1:T:181:GLN:HG3	1.96	0.66
1:Q:134:SER:HB3	1:Q:137:LEU:HB2	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:167:LEU:CD1	1:K:167:LEU:H	2.07	0.66
1:O:167:LEU:H	1:O:167:LEU:CD1	2.07	0.66
1:A:147:VAL:HG21	1:B:124:VAL:HG22	1.78	0.66
1:M:49:PRO:HD2	1:M:50:GLU:OE1	1.96	0.66
1:O:40:GLN:CA	1:O:40:GLN:HE21	2.09	0.66
1:Q:110:PHE:CE2	1:Q:124:VAL:HG13	2.30	0.66
1:G:47:LEU:HD23	1:G:47:LEU:H	1.61	0.66
1:D:208:CYS:HB2	1:F:33:ALA:HB2	1.77	0.66
1:O:195:ASP:HB3	1:P:77:GLU:HG3	1.78	0.66
1:S:113:VAL:HG12	1:S:154:ALA:HB1	1.77	0.66
1:L:69:HIS:HB3	1:M:167:LEU:HD21	1.78	0.66
1:E:47:LEU:N	1:E:47:LEU:HD23	2.10	0.66
1:T:69:HIS:HB3	1:U:167:LEU:HD21	1.76	0.66
1:F:192:LYS:HG2	1:G:51:TYR:CE1	2.31	0.66
1:B:69:HIS:HB3	1:C:167:LEU:HD21	1.78	0.66
1:H:134:SER:HB3	1:H:137:LEU:HB2	1.77	0.66
1:N:184:LEU:O	1:O:173:ARG:NH2	2.28	0.66
1:K:139:LEU:O	1:K:143:ARG:HG3	1.95	0.66
1:B:47:LEU:HD23	1:B:47:LEU:N	2.11	0.66
1:O:49:PRO:HD2	1:O:50:GLU:OE1	1.96	0.66
1:A:86:HIS:ND1	1:B:121:HIS:HD2	1.93	0.66
1:A:184:LEU:CD2	1:A:185:GLU:N	2.59	0.65
1:R:196:LEU:HD12	1:R:198:PRO:HG3	1.77	0.65
1:K:166:ILE:HG22	1:K:167:LEU:HD12	1.76	0.65
1:T:134:SER:HB3	1:T:137:LEU:HB2	1.78	0.65
1:M:47:LEU:H	1:M:47:LEU:HD23	1.61	0.65
1:H:86:HIS:ND1	1:I:121:HIS:HD2	1.94	0.65
1:S:86:HIS:ND1	1:T:121:HIS:HD2	1.94	0.65
1:N:182:LEU:N	1:N:182:LEU:CD2	2.55	0.65
1:N:40:GLN:CA	1:N:40:GLN:HE21	2.09	0.65
1:K:193:ARG:HB3	1:L:180:ARG:HE	1.61	0.65
1:J:166:ILE:HG22	1:J:167:LEU:HD12	1.79	0.65
1:P:52:ILE:HG13	1:P:175:LEU:HD11	1.77	0.65
1:C:86:HIS:ND1	1:D:121:HIS:HD2	1.95	0.65
1:J:167:LEU:H	1:J:167:LEU:CD1	2.09	0.65
1:K:193:ARG:NE	1:L:180:ARG:CZ	2.59	0.65
1:S:204:ARG:HG3	1:T:35:GLU:OE1	1.97	0.65
1:M:69:HIS:HB3	1:N:167:LEU:HD21	1.79	0.65
1:L:184:LEU:HD23	1:L:185:GLU:H	1.62	0.65
1:O:166:ILE:HG22	1:O:167:LEU:HD12	1.78	0.65
1:V:100:ASN:HD21	1:V:102:LYS:HB2	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:40:GLN:HE21	1:H:40:GLN:CA	2.10	0.65
1:I:110:PHE:CE2	1:I:124:VAL:HG13	2.32	0.65
1:D:49:PRO:HD2	1:D:50:GLU:OE1	1.96	0.65
1:C:82:ASN:HB2	1:D:117:ASP:OD1	1.96	0.65
1:L:167:LEU:CD1	1:L:167:LEU:H	2.10	0.64
1:U:167:LEU:CD1	1:U:167:LEU:H	2.09	0.64
1:D:182:LEU:H	1:D:182:LEU:CD2	2.10	0.64
1:Q:184:LEU:HD22	1:Q:185:GLU:H	1.62	0.64
1:Q:166:ILE:HG22	1:Q:167:LEU:HD12	1.77	0.64
1:J:134:SER:HB3	1:J:137:LEU:HB2	1.80	0.64
1:F:196:LEU:C	1:F:196:LEU:HD13	2.18	0.64
1:M:47:LEU:HD23	1:M:47:LEU:N	2.13	0.64
1:M:82:ASN:HD22	1:M:82:ASN:H	1.45	0.64
1:T:182:LEU:H	1:T:182:LEU:HD23	1.60	0.64
1:B:47:LEU:HD23	1:B:47:LEU:H	1.62	0.64
1:O:82:ASN:H	1:O:82:ASN:HD22	1.45	0.64
1:P:50:GLU:HA	1:P:181:GLN:HE22	1.63	0.64
1:S:134:SER:HB3	1:S:137:LEU:HB2	1.78	0.64
1:G:69:HIS:HB3	1:H:167:LEU:HD21	1.79	0.64
1:S:40:GLN:HE21	1:S:40:GLN:CA	2.10	0.64
1:F:167:LEU:H	1:F:167:LEU:CD1	2.11	0.64
1:C:182:LEU:N	1:C:182:LEU:CD2	2.47	0.64
1:K:82:ASN:HD22	1:K:82:ASN:H	1.44	0.64
1:T:70:ARG:HH11	1:T:70:ARG:HG3	1.63	0.64
1:A:167:LEU:N	1:A:167:LEU:HD13	2.11	0.64
1:U:47:LEU:HD23	1:U:47:LEU:H	1.62	0.64
1:M:86:HIS:ND1	1:N:121:HIS:HD2	1.96	0.64
1:E:167:LEU:H	1:E:167:LEU:CD1	2.09	0.64
1:Q:207:SER:C	1:Q:209:ARG:H	2.00	0.64
1:Q:192:LYS:HB2	1:R:45:GLN:HE21	1.63	0.64
1:E:40:GLN:CA	1:E:40:GLN:HE21	2.11	0.64
1:H:204:ARG:HG3	1:I:35:GLU:OE1	1.98	0.64
1:K:47:LEU:HD23	1:K:47:LEU:H	1.61	0.63
1:Q:52:ILE:HG13	1:Q:175:LEU:HD11	1.80	0.63
1:T:40:GLN:CA	1:T:40:GLN:HE21	2.11	0.63
1:C:36:TYR:OH	1:C:40:GLN:HG3	1.98	0.63
1:P:47:LEU:HD23	1:P:47:LEU:H	1.61	0.63
1:C:204:ARG:HG3	1:C:204:ARG:HH21	1.63	0.63
1:B:70:ARG:HH11	1:B:70:ARG:HG3	1.64	0.63
1:M:166:ILE:HG22	1:M:167:LEU:HD12	1.79	0.63
1:S:166:ILE:HG22	1:S:167:LEU:HD12	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:47:LEU:H	1:J:47:LEU:HD23	1.63	0.63
1:O:47:LEU:H	1:O:47:LEU:HD23	1.61	0.63
1:V:167:LEU:H	1:V:167:LEU:CD1	2.12	0.63
1:P:69:HIS:HB3	1:Q:167:LEU:HD21	1.81	0.63
1:D:167:LEU:N	1:D:167:LEU:CD1	2.62	0.63
1:U:205:TYR:HE2	1:U:209:ARG:HH22	1.46	0.63
1:G:82:ASN:HD22	1:G:82:ASN:H	1.47	0.63
1:M:123:ASP:OD1	1:M:153:ARG:NH1	2.32	0.63
1:R:82:ASN:H	1:R:82:ASN:HD22	1.44	0.63
1:G:40:GLN:CA	1:G:40:GLN:HE21	2.12	0.62
1:Q:193:ARG:NH1	1:Q:193:ARG:HG2	2.10	0.62
1:E:52:ILE:HG13	1:E:175:LEU:HD11	1.81	0.62
1:R:193:ARG:HH11	1:R:193:ARG:HG2	1.64	0.62
1:B:82:ASN:HD22	1:B:82:ASN:H	1.47	0.62
1:Q:204:ARG:HG3	1:R:35:GLU:OE1	1.99	0.62
1:P:70:ARG:HH11	1:P:70:ARG:HG3	1.64	0.62
1:G:195:ASP:HB3	1:H:77:GLU:HG3	1.80	0.62
1:G:47:LEU:HD23	1:G:47:LEU:N	2.13	0.62
1:S:82:ASN:HD22	1:S:82:ASN:H	1.47	0.62
1:F:208:CYS:HB3	1:H:33:ALA:HB2	1.81	0.62
1:G:52:ILE:HG13	1:G:175:LEU:HD11	1.79	0.62
1:J:70:ARG:HG3	1:J:70:ARG:HH11	1.64	0.62
1:S:180:ARG:HH11	1:S:180:ARG:HG2	1.64	0.62
1:K:193:ARG:NE	1:L:180:ARG:NH2	2.47	0.62
1:R:167:LEU:CD1	1:R:167:LEU:H	2.12	0.62
1:U:82:ASN:H	1:U:82:ASN:HD22	1.47	0.62
1:V:197:GLU:O	1:V:200:VAL:HB	1.99	0.62
1:K:193:ARG:CB	1:L:180:ARG:HE	2.13	0.62
1:P:182:LEU:N	1:P:182:LEU:HD23	2.12	0.62
1:I:134:SER:HB3	1:I:137:LEU:HB2	1.82	0.62
1:P:82:ASN:HD22	1:P:82:ASN:H	1.48	0.62
1:H:167:LEU:CD1	1:H:167:LEU:H	2.13	0.62
1:K:134:SER:HB3	1:K:137:LEU:HB2	1.82	0.62
1:A:100:ASN:HD22	1:A:102:LYS:HB2	1.64	0.62
1:P:110:PHE:CE2	1:P:124:VAL:HG13	2.34	0.62
1:J:47:LEU:N	1:J:47:LEU:HD23	2.15	0.62
1:C:134:SER:HB3	1:C:137:LEU:HB2	1.80	0.62
1:A:196:LEU:CD1	1:A:198:PRO:HG3	2.30	0.62
1:I:24:LEU:HB3	1:J:30:GLN:NE2	2.14	0.62
1:O:70:ARG:HH11	1:O:70:ARG:HG3	1.64	0.62
1:L:47:LEU:HD23	1:L:47:LEU:H	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:167:LEU:HD13	1:C:167:LEU:N	2.12	0.62
1:T:24:LEU:HB3	1:U:30:GLN:NE2	2.13	0.62
1:K:182:LEU:N	1:K:182:LEU:HD23	2.15	0.61
1:I:47:LEU:H	1:I:47:LEU:HD23	1.65	0.61
1:E:207:SER:C	1:E:209:ARG:H	2.04	0.61
1:L:47:LEU:N	1:L:47:LEU:HD23	2.14	0.61
1:N:47:LEU:HD23	1:N:47:LEU:H	1.64	0.61
1:H:82:ASN:HD22	1:H:82:ASN:H	1.46	0.61
1:Q:167:LEU:CD1	1:Q:167:LEU:H	2.14	0.61
1:F:82:ASN:H	1:F:82:ASN:HD22	1.46	0.61
1:B:86:HIS:ND1	1:C:121:HIS:HD2	1.98	0.61
1:A:70:ARG:HG3	1:A:70:ARG:HH11	1.64	0.61
1:Q:47:LEU:N	1:Q:47:LEU:HD23	2.15	0.61
1:H:204:ARG:HH21	1:H:204:ARG:HG3	1.65	0.61
1:V:52:ILE:HG13	1:V:175:LEU:HD11	1.82	0.61
1:Q:24:LEU:HB3	1:R:30:GLN:NE2	2.16	0.61
1:F:113:VAL:HG12	1:F:154:ALA:HB1	1.82	0.61
1:A:113:VAL:HG12	1:A:154:ALA:HB1	1.82	0.61
1:D:86:HIS:ND1	1:E:121:HIS:HD2	1.98	0.61
1:B:196:LEU:CD1	1:B:198:PRO:HG3	2.29	0.61
1:F:52:ILE:HG13	1:F:175:LEU:HD11	1.81	0.61
1:H:195:ASP:HB3	1:I:77:GLU:HG3	1.83	0.61
1:S:204:ARG:HG3	1:S:204:ARG:HH21	1.65	0.61
1:B:166:ILE:HG22	1:B:167:LEU:HD12	1.81	0.61
1:B:182:LEU:H	1:B:182:LEU:CD2	2.12	0.61
1:T:208:CYS:CB	1:V:33:ALA:HB2	2.31	0.61
1:T:49:PRO:HD2	1:T:50:GLU:OE1	2.00	0.61
1:B:187:ASP:OD2	1:B:189:THR:HB	2.01	0.61
1:C:192:LYS:HB2	1:D:45:GLN:NE2	2.15	0.61
1:C:167:LEU:N	1:C:167:LEU:CD1	2.64	0.61
1:A:36:TYR:OH	1:A:40:GLN:HG3	2.01	0.61
1:U:192:LYS:HB2	1:V:45:GLN:HE21	1.63	0.61
1:T:165:CYS:HA	2:T:2022:HOH:O	2.00	0.61
1:N:47:LEU:HD23	1:N:47:LEU:N	2.15	0.61
1:J:195:ASP:HB3	1:K:77:GLU:HG3	1.81	0.61
1:S:208:CYS:HB2	1:U:33:ALA:HB2	1.83	0.60
1:Q:113:VAL:HG12	1:Q:154:ALA:HB1	1.83	0.60
1:A:82:ASN:HB2	1:B:117:ASP:OD1	2.01	0.60
1:N:86:HIS:ND1	1:O:121:HIS:HD2	1.99	0.60
1:H:52:ILE:HG13	1:H:175:LEU:HD11	1.83	0.60
1:H:47:LEU:HD23	1:H:47:LEU:N	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:70:ARG:HG3	1:C:70:ARG:HH11	1.64	0.60
1:Q:205:TYR:HE1	1:S:37:GLN:HB2	1.63	0.60
1:L:121:HIS:HD2	1:V:86:HIS:ND1	1.99	0.60
1:G:192:LYS:HE2	1:H:45:GLN:HE22	1.65	0.60
1:E:195:ASP:HB3	1:F:77:GLU:HG3	1.83	0.60
1:M:40:GLN:CA	1:M:40:GLN:HE21	2.12	0.60
1:O:100:ASN:HD21	1:O:102:LYS:HB2	1.62	0.60
1:U:100:ASN:HD21	1:U:102:LYS:HB2	1.66	0.60
1:I:182:LEU:H	1:I:182:LEU:CD2	2.13	0.60
1:N:124:VAL:O	1:N:153:ARG:HD3	2.01	0.60
1:T:196:LEU:HD13	1:T:198:PRO:HG3	1.82	0.60
1:D:69:HIS:HB3	1:E:167:LEU:HD21	1.83	0.60
1:M:167:LEU:CD1	1:M:167:LEU:H	2.14	0.60
1:P:166:ILE:HG22	1:P:167:LEU:HD12	1.82	0.60
1:G:113:VAL:HG12	1:G:154:ALA:HB1	1.82	0.60
1:N:36:TYR:OH	1:N:40:GLN:HG3	2.01	0.60
1:V:192:LYS:NZ	1:V:197:GLU:OE2	2.34	0.60
1:I:47:LEU:N	1:I:47:LEU:HD23	2.16	0.60
1:L:35:GLU:OE1	1:V:204:ARG:HG3	2.02	0.60
1:A:134:SER:HB3	1:A:137:LEU:HB2	1.84	0.60
1:C:49:PRO:HD2	1:C:50:GLU:OE1	2.02	0.60
1:J:167:LEU:HD13	1:J:167:LEU:N	2.14	0.60
1:D:52:ILE:HG13	1:D:175:LEU:HD11	1.83	0.60
1:J:52:ILE:HG13	1:J:175:LEU:HD11	1.83	0.60
1:J:86:HIS:ND1	1:K:121:HIS:HD2	2.00	0.60
1:G:70:ARG:HH11	1:G:70:ARG:HG3	1.66	0.60
1:F:36:TYR:OH	1:F:40:GLN:HG3	2.01	0.59
1:L:82:ASN:HB2	1:M:117:ASP:OD1	2.02	0.59
1:D:134:SER:HB3	1:D:137:LEU:HB2	1.83	0.59
1:U:52:ILE:HG13	1:U:175:LEU:HD11	1.84	0.59
1:E:47:LEU:H	1:E:47:LEU:HD23	1.65	0.59
1:L:45:GLN:HE21	1:V:192:LYS:HB2	1.67	0.59
1:K:52:ILE:HG13	1:K:175:LEU:HD11	1.83	0.59
1:O:167:LEU:N	1:O:167:LEU:CD1	2.65	0.59
1:F:134:SER:HB3	1:F:137:LEU:HB2	1.83	0.59
1:T:167:LEU:CD1	1:T:167:LEU:H	2.14	0.59
1:K:182:LEU:CD2	1:K:182:LEU:H	2.14	0.59
1:Q:182:LEU:N	1:Q:182:LEU:CD2	2.57	0.59
1:G:186:VAL:HG21	1:H:170:ASP:C	2.22	0.59
1:N:70:ARG:NH1	1:N:70:ARG:HG3	2.17	0.59
1:D:70:ARG:HH11	1:D:70:ARG:HG3	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:70:ARG:HG3	1:F:70:ARG:HH11	1.67	0.59
1:Q:69:HIS:HB3	1:R:167:LEU:HD21	1.84	0.59
1:M:167:LEU:N	1:M:167:LEU:HD13	2.17	0.59
1:H:47:LEU:HD23	1:H:47:LEU:H	1.66	0.59
1:I:82:ASN:HD22	1:I:82:ASN:H	1.50	0.59
1:B:204:ARG:HG3	1:C:35:GLU:OE1	2.01	0.59
1:V:196:LEU:O	1:V:198:PRO:HD3	2.03	0.59
1:A:167:LEU:N	1:A:167:LEU:CD1	2.65	0.59
1:A:100:ASN:HD21	1:A:102:LYS:HB2	1.67	0.59
1:D:123:ASP:OD1	1:D:153:ARG:NH1	2.36	0.59
1:R:196:LEU:CD1	1:R:198:PRO:HG3	2.32	0.59
1:R:193:ARG:HG2	1:S:50:GLU:OE2	2.02	0.59
1:M:36:TYR:OH	1:M:40:GLN:HG3	2.02	0.59
1:B:167:LEU:CD1	1:B:167:LEU:N	2.65	0.59
1:U:183:PRO:HB3	1:V:170:ASP:OD1	2.02	0.59
1:M:192:LYS:HG3	1:N:45:GLN:NE2	2.17	0.59
1:A:52:ILE:HG13	1:A:175:LEU:HD11	1.85	0.59
1:I:52:ILE:HG13	1:I:175:LEU:HD11	1.84	0.59
1:M:134:SER:HB3	1:M:137:LEU:HB2	1.84	0.59
1:E:100:ASN:HD21	1:E:102:LYS:HB2	1.65	0.59
1:A:45:GLN:HE21	1:K:192:LYS:HB2	1.68	0.59
1:E:182:LEU:O	1:E:184:LEU:N	2.36	0.59
1:L:52:ILE:HG13	1:L:175:LEU:HD11	1.84	0.59
1:C:52:ILE:HG13	1:C:175:LEU:HD11	1.84	0.59
1:J:82:ASN:HD22	1:J:82:ASN:H	1.50	0.59
1:B:192:LYS:HB2	1:C:45:GLN:NE2	2.18	0.58
1:K:36:TYR:OH	1:K:40:GLN:HG3	2.03	0.58
1:U:69:HIS:HB3	1:V:167:LEU:HD21	1.85	0.58
1:V:192:LYS:HE2	1:V:197:GLU:OE2	2.02	0.58
1:Q:47:LEU:HD23	1:Q:47:LEU:H	1.67	0.58
1:J:192:LYS:HB2	1:K:45:GLN:HE21	1.67	0.58
1:L:139:LEU:O	1:L:143:ARG:HG3	2.03	0.58
1:M:52:ILE:HG13	1:M:175:LEU:HD11	1.85	0.58
1:V:70:ARG:HH11	1:V:70:ARG:HG3	1.66	0.58
1:H:113:VAL:HG12	1:H:154:ALA:HB1	1.85	0.58
1:H:208:CYS:HB3	1:J:33:ALA:HB2	1.84	0.58
1:M:100:ASN:HD22	1:M:102:LYS:HB2	1.66	0.58
1:L:117:ASP:OD1	1:V:82:ASN:HB2	2.03	0.58
1:G:196:LEU:HD13	1:G:197:GLU:H	1.66	0.58
1:B:52:ILE:HG13	1:B:175:LEU:HD11	1.86	0.58
1:E:204:ARG:HH21	1:E:204:ARG:HG3	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:179:PRO:C	1:N:180:ARG:O	2.42	0.58
1:O:86:HIS:ND1	1:P:121:HIS:HD2	2.00	0.58
1:Q:70:ARG:HH11	1:Q:70:ARG:HG3	1.68	0.58
1:Q:100:ASN:HD21	1:Q:102:LYS:HB2	1.66	0.58
1:M:70:ARG:HG3	1:M:70:ARG:NH1	2.18	0.58
1:M:33:ALA:HB2	1:V:208:CYS:HB2	1.84	0.58
1:V:134:SER:HB3	1:V:137:LEU:HB2	1.85	0.58
1:L:50:GLU:CD	1:V:193:ARG:HG2	2.24	0.58
1:H:36:TYR:OH	1:H:40:GLN:HG3	2.04	0.58
1:U:49:PRO:HD2	1:U:50:GLU:OE1	2.03	0.58
1:B:113:VAL:HG12	1:B:154:ALA:HB1	1.85	0.58
1:D:192:LYS:HG3	1:E:45:GLN:HE22	1.69	0.58
1:J:100:ASN:HD21	1:J:102:LYS:HB2	1.66	0.58
1:T:124:VAL:O	1:T:153:ARG:HD3	2.04	0.58
1:B:57:ALA:HB3	1:B:61:GLN:HG3	1.86	0.58
1:J:69:HIS:HB3	1:K:167:LEU:HD21	1.84	0.58
1:G:184:LEU:HD23	1:G:185:GLU:H	1.68	0.58
1:D:192:LYS:HB2	1:E:45:GLN:HE21	1.69	0.58
1:R:49:PRO:HD2	1:R:50:GLU:OE1	2.04	0.58
1:F:123:ASP:OD1	1:F:153:ARG:NH1	2.37	0.57
1:T:204:ARG:HH21	1:T:204:ARG:HG3	1.68	0.57
1:N:205:TYR:HE2	1:N:209:ARG:NH2	2.02	0.57
1:I:204:ARG:HG3	1:J:35:GLU:OE1	2.04	0.57
1:R:204:ARG:HD2	1:T:36:TYR:CZ	2.38	0.57
1:R:167:LEU:CD1	1:R:167:LEU:N	2.67	0.57
1:N:204:ARG:HG3	1:N:204:ARG:HH21	1.69	0.57
1:J:139:LEU:O	1:J:143:ARG:HG3	2.03	0.57
1:T:192:LYS:HB2	1:U:45:GLN:HE21	1.69	0.57
1:F:182:LEU:O	1:F:182:LEU:HG	2.02	0.57
1:I:100:ASN:HD21	1:I:102:LYS:HB2	1.68	0.57
1:E:139:LEU:O	1:E:143:ARG:HG3	2.04	0.57
1:E:70:ARG:HG3	1:E:70:ARG:HH11	1.67	0.57
1:K:167:LEU:N	1:K:167:LEU:CD1	2.68	0.57
1:F:40:GLN:HE21	1:F:40:GLN:CA	2.15	0.57
1:C:184:LEU:CD1	1:C:185:GLU:O	2.52	0.57
1:R:139:LEU:O	1:R:143:ARG:HG3	2.04	0.57
1:U:70:ARG:HG3	1:U:70:ARG:HH11	1.69	0.57
1:E:36:TYR:OH	1:E:40:GLN:HG3	2.04	0.57
1:D:179:PRO:O	1:D:180:ARG:C	2.42	0.57
1:E:167:LEU:N	1:E:167:LEU:CD1	2.68	0.57
1:U:167:LEU:CD1	1:U:167:LEU:N	2.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:100:ASN:HD22	1:S:102:LYS:HB2	1.68	0.57
1:R:69:HIS:HB3	1:S:167:LEU:HD21	1.85	0.57
1:F:147:VAL:HG21	1:G:124:VAL:CG2	2.32	0.57
1:O:52:ILE:HG13	1:O:175:LEU:HD11	1.85	0.57
1:B:208:CYS:HB2	1:D:33:ALA:HB2	1.87	0.57
1:L:182:LEU:CD2	1:L:182:LEU:H	2.16	0.57
1:R:184:LEU:HD22	1:R:185:GLU:N	2.17	0.57
1:E:192:LYS:NZ	1:E:195:ASP:O	2.38	0.57
1:G:24:LEU:HB3	1:H:30:GLN:NE2	2.19	0.57
1:O:204:ARG:HD2	1:Q:36:TYR:CZ	2.40	0.57
1:T:167:LEU:N	1:T:167:LEU:HD13	2.15	0.57
1:F:167:LEU:CD1	1:F:167:LEU:N	2.68	0.57
1:U:40:GLN:NE2	1:U:40:GLN:HA	2.15	0.57
1:Q:82:ASN:HB2	1:R:117:ASP:OD1	2.05	0.57
1:Q:49:PRO:HD2	1:Q:50:GLU:OE1	2.04	0.57
1:A:40:GLN:HA	1:A:40:GLN:NE2	2.16	0.56
1:L:36:TYR:OH	1:L:40:GLN:HG3	2.05	0.56
1:I:124:VAL:O	1:I:153:ARG:HD3	2.04	0.56
1:K:196:LEU:HD13	1:K:198:PRO:HG3	1.87	0.56
1:P:40:GLN:HE21	1:P:40:GLN:CA	2.17	0.56
1:E:192:LYS:HB2	1:F:45:GLN:HE21	1.70	0.56
1:M:192:LYS:HG3	1:N:45:GLN:HE22	1.68	0.56
1:E:49:PRO:HD2	1:E:50:GLU:OE1	2.04	0.56
1:T:184:LEU:HD23	1:T:185:GLU:H	1.69	0.56
1:I:70:ARG:HG3	1:I:70:ARG:HH11	1.70	0.56
1:J:167:LEU:N	1:J:167:LEU:CD1	2.68	0.56
1:L:167:LEU:HD21	1:V:69:HIS:HB3	1.87	0.56
1:P:100:ASN:HD22	1:P:102:LYS:HB2	1.70	0.56
1:D:100:ASN:HD21	1:D:102:LYS:HB2	1.70	0.56
1:S:192:LYS:HB2	1:T:45:GLN:HE21	1.69	0.56
