



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 02:42 AM UTC

PDB ID : 7EY9 / pdb_00007ey9
EMDB ID : EMD-31319
Title : tail proteins
Authors : Liu, H.R.; Chen, W.Y.
Deposited on : 2021-05-30
Resolution : 3.40 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

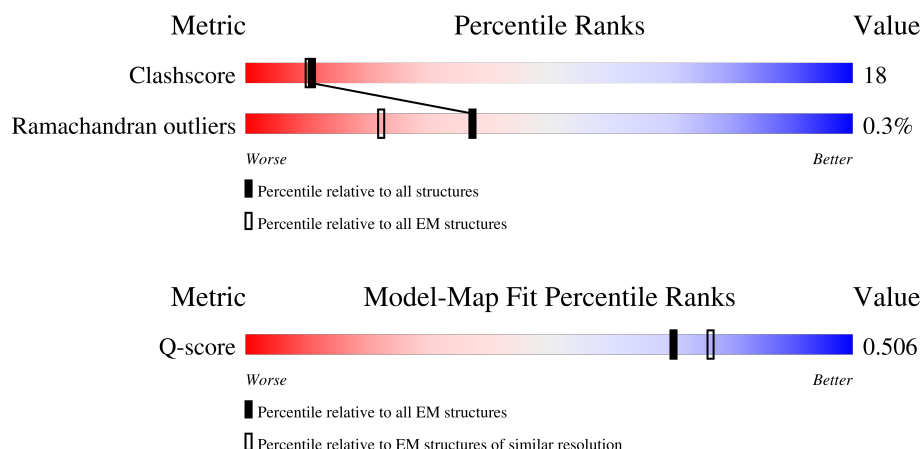
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	553	
1	b	553	
1	c	553	
1	d	553	
1	e	553	

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Mol	Chain	Length	Quality of chain
1	f	553	
1	g	553	
1	h	553	
1	i	553	
1	j	553	
1	k	553	
1	l	553	
1	m	553	
1	n	553	
1	o	553	
1	p	553	
1	q	553	
1	r	553	
2	s	794	
2	t	794	
2	u	794	
2	v	794	
2	w	794	
2	x	794	
3	M	196	
3	N	196	
3	O	196	
3	P	196	
3	Q	196	
3	R	196	

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Mol	Chain	Length	Quality of chain
3	S	196	66%32%..
3	T	196	64%33%..
3	U	196	65%32%..
3	V	196	64%33%..
3	W	196	66%31%..
3	X	196	63%34%..

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 76038 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Tail fiber protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	141	Total	C	N	O	S	0	0
			1115	698	201	215	1		
1	b	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		
1	c	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		
1	d	141	Total	C	N	O	S	0	0
			1115	698	201	215	1		
1	e	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		
1	f	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		
1	g	141	Total	C	N	O	S	0	0
			1115	698	201	215	1		
1	h	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		
1	i	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		
1	j	141	Total	C	N	O	S	0	0
			1115	698	201	215	1		
1	k	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		
1	l	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		
1	m	141	Total	C	N	O	S	0	0
			1115	698	201	215	1		
1	n	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		
1	o	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		
1	p	141	Total	C	N	O	S	0	0
			1115	698	201	215	1		
1	q	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	r	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		

- Molecule 2 is a protein called Tail tubular protein gp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	s	792	Total	C	N	O	S	0	0
			6308	4000	1086	1207	15		
2	t	792	Total	C	N	O	S	0	0
			6308	4000	1086	1207	15		
2	u	792	Total	C	N	O	S	0	0
			6308	4000	1086	1207	15		
2	v	792	Total	C	N	O	S	0	0
			6308	4000	1086	1207	15		
2	w	792	Total	C	N	O	S	0	0
			6308	4000	1086	1207	15		
2	x	792	Total	C	N	O	S	0	0
			6308	4000	1086	1207	15		

- Molecule 3 is a protein called Tail tubular protein gp11.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
3	N	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
3	O	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
3	P	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
3	Q	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
3	R	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
3	S	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
3	T	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
3	U	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
3	V	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		

