



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:39 PM UTC

PDB ID : 1H2I / pdb_00001h2i
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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

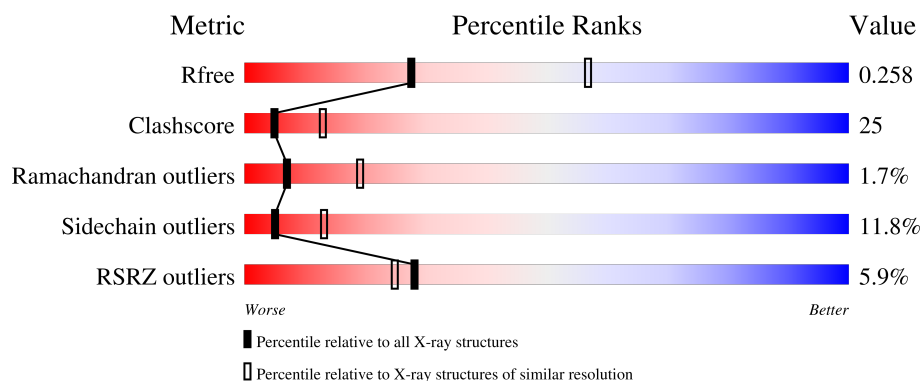
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	209	4% 51% 29% 8% 11%
1	B	209	4% 54% 24% 10% 11%
1	C	209	4% 54% 25% 8% 11%
1	D	209	6% 53% 28% 7% 11%
1	E	209	5% 51% 28% 8% 11%

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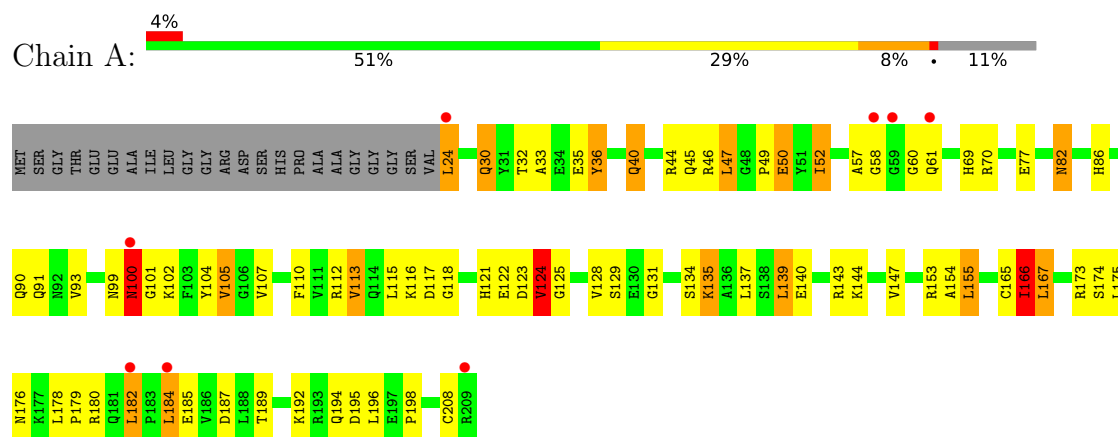
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	N	26	Total 26	O 26	0	0
2	O	17	Total 17	O 17	0	0
2	P	24	Total 24	O 24	0	0
2	Q	21	Total 21	O 21	0	0
2	R	22	Total 22	O 22	0	0
2	S	22	Total 22	O 22	0	0
2	T	22	Total 22	O 22	0	0
2	U	23	Total 23	O 23	0	0
2	V	21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

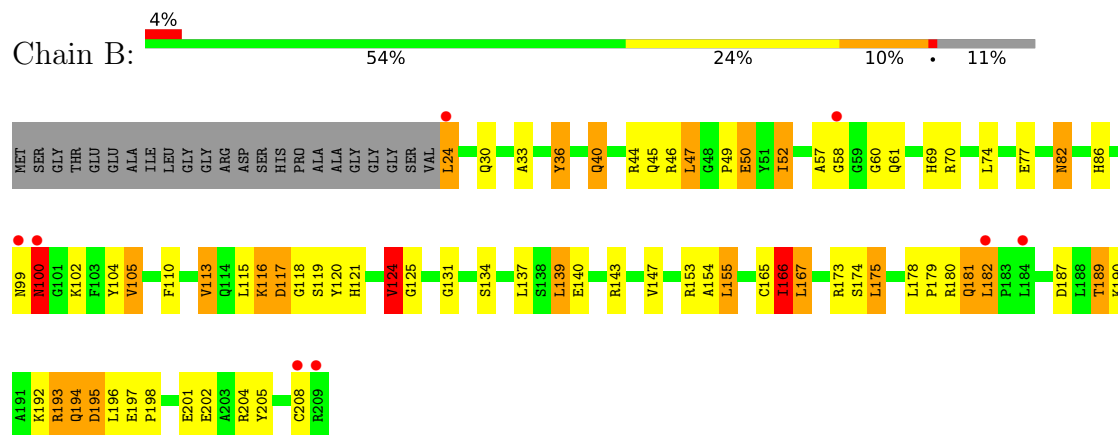
3 Residue-property plots [i](#)

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

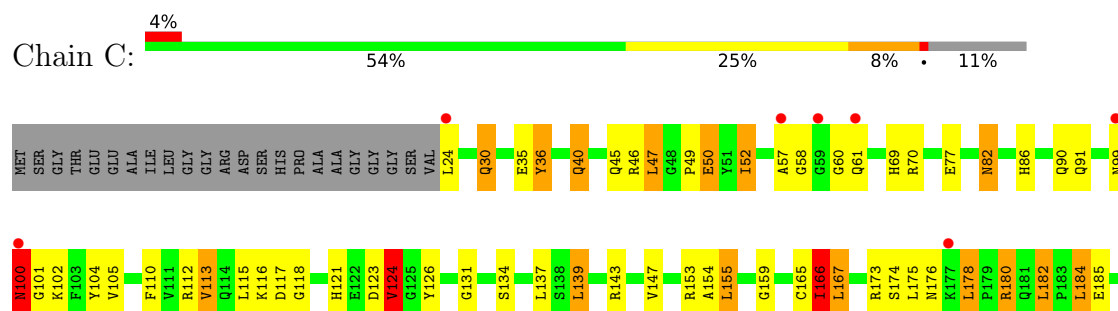
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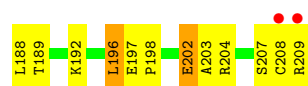


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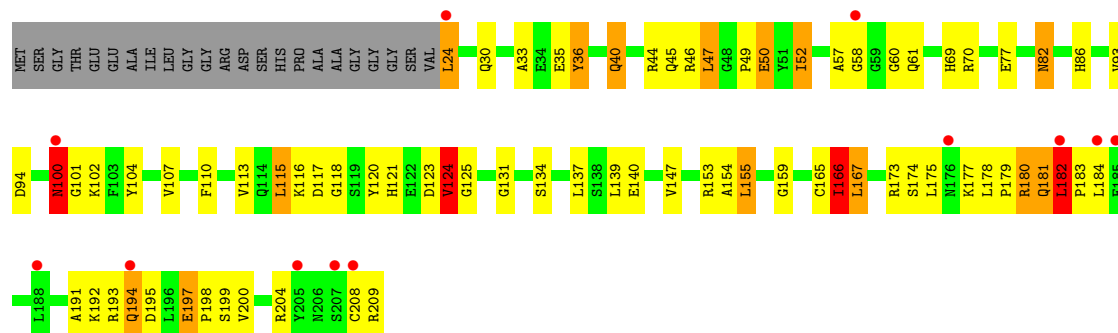


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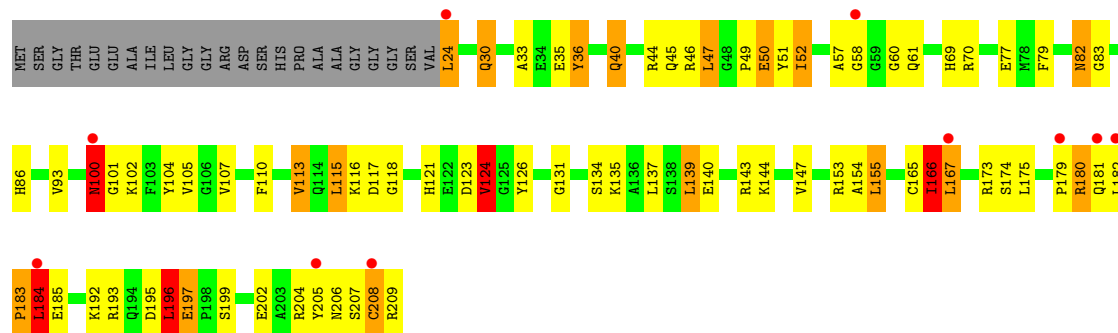




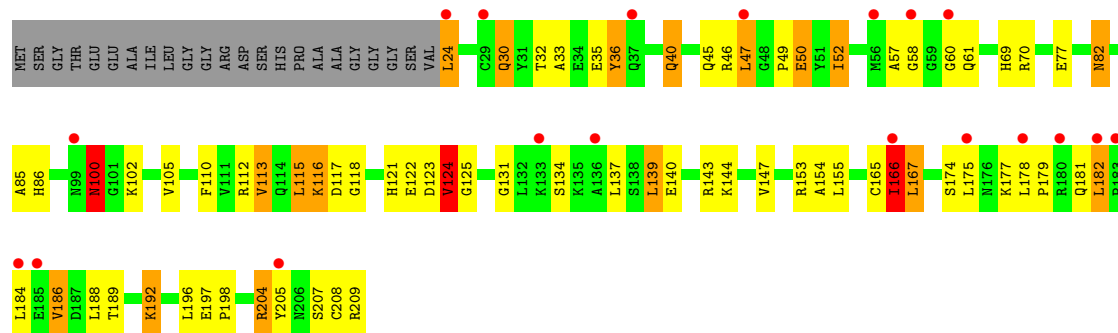
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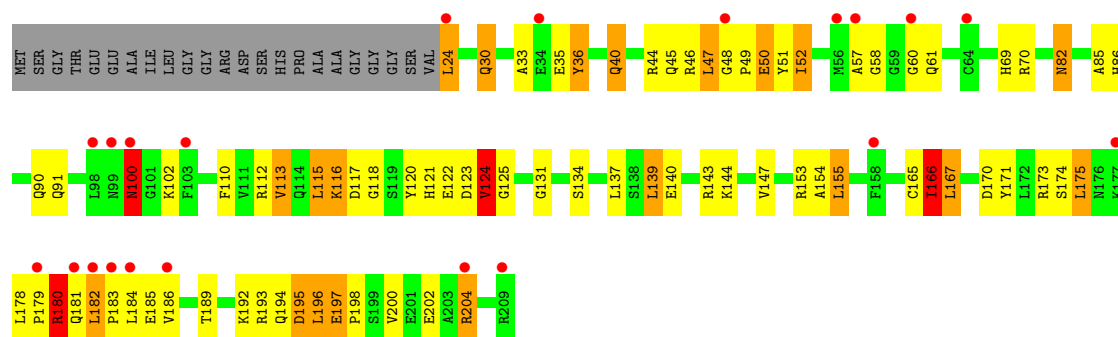


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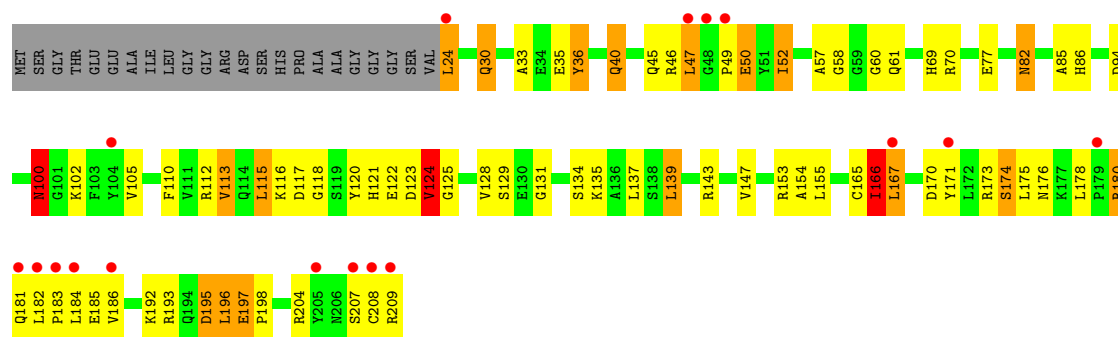


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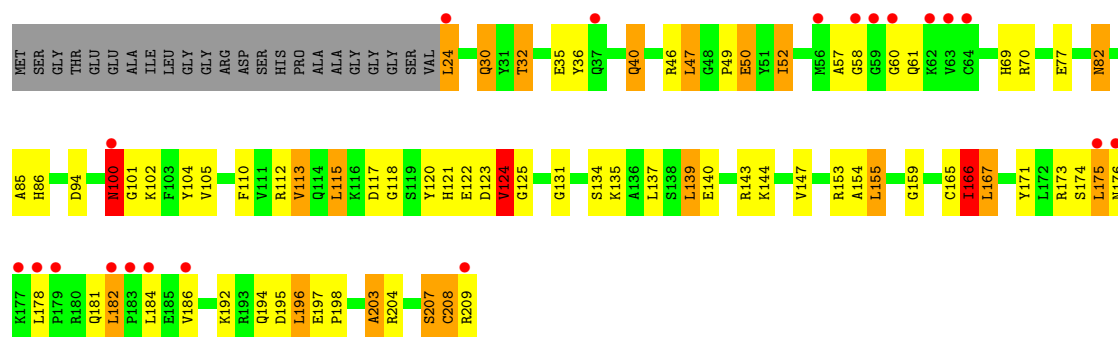




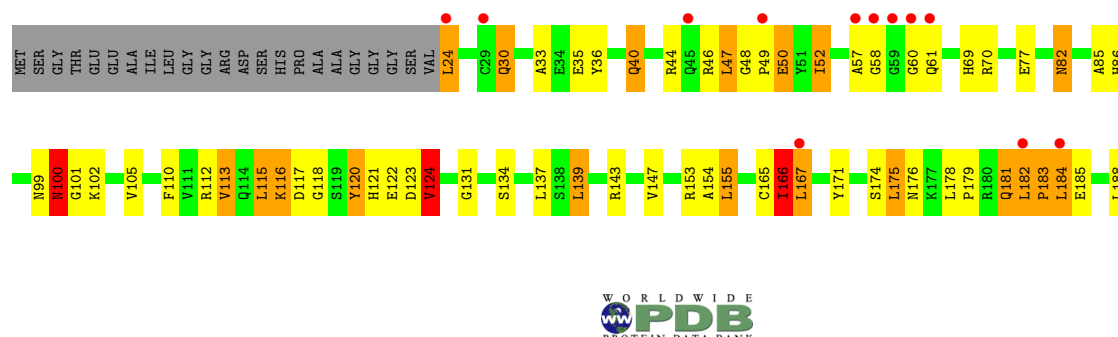
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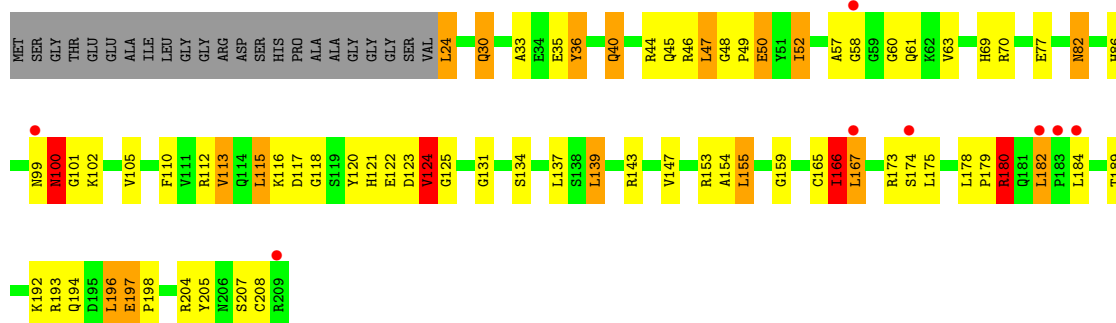


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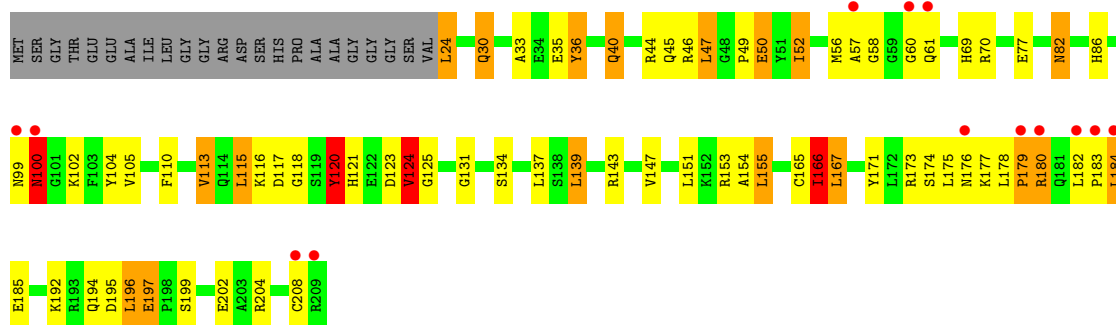




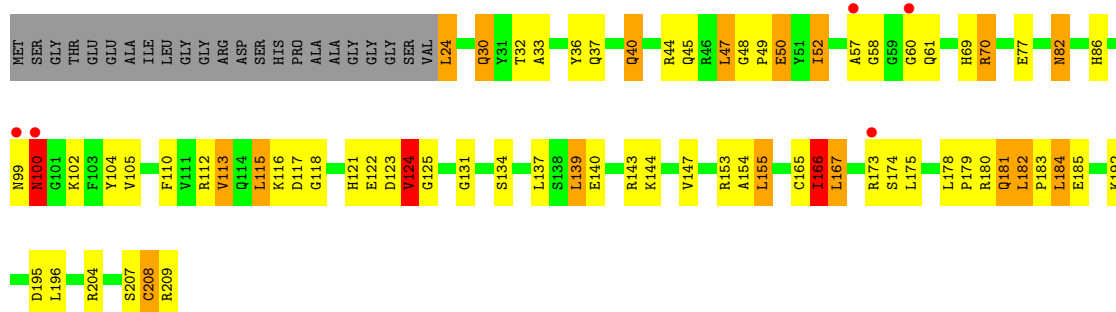
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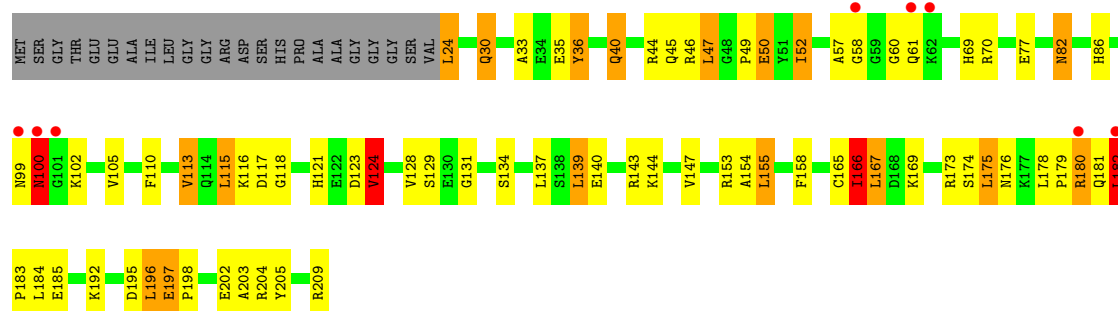


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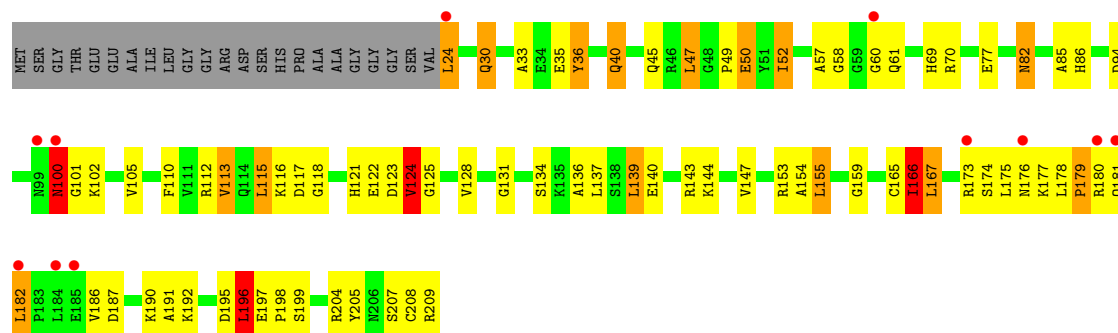


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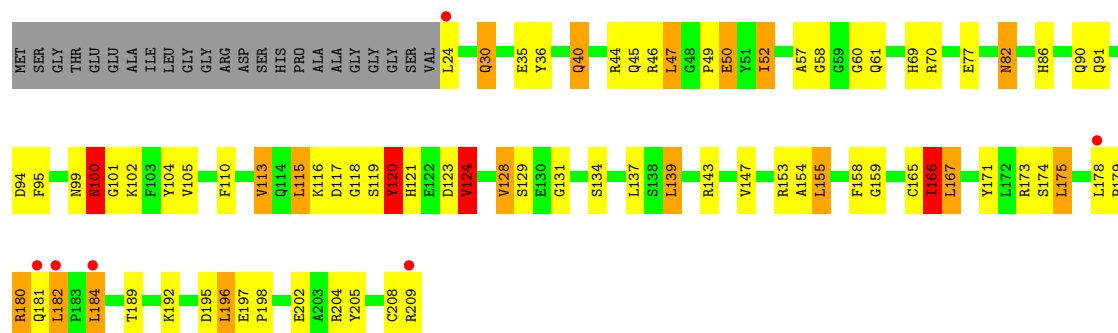




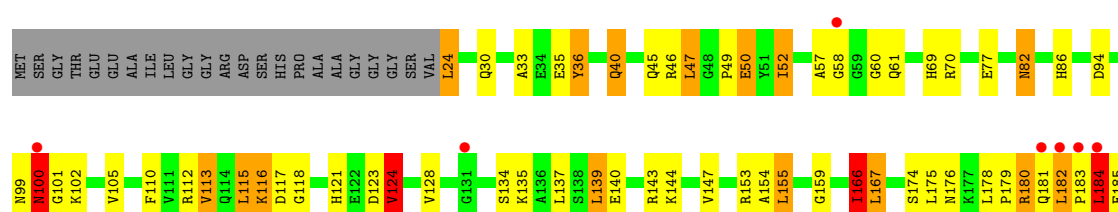
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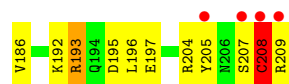