1:S:195:ASP:HB3	1:T:77:GLU:HG3	1.86	0.56
1:E:113:VAL:HG12	1:E:154:ALA:HB1	1.86	0.56
1:S:70:ARG:HG3	1:S:70:ARG:HH11	1.69	0.56
1:S:204:ARG:HD2	1:U:36:TYR:CZ	2.40	0.56
1:E:69:HIS:HB3	1:F:167:LEU:HD21	1.87	0.56
1:P:113:VAL:HG12	1:P:154:ALA:HB1	1.87	0.56
1:O:24:LEU:HB3	1:P:30:GLN:NE2	2.20	0.56
1:T:176:ASN:C	1:T:178:LEU:H	2.08	0.56
1:K:193:ARG:NE	1:L:180:ARG:NE	2.53	0.56
1:V:124:VAL:O	1:V:153:ARG:HD3	2.06	0.56
1:P:124:VAL:O	1:P:153:ARG:HD3	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:192:LYS:HB2	1:P:45:GLN:HE21	1.70	0.56
1:C:207:SER:C	1:C:209:ARG:H	2.07	0.56
1:P:134:SER:HB3	1:P:137:LEU:HB2	1.87	0.56
1:L:113:VAL:HG12	1:L:154:ALA:HB1	1.86	0.56
1:V:180:ARG:CG	1:V:181:GLN:N	2.67	0.56
1:L:167:LEU:HD13	1:L:167:LEU:N	2.16	0.56
1:N:100:ASN:HD22	1:N:102:LYS:HB2	1.71	0.56
1:H:186:VAL:HG21	1:I:171:TYR:CA	2.36	0.56
1:J:123:ASP:OD1	1:J:153:ARG:NH1	2.38	0.56
1:K:179:PRO:O	1:K:180:ARG:O	2.24	0.56
1:K:113:VAL:HG12	1:K:154:ALA:HB1	1.88	0.56
1:N:49:PRO:HD2	1:N:50:GLU:OE1	2.04	0.56
1:E:123:ASP:OD1	1:E:153:ARG:NH1	2.39	0.56
1:G:192:LYS:HE2	1:H:45:GLN:NE2	2.21	0.56
1:A:49:PRO:HG3	1:A:178:LEU:HD12	1.88	0.56
1:G:124:VAL:O	1:G:153:ARG:HD3	2.05	0.56
1:P:167:LEU:CD1	1:P:167:LEU:H	2.18	0.56
1:E:184:LEU:CD2	1:E:185:GLU:H	2.19	0.56
1:P:113:VAL:HG21	1:P:155:LEU:HD13	1.87	0.56
1:P:49:PRO:HD2	1:P:50:GLU:OE1	2.06	0.56
1:O:196:LEU:HD12	1:O:198:PRO:HG3	1.88	0.56
1:L:204:ARG:HD2	1:N:36:TYR:CZ	2.41	0.55
1:E:167:LEU:N	1:E:167:LEU:HD13	2.16	0.55
1:P:82:ASN:HB2	1:Q:117:ASP:OD1	2.06	0.55
1:K:193:ARG:CB	1:L:180:ARG:NH2	2.43	0.55
1:E:204:ARG:HD2	1:G:36:TYR:CZ	2.41	0.55
1:S:124:VAL:O	1:S:153:ARG:HD3	2.06	0.55
1:G:167:LEU:H	1:G:167:LEU:CD1	2.16	0.55
1:I:36:TYR:OH	1:I:40:GLN:HG3	2.05	0.55
1:C:100:ASN:HD21	1:C:102:LYS:HB2	1.70	0.55
1:C:57:ALA:HB3	1:C:61:GLN:HG3	1.88	0.55
1:E:57:ALA:HB3	1:E:61:GLN:HG3	1.88	0.55
1:O:204:ARG:HG3	1:P:35:GLU:OE1	2.06	0.55
1:L:123:ASP:OD1	1:L:153:ARG:NH1	2.40	0.55
1:H:167:LEU:N	1:H:167:LEU:CD1	2.70	0.55
1:R:70:ARG:HG3	1:R:70:ARG:NH1	2.20	0.55
1:M:139:LEU:O	1:M:143:ARG:HG3	2.07	0.55
1:A:30:GLN:NE2	1:K:24:LEU:HB3	2.22	0.55
1:N:167:LEU:CD1	1:N:167:LEU:H	2.19	0.55
1:H:100:ASN:HD21	1:H:102:LYS:HB2	1.70	0.55
1:C:204:ARG:HG3	1:D:35:GLU:OE1	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:139:LEU:O	1:V:143:ARG:HG3	2.06	0.55
1:V:100:ASN:HD22	1:V:102:LYS:HB2	1.69	0.55
1:R:124:VAL:O	1:R:153:ARG:HD3	2.07	0.55
1:A:77:GLU:OE2	1:B:44:ARG:NH1	2.40	0.55
1:I:167:LEU:H	1:I:167:LEU:CD1	2.18	0.55
1:F:100:ASN:HD21	1:F:102:LYS:HB2	1.70	0.55
1:M:124:VAL:O	1:M:153:ARG:HD3	2.06	0.55
1:V:82:ASN:HD22	1:V:82:ASN:N	2.02	0.55
1:S:49:PRO:HD2	1:S:50:GLU:OE1	2.07	0.55
1:J:49:PRO:HD2	1:J:50:GLU:OE1	2.07	0.55
1:G:100:ASN:HD21	1:G:102:LYS:HB2	1.72	0.55
1:T:186:VAL:HG21	1:U:171:TYR:CA	2.37	0.55
1:E:134:SER:HB3	1:E:137:LEU:HB2	1.88	0.55
1:I:69:HIS:HB3	1:J:167:LEU:HD21	1.88	0.55
1:Q:192:LYS:HB2	1:R:45:GLN:NE2	2.22	0.55
1:R:86:HIS:ND1	1:S:121:HIS:CD2	2.73	0.55
1:S:69:HIS:HB3	1:T:167:LEU:HD21	1.88	0.54
1:L:167:LEU:N	1:L:167:LEU:CD1	2.69	0.54
1:K:100:ASN:HD21	1:K:102:LYS:HB2	1.70	0.54
1:U:50:GLU:HA	1:U:181:GLN:HE21	1.71	0.54
1:B:205:TYR:CE1	1:D:33:ALA:HB1	2.42	0.54
1:B:134:SER:HB3	1:B:137:LEU:HB2	1.89	0.54
1:Q:195:ASP:HB3	1:R:77:GLU:HG3	1.89	0.54
1:A:49:PRO:HD2	1:A:50:GLU:OE1	2.07	0.54
1:B:36:TYR:OH	1:B:40:GLN:HG3	2.07	0.54
1:C:82:ASN:H	1:C:82:ASN:HD22	1.54	0.54
1:U:24:LEU:HB3	1:V:30:GLN:NE2	2.21	0.54
1:M:182:LEU:CD2	1:M:182:LEU:H	2.01	0.54
1:J:40:GLN:HA	1:J:40:GLN:NE2	2.16	0.54
1:R:36:TYR:OH	1:R:40:GLN:HG3	2.07	0.54
1:C:192:LYS:HB2	1:D:45:GLN:HE21	1.70	0.54
1:S:192:LYS:HG3	1:T:45:GLN:HE22	1.72	0.54
1:C:113:VAL:HG12	1:C:154:ALA:HB1	1.89	0.54
1:S:52:ILE:HG13	1:S:175:LEU:HD11	1.88	0.54
1:H:167:LEU:HD13	1:H:167:LEU:N	2.16	0.54
1:E:208:CYS:HB2	1:G:33:ALA:HB2	1.90	0.54
1:M:167:LEU:CD1	1:M:167:LEU:N	2.70	0.54
1:P:147:VAL:HG21	1:Q:124:VAL:CG2	2.36	0.54
1:L:100:ASN:HD21	1:L:102:LYS:HB2	1.70	0.54
1:T:52:ILE:HG13	1:T:175:LEU:HD11	1.89	0.54
1:T:82:ASN:H	1:T:82:ASN:HD22	1.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:205:TYR:CE2	1:V:209:ARG:NH2	2.76	0.54
1:T:113:VAL:HG12	1:T:154:ALA:HB1	1.90	0.54
1:H:70:ARG:HH11	1:H:70:ARG:HG3	1.71	0.54
1:K:40:GLN:HA	1:K:40:GLN:NE2	2.16	0.54
1:G:196:LEU:HD13	1:G:197:GLU:N	2.23	0.54
1:K:70:ARG:HG3	1:K:70:ARG:HH11	1.71	0.54
1:T:167:LEU:CD1	1:T:167:LEU:N	2.71	0.54
1:S:100:ASN:HD21	1:S:102:LYS:HB2	1.69	0.54
1:U:123:ASP:OD1	1:U:153:ARG:NH1	2.41	0.54
1:O:123:ASP:OD1	1:O:153:ARG:NH1	2.41	0.54
1:R:123:ASP:OD1	1:R:153:ARG:NH1	2.41	0.54
1:N:50:GLU:HB3	1:N:181:GLN:HE21	1.72	0.54
1:F:57:ALA:HB3	1:F:61:GLN:HG3	1.89	0.54
1:U:178:LEU:HD23	1:U:179:PRO:HD3	1.90	0.54
1:I:40:GLN:HA	1:I:40:GLN:NE2	2.16	0.54
1:L:124:VAL:O	1:L:153:ARG:HD3	2.08	0.54
1:E:204:ARG:HG3	1:F:35:GLU:OE1	2.07	0.54
1:V:167:LEU:CD1	1:V:167:LEU:N	2.71	0.54
1:O:82:ASN:HD22	1:O:82:ASN:N	2.06	0.54
1:V:70:ARG:HG3	1:V:70:ARG:NH1	2.23	0.54
1:M:113:VAL:HG12	1:M:154:ALA:HB1	1.90	0.54
1:A:184:LEU:HD22	1:A:185:GLU:N	2.24	0.54
1:E:124:VAL:O	1:E:153:ARG:HD3	2.08	0.54
1:O:113:VAL:HG21	1:O:155:LEU:HD13	1.90	0.54
1:R:24:LEU:HB3	1:S:30:GLN:NE2	2.23	0.54
1:H:85:ALA:HB1	1:I:120:TYR:O	2.09	0.54
1:F:49:PRO:HD2	1:F:50:GLU:OE1	2.08	0.54
1:T:195:ASP:HB3	1:U:77:GLU:HG3	1.89	0.54
1:U:188:LEU:HD12	1:V:178:LEU:HD11	1.90	0.54
1:P:100:ASN:HD21	1:P:102:LYS:HB2	1.69	0.53
1:U:182:LEU:CD2	1:U:182:LEU:H	2.21	0.53
1:C:124:VAL:O	1:C:153:ARG:HD3	2.08	0.53
1:J:192:LYS:HB2	1:K:45:GLN:NE2	2.22	0.53
1:N:134:SER:HB3	1:N:137:LEU:HB2	1.89	0.53
1:K:49:PRO:HD2	1:K:50:GLU:OE1	2.08	0.53
1:A:49:PRO:HD2	1:L:180:ARG:NH1	2.24	0.53
1:R:100:ASN:HD21	1:R:102:LYS:HB2	1.69	0.53
1:C:139:LEU:O	1:C:143:ARG:HG3	2.07	0.53
1:R:147:VAL:HG21	1:S:124:VAL:CG2	2.35	0.53
1:K:123:ASP:OD1	1:K:153:ARG:NH1	2.41	0.53
1:P:86:HIS:ND1	1:Q:121:HIS:CD2	2.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:113:VAL:HG21	1:C:155:LEU:HD13	1.91	0.53
1:O:113:VAL:HG12	1:O:154:ALA:HB1	1.91	0.53
1:J:205:TYR:CE2	1:J:209:ARG:NH2	2.76	0.53
1:K:167:LEU:N	1:K:167:LEU:HD13	2.17	0.53
1:C:184:LEU:O	1:D:173:ARG:NH2	2.40	0.53
1:N:113:VAL:HG12	1:N:154:ALA:HB1	1.90	0.53
1:V:180:ARG:CG	1:V:181:GLN:H	2.17	0.53
1:J:124:VAL:O	1:J:153:ARG:HD3	2.07	0.53
1:Q:86:HIS:ND1	1:R:121:HIS:CD2	2.76	0.53
1:T:70:ARG:NH1	1:T:70:ARG:HG3	2.23	0.53
1:R:193:ARG:HG2	1:R:193:ARG:NH1	2.22	0.53
1:A:70:ARG:HG3	1:A:70:ARG:NH1	2.24	0.53
1:Q:167:LEU:N	1:Q:167:LEU:CD1	2.71	0.53
1:D:82:ASN:HB2	1:E:117:ASP:OD1	2.09	0.53
1:I:113:VAL:HG12	1:I:154:ALA:HB1	1.90	0.53
1:H:57:ALA:HB3	1:H:61:GLN:HG3	1.91	0.53
1:H:49:PRO:HD2	1:H:50:GLU:OE1	2.09	0.53
1:R:195:ASP:HB3	1:S:77:GLU:HG3	1.90	0.53
1:P:179:PRO:O	1:P:180:ARG:C	2.45	0.53
1:P:180:ARG:HG3	1:P:180:ARG:O	2.08	0.53
1:F:69:HIS:HB3	1:G:167:LEU:HD21	1.90	0.53
1:A:45:GLN:NE2	1:K:192:LYS:HB2	2.23	0.53
1:F:112:ARG:HG3	1:F:122:GLU:HB2	1.90	0.53
1:O:100:ASN:HD22	1:O:102:LYS:HB2	1.71	0.53
1:S:167:LEU:H	1:S:167:LEU:CD1	2.19	0.53
1:T:100:ASN:HD21	1:T:102:LYS:HB2	1.74	0.53
1:P:70:ARG:NH1	1:P:70:ARG:HG3	2.24	0.53
1:S:180:ARG:HG2	1:S:180:ARG:NH1	2.23	0.53
1:Q:57:ALA:HB3	1:Q:61:GLN:HG3	1.91	0.53
1:O:180:ARG:O	1:O:180:ARG:HD2	2.09	0.53
1:F:139:LEU:O	1:F:143:ARG:HG3	2.09	0.53
1:N:40:GLN:NE2	1:N:40:GLN:HA	2.18	0.53
1:P:165:CYS:HA	2:P:2023:HOH:O	2.09	0.53
1:B:124:VAL:O	1:B:153:ARG:HD3	2.09	0.53
1:H:124:VAL:O	1:H:153:ARG:HD3	2.09	0.53
1:S:196:LEU:HD22	1:S:197:GLU:N	2.24	0.53
1:P:57:ALA:HB3	1:P:61:GLN:HG3	1.90	0.52
1:D:113:VAL:HG12	1:D:154:ALA:HB1	1.91	0.52
1:C:100:ASN:HD22	1:C:102:LYS:HB2	1.71	0.52
1:U:178:LEU:CD2	1:U:179:PRO:HD3	2.40	0.52
1:Q:179:PRO:O	1:Q:180:ARG:O	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:139:LEU:O	1:H:143:ARG:HG3	2.08	0.52
1:L:70:ARG:HH11	1:L:70:ARG:HG3	1.73	0.52
1:T:36:TYR:OH	1:T:40:GLN:HG3	2.10	0.52
1:O:36:TYR:OH	1:O:40:GLN:HG3	2.10	0.52
1:P:36:TYR:OH	1:P:40:GLN:HG3	2.09	0.52
1:D:177:LYS:O	1:D:178:LEU:HD23	2.09	0.52
1:C:112:ARG:HD2	2:C:2005:HOH:O	2.09	0.52
1:Q:40:GLN:NE2	1:Q:40:GLN:HA	2.16	0.52
1:A:184:LEU:HD23	1:A:185:GLU:N	2.18	0.52
1:G:186:VAL:HG21	1:H:171:TYR:N	2.25	0.52
1:H:180:ARG:CG	1:H:181:GLN:N	2.72	0.52
1:H:196:LEU:HD12	1:H:198:PRO:HD3	1.90	0.52
1:N:182:LEU:HB2	1:N:183:PRO:HD2	1.90	0.52
1:C:69:HIS:HB3	1:D:167:LEU:HD21	1.91	0.52
1:G:167:LEU:N	1:G:167:LEU:HD13	2.20	0.52
1:G:167:LEU:N	1:G:167:LEU:CD1	2.73	0.52
1:A:182:LEU:N	1:A:182:LEU:CD2	2.72	0.52
1:H:82:ASN:HD22	1:H:82:ASN:N	2.06	0.52
1:L:195:ASP:HB3	1:M:77:GLU:HG3	1.90	0.52
1:Q:140:GLU:HG3	1:Q:144:LYS:HE3	1.90	0.52
1:J:181:GLN:O	1:J:181:GLN:CG	2.58	0.52
1:R:204:ARG:HG3	1:S:35:GLU:OE1	2.10	0.52
1:A:77:GLU:OE1	1:B:44:ARG:HD3	2.09	0.52
1:U:192:LYS:HE2	1:U:197:GLU:OE2	2.10	0.52
1:C:47:LEU:CD2	1:C:47:LEU:N	2.71	0.52
1:E:192:LYS:HE2	1:E:197:GLU:OE2	2.10	0.52
1:G:196:LEU:HD12	1:G:198:PRO:HD3	1.90	0.52
1:J:113:VAL:HG12	1:J:154:ALA:HB1	1.91	0.52
1:V:182:LEU:HD23	1:V:182:LEU:H	1.75	0.52
1:H:207:SER:HB2	1:I:32:THR:HG21	1.92	0.52
1:V:36:TYR:OH	1:V:40:GLN:HG3	2.10	0.52
1:O:124:VAL:O	1:O:153:ARG:HD3	2.09	0.52
1:N:82:ASN:HD22	1:N:82:ASN:N	2.07	0.52
1:L:77:GLU:HG3	1:V:195:ASP:HB3	1.91	0.52
1:G:49:PRO:HD2	1:G:50:GLU:OE1	2.09	0.52
1:I:49:PRO:HD2	1:I:50:GLU:OE1	2.10	0.52
1:R:57:ALA:HB3	1:R:61:GLN:HG3	1.91	0.52
1:L:120:TYR:O	1:V:85:ALA:HB1	2.09	0.52
1:S:167:LEU:N	1:S:167:LEU:HD13	2.22	0.52
1:N:166:ILE:HD13	1:N:166:ILE:O	2.10	0.52
1:A:82:ASN:N	1:A:82:ASN:HD22	2.01	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:LYS:HD2	1:B:45:GLN:NE2	2.25	0.52
1:J:196:LEU:HD13	1:J:198:PRO:HG3	1.92	0.52
1:S:139:LEU:O	1:S:143:ARG:HG3	2.09	0.51
1:E:100:ASN:HD22	1:E:102:LYS:HB2	1.73	0.51
1:N:204:ARG:HG3	1:O:35:GLU:OE1	2.10	0.51
1:O:70:ARG:NH1	1:O:70:ARG:HG3	2.25	0.51
1:U:70:ARG:HG3	1:U:70:ARG:NH1	2.25	0.51
1:B:49:PRO:HD2	1:B:50:GLU:OE1	2.10	0.51
1:D:165:CYS:HA	2:D:2024:HOH:O	2.09	0.51
1:I:181:GLN:HG3	1:I:181:GLN:O	2.09	0.51
1:D:124:VAL:O	1:D:153:ARG:HD3	2.09	0.51
1:J:70:ARG:HG3	1:J:70:ARG:NH1	2.23	0.51
1:E:183:PRO:O	1:E:184:LEU:O	2.28	0.51
1:V:40:GLN:NE2	1:V:40:GLN:HA	2.16	0.51
1:Q:123:ASP:OD1	1:Q:153:ARG:NH1	2.43	0.51
1:S:40:GLN:NE2	1:S:40:GLN:HA	2.20	0.51
1:O:82:ASN:HB2	1:P:117:ASP:OD1	2.11	0.51
1:B:70:ARG:NH1	1:B:70:ARG:HG3	2.23	0.51
1:S:85:ALA:HB1	1:T:120:TYR:O	2.09	0.51
1:A:135:LYS:HE2	2:A:2014:HOH:O	2.10	0.51
1:S:47:LEU:CD2	1:S:47:LEU:N	2.72	0.51
1:H:123:ASP:OD1	1:H:153:ARG:NH1	2.44	0.51
1:F:86:HIS:ND1	1:G:121:HIS:CD2	2.75	0.51
1:G:196:LEU:HD12	1:G:198:PRO:CD	2.41	0.51
1:F:100:ASN:HD22	1:F:102:LYS:HB2	1.75	0.51
1:G:204:ARG:CG	1:G:204:ARG:HH21	2.18	0.51
1:F:192:LYS:HE2	1:G:45:GLN:NE2	2.26	0.51
1:P:82:ASN:HD22	1:P:82:ASN:N	2.09	0.51
1:H:207:SER:HB2	1:I:32:THR:CG2	2.40	0.51
1:V:57:ALA:HB3	1:V:61:GLN:HG3	1.92	0.51
1:N:52:ILE:HG13	1:N:175:LEU:HD11	1.92	0.51
1:T:57:ALA:HB3	1:T:61:GLN:HG3	1.92	0.51
1:V:100:ASN:ND2	1:V:102:LYS:CB	2.71	0.51
1:Q:50:GLU:HA	1:Q:181:GLN:HE22	1.75	0.51
1:O:179:PRO:O	1:O:180:ARG:C	2.49	0.51
1:A:179:PRO:HD3	1:L:183:PRO:HG3	1.93	0.51
1:H:24:LEU:HB3	1:I:30:GLN:NE2	2.25	0.51
1:B:33:ALA:HB2	1:K:208:CYS:HB2	1.92	0.51
1:P:196:LEU:CD1	1:P:198:PRO:HG3	2.40	0.51
1:A:100:ASN:HD22	1:A:102:LYS:CB	2.24	0.51
1:J:100:ASN:HD22	1:J:102:LYS:HB2	1.72	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:196:LEU:HD13	1:F:198:PRO:HD3	1.93	0.51
1:F:124:VAL:O	1:F:153:ARG:HD3	2.11	0.51
1:E:184:LEU:HD23	1:E:185:GLU:H	1.75	0.51
1:T:192:LYS:HG3	1:U:45:GLN:HE22	1.76	0.51
1:T:113:VAL:HG21	1:T:155:LEU:HD13	1.93	0.51
1:M:57:ALA:HB3	1:M:61:GLN:HG3	1.93	0.51
1:A:195:ASP:HB3	1:B:77:GLU:HG3	1.93	0.51
1:A:49:PRO:CD	1:L:180:ARG:NH1	2.74	0.51
1:N:196:LEU:HD13	1:N:197:GLU:N	2.25	0.51
1:M:40:GLN:NE2	1:M:40:GLN:HA	2.18	0.51
1:S:123:ASP:OD1	1:S:153:ARG:NH1	2.44	0.51
1:B:182:LEU:HD23	1:B:182:LEU:N	2.21	0.51
1:K:124:VAL:O	1:K:153:ARG:HD3	2.11	0.51
1:O:173:ARG:HG2	1:O:173:ARG:HH11	1.75	0.51
1:A:117:ASP:OD1	1:K:82:ASN:HB2	2.10	0.51
1:Q:139:LEU:O	1:Q:143:ARG:HG3	2.11	0.51
1:B:189:THR:HG22	1:B:190:LYS:CG	2.28	0.51
1:A:167:LEU:HD21	1:K:69:HIS:HB3	1.92	0.51
1:F:47:LEU:CD2	1:F:47:LEU:N	2.74	0.51
1:V:192:LYS:NZ	1:V:194:GLN:O	2.36	0.51
1:O:205:TYR:CE2	1:O:209:ARG:NH2	2.79	0.51
1:N:192:LYS:CE	1:N:197:GLU:OE2	2.52	0.50
1:V:100:ASN:HD22	1:V:102:LYS:CB	2.24	0.50
1:M:100:ASN:HD21	1:M:102:LYS:HB2	1.68	0.50
1:P:167:LEU:CD1	1:P:167:LEU:N	2.74	0.50
1:V:192:LYS:CE	1:V:197:GLU:OE2	2.58	0.50
1:S:57:ALA:HB3	1:S:61:GLN:HG3	1.93	0.50
1:K:165:CYS:HA	2:K:2023:HOH:O	2.10	0.50
1:J:204:ARG:HH21	1:J:204:ARG:HG3	1.76	0.50
1:F:82:ASN:N	1:F:82:ASN:HD22	2.07	0.50
1:K:193:ARG:NH1	1:L:182:LEU:HD22	2.25	0.50
1:S:203:ALA:HB1	1:T:35:GLU:N	2.26	0.50
1:S:167:LEU:CD1	1:S:167:LEU:N	2.75	0.50
1:G:183:PRO:HB2	1:H:170:ASP:OD1	2.11	0.50
1:R:47:LEU:N	1:R:47:LEU:CD2	2.73	0.50
1:L:45:GLN:NE2	1:V:192:LYS:HB2	2.26	0.50
1:H:182:LEU:HD23	1:H:182:LEU:H	1.77	0.50
1:G:193:ARG:HG2	1:G:193:ARG:HH11	1.76	0.50
1:S:47:LEU:HD23	1:S:165:CYS:SG	2.51	0.50
1:C:184:LEU:CD1	1:C:185:GLU:N	2.74	0.50
1:T:86:HIS:ND1	1:U:121:HIS:CD2	2.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:50:GLU:HA	1:U:181:GLN:NE2	2.26	0.50
1:D:113:VAL:HG21	1:D:155:LEU:HD13	1.92	0.50
1:N:24:LEU:HB3	1:O:30:GLN:NE2	2.27	0.50
1:E:82:ASN:HB2	1:F:117:ASP:OD1	2.11	0.50
1:E:192:LYS:HB2	1:F:45:GLN:NE2	2.26	0.50
1:V:196:LEU:C	1:V:198:PRO:HD3	2.32	0.50
1:I:204:ARG:HG3	1:I:204:ARG:HH21	1.75	0.50
1:J:188:LEU:HB3	1:J:191:ALA:HB2	1.92	0.50
1:A:124:VAL:O	1:A:153:ARG:HD3	2.12	0.50
1:U:112:ARG:HG3	1:U:122:GLU:HB2	1.94	0.50
1:O:57:ALA:HB3	1:O:61:GLN:HG3	1.94	0.50
1:L:30:GLN:NE2	1:V:24:LEU:HB3	2.27	0.50
1:C:196:LEU:HD12	1:C:198:PRO:HG3	1.92	0.50
1:T:40:GLN:NE2	1:T:40:GLN:HA	2.20	0.50
1:B:40:GLN:NE2	1:B:40:GLN:HA	2.19	0.50
1:F:192:LYS:O	1:G:48:GLY:N	2.35	0.50
1:L:57:ALA:HB3	1:L:61:GLN:HG3	1.94	0.50
1:B:193:ARG:NH1	1:C:50:GLU:OE2	2.43	0.50
1:G:112:ARG:HG3	1:G:122:GLU:HB2	1.93	0.50
1:N:192:LYS:HB2	1:O:45:GLN:HE21	1.77	0.50
1:J:36:TYR:OH	1:J:40:GLN:HG3	2.12	0.50