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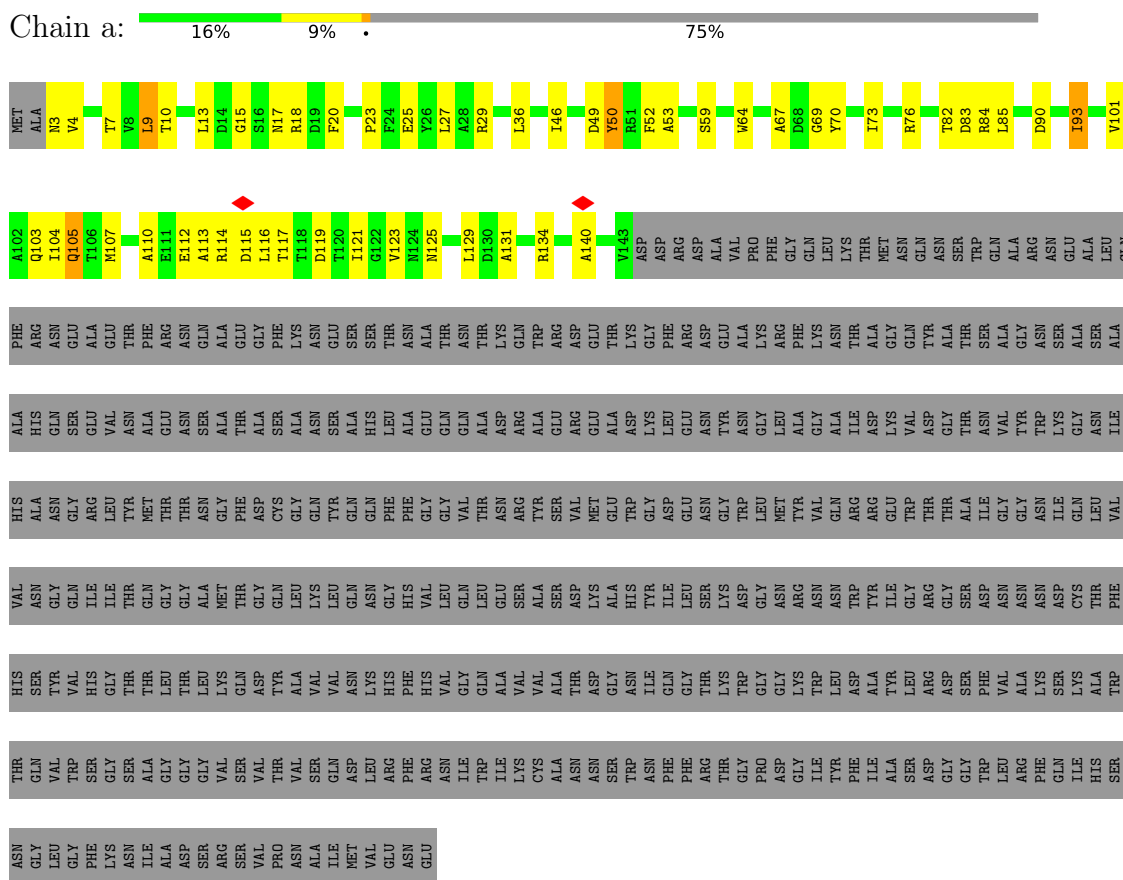
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	W	194	Total	C	N	O	S	0	0
			1546	960	262	316	8		
3	X	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		

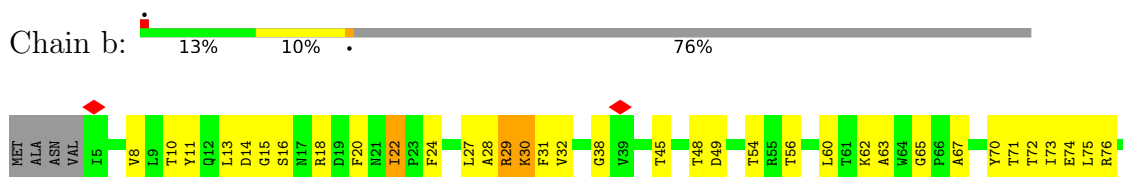
3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