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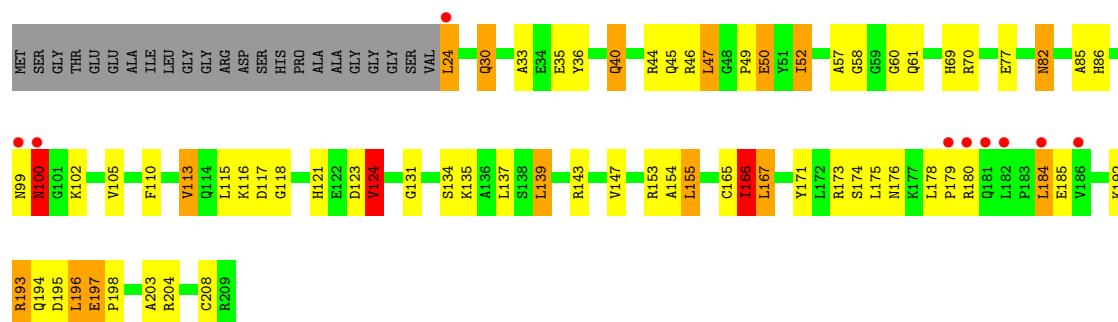


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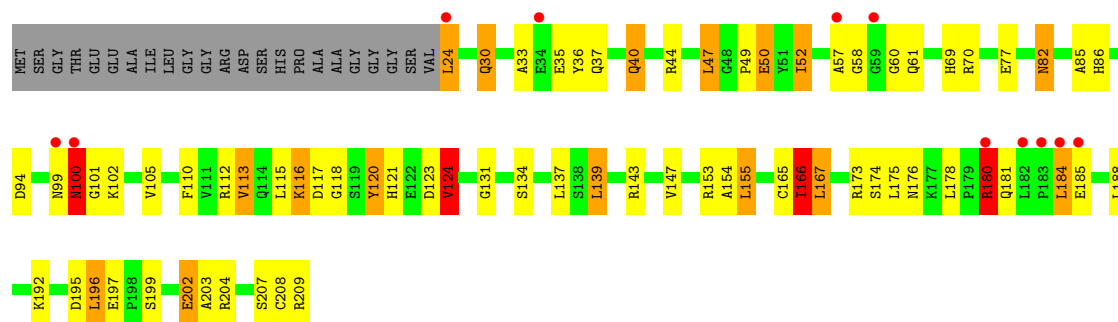




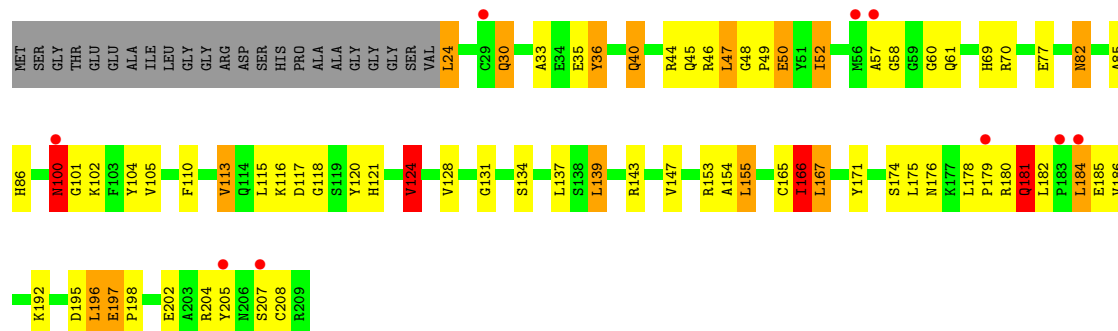
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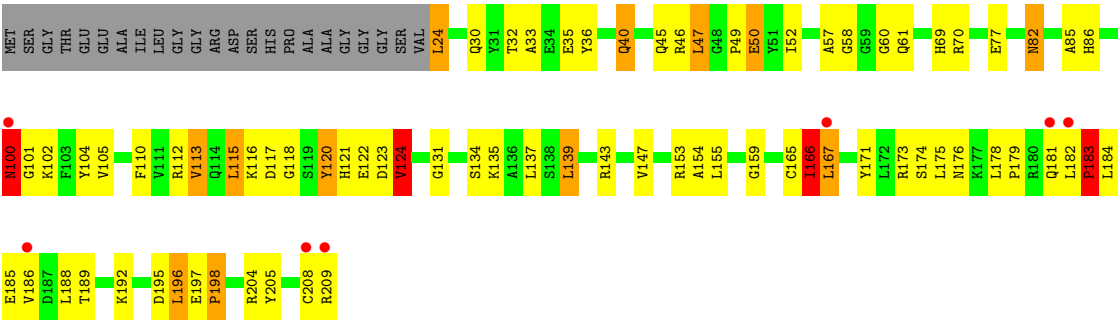


• Molecule 1: DNA REPAIR PROTEIN RAD52 HOMOLOG

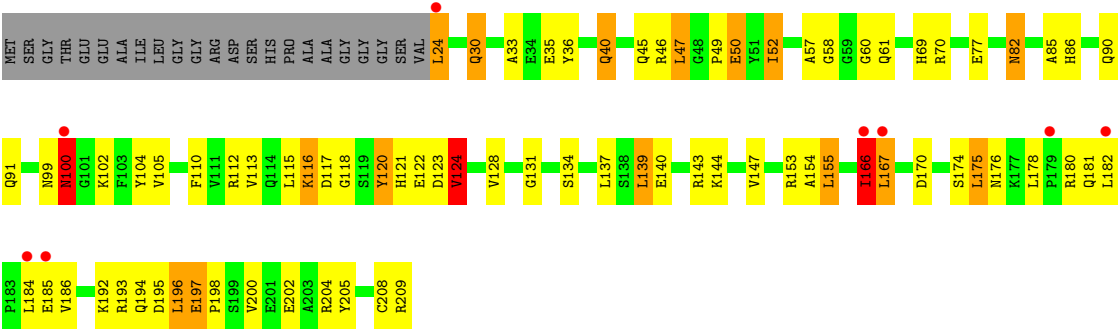


• Molecule 1: DNA REPAIR PROTEIN RAD52 HOMOLOG





● 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, α , β , γ	117.26Å 127.32Å 191.23Å 90.00° 90.29° 90.00°	Depositor
Resolution (Å)	30.00 – 2.70 30.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.9 (30.00-2.70) 96.9 (30.00-2.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	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%)	wwPDB-VP
Wilson B-factor (Å ²)	46.4	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 51.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.015 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	32802	wwPDB-VP
Average B, all atoms (Å ²)	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.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.88	0/1493	1.19	13/2006 (0.6%)
1	B	0.94	1/1493 (0.1%)	1.29	18/2006 (0.9%)
1	C	0.88	0/1493	1.23	15/2006 (0.7%)
1	D	0.80	0/1493	1.23	19/2006 (0.9%)
1	E	0.72	0/1493	1.14	14/2006 (0.7%)
1	F	0.65	0/1493	1.15	18/2006 (0.9%)
1	G	0.64	0/1493	1.13	16/2006 (0.8%)
1	H	0.63	0/1493	1.14	16/2006 (0.8%)
1	I	0.63	0/1493	1.16	16/2006 (0.8%)
1	J	0.69	0/1493	1.15	14/2006 (0.7%)
1	K	0.78	0/1493	1.16	17/2006 (0.8%)
1	L	0.89	0/1493	1.24	17/2006 (0.8%)
1	M	0.87	0/1493	1.23	16/2006 (0.8%)
1	N	0.90	0/1493	1.24	15/2006 (0.7%)
1	O	0.83	0/1493	1.20	14/2006 (0.7%)
1	P	0.78	0/1493	1.22	18/2006 (0.9%)
1	Q	0.79	0/1493	1.17	15/2006 (0.7%)
1	R	0.83	0/1493	1.20	14/2006 (0.7%)
1	S	0.85	0/1493	1.20	13/2006 (0.6%)
1	T	0.80	0/1493	1.20	18/2006 (0.9%)
1	U	0.80	0/1493	1.15	13/2006 (0.6%)
1	V	0.82	0/1493	1.18	15/2006 (0.7%)
All	All	0.80	1/32846 (0.0%)	1.19	344/44132 (0.8%)

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 (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	117	ASP	CB-CG	-5.29	1.38	1.52

All (344) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	197	GLU	CA-C-N	11.98	134.81	119.84
1	D	197	GLU	C-N-CA	11.98	134.81	119.84
1	B	180	ARG	N-CA-C	-9.68	97.66	110.24
1	I	208	CYS	N-CA-C	-9.56	101.55	113.02
1	C	124	VAL	CB-CA-C	-8.61	98.31	111.31
1	P	124	VAL	CB-CA-C	-8.58	98.36	111.31
1	T	197	GLU	CA-C-N	8.53	130.51	119.84
1	T	197	GLU	C-N-CA	8.53	130.51	119.84
1	P	118	GLY	N-CA-C	-8.25	103.09	114.64
1	D	124	VAL	CB-CA-C	-8.20	98.93	111.31
1	N	124	VAL	CB-CA-C	-8.17	98.97	111.31
1	B	124	VAL	CB-CA-C	-8.07	99.13	111.31
1	L	124	VAL	CB-CA-C	-7.95	99.30	111.31
1	U	124	VAL	CB-CA-C	-7.95	99.31	111.31
1	M	124	VAL	CB-CA-C	-7.93	99.34	111.31
1	A	124	VAL	CB-CA-C	-7.92	99.35	111.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	124	VAL	CB-CA-C	-7.92	99.35	111.31
1	F	197	GLU	CA-C-N	7.88	127.44	119.24
1	F	197	GLU	C-N-CA	7.88	127.44	119.24
1	E	197	GLU	CA-C-N	7.87	127.42	119.24
1	E	197	GLU	C-N-CA	7.87	127.42	119.24
1	E	124	VAL	CB-CA-C	-7.86	99.44	111.31
1	V	124	VAL	CB-CA-C	-7.78	99.56	111.31
1	G	200	VAL	N-CA-C	-7.74	103.26	110.53
1	O	124	VAL	CB-CA-C	-7.74	99.63	111.31
1	F	124	VAL	CB-CA-C	-7.73	99.64	111.31
1	S	116	LYS	CA-C-N	7.71	131.24	120.29
1	S	116	LYS	C-N-CA	7.71	131.24	120.29
1	P	52	ILE	N-CA-C	7.61	118.94	108.89
1	K	124	VAL	CB-CA-C	-7.53	99.94	111.31
1	H	124	VAL	CB-CA-C	-7.44	100.08	111.31
1	P	180	ARG	N-CA-C	-7.39	99.82	110.24
1	P	116	LYS	CA-C-N	7.32	130.09	120.28
1	P	116	LYS	C-N-CA	7.32	130.09	120.28
1	O	131	GLY	N-CA-C	7.25	123.32	114.69
1	T	124	VAL	CB-CA-C	-7.23	100.39	111.31
1	J	189	THR	N-CA-C	-7.21	103.11	110.97
1	U	100	ASN	N-CA-C	-7.20	95.46	110.80
1	A	118	GLY	N-CA-C	-7.20	104.57	114.64
1	O	30	GLN	N-CA-C	-7.18	97.24	109.24
1	S	30	GLN	N-CA-C	-7.02	97.12	109.06
1	S	124	VAL	CB-CA-C	-7.00	100.74	111.31
1	B	30	GLN	N-CA-C	-6.99	97.57	109.24
1	D	52	ILE	N-CA-C	6.99	118.11	108.89
1	G	118	GLY	N-CA-C	-6.98	104.87	114.64
1	V	197	GLU	CA-C-N	6.97	128.56	119.84
1	V	197	GLU	C-N-CA	6.97	128.56	119.84
1	G	124	VAL	CB-CA-C	-6.97	100.78	111.31
1	Q	124	VAL	CB-CA-C	-6.96	100.80	111.31
1	H	46	ARG	N-CA-C	-6.94	100.25	110.52
1	E	118	GLY	N-CA-C	-6.93	105.64	114.37
1	L	116	LYS	CA-C-N	6.89	130.07	120.29
1	L	116	LYS	C-N-CA	6.89	130.07	120.29
1	T	131	GLY	N-CA-C	6.88	122.88	114.69
1	V	100	ASN	N-CA-C	-6.87	96.16	110.80
1	S	52	ILE	N-CA-C	6.86	117.95	108.89
1	F	118	GLY	N-CA-C	-6.81	105.11	114.64
1	L	131	GLY	N-CA-C	6.80	122.78	114.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	118	GLY	N-CA-C	-6.80	105.12	114.64
1	N	166	ILE	N-CA-C	6.80	123.48	109.34
1	I	207	SER	N-CA-C	-6.80	106.19	114.75
1	H	118	GLY	N-CA-C	-6.78	105.83	114.37
1	V	30	GLN	N-CA-C	-6.77	97.93	109.24
1	D	118	GLY	N-CA-C	-6.76	105.18	114.64
1	I	118	GLY	N-CA-C	-6.73	105.89	114.37
1	C	100	ASN	N-CA-C	-6.72	96.48	110.80
1	M	52	ILE	N-CA-C	6.72	117.76	108.89
1	V	118	GLY	N-CA-C	-6.71	105.25	114.64
1	T	181	GLN	N-CA-C	-6.70	97.35	108.34
1	C	116	LYS	CA-C-N	6.70	129.80	120.29
1	C	116	LYS	C-N-CA	6.70	129.80	120.29
1	S	131	GLY	N-CA-C	6.69	122.66	114.69
1	L	100	ASN	N-CA-C	-6.66	96.61	110.80
1	O	100	ASN	N-CA-C	-6.66	96.61	110.80
1	R	116	LYS	CA-C-N	6.66	129.74	120.29
1	R	116	LYS	C-N-CA	6.66	129.74	120.29
1	O	118	GLY	N-CA-C	-6.63	105.36	114.64
1	I	203	ALA	N-CA-C	-6.62	104.09	111.71
1	C	180	ARG	N-CA-C	-6.62	101.75	110.43
1	L	197	GLU	CA-C-N	6.61	128.10	119.84
1	L	197	GLU	C-N-CA	6.61	128.10	119.84
1	M	116	LYS	CA-C-N	6.61	129.67	120.29
1	M	116	LYS	C-N-CA	6.61	129.67	120.29
1	B	100	ASN	N-CA-C	-6.59	96.75	110.80
1	T	52	ILE	N-CA-C	6.59	117.59	108.89
1	A	100	ASN	N-CA-C	-6.59	96.77	110.80
1	L	30	GLN	N-CA-C	-6.58	98.25	109.24
1	Q	100	ASN	N-CA-C	-6.57	96.81	110.80
1	M	118	GLY	N-CA-C	-6.57	106.10	114.37
1	N	131	GLY	N-CA-C	6.55	122.49	114.69
1	P	197	GLU	CA-C-N	6.55	126.05	119.24
1	P	197	GLU	C-N-CA	6.55	126.05	119.24
1	A	116	LYS	CA-C-N	6.54	129.57	120.29
1	A	116	LYS	C-N-CA	6.54	129.57	120.29
1	L	52	ILE	N-CA-C	6.53	117.52	108.89
1	V	116	LYS	CA-C-N	6.53	129.03	120.28
1	V	116	LYS	C-N-CA	6.53	129.03	120.28
1	S	180	ARG	N-CA-C	-6.50	101.51	110.35
1	E	100	ASN	N-CA-C	-6.49	96.97	110.80
1	G	180	ARG	N-CA-C	-6.49	101.96	110.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	100	ASN	N-CA-C	-6.48	96.99	110.80
1	R	131	GLY	N-CA-C	6.48	122.53	114.37
1	N	118	GLY	N-CA-C	-6.45	106.24	114.37
1	J	124	VAL	CB-CA-C	-6.43	101.59	111.31
1	B	131	GLY	N-CA-C	6.42	122.33	114.69
1	Q	118	GLY	N-CA-C	-6.41	105.67	114.64
1	R	52	ILE	N-CA-C	6.39	117.33	108.89
1	M	125	GLY	N-CA-C	-6.38	101.36	111.18
1	J	100	ASN	N-CA-C	-6.37	97.24	110.80
1	R	197	GLU	CA-C-N	6.35	126.56	119.32
1	R	197	GLU	C-N-CA	6.35	126.56	119.32
1	O	116	LYS	CA-C-N	6.35	129.31	120.29
1	O	116	LYS	C-N-CA	6.35	129.31	120.29
1	F	178	LEU	CA-C-N	6.33	127.75	119.84
1	F	178	LEU	C-N-CA	6.33	127.75	119.84
1	B	105	VAL	N-CA-C	6.31	117.21	108.12
1	Q	208	CYS	N-CA-C	-6.31	104.66	113.37
1	I	46	ARG	N-CA-C	-6.30	101.20	110.52
1	G	195	ASP	N-CA-C	-6.28	103.73	111.40
1	J	131	GLY	N-CA-C	6.28	122.16	114.69
1	L	125	GLY	N-CA-C	-6.28	101.52	111.18
1	D	100	ASN	N-CA-C	-6.27	97.45	110.80
1	J	46	ARG	N-CA-C	-6.25	101.28	110.52
1	I	124	VAL	CB-CA-C	-6.25	101.88	111.31
1	K	118	GLY	N-CA-C	-6.24	105.90	114.64
1	B	195	ASP	N-CA-C	6.24	117.87	111.14
1	E	105	VAL	N-CA-C	6.23	117.09	108.12
1	A	105	VAL	N-CA-C	6.22	117.08	108.12
1	F	100	ASN	N-CA-C	-6.22	97.56	110.80
1	L	105	VAL	N-CA-C	6.21	117.06	108.12
1	Q	30	GLN	N-CA-C	-6.19	98.30	108.76
1	D	166	ILE	N-CA-C	6.18	122.20	109.34
1	T	100	ASN	N-CA-C	-6.18	97.63	110.80
1	U	198	PRO	N-CA-C	6.18	122.11	113.53
1	E	52	ILE	N-CA-C	6.17	117.04	108.89
1	V	52	ILE	N-CA-C	6.17	117.04	108.89
1	H	197	GLU	CA-C-N	6.17	127.55	119.84
1	H	197	GLU	C-N-CA	6.17	127.55	119.84
1	F	30	GLN	N-CA-C	-6.15	98.97	109.24
1	P	100	ASN	N-CA-C	-6.15	97.70	110.80
1	S	100	ASN	N-CA-C	-6.14	97.72	110.80
1	F	52	ILE	N-CA-C	6.13	116.98	108.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	116	LYS	CA-C-N	6.12	128.49	120.28
1	B	116	LYS	C-N-CA	6.12	128.49	120.28
1	A	46	ARG	N-CA-C	-6.12	101.46	110.52
1	K	100	ASN	N-CA-C	-6.12	97.78	110.80
1	S	118	GLY	N-CA-C	-6.10	106.68	114.37
1	L	118	GLY	N-CA-C	-6.08	106.71	114.37
1	G	131	GLY	N-CA-C	6.08	121.92	114.69
1	A	52	ILE	N-CA-C	6.06	116.89	108.89
1	N	100	ASN	N-CA-C	-6.05	97.92	110.80
1	F	105	VAL	N-CA-C	6.04	116.83	108.12
1	K	125	GLY	N-CA-C	-6.04	101.87	111.18
1	L	196	LEU	N-CA-C	6.04	119.13	110.24
1	M	131	GLY	N-CA-C	6.04	121.88	114.69
1	B	166	ILE	N-CA-C	6.04	121.90	109.34
1	P	46	ARG	N-CA-C	-6.04	101.59	110.52
1	V	131	GLY	N-CA-C	6.03	121.86	114.69
1	H	125	GLY	N-CA-C	-6.02	101.57	111.38
1	Q	105	VAL	N-CA-C	6.01	116.78	108.12
1	H	116	LYS	CA-C-N	6.01	128.82	120.29
1	H	116	LYS	C-N-CA	6.01	128.82	120.29
1	D	116	LYS	CA-C-N	6.00	128.81	120.29
1	D	116	LYS	C-N-CA	6.00	128.81	120.29
1	I	166	ILE	N-CA-C	6.00	121.81	109.34
1	G	46	ARG	N-CA-C	-5.99	101.65	110.52
1	P	131	GLY	N-CA-C	5.99	121.81	114.69
1	A	125	GLY	N-CA-C	-5.96	102.01	111.18
1	F	131	GLY	N-CA-C	5.96	121.78	114.69
1	F	46	ARG	N-CA-C	-5.95	101.71	110.52
1	R	46	ARG	N-CA-C	-5.94	101.73	110.52
1	M	30	GLN	N-CA-C	-5.92	98.76	108.76
1	U	120	TYR	N-CA-C	5.92	117.84	108.79
1	T	30	GLN	N-CA-C	-5.91	98.77	108.76
1	K	46	ARG	N-CA-C	-5.90	101.78	110.52
1	M	178	LEU	CA-C-N	5.90	127.22	119.84
1	M	178	LEU	C-N-CA	5.90	127.22	119.84
1	A	135	LYS	N-CA-C	-5.90	104.77	111.14
1	C	52	ILE	N-CA-C	5.90	117.07	108.58
1	I	135	LYS	N-CA-C	-5.89	104.77	111.14
1	C	178	LEU	CA-C-N	5.89	125.83	119.76
1	C	178	LEU	C-N-CA	5.89	125.83	119.76
1	K	52	ILE	N-CA-C	5.89	116.66	108.89
1	I	100	ASN	N-CA-C	-5.88	98.27	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	118	GLY	N-CA-C	-5.88	106.40	114.64
1	T	166	ILE	N-CA-C	5.88	121.57	109.34
1	E	131	GLY	N-CA-C	5.86	121.67	114.69
1	M	100	ASN	N-CA-C	-5.84	98.36	110.80
1	B	197	GLU	CA-C-N	5.83	127.13	119.84
1	B	197	GLU	C-N-CA	5.83	127.13	119.84
1	I	30	GLN	N-CA-C	-5.83	99.50	109.24
1	J	52	ILE	N-CA-C	5.81	116.56	108.89
1	O	159	GLY	N-CA-C	5.80	118.44	110.56
1	V	166	ILE	N-CA-C	5.78	121.36	109.34
1	M	166	ILE	N-CA-C	5.77	121.34	109.34
1	R	166	ILE	N-CA-C	5.76	121.33	109.34
1	G	197	GLU	CA-C-N	5.76	127.04	119.84
1	G	197	GLU	C-N-CA	5.76	127.04	119.84
1	A	131	GLY	N-CA-C	5.75	121.53	114.69
1	K	116	LYS	CA-C-N	5.75	128.46	120.29
1	K	116	LYS	C-N-CA	5.75	128.46	120.29
1	N	52	ILE	N-CA-C	5.75	116.47	108.89
1	K	166	ILE	N-CA-C	5.74	121.29	109.34
1	U	105	VAL	N-CA-C	5.73	116.37	108.12
1	H	105	VAL	N-CA-C	5.72	116.36	108.12
1	J	30	GLN	N-CA-C	-5.72	99.08	108.76
1	N	105	VAL	N-CA-C	5.72	116.36	108.12
1	O	125	GLY	N-CA-C	-5.72	102.38	111.18
1	K	105	VAL	N-CA-C	5.71	116.35	108.12
1	U	46	ARG	N-CA-C	-5.71	102.07	110.52
1	C	118	GLY	N-CA-C	-5.69	106.67	114.64
1	O	52	ILE	N-CA-C	5.69	116.77	108.58
1	A	166	ILE	N-CA-C	5.67	121.13	109.34
1	H	166	ILE	N-CA-C	5.67	121.13	109.34
1	I	105	VAL	N-CA-C	5.67	116.28	108.12
1	I	131	GLY	N-CA-C	5.66	121.50	114.37
1	O	166	ILE	N-CA-C	5.65	121.09	109.34
1	D	120	TYR	N-CA-C	5.65	117.43	108.79
1	E	166	ILE	N-CA-C	5.65	121.08	109.34
1	J	116	LYS	CA-C-N	5.64	128.31	120.29
1	J	116	LYS	C-N-CA	5.64	128.31	120.29
1	M	32	THR	N-CA-C	-5.64	102.93	110.55
1	G	52	ILE	N-CA-C	5.64	116.33	108.89
1	I	52	ILE	N-CA-C	5.64	116.88	109.21
1	D	184	LEU	N-CA-C	5.63	118.00	110.35
1	G	100	ASN	N-CA-C	-5.62	98.82	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	P	105	VAL	N-CA-C	5.62	116.22	108.12
1	D	182	LEU	CA-C-N	5.62	126.86	119.84
1	D	182	LEU	C-N-CA	5.62	126.86	119.84
1	V	46	ARG	N-CA-C	-5.61	102.22	110.52
1	R	105	VAL	N-CA-C	5.60	116.19	108.12
1	U	166	ILE	N-CA-C	5.60	120.98	109.34
1	Q	116	LYS	CA-C-N	5.59	128.23	120.29
1	Q	116	LYS	C-N-CA	5.59	128.23	120.29
1	G	166	ILE	N-CA-C	5.59	120.97	109.34
1	T	116	LYS	CA-C-N	5.58	128.80	120.31
1	T	116	LYS	C-N-CA	5.58	128.80	120.31
1	A	30	GLN	N-CA-C	-5.58	98.81	108.69
1	U	116	LYS	CA-C-N	5.58	128.21	120.29
1	U	116	LYS	C-N-CA	5.58	128.21	120.29
1	N	116	LYS	CA-C-N	5.57	128.19	120.29
1	N	116	LYS	C-N-CA	5.57	128.19	120.29
1	J	166	ILE	N-CA-C	5.56	120.91	109.34
1	P	30	GLN	N-CA-C	-5.56	99.36	108.76
1	E	46	ARG	N-CA-C	-5.56	102.30	110.52
1	J	120	TYR	N-CA-C	5.56	117.52	109.07
1	R	30	GLN	N-CA-C	-5.56	99.37	108.76
1	Q	52	ILE	N-CA-C	5.55	116.77	109.21
1	C	105	VAL	N-CA-C	5.55	116.11	108.12
1	H	100	ASN	N-CA-C	-5.54	99.00	110.80
1	H	131	GLY	N-CA-C	5.54	121.28	114.69
1	P	166	ILE	N-CA-C	5.54	120.85	109.34
1	K	30	GLN	N-CA-C	-5.53	99.41	108.76
1	Q	166	ILE	N-CA-C	5.53	120.84	109.34
1	U	131	GLY	N-CA-C	5.51	121.32	114.37
1	O	196	LEU	N-CA-C	5.51	118.06	110.35
1	J	105	VAL	N-CA-C	5.50	116.04	108.12
1	L	202	GLU	CB-CA-C	-5.50	102.50	110.96
1	S	202	GLU	CB-CA-C	-5.49	102.44	110.95
1	J	182	LEU	N-CA-C	5.48	117.37	109.48
1	F	166	ILE	N-CA-C	5.48	120.73	109.34
1	I	125	GLY	N-CA-C	-5.48	102.45	111.38
1	B	125	GLY	N-CA-C	-5.46	101.63	111.19
1	C	46	ARG	N-CA-C	-5.46	102.43	110.52
1	L	166	ILE	N-CA-C	5.45	120.68	109.34
1	O	105	VAL	N-CA-C	5.45	115.96	108.12
1	P	184	LEU	N-CA-C	5.44	117.56	110.43
1	C	166	ILE	N-CA-C	5.44	120.66	109.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	125	GLY	N-CA-C	-5.44	101.67	111.19
1	Q	128	VAL	N-CA-C	5.44	116.31	108.48
1	V	105	VAL	N-CA-C	5.44	115.95	108.12
1	D	30	GLN	N-CA-C	-5.43	99.07	108.69
1	N	197	GLU	CA-C-N	5.43	126.63	119.84
1	N	197	GLU	C-N-CA	5.43	126.63	119.84
1	K	131	GLY	N-CA-C	5.42	121.21	114.37
1	U	118	GLY	N-CA-C	-5.42	107.05	114.64
1	L	46	ARG	N-CA-C	-5.42	102.50	110.52
1	S	105	VAL	N-CA-C	5.42	115.92	108.12
1	D	125	GLY	N-CA-C	-5.41	102.84	111.18
1	T	105	VAL	N-CA-C	5.40	115.89	108.12
1	N	169	LYS	N-CA-C	5.39	118.66	111.75
1	B	46	ARG	N-CA-C	-5.39	102.54	110.52
1	C	30	GLN	N-CA-C	-5.38	99.66	108.76
1	F	178	LEU	N-CA-C	-5.38	101.87	110.10
1	I	159	GLY	N-CA-C	5.38	117.88	110.56
1	N	46	ARG	N-CA-C	-5.38	102.56	110.52
1	Q	46	ARG	N-CA-C	-5.37	102.57	110.52
1	C	131	GLY	N-CA-C	5.37	121.14	114.37
1	S	120	TYR	N-CA-C	5.37	117.00	108.79
1	D	131	GLY	N-CA-C	5.35	121.11	114.37
1	G	125	GLY	N-CA-C	-5.33	102.69	111.38
1	M	105	VAL	N-CA-C	5.33	115.79	108.12
1	G	116	LYS	CA-C-N	5.32	127.85	120.29
1	G	116	LYS	C-N-CA	5.32	127.85	120.29
1	V	128	VAL	N-CA-C	5.32	116.39	108.46
1	H	30	GLN	N-CA-C	-5.32	99.78	108.76
1	N	30	GLN	N-CA-C	-5.27	99.85	108.76
1	D	159	GLY	N-CA-C	5.26	117.72	110.56
1	P	120	TYR	N-CA-C	5.26	116.28	108.60
1	G	30	GLN	N-CA-C	-5.26	99.87	108.76
1	H	195	ASP	N-CA-C	-5.26	102.89	111.04
1	D	181	GLN	N-CA-C	5.25	117.80	109.24
1	T	207	SER	N-CA-C	-5.25	107.00	113.41
1	F	32	THR	N-CA-C	-5.25	103.46	110.55
1	H	52	ILE	N-CA-C	5.25	116.35	109.21
1	S	166	ILE	N-CA-C	5.25	120.25	109.34
1	T	46	ARG	N-CA-C	-5.24	102.76	110.52
1	K	197	GLU	CA-C-N	5.24	126.39	119.84
1	K	197	GLU	C-N-CA	5.24	126.39	119.84
1	B	52	ILE	N-CA-C	5.22	116.81	108.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	135	LYS	N-CA-C	-5.21	105.52	111.14
1	E	135	LYS	N-CA-C	-5.20	105.52	111.14
1	F	116	LYS	CA-C-N	5.20	127.67	120.29
1	F	116	LYS	C-N-CA	5.20	127.67	120.29
1	K	159	GLY	N-CA-C	5.20	117.63	110.56
1	T	128	VAL	N-CA-C	5.20	116.21	108.46
1	Q	135	LYS	N-CA-C	-5.19	105.53	111.14
1	L	120	TYR	N-CA-C	5.19	116.72	108.79
1	N	182	LEU	N-CA-C	5.17	117.29	110.36
1	T	118	GLY	N-CA-C	-5.15	108.22	114.92
1	P	128	VAL	N-CA-C	5.15	116.13	108.46
1	B	74	LEU	N-CA-C	-5.14	105.57	111.07
1	E	30	GLN	N-CA-C	-5.12	100.11	108.76
1	Q	159	GLY	N-CA-C	5.12	117.52	110.56
1	D	46	ARG	N-CA-C	-5.11	102.95	110.52
1	R	135	LYS	N-CA-C	-5.10	105.63	111.14
1	I	32	THR	N-CA-C	-5.10	102.94	110.48
1	B	120	TYR	N-CA-C	5.09	116.58	108.79
1	C	159	GLY	N-CA-C	5.09	117.48	110.56
1	U	135	LYS	N-CA-C	-5.08	105.66	111.14
1	P	159	GLY	N-CA-C	5.07	117.46	110.56
1	E	116	LYS	CA-C-N	5.07	127.49	120.29
1	E	116	LYS	C-N-CA	5.07	127.49	120.29
1	T	48	GLY	CA-C-N	5.06	124.85	119.28
1	T	48	GLY	C-N-CA	5.06	124.85	119.28
1	O	128	VAL	N-CA-C	5.06	116.00	108.46
1	M	48	GLY	CA-C-N	5.06	124.84	119.28
1	M	48	GLY	C-N-CA	5.06	124.84	119.28
1	R	118	GLY	N-CA-C	-5.04	107.58	114.64
1	V	120	TYR	N-CA-C	5.04	115.96	108.60
1	Q	184	LEU	N-CA-C	5.02	116.80	110.33
1	U	159	GLY	N-CA-C	5.01	117.37	110.56
1	K	48	GLY	CA-C-N	5.00	124.66	119.56
1	K	48	GLY	C-N-CA	5.00	124.66	119.56