1:D:40:GLN:NE2	1:D:40:GLN:HA	2.20	0.50
1:Q:167:LEU:N	1:Q:167:LEU:HD13	2.19	0.50
1:A:121:HIS:CD2	1:K:86:HIS:ND1	2.77	0.50
1:R:82:ASN:HB2	1:S:117:ASP:OD1	2.12	0.50
1:B:82:ASN:N	1:B:82:ASN:HD22	2.07	0.50
1:D:57:ALA:HB3	1:D:61:GLN:HG3	1.93	0.50
1:M:100:ASN:HD22	1:M:102:LYS:CB	2.25	0.49
1:S:36:TYR:OH	1:S:40:GLN:HG3	2.11	0.49
1:G:139:LEU:O	1:G:143:ARG:HG3	2.12	0.49
1:B:189:THR:CG2	1:B:190:LYS:HG3	2.30	0.49
1:M:47:LEU:HD23	1:M:165:CYS:SG	2.52	0.49
1:P:117:ASP:HB3	1:P:119:SER:H	1.77	0.49
1:G:182:LEU:N	1:G:182:LEU:HD23	2.16	0.49
1:A:69:HIS:HB3	1:B:167:LEU:HD21	1.94	0.49
1:D:147:VAL:HG21	1:E:124:VAL:CG2	2.40	0.49
1:A:47:LEU:N	1:A:47:LEU:CD2	2.75	0.49
1:L:40:GLN:HA	1:L:40:GLN:NE2	2.18	0.49
1:Q:124:VAL:O	1:Q:153:ARG:HD3	2.11	0.49
1:Q:166:ILE:HD13	1:Q:166:ILE:O	2.13	0.49
1:S:184:LEU:CD2	1:S:185:GLU:N	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:47:LEU:HD23	1:T:165:CYS:SG	2.53	0.49
1:L:86:HIS:ND1	1:M:121:HIS:CD2	2.78	0.49
1:L:177:LYS:NZ	1:V:185:GLU:OE1	2.45	0.49
1:G:116:LYS:HE2	2:G:2004:HOH:O	2.11	0.49
1:B:192:LYS:HG3	1:C:45:GLN:HE22	1.76	0.49
1:R:176:ASN:C	1:R:178:LEU:H	2.16	0.49
1:F:70:ARG:HG3	1:F:70:ARG:NH1	2.27	0.49
1:D:192:LYS:HG3	1:E:45:GLN:NE2	2.28	0.49
1:N:139:LEU:O	1:N:143:ARG:HG3	2.11	0.49
1:F:24:LEU:HB3	1:G:30:GLN:NE2	2.28	0.49
1:D:182:LEU:N	1:D:182:LEU:HD23	2.19	0.49
1:Q:184:LEU:CD2	1:Q:185:GLU:N	2.68	0.49
1:L:100:ASN:HD22	1:L:102:LYS:HB2	1.72	0.49
1:G:82:ASN:HD22	1:G:82:ASN:N	2.06	0.49
1:U:192:LYS:CE	1:U:197:GLU:OE2	2.60	0.49
1:N:167:LEU:CD1	1:N:167:LEU:N	2.76	0.49
1:D:82:ASN:N	1:D:82:ASN:HD22	2.00	0.49
1:S:82:ASN:HB2	1:T:117:ASP:OD1	2.13	0.49
1:I:203:ALA:HB1	1:J:35:GLU:HA	1.95	0.49
1:M:113:VAL:HG21	1:M:155:LEU:HD13	1.93	0.49
1:K:47:LEU:N	1:K:47:LEU:CD2	2.76	0.49
1:S:147:VAL:HG21	1:T:124:VAL:CG2	2.40	0.49
1:J:184:LEU:HD13	1:J:185:GLU:N	2.26	0.49
1:B:100:ASN:HD21	1:B:102:LYS:HB2	1.77	0.49
1:E:82:ASN:HD22	1:E:82:ASN:N	2.04	0.49
1:L:77:GLU:OE2	1:M:44:ARG:NH1	2.46	0.49
1:T:139:LEU:O	1:T:143:ARG:HG3	2.13	0.49
1:G:57:ALA:HB3	1:G:61:GLN:HG3	1.94	0.49
1:A:182:LEU:HB2	1:L:56:MET:HE3	1.94	0.49
1:E:86:HIS:ND1	1:F:121:HIS:CD2	2.73	0.49
1:D:47:LEU:N	1:D:47:LEU:CD2	2.74	0.49
1:B:100:ASN:HD22	1:B:102:LYS:HB2	1.76	0.49
1:R:113:VAL:HG21	1:R:155:LEU:HD13	1.94	0.49
1:N:113:VAL:HG21	1:N:155:LEU:HD13	1.95	0.49
1:H:112:ARG:HG3	1:H:122:GLU:HB2	1.94	0.49
1:Q:100:ASN:HD22	1:Q:102:LYS:CB	2.26	0.49
1:U:165:CYS:HA	2:U:2023:HOH:O	2.11	0.49
1:B:33:ALA:HB2	1:K:208:CYS:CB	2.43	0.49
1:J:24:LEU:HB3	1:K:30:GLN:NE2	2.28	0.49
1:D:24:LEU:HB3	1:E:30:GLN:NE2	2.27	0.49
1:O:100:ASN:HD22	1:O:102:LYS:CB	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:100:ASN:HD22	1:D:102:LYS:HB2	1.74	0.48
1:C:70:ARG:NH1	1:C:70:ARG:HG3	2.27	0.48
1:K:57:ALA:HB3	1:K:61:GLN:HG3	1.94	0.48
1:O:186:VAL:HG21	1:P:171:TYR:HA	1.95	0.48
1:V:49:PRO:HD2	1:V:50:GLU:OE1	2.13	0.48
1:E:100:ASN:HD22	1:E:102:LYS:CB	2.26	0.48
1:G:204:ARG:NH2	1:H:35:GLU:OE1	2.47	0.48
1:Q:82:ASN:HD22	1:Q:82:ASN:N	2.02	0.48
1:E:185:GLU:OE1	1:F:177:LYS:NZ	2.47	0.48
1:S:70:ARG:NH1	1:S:70:ARG:HG3	2.28	0.48
1:T:175:LEU:O	1:T:178:LEU:HD12	2.13	0.48
1:I:113:VAL:HG21	1:I:155:LEU:HD13	1.94	0.48
1:U:195:ASP:HB3	1:V:77:GLU:HG3	1.95	0.48
1:I:167:LEU:N	1:I:167:LEU:CD1	2.74	0.48
1:P:167:LEU:HD13	1:P:167:LEU:N	2.23	0.48
1:P:47:LEU:CD2	1:P:47:LEU:N	2.76	0.48
1:I:86:HIS:ND1	1:J:121:HIS:CD2	2.79	0.48
1:E:70:ARG:NH1	1:E:70:ARG:HG3	2.28	0.48
1:O:139:LEU:O	1:O:143:ARG:HG3	2.12	0.48
1:D:140:GLU:HB2	1:E:126:TYR:CD2	2.47	0.48
1:R:40:GLN:HA	1:R:40:GLN:NE2	2.20	0.48
1:T:182:LEU:H	1:T:182:LEU:CD2	2.24	0.48
1:R:193:ARG:HG2	1:S:50:GLU:CD	2.34	0.48
1:E:207:SER:O	1:E:209:ARG:N	2.46	0.48
1:H:70:ARG:NH1	1:H:70:ARG:HG3	2.29	0.48
1:F:116:LYS:HE2	2:F:2005:HOH:O	2.13	0.48
1:J:100:ASN:HD22	1:J:102:LYS:CB	2.27	0.48
1:C:47:LEU:HD23	1:C:165:CYS:SG	2.54	0.48
1:H:196:LEU:HD13	1:H:197:GLU:N	2.29	0.48
1:V:116:LYS:HE2	2:V:2003:HOH:O	2.14	0.48
1:B:116:LYS:HE2	2:B:2001:HOH:O	2.12	0.48
1:G:123:ASP:OD1	1:G:153:ARG:NH1	2.47	0.48
1:V:47:LEU:N	1:V:47:LEU:CD2	2.75	0.48
1:D:191:ALA:O	1:D:193:ARG:HG3	2.14	0.48
1:D:195:ASP:HB3	1:E:77:GLU:HG3	1.95	0.48
1:J:182:LEU:H	1:J:182:LEU:CD2	2.26	0.48
1:F:196:LEU:CD1	1:F:198:PRO:HG3	2.42	0.48
1:G:204:ARG:O	1:G:204:ARG:HG2	2.12	0.48
1:G:204:ARG:HG3	1:H:35:GLU:OE1	2.13	0.48
1:Q:82:ASN:H	1:Q:82:ASN:ND2	2.10	0.48
1:Q:113:VAL:HG21	1:Q:155:LEU:HD13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:182:LEU:N	1:V:182:LEU:HD23	2.29	0.48
1:F:205:TYR:CE2	1:F:209:ARG:NH2	2.81	0.48
1:L:182:LEU:HD23	1:L:182:LEU:N	2.25	0.48
1:T:166:ILE:HD13	1:T:166:ILE:O	2.14	0.48
1:O:40:GLN:HA	1:O:40:GLN:NE2	2.21	0.48
1:M:166:ILE:HD13	1:M:166:ILE:O	2.14	0.48
1:V:167:LEU:N	1:V:167:LEU:HD13	2.19	0.48
1:U:47:LEU:CD2	1:U:47:LEU:N	2.77	0.48
1:M:82:ASN:HB2	1:N:117:ASP:OD1	2.14	0.48
1:T:192:LYS:NZ	1:T:197:GLU:OE2	2.45	0.48
1:G:140:GLU:HG3	1:G:144:LYS:HE3	1.95	0.48
1:B:195:ASP:HB3	1:C:77:GLU:HG3	1.95	0.48
1:N:57:ALA:HB3	1:N:61:GLN:HG3	1.96	0.48
1:L:40:GLN:NE2	1:L:40:GLN:CA	2.76	0.48
1:L:82:ASN:N	1:L:82:ASN:HD22	2.06	0.48
1:Q:207:SER:C	1:Q:209:ARG:N	2.66	0.48
1:G:70:ARG:NH1	1:G:70:ARG:HG3	2.26	0.48
1:Q:70:ARG:HG3	1:Q:70:ARG:NH1	2.29	0.48
1:A:35:GLU:OE1	1:K:204:ARG:HG3	2.13	0.48
1:H:100:ASN:HD22	1:H:102:LYS:HB2	1.76	0.48
1:I:139:LEU:O	1:I:143:ARG:HG3	2.14	0.48
1:N:123:ASP:OD1	1:N:153:ARG:NH1	2.47	0.47
1:N:100:ASN:HD21	1:N:102:LYS:HB2	1.75	0.47
1:T:47:LEU:N	1:T:47:LEU:CD2	2.75	0.47
1:I:57:ALA:HB3	1:I:61:GLN:HG3	1.96	0.47
1:V:113:VAL:HG12	1:V:154:ALA:HB1	1.96	0.47
1:J:116:LYS:HE2	2:J:2001:HOH:O	2.13	0.47
1:N:184:LEU:C	1:O:173:ARG:HH22	2.15	0.47
1:B:82:ASN:HB2	1:C:117:ASP:OD1	2.14	0.47
1:A:192:LYS:HB2	1:B:45:GLN:HE21	1.80	0.47
1:M:112:ARG:HG3	1:M:122:GLU:HB2	1.96	0.47
1:U:166:ILE:O	1:U:166:ILE:HD13	2.14	0.47
1:R:196:LEU:HD13	1:R:197:GLU:N	2.29	0.47
1:O:47:LEU:N	1:O:47:LEU:CD2	2.76	0.47
1:C:123:ASP:OD1	1:C:153:ARG:NH1	2.48	0.47
1:L:49:PRO:HD2	1:L:50:GLU:OE1	2.14	0.47
1:E:40:GLN:NE2	1:E:40:GLN:HA	2.22	0.47
1:E:140:GLU:HG3	1:E:144:LYS:HE3	1.95	0.47
1:F:100:ASN:HD22	1:F:102:LYS:CB	2.28	0.47
1:U:182:LEU:O	1:U:183:PRO:C	2.52	0.47
1:F:192:LYS:HE2	1:G:45:GLN:HE22	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:82:ASN:HB2	1:V:117:ASP:OD1	2.15	0.47
1:N:47:LEU:HD23	1:N:165:CYS:SG	2.55	0.47
1:I:70:ARG:NH1	1:I:70:ARG:HG3	2.29	0.47
1:V:182:LEU:CD2	1:V:182:LEU:H	2.28	0.47
1:M:182:LEU:O	1:M:183:PRO:C	2.52	0.47
1:H:208:CYS:C	1:H:209:ARG:HG3	2.34	0.47
1:T:175:LEU:HA	1:T:178:LEU:HD12	1.97	0.47
1:N:182:LEU:N	1:N:182:LEU:HD22	2.06	0.47
1:Q:100:ASN:HD22	1:Q:102:LYS:HB2	1.74	0.47
1:M:82:ASN:N	1:M:82:ASN:HD22	2.07	0.47
1:B:175:LEU:O	1:B:178:LEU:HB2	2.15	0.47
1:L:50:GLU:OE1	1:V:193:ARG:HG2	2.15	0.47
1:J:85:ALA:HB1	1:K:120:TYR:O	2.15	0.47
1:A:128:VAL:HG12	1:A:129:SER:N	2.29	0.47
1:D:40:GLN:HE21	1:D:40:GLN:CA	2.19	0.47
1:I:100:ASN:HB2	1:I:101:GLY:H	1.49	0.47
1:H:147:VAL:HG21	1:I:124:VAL:CG2	2.41	0.47
1:G:100:ASN:HD22	1:G:102:LYS:HB2	1.78	0.47
1:D:70:ARG:HG3	1:D:70:ARG:NH1	2.29	0.47
1:K:113:VAL:HG21	1:K:155:LEU:HD13	1.96	0.47
1:U:40:GLN:CA	1:U:40:GLN:NE2	2.75	0.46
1:U:124:VAL:O	1:U:153:ARG:HD3	2.14	0.46
1:G:113:VAL:HG21	1:G:155:LEU:HD13	1.97	0.46
1:J:82:ASN:HB2	1:K:117:ASP:OD1	2.15	0.46
1:A:57:ALA:HB3	1:A:61:GLN:HG3	1.96	0.46
1:J:100:ASN:HB2	1:J:101:GLY:H	1.51	0.46
1:L:100:ASN:HD22	1:L:102:LYS:CB	2.27	0.46
1:D:100:ASN:HB2	1:D:101:GLY:H	1.57	0.46
1:I:123:ASP:OD1	1:I:153:ARG:NH1	2.48	0.46
1:E:47:LEU:HD23	1:E:165:CYS:SG	2.54	0.46
1:B:86:HIS:ND1	1:C:121:HIS:CD2	2.83	0.46
1:K:173:ARG:HG2	1:K:173:ARG:HH11	1.80	0.46
1:D:36:TYR:CZ	1:D:40:GLN:HG3	2.51	0.46
1:O:69:HIS:HB3	1:P:167:LEU:CD2	2.44	0.46
1:C:86:HIS:ND1	1:D:121:HIS:CD2	2.80	0.46
1:J:57:ALA:HB3	1:J:61:GLN:HG3	1.97	0.46
1:S:100:ASN:HB2	1:S:101:GLY:H	1.59	0.46
1:O:134:SER:OG	1:O:137:LEU:HD23	2.15	0.46
1:C:192:LYS:HE2	1:C:197:GLU:OE2	2.15	0.46
1:N:50:GLU:HA	1:N:181:GLN:HG2	1.96	0.46
1:U:57:ALA:HB3	1:U:61:GLN:HG3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:193:ARG:CZ	1:L:180:ARG:CZ	2.93	0.46
1:H:100:ASN:HD22	1:H:102:LYS:CB	2.29	0.46
1:O:24:LEU:HA	1:O:24:LEU:HD22	1.80	0.46
1:P:134:SER:OG	1:P:137:LEU:HD23	2.16	0.46
1:B:139:LEU:O	1:B:143:ARG:HG3	2.15	0.46
1:L:24:LEU:HB3	1:M:30:GLN:NE2	2.31	0.46
1:P:139:LEU:O	1:P:143:ARG:HG3	2.16	0.46
1:N:82:ASN:HB2	1:O:117:ASP:OD1	2.16	0.46
1:E:207:SER:C	1:E:209:ARG:N	2.68	0.46
1:D:194:GLN:C	1:E:51:TYR:OH	2.53	0.46
1:L:33:ALA:HB2	1:U:208:CYS:HB2	1.96	0.46
1:A:139:LEU:O	1:A:143:ARG:HG3	2.15	0.46
1:E:24:LEU:HB3	1:F:30:GLN:NE2	2.30	0.46
1:V:40:GLN:NE2	1:V:40:GLN:CA	2.76	0.46
1:H:134:SER:OG	1:H:137:LEU:HD23	2.15	0.46
1:G:196:LEU:HD12	1:G:198:PRO:HG3	1.97	0.46
1:D:180:ARG:O	1:D:180:ARG:HG3	2.15	0.46
1:L:173:ARG:HG2	1:L:173:ARG:HH11	1.81	0.46
1:N:173:ARG:HH11	1:N:173:ARG:HG2	1.81	0.46
1:P:192:LYS:NZ	1:P:195:ASP:O	2.49	0.46
1:I:173:ARG:HH11	1:I:173:ARG:HG2	1.81	0.46
1:A:49:PRO:CG	1:A:178:LEU:HD12	2.46	0.46
1:K:193:ARG:CZ	1:L:180:ARG:NE	2.79	0.46
1:K:100:ASN:HD22	1:K:102:LYS:CB	2.27	0.46
1:A:86:HIS:ND1	1:B:121:HIS:CD2	2.80	0.46
1:M:47:LEU:N	1:M:47:LEU:CD2	2.79	0.46
1:S:77:GLU:OE2	1:T:44:ARG:NH1	2.49	0.46
1:F:140:GLU:HG3	1:F:144:LYS:HE3	1.98	0.46
1:P:100:ASN:HD22	1:P:102:LYS:CB	2.28	0.46
1:D:173:ARG:HG2	1:D:173:ARG:HH11	1.81	0.46
1:B:47:LEU:CD2	1:B:47:LEU:N	2.78	0.46
1:E:184:LEU:HD22	1:E:185:GLU:N	2.31	0.46
1:O:112:ARG:HG3	1:O:122:GLU:HB2	1.98	0.46
1:N:196:LEU:HD12	1:N:198:PRO:HG3	1.98	0.45
1:O:204:ARG:HH21	1:O:204:ARG:HG3	1.82	0.45
1:P:182:LEU:CD2	1:P:182:LEU:N	2.67	0.45
1:S:100:ASN:HD22	1:S:102:LYS:CB	2.27	0.45
1:N:147:VAL:HG21	1:O:124:VAL:CG2	2.40	0.45
1:S:113:VAL:HG21	1:S:155:LEU:HD13	1.99	0.45
1:A:77:GLU:CD	1:B:44:ARG:HH11	2.20	0.45
1:D:194:GLN:HB2	1:D:194:GLN:HE21	1.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:85:ALA:HB1	1:V:120:TYR:O	2.15	0.45
1:O:176:ASN:C	1:O:178:LEU:H	2.20	0.45
1:H:86:HIS:ND1	1:I:121:HIS:CD2	2.81	0.45
1:T:182:LEU:N	1:T:182:LEU:HD23	2.30	0.45
1:I:175:LEU:O	1:I:178:LEU:HB2	2.15	0.45
1:K:70:ARG:NH1	1:K:70:ARG:HG3	2.31	0.45
1:K:193:ARG:CA	1:L:180:ARG:HH21	2.28	0.45
1:O:100:ASN:HB2	1:O:101:GLY:H	1.54	0.45
1:H:24:LEU:HA	1:H:24:LEU:HD22	1.82	0.45
1:K:112:ARG:HG3	1:K:122:GLU:HB2	1.97	0.45
1:K:192:LYS:NZ	1:K:194:GLN:O	2.47	0.45
1:Q:204:ARG:HG3	1:R:35:GLU:CD	2.37	0.45
1:F:82:ASN:HB2	1:G:117:ASP:OD1	2.17	0.45
1:B:113:VAL:HG21	1:B:155:LEU:HD13	1.98	0.45
1:O:85:ALA:HB1	1:P:120:TYR:O	2.16	0.45
1:U:192:LYS:NZ	1:U:197:GLU:OE2	2.49	0.45
1:D:82:ASN:H	1:D:82:ASN:ND2	2.10	0.45
1:V:82:ASN:H	1:V:82:ASN:ND2	2.10	0.45
1:R:82:ASN:N	1:R:82:ASN:HD22	2.09	0.45
1:B:196:LEU:HD13	1:B:198:PRO:HD3	1.99	0.45
1:M:113:VAL:HG21	1:M:155:LEU:CD1	2.47	0.45
1:B:40:GLN:NE2	1:B:40:GLN:CA	2.78	0.45
1:I:100:ASN:HD22	1:I:102:LYS:CB	2.29	0.45
1:H:180:ARG:HG3	1:H:181:GLN:N	2.32	0.45
1:I:40:GLN:CA	1:I:40:GLN:NE2	2.75	0.45
1:O:166:ILE:HD13	1:O:166:ILE:O	2.17	0.45
1:P:47:LEU:HD23	1:P:165:CYS:SG	2.57	0.45
1:E:47:LEU:CD2	1:E:47:LEU:N	2.78	0.45
1:M:86:HIS:ND1	1:N:121:HIS:CD2	2.82	0.45
1:E:184:LEU:CD2	1:E:185:GLU:N	2.78	0.45
1:G:143:ARG:NH1	1:H:94:ASP:OD2	2.49	0.45
1:M:140:GLU:HG3	1:M:144:LYS:HE3	1.98	0.45
1:K:47:LEU:HD23	1:K:165:CYS:SG	2.57	0.45
1:N:100:ASN:HD22	1:N:102:LYS:CB	2.30	0.45
1:G:47:LEU:HD23	1:G:165:CYS:SG	2.57	0.45
1:B:196:LEU:HD13	1:B:198:PRO:CD	2.46	0.45
1:T:192:LYS:HB2	1:U:45:GLN:NE2	2.31	0.45
1:L:24:LEU:HD22	1:L:24:LEU:HA	1.82	0.45
1:G:204:ARG:CG	1:G:204:ARG:NH2	2.79	0.45
1:O:47:LEU:HD23	1:O:165:CYS:SG	2.57	0.45
1:I:47:LEU:HD23	1:I:165:CYS:SG	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:192:LYS:HG3	1:U:45:GLN:NE2	2.32	0.45
1:H:192:LYS:HE2	1:H:197:GLU:OE2	2.16	0.45
1:I:85:ALA:HB1	1:J:120:TYR:O	2.16	0.45
1:U:36:TYR:OH	1:U:40:GLN:HG3	2.17	0.45
1:A:40:GLN:NE2	1:A:40:GLN:CA	2.76	0.45
1:S:40:GLN:NE2	1:S:40:GLN:CA	2.80	0.45
1:G:40:GLN:HA	1:G:40:GLN:NE2	2.22	0.45
1:M:37:GLN:OE1	1:V:205:TYR:CE1	2.70	0.45
1:N:195:ASP:HB3	1:O:77:GLU:HG3	1.97	0.45
1:H:173:ARG:HG2	1:H:173:ARG:HH11	1.80	0.45
1:C:100:ASN:HD22	1:C:102:LYS:CB	2.28	0.44
1:E:193:ARG:HG2	1:F:50:GLU:CD	2.38	0.44
1:H:128:VAL:HG12	1:H:129:SER:N	2.32	0.44
1:I:208:CYS:HB2	1:K:33:ALA:HB2	1.99	0.44
1:Q:181:GLN:O	1:Q:181:GLN:HG3	2.18	0.44
1:S:192:LYS:HG3	1:T:45:GLN:NE2	2.32	0.44
1:P:100:ASN:HB2	1:P:101:GLY:H	1.56	0.44
1:R:47:LEU:HD23	1:R:165:CYS:SG	2.57	0.44
1:D:208:CYS:C	1:D:209:ARG:HG3	2.38	0.44
1:D:192:LYS:HB2	1:E:45:GLN:NE2	2.32	0.44
1:B:181:GLN:HG3	1:B:181:GLN:O	2.17	0.44
1:A:173:ARG:HG2	1:A:173:ARG:HH11	1.82	0.44
1:C:173:ARG:HH11	1:C:173:ARG:HG2	1.81	0.44
1:I:192:LYS:O	1:J:48:GLY:N	2.36	0.44
1:N:128:VAL:HG12	1:N:129:SER:N	2.33	0.44
1:G:179:PRO:C	1:G:180:ARG:O	2.56	0.44
1:G:47:LEU:CD2	1:G:47:LEU:N	2.79	0.44
1:B:47:LEU:HD23	1:B:165:CYS:SG	2.57	0.44
1:Q:186:VAL:HG21	1:R:171:TYR:HA	2.00	0.44
1:G:173:ARG:HH11	1:G:173:ARG:HG2	1.81	0.44
1:D:100:ASN:HD22	1:D:102:LYS:CB	2.30	0.44
1:K:100:ASN:HB2	1:K:101:GLY:H	1.54	0.44
1:J:112:ARG:HG3	1:J:122:GLU:HB2	2.00	0.44
1:S:207:SER:C	1:S:209:ARG:H	2.21	0.44
1:I:100:ASN:HD22	1:I:102:LYS:HB2	1.77	0.44
1:I:196:LEU:HD13	1:I:197:GLU:H	1.82	0.44
1:M:204:ARG:HG3	1:N:35:GLU:OE1	2.16	0.44
1:V:50:GLU:HA	1:V:181:GLN:NE2	2.33	0.44
1:G:166:ILE:O	1:G:166:ILE:HD13	2.18	0.44
1:P:40:GLN:NE2	1:P:40:GLN:HA	2.25	0.44
1:U:100:ASN:HD22	1:U:102:LYS:CB	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:86:HIS:ND1	1:H:121:HIS:CD2	2.79	0.44
1:A:113:VAL:HG21	1:A:155:LEU:HD13	2.00	0.44
1:B:113:VAL:HG21	1:B:155:LEU:CD1	2.48	0.44
1:T:82:ASN:HB2	1:U:117:ASP:OD1	2.18	0.44
1:C:208:CYS:HB2	1:E:33:ALA:HB2	1.98	0.44
1:Q:116:LYS:HE2	2:Q:2001:HOH:O	2.18	0.44
1:S:24:LEU:HB3	1:T:30:GLN:NE2	2.33	0.44
1:C:40:GLN:CA	1:C:40:GLN:NE2	2.78	0.44
1:E:100:ASN:ND2	1:E:102:LYS:CB	2.74	0.44
1:B:192:LYS:NZ	1:B:194:GLN:O	2.46	0.44
1:L:47:LEU:N	1:L:47:LEU:CD2	2.80	0.44
1:F:77:GLU:OE2	1:G:44:ARG:NH1	2.51	0.44
1:E:113:VAL:HG21	1:E:155:LEU:HD13	1.99	0.44