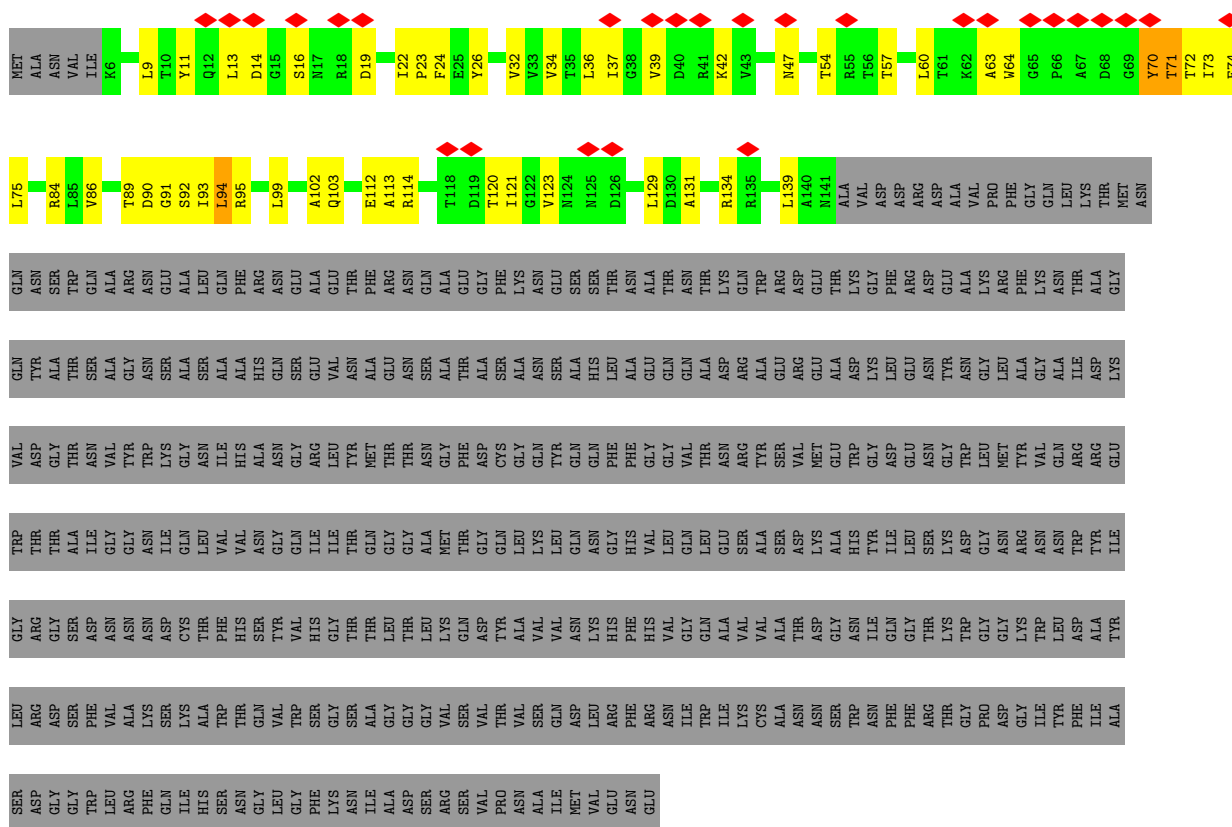
• Molecule 1: Tail fiber protein



• Molecule 1: Tail fiber protein



- Molecule 1: Tail fiber protein