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

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Mol	Chain	Res	Type	Group
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
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	89	0
1	B	1469	0	1457	96	0
1	C	1469	0	1457	84	0
1	D	1469	0	1457	85	0
1	E	1469	0	1457	91	0
1	F	1469	0	1457	77	0
1	G	1469	0	1457	107	0
1	H	1469	0	1457	94	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	1469	0	1457	86	0
1	J	1469	0	1457	88	0
1	K	1469	0	1457	102	0
1	L	1469	0	1457	107	0
1	M	1469	0	1457	76	0
1	N	1469	0	1457	88	0
1	O	1469	0	1457	87	0
1	P	1469	0	1457	89	0
1	Q	1469	0	1457	95	0
1	R	1469	0	1457	87	0
1	S	1469	0	1457	95	0
1	T	1469	0	1457	89	0
1	U	1469	0	1457	88	0
1	V	1469	0	1457	96	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	1616	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 25.

All (1616) 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:H	1:C:182:LEU:HD23	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:I:50:GLU:HA	1:I:181:GLN:HE22	1.25	1.01
1:Q:182:LEU:H	1:Q:182:LEU:HD23	1.20	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:HD23	1:M:182:LEU:H	1.25	0.99
1:Q:182:LEU:H	1:Q:182:LEU:CD2	1.77	0.97
1:F:204:ARG:HH21	1:F:204:ARG:HG3	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:HH11	1:B:193:ARG:CG	1.79	0.92
1:G:182:LEU:H	1:G:182:LEU:HD23	1.34	0.92
1:N:182:LEU:H	1:N:182:LEU:CD2	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:HD13	1:D:167:LEU:H	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:HD23	1:P:182:LEU:H	1.35	0.89
1:V:40:GLN:HA	1:V:40:GLN:HE21	1.37	0.89
1:I:40:GLN:HE21	1:I:40:GLN:HA	1.39	0.88
1:J:50:GLU:HA	1:J:181:GLN:NE2	1.88	0.88
1:J:167:LEU:HD13	1:J:167:LEU:H	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:HE21	1:J:40:GLN:HA	1.38	0.88
1:A:40:GLN:HE21	1:A:40:GLN:HA	1.38	0.87
1:O:167:LEU:HD13	1:O:167:LEU:H	1.38	0.87
1:D:182:LEU:HD23	1:D:182:LEU:H	1.39	0.87
1:R:184:LEU:HD22	1:R:185:GLU:H	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:HD13	1:T:167:LEU:H	1.40	0.86
1:K:40:GLN:HE21	1:K:40:GLN:HA	1.40	0.86
1:B:40:GLN:HE21	1:B:40:GLN:HA	1.40	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:192:LYS:HB2	1:M:45:GLN:HE21	1.41	0.86
1:N:40:GLN:HA	1:N:40:GLN:HE21	1.40	0.86
1:T:40:GLN:HE21	1:T:40:GLN:HA	1.40	0.86
1:V:100:ASN:ND2	1:V:102:LYS:HB2	1.90	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
1:F:167:LEU:HD13	1:F:167:LEU:H	1.39	0.86
1:B:167:LEU:H	1:B:167:LEU:HD13	1.38	0.86
1:V:180:ARG:HG2	1:V:181:GLN:H	1.41	0.86
1:Q:192:LYS:HE2	1:Q:197:GLU:OE2	1.76	0.85
1:R:167:LEU:HD13	1:R:167:LEU:H	1.39	0.85
1:O:40:GLN:HA	1:O:40:GLN:HE21	1.42	0.85
1:H:167:LEU:HD13	1:H:167:LEU:H	1.41	0.85
1:L:167:LEU:HD13	1:L:167:LEU:H	1.39	0.85
1:O:100:ASN:ND2	1:O:102:LYS:HB2	1.92	0.85
1:B:193:ARG:HG2	1:B:193:ARG:NH1	1.79	0.84
1:C:40:GLN:HE21	1:C:40:GLN:HA	1.42	0.84
1:Q:184:LEU:CD2	1:Q:185:GLU:H	1.89	0.84
1:L:40:GLN:HE21	1:L:40:GLN:HA	1.40	0.84
1:L:192:LYS:HE2	1:L:197:GLU:OE2	1.77	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:M:167:LEU:HD13	1:M:167:LEU:H	1.42	0.84
1:P:182:LEU:H	1:P:182:LEU:CD2	1.91	0.84
1:G:184:LEU:HD23	1:G:185:GLU:N	1.92	0.84
1:U:167:LEU:HD13	1:U:167:LEU:H	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:HE21	1:R:40:GLN:HA	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:HD13	1:V:167:LEU:H	1.42	0.82
1:R:147:VAL:HG21	1:S:124:VAL:HG22	1.61	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:G:167:LEU:H	1:G:167:LEU:HD13	1.45	0.81
1:P:100:ASN:ND2	1:P:102:LYS:HB2	1.95	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:I:167:LEU:HD13	1:I:167:LEU:H	1.46	0.80
1:S:100:ASN:ND2	1:S:102:LYS:HB2	1.95	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
1:R:208:CYS:HB2	1:T:33:ALA:HB2	1.64	0.80
1:B:182:LEU:HD23	1:B:182:LEU:H	1.47	0.80
1:S:167:LEU:HD13	1:S:167:LEU:H	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:C:100:ASN:ND2	1:C:102:LYS:HB2	1.96	0.78
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: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:A:33:ALA:HB2	1:J:208:CYS:HB2	1.64	0.78
1:T:166:ILE:HG22	1:T:167:LEU:HD12	1.66	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:H:147:VAL:HG21	1:I:124:VAL:HG22	1.66	0.77
1:N:69:HIS:HB3	1:O:167:LEU:HD21	1.66	0.77
1:N:100:ASN:ND2	1:N:102:LYS:HB2	1.99	0.77
1:U:204:ARG:HG3	1:V:35:GLU:OE1	1.83	0.77
1:R:192:LYS:HE2	1:R:197:GLU:OE2	1.83	0.77
1:D:147:VAL:HG21	1:E:124:VAL:HG22	1.66	0.77
1:I:182:LEU:HD23	1:I:182:LEU:H	1.49	0.77
1:V:110:PHE:CE2	1:V:124:VAL:HG13	2.19	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:E:86:HIS:ND1	1:F:121:HIS:HD2	1.84	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:100:ASN:ND2	1:H:102:LYS:HB2	1.99	0.76
1:B:110:PHE:CE2	1:B:124:VAL:HG13	2.19	0.76
1:L:192:LYS:HB2	1:M:45:GLN:NE2	1.99	0.76
1:J:40:GLN:HE21	1:J:40:GLN:CA	1.99	0.76
1:M:208:CYS:HB3	1:O:33:ALA:HB2	1.66	0.76
1:Q:193:ARG:HG2	1:Q:193:ARG:HH11	1.50	0.76
1:U:147:VAL:HG21	1:V:124:VAL:HG22	1.68	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:G:100:ASN:ND2	1:G:102:LYS:HB2	2.01	0.75
1:K:193:ARG:HB3	1:L:180:ARG:NE	2.01	0.75
1:I:195:ASP:HB3	1:J:77:GLU:HG3	1.68	0.75
1:M:182:LEU:HD23	1:M:182:LEU:N	2.02	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:J:147:VAL:HG21	1:K:124:VAL:HG22	1.69	0.74
1:Q:205:TYR:CE1	1:S:37:GLN:HB2	2.22	0.74
1:F:166:ILE:HG22	1:F:167:LEU:HD12	1.69	0.74
1:G:204:ARG:HH21	1:G:204:ARG:HG3	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:K:192:LYS:HE2	1:K:197:GLU:OE2	1.87	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: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:HD23	1:U:182:LEU:H	1.51	0.74
1:H:110:PHE:CE2	1:H:124:VAL:HG13	2.23	0.74
1:I:166:ILE:HG22	1:I:167:LEU:HD12	1.70	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:HD23	1:C:47:LEU:N	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:186:VAL:HG21	1:I:171:TYR:HA	1.71	0.72
1:M:70:ARG:HG3	1:M:70:ARG:HH11	1.54	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:D:82:ASN:HD22	1:D:82:ASN:H	1.36	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:K:193:ARG:HE	1:L:180:ARG:NH2	1.87	0.72
1:Q:40:GLN:HE21	1:Q:40:GLN:CA	2.02	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:A:82:ASN:HD22	1:A:82:ASN:H	1.36	0.72
1:K:40:GLN:HE21	1:K:40:GLN:CA	2.01	0.72
1:M:110:PHE:CE2	1:M:124:VAL:HG13	2.25	0.72
1:I:147:VAL:HG21	1:J:124:VAL:HG22	1.71	0.71
1:J:181:GLN:HG3	1:J:181:GLN:O	1.90	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:N:185:GLU:OE1	1:O:177:LYS:NZ	2.23	0.71
1:R:47:LEU:N	1:R:47:LEU:HD23	2.05	0.71
1:D:167:LEU:H	1:D:167:LEU:CD1	2.01	0.71
1:G:180:ARG:HG2	1:G:181:GLN:H	1.54	0.71
1:T:147:VAL:HG21	1:U:124:VAL:HG22	1.71	0.71
1:J:110:PHE:CE2	1:J:124:VAL:HG13	2.26	0.71
1:R:110:PHE:CE2	1:R:124:VAL:HG13	2.25	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:C:184:LEU:HD12	1:C:185:GLU:O	1.89	0.71
1:E:147:VAL:HG21	1:F:124:VAL:HG22	1.70	0.71
1:E:166:ILE:HG22	1:E:167:LEU:HD12	1.72	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:M:184:LEU:HD23	1:M:185:GLU:H	1.55	0.71
1:O:147:VAL:HG21	1:P:124:VAL:HG22	1.73	0.71
1:A:47:LEU:HD23	1:A:47:LEU:H	1.56	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:N:110:PHE:CE2	1:N:124:VAL:HG13	2.26	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:40:GLN:HE21	1:U:40:GLN:CA	2.03	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
1:L:182:LEU:H	1:L:182:LEU:HD23	1.55	0.70
1:Q:182:LEU:HD23	1:Q:182:LEU:N	2.02	0.70
1:G:166:ILE:HG22	1:G:167:LEU:HD12	1.73	0.70
1:R:40:GLN:HE21	1:R:40:GLN:CA	2.05	0.70
1:F:47:LEU:HD23	1:F:47:LEU:H	1.56	0.70
1:J:50:GLU:HA	1:J:181:GLN:HE22	1.57	0.70
1:S:47:LEU:HD23	1:S:47:LEU:N	2.07	0.70
1:T:204:ARG:HG3	1:U:35:GLU:OE1	1.92	0.70
1:O:47:LEU:HD23	1:O:47:LEU:N	2.07	0.69
1:P:86:HIS:ND1	1:Q:121:HIS:HD2	1.89	0.69
1:R:47:LEU:HD23	1:R:47:LEU:H	1.56	0.69
1:B:167:LEU:H	1:B:167:LEU:CD1	2.04	0.69
1:F:47:LEU:HD23	1:F:47:LEU:N	2.07	0.69
1:M:147:VAL:HG21	1:N:124:VAL:HG22	1.73	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:HD23	1:V:47:LEU:H	1.56	0.69
1:B:40:GLN:HE21	1:B:40:GLN:CA	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:Q:86:HIS:ND1	1:R:121:HIS:HD2	1.90	0.69
1:V:47:LEU:HD23	1:V:47:LEU:N	2.07	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:C:167:LEU:H	1:C:167:LEU:CD1	2.06	0.69
1:D:166:ILE:HG22	1:D:167:LEU:HD12	1.75	0.69
1:G:36:TYR:OH	1:G:40:GLN:HG3	1.91	0.69
1:K:182:LEU:HD23	1:K:182:LEU:H	1.57	0.69
1:O:192:LYS:HB2	1:P:45:GLN:NE2	2.08	0.69
1:T:208:CYS:HB3	1:V:33:ALA:HB2	1.75	0.69
1:U:86:HIS:ND1	1:V:121:HIS:HD2	1.91	0.69
1:U:196:LEU:CD1	1:U:198:PRO:HG3	2.23	0.69
1:V:166:ILE:HG22	1:V:167:LEU:HD12	1.75	0.69
1:F:196:LEU:HD13	1:F:196:LEU:C	2.18	0.69
1:G:86:HIS:ND1	1:H:121:HIS:HD2	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:134:SER:HB3	1:O:137:LEU:HB2	1.74	0.69
1:T:47:LEU:HD23	1:T:47:LEU:H	1.58	0.69
1:V:82:ASN:H	1:V:82:ASN:HD22	1.40	0.69
1:I:40:GLN:HE21	1:I:40:GLN:CA	2.04	0.69
1:P:47:LEU:N	1:P:47:LEU:HD23	2.08	0.68
1:E:82:ASN:H	1:E:82:ASN:HD22	1.41	0.68
1:T:186:VAL:HG21	1:U:171:TYR:HA	1.74	0.68
1:F:192:LYS:HB3	1:G:47:LEU:HA	1.76	0.68
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: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:A:121:HIS:HD2	1:K:86:HIS:ND1	1.91	0.67
1:B:147:VAL:HG21	1:C:124:VAL:HG22	1.76	0.67
1:G:186:VAL:HB	1:H:174:SER:HB3	1.76	0.67
1:N:179:PRO:O	1:N:180:ARG:O	2.11	0.67
1:G:180:ARG:HG2	1:G:181:GLN:N	2.08	0.67
1:H:166:ILE:HG22	1:H:167:LEU:HD12	1.75	0.67
1:L:166:ILE:HG22	1:L:167:LEU:HD12	1.75	0.67
1:L:184:LEU:HD23	1:L:185:GLU:N	2.09	0.67
1:Q:207:SER:C	1:Q:209:ARG:H	2.00	0.67
1:R:113:VAL:HG12	1:R:154:ALA:HB1	1.77	0.67
1:C:147:VAL:HG21	1:D:124:VAL:HG22	1.77	0.67
1:N:70:ARG:HG3	1:N:70:ARG:HH11	1.60	0.67
1:T:50:GLU:HA	1:T:181:GLN:NE2	2.10	0.67
1:T:86:HIS:ND1	1:U:121:HIS:HD2	1.92	0.67
1:U:166:ILE:HG22	1:U:167:LEU:HD12	1.76	0.67
1:G:134:SER:HB3	1:G:137:LEU:HB2	1.77	0.67
1:R:52:ILE:HG13	1:R:175:LEU:HD11	1.77	0.67
1:G:182:LEU:H	1:G:182:LEU:CD2	2.06	0.67
1:C:40:GLN:HE21	1:C:40:GLN:CA	2.06	0.67
1:C:184:LEU:HD13	1:C:185:GLU:H	1.59	0.67
1:K:47:LEU:N	1:K:47:LEU:HD23	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:N	1:U:47:LEU:HD23	2.10	0.66
1:E:207:SER:C	1:E:209:ARG:H	2.04	0.66
1:O:192:LYS:HE2	1:O:197:GLU:OE2	1.95	0.66
1:Q:134:SER:HB3	1:Q:137:LEU:HB2	1.76	0.66
1:T:181:GLN:HG3	1:T:181:GLN:O	1.96	0.66
1:A:147:VAL:HG21	1:B:124:VAL:HG22	1.78	0.66
1:K:167:LEU:H	1:K:167:LEU:CD1	2.07	0.66
1:M:49:PRO:HD2	1:M:50:GLU:OE1	1.96	0.66
1:O:167:LEU:H	1:O:167:LEU:CD1	2.07	0.66
1:D:208:CYS:HB2	1:F:33:ALA:HB2	1.77	0.66
1:G:47:LEU:H	1:G:47:LEU:HD23	1.61	0.66
1:O:40:GLN:HE21	1:O:40:GLN:CA	2.09	0.66
1:O:195:ASP:HB3	1:P:77:GLU:HG3	1.78	0.66
1:Q:110:PHE:CE2	1:Q:124:VAL:HG13	2.30	0.66
1:S:113:VAL:HG12	1:S:154:ALA:HB1	1.77	0.66
1:E:47:LEU:HD23	1:E:47:LEU:N	2.10	0.66
1:L:69:HIS:HB3	1:M:167:LEU:HD21	1.78	0.66
1:F:192:LYS:HG2	1:G:51:TYR:CE1	2.31	0.66
1:T:69:HIS:HB3	1:U:167:LEU:HD21	1.76	0.66
1:A:86:HIS:ND1	1:B:121:HIS:HD2	1.93	0.66
1:B:47:LEU:N	1:B:47:LEU:HD23	2.11	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:K:139:LEU:O	1:K:143:ARG:HG3	1.95	0.66
1:N:184:LEU:O	1:O:173:ARG:NH2	2.28	0.66
1:O:49:PRO:HD2	1:O:50:GLU:OE1	1.96	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:M:47:LEU:HD23	1:M:47:LEU:H	1.61	0.65
1:T:134:SER:HB3	1:T:137:LEU:HB2	1.78	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:40:GLN:HE21	1:N:40:GLN:CA	2.09	0.65
1:N:182:LEU:CD2	1:N:182:LEU:N	2.55	0.65
1:C:86:HIS:ND1	1:D:121:HIS:HD2	1.95	0.65
1:G:186:VAL:HG21	1:H:170:ASP:C	2.22	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:166:ILE:HG22	1:J:167:LEU:HD12	1.79	0.65
1:K:193:ARG:HB3	1:L:180:ARG:HE	1.61	0.65
1:P:52:ILE:HG13	1:P:175:LEU:HD11	1.77	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:L:184:LEU:HD23	1:L:185:GLU:H	1.62	0.65
1:M:69:HIS:HB3	1:N:167:LEU:HD21	1.79	0.65
1:S:204:ARG:HG3	1:T:35:GLU:OE1	1.97	0.65
1:C:82:ASN:HB2	1:D:117:ASP:OD1	1.96	0.65
1:D:49:PRO:HD2	1:D:50:GLU:OE1	1.96	0.65
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: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
1:L:167:LEU:H	1:L:167:LEU:CD1	2.10	0.64
1:U:167:LEU:H	1:U:167:LEU:CD1	2.09	0.64
1:D:182:LEU:H	1:D:182:LEU:CD2	2.10	0.64
1:J:134:SER:HB3	1:J:137:LEU:HB2	1.80	0.64
1:Q:166:ILE:HG22	1:Q:167:LEU:HD12	1.77	0.64
1:Q:184:LEU:HD22	1:Q:185:GLU:H	1.62	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:HD23	1:T:182:LEU:H	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:CD2	1:C:182:LEU:N	2.47	0.64
1:K:82:ASN:HD22	1:K:82:ASN:H	1.44	0.64
1:T:70:ARG:HG3	1:T:70:ARG:HH11	1.63	0.64
1:A:167:LEU:HD13	1:A:167:LEU:N	2.11	0.64
1:M:86:HIS:ND1	1:N:121:HIS:HD2	1.96	0.64
1:U:47:LEU:HD23	1:U:47:LEU:H	1.62	0.64
1:E:167:LEU:H	1:E:167:LEU:CD1	2.09	0.64
1:E:40:GLN:HE21	1:E:40:GLN:CA	2.11	0.64
1:H:204:ARG:HG3	1:I:35:GLU:OE1	1.98	0.64
1:Q:192:LYS:HB2	1:R:45:GLN:HE21	1.63	0.64
1:K:47:LEU:HD23	1:K:47:LEU:H	1.61	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:52:ILE:HG13	1:Q:175:LEU:HD11	1.80	0.63
1:B:70:ARG:HG3	1:B:70:ARG:HH11	1.64	0.63
1:C:36:TYR:OH	1:C:40:GLN:HG3	1.98	0.63
1:C:204:ARG:HH21	1:C:204:ARG:HG3	1.63	0.63
1:P:47:LEU:HD23	1:P:47:LEU:H	1.61	0.63
1:T:40:GLN:HE21	1:T:40:GLN:CA	2.11	0.63
1:J:47:LEU:HD23	1:J:47:LEU:H	1.63	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
1:O:47:LEU:HD23	1:O:47:LEU:H	1.61	0.63
1:V:167:LEU:H	1:V:167:LEU:CD1	2.12	0.63
1:N:179:PRO:C	1:N:180:ARG:O	2.42	0.63
1:P:69:HIS:HB3	1:Q:167:LEU:HD21	1.81	0.63
1:D:167:LEU:CD1	1:D:167:LEU:N	2.62	0.63
1:G:82:ASN:H	1:G:82:ASN:HD22	1.47	0.63
1:L:50:GLU:CD	1:V:193:ARG:HG2	2.24	0.63
1:U:205:TYR:HE2	1:U:209:ARG:HH22	1.46	0.63
1:M:123:ASP:OD1	1:M:153:ARG:NH1	2.32	0.63
1:R:82:ASN:HD22	1:R:82:ASN:H	1.44	0.63
1:C:207:SER:C	1:C:209:ARG:H	2.07	0.62
1:E:52:ILE:HG13	1:E:175:LEU:HD11	1.81	0.62
1:G:40:GLN:HE21	1:G:40:GLN:CA	2.12	0.62
1:Q:193:ARG:HG2	1:Q:193:ARG:NH1	2.10	0.62
1:R:193:ARG:HG2	1:R:193:ARG:HH11	1.64	0.62
1:B:82:ASN:H	1:B:82:ASN:HD22	1.47	0.62
1:G:195:ASP:HB3	1:H:77:GLU:HG3	1.80	0.62
1:P:70:ARG:HG3	1:P:70:ARG:HH11	1.64	0.62
1:Q:204:ARG:HG3	1:R:35:GLU:OE1	1.99	0.62
1:F:208:CYS:HB3	1:H:33:ALA:HB2	1.81	0.62
1:G:47:LEU:HD23	1:G:47:LEU:N	2.13	0.62
1:G:52:ILE:HG13	1:G:175:LEU:HD11	1.79	0.62
1:J:70:ARG:HH11	1:J:70:ARG:HG3	1.64	0.62
1:S:82:ASN:HD22	1:S:82:ASN:H	1.47	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:H	1:R:167:LEU:CD1	2.12	0.62
1:U:82:ASN:HD22	1:U:82:ASN:H	1.47	0.62
1:V:197:GLU:O	1:V:200:VAL:HB	1.99	0.62
1:I:134:SER:HB3	1:I:137:LEU:HB2	1.82	0.62
1:K:193:ARG:CB	1:L:180:ARG:HE	2.13	0.62
1:P:82:ASN:HD22	1:P:82:ASN:H	1.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:182:LEU:HD23	1:P:182:LEU:N	2.12	0.62
1:H:167:LEU:H	1:H:167:LEU:CD1	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:A:196:LEU:CD1	1:A:198:PRO:HG3	2.30	0.62
1:C:134:SER:HB3	1:C:137:LEU:HB2	1.80	0.62
1:D:179:PRO:O	1:D:180:ARG:C	2.42	0.62
1:I:24:LEU:HB3	1:J:30:GLN:NE2	2.14	0.62
1:J:47:LEU:HD23	1:J:47:LEU:N	2.15	0.62
1:O:70:ARG:HG3	1:O:70:ARG:HH11	1.64	0.62
1:P:110:PHE:CE2	1:P:124:VAL:HG13	2.34	0.62
1:L:47:LEU:H	1:L:47:LEU:HD23	1.65	0.62
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:I:47:LEU:H	1:I:47:LEU:HD23	1.65	0.61
1:K:182:LEU:HD23	1:K:182:LEU:N	2.15	0.61
1:H:82:ASN:H	1:H:82:ASN:HD22	1.46	0.61
1:L:47:LEU:HD23	1:L:47:LEU:N	2.14	0.61
1:N:47:LEU:H	1:N:47:LEU:HD23	1.64	0.61
1:F:82:ASN:HD22	1:F:82:ASN:H	1.46	0.61
1:Q:167:LEU:H	1:Q:167:LEU:CD1	2.14	0.61
1:A:70:ARG:HG3	1:A:70:ARG:HH11	1.64	0.61
1:B:86:HIS:ND1	1:C:121:HIS:HD2	1.98	0.61
1:Q:47:LEU:HD23	1:Q:47:LEU:N	2.15	0.61
1:F:113:VAL:HG12	1:F:154:ALA:HB1	1.82	0.61
1:H:204:ARG:HG3	1:H:204:ARG:HH21	1.65	0.61
1:Q:24:LEU:HB3	1:R:30:GLN:NE2	2.16	0.61
1:V:52:ILE:HG13	1:V:175:LEU:HD11	1.82	0.61
1:A:113:VAL:HG12	1:A:154:ALA:HB1	1.82	0.61