1:T:82:ASN:HD22	1:T:82:ASN:N	2.14	0.44
1:A:49:PRO:HD3	1:L:180:ARG:HH12	1.83	0.44
1:F:204:ARG:HG3	1:G:35:GLU:OE1	2.18	0.44
1:M:77:GLU:OE2	1:N:44:ARG:NH1	2.51	0.44
1:B:33:ALA:HB1	1:K:205:TYR:CE1	2.53	0.44
1:F:186:VAL:HG21	1:G:171:TYR:HA	2.00	0.44
1:T:58:GLY:C	1:T:60:GLY:H	2.21	0.44
1:D:77:GLU:OE2	1:E:44:ARG:NH1	2.51	0.44
1:E:202:GLU:HG2	1:E:206:ASN:HD21	1.83	0.44
1:H:58:GLY:C	1:H:60:GLY:H	2.22	0.44
1:U:173:ARG:HH11	1:U:173:ARG:HG2	1.83	0.44
1:L:192:LYS:NZ	1:L:194:GLN:O	2.40	0.43
1:U:47:LEU:HD23	1:U:165:CYS:SG	2.57	0.43
1:L:151:LEU:CD1	1:L:155:LEU:HD22	2.48	0.43
1:K:178:LEU:HB3	1:K:179:PRO:CD	2.48	0.43
1:A:192:LYS:HB2	1:B:45:GLN:NE2	2.32	0.43
1:O:77:GLU:OE2	1:P:44:ARG:NH1	2.51	0.43
1:G:186:VAL:HG21	1:H:171:TYR:HA	2.00	0.43
1:D:113:VAL:HG21	1:D:155:LEU:CD1	2.48	0.43
1:E:179:PRO:C	1:E:180:ARG:O	2.56	0.43
1:N:140:GLU:HG3	1:N:144:LYS:HE3	1.99	0.43
1:E:93:VAL:HA	1:E:107:VAL:HG22	2.00	0.43
1:U:58:GLY:C	1:U:60:GLY:H	2.22	0.43
1:N:40:GLN:CA	1:N:40:GLN:NE2	2.79	0.43
1:R:166:ILE:O	1:R:166:ILE:HD13	2.17	0.43
1:I:166:ILE:O	1:I:166:ILE:HD13	2.19	0.43
1:J:113:VAL:HG21	1:J:155:LEU:HD13	2.00	0.43
1:P:173:ARG:HG2	1:P:173:ARG:HH11	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:100:ASN:HD22	1:G:102:LYS:CB	2.30	0.43
1:O:113:VAL:HG21	1:O:155:LEU:CD1	2.48	0.43
1:P:143:ARG:NH1	1:Q:94:ASP:OD2	2.51	0.43
1:L:178:LEU:O	1:L:179:PRO:C	2.57	0.43
1:L:178:LEU:O	1:L:179:PRO:O	2.36	0.43
1:G:186:VAL:HG21	1:H:171:TYR:CA	2.49	0.43
1:G:115:LEU:C	1:G:117:ASP:H	2.22	0.43
1:N:175:LEU:O	1:N:178:LEU:HB2	2.18	0.43
1:N:143:ARG:NH1	1:O:94:ASP:OD2	2.51	0.43
1:D:24:LEU:HA	1:D:24:LEU:HD22	1.81	0.43
1:M:204:ARG:HH21	1:M:204:ARG:HG3	1.83	0.43
1:I:115:LEU:C	1:I:117:ASP:H	2.21	0.43
1:T:202:GLU:O	1:T:205:TYR:N	2.51	0.43
1:B:193:ARG:HH12	1:C:50:GLU:CD	2.22	0.43
1:R:143:ARG:NH1	1:S:94:ASP:OD2	2.52	0.43
1:L:70:ARG:NH1	1:L:70:ARG:HG3	2.31	0.43
1:A:105:VAL:HG11	1:A:139:LEU:HD13	1.99	0.43
1:L:58:GLY:C	1:L:60:GLY:H	2.22	0.43
1:A:32:THR:CG2	1:K:207:SER:HB2	2.48	0.43
1:B:24:LEU:HB3	1:C:30:GLN:NE2	2.34	0.43
1:M:173:ARG:HH11	1:M:173:ARG:HG2	1.83	0.43
1:G:36:TYR:CZ	1:G:40:GLN:HG3	2.53	0.43
1:D:179:PRO:O	1:D:180:ARG:O	2.37	0.43
1:K:24:LEU:HD22	1:K:24:LEU:HA	1.81	0.43
1:B:140:GLU:HB2	1:C:126:TYR:CD2	2.53	0.43
1:G:85:ALA:HB1	1:H:120:TYR:O	2.19	0.43
1:I:186:VAL:HG21	1:J:171:TYR:HA	2.00	0.43
1:G:178:LEU:HA	1:G:178:LEU:HD23	1.78	0.43
1:A:166:ILE:HD13	1:A:166:ILE:O	2.18	0.43
1:O:100:ASN:HD22	1:O:102:LYS:H	1.67	0.43
1:B:192:LYS:CB	1:C:45:GLN:NE2	2.81	0.43
1:R:113:VAL:CG1	1:R:154:ALA:HB1	2.47	0.43
1:R:178:LEU:HA	1:R:178:LEU:HD23	1.79	0.43
1:I:77:GLU:OE1	1:J:44:ARG:HD3	2.18	0.43
1:S:196:LEU:HD22	1:S:197:GLU:H	1.82	0.43
1:J:113:VAL:HG21	1:J:155:LEU:CD1	2.49	0.43
1:L:44:ARG:HD3	1:V:77:GLU:OE1	2.19	0.43
1:Q:186:VAL:HG21	1:R:171:TYR:CA	2.49	0.43
1:D:93:VAL:HA	1:D:107:VAL:HG22	2.00	0.43
1:Q:208:CYS:HB3	1:S:33:ALA:HB2	2.01	0.43
1:B:166:ILE:HD13	1:B:166:ILE:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:100:ASN:HB2	1:Q:101:GLY:H	1.55	0.43
1:F:100:ASN:ND2	1:F:102:LYS:CB	2.77	0.43
1:A:123:ASP:OD1	1:A:153:ARG:NH1	2.51	0.43
1:D:204:ARG:HG3	1:E:35:GLU:CD	2.39	0.43
1:R:70:ARG:NH1	1:R:70:ARG:CG	2.82	0.43
1:T:85:ALA:HB1	1:U:120:TYR:O	2.19	0.43
1:V:112:ARG:HG3	1:V:122:GLU:HB2	2.00	0.43
1:P:128:VAL:HG12	1:P:129:SER:N	2.33	0.43
1:V:140:GLU:HG3	1:V:144:LYS:HE3	2.01	0.43
1:Q:40:GLN:CA	1:Q:40:GLN:NE2	2.75	0.43
1:V:50:GLU:HA	1:V:181:GLN:HE21	1.83	0.43
1:F:40:GLN:HA	1:F:40:GLN:NE2	2.26	0.43
1:T:134:SER:OG	1:T:137:LEU:HD23	2.18	0.43
1:G:82:ASN:HB2	1:H:117:ASP:OD1	2.19	0.43
1:S:192:LYS:HB2	1:T:45:GLN:NE2	2.34	0.43
1:C:113:VAL:HG21	1:C:155:LEU:CD1	2.49	0.43
1:C:77:GLU:OE2	1:D:44:ARG:NH1	2.51	0.43
1:P:205:TYR:CE2	1:P:209:ARG:NH2	2.86	0.43
1:K:58:GLY:C	1:K:60:GLY:H	2.22	0.43
1:P:90:GLN:HG2	1:P:91:GLN:N	2.34	0.43
1:G:58:GLY:C	1:G:60:GLY:H	2.22	0.43
1:H:69:HIS:HB3	1:I:167:LEU:CD2	2.47	0.42
1:R:175:LEU:O	1:R:178:LEU:HB2	2.18	0.42
1:F:58:GLY:C	1:F:60:GLY:H	2.21	0.42
1:M:40:GLN:CA	1:M:40:GLN:NE2	2.81	0.42
1:R:36:TYR:CE1	1:R:40:GLN:HG2	2.54	0.42
1:S:166:ILE:O	1:S:166:ILE:HD13	2.18	0.42
1:P:189:THR:HG22	1:P:189:THR:O	2.19	0.42
1:R:113:VAL:HG21	1:R:155:LEU:CD1	2.49	0.42
1:K:179:PRO:C	1:K:180:ARG:O	2.58	0.42
1:L:44:ARG:NH1	1:V:77:GLU:OE2	2.52	0.42
1:U:139:LEU:O	1:U:143:ARG:HG3	2.19	0.42
1:U:86:HIS:HA	1:U:112:ARG:O	2.19	0.42
1:J:47:LEU:N	1:J:47:LEU:CD2	2.80	0.42
1:K:134:SER:OG	1:K:137:LEU:HD23	2.19	0.42
1:E:205:TYR:CE2	1:E:209:ARG:NH2	2.87	0.42
1:N:47:LEU:N	1:N:47:LEU:CD2	2.80	0.42
1:G:198:PRO:O	1:G:202:GLU:HG3	2.20	0.42
1:B:50:GLU:HA	1:B:181:GLN:HE22	1.85	0.42
1:I:112:ARG:NH1	2:I:2007:HOH:O	2.51	0.42
1:D:197:GLU:HB3	1:D:200:VAL:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:188:LEU:HD21	1:T:171:TYR:CE1	2.54	0.42
1:S:58:GLY:C	1:S:60:GLY:H	2.22	0.42
1:F:204:ARG:CG	1:F:204:ARG:NH2	2.75	0.42
1:Q:184:LEU:HD22	1:Q:185:GLU:N	2.32	0.42
1:B:196:LEU:HD13	1:B:198:PRO:HG3	1.99	0.42
1:O:40:GLN:CA	1:O:40:GLN:NE2	2.80	0.42
1:L:36:TYR:CE1	1:L:40:GLN:HG2	2.55	0.42
1:E:100:ASN:HB2	1:E:101:GLY:H	1.57	0.42
1:J:77:GLU:OE2	1:K:44:ARG:NH1	2.52	0.42
1:I:147:VAL:HG21	1:J:124:VAL:CG2	2.43	0.42
1:T:100:ASN:HB2	1:T:101:GLY:H	1.57	0.42
1:L:113:VAL:HG21	1:L:155:LEU:HD13	2.00	0.42
1:M:180:ARG:O	1:M:181:GLN:HB3	2.19	0.42
1:B:173:ARG:HH11	1:B:173:ARG:HG2	1.84	0.42
1:G:90:GLN:HG2	1:G:91:GLN:N	2.35	0.42
1:K:100:ASN:ND2	1:K:102:LYS:CB	2.77	0.42
1:J:77:GLU:OE1	1:K:44:ARG:HD3	2.20	0.42
1:Q:77:GLU:OE2	1:R:44:ARG:NH1	2.52	0.42
1:A:82:ASN:ND2	1:A:82:ASN:H	2.10	0.42
1:D:115:LEU:C	1:D:117:ASP:N	2.72	0.42
1:D:134:SER:OG	1:D:137:LEU:HD23	2.20	0.42
1:S:24:LEU:HD22	1:S:24:LEU:HA	1.82	0.42
1:I:112:ARG:HG3	1:I:122:GLU:HB2	2.02	0.42
1:I:207:SER:C	1:I:209:ARG:H	2.21	0.42
1:R:173:ARG:HG2	1:R:173:ARG:HH11	1.84	0.42
1:G:36:TYR:CE1	1:G:40:GLN:HG2	2.55	0.42
1:U:100:ASN:HB2	1:U:101:GLY:H	1.53	0.42
1:L:134:SER:OG	1:L:137:LEU:HD23	2.20	0.42
1:B:165:CYS:HA	2:B:2021:HOH:O	2.19	0.42
1:Q:24:LEU:HD22	1:Q:24:LEU:HA	1.89	0.42
1:J:82:ASN:HD22	1:J:82:ASN:N	2.11	0.42
1:N:176:ASN:C	1:N:178:LEU:H	2.22	0.42
1:V:113:VAL:HG21	1:V:155:LEU:HD13	2.02	0.42
1:M:24:LEU:HB3	1:N:30:GLN:NE2	2.34	0.42
1:R:85:ALA:HB1	1:S:120:TYR:O	2.20	0.42
1:Q:182:LEU:O	1:Q:183:PRO:C	2.58	0.42
1:N:204:ARG:HD2	1:P:36:TYR:CZ	2.55	0.42
1:I:115:LEU:C	1:I:117:ASP:N	2.73	0.42
1:U:32:THR:HG23	2:U:2002:HOH:O	2.19	0.42
1:L:179:PRO:O	1:L:180:ARG:O	2.38	0.42
1:K:192:LYS:CE	1:K:197:GLU:OE2	2.65	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:204:ARG:HG3	1:D:204:ARG:HH21	1.85	0.42
1:H:204:ARG:HG3	1:I:35:GLU:CD	2.41	0.42
1:S:82:ASN:HD22	1:S:82:ASN:N	2.11	0.42
1:F:186:VAL:HG21	1:G:170:ASP:C	2.40	0.42
1:B:193:ARG:NH1	1:B:193:ARG:CG	2.51	0.41
1:H:40:GLN:NE2	1:H:40:GLN:HA	2.23	0.41
1:R:100:ASN:HD22	1:R:102:LYS:CB	2.32	0.41
1:D:86:HIS:ND1	1:E:121:HIS:CD2	2.85	0.41
1:G:192:LYS:HB2	1:H:45:GLN:HE21	1.85	0.41
1:K:113:VAL:HG21	1:K:155:LEU:CD1	2.50	0.41
1:R:77:GLU:OE1	1:S:44:ARG:HD3	2.20	0.41
1:A:140:GLU:HG3	1:A:144:LYS:HE3	2.01	0.41
1:O:136:ALA:HB2	1:P:95:PHE:HZ	1.85	0.41
1:I:140:GLU:HG3	1:I:144:LYS:HE3	2.01	0.41
1:Q:86:HIS:HA	1:Q:112:ARG:O	2.20	0.41
1:O:192:LYS:CE	1:O:197:GLU:OE2	2.66	0.41
1:G:24:LEU:HA	1:G:24:LEU:HD22	1.82	0.41
1:O:143:ARG:NH1	1:P:94:ASP:OD2	2.53	0.41
1:V:90:GLN:HG2	1:V:91:GLN:N	2.35	0.41
1:E:173:ARG:HG2	1:E:173:ARG:HH11	1.85	0.41
1:F:181:GLN:O	1:F:181:GLN:HG3	2.20	0.41
1:P:178:LEU:HA	1:P:178:LEU:HD23	1.78	0.41
1:S:203:ALA:CB	1:T:35:GLU:HA	2.51	0.41
1:Q:36:TYR:CE1	1:Q:40:GLN:HG2	2.55	0.41
1:E:40:GLN:CA	1:E:40:GLN:NE2	2.81	0.41
1:I:182:LEU:HD23	1:I:182:LEU:N	2.24	0.41
1:S:208:CYS:CB	1:U:33:ALA:HB2	2.49	0.41
1:B:178:LEU:HD22	1:B:179:PRO:HD3	2.02	0.41
1:I:113:VAL:HG21	1:I:155:LEU:CD1	2.50	0.41
1:O:140:GLU:HG3	1:O:144:LYS:HE3	2.01	0.41
1:A:100:ASN:HB2	1:A:101:GLY:H	1.55	0.41
1:H:40:GLN:NE2	1:H:40:GLN:CA	2.81	0.41
1:J:184:LEU:HA	1:J:184:LEU:HD22	1.75	0.41
1:A:47:LEU:HD23	1:A:165:CYS:SG	2.61	0.41
1:F:47:LEU:HD23	1:F:165:CYS:SG	2.61	0.41
1:V:204:ARG:HG3	1:V:204:ARG:HH21	1.84	0.41
1:E:193:ARG:HH11	1:E:193:ARG:HG2	1.85	0.41
1:A:112:ARG:HG3	1:A:122:GLU:HB2	2.03	0.41
1:K:193:ARG:CD	1:L:180:ARG:HE	2.32	0.41
1:R:100:ASN:HD22	1:R:102:LYS:H	1.68	0.41
1:U:204:ARG:HG3	1:U:204:ARG:HH21	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:47:LEU:HD23	1:J:165:CYS:SG	2.60	0.41
1:H:208:CYS:CB	1:J:33:ALA:HB2	2.50	0.41
1:B:105:VAL:HG11	1:B:139:LEU:HD13	2.02	0.41
1:D:58:GLY:C	1:D:60:GLY:H	2.24	0.41
1:O:58:GLY:C	1:O:60:GLY:H	2.23	0.41
1:J:50:GLU:CD	1:J:50:GLU:H	2.24	0.41
1:V:123:ASP:OD1	1:V:153:ARG:NH1	2.54	0.41
1:R:77:GLU:OE2	1:S:44:ARG:NH1	2.54	0.41
1:K:57:ALA:HB2	1:K:63:VAL:CG2	2.51	0.41
1:E:58:GLY:C	1:E:60:GLY:H	2.24	0.41
1:C:188:LEU:HD23	1:C:188:LEU:HA	1.69	0.41
1:M:195:ASP:HB3	1:N:77:GLU:HG3	2.02	0.41
1:E:166:ILE:O	1:E:166:ILE:HD13	2.21	0.41
1:D:36:TYR:CE1	1:D:40:GLN:HG2	2.55	0.41
1:P:36:TYR:CE1	1:P:40:GLN:HG2	2.56	0.41
1:C:100:ASN:HB2	1:C:101:GLY:H	1.56	0.41
1:V:24:LEU:HA	1:V:24:LEU:HD22	1.88	0.41
1:A:24:LEU:HD22	1:A:24:LEU:HA	1.81	0.41
1:S:203:ALA:HB1	1:T:35:GLU:CA	2.51	0.41
1:K:165:CYS:O	1:K:167:LEU:N	2.54	0.41
1:I:100:ASN:ND2	1:I:102:LYS:CB	2.77	0.41
1:Q:77:GLU:OE1	1:R:44:ARG:HD3	2.21	0.41
1:B:117:ASP:HB3	1:B:119:SER:H	1.86	0.41
1:B:70:ARG:NH1	1:B:70:ARG:CG	2.81	0.41
1:L:45:GLN:HE22	1:V:192:LYS:HG3	1.85	0.41
1:K:178:LEU:HD23	1:K:178:LEU:HA	1.90	0.41
1:T:113:VAL:HG21	1:T:155:LEU:CD1	2.50	0.41
1:H:143:ARG:NH1	1:I:94:ASP:OD2	2.54	0.41
1:J:182:LEU:N	1:J:182:LEU:HD23	2.35	0.41
1:C:188:LEU:O	1:C:189:THR:C	2.58	0.41
1:N:115:LEU:HD22	1:N:158:PHE:CE2	2.56	0.41
1:E:79:PHE:O	1:E:83:GLY:HA3	2.21	0.41
1:R:204:ARG:HG3	1:R:204:ARG:HH21	1.85	0.41
1:P:165:CYS:O	1:P:167:LEU:N	2.54	0.41
1:N:82:ASN:ND2	1:N:82:ASN:H	2.15	0.41
1:T:50:GLU:HA	1:T:181:GLN:HE22	1.82	0.41
1:S:134:SER:OG	1:S:137:LEU:HD23	2.21	0.41
1:L:47:LEU:HD23	1:L:165:CYS:SG	2.61	0.41
1:A:44:ARG:HD3	1:K:77:GLU:OE1	2.21	0.41
1:H:47:LEU:HD23	1:H:165:CYS:SG	2.61	0.41
1:H:47:LEU:CD2	1:H:47:LEU:N	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:121:HIS:CD2	1:V:86:HIS:ND1	2.85	0.41
1:J:192:LYS:HG3	1:K:45:GLN:HE22	1.86	0.41
1:U:115:LEU:C	1:U:117:ASP:H	2.24	0.41
1:J:196:LEU:HD22	1:J:197:GLU:H	1.85	0.41
1:H:182:LEU:HD23	1:H:182:LEU:N	2.36	0.41
1:J:191:ALA:O	1:J:193:ARG:HG3	2.20	0.41
1:A:93:VAL:HA	1:A:107:VAL:HG22	2.02	0.41
1:A:194:GLN:HE21	1:A:194:GLN:HB3	1.57	0.41
1:A:90:GLN:HG2	1:A:91:GLN:N	2.35	0.41
1:C:90:GLN:HG2	1:C:91:GLN:N	2.34	0.41
1:U:113:VAL:HG12	1:U:154:ALA:HB1	2.02	0.41
1:B:58:GLY:C	1:B:60:GLY:H	2.23	0.41
1:N:192:LYS:HB2	1:O:45:GLN:NE2	2.36	0.41
1:R:203:ALA:HB1	1:S:35:GLU:HA	2.03	0.41
1:B:36:TYR:CZ	1:K:204:ARG:HD2	2.56	0.41
1:L:166:ILE:O	1:L:166:ILE:HD13	2.20	0.41
1:U:184:LEU:HD13	1:U:185:GLU:C	2.41	0.41
1:P:195:ASP:HB3	1:Q:77:GLU:HG3	2.02	0.41
1:Q:115:LEU:C	1:Q:117:ASP:H	2.24	0.41
1:G:192:LYS:HB2	1:H:45:GLN:NE2	2.36	0.41
1:G:113:VAL:HG21	1:G:155:LEU:CD1	2.51	0.41
1:H:182:LEU:HA	1:H:183:PRO:HD3	1.98	0.41
1:S:116:LYS:HE2	2:S:2001:HOH:O	2.21	0.41
1:D:166:ILE:HD13	1:D:166:ILE:O	2.21	0.40
1:F:166:ILE:O	1:F:166:ILE:HD13	2.21	0.40
1:V:166:ILE:O	1:V:166:ILE:HD13	2.21	0.40
1:T:110:PHE:CD2	1:T:124:VAL:HG13	2.54	0.40
1:B:178:LEU:HA	1:B:178:LEU:HD23	1.88	0.40
1:O:208:CYS:HB2	1:Q:33:ALA:HB2	2.01	0.40
1:L:171:TYR:HA	1:V:186:VAL:HG21	2.04	0.40
1:P:184:LEU:HA	1:P:184:LEU:HD23	1.87	0.40
1:N:36:TYR:CE1	1:N:40:GLN:HG2	2.56	0.40
1:T:24:LEU:HD22	1:T:24:LEU:HA	1.74	0.40
1:H:82:ASN:ND2	1:H:82:ASN:H	2.15	0.40
1:C:143:ARG:NH1	1:D:94:ASP:OD2	2.55	0.40
1:F:207:SER:C	1:F:209:ARG:H	2.24	0.40
1:F:85:ALA:HB1	1:G:120:TYR:O	2.22	0.40
1:A:58:GLY:C	1:A:60:GLY:H	2.25	0.40
1:S:173:ARG:HH11	1:S:173:ARG:HG2	1.86	0.40
1:C:166:ILE:HD13	1:C:166:ILE:O	2.22	0.40
1:J:166:ILE:O	1:J:166:ILE:HD13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:100:ASN:HD22	1:K:102:LYS:HB2	1.73	0.40
1:Q:175:LEU:O	1:Q:178:LEU:HB2	2.22	0.40
1:I:82:ASN:HB2	1:J:117:ASP:OD1	2.21	0.40
1:N:58:GLY:C	1:N:60:GLY:H	2.24	0.40
1:G:189:THR:HG22	1:G:190:LYS:N	2.37	0.40
1:P:123:ASP:OD1	1:P:153:ARG:NH1	2.55	0.40
1:S:86:HIS:HA	1:S:112:ARG:O	2.22	0.40
1:O:86:HIS:ND1	1:P:121:HIS:CD2	2.86	0.40
1:N:113:VAL:HG21	1:N:155:LEU:CD1	2.51	0.40
1:P:115:LEU:HD22	1:P:158:PHE:CE2	2.56	0.40
1:V:181:GLN:OE1	1:V:181:GLN:HA	2.21	0.40
1:G:184:LEU:CD2	1:G:185:GLU:O	2.69	0.40
1:D:115:LEU:C	1:D:117:ASP:H	2.23	0.40
1:P:50:GLU:CA	1:P:181:GLN:HE22	2.30	0.40
1:P:50:GLU:H	1:P:50:GLU:CD	2.24	0.40
1:B:178:LEU:HD22	1:B:179:PRO:CD	2.52	0.40
1:A:187:ASP:OD1	1:L:177:LYS:CE	2.70	0.40
1:I:196:LEU:HD12	1:I:198:PRO:HG3	2.03	0.40
1:M:24:LEU:HD22	1:M:24:LEU:HA	1.82	0.40
1:R:179:PRO:O	1:R:180:ARG:C	2.59	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	A	184/209 (88%)	177 (96%)	4 (2%)	3 (2%)	12	30
1	B	184/209 (88%)	178 (97%)	4 (2%)	2 (1%)	17	42
1	C	184/209 (88%)	172 (94%)	9 (5%)	3 (2%)	12	30
1	D	184/209 (88%)	173 (94%)	6 (3%)	5 (3%)	6	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	184/209 (88%)	171 (93%)	6 (3%)	7 (4%)	4	9
1	F	184/209 (88%)	171 (93%)	8 (4%)	5 (3%)	6	16
1	G	184/209 (88%)	169 (92%)	12 (6%)	3 (2%)	12	30
1	H	184/209 (88%)	171 (93%)	11 (6%)	2 (1%)	17	42
1	I	184/209 (88%)	174 (95%)	8 (4%)	2 (1%)	17	42
1	J	184/209 (88%)	175 (95%)	5 (3%)	4 (2%)	8	22
1	K	184/209 (88%)	176 (96%)	5 (3%)	3 (2%)	12	30
1	L	184/209 (88%)	175 (95%)	5 (3%)	4 (2%)	8	22
1	M	184/209 (88%)	173 (94%)	6 (3%)	5 (3%)	6	16
1	N	184/209 (88%)	173 (94%)	8 (4%)	3 (2%)	12	30
1	O	184/209 (88%)	173 (94%)	9 (5%)	2 (1%)	17	42
1	P	184/209 (88%)	179 (97%)	3 (2%)	2 (1%)	17	42
1	Q	184/209 (88%)	173 (94%)	8 (4%)	3 (2%)	12	30
1	R	184/209 (88%)	178 (97%)	4 (2%)	2 (1%)	17	42
1	S	184/209 (88%)	175 (95%)	7 (4%)	2 (1%)	17	42
1	T	184/209 (88%)	173 (94%)	8 (4%)	3 (2%)	12	30
1	U	184/209 (88%)	175 (95%)	6 (3%)	3 (2%)	12	30
1	V	184/209 (88%)	173 (94%)	9 (5%)	2 (1%)	17	42
All	All	4048/4598 (88%)	3827 (94%)	151 (4%)	70 (2%)	11	29