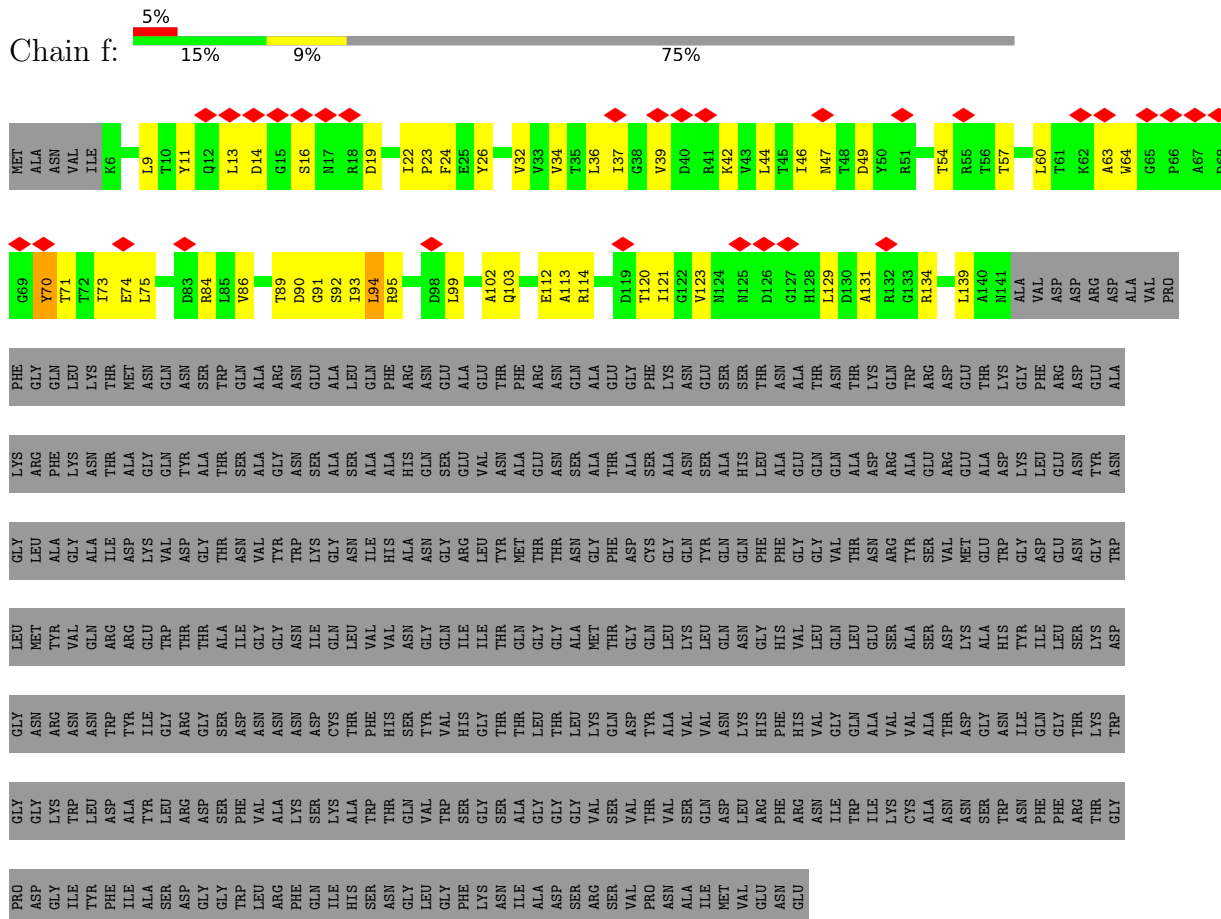


- Molecule 1: Tail fiber protein

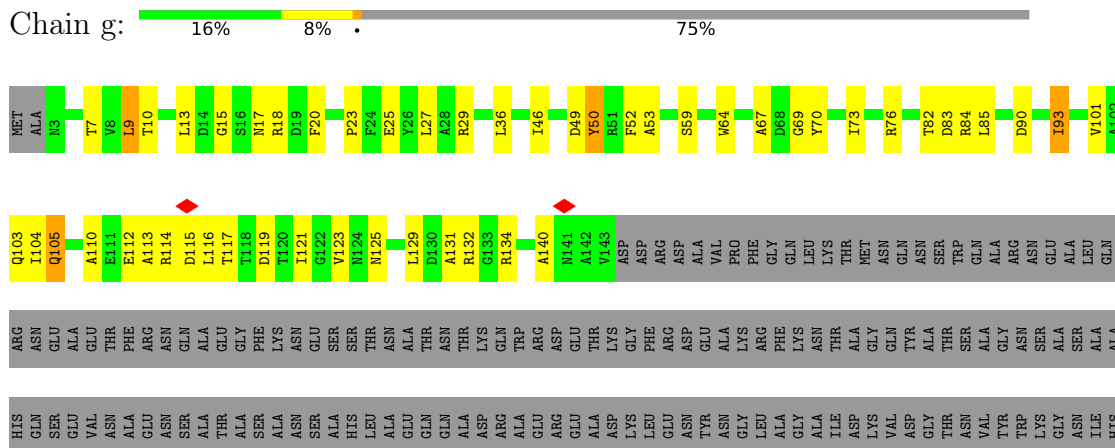


[illegible]