1:B:196:LEU:CD1	1:B:198:PRO:HG3	2.29	0.61
1:D:86:HIS:ND1	1:E:121:HIS:HD2	1.98	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: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:S:204:ARG:HG3	1:S:204:ARG:HH21	1.65	0.61
1:T:49:PRO:HD2	1:T:50:GLU:OE1	2.00	0.61
1:T:176:ASN:C	1:T:178:LEU:H	2.08	0.61
1:T:208:CYS:CB	1:V:33:ALA:HB2	2.31	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:TYR:OH	1:A:40:GLN:HG3	2.01	0.61
1:C:167:LEU:CD1	1:C:167:LEU:N	2.64	0.61
1:J:195:ASP:HB3	1:K:77:GLU:HG3	1.81	0.61
1:N:47:LEU:HD23	1:N:47:LEU:N	2.15	0.61
1:T:165:CYS:HA	2:T:2022:HOH:O	2.00	0.61
1:U:192:LYS:HB2	1:V:45:GLN:HE21	1.63	0.61
1:Q:113:VAL:HG12	1:Q:154:ALA:HB1	1.83	0.60
1:S:208:CYS:HB2	1:U:33:ALA:HB2	1.83	0.60
1:A:82:ASN:HB2	1:B:117:ASP:OD1	2.01	0.60
1:H:52:ILE:HG13	1:H:175:LEU:HD11	1.83	0.60
1:N:86:HIS:ND1	1:O:121:HIS:HD2	1.99	0.60
1:C:70:ARG:HG3	1:C:70:ARG:HH11	1.64	0.60
1:H:47:LEU:N	1:H:47:LEU:HD23	2.16	0.60
1:G:192:LYS:HE2	1:H:45:GLN:HE22	1.65	0.60
1:L:121:HIS:HD2	1:V:86:HIS:ND1	1.99	0.60
1:Q:205:TYR:HE1	1:S:37:GLN:HB2	1.63	0.60
1:E:195:ASP:HB3	1:F:77:GLU:HG3	1.83	0.60
1:I:182:LEU:H	1:I:182:LEU:CD2	2.13	0.60
1:M:40:GLN:HE21	1:M:40:GLN:CA	2.12	0.60
1:N:124:VAL:O	1:N:153:ARG:HD3	2.01	0.60
1:O:100:ASN:HD21	1:O:102:LYS:HB2	1.62	0.60
1:T:196:LEU:HD13	1:T:198:PRO:HG3	1.82	0.60
1:U:100:ASN:HD21	1:U:102:LYS:HB2	1.66	0.60
1:D:69:HIS:HB3	1:E:167:LEU:HD21	1.83	0.60
1:G:113:VAL:HG12	1:G:154:ALA:HB1	1.82	0.60
1:M:167:LEU:H	1:M:167:LEU:CD1	2.14	0.60
1:P:166:ILE:HG22	1:P:167:LEU:HD12	1.82	0.60
1:A:134:SER:HB3	1:A:137:LEU:HB2	1.84	0.60
1:I:47:LEU:HD23	1:I:47:LEU:N	2.16	0.60
1:L:35:GLU:OE1	1:V:204:ARG:HG3	2.02	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:C:49:PRO:HD2	1:C:50:GLU:OE1	2.02	0.60
1:D:52:ILE:HG13	1:D:175:LEU:HD11	1.83	0.60
1:J:167:LEU:HD13	1:J:167:LEU:N	2.14	0.60
1:G:70:ARG:HG3	1:G:70:ARG:HH11	1.66	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:D:134:SER:HB3	1:D:137:LEU:HB2	1.83	0.59
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:52:ILE:HG13	1:U:175:LEU:HD11	1.84	0.59
1:E:47:LEU:HD23	1:E:47:LEU:H	1.65	0.59
1:K:52:ILE:HG13	1:K:175:LEU:HD11	1.83	0.59
1:L:45:GLN:HE21	1:V:192:LYS:HB2	1.67	0.59
1:F:134:SER:HB3	1:F:137:LEU:HB2	1.83	0.59
1:O:167:LEU:CD1	1:O:167:LEU:N	2.65	0.59
1:K:182:LEU:H	1:K:182:LEU:CD2	2.14	0.59
1:T:167:LEU:H	1:T:167:LEU:CD1	2.14	0.59
1:D:70:ARG:HG3	1:D:70:ARG:HH11	1.68	0.59
1:F:70:ARG:HG3	1:F:70:ARG:HH11	1.67	0.59
1:N:70:ARG:HG3	1:N:70:ARG:NH1	2.17	0.59
1:Q:182:LEU:CD2	1:Q:182:LEU:N	2.57	0.59
1:B:204:ARG:HG3	1:C:35:GLU:OE1	2.01	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:M:167:LEU:HD13	1:M:167:LEU:N	2.17	0.59
1:Q:69:HIS:HB3	1:R:167:LEU:HD21	1.84	0.59
1:V:196:LEU:O	1:V:198:PRO:HD3	2.03	0.59
1:A:100:ASN:HD21	1:A:102:LYS:HB2	1.67	0.59
1:A:167:LEU:CD1	1:A:167:LEU:N	2.65	0.59
1:D:123:ASP:OD1	1:D:153:ARG:NH1	2.36	0.59
1:R:193:ARG:HG2	1:S:50:GLU:OE2	2.02	0.59
1:R:196:LEU:CD1	1:R:198:PRO:HG3	2.32	0.59
1:A:52:ILE:HG13	1:A:175:LEU:HD11	1.85	0.59
1:B:167:LEU:CD1	1:B:167:LEU:N	2.65	0.59
1:I:52:ILE:HG13	1:I:175:LEU:HD11	1.84	0.59
1:M:36:TYR:OH	1:M:40:GLN:HG3	2.02	0.59
1:M:134:SER:HB3	1:M:137:LEU:HB2	1.84	0.59
1:M:192:LYS:HG3	1:N:45:GLN:NE2	2.17	0.59
1:U:183:PRO:HB3	1:V:170:ASP:OD1	2.02	0.59
1:A:45:GLN:HE21	1:K:192:LYS:HB2	1.68	0.59
1:C:52:ILE:HG13	1:C:175:LEU:HD11	1.84	0.59
1:E:100:ASN:HD21	1:E:102:LYS:HB2	1.65	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:J:82:ASN:H	1:J:82:ASN:HD22	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:H:113:VAL:HG12	1:H:154:ALA:HB1	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:208:CYS:HB3	1:J:33:ALA:HB2	1.84	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:Q:47:LEU:HD23	1:Q:47:LEU:H	1.67	0.58
1:V:70:ARG:HH11	1:V:70:ARG:HG3	1.66	0.58
1:B:52:ILE:HG13	1:B:175:LEU:HD11	1.86	0.58
1:G:196:LEU:HD13	1:G:197:GLU:H	1.66	0.58
1:L:117:ASP:OD1	1:V:82:ASN:HB2	2.03	0.58
1:M:100:ASN:HD22	1:M:102:LYS:HB2	1.66	0.58
1:E:204:ARG:HH21	1:E:204:ARG:HG3	1.68	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:M:33:ALA:HB2	1:V:208:CYS:HB2	1.84	0.58
1:M:70:ARG:HG3	1:M:70:ARG:NH1	2.18	0.58
1:Q:100:ASN:HD21	1:Q:102:LYS:HB2	1.66	0.58
1:V:134:SER:HB3	1:V:137:LEU:HB2	1.85	0.58
1:B:113:VAL:HG12	1:B:154:ALA:HB1	1.85	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:D:192:LYS:HG3	1:E:45:GLN:HE22	1.69	0.58
1:B:57:ALA:HB3	1:B:61:GLN:HG3	1.86	0.58
1:J:100:ASN:HD21	1:J:102:LYS:HB2	1.66	0.58
1:P:179:PRO:O	1:P:180:ARG:C	2.45	0.58
1:T:124:VAL:O	1:T:153:ARG:HD3	2.04	0.58
1:D:192:LYS:HB2	1:E:45:GLN:HE21	1.69	0.58
1:G:184:LEU:HD23	1:G:185:GLU:H	1.68	0.58
1:J:69:HIS:HB3	1:K:167:LEU:HD21	1.84	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:I:204:ARG:HG3	1:J:35:GLU:OE1	2.04	0.57
1:N:205:TYR:HE2	1:N:209:ARG:NH2	2.02	0.57
1:T:204:ARG:HG3	1:T:204:ARG:HH21	1.68	0.57
1:F:182:LEU:O	1:F:182:LEU:HG	2.02	0.57
1:J:139:LEU:O	1:J:143:ARG:HG3	2.03	0.57
1:N:204:ARG:HH21	1:N:204:ARG:HG3	1.69	0.57
1:R:167:LEU:CD1	1:R:167:LEU:N	2.67	0.57
1:R:204:ARG:HD2	1:T:36:TYR:CZ	2.38	0.57
1:T:192:LYS:HB2	1:U:45:GLN:HE21	1.69	0.57
1:E:70:ARG:HH11	1:E:70:ARG:HG3	1.67	0.57
1:E:139:LEU:O	1:E:143:ARG:HG3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:100:ASN:HD21	1:I:102:LYS:HB2	1.68	0.57
1:C:184:LEU:CD1	1:C:185:GLU:O	2.52	0.57
1:F:40:GLN:HE21	1:F:40:GLN:CA	2.15	0.57
1:K:167:LEU:CD1	1:K:167:LEU:N	2.68	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:B:208:CYS:HB2	1:D:33:ALA:HB2	1.87	0.57
1:E:167:LEU:CD1	1:E:167:LEU:N	2.68	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:R:69:HIS:HB3	1:S:167:LEU:HD21	1.85	0.57
1:S:100:ASN:HD22	1:S:102:LYS:HB2	1.68	0.57
1:U:167:LEU:CD1	1:U:167:LEU:N	2.68	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:L:182:LEU:H	1:L:182:LEU:CD2	2.16	0.57
1:R:184:LEU:HD22	1:R:185:GLU:N	2.17	0.57
1:O:204:ARG:HD2	1:Q:36:TYR:CZ	2.40	0.57
1:T:167:LEU:HD13	1:T:167:LEU:N	2.15	0.57
1:F:167:LEU:CD1	1:F:167:LEU:N	2.68	0.57
1:Q:49:PRO:HD2	1:Q:50:GLU:OE1	2.04	0.57
1:Q:82:ASN:HB2	1:R:117:ASP:OD1	2.05	0.57
1:U:40:GLN:HA	1:U:40:GLN:NE2	2.15	0.57
1:A:40:GLN:HA	1:A:40:GLN:NE2	2.16	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:L:36:TYR:OH	1:L:40:GLN:HG3	2.05	0.56
1:E:49:PRO:HD2	1:E:50:GLU:OE1	2.04	0.56
1:E:192:LYS:HB2	1:F:45:GLN:HE21	1.70	0.56
1:I:70:ARG:HG3	1:I:70:ARG:HH11	1.70	0.56
1:M:192:LYS:HG3	1:N:45:GLN:HE22	1.68	0.56
1:P:40:GLN:HE21	1:P:40:GLN:CA	2.17	0.56
1:T:184:LEU:HD23	1:T:185:GLU:H	1.69	0.56
1:D:100:ASN:HD21	1:D:102:LYS:HB2	1.70	0.56
1:E:113:VAL:HG12	1:E:154:ALA:HB1	1.86	0.56
1:J:167:LEU:CD1	1:J:167:LEU:N	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:S:70:ARG:HG3	1:S:70:ARG:HH11	1.69	0.56
1:S:192:LYS:HB2	1:T:45:GLN:HE21	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:195:ASP:HB3	1:T:77:GLU:HG3	1.86	0.56
1:E:69:HIS:HB3	1:F:167:LEU:HD21	1.87	0.56
1:O:24:LEU:HB3	1:P:30:GLN:NE2	2.20	0.56
1:P:113:VAL:HG12	1:P:154:ALA:HB1	1.87	0.56
1:S:204:ARG:HD2	1:U:36:TYR:CZ	2.40	0.56
1:K:193:ARG:NE	1:L:180:ARG:NE	2.53	0.56
1:L:113:VAL:HG12	1:L:154:ALA:HB1	1.86	0.56
1:O:192:LYS:HB2	1:P:45:GLN:HE21	1.70	0.56
1:P:124:VAL:O	1:P:153:ARG:HD3	2.06	0.56
1:P:134:SER:HB3	1:P:137:LEU:HB2	1.87	0.56
1:V:124:VAL:O	1:V:153:ARG:HD3	2.06	0.56
1:H:186:VAL:HG21	1:I:171:TYR:CA	2.36	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:V:180:ARG:CG	1:V:181:GLN:N	2.67	0.56
1:J:123:ASP:OD1	1:J:153:ARG:NH1	2.38	0.56
1:K:113:VAL:HG12	1:K:154:ALA:HB1	1.88	0.56
1:K:179:PRO:O	1:K:180:ARG:O	2.24	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:E:184:LEU:CD2	1:E:185:GLU:H	2.19	0.56
1:G:124:VAL:O	1:G:153:ARG:HD3	2.05	0.56
1:P:113:VAL:HG21	1:P:155:LEU:HD13	1.87	0.56
1:P:167:LEU:H	1:P:167:LEU:CD1	2.18	0.56
1:O:179:PRO:O	1:O:180:ARG:C	2.49	0.56
1:O:196:LEU:HD12	1:O:198:PRO:HG3	1.88	0.56
1:P:49:PRO:HD2	1:P:50:GLU:OE1	2.06	0.56
1:E:167:LEU:HD13	1:E:167:LEU:N	2.16	0.55
1:L:204:ARG:HD2	1:N:36:TYR:CZ	2.41	0.55
1:P:82:ASN:HB2	1:Q:117:ASP:OD1	2.06	0.55
1:E:204:ARG:HD2	1:G:36:TYR:CZ	2.41	0.55
1:G:167:LEU:H	1:G:167:LEU:CD1	2.16	0.55
1:K:193:ARG:CB	1:L:180:ARG:NH2	2.43	0.55
1:S:124:VAL:O	1:S:153:ARG:HD3	2.06	0.55
1:C:57:ALA:HB3	1:C:61:GLN:HG3	1.88	0.55
1:C:100:ASN:HD21	1:C:102:LYS:HB2	1.70	0.55
1:E:57:ALA:HB3	1:E:61:GLN:HG3	1.88	0.55
1:I:36:TYR:OH	1:I:40:GLN:HG3	2.05	0.55
1:A:30:GLN:NE2	1:K:24:LEU:HB3	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:167:LEU:CD1	1:H:167:LEU:N	2.70	0.55
1:L:123:ASP:OD1	1:L:153:ARG:NH1	2.40	0.55
1:M:139:LEU:O	1:M:143:ARG:HG3	2.07	0.55
1:O:204:ARG:HG3	1:P:35:GLU:OE1	2.06	0.55
1:R:70:ARG:HG3	1:R:70:ARG:NH1	2.20	0.55
1:C:204:ARG:HG3	1:D:35:GLU:OE1	2.07	0.55
1:H:100:ASN:HD21	1:H:102:LYS:HB2	1.70	0.55
1:N:167:LEU:H	1:N:167:LEU:CD1	2.19	0.55
1:V:139:LEU:O	1:V:143:ARG:HG3	2.06	0.55
1:A:77:GLU:OE2	1:B:44:ARG:NH1	2.40	0.55
1:R:124:VAL:O	1:R:153:ARG:HD3	2.07	0.55
1:V:100:ASN:HD22	1:V:102:LYS:HB2	1.69	0.55
1:V:196:LEU:C	1:V:198:PRO:HD3	2.32	0.55
1:F:100:ASN:HD21	1:F:102:LYS:HB2	1.70	0.55
1:I:167:LEU:H	1:I:167:LEU:CD1	2.18	0.55
1:M:124:VAL:O	1:M:153:ARG:HD3	2.06	0.55
1:S:49:PRO:HD2	1:S:50:GLU:OE1	2.07	0.55
1:V:82:ASN:HD22	1:V:82:ASN:N	2.02	0.55
1:E:134:SER:HB3	1:E:137:LEU:HB2	1.88	0.55
1:G:100:ASN:HD21	1:G:102:LYS:HB2	1.72	0.55
1:J:49:PRO:HD2	1:J:50:GLU:OE1	2.07	0.55
1:T:186:VAL:HG21	1:U:171:TYR:CA	2.37	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:B:134:SER:HB3	1:B:137:LEU:HB2	1.89	0.54
1:B:205:TYR:CE1	1:D:33:ALA:HB1	2.42	0.54
1:K:100:ASN:HD21	1:K:102:LYS:HB2	1.70	0.54
1:L:167:LEU:CD1	1:L:167:LEU:N	2.69	0.54
1:Q:195:ASP:HB3	1:R:77:GLU:HG3	1.89	0.54
1:S:69:HIS:HB3	1:T:167:LEU:HD21	1.88	0.54
1:U:50:GLU:HA	1:U:181:GLN:HE21	1.71	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:C:113:VAL:HG12	1:C:154:ALA:HB1	1.89	0.54
1:C:192:LYS:HB2	1:D:45:GLN:HE21	1.70	0.54
1:M:182:LEU:H	1:M:182:LEU:CD2	2.01	0.54
1:R:36:TYR:OH	1:R:40:GLN:HG3	2.07	0.54
1:S:52:ILE:HG13	1:S:175:LEU:HD11	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:192:LYS:HG3	1:T:45:GLN:HE22	1.72	0.54
1:E:208:CYS:HB2	1:G:33:ALA:HB2	1.90	0.54
1:H:167:LEU:HD13	1:H:167:LEU:N	2.16	0.54
1:H:70:ARG:HG3	1:H:70:ARG:HH11	1.71	0.54
1:L:100:ASN:HD21	1:L:102:LYS:HB2	1.70	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: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
1:T:113:VAL:HG12	1:T:154:ALA:HB1	1.90	0.54
1:V:205:TYR:CE2	1:V:209:ARG:NH2	2.76	0.54
1:G:196:LEU:HD13	1:G:197:GLU:N	2.23	0.54
1:K:40:GLN:HA	1:K:40:GLN:NE2	2.16	0.54
1:K:70:ARG:HG3	1:K:70:ARG:HH11	1.71	0.54
1:F:57:ALA:HB3	1:F:61:GLN:HG3	1.89	0.54
1:N:50:GLU:HB3	1:N:181:GLN:HE21	1.72	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:S:100:ASN:HD21	1:S:102:LYS:HB2	1.69	0.54
1:T:167:LEU:CD1	1:T:167:LEU:N	2.71	0.54
1:U:123:ASP:OD1	1:U:153:ARG:NH1	2.41	0.54
1:U:178:LEU:HD23	1:U:179:PRO:HD3	1.90	0.54
1:E:204:ARG:HG3	1:F:35:GLU:OE1	2.07	0.54
1:L:124:VAL:O	1:L:153:ARG:HD3	2.08	0.54
1:M:113:VAL:HG12	1:M:154:ALA:HB1	1.90	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:V:167:LEU:CD1	1:V:167:LEU:N	2.71	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:F:49:PRO:HD2	1:F:50:GLU:OE1	2.08	0.54
1:H:85:ALA:HB1	1:I:120:TYR:O	2.09	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: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: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:K:49:PRO:HD2	1:K:50:GLU:OE1	2.08	0.53
1:N:134:SER:HB3	1:N:137:LEU:HB2	1.89	0.53
1:P:100:ASN:HD21	1:P:102:LYS:HB2	1.69	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:182:LEU:H	1:U:182:LEU:CD2	2.21	0.53
1:A:49:PRO:HD2	1:L:180:ARG:NH1	2.24	0.53
1:C:139:LEU:O	1:C:143:ARG:HG3	2.07	0.53
1:N:184:LEU:C	1:O:173:ARG:HH22	2.15	0.53
1:R:100:ASN:HD21	1:R:102:LYS:HB2	1.69	0.53
1:R:193:ARG:HG2	1:S:50:GLU:CD	2.34	0.53
1:C:113:VAL:HG21	1:C:155:LEU:HD13	1.91	0.53
1:J:205:TYR:CE2	1:J:209:ARG:NH2	2.76	0.53
1:K:123:ASP:OD1	1:K:153:ARG:NH1	2.41	0.53
1:O:113:VAL:HG12	1:O:154:ALA:HB1	1.91	0.53
1:P:86:HIS:ND1	1:Q:121:HIS:CD2	2.74	0.53
1:R:147:VAL:HG21	1:S:124:VAL:CG2	2.35	0.53
1:C:184:LEU:O	1:D:173:ARG:NH2	2.40	0.53
1:K:167:LEU:HD13	1:K:167:LEU:N	2.17	0.53
1:N:113:VAL:HG12	1:N:154:ALA:HB1	1.90	0.53
1:A:70:ARG:HG3	1:A:70:ARG:NH1	2.24	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:R:193:ARG:HG2	1:R:193:ARG:NH1	2.22	0.53
1:T:70:ARG:HG3	1:T:70:ARG:NH1	2.23	0.53
1:V:180:ARG:CG	1:V:181:GLN:H	2.17	0.53
1:D:82:ASN:HB2	1:E:117:ASP:OD1	2.09	0.53
1:H:49:PRO:HD2	1:H:50:GLU:OE1	2.09	0.53
1:H:57:ALA:HB3	1:H:61:GLN:HG3	1.91	0.53
1:I:113:VAL:HG12	1:I:154:ALA:HB1	1.90	0.53
1:P:180:ARG:HG3	1:P:180:ARG:O	2.08	0.53
1:Q:167:LEU:CD1	1:Q:167:LEU:N	2.71	0.53
1:R:195:ASP:HB3	1:S:77:GLU:HG3	1.90	0.53
1:A:45:GLN:NE2	1:K:192:LYS:HB2	2.23	0.53
1:F:69:HIS:HB3	1:G:167:LEU:HD21	1.90	0.53
1:F:112:ARG:HG3	1:F:122:GLU:HB2	1.90	0.53
1:R:176:ASN:C	1:R:178:LEU:H	2.16	0.53
1:F:139:LEU:O	1:F:143:ARG:HG3	2.09	0.53
1:O:100:ASN:HD22	1:O:102:LYS:HB2	1.71	0.53
1:O:180:ARG:HD2	1:O:180:ARG:O	2.09	0.53
1:P:70:ARG:HG3	1:P:70:ARG:NH1	2.24	0.53
1:Q:57:ALA:HB3	1:Q:61:GLN:HG3	1.91	0.53
1:S:167:LEU:H	1:S:167:LEU:CD1	2.19	0.53
1:S:180:ARG:HG2	1:S:180:ARG:NH1	2.23	0.53
1:T:100:ASN:HD21	1:T:102:LYS:HB2	1.74	0.53
1:B:124:VAL:O	1:B:153:ARG:HD3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:124:VAL:O	1:H:153:ARG:HD3	2.09	0.53
1:P:165:CYS:HA	2:P:2023:HOH:O	2.09	0.53
1:S:196:LEU:HD22	1:S:197:GLU:N	2.24	0.53
1:D:113:VAL:HG12	1:D:154:ALA:HB1	1.91	0.52
1:P:57:ALA:HB3	1:P:61:GLN:HG3	1.90	0.52
1:C:100:ASN:HD22	1:C:102:LYS:HB2	1.71	0.52
1:H:139:LEU:O	1:H:143:ARG:HG3	2.08	0.52
1:L:70:ARG:HG3	1:L:70:ARG:HH11	1.73	0.52
1:Q:179:PRO:O	1:Q:180:ARG:O	2.27	0.52
1:U:178:LEU:CD2	1:U:179:PRO:HD3	2.40	0.52
1:C:112:ARG:HD2	2:C:2005:HOH:O	2.09	0.52
1:D:177:LYS:O	1:D:178:LEU:HD23	2.09	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:T:36:TYR:OH	1:T:40:GLN:HG3	2.10	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:A:182:LEU:CD2	1:A:182:LEU:N	2.72	0.52
1:C:69:HIS:HB3	1:D:167:LEU:HD21	1.91	0.52
1:G:167:LEU:HD13	1:G:167:LEU:N	2.20	0.52
1:G:167:LEU:CD1	1:G:167:LEU:N	2.73	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:N:182:LEU:HB2	1:N:183:PRO:HD2	1.90	0.52
1:Q:140:GLU:HG3	1:Q:144:LYS:HE3	1.90	0.52
1:A:77:GLU:OE1	1:B:44:ARG:HD3	2.09	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:C:47:LEU:N	1:C:47:LEU:CD2	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:H:207:SER:HB2	1:I:32:THR:HG21	1.92	0.52
1:J:113:VAL:HG12	1:J:154:ALA:HB1	1.91	0.52
1:U:192:LYS:HE2	1:U:197:GLU:OE2	2.10	0.52
1:V:182:LEU:H	1:V:182:LEU:HD23	1.75	0.52
1:G:49:PRO:HD2	1:G:50:GLU:OE1	2.09	0.52
1:L:77:GLU:HG3	1:V:195:ASP:HB3	1.91	0.52
1:N:82:ASN:HD22	1:N:82:ASN:N	2.07	0.52
1:O:124:VAL:O	1:O:153:ARG:HD3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:36:TYR:OH	1:V:40:GLN:HG3	2.10	0.52
1:I:49:PRO:HD2	1:I:50:GLU:OE1	2.10	0.52
1:L:120:TYR:O	1:V:85:ALA:HB1	2.09	0.52
1:R:57:ALA:HB3	1:R:61:GLN:HG3	1.91	0.52
1:U:182:LEU:O	1:U:183:PRO:C	2.52	0.52
1:A:82:ASN:HD22	1:A:82:ASN:N	2.01	0.52
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:N:40:GLN:HA	1:N:40:GLN:NE2	2.18	0.52
1:N:166:ILE:HD13	1:N:166:ILE:O	2.10	0.52
1:S:167:LEU:HD13	1:S:167:LEU:N	2.22	0.52
1:S:139:LEU:O	1:S:143:ARG:HG3	2.09	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: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:HG3	1:O:70:ARG:NH1	2.25	0.51
1:U:70:ARG:HG3	1:U:70:ARG:NH1	2.25	0.51
1:D:124:VAL:O	1:D:153:ARG:HD3	2.09	0.51
1:E:183:PRO:O	1:E:184:LEU:O	2.28	0.51
1:H:208:CYS:C	1:H:209:ARG:HG3	2.34	0.51
1:I:181:GLN:O	1:I:181:GLN:HG3	2.09	0.51
1:J:70:ARG:HG3	1:J:70:ARG:NH1	2.23	0.51
1:A:135:LYS:HE2	2:A:2014:HOH:O	2.10	0.51
1:B:70:ARG:HG3	1:B:70:ARG:NH1	2.23	0.51
1:D:194:GLN:C	1:E:51:TYR:OH	2.53	0.51
1:O:82:ASN:HB2	1:P:117:ASP:OD1	2.11	0.51
1:Q:123:ASP:OD1	1:Q:153:ARG:NH1	2.43	0.51
1:S:85:ALA:HB1	1:T:120:TYR:O	2.09	0.51