All (70) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	166	ILE
1	E	184	LEU
1	F	166	ILE
1	G	166	ILE
1	G	189	THR
1	H	166	ILE
1	I	166	ILE
1	J	166	ILE
1	J	179	PRO
1	K	166	ILE
1	K	180	ARG
1	L	180	ARG
1	M	179	PRO

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Mol	Chain	Res	Type
1	M	208	CYS
1	N	166	ILE
1	N	180	ARG
1	P	166	ILE
1	Q	180	ARG
1	R	166	ILE
1	T	166	ILE
1	V	166	ILE
1	A	100	ASN
1	A	166	ILE
1	B	166	ILE
1	C	100	ASN
1	D	100	ASN
1	D	183	PRO
1	E	166	ILE
1	E	183	PRO
1	E	208	CYS
1	F	100	ASN
1	F	179	PRO
1	I	100	ASN
1	J	100	ASN
1	K	100	ASN
1	L	100	ASN
1	L	166	ILE
1	M	100	ASN
1	M	166	ILE
1	N	100	ASN
1	O	100	ASN
1	O	166	ILE
1	P	100	ASN
1	Q	100	ASN
1	Q	166	ILE
1	R	100	ASN
1	S	100	ASN
1	S	166	ILE
1	T	180	ARG
1	U	166	ILE
1	V	100	ASN
1	B	100	ASN
1	D	180	ARG
1	E	100	ASN
1	E	180	ARG