- Molecule 1: Tail fiber protein

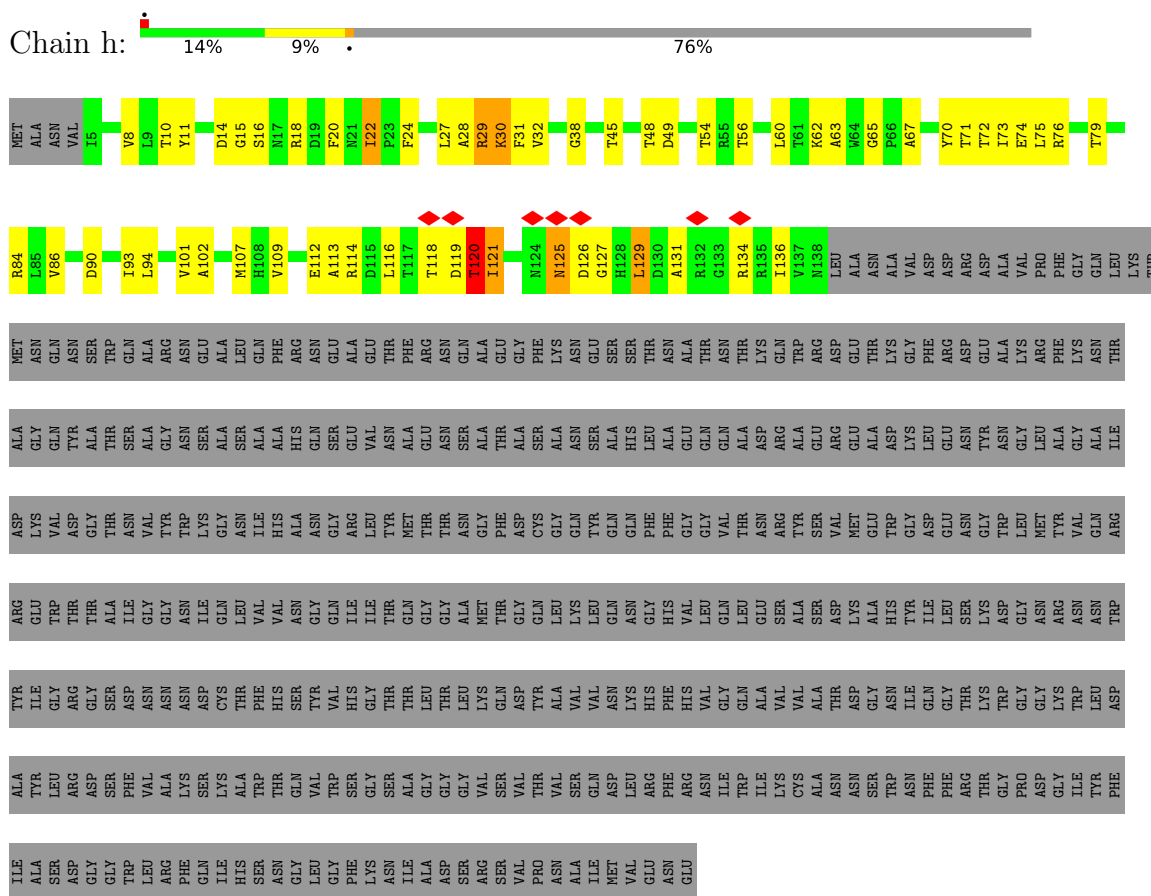


- Molecule 1: Tail fiber protein

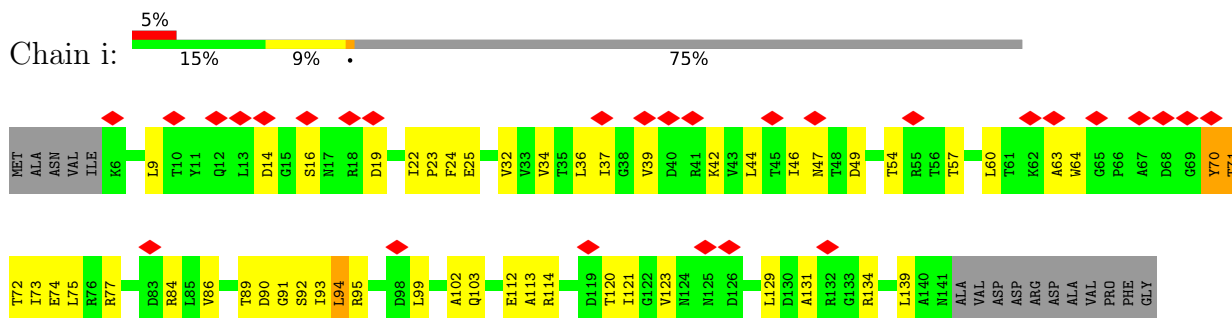


GLN	VAL	GLN	SER	ASN	ALA
VAL	TRP	GLN	TYR	GLY	ASN
TRP	SER	LYS	HIS	ILE	ARG
GLY	SER	GLY	THR	THR	TYR
ALA	ALA	ASN	THR	GLN	MET
GLY	GLY	ALA	LEU	GLY	THR
ASP	ASP	ASP	THR	GLY	ASN
SER	SER	GLY	LEU	ALA	ASN
ARG	VAL	VAL	LYS	MET	GLY
SER	SER	SER	GLN	THR	PHE
VAL	VAL	ASP	ASP	GLY	ASP
THR	THR	TYR	TYR	GLN	CYS
ASN	VAL	ASN	ALA	LEU	GLY
ALA	SER	VAL	VAL	LYS	GLN
ILE	GLN	VAL	VAL	LEU	TYR
ASP	ASP	ASN	ASN	GLN	GLN
LEU	LEU	LYS	VAL	ASN	GLN
ARG	PHE	HIS	HIS	GLY	PHE
ASN	ARG	PHE	HIS	VAL	PHE
GLU	ASN	GLY	HIS	VAL	GLY
	ASN	ASN	ASN	LEU	GLY
	ILE	GLN	GLY	GLN	VAL
	TRP	GLN	GLN	LEU	THR