1:V:40:GLN:HA	1:V:40:GLN:NE2	2.16	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:H:123:ASP:OD1	1:H:153:ARG:NH1	2.44	0.51
1:S:47:LEU:N	1:S:47:LEU:CD2	2.72	0.51
1:F:100:ASN:HD22	1:F:102:LYS:HB2	1.75	0.51
1:F:192:LYS:HE2	1:G:45:GLN:NE2	2.26	0.51
1:G:204:ARG:HH21	1:G:204:ARG:CG	2.18	0.51
1:H:207:SER:HB2	1:I:32:THR:CG2	2.40	0.51
1:N:52:ILE:HG13	1:N:175:LEU:HD11	1.92	0.51
1:P:82:ASN:HD22	1:P:82:ASN:N	2.09	0.51
1:T:57:ALA:HB3	1:T:61:GLN:HG3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:57:ALA:HB3	1:V:61:GLN:HG3	1.92	0.51
1:A:179:PRO:HD3	1:L:183:PRO:HG3	1.93	0.51
1:B:33:ALA:HB2	1:K:208:CYS:HB2	1.92	0.51
1:H:24:LEU:HB3	1:I:30:GLN:NE2	2.25	0.51
1:P:196:LEU:CD1	1:P:198:PRO:HG3	2.40	0.51
1:Q:50:GLU:HA	1:Q:181:GLN:HE22	1.75	0.51
1:V:100:ASN:ND2	1:V:102:LYS:CB	2.71	0.51
1:A:100:ASN:HD22	1:A:102:LYS:CB	2.24	0.51
1:A:195:ASP:HB3	1:B:77:GLU:HG3	1.93	0.51
1:E:184:LEU:HD23	1:E:185:GLU:H	1.75	0.51
1:F:124:VAL:O	1:F:153:ARG:HD3	2.11	0.51
1:F:196:LEU:HD13	1:F:198:PRO:HD3	1.93	0.51
1:J:100:ASN:HD22	1:J:102:LYS:HB2	1.72	0.51
1:M:57:ALA:HB3	1:M:61:GLN:HG3	1.93	0.51
1:M:182:LEU:O	1:M:183:PRO:C	2.52	0.51
1:T:113:VAL:HG21	1:T:155:LEU:HD13	1.93	0.51
1:T:192:LYS:HG3	1:U:45:GLN:HE22	1.76	0.51
1:A:49:PRO:CD	1:L:180:ARG:NH1	2.74	0.51
1:A:117:ASP:OD1	1:K:82:ASN:HB2	2.10	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:M:40:GLN:HA	1:M:40:GLN:NE2	2.18	0.51
1:N:196:LEU:HD13	1:N:197:GLU:N	2.25	0.51
1:O:173:ARG:HH11	1:O:173:ARG:HG2	1.75	0.51
1:Q:139:LEU:O	1:Q:143:ARG:HG3	2.11	0.51
1:S:123:ASP:OD1	1:S:153:ARG:NH1	2.44	0.51
1:A:167:LEU:HD21	1:K:69:HIS:HB3	1.92	0.51
1:B:189:THR:HG22	1:B:190:LYS:CG	2.28	0.51
1:F:47:LEU:N	1:F:47:LEU:CD2	2.74	0.51
1:O:205:TYR:CE2	1:O:209:ARG:NH2	2.79	0.51
1:Q:207:SER:C	1:Q:209:ARG:N	2.66	0.51
1:V:192:LYS:NZ	1:V:194:GLN:O	2.36	0.51
1:M:100:ASN:HD21	1:M:102:LYS:HB2	1.68	0.50
1:N:192:LYS:CE	1:N:197:GLU:OE2	2.52	0.50
1:P:167:LEU:CD1	1:P:167:LEU:N	2.74	0.50
1:S:57:ALA:HB3	1:S:61:GLN:HG3	1.93	0.50
1:V:100:ASN:HD22	1:V:102:LYS:CB	2.24	0.50
1:V:192:LYS:CE	1:V:197:GLU:OE2	2.58	0.50
1:F:82:ASN:HD22	1:F:82:ASN:N	2.07	0.50
1:J:204:ARG:HG3	1:J:204:ARG:HH21	1.76	0.50
1:K:165:CYS:HA	2:K:2023:HOH:O	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:183:PRO:HB2	1:H:170:ASP:OD1	2.11	0.50
1:G:193:ARG:HG2	1:G:193:ARG:HH11	1.76	0.50
1:H:182:LEU:HD23	1:H:182:LEU:H	1.77	0.50
1:K:193:ARG:NH1	1:L:182:LEU:HD22	2.25	0.50
1:L:45:GLN:NE2	1:V:192:LYS:HB2	2.26	0.50
1:R:47:LEU:N	1:R:47:LEU:CD2	2.73	0.50
1:S:167:LEU:CD1	1:S:167:LEU:N	2.75	0.50
1:S:203:ALA:HB1	1:T:35:GLU:N	2.26	0.50
1:A:77:GLU:CD	1:B:44:ARG:HH11	2.20	0.50
1:C:184:LEU:CD1	1:C:185:GLU:N	2.74	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:S:47:LEU:HD23	1:S:165:CYS:SG	2.51	0.50
1:T:86:HIS:ND1	1:U:121:HIS:CD2	2.77	0.50
1:U:50:GLU:HA	1:U:181:GLN:NE2	2.26	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: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:O:176:ASN:C	1:O:178:LEU:H	2.20	0.50
1:A:124:VAL:O	1:A:153:ARG:HD3	2.12	0.50
1:C:196:LEU:HD12	1:C:198:PRO:HG3	1.92	0.50
1:L:30:GLN:NE2	1:V:24:LEU:HB3	2.27	0.50
1:O:57:ALA:HB3	1:O:61:GLN:HG3	1.94	0.50
1:U:112:ARG:HG3	1:U:122:GLU:HB2	1.94	0.50
1:B:40:GLN:HA	1:B:40:GLN:NE2	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:Q:204:ARG:HG3	1:R:35:GLU:CD	2.37	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:A:121:HIS:CD2	1:K:86:HIS:ND1	2.77	0.50
1:B:82:ASN:HD22	1:B:82:ASN:N	2.07	0.50
1:D:57:ALA:HB3	1:D:61:GLN:HG3	1.93	0.50
1:J:36:TYR:OH	1:J:40:GLN:HG3	2.12	0.50
1:N:192:LYS:HB2	1:O:45:GLN:HE21	1.77	0.50
1:Q:167:LEU:HD13	1:Q:167:LEU:N	2.19	0.50
1:R:82:ASN:HB2	1:S:117:ASP:OD1	2.12	0.50
1:G:139:LEU:O	1:G:143:ARG:HG3	2.12	0.49
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:47:LEU:N	1:A:47:LEU:CD2	2.75	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:G:182:LEU:HD23	1:G:182:LEU:N	2.16	0.49
1:E:193:ARG:HG2	1:F:50:GLU:CD	2.38	0.49
1:G:116:LYS:HE2	2:G:2004:HOH:O	2.11	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: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
1:T:47:LEU:HD23	1:T:165:CYS:SG	2.53	0.49
1:B:192:LYS:HG3	1:C:45:GLN:HE22	1.76	0.49
1:D:192:LYS:HG3	1:E:45:GLN:NE2	2.28	0.49
1:F:24:LEU:HB3	1:G:30:GLN:NE2	2.28	0.49
1:F:70:ARG:HG3	1:F:70:ARG:NH1	2.27	0.49
1:N:139:LEU:O	1:N:143:ARG:HG3	2.11	0.49
1:D:182:LEU:HD23	1:D:182:LEU:N	2.19	0.49
1:G:82:ASN:HD22	1:G:82:ASN:N	2.06	0.49
1:L:100:ASN:HD22	1:L:102:LYS:HB2	1.72	0.49
1:Q:184:LEU:CD2	1:Q:185:GLU:N	2.68	0.49
1:D:82:ASN:HD22	1:D:82:ASN:N	2.00	0.49
1:D:208:CYS:C	1:D:209:ARG:HG3	2.38	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:N:167:LEU:CD1	1:N:167:LEU:N	2.76	0.49
1:S:82:ASN:HB2	1:T:117:ASP:OD1	2.13	0.49
1:U:192:LYS:CE	1:U:197:GLU:OE2	2.60	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:G:57:ALA:HB3	1:G:61:GLN:HG3	1.94	0.49
1:G:179:PRO:C	1:G:180:ARG:O	2.56	0.49
1:J:184:LEU:HD13	1:J:185:GLU:N	2.26	0.49
1:K:47:LEU:N	1:K:47:LEU:CD2	2.76	0.49
1:L:77:GLU:OE2	1:M:44:ARG:NH1	2.46	0.49
1:S:147:VAL:HG21	1:T:124:VAL:CG2	2.40	0.49
1:T:139:LEU:O	1:T:143:ARG:HG3	2.13	0.49
1:B:100:ASN:HD22	1:B:102:LYS:HB2	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:47:LEU:N	1:D:47:LEU:CD2	2.74	0.49
1:E:86:HIS:ND1	1:F:121:HIS:CD2	2.73	0.49
1:H:112:ARG:HG3	1:H:122:GLU:HB2	1.94	0.49
1:N:113:VAL:HG21	1:N:155:LEU:HD13	1.95	0.49
1:R:113:VAL:HG21	1:R:155:LEU:HD13	1.94	0.49
1:S:207:SER:C	1:S:209:ARG:H	2.21	0.49
1:B:33:ALA:HB2	1:K:208:CYS:CB	2.43	0.49
1:D:24:LEU:HB3	1:E:30:GLN:NE2	2.27	0.49
1:J:24:LEU:HB3	1:K:30:GLN:NE2	2.28	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:C:70:ARG:HG3	1:C:70:ARG:NH1	2.27	0.48
1:D:100:ASN:HD22	1:D:102:LYS:HB2	1.74	0.48
1:F:58:GLY:C	1:F:60:GLY:H	2.21	0.48
1:K:57:ALA:HB3	1:K:61:GLN:HG3	1.94	0.48
1:O:100:ASN:HD22	1:O:102:LYS:CB	2.26	0.48
1:O:186:VAL:HG21	1:P:171:TYR:HA	1.95	0.48
1:E:100:ASN:HD22	1:E:102:LYS:CB	2.26	0.48
1:E:185:GLU:OE1	1:F:177:LYS:NZ	2.47	0.48
1:G:204:ARG:NH2	1:H:35:GLU:OE1	2.47	0.48
1:I:113:VAL:HG21	1:I:155:LEU:HD13	1.94	0.48
1:Q:82:ASN:HD22	1:Q:82:ASN:N	2.02	0.48
1:S:70:ARG:HG3	1:S:70:ARG:NH1	2.28	0.48
1:T:175:LEU:O	1:T:178:LEU:HD12	2.13	0.48
1:U:195:ASP:HB3	1:V:77:GLU:HG3	1.95	0.48
1:V:49:PRO:HD2	1:V:50:GLU:OE1	2.13	0.48
1:D:140:GLU:HB2	1:E:126:TYR:CD2	2.47	0.48
1:E:70:ARG:HG3	1:E:70:ARG:NH1	2.28	0.48
1:H:58:GLY:C	1:H:60:GLY:H	2.22	0.48
1:I:86:HIS:ND1	1:J:121:HIS:CD2	2.79	0.48
1:I:167:LEU:CD1	1:I:167:LEU:N	2.74	0.48
1:L:192:LYS:NZ	1:L:194:GLN:O	2.40	0.48
1:O:139:LEU:O	1:O:143:ARG:HG3	2.12	0.48
1:P:47:LEU:N	1:P:47:LEU:CD2	2.76	0.48
1:P:167:LEU:HD13	1:P:167:LEU:N	2.23	0.48
1:T:58:GLY:C	1:T:60:GLY:H	2.21	0.48
1:E:207:SER:O	1:E:209:ARG:N	2.46	0.48
1:F:116:LYS:HE2	2:F:2005:HOH:O	2.13	0.48
1:H:70:ARG:HG3	1:H:70:ARG:NH1	2.29	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:LYS:HE2	2:B:2001:HOH:O	2.12	0.48
1:C:47:LEU:HD23	1:C:165:CYS:SG	2.54	0.48
1:E:179:PRO:C	1:E:180:ARG:O	2.56	0.48
1:H:196:LEU:HD13	1:H:197:GLU:N	2.29	0.48
1:J:100:ASN:HD22	1:J:102:LYS:CB	2.27	0.48
1:U:58:GLY:C	1:U:60:GLY:H	2.22	0.48
1:V:116:LYS:HE2	2:V:2003:HOH:O	2.14	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:G:123:ASP:OD1	1:G:153:ARG:NH1	2.47	0.48
1:J:182:LEU:H	1:J:182:LEU:CD2	2.26	0.48
1:V:47:LEU:N	1:V:47:LEU:CD2	2.75	0.48
1:F:196:LEU:CD1	1:F:198:PRO:HG3	2.42	0.48
1:F:205:TYR:CE2	1:F:209:ARG:NH2	2.81	0.48
1:G:204:ARG:HG3	1:H:35:GLU:OE1	2.13	0.48
1:G:204:ARG:O	1:G:204:ARG:HG2	2.12	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
1:V:182:LEU:HD23	1:V:182:LEU:N	2.29	0.48
1:B:195:ASP:HB3	1:C:77:GLU:HG3	1.95	0.48
1:G:115:LEU:C	1:G:117:ASP:H	2.22	0.48
1:G:140:GLU:HG3	1:G:144:LYS:HE3	1.95	0.48
1:L:178:LEU:O	1:L:179:PRO:C	2.57	0.48
1:L:182:LEU:HD23	1:L:182:LEU:N	2.25	0.48
1:M:82:ASN:HB2	1:N:117:ASP:OD1	2.14	0.48
1:M:166:ILE:HD13	1:M:166:ILE:O	2.14	0.48
1:N:57:ALA:HB3	1:N:61:GLN:HG3	1.96	0.48
1:T:166:ILE:HD13	1:T:166:ILE:O	2.14	0.48
1:T:192:LYS:NZ	1:T:197:GLU:OE2	2.45	0.48
1:U:47:LEU:N	1:U:47:LEU:CD2	2.77	0.48
1:V:167:LEU:HD13	1:V:167:LEU:N	2.19	0.48
1:B:193:ARG:HH12	1:C:50:GLU:CD	2.22	0.48
1:G:70:ARG:HG3	1:G:70:ARG:NH1	2.26	0.48
1:L:40:GLN:CA	1:L:40:GLN:NE2	2.76	0.48
1:L:82:ASN:HD22	1:L:82:ASN:N	2.06	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:D:204:ARG:HG3	1:E:35:GLU:CD	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:57:ALA:HB3	1:I:61:GLN:HG3	1.96	0.47
1:L:40:GLN:HA	1:L:40:GLN:NE2	2.18	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:J:116:LYS:HE2	2:J:2001:HOH:O	2.13	0.47
1:K:58:GLY:C	1:K:60:GLY:H	2.22	0.47
1:V:113:VAL:HG12	1:V:154:ALA:HB1	1.96	0.47
1:A:192:LYS:HB2	1:B:45:GLN:HE21	1.80	0.47
1:B:82:ASN:HB2	1:C:117:ASP:OD1	2.14	0.47
1:G:58:GLY:C	1:G:60:GLY:H	2.22	0.47
1:J:40:GLN:HA	1:J:40:GLN:NE2	2.16	0.47
1:L:58:GLY:C	1:L:60:GLY:H	2.22	0.47
1:M:112:ARG:HG3	1:M:122:GLU:HB2	1.96	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:O:47:LEU:N	1:O:47:LEU:CD2	2.76	0.47
1:R:196:LEU:HD13	1:R:197:GLU:N	2.29	0.47
1:U:166:ILE:HD13	1:U:166:ILE:O	2.14	0.47
1:E:40:GLN:HA	1:E:40:GLN:NE2	2.22	0.47
1:E:140:GLU:HG3	1:E:144:LYS:HE3	1.95	0.47
1:I:207:SER:C	1:I:209:ARG:H	2.21	0.47
1:D:115:LEU:C	1:D:117:ASP:H	2.23	0.47
1:F:100:ASN:HD22	1:F:102:LYS:CB	2.28	0.47
1:F:192:LYS:HE2	1:G:45:GLN:HE22	1.79	0.47
1:I:70:ARG:HG3	1:I:70:ARG:NH1	2.29	0.47
1:I:115:LEU:C	1:I:117:ASP:H	2.21	0.47
1:N:47:LEU:HD23	1:N:165:CYS:SG	2.55	0.47
1:S:58:GLY:C	1:S:60:GLY:H	2.22	0.47
1:U:82:ASN:HB2	1:V:117:ASP:OD1	2.15	0.47
1:V:182:LEU:H	1:V:182:LEU:CD2	2.28	0.47
1:T:175:LEU:HA	1:T:178:LEU:HD12	1.97	0.47
1:A:128:VAL:HG12	1:A:129:SER:N	2.29	0.47
1:B:175:LEU:O	1:B:178:LEU:HB2	2.15	0.47
1:J:85:ALA:HB1	1:K:120:TYR:O	2.15	0.47
1:L:50:GLU:OE1	1:V:193:ARG:HG2	2.15	0.47
1:M:82:ASN:HD22	1:M:82:ASN:N	2.07	0.47
1:N:182:LEU:HD22	1:N:182:LEU:N	2.06	0.47
1:Q:100:ASN:HD22	1:Q:102:LYS:HB2	1.74	0.47
1:D:40:GLN:HE21	1:D:40:GLN:CA	2.19	0.47
1:D:70:ARG:HG3	1:D:70:ARG:NH1	2.29	0.47
1:G:100:ASN:HD22	1:G:102:LYS:HB2	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:147:VAL:HG21	1:I:124:VAL:CG2	2.41	0.47
1:I:100:ASN:HB2	1:I:101:GLY:H	1.49	0.47
1:K:113:VAL:HG21	1:K:155:LEU:HD13	1.96	0.47
1:Q:182:LEU:O	1:Q:183:PRO:C	2.58	0.47
1:A:57:ALA:HB3	1:A:61:GLN:HG3	1.96	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:N:176:ASN:C	1:N:178:LEU:H	2.22	0.46
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:B:86:HIS:ND1	1:C:121:HIS:CD2	2.83	0.46
1:D:100:ASN:HB2	1:D:101:GLY:H	1.57	0.46
1:E:47:LEU:HD23	1:E:165:CYS:SG	2.54	0.46
1:F:186:VAL:HG21	1:G:170:ASP:C	2.40	0.46
1:H:204:ARG:HG3	1:I:35:GLU:CD	2.41	0.46
1:I:123:ASP:OD1	1:I:153:ARG:NH1	2.48	0.46
1:J:100:ASN:HB2	1:J:101:GLY:H	1.51	0.46
1:K:173:ARG:HG2	1:K:173:ARG:HH11	1.80	0.46
1:K:179:PRO:C	1:K:180:ARG:O	2.58	0.46
1:L:100:ASN:HD22	1:L:102:LYS:CB	2.27	0.46
1:C:86:HIS:ND1	1:D:121:HIS:CD2	2.80	0.46
1:D:36:TYR:CZ	1:D:40:GLN:HG3	2.51	0.46
1:J:57:ALA:HB3	1:J:61:GLN:HG3	1.97	0.46
1:O:69:HIS:HB3	1:P:167:LEU:CD2	2.44	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:O:134:SER:OG	1:O:137:LEU:HD23	2.15	0.46
1:S:100:ASN:HB2	1:S:101:GLY:H	1.59	0.46
1:U:57:ALA:HB3	1:U:61:GLN:HG3	1.96	0.46
1:B:139:LEU:O	1:B:143:ARG:HG3	2.15	0.46
1:H:100:ASN:HD22	1:H:102:LYS:CB	2.29	0.46
1:K:193:ARG:CZ	1:L:180:ARG:CZ	2.93	0.46
1:L:24:LEU:HB3	1:M:30:GLN:NE2	2.31	0.46
1:O:24:LEU:HD22	1:O:24:LEU:HA	1.80	0.46
1:P:134:SER:OG	1:P:137:LEU:HD23	2.16	0.46
1:P:139:LEU:O	1:P:143:ARG:HG3	2.16	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:L:33:ALA:HB2	1:U:208:CYS:HB2	1.96	0.46
1:N:82:ASN:HB2	1:O:117:ASP:OD1	2.16	0.46
1:O:58:GLY:C	1:O:60:GLY:H	2.23	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:58:GLY:C	1:D:60:GLY:H	2.24	0.46
1:G:196:LEU:HD12	1:G:198:PRO:HG3	1.97	0.46
1:H:134:SER:OG	1:H:137:LEU:HD23	2.15	0.46
1:L:173:ARG:HG2	1:L:173:ARG:HH11	1.81	0.46
1:N:173:ARG:HG2	1:N:173:ARG:HH11	1.81	0.46
1:V:40:GLN:CA	1:V:40:GLN:NE2	2.76	0.46
1:E:58:GLY:C	1:E:60:GLY:H	2.24	0.46
1:I:173:ARG:HG2	1:I:173:ARG:HH11	1.81	0.46
1:J:50:GLU:H	1:J:50:GLU:CD	2.24	0.46
1:P:192:LYS:NZ	1:P:195:ASP:O	2.49	0.46
1:A:49:PRO:CG	1:A:178:LEU:HD12	2.46	0.46
1:A:86:HIS:ND1	1:B:121:HIS:CD2	2.80	0.46
1:A:182:LEU:HB2	1:L:56:MET:HE3	1.97	0.46
1:F:140:GLU:HG3	1:F:144:LYS:HE3	1.98	0.46
1:I:115:LEU:C	1:I:117:ASP:N	2.73	0.46
1:K:100:ASN:HD22	1:K:102:LYS:CB	2.27	0.46
1:K:193:ARG:CZ	1:L:180:ARG:NE	2.79	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:B:47:LEU:N	1:B:47:LEU:CD2	2.78	0.46
1:C:188:LEU:O	1:C:189:THR:C	2.58	0.46
1:D:173:ARG:HG2	1:D:173:ARG:HH11	1.81	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:P:100:ASN:HD22	1:P:102:LYS:CB	2.28	0.46
1:D:194:GLN:HE21	1:D:194:GLN:HB2	1.48	0.45
1:N:147:VAL:HG21	1:O:124:VAL:CG2	2.40	0.45
1:N:196:LEU:HD12	1:N:198:PRO:HG3	1.98	0.45
1:O:204:ARG:HG3	1:O:204:ARG:HH21	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:S:113:VAL:HG21	1:S:155:LEU:HD13	1.99	0.45
1:U:85:ALA:HB1	1:V:120:TYR:O	2.15	0.45
1:B:58:GLY:C	1:B:60:GLY:H	2.23	0.45
1:H:86:HIS:ND1	1:I:121:HIS:CD2	2.81	0.45
1:I:175:LEU:O	1:I:178:LEU:HB2	2.15	0.45
1:K:70:ARG:HG3	1:K:70:ARG:NH1	2.31	0.45
1:T:182:LEU:HD23	1:T:182:LEU:N	2.30	0.45
1:F:207:SER:C	1:F:209:ARG:H	2.24	0.45
1:H:24:LEU:HD22	1:H:24:LEU:HA	1.82	0.45
1:K:112:ARG:HG3	1:K:122:GLU:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:Q:115:LEU:C	1:Q:117:ASP:H	2.24	0.45
1:U:115:LEU:C	1:U:117:ASP:H	2.24	0.45
1:U:184:LEU:HD13	1:U:185:GLU:C	2.41	0.45
1:B:113:VAL:HG21	1:B:155:LEU:HD13	1.98	0.45
1:D:180:ARG:O	1:D:180:ARG:HG3	2.15	0.45
1:F:82:ASN:HB2	1:G:117:ASP:OD1	2.17	0.45
1:K:192:LYS:NZ	1:K:194:GLN:O	2.47	0.45
1:O:85:ALA:HB1	1:P:120:TYR:O	2.16	0.45
1:A:58:GLY:C	1:A:60:GLY:H	2.25	0.45
1:B:196:LEU:HD13	1:B:198:PRO:HD3	1.99	0.45
1:D:82:ASN:H	1:D:82:ASN:ND2	2.10	0.45
1:M:113:VAL:HG21	1:M:155:LEU:CD1	2.47	0.45
1:N:58:GLY:C	1:N:60:GLY:H	2.24	0.45
1:R:82:ASN:HD22	1:R:82:ASN:N	2.09	0.45
1:U:192:LYS:NZ	1:U:197:GLU:OE2	2.49	0.45
1:V:82:ASN:H	1:V:82:ASN:ND2	2.10	0.45
1:H:180:ARG:HG3	1:H:181:GLN:N	2.32	0.45
1:I:100:ASN:HD22	1:I:102:LYS:CB	2.29	0.45
1:E:47:LEU:N	1:E:47:LEU:CD2	2.78	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:L:99:ASN:C	1:L:100:ASN:CG	2.85	0.45
1:M:86:HIS:ND1	1:N:121:HIS:CD2	2.82	0.45
1:M:140:GLU:HG3	1:M:144:LYS:HE3	1.98	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:R:179:PRO:O	1:R:180:ARG:C	2.59	0.45
1:B:196:LEU:HD13	1:B:198:PRO:CD	2.46	0.45
1:C:99:ASN:C	1:C:100:ASN:OD1	2.60	0.45
1:G:47:LEU:HD23	1:G:165:CYS:SG	2.57	0.45
1:K:47:LEU:HD23	1:K:165:CYS:SG	2.57	0.45
1:L:24:LEU:HD22	1:L:24:LEU:HA	1.82	0.45
1:N:100:ASN:HD22	1:N:102:LYS:CB	2.30	0.45
1:P:50:GLU:H	1:P:50:GLU:CD	2.24	0.45
1:T:192:LYS:HB2	1:U:45:GLN:NE2	2.31	0.45
1:G:204:ARG:CG	1:G:204:ARG:NH2	2.79	0.45
1:H:192:LYS:HE2	1:H:197:GLU:OE2	2.16	0.45
1:I:47:LEU:HD23	1:I:165:CYS:SG	2.57	0.45
1:I:85:ALA:HB1	1:J:120:TYR:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:204:ARG:O	1:J:207:SER:OG	2.33	0.45
1:O:47:LEU:HD23	1:O:165:CYS:SG	2.57	0.45
1:S:202:GLU:O	1:S:203:ALA:C	2.59	0.45
1:T:192:LYS:HG3	1:U:45:GLN:NE2	2.32	0.45
1:H:173:ARG:HH11	1:H:173:ARG:HG2	1.80	0.45
1:M:37:GLN:OE1	1:V:205:TYR:CE1	2.70	0.45
1:M:58:GLY:C	1:M:60:GLY:H	2.25	0.45
1:N:195:ASP:HB3	1:O:77:GLU:HG3	1.97	0.45
1:S:40:GLN:CA	1:S:40:GLN:NE2	2.80	0.45
1:U:36:TYR:OH	1:U:40:GLN:HG3	2.17	0.45
1:V:99:ASN:C	1:V:100:ASN:OD1	2.60	0.45
1:A:50:GLU:H	1:A:50:GLU:CD	2.25	0.44
1:B:40:GLN:CA	1:B:40:GLN:NE2	2.78	0.44
1:C:100:ASN:HD22	1:C:102:LYS:CB	2.28	0.44
1:E:183:PRO:O	1:E:184:LEU:C	2.59	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:O:190:LYS:O	1:O:191:ALA:C	2.59	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:U:115:LEU:C	1:U:117:ASP:N	2.75	0.44
1:A:173:ARG:HG2	1:A:173:ARG:HH11	1.82	0.44
1:B:181:GLN:O	1:B:181:GLN:HG3	2.17	0.44
1:C:173:ARG:HH11	1:C:173:ARG:HG2	1.81	0.44