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Mol	Chain	Res	Type
1	F	188	LEU
1	F	189	THR
1	G	100	ASN
1	H	100	ASN
1	J	183	PRO
1	T	100	ASN
1	U	100	ASN
1	A	180	ARG
1	C	166	ILE
1	M	181	GLN
1	U	183	PRO
1	C	202	GLU
1	E	196	LEU
1	L	179	PRO
1	D	198	PRO

### 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	A	155/169 (92%)	139 (90%)	16 (10%)	9	20
1	B	155/169 (92%)	136 (88%)	19 (12%)	6	14
1	C	155/169 (92%)	138 (89%)	17 (11%)	8	18
1	D	155/169 (92%)	138 (89%)	17 (11%)	8	18
1	E	155/169 (92%)	136 (88%)	19 (12%)	6	14
1	F	155/169 (92%)	138 (89%)	17 (11%)	8	18
1	G	155/169 (92%)	137 (88%)	18 (12%)	7	16
1	H	155/169 (92%)	140 (90%)	15 (10%)	10	23
1	I	155/169 (92%)	138 (89%)	17 (11%)	8	18
1	J	155/169 (92%)	135 (87%)	20 (13%)	5	12
1	K	155/169 (92%)	136 (88%)	19 (12%)	6	14
1	L	155/169 (92%)	138 (89%)	17 (11%)	8	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	155/169 (92%)	140 (90%)	15 (10%)	10	23
1	N	155/169 (92%)	139 (90%)	16 (10%)	9	20
1	O	155/169 (92%)	138 (89%)	17 (11%)	8	18
1	P	155/169 (92%)	138 (89%)	17 (11%)	8	18
1	Q	155/169 (92%)	137 (88%)	18 (12%)	7	16
1	R	155/169 (92%)	138 (89%)	17 (11%)	8	18
1	S	155/169 (92%)	136 (88%)	19 (12%)	6	14
1	T	155/169 (92%)	137 (88%)	18 (12%)	7	16
1	U	155/169 (92%)	140 (90%)	15 (10%)	10	23
1	V	155/169 (92%)	138 (89%)	17 (11%)	8	18
All	All	3410/3718 (92%)	3030 (89%)	380 (11%)	8	17