	ILE	ALA	VAL	GLU	ASN
	LYS	VAL	VAL	SER	ARG
	CYS	VAL	VAL	ALA	TYR
	ALA	ALA	THR	SER	SER
	ASN	ASN	ASP	ASP	VAL
	ASN	SER	ASP	LYS	MET
	SER	SER	GLY	ALA	GLU
	TRP	ASN	ASN	HIS	TRP
	ASN	ASN	ILE	TYR	GLY
	PHE	GLN	GLN	ILE	ASP
	PHE	GLY	GLY	LEU	GLU
	ARG	THR	THR	SER	ASN
	THR	LYS	TRP	ASP	GLY
	PRO	GLY	GLY	GLY	LEU
	ASP	ASP	GLY	ASN	MET
	GLY	LYS	LYS	ARG	TYR
	ILE	TRP	TRP	ASN	VAL
	PHE	LEU	ASP	ASN	GLN
	ILE	ALA	ALA	TYR	ARG
	SER	THR	LEU	ILE	GLY
	ASP	ARG	LEU	GLY	TRP
	GLY	GLY	ASP	SER	THR
	GLY	THR	PHE	ASN	THR
	THR	ALA	VAL	ASP	ALA
	ILE	GLY	THR	ILE	ILE
	LEU	ASN	ASN	ASN	GLY
	ARG	ASN	ALA	ASN	GLY
	PHE	LYS	VAL	ASN	GLY
	ILE	LYS	SER	ASN	ILE
	ILE	LYS	CYS	GLN	GLN
	HIS	ALA	THR	THR	LEU
	SER	ASN	TRP	PHE	VAL
	ASN	THR	THR	HIS	VAL