1:D:192:LYS:HB2	1:E:45:GLN:NE2	2.32	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: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:A:176:ASN:C	1:A:178:LEU:H	2.25	0.44
1:B:47:LEU:HD23	1:B:165:CYS:SG	2.57	0.44
1:D:115:LEU:C	1:D:117:ASP:N	2.72	0.44
1:G:47:LEU:N	1:G:47:LEU:CD2	2.79	0.44
1:G:173:ARG:HG2	1:G:173:ARG:HH11	1.81	0.44
1:Q:186:VAL:HG21	1:R:171:TYR:HA	2.00	0.44
1:D:100:ASN:HD22	1:D:102:LYS:CB	2.30	0.44
1:J:58:GLY:C	1:J:60:GLY:H	2.25	0.44
1:J:112:ARG:HG3	1:J:122:GLU:HB2	2.00	0.44
1:K:100:ASN:HB2	1:K:101:GLY:H	1.54	0.44
1:S:99:ASN:C	1:S:100:ASN:CG	2.85	0.44
1:I:100:ASN:HD22	1:I:102:LYS:HB2	1.77	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:B:201:GLU:O	1:B:202:GLU:C	2.60	0.44
1:C:58:GLY:C	1:C:60:GLY:H	2.26	0.44
1:C:208:CYS:HB2	1:E:33:ALA:HB2	1.98	0.44
1:G:86:HIS:ND1	1:H:121:HIS:CD2	2.79	0.44
1:G:166:ILE:HD13	1:G:166:ILE:O	2.18	0.44
1:P:40:GLN:HA	1:P:40:GLN:NE2	2.25	0.44
1:Q:58:GLY:C	1:Q:60:GLY:H	2.25	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:T:82:ASN:HB2	1:U:117:ASP:OD1	2.18	0.44
1:U:100:ASN:HD22	1:U:102:LYS:CB	2.30	0.44
1:V:50:GLU:HA	1:V:181:GLN:NE2	2.33	0.44
1:B:192:LYS:NZ	1:B:194:GLN:O	2.46	0.44
1:E:100:ASN:ND2	1:E:102:LYS:CB	2.74	0.44
1:E:113:VAL:HG21	1:E:155:LEU:HD13	1.99	0.44
1:F:77:GLU:OE2	1:G:44:ARG:NH1	2.51	0.44
1:I:58:GLY:C	1:I:60:GLY:H	2.25	0.44
1:L:47:LEU:N	1:L:47:LEU:CD2	2.80	0.44
1:T:82:ASN:HD22	1:T:82:ASN:N	2.14	0.44
1:T:196:LEU:C	1:T:198:PRO:HD3	2.43	0.44
1:A:49:PRO:HD3	1:L:180:ARG:HH12	1.83	0.44
1:B:33:ALA:HB1	1:K:205:TYR:CE1	2.53	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:F:186:VAL:HG21	1:G:171:TYR:HA	2.00	0.44
1:F:204:ARG:HG3	1:G:35:GLU:OE1	2.18	0.44
1:H:193:ARG:HG2	1:I:50:GLU:CD	2.43	0.44
1:M:77:GLU:OE2	1:N:44:ARG:NH1	2.51	0.44
1:U:173:ARG:HG2	1:U:173:ARG:HH11	1.83	0.44
1:V:58:GLY:C	1:V:60:GLY:H	2.25	0.44
1:A:192:LYS:HB2	1:B:45:GLN:NE2	2.32	0.43
1:G:115:LEU:C	1:G:117:ASP:N	2.76	0.43
1:I:192:LYS:NZ	1:I:194:GLN:O	2.36	0.43
1:K:178:LEU:HB3	1:K:179:PRO:CD	2.48	0.43
1:L:151:LEU:CD1	1:L:155:LEU:HD22	2.48	0.43
1:O:77:GLU:OE2	1:P:44:ARG:NH1	2.51	0.43
1:U:47:LEU:HD23	1:U:165:CYS:SG	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:99:ASN:C	1:C:100:ASN:CG	2.84	0.43
1:D:113:VAL:HG21	1:D:155:LEU:CD1	2.48	0.43
1:E:93:VAL:HA	1:E:107:VAL:HG22	2.00	0.43
1:G:186:VAL:HG21	1:H:171:TYR:HA	2.00	0.43
1:N:140:GLU:HG3	1:N:144:LYS:HE3	1.99	0.43
1:I:166:ILE:HD13	1:I:166:ILE:O	2.19	0.43
1:I:176:ASN:C	1:I:178:LEU:H	2.26	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
1:R:166:ILE:HD13	1:R:166:ILE:O	2.17	0.43
1:C:40:GLN:CA	1:C:40:GLN:NE2	2.78	0.43
1:G:100:ASN:HD22	1:G:102:LYS:CB	2.30	0.43
1:J:176:ASN:C	1:J:178:LEU:H	2.26	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:D:24:LEU:HD22	1:D:24:LEU:HA	1.81	0.43
1:G:186:VAL:HG21	1:H:171:TYR:CA	2.49	0.43
1:H:115:LEU:C	1:H:117:ASP:N	2.77	0.43
1:L:178:LEU:O	1:L:179:PRO:O	2.36	0.43
1:M:204:ARG:HG3	1:M:204:ARG:HH21	1.83	0.43
1:N:143:ARG:NH1	1:O:94:ASP:OD2	2.51	0.43
1:N:175:LEU:O	1:N:178:LEU:HB2	2.18	0.43
1:T:202:GLU:O	1:T:205:TYR:N	2.51	0.43
1:U:176:ASN:C	1:U:178:LEU:H	2.26	0.43
1:A:32:THR:CG2	1:K:207:SER:HB2	2.48	0.43
1:A:105:VAL:HG11	1:A:139:LEU:HD13	1.99	0.43
1:B:24:LEU:HB3	1:C:30:GLN:NE2	2.34	0.43
1:H:115:LEU:C	1:H:117:ASP:H	2.24	0.43
1:L:70:ARG:HG3	1:L:70:ARG:NH1	2.31	0.43
1:M:173:ARG:HG2	1:M:173:ARG:HH11	1.83	0.43
1:R:143:ARG:NH1	1:S:94:ASP:OD2	2.52	0.43
1:B:140:GLU:HB2	1:C:126:TYR:CD2	2.53	0.43
1:C:176:ASN:C	1:C:178:LEU:H	2.25	0.43
1:D:179:PRO:O	1:D:180:ARG:O	2.37	0.43
1:G:36:TYR:CZ	1:G:40:GLN:HG3	2.53	0.43
1:G:85:ALA:HB1	1:H:120:TYR:O	2.19	0.43
1:G:178:LEU:HD23	1:G:178:LEU:HA	1.78	0.43
1:I:186:VAL:HG21	1:J:171:TYR:HA	2.00	0.43
1:J:115:LEU:C	1:J:117:ASP:H	2.25	0.43
1:K:24:LEU:HD22	1:K:24:LEU:HA	1.81	0.43
1:S:99:ASN:C	1:S:100:ASN:OD1	2.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:176:ASN:C	1:V:178:LEU:H	2.27	0.43
1:A:166:ILE:HD13	1:A:166:ILE:O	2.18	0.43
1:B:192:LYS:CB	1:C:45:GLN:NE2	2.81	0.43
1:D:93:VAL:HA	1:D:107:VAL:HG22	2.00	0.43
1:I:77:GLU:OE1	1:J:44:ARG:HD3	2.18	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:N:40:GLN:CA	1:N:40:GLN:NE2	2.79	0.43
1:O:100:ASN:HD22	1:O:102:LYS:H	1.67	0.43
1:O:207:SER:C	1:O:209:ARG:H	2.26	0.43
1:Q:186:VAL:HG21	1:R:171:TYR:CA	2.49	0.43
1:Q:208:CYS:HB3	1:S:33:ALA:HB2	2.01	0.43
1:R:113:VAL:CG1	1:R:154:ALA:HB1	2.47	0.43
1:R:178:LEU:HD23	1:R:178:LEU:HA	1.79	0.43
1:S:196:LEU:HD22	1:S:197:GLU:H	1.82	0.43
1:A:123:ASP:OD1	1:A:153:ARG:NH1	2.51	0.43
1:B:166:ILE:HD13	1:B:166:ILE:O	2.18	0.43
1:F:100:ASN:ND2	1:F:102:LYS:CB	2.77	0.43
1:L:115:LEU:C	1:L:117:ASP:H	2.27	0.43
1:P:128:VAL:HG12	1:P:129:SER:N	2.33	0.43
1:Q:100:ASN:HB2	1:Q:101:GLY:H	1.55	0.43
1:R:58:GLY:C	1:R:60:GLY:H	2.26	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:V:140:GLU:HG3	1:V:144:LYS:HE3	2.01	0.43
1:C:77:GLU:OE2	1:D:44:ARG:NH1	2.51	0.43
1:C:113:VAL:HG21	1:C:155:LEU:CD1	2.49	0.43
1:G:82:ASN:HB2	1:H:117:ASP:OD1	2.19	0.43
1:P:90:GLN:HG2	1:P:91:GLN:N	2.34	0.43
1:P:205:TYR:CE2	1:P:209:ARG:NH2	2.86	0.43
1:Q:40:GLN:CA	1:Q:40:GLN:NE2	2.75	0.43
1:S:192:LYS:HB2	1:T:45:GLN:NE2	2.34	0.43
1:T:134:SER:OG	1:T:137:LEU:HD23	2.18	0.43
1:V:50:GLU:HA	1:V:181:GLN:HE21	1.83	0.43
1:E:115:LEU:C	1:E:117:ASP:N	2.77	0.42
1:H:69:HIS:HB3	1:I:167:LEU:CD2	2.47	0.42
1:H:176:ASN:C	1:H:178:LEU:H	2.27	0.42
1:R:175:LEU:O	1:R:178:LEU:HB2	2.18	0.42
1:M:40:GLN:CA	1:M:40:GLN:NE2	2.81	0.42
1:N:99:ASN:C	1:N:100:ASN:OD1	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:58:GLY:C	1:P:60:GLY:H	2.26	0.42
1:R:36:TYR:CE1	1:R:40:GLN:HG2	2.54	0.42
1:S:166:ILE:HD13	1:S:166:ILE:O	2.18	0.42
1:S:176:ASN:C	1:S:178:LEU:H	2.26	0.42
1:L:44:ARG:NH1	1:V:77:GLU:OE2	2.52	0.42
1:M:99:ASN:C	1:M:100:ASN:CG	2.87	0.42
1:R:113:VAL:HG21	1:R:155:LEU:CD1	2.49	0.42
1:U:139:LEU:O	1:U:143:ARG:HG3	2.19	0.42
1:B:50:GLU:HA	1:B:181:GLN:HE22	1.85	0.42
1:D:197:GLU:HB3	1:D:200:VAL:HB	2.01	0.42
1:E:205:TYR:CE2	1:E:209:ARG:NH2	2.87	0.42
1:G:198:PRO:O	1:G:202:GLU:HG3	2.20	0.42
1:I:112:ARG:NH1	2:I:2007:HOH:O	2.51	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:N:47:LEU:N	1:N:47:LEU:CD2	2.80	0.42
1:P:189:THR:O	1:P:189:THR:HG22	2.19	0.42
1:Q:115:LEU:C	1:Q:117:ASP:N	2.76	0.42
1:S:188:LEU:HD21	1:T:171:TYR:CE1	2.54	0.42
1:U:86:HIS:HA	1:U:112:ARG:O	2.19	0.42
1:B:196:LEU:HD13	1:B:198:PRO:HG3	1.99	0.42
1:D:40:GLN:HA	1:D:40:GLN:NE2	2.20	0.42
1:F:204:ARG:NH2	1:F:204:ARG:CG	2.75	0.42
1:Q:184:LEU:HD22	1:Q:185:GLU:N	2.32	0.42
1:V:99:ASN:C	1:V:100:ASN:CG	2.86	0.42
1:B:173:ARG:HG2	1:B:173:ARG:HH11	1.84	0.42
1:E:100:ASN:HB2	1:E:101:GLY:H	1.57	0.42
1:G:90:GLN:HG2	1:G:91:GLN:N	2.35	0.42
1:I:147:VAL:HG21	1:J:124:VAL:CG2	2.43	0.42
1:J:77:GLU:OE2	1:K:44:ARG:NH1	2.52	0.42
1:L:36:TYR:CE1	1:L:40:GLN:HG2	2.55	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:O:40:GLN:CA	1:O:40:GLN:NE2	2.80	0.42
1:Q:99:ASN:C	1:Q:100:ASN:OD1	2.63	0.42
1:T:100:ASN:HB2	1:T:101:GLY:H	1.57	0.42
1:A:82:ASN:H	1:A:82:ASN:ND2	2.10	0.42
1:D:134:SER:OG	1:D:137:LEU:HD23	2.20	0.42
1:I:112:ARG:HG3	1:I:122:GLU:HB2	2.02	0.42
1:J:77:GLU:OE1	1:K:44:ARG:HD3	2.20	0.42
1:J:99:ASN:C	1:J:100:ASN:CG	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:99:ASN:C	1:J:100:ASN:OD1	2.63	0.42
1:K:100:ASN:ND2	1:K:102:LYS:CB	2.77	0.42
1:L:176:ASN:C	1:L:178:LEU:H	2.28	0.42
1:Q:77:GLU:OE2	1:R:44:ARG:NH1	2.52	0.42
1:R:173:ARG:HG2	1:R:173:ARG:HH11	1.84	0.42
1:S:24:LEU:HA	1:S:24:LEU:HD22	1.82	0.42
1:B:165:CYS:HA	2:B:2021:HOH:O	2.19	0.42
1:G:36:TYR:CE1	1:G:40:GLN:HG2	2.55	0.42
1:J:82:ASN:HD22	1:J:82:ASN:N	2.11	0.42
1:K:50:GLU:H	1:K:50:GLU:CD	2.27	0.42
1:L:134:SER:OG	1:L:137:LEU:HD23	2.20	0.42
1:M:24:LEU:HB3	1:N:30:GLN:NE2	2.34	0.42
1:Q:24:LEU:HD22	1:Q:24:LEU:HA	1.89	0.42
1:R:85:ALA:HB1	1:S:120:TYR:O	2.20	0.42
1:U:100:ASN:HB2	1:U:101:GLY:H	1.53	0.42
1:V:113:VAL:HG21	1:V:155:LEU:HD13	2.02	0.42
1:G:50:GLU:H	1:G:50:GLU:CD	2.28	0.42
1:G:186:VAL:CG2	1:H:170:ASP:C	2.90	0.42
1:N:204:ARG:HD2	1:P:36:TYR:CZ	2.55	0.42
1:U:32:THR:HG23	2:U:2002:HOH:O	2.19	0.42
1:D:204:ARG:HG3	1:D:204:ARG:HH21	1.85	0.42
1:K:192:LYS:CE	1:K:197:GLU:OE2	2.65	0.42
1:L:179:PRO:O	1:L:180:ARG:O	2.38	0.42
1:S:82:ASN:HD22	1:S:82:ASN:N	2.11	0.42
1:A:140:GLU:HG3	1:A:144:LYS:HE3	2.01	0.41
1:B:193:ARG:CG	1:B:193:ARG:NH1	2.51	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:I:140:GLU:HG3	1:I:144:LYS:HE3	2.01	0.41
1:K:113:VAL:HG21	1:K:155:LEU:CD1	2.50	0.41
1:N:99:ASN:C	1:N:100:ASN:CG	2.86	0.41
1:O:136:ALA:HB2	1:P:95:PHE:HZ	1.85	0.41
1:R:77:GLU:OE1	1:S:44:ARG:HD3	2.20	0.41
1:R:100:ASN:HD22	1:R:102:LYS:CB	2.32	0.41
1:E:173:ARG:HH11	1:E:173:ARG:HG2	1.85	0.41
1:F:181:GLN:O	1:F:181:GLN:HG3	2.20	0.41
1:G:24:LEU:HD22	1:G:24:LEU:HA	1.82	0.41
1:K:99:ASN:C	1:K:100:ASN:CG	2.87	0.41
1:N:202:GLU:O	1:N:203:ALA:C	2.62	0.41
1:O:143:ARG:NH1	1:P:94:ASP:OD2	2.53	0.41
1:O:192:LYS:CE	1:O:197:GLU:OE2	2.66	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:178:LEU:HD23	1:P:178:LEU:HA	1.78	0.41
1:Q:86:HIS:HA	1:Q:112:ARG:O	2.20	0.41
1:V:90:GLN:HG2	1:V:91:GLN:N	2.35	0.41
1:B:178:LEU:HD22	1:B:179:PRO:HD3	2.02	0.41
1:E:40:GLN:CA	1:E:40:GLN:NE2	2.81	0.41
1:E:115:LEU:C	1:E:117:ASP:H	2.26	0.41
1:I:113:VAL:HG21	1:I:155:LEU:CD1	2.50	0.41
1:I:182:LEU:HD23	1:I:182:LEU:N	2.24	0.41
1:O:140:GLU:HG3	1:O:144:LYS:HE3	2.01	0.41
1:Q:36:TYR:CE1	1:Q:40:GLN:HG2	2.55	0.41
1:S:203:ALA:CB	1:T:35:GLU:HA	2.51	0.41
1:S:208:CYS:CB	1:U:33:ALA:HB2	2.49	0.41
1:A:47:LEU:HD23	1:A:165:CYS:SG	2.61	0.41
1:A:100:ASN:HB2	1:A:101:GLY:H	1.55	0.41
1:A:112:ARG:HG3	1:A:122:GLU:HB2	2.03	0.41
1:E:193:ARG:HG2	1:E:193:ARG:HH11	1.85	0.41
1:F:47:LEU:HD23	1:F:165:CYS:SG	2.61	0.41
1:H:40:GLN:CA	1:H:40:GLN:NE2	2.81	0.41
1:J:184:LEU:HD22	1:J:184:LEU:HA	1.75	0.41
1:M:115:LEU:C	1:M:117:ASP:H	2.28	0.41
1:S:40:GLN:HA	1:S:40:GLN:NE2	2.20	0.41
1:V:204:ARG:HG3	1:V:204:ARG:HH21	1.84	0.41
1:B:105:VAL:HG11	1:B:139:LEU:HD13	2.02	0.41
1:H:208:CYS:CB	1:J:33:ALA:HB2	2.50	0.41
1:J:47:LEU:HD23	1:J:165:CYS:SG	2.60	0.41
1:K:193:ARG:CD	1:L:180:ARG:HE	2.32	0.41
1:M:207:SER:C	1:M:209:ARG:H	2.29	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
1:C:188:LEU:HA	1:C:188:LEU:HD23	1.69	0.41
1:K:57:ALA:HB2	1:K:63:VAL:CG2	2.51	0.41
1:M:195:ASP:HB3	1:N:77:GLU:HG3	2.02	0.41
1:O:115:LEU:C	1:O:117:ASP:N	2.79	0.41
1:R:77:GLU:OE2	1:S:44:ARG:NH1	2.54	0.41
1:V:123:ASP:OD1	1:V:153:ARG:NH1	2.54	0.41
1:A:24:LEU:HD22	1:A:24:LEU:HA	1.81	0.41
1:C:100:ASN:HB2	1:C:101:GLY:H	1.56	0.41
1:D:36:TYR:CE1	1:D:40:GLN:HG2	2.55	0.41
1:E:166:ILE:HD13	1:E:166:ILE:O	2.21	0.41
1:I:50:GLU:CD	1:I:50:GLU:H	2.29	0.41
1:P:36:TYR:CE1	1:P:40:GLN:HG2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:24:LEU:HD22	1:V:24:LEU:HA	1.88	0.41
1:B:70:ARG:NH1	1:B:70:ARG:CG	2.81	0.41
1:B:117:ASP:HB3	1:B:119:SER:H	1.86	0.41
1:E:79:PHE:O	1:E:83:GLY:HA3	2.21	0.41
1:E:195:ASP:O	1:E:196:LEU:C	2.62	0.41
1:H:143:ARG:NH1	1:I:94:ASP:OD2	2.54	0.41
1:I:100:ASN:ND2	1:I:102:LYS:CB	2.77	0.41
1:J:182:LEU:HD23	1:J:182:LEU:N	2.35	0.41
1:K:165:CYS:O	1:K:167:LEU:N	2.54	0.41
1:K:178:LEU:HD23	1:K:178:LEU:HA	1.90	0.41
1:L:45:GLN:HE22	1:V:192:LYS:HG3	1.85	0.41
1:M:50:GLU:H	1:M:50:GLU:CD	2.26	0.41
1:M:99:ASN:C	1:M:100:ASN:OD1	2.64	0.41
1:N:115:LEU:HD22	1:N:158:PHE:CE2	2.56	0.41
1:Q:40:GLN:HA	1:Q:40:GLN:NE2	2.16	0.41
1:Q:50:GLU:H	1:Q:50:GLU:CD	2.29	0.41
1:Q:77:GLU:OE1	1:R:44:ARG:HD3	2.21	0.41
1:Q:176:ASN:C	1:Q:178:LEU:H	2.29	0.41
1:R:193:ARG:C	1:R:194:GLN:HG3	2.45	0.41
1:S:203:ALA:HB1	1:T:35:GLU:CA	2.51	0.41
1:T:113:VAL:HG21	1:T:155:LEU:CD1	2.50	0.41
1:A:44:ARG:HD3	1:K:77:GLU:OE1	2.21	0.41
1:A:90:GLN:HG2	1:A:91:GLN:N	2.35	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:B:193:ARG:NH1	1:C:50:GLU:CD	2.79	0.41
1:C:90:GLN:HG2	1:C:91:GLN:N	2.34	0.41
1:H:47:LEU:N	1:H:47:LEU:CD2	2.83	0.41
1:H:47:LEU:HD23	1:H:165:CYS:SG	2.61	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:J:192:LYS:HG3	1:K:45:GLN:HE22	1.86	0.41
1:J:196:LEU:HD22	1:J:197:GLU:H	1.85	0.41
1:K:115:LEU:C	1:K:117:ASP:H	2.27	0.41
1:L:47:LEU:HD23	1:L:165:CYS:SG	2.61	0.41
1:L:121:HIS:CD2	1:V:86:HIS:ND1	2.85	0.41
1:N:82:ASN:H	1:N:82:ASN:ND2	2.15	0.41
1:O:40:GLN:HA	1:O:40:GLN:NE2	2.21	0.41
1:P:165:CYS:O	1:P:167:LEU:N	2.54	0.41
1:R:204:ARG:HG3	1:R:204:ARG:HH21	1.85	0.41
1:S:134:SER:OG	1:S:137:LEU:HD23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:50:GLU:HA	1:T:181:GLN:HE22	1.82	0.41
1:U:113:VAL:HG12	1:U:154:ALA:HB1	2.02	0.41
1:B:36:TYR:CZ	1:K:204:ARG:HD2	2.56	0.41
1:C:202:GLU:O	1:C:203:ALA:C	2.64	0.41
1:G:113:VAL:HG21	1:G:155:LEU:CD1	2.51	0.41
1:G:192:LYS:HB2	1:H:45:GLN:NE2	2.36	0.41
1:H:182:LEU:HA	1:H:183:PRO:HD3	1.98	0.41
1:L:166:ILE:HD13	1:L:166:ILE:O	2.20	0.41
1:N:192:LYS:HB2	1:O:45:GLN:NE2	2.36	0.41
1:P:49:PRO:C	1:P:181:GLN:NE2	2.79	0.41
1:P:195:ASP:HB3	1:Q:77:GLU:HG3	2.02	0.41
1:Q:179:PRO:O	1:Q:180:ARG:C	2.64	0.41
1:R:203:ALA:HB1	1:S:35:GLU:HA	2.03	0.41
1:S:116:LYS:HE2	2:S:2001:HOH:O	2.21	0.41
1:B:178:LEU:HD23	1:B:178:LEU:HA	1.88	0.40
1:D:166:ILE:HD13	1:D:166:ILE:O	2.21	0.40
1:F:166:ILE:HD13	1:F:166:ILE:O	2.21	0.40
1:L:171:TYR:HA	1:V:186:VAL:HG21	2.04	0.40
1:O:208:CYS:HB2	1:Q:33:ALA:HB2	2.01	0.40
1:P:184:LEU:HD23	1:P:184:LEU:HA	1.87	0.40
1:S:50:GLU:CD	1:S:50:GLU:H	2.26	0.40
1:T:110:PHE:CD2	1:T:124:VAL:HG13	2.54	0.40
1:T:176:ASN:C	1:T:178:LEU:N	2.77	0.40
1:V:166:ILE:HD13	1:V:166:ILE:O	2.21	0.40
1:A:99:ASN:C	1:A:100:ASN:OD1	2.64	0.40
1:C:143:ARG:NH1	1:D:94:ASP:OD2	2.55	0.40
1:F:85:ALA:HB1	1:G:120:TYR:O	2.22	0.40
1:H:82:ASN:H	1:H:82:ASN:ND2	2.15	0.40
1:H:185:GLU:CD	1:I:173:ARG:HH12	2.28	0.40
1:N:36:TYR:CE1	1:N:40:GLN:HG2	2.56	0.40
1:O:187:ASP:OD2	1:O:187:ASP:C	2.64	0.40
1:R:99:ASN:C	1:R:100:ASN:OD1	2.65	0.40
1:S:173:ARG:HG2	1:S:173:ARG:HH11	1.86	0.40
1:T:24:LEU:HD22	1:T:24:LEU:HA	1.74	0.40
1:C:166:ILE:HD13	1:C:166:ILE:O	2.22	0.40
1:F:115:LEU:C	1:F:117:ASP:H	2.29	0.40
1:I:82:ASN:HB2	1:J:117:ASP:OD1	2.21	0.40
1:J:166:ILE:HD13	1:J:166:ILE:O	2.21	0.40
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:R:99:ASN:C	1:R:100:ASN:CG	2.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:113:VAL:HG21	1:N:155:LEU:CD1	2.51	0.40
1:O:86:HIS:ND1	1:P:121:HIS:CD2	2.86	0.40
1:P:115:LEU:HD22	1:P:158:PHE:CE2	2.56	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:A:187:ASP:OD1	1:L:177:LYS:CE	2.70	0.40
1:B:99:ASN:C	1:B:100:ASN:OD1	2.64	0.40
1:B:178:LEU:HD22	1:B:179:PRO:CD	2.52	0.40
1:G:184:LEU:CD2	1:G:185:GLU:O	2.69	0.40
1:I:196:LEU:HD12	1:I:198:PRO:HG3	2.03	0.40
1:M:24:LEU:HA	1:M:24:LEU:HD22	1.82	0.40
1:P:50:GLU:CA	1:P:181:GLN:HE22	2.30	0.40
1:P:99:ASN:C	1:P:100:ASN:CG	2.89	0.40
1:P:99:ASN:C	1:P:100:ASN:OD1	2.65	0.40
1:S:77:GLU:CD	1:T:44:ARG:HH11	2.29	0.40
1:V:181:GLN:HA	1:V:181:GLN:OE1	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	184/209 (88%)	177 (96%)	4 (2%)	3 (2%)	7	20
1	B	184/209 (88%)	178 (97%)	4 (2%)	2 (1%)	11	29
1	C	184/209 (88%)	172 (94%)	9 (5%)	3 (2%)	7	20
1	D	184/209 (88%)	173 (94%)	6 (3%)	5 (3%)	4	10
1	E	184/209 (88%)	171 (93%)	6 (3%)	7 (4%)	2	5
1	F	184/209 (88%)	171 (93%)	8 (4%)	5 (3%)	4	10
1	G	184/209 (88%)	169 (92%)	12 (6%)	3 (2%)	7	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	184/209 (88%)	171 (93%)	11 (6%)	2 (1%)	11	29
1	I	184/209 (88%)	174 (95%)	8 (4%)	2 (1%)	11	29
1	J	184/209 (88%)	175 (95%)	5 (3%)	4 (2%)	5	14
1	K	184/209 (88%)	176 (96%)	5 (3%)	3 (2%)	7	20
1	L	184/209 (88%)	175 (95%)	5 (3%)	4 (2%)	5	14
1	M	184/209 (88%)	173 (94%)	6 (3%)	5 (3%)	4	10
1	N	184/209 (88%)	173 (94%)	8 (4%)	3 (2%)	7	20
1	O	184/209 (88%)	173 (94%)	9 (5%)	2 (1%)	11	29
1	P	184/209 (88%)	179 (97%)	3 (2%)	2 (1%)	11	29
1	Q	184/209 (88%)	173 (94%)	8 (4%)	3 (2%)	7	20
1	R	184/209 (88%)	178 (97%)	4 (2%)	2 (1%)	11	29
1	S	184/209 (88%)	175 (95%)	7 (4%)	2 (1%)	11	29
1	T	184/209 (88%)	173 (94%)	8 (4%)	3 (2%)	7	20
1	U	184/209 (88%)	175 (95%)	6 (3%)	3 (2%)	7	20
1	V	184/209 (88%)	173 (94%)	9 (5%)	2 (1%)	11	29
All	All	4048/4598 (88%)	3827 (94%)	151 (4%)	70 (2%)	7	19