All (380) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	LEU
1	A	40	GLN
1	A	47	LEU
1	A	70	ARG
1	A	82	ASN
1	A	100	ASN
1	A	115	LEU
1	A	124	VAL
1	A	139	LEU
1	A	155	LEU
1	A	166	ILE
1	A	167	LEU
1	A	174	SER
1	A	182	LEU
1	A	184	LEU
1	A	208	CYS
1	B	24	LEU
1	B	40	GLN
1	B	47	LEU
1	B	70	ARG
1	B	82	ASN
1	B	100	ASN
1	B	112	ARG

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Mol	Chain	Res	Type
1	B	115	LEU
1	B	124	VAL
1	B	139	LEU
1	B	155	LEU
1	B	166	ILE
1	B	167	LEU
1	B	174	SER
1	B	175	LEU
1	B	182	LEU
1	B	189	THR
1	B	193	ARG
1	B	194	GLN
1	C	24	LEU
1	C	40	GLN
1	C	47	LEU
1	C	70	ARG
1	C	82	ASN
1	C	100	ASN
1	C	115	LEU
1	C	124	VAL
1	C	139	LEU
1	C	155	LEU
1	C	166	ILE
1	C	167	LEU
1	C	174	SER
1	C	180	ARG
1	C	182	LEU
1	C	184	LEU
1	C	196	LEU
1	D	24	LEU
1	D	40	GLN
1	D	47	LEU
1	D	70	ARG
1	D	82	ASN
1	D	100	ASN
1	D	112	ARG
1	D	115	LEU
1	D	124	VAL
1	D	139	LEU
1	D	155	LEU
1	D	166	ILE
1	D	167	LEU

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Mol	Chain	Res	Type
1	D	174	SER
1	D	181	GLN
1	D	194	GLN
1	D	199	SER
1	E	24	LEU
1	E	40	GLN
1	E	47	LEU
1	E	70	ARG
1	E	82	ASN
1	E	100	ASN
1	E	112	ARG
1	E	115	LEU
1	E	124	VAL
1	E	139	LEU
1	E	155	LEU
1	E	166	ILE
1	E	167	LEU
1	E	174	SER
1	E	175	LEU
1	E	181	GLN
1	E	184	LEU
1	E	196	LEU
1	E	199	SER
1	F	24	LEU
1	F	40	GLN
1	F	47	LEU
1	F	70	ARG
1	F	82	ASN
1	F	100	ASN
1	F	115	LEU
1	F	124	VAL
1	F	139	LEU
1	F	155	LEU
1	F	166	ILE
1	F	167	LEU
1	F	174	SER
1	F	175	LEU
1	F	182	LEU
1	F	184	LEU
1	F	204	ARG
1	G	24	LEU
1	G	40	GLN

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Mol	Chain	Res	Type
1	G	47	LEU
1	G	82	ASN
1	G	100	ASN
1	G	115	LEU
1	G	124	VAL
1	G	139	LEU
1	G	155	LEU
1	G	166	ILE
1	G	167	LEU
1	G	174	SER
1	G	175	LEU
1	G	180	ARG
1	G	182	LEU
1	G	194	GLN
1	G	196	LEU
1	G	204	ARG
1	H	24	LEU
1	H	40	GLN
1	H	47	LEU
1	H	82	ASN
1	H	100	ASN
1	H	115	LEU
1	H	124	VAL
1	H	139	LEU
1	H	155	LEU
1	H	166	ILE
1	H	167	LEU
1	H	174	SER
1	H	180	ARG
1	H	184	LEU
1	H	196	LEU
1	I	24	LEU
1	I	40	GLN
1	I	47	LEU
1	I	70	ARG
1	I	82	ASN
1	I	100	ASN
1	I	115	LEU
1	I	124	VAL
1	I	139	LEU
1	I	155	LEU
1	I	166	ILE

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Mol	Chain	Res	Type
1	I	167	LEU
1	I	174	SER
1	I	175	LEU
1	I	182	LEU
1	I	184	LEU
1	I	196	LEU
1	J	24	LEU
1	J	40	GLN
1	J	47	LEU
1	J	70	ARG
1	J	82	ASN
1	J	100	ASN
1	J	115	LEU
1	J	124	VAL
1	J	139	LEU
1	J	155	LEU
1	J	166	ILE
1	J	167	LEU
1	J	174	SER
1	J	175	LEU
1	J	181	GLN
1	J	182	LEU
1	J	183	PRO
1	J	184	LEU
1	J	196	LEU
1	J	202	GLU
1	K	24	LEU
1	K	40	GLN
1	K	47	LEU
1	K	70	ARG
1	K	82	ASN
1	K	100	ASN
1	K	115	LEU
1	K	124	VAL
1	K	139	LEU
1	K	155	LEU
1	K	166	ILE
1	K	167	LEU
1	K	174	SER
1	K	175	LEU
1	K	180	ARG
1	K	182	LEU

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Mol	Chain	Res	Type
1	K	184	LEU
1	K	189	THR
1	K	196	LEU
1	L	24	LEU
1	L	40	GLN
1	L	47	LEU
1	L	82	ASN
1	L	100	ASN
1	L	112	ARG
1	L	115	LEU
1	L	124	VAL
1	L	139	LEU
1	L	155	LEU
1	L	166	ILE
1	L	167	LEU
1	L	174	SER
1	L	175	LEU
1	L	196	LEU
1	L	199	SER
1	L	204	ARG
1	M	24	LEU
1	M	40	GLN
1	M	47	LEU
1	M	70	ARG
1	M	82	ASN
1	M	100	ASN
1	M	115	LEU
1	M	124	VAL
1	M	139	LEU
1	M	155	LEU
1	M	166	ILE
1	M	167	LEU
1	M	174	SER
1	M	182	LEU
1	M	196	LEU
1	N	24	LEU
1	N	40	GLN
1	N	47	LEU
1	N	70	ARG
1	N	82	ASN
1	N	100	ASN
1	N	115	LEU

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Mol	Chain	Res	Type
1	N	124	VAL
1	N	139	LEU
1	N	155	LEU
1	N	166	ILE
1	N	167	LEU
1	N	174	SER
1	N	175	LEU
1	N	182	LEU
1	N	196	LEU
1	O	24	LEU
1	O	40	GLN
1	O	47	LEU
1	O	70	ARG
1	O	82	ASN
1	O	100	ASN
1	O	115	LEU
1	O	124	VAL
1	O	139	LEU
1	O	155	LEU
1	O	166	ILE
1	O	167	LEU
1	O	174	SER
1	O	179	PRO
1	O	181	GLN
1	O	182	LEU
1	O	196	LEU
1	P	24	LEU
1	P	40	GLN
1	P	47	LEU
1	P	70	ARG
1	P	82	ASN
1	P	100	ASN
1	P	112	ARG
1	P	115	LEU
1	P	124	VAL
1	P	139	LEU
1	P	155	LEU
1	P	166	ILE
1	P	167	LEU
1	P	174	SER
1	P	175	LEU
1	P	182	LEU

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Mol	Chain	Res	Type
1	P	196	LEU
1	Q	24	LEU
1	Q	40	GLN
1	Q	47	LEU
1	Q	70	ARG
1	Q	82	ASN
1	Q	100	ASN
1	Q	115	LEU
1	Q	124	VAL
1	Q	139	LEU
1	Q	155	LEU
1	Q	166	ILE
1	Q	167	LEU
1	Q	174	SER
1	Q	182	LEU
1	Q	184	LEU
1	Q	193	ARG
1	Q	196	LEU
1	Q	208	CYS
1	R	24	LEU
1	R	40	GLN
1	R	47	LEU
1	R	70	ARG
1	R	82	ASN
1	R	100	ASN
1	R	115	LEU
1	R	124	VAL
1	R	139	LEU
1	R	155	LEU
1	R	166	ILE
1	R	167	LEU
1	R	174	SER
1	R	175	LEU
1	R	184	LEU
1	R	193	ARG
1	R	196	LEU
1	S	24	LEU
1	S	40	GLN
1	S	47	LEU
1	S	70	ARG
1	S	82	ASN
1	S	100	ASN

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Mol	Chain	Res	Type
1	S	115	LEU
1	S	124	VAL
1	S	139	LEU
1	S	155	LEU
1	S	166	ILE
1	S	167	LEU
1	S	174	SER
1	S	175	LEU
1	S	180	ARG
1	S	181	GLN
1	S	184	LEU
1	S	196	LEU
1	S	199	SER
1	T	24	LEU
1	T	40	GLN
1	T	47	LEU
1	T	70	ARG
1	T	82	ASN
1	T	100	ASN
1	T	115	LEU
1	T	124	VAL
1	T	139	LEU
1	T	155	LEU
1	T	166	ILE
1	T	167	LEU
1	T	174	SER
1	T	175	LEU
1	T	179	PRO
1	T	181	GLN
1	T	184	LEU
1	T	196	LEU
1	U	24	LEU
1	U	40	GLN
1	U	47	LEU
1	U	70	ARG
1	U	82	ASN
1	U	100	ASN
1	U	115	LEU
1	U	124	VAL
1	U	139	LEU
1	U	155	LEU
1	U	166	ILE

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Mol	Chain	Res	Type
1	U	167	LEU
1	U	174	SER
1	U	183	PRO
1	U	196	LEU
1	V	24	LEU
1	V	40	GLN
1	V	47	LEU
1	V	70	ARG
1	V	82	ASN
1	V	100	ASN
1	V	115	LEU
1	V	124	VAL
1	V	139	LEU
1	V	155	LEU
1	V	166	ILE
1	V	167	LEU
1	V	174	SER
1	V	175	LEU
1	V	184	LEU
1	V	196	LEU
1	V	202	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (285) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	GLN
1	A	30	GLN
1	A	37	GLN
1	A	40	GLN
1	A	45	GLN
1	A	61	GLN
1	A	82	ASN
1	A	99	ASN
1	A	100	ASN
1	A	121	HIS
1	A	164	ASN
1	A	194	GLN
1	B	28	GLN
1	B	30	GLN
1	B	37	GLN
1	B	40	GLN
1	B	45	GLN

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Mol	Chain	Res	Type
1	B	61	GLN
1	B	82	ASN
1	B	90	GLN
1	B	99	ASN
1	B	100	ASN
1	B	121	HIS
1	B	164	ASN
1	C	28	GLN
1	C	30	GLN
1	C	40	GLN
1	C	45	GLN
1	C	61	GLN
1	C	82	ASN
1	C	90	GLN
1	C	99	ASN
1	C	100	ASN
1	C	121	HIS
1	C	164	ASN
1	C	181	GLN
1	C	194	GLN
1	D	28	GLN
1	D	30	GLN
1	D	37	GLN
1	D	40	GLN
1	D	45	GLN
1	D	61	GLN
1	D	82	ASN
1	D	90	GLN
1	D	99	ASN
1	D	100	ASN
1	D	121	HIS
1	D	164	ASN
1	D	194	GLN
1	E	28	GLN
1	E	30	GLN
1	E	37	GLN
1	E	40	GLN
1	E	45	GLN
1	E	61	GLN
1	E	82	ASN
1	E	90	GLN
1	E	99	ASN

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Mol	Chain	Res	Type
1	E	100	ASN
1	E	121	HIS
1	E	164	ASN
1	E	194	GLN
1	E	206	ASN
1	F	28	GLN
1	F	30	GLN
1	F	37	GLN
1	F	40	GLN
1	F	45	GLN
1	F	61	GLN
1	F	82	ASN
1	F	90	GLN
1	F	99	ASN
1	F	100	ASN
1	F	121	HIS
1	F	164	ASN
1	F	181	GLN
1	F	194	GLN
1	G	28	GLN
1	G	30	GLN
1	G	40	GLN
1	G	45	GLN
1	G	61	GLN
1	G	82	ASN
1	G	90	GLN
1	G	99	ASN
1	G	100	ASN
1	G	121	HIS
1	G	164	ASN
1	G	181	GLN
1	G	194	GLN
1	H	28	GLN
1	H	30	GLN
1	H	37	GLN
1	H	40	GLN
1	H	45	GLN
1	H	61	GLN
1	H	82	ASN
1	H	90	GLN
1	H	99	ASN
1	H	100	ASN