- Molecule 1: Tail fiber protein



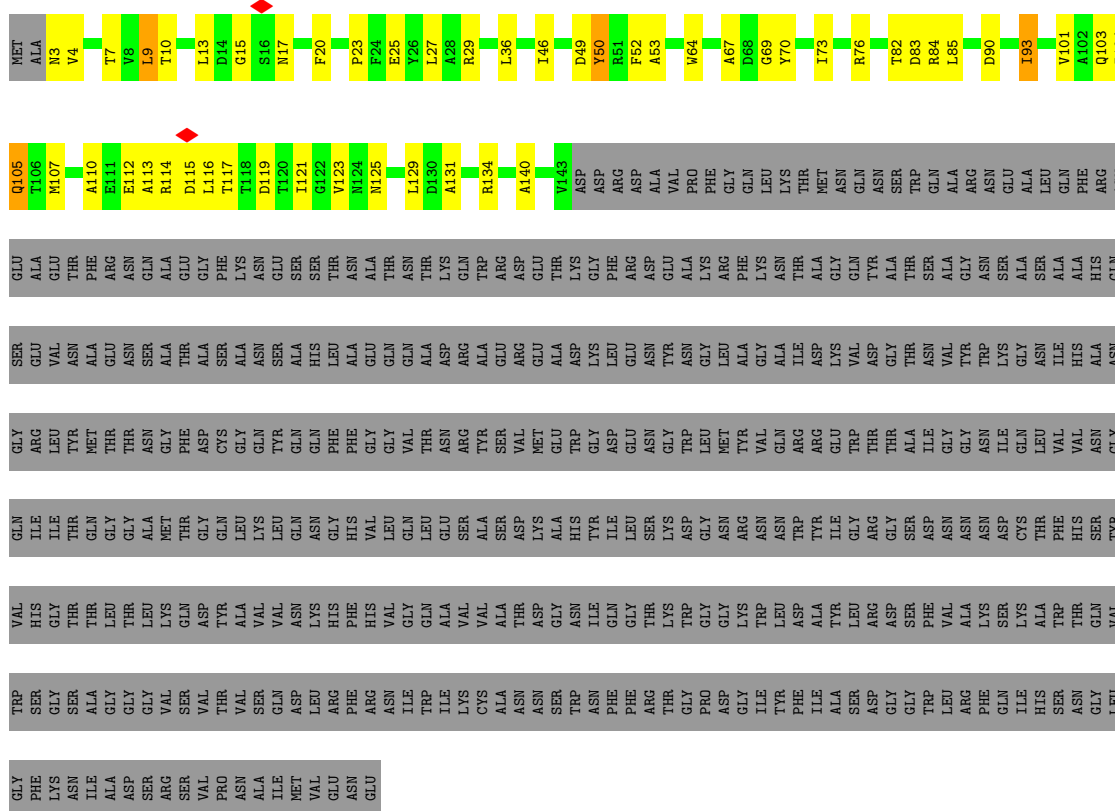
- Molecule 1: Tail fiber protein



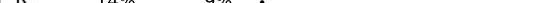
[illegible]

- Molecule 1: Tail fiber protein

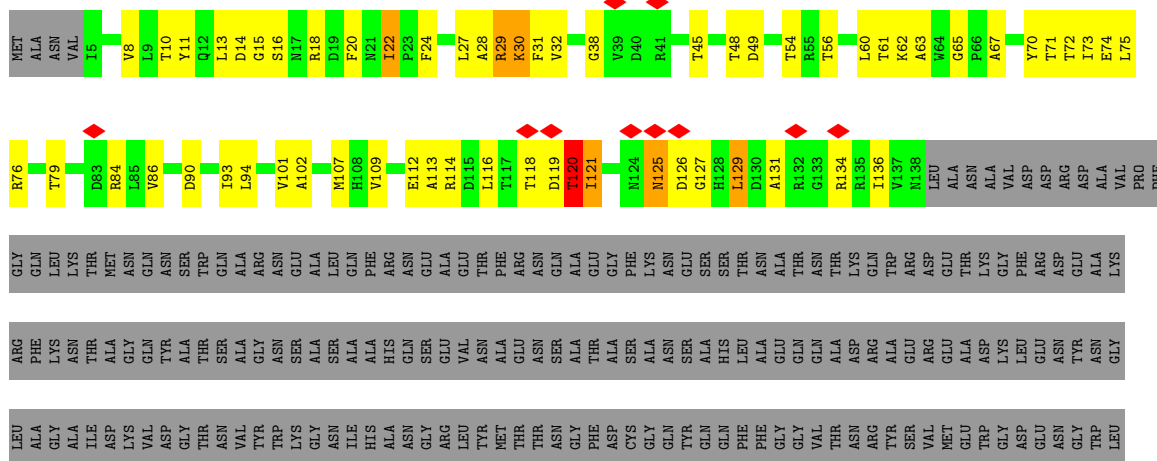
Chain j:  16% 8% . 75%



- Molecule 1: Tail fiber protein