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
1	M	208	CYS
1	N	166	ILE
1	N	180	ARG
1	P	166	ILE

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Mol	Chain	Res	Type
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
1	F	188	LEU
1	F	189	THR
1	G	100	ASN
1	H	100	ASN

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Mol	Chain	Res	Type
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%)	137 (88%)	18 (12%)	5	13
1	B	155/169 (92%)	135 (87%)	20 (13%)	4	10
1	C	155/169 (92%)	137 (88%)	18 (12%)	5	13
1	D	155/169 (92%)	138 (89%)	17 (11%)	6	15
1	E	155/169 (92%)	137 (88%)	18 (12%)	5	13
1	F	155/169 (92%)	136 (88%)	19 (12%)	4	12
1	G	155/169 (92%)	135 (87%)	20 (13%)	4	10
1	H	155/169 (92%)	138 (89%)	17 (11%)	6	15
1	I	155/169 (92%)	137 (88%)	18 (12%)	5	13
1	J	155/169 (92%)	135 (87%)	20 (13%)	4	10
1	K	155/169 (92%)	136 (88%)	19 (12%)	4	12
1	L	155/169 (92%)	138 (89%)	17 (11%)	6	15
1	M	155/169 (92%)	137 (88%)	18 (12%)	5	13
1	N	155/169 (92%)	138 (89%)	17 (11%)	6	15
1	O	155/169 (92%)	136 (88%)	19 (12%)	4	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	P	155/169 (92%)	137 (88%)	18 (12%)	5	13
1	Q	155/169 (92%)	136 (88%)	19 (12%)	4	12
1	R	155/169 (92%)	138 (89%)	17 (11%)	6	15
1	S	155/169 (92%)	136 (88%)	19 (12%)	4	12
1	T	155/169 (92%)	137 (88%)	18 (12%)	5	13
1	U	155/169 (92%)	137 (88%)	18 (12%)	5	13
1	V	155/169 (92%)	138 (89%)	17 (11%)	6	15
All	All	3410/3718 (92%)	3009 (88%)	401 (12%)	5	13