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Mol	Chain	Res	Type
1	H	121	HIS
1	H	164	ASN
1	H	194	GLN
1	I	28	GLN
1	I	30	GLN
1	I	37	GLN
1	I	40	GLN
1	I	45	GLN
1	I	61	GLN
1	I	82	ASN
1	I	90	GLN
1	I	99	ASN
1	I	100	ASN
1	I	121	HIS
1	I	164	ASN
1	I	181	GLN
1	I	194	GLN
1	J	28	GLN
1	J	30	GLN
1	J	37	GLN
1	J	40	GLN
1	J	45	GLN
1	J	61	GLN
1	J	82	ASN
1	J	90	GLN
1	J	99	ASN
1	J	100	ASN
1	J	121	HIS
1	J	164	ASN
1	J	194	GLN
1	K	28	GLN
1	K	30	GLN
1	K	37	GLN
1	K	40	GLN
1	K	45	GLN
1	K	61	GLN
1	K	82	ASN
1	K	90	GLN
1	K	99	ASN
1	K	100	ASN
1	K	121	HIS
1	K	164	ASN

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Mol	Chain	Res	Type
1	K	194	GLN
1	L	28	GLN
1	L	30	GLN
1	L	40	GLN
1	L	45	GLN
1	L	61	GLN
1	L	82	ASN
1	L	90	GLN
1	L	99	ASN
1	L	100	ASN
1	L	121	HIS
1	L	164	ASN
1	L	194	GLN
1	M	28	GLN
1	M	30	GLN
1	M	37	GLN
1	M	40	GLN
1	M	45	GLN
1	M	61	GLN
1	M	82	ASN
1	M	99	ASN
1	M	100	ASN
1	M	121	HIS
1	M	164	ASN
1	M	194	GLN
1	N	28	GLN
1	N	30	GLN
1	N	37	GLN
1	N	40	GLN
1	N	45	GLN
1	N	61	GLN
1	N	82	ASN
1	N	90	GLN
1	N	99	ASN
1	N	100	ASN
1	N	121	HIS
1	N	164	ASN
1	N	194	GLN
1	O	28	GLN
1	O	30	GLN
1	O	37	GLN
1	O	40	GLN

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Mol	Chain	Res	Type
1	O	45	GLN
1	O	61	GLN
1	O	82	ASN
1	O	99	ASN
1	O	100	ASN
1	O	121	HIS
1	O	164	ASN
1	O	194	GLN
1	P	28	GLN
1	P	30	GLN
1	P	37	GLN
1	P	40	GLN
1	P	45	GLN
1	P	61	GLN
1	P	82	ASN
1	P	99	ASN
1	P	100	ASN
1	P	121	HIS
1	P	164	ASN
1	P	181	GLN
1	P	194	GLN
1	Q	28	GLN
1	Q	30	GLN
1	Q	37	GLN
1	Q	40	GLN
1	Q	45	GLN
1	Q	61	GLN
1	Q	82	ASN
1	Q	90	GLN
1	Q	99	ASN
1	Q	100	ASN
1	Q	121	HIS
1	Q	164	ASN
1	Q	194	GLN
1	R	28	GLN
1	R	30	GLN
1	R	37	GLN
1	R	40	GLN
1	R	45	GLN
1	R	61	GLN
1	R	82	ASN
1	R	90	GLN

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Mol	Chain	Res	Type
1	R	99	ASN
1	R	100	ASN
1	R	121	HIS
1	R	164	ASN
1	R	194	GLN
1	S	28	GLN
1	S	30	GLN
1	S	37	GLN
1	S	40	GLN
1	S	45	GLN
1	S	61	GLN
1	S	82	ASN
1	S	90	GLN
1	S	99	ASN
1	S	100	ASN
1	S	121	HIS
1	S	164	ASN
1	S	194	GLN
1	T	28	GLN
1	T	30	GLN
1	T	37	GLN
1	T	40	GLN
1	T	45	GLN
1	T	61	GLN
1	T	82	ASN
1	T	99	ASN
1	T	100	ASN
1	T	121	HIS
1	T	164	ASN
1	T	181	GLN
1	T	194	GLN
1	U	28	GLN
1	U	30	GLN
1	U	37	GLN
1	U	40	GLN
1	U	45	GLN
1	U	61	GLN
1	U	82	ASN
1	U	90	GLN
1	U	99	ASN
1	U	100	ASN
1	U	121	HIS

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Mol	Chain	Res	Type
1	U	164	ASN
1	U	181	GLN
1	U	194	GLN
1	V	28	GLN
1	V	30	GLN
1	V	37	GLN
1	V	40	GLN
1	V	45	GLN
1	V	61	GLN
1	V	82	ASN
1	V	90	GLN
1	V	99	ASN
1	V	100	ASN
1	V	121	HIS
1	V	164	ASN
1	V	194	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

### 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	186/209 (88%)	-0.13	7 (3%) 44 44	19, 37, 80, 95	0
1	B	186/209 (88%)	-0.12	13 (6%) 19 17	14, 32, 84, 98	0
1	C	186/209 (88%)	-0.12	10 (5%) 29 28	16, 35, 82, 101	0
1	D	186/209 (88%)	0.08	14 (7%) 17 15	22, 46, 91, 105	0
1	E	186/209 (88%)	0.31	13 (6%) 19 17	32, 58, 98, 108	0
1	F	186/209 (88%)	0.64	25 (13%) 4 3	39, 67, 102, 116	0
1	G	186/209 (88%)	0.59	20 (10%) 8 6	45, 73, 105, 118	0
1	H	186/209 (88%)	0.73	32 (17%) 2 1	42, 74, 103, 120	0
1	I	186/209 (88%)	0.56	21 (11%) 7 5	41, 69, 107, 116	0
1	J	186/209 (88%)	0.35	15 (8%) 15 12	33, 61, 101, 108	0
1	K	186/209 (88%)	0.17	13 (6%) 19 17	25, 48, 96, 105	0
1	L	186/209 (88%)	-0.15	10 (5%) 29 28	18, 37, 85, 97	0
1	M	186/209 (88%)	-0.07	9 (4%) 34 33	16, 35, 81, 94	0
1	N	186/209 (88%)	-0.10	10 (5%) 29 28	19, 36, 82, 104	0
1	O	186/209 (88%)	-0.03	15 (8%) 15 12	18, 38, 91, 100	0
1	P	186/209 (88%)	0.06	12 (6%) 22 20	21, 44, 91, 100	0
1	Q	186/209 (88%)	0.12	15 (8%) 15 12	23, 45, 95, 111	0
1	R	186/209 (88%)	0.04	16 (8%) 13 10	22, 43, 93, 100	0
1	S	186/209 (88%)	0.07	17 (9%) 11 9	21, 42, 91, 107	0
1	T	186/209 (88%)	0.10	13 (6%) 19 17	22, 46, 95, 109	0
1	U	186/209 (88%)	-0.03	11 (5%) 26 24	21, 46, 89, 106	0
1	V	186/209 (88%)	-0.04	12 (6%) 22 20	20, 42, 86, 98	0
All	All	4092/4598 (88%)	0.14	323 (7%) 15 13	14, 49, 95, 120	0

All (323) RSRZ outliers are listed below:



Mol	Chain	Res	Type	RSRZ
1	E	58	GLY	7.4
1	Q	209	ARG	6.8
1	H	208	CYS	6.7
1	I	209	ARG	6.6
1	M	58	GLY	6.3
1	N	58	GLY	6.2
1	C	57	ALA	6.1
1	E	180	ARG	6.1
1	I	60	GLY	5.6
1	F	209	ARG	5.5
1	L	209	ARG	5.4
1	T	180	ARG	5.4
1	C	61	GLN	5.4
1	F	56	MET	5.3
1	F	60	GLY	5.3
1	J	57	ALA	5.2
1	T	179	PRO	5.2
1	J	58	GLY	5.2
1	R	58	GLY	5.1
1	S	209	ARG	5.1
1	A	58	GLY	5.1
1	F	58	GLY	5.1
1	P	209	ARG	5.1
1	O	60	GLY	5.0
1	G	59	GLY	4.9
1	L	60	GLY	4.9
1	F	180	ARG	4.9
1	K	182	LEU	4.8
1	B	209	ARG	4.8
1	D	209	ARG	4.8
1	J	181	GLN	4.8
1	G	56	MET	4.8
1	B	180	ARG	4.7
1	Q	208	CYS	4.6
1	J	209	ARG	4.6
1	B	57	ALA	4.5
1	H	183	PRO	4.5
1	G	209	ARG	4.5
1	K	180	ARG	4.5
1	K	183	PRO	4.4
1	H	58	GLY	4.4
1	N	61	GLN	4.4
1	T	209	ARG	4.4

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Mol	Chain	Res	Type	RSRZ
1	O	57	ALA	4.3
1	R	57	ALA	4.3
1	R	184	LEU	4.3
1	Q	180	ARG	4.2
1	Q	61	GLN	4.2
1	M	209	ARG	4.2
1	D	184	LEU	4.2
1	I	183	PRO	4.2
1	J	180	ARG	4.1
1	O	58	GLY	4.1
1	I	61	GLN	4.1
1	A	61	GLN	4.1
1	J	56	MET	4.1
1	H	209	ARG	4.0
1	U	180	ARG	4.0
1	H	56	MET	4.0
1	M	57	ALA	4.0
1	B	60	GLY	3.9
1	C	58	GLY	3.9
1	Q	57	ALA	3.9
1	U	209	ARG	3.9
1	V	208	CYS	3.9
1	Q	58	GLY	3.9
1	H	207	SER	3.9
1	K	61	GLN	3.9
1	S	58	GLY	3.9
1	I	56	MET	3.9
1	S	61	GLN	3.9
1	C	60	GLY	3.8
1	I	59	GLY	3.8
1	O	185	GLU	3.8
1	C	56	MET	3.8
1	J	60	GLY	3.8
1	K	58	GLY	3.8
1	M	180	ARG	3.8
1	B	58	GLY	3.8
1	P	181	GLN	3.8
1	H	60	GLY	3.7
1	G	184	LEU	3.7
1	O	100	ASN	3.7
1	G	58	GLY	3.6
1	I	180	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
1	I	64	CYS	3.6
1	P	59	GLY	3.6
1	N	59	GLY	3.6
1	C	59	GLY	3.6
1	I	62	LYS	3.5
1	Q	59	GLY	3.5
1	H	61	GLN	3.5
1	A	59	GLY	3.5
1	O	59	GLY	3.5
1	T	184	LEU	3.5
1	G	61	GLN	3.5
1	A	180	ARG	3.5
1	P	24	LEU	3.5
1	T	205	TYR	3.5
1	H	191	ALA	3.4
1	V	59	GLY	3.4
1	E	61	GLN	3.4
1	O	56	MET	3.4
1	T	182	LEU	3.4
1	R	60	GLY	3.4
1	I	184	LEU	3.4
1	G	57	ALA	3.4
1	O	182	LEU	3.4
1	E	209	ARG	3.4
1	M	181	GLN	3.4
1	F	102	LYS	3.4
1	R	180	ARG	3.4
1	R	209	ARG	3.3
1	D	58	GLY	3.3
1	S	57	ALA	3.3
1	I	58	GLY	3.3
1	S	180	ARG	3.3
1	H	181	GLN	3.3
1	I	57	ALA	3.3
1	D	180	ARG	3.3
1	R	61	GLN	3.2
1	F	183	PRO	3.2
1	Q	184	LEU	3.2
1	G	60	GLY	3.2
1	G	182	LEU	3.2
1	H	24	LEU	3.2
1	F	57	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	O	179	PRO	3.2
1	O	180	ARG	3.2
1	K	209	ARG	3.2
1	J	182	LEU	3.1
1	R	183	PRO	3.1
1	V	209	ARG	3.1
1	G	179	PRO	3.1
1	E	181	GLN	3.1
1	G	99	ASN	3.1
1	T	207	SER	3.1
1	A	56	MET	3.1
1	N	60	GLY	3.1
1	K	57	ALA	3.1
1	B	99	ASN	3.1
1	C	62	LYS	3.1
1	T	183	PRO	3.1
1	G	205	TYR	3.1
1	R	179	PRO	3.0
1	F	188	LEU	3.0
1	H	182	LEU	3.0
1	F	208	CYS	3.0
1	U	181	GLN	3.0
1	A	209	ARG	3.0
1	K	56	MET	3.0
1	V	57	ALA	3.0
1	E	179	PRO	3.0
1	Q	60	GLY	3.0
1	O	184	LEU	3.0
1	E	56	MET	3.0
1	B	184	LEU	3.0
1	G	24	LEU	3.0
1	F	62	LYS	3.0
1	H	190	LYS	3.0
1	B	56	MET	2.9
1	J	61	GLN	2.9
1	P	60	GLY	2.9
1	V	58	GLY	2.9
1	U	184	LEU	2.9
1	R	56	MET	2.9
1	H	104	TYR	2.9
1	Q	181	GLN	2.9
1	F	99	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	H	64	CYS	2.9
1	T	208	CYS	2.9
1	P	184	LEU	2.9
1	F	59	GLY	2.9
1	I	189	THR	2.9
1	J	183	PRO	2.9
1	V	60	GLY	2.9
1	H	205	TYR	2.9
1	O	209	ARG	2.8
1	U	182	LEU	2.8
1	M	182	LEU	2.8
1	K	59	GLY	2.8
1	H	57	ALA	2.8
1	E	205	TYR	2.8
1	O	61	GLN	2.8
1	I	181	GLN	2.8
1	H	48	GLY	2.8
1	K	60	GLY	2.8
1	F	133	LYS	2.8
1	D	205	TYR	2.8
1	L	99	ASN	2.8
1	S	60	GLY	2.8
1	F	205	TYR	2.7
1	V	24	LEU	2.7
1	V	180	ARG	2.7
1	B	100	ASN	2.7
1	A	57	ALA	2.7
1	N	209	ARG	2.7
1	K	184	LEU	2.7
1	D	183	PRO	2.7
1	C	209	ARG	2.7
1	E	60	GLY	2.7
1	N	57	ALA	2.7
1	Q	207	SER	2.7
1	E	182	LEU	2.7
1	Q	205	TYR	2.7
1	G	48	GLY	2.7
1	F	104	TYR	2.7
1	H	59	GLY	2.7
1	Q	179	PRO	2.7
1	L	184	LEU	2.6
1	L	208	CYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	G	181	GLN	2.6
1	I	176	ASN	2.6
1	F	179	PRO	2.6
1	P	56	MET	2.6
1	G	191	ALA	2.6
1	F	61	GLN	2.6
1	F	193	ARG	2.6
1	H	99	ASN	2.6
1	N	99	ASN	2.6
1	F	24	LEU	2.6
1	R	182	LEU	2.6
1	P	61	GLN	2.6
1	G	180	ARG	2.5
1	F	181	GLN	2.5
1	E	57	ALA	2.5
1	B	182	LEU	2.5
1	E	177	LYS	2.5
1	D	99	ASN	2.5
1	H	179	PRO	2.5
1	S	24	LEU	2.5
1	B	59	GLY	2.5
1	I	99	ASN	2.5
1	P	182	LEU	2.4
1	B	61	GLN	2.4
1	S	56	MET	2.4
1	I	205	TYR	2.4
1	H	55	ARG	2.4
1	B	208	CYS	2.4
1	H	175	LEU	2.4
1	H	184	LEU	2.4
1	L	57	ALA	2.4
1	G	103	PHE	2.4
1	H	186	VAL	2.4
1	P	99	ASN	2.4
1	Q	24	LEU	2.4
1	U	58	GLY	2.4
1	T	173	ARG	2.3
1	U	57	ALA	2.3
1	H	187	ASP	2.3
1	F	172	LEU	2.3
1	N	185	GLU	2.3
1	H	177	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	F	189	THR	2.3
1	D	24	LEU	2.3
1	O	183	PRO	2.3
1	E	178	LEU	2.3
1	V	61	GLN	2.3
1	K	99	ASN	2.3
1	J	59	GLY	2.3
1	J	188	LEU	2.3
1	U	183	PRO	2.3
1	G	131	GLY	2.3
1	L	180	ARG	2.3
1	D	182	LEU	2.3
1	L	61	GLN	2.3
1	I	185	GLU	2.3
1	S	179	PRO	2.3
1	L	56	MET	2.3
1	I	175	LEU	2.2
1	I	182	LEU	2.2
1	F	207	SER	2.2
1	M	99	ASN	2.2
1	M	60	GLY	2.2
1	N	205	TYR	2.2
1	R	185	GLU	2.2
1	V	184	LEU	2.2
1	T	57	ALA	2.2
1	C	24	LEU	2.2
1	I	24	LEU	2.2
1	H	100	ASN	2.2
1	P	57	ALA	2.2
1	J	186	VAL	2.2
1	G	190	LYS	2.2
1	T	189	THR	2.2
1	M	61	GLN	2.2
1	F	190	LYS	2.2
1	S	208	CYS	2.2
1	S	178	LEU	2.2
1	D	177	LYS	2.2
1	H	133	LYS	2.2
1	R	181	GLN	2.1
1	S	62	LYS	2.1
1	T	56	MET	2.1
1	D	57	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	N	62	LYS	2.1
1	O	181	GLN	2.1
1	S	59	GLY	2.1
1	V	56	MET	2.1
1	S	205	TYR	2.1
1	Q	56	MET	2.1
1	D	207	SER	2.1
1	C	55	ARG	2.1
1	P	185	GLU	2.1
1	R	24	LEU	2.1
1	D	176	ASN	2.1
1	K	189	THR	2.1
1	R	99	ASN	2.1
1	S	100	ASN	2.1
1	U	208	CYS	2.1
1	H	62	LYS	2.0
1	U	56	MET	2.0
1	H	180	ARG	2.0
1	J	49	PRO	2.0
1	D	185	GLU	2.0
1	R	55	ARG	2.0
1	L	59	GLY	2.0
1	S	99	ASN	2.0
1	V	182	LEU	2.0
1	H	185	GLU	2.0
1	S	181	GLN	2.0
1	J	208	CYS	2.0
1	U	179	PRO	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.



## 6.5 Other polymers

There are no such residues in this entry.