All (401) 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	50	GLU
1	A	82	ASN
1	A	100	ASN
1	A	113	VAL
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	189	THR
1	A	208	CYS
1	B	24	LEU
1	B	40	GLN
1	B	47	LEU
1	B	50	GLU
1	B	82	ASN
1	B	100	ASN
1	B	113	VAL
1	B	115	LEU
1	B	124	VAL
1	B	139	LEU

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Mol	Chain	Res	Type
1	B	155	LEU
1	B	166	ILE
1	B	167	LEU
1	B	174	SER
1	B	175	LEU
1	B	181	GLN
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	50	GLU
1	C	82	ASN
1	C	100	ASN
1	C	113	VAL
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	50	GLU
1	D	82	ASN
1	D	100	ASN
1	D	115	LEU
1	D	124	VAL
1	D	139	LEU
1	D	155	LEU
1	D	166	ILE
1	D	167	LEU
1	D	174	SER
1	D	181	GLN

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Mol	Chain	Res	Type
1	D	182	LEU
1	D	194	GLN
1	D	199	SER
1	E	24	LEU
1	E	40	GLN
1	E	47	LEU
1	E	50	GLU
1	E	82	ASN
1	E	100	ASN
1	E	113	VAL
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	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	50	GLU
1	F	82	ASN
1	F	100	ASN
1	F	113	VAL
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	182	LEU
1	F	184	LEU
1	F	186	VAL
1	F	192	LYS
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	50	GLU
1	G	82	ASN
1	G	100	ASN
1	G	113	VAL
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	50	GLU
1	H	82	ASN
1	H	100	ASN
1	H	113	VAL
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	50	GLU
1	I	82	ASN
1	I	100	ASN
1	I	113	VAL

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Mol	Chain	Res	Type
1	I	115	LEU
1	I	124	VAL
1	I	139	LEU
1	I	155	LEU
1	I	166	ILE
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	50	GLU
1	J	82	ASN
1	J	100	ASN
1	J	113	VAL
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	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	50	GLU
1	K	82	ASN
1	K	100	ASN
1	K	113	VAL
1	K	115	LEU
1	K	124	VAL
1	K	139	LEU
1	K	155	LEU

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Mol	Chain	Res	Type
1	K	166	ILE
1	K	167	LEU
1	K	174	SER
1	K	180	ARG
1	K	182	LEU
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	50	GLU
1	L	82	ASN
1	L	100	ASN
1	L	113	VAL
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	184	LEU
1	L	196	LEU
1	L	199	SER
1	M	24	LEU
1	M	40	GLN
1	M	47	LEU
1	M	50	GLU
1	M	70	ARG
1	M	82	ASN
1	M	100	ASN
1	M	113	VAL
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	184	LEU

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Mol	Chain	Res	Type
1	M	196	LEU
1	N	24	LEU
1	N	40	GLN
1	N	47	LEU
1	N	50	GLU
1	N	82	ASN
1	N	100	ASN
1	N	113	VAL
1	N	115	LEU
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	50	GLU
1	O	82	ASN
1	O	100	ASN
1	O	113	VAL
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	O	199	SER
1	P	24	LEU
1	P	40	GLN
1	P	47	LEU
1	P	50	GLU
1	P	82	ASN

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Mol	Chain	Res	Type
1	P	100	ASN
1	P	113	VAL
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
1	P	196	LEU
1	P	202	GLU
1	Q	24	LEU
1	Q	40	GLN
1	Q	47	LEU
1	Q	50	GLU
1	Q	82	ASN
1	Q	100	ASN
1	Q	113	VAL
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	50	GLU
1	R	82	ASN
1	R	100	ASN
1	R	113	VAL
1	R	115	LEU
1	R	124	VAL
1	R	139	LEU

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Mol	Chain	Res	Type
1	R	155	LEU
1	R	166	ILE
1	R	167	LEU
1	R	174	SER
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	50	GLU
1	S	82	ASN
1	S	100	ASN
1	S	113	VAL
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	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	50	GLU
1	T	82	ASN
1	T	100	ASN
1	T	113	VAL
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	179	PRO
1	T	181	GLN

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Mol	Chain	Res	Type
1	T	184	LEU
1	T	196	LEU
1	U	24	LEU
1	U	40	GLN
1	U	47	LEU
1	U	50	GLU
1	U	82	ASN
1	U	100	ASN
1	U	113	VAL
1	U	115	LEU
1	U	124	VAL
1	U	139	LEU
1	U	155	LEU
1	U	166	ILE
1	U	167	LEU
1	U	174	SER
1	U	183	PRO
1	U	186	VAL
1	U	189	THR
1	U	196	LEU
1	V	24	LEU
1	V	40	GLN
1	V	47	LEU
1	V	50	GLU
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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (291) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	GLN

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Mol	Chain	Res	Type
1	A	30	GLN
1	A	37	GLN
1	A	40	GLN
1	A	45	GLN
1	A	61	GLN
1	A	69	HIS
1	A	82	ASN
1	A	92	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
1	B	61	GLN
1	B	69	HIS
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	37	GLN
1	C	40	GLN
1	C	45	GLN
1	C	61	GLN
1	C	82	ASN
1	C	90	GLN
1	C	92	ASN
1	C	99	ASN
1	C	100	ASN
1	C	121	HIS
1	C	164	ASN
1	C	194	GLN
1	D	28	GLN
1	D	30	GLN

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Mol	Chain	Res	Type
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	181	GLN
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	92	ASN
1	E	99	ASN
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

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Mol	Chain	Res	Type
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
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	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

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Mol	Chain	Res	Type
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
1	K	194	GLN
1	L	28	GLN
1	L	30	GLN
1	L	37	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

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Mol	Chain	Res	Type
1	M	99	ASN
1	M	100	ASN
1	M	121	HIS
1	M	164	ASN
1	M	181	GLN
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	92	ASN
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
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	100	ASN
1	P	121	HIS
1	P	164	ASN

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Mol	Chain	Res	Type
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	181	GLN
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
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	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

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Mol	Chain	Res	Type
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	99	ASN
1	U	100	ASN
1	U	121	HIS
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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	186/209 (88%)	-0.06	8 (4%) 40 36	19, 37, 80, 95	0
1	B	186/209 (88%)	-0.19	8 (4%) 40 36	14, 32, 84, 98	0
1	C	186/209 (88%)	-0.08	9 (4%) 35 32	16, 35, 82, 101	0
1	D	186/209 (88%)	0.18	12 (6%) 25 22	22, 46, 91, 105	0
1	E	186/209 (88%)	0.58	10 (5%) 31 27	32, 58, 98, 108	0
1	F	186/209 (88%)	0.95	19 (10%) 12 10	39, 67, 102, 116	0
1	G	186/209 (88%)	1.03	21 (11%) 10 8	45, 73, 105, 118	0
1	H	186/209 (88%)	1.00	17 (9%) 15 12	42, 74, 103, 120	0
1	I	186/209 (88%)	0.95	20 (10%) 11 9	41, 69, 107, 116	0
1	J	186/209 (88%)	0.58	13 (6%) 22 19	33, 61, 101, 108	0
1	K	186/209 (88%)	0.23	8 (4%) 40 36	25, 48, 96, 105	0
1	L	186/209 (88%)	-0.06	13 (6%) 22 19	18, 37, 85, 97	0
1	M	186/209 (88%)	-0.15	5 (2%) 56 53	16, 35, 81, 94	0
1	N	186/209 (88%)	-0.05	8 (4%) 40 36	19, 36, 82, 104	0
1	O	186/209 (88%)	0.07	11 (5%) 28 25	18, 38, 91, 100	0
1	P	186/209 (88%)	0.06	6 (3%) 50 46	21, 44, 91, 100	0
1	Q	186/209 (88%)	0.19	11 (5%) 28 25	23, 45, 95, 111	0
1	R	186/209 (88%)	0.09	9 (4%) 35 32	22, 43, 93, 100	0
1	S	186/209 (88%)	0.14	11 (5%) 28 25	21, 42, 91, 107	0
1	T	186/209 (88%)	0.17	9 (4%) 35 32	22, 46, 95, 109	0
1	U	186/209 (88%)	0.04	7 (3%) 44 40	21, 46, 89, 106	0
1	V	186/209 (88%)	0.07	8 (4%) 40 36	20, 42, 86, 98	0
All	All	4092/4598 (88%)	0.26	243 (5%) 28 25	14, 49, 95, 120	0

All (243) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	100	ASN	6.7
1	Q	209	ARG	5.0
1	L	184	LEU	4.8
1	B	99	ASN	4.7
1	B	100	ASN	4.5
1	I	60	GLY	4.2
1	I	182	LEU	4.2
1	N	58	GLY	3.9
1	A	184	LEU	3.8
1	I	184	LEU	3.7
1	K	184	LEU	3.7
1	E	58	GLY	3.7
1	L	60	GLY	3.7
1	A	24	LEU	3.6
1	L	180	ARG	3.6
1	D	184	LEU	3.6
1	C	100	ASN	3.6
1	S	100	ASN	3.5
1	G	182	LEU	3.5
1	R	100	ASN	3.4
1	O	181	GLN	3.4
1	H	184	LEU	3.4
1	E	208	CYS	3.3
1	E	167	LEU	3.3
1	U	100	ASN	3.2
1	L	182	LEU	3.2
1	I	64	CYS	3.2
1	H	183	PRO	3.2
1	G	48	GLY	3.2
1	B	24	LEU	3.1
1	Q	208	CYS	3.1
1	T	205	TYR	3.1
1	I	62	LYS	3.1
1	K	209	ARG	3.1
1	O	24	LEU	3.1
1	M	60	GLY	3.1
1	O	60	GLY	3.1
1	K	182	LEU	3.1
1	R	184	LEU	3.1
1	S	24	LEU	3.1
1	S	99	ASN	3.1
1	I	179	PRO	3.1
1	J	49	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
1	J	59	GLY	3.1
1	Q	182	LEU	3.0
1	L	99	ASN	3.0
1	R	99	ASN	3.0
1	J	184	LEU	3.0
1	P	24	LEU	3.0
1	Q	184	LEU	3.0
1	V	24	LEU	3.0
1	N	99	ASN	3.0
1	V	166	ILE	3.0
1	S	34	GLU	3.0
1	D	176	ASN	3.0
1	Q	181	GLN	3.0
1	C	57	ALA	3.0
1	A	209	ARG	2.9
1	D	182	LEU	2.9
1	G	179	PRO	2.9
1	L	176	ASN	2.9
1	L	209	ARG	2.9
1	I	58	GLY	2.9
1	G	24	LEU	2.9
1	H	47	LEU	2.9
1	I	175	LEU	2.9
1	T	179	PRO	2.9
1	O	99	ASN	2.9
1	G	60	GLY	2.9
1	B	182	LEU	2.9
1	I	177	LYS	2.9
1	I	63	VAL	2.9
1	U	181	GLN	2.8
1	D	24	LEU	2.8
1	H	167	LEU	2.8
1	O	184	LEU	2.8
1	R	24	LEU	2.8
1	G	186	VAL	2.8
1	P	209	ARG	2.8
1	F	47	LEU	2.8
1	D	208	CYS	2.8
1	Q	205	TYR	2.8
1	E	181	GLN	2.8
1	G	181	GLN	2.8
1	E	100	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	G	184	LEU	2.7
1	L	57	ALA	2.7
1	I	183	PRO	2.7
1	C	61	GLN	2.7
1	E	24	LEU	2.7
1	N	100	ASN	2.7
1	H	104	TYR	2.7
1	P	181	GLN	2.7
1	F	184	LEU	2.7
1	F	178	LEU	2.7
1	M	173	ARG	2.7
1	R	180	ARG	2.7
1	Q	100	ASN	2.7
1	C	177	LYS	2.7
1	V	179	PRO	2.7
1	H	205	TYR	2.6
1	J	208	CYS	2.6
1	V	167	LEU	2.6
1	E	184	LEU	2.6
1	K	167	LEU	2.6
1	B	58	GLY	2.6
1	J	60	GLY	2.6
1	O	185	GLU	2.6
1	L	183	PRO	2.6
1	T	184	LEU	2.6
1	G	209	ARG	2.6
1	I	59	GLY	2.6
1	L	179	PRO	2.6
1	H	208	CYS	2.6
1	I	186	VAL	2.6
1	I	100	ASN	2.6
1	D	207	SER	2.5
1	H	207	SER	2.5
1	G	56	MET	2.5
1	J	182	LEU	2.5
1	A	58	GLY	2.5
1	R	181	GLN	2.5
1	P	182	LEU	2.5
1	E	205	TYR	2.5
1	Q	183	PRO	2.5
1	A	100	ASN	2.5
1	F	166	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	F	182	LEU	2.5
1	V	184	LEU	2.5
1	G	57	ALA	2.5
1	L	100	ASN	2.5
1	V	100	ASN	2.5
1	F	29	CYS	2.5
1	C	209	ARG	2.5
1	I	178	LEU	2.5
1	H	48	GLY	2.5
1	H	181	GLN	2.5
1	A	182	LEU	2.4
1	N	182	LEU	2.4
1	U	208	CYS	2.4
1	F	56	MET	2.4
1	S	59	GLY	2.4
1	G	34	GLU	2.4
1	H	186	VAL	2.4
1	P	184	LEU	2.4
1	M	99	ASN	2.4
1	Q	207	SER	2.4
1	C	208	CYS	2.4
1	F	183	PRO	2.4
1	A	61	GLN	2.4
1	H	182	LEU	2.4
1	G	99	ASN	2.4
1	F	24	LEU	2.3
1	J	167	LEU	2.3
1	O	182	LEU	2.3
1	D	58	GLY	2.3
1	H	209	ARG	2.3
1	N	180	ARG	2.3
1	F	175	LEU	2.3
1	J	24	LEU	2.3
1	J	57	ALA	2.3
1	S	184	LEU	2.3
1	F	185	GLU	2.3
1	I	37	GLN	2.3
1	J	29	CYS	2.3
1	C	24	LEU	2.3
1	I	24	LEU	2.3
1	F	205	TYR	2.3
1	I	176	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	O	176	ASN	2.3
1	T	207	SER	2.3
1	H	49	PRO	2.3
1	N	61	GLN	2.3
1	G	98	LEU	2.3
1	L	208	CYS	2.3
1	U	167	LEU	2.3
1	V	182	LEU	2.3
1	D	185	GLU	2.3
1	S	185	GLU	2.3
1	M	100	ASN	2.3
1	T	100	ASN	2.3
1	Q	58	GLY	2.3
1	Q	131	GLY	2.3
1	H	24	LEU	2.3
1	C	99	ASN	2.2
1	K	99	ASN	2.2
1	K	58	GLY	2.2
1	D	188	LEU	2.2
1	U	186	VAL	2.2
1	F	136	ALA	2.2
1	T	56	MET	2.2
1	G	64	CYS	2.2
1	D	100	ASN	2.2
1	U	209	ARG	2.2
1	T	183	PRO	2.2
1	J	58	GLY	2.2
1	T	57	ALA	2.2
1	I	209	ARG	2.2
1	O	173	ARG	2.2
1	S	180	ARG	2.2
1	H	171	TYR	2.2
1	R	179	PRO	2.2
1	K	174	SER	2.2
1	N	62	LYS	2.2
1	G	103	PHE	2.2
1	V	185	GLU	2.2
1	D	194	GLN	2.2
1	F	58	GLY	2.2
1	F	60	GLY	2.2
1	F	99	ASN	2.1
1	E	182	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	I	56	MET	2.1
1	A	59	GLY	2.1
1	G	204	ARG	2.1
1	E	179	PRO	2.1
1	G	183	PRO	2.1
1	K	183	PRO	2.1
1	G	100	ASN	2.1
1	J	45	GLN	2.1
1	J	61	GLN	2.1
1	S	182	LEU	2.1
1	O	180	ARG	2.1
1	G	177	LYS	2.1
1	L	61	GLN	2.1
1	U	182	LEU	2.1
1	C	59	GLY	2.1
1	F	180	ARG	2.1
1	S	57	ALA	2.1
1	F	133	LYS	2.1
1	F	37	GLN	2.1
1	B	184	LEU	2.1
1	R	182	LEU	2.1
1	D	205	TYR	2.1
1	G	158	PHE	2.1
1	M	57	ALA	2.0
1	H	179	PRO	2.0
1	S	183	PRO	2.0
1	B	208	CYS	2.0
1	T	29	CYS	2.0
1	P	178	LEU	2.0
1	N	101	GLY	2.0
1	B	209	ARG	2.0
1	R	186	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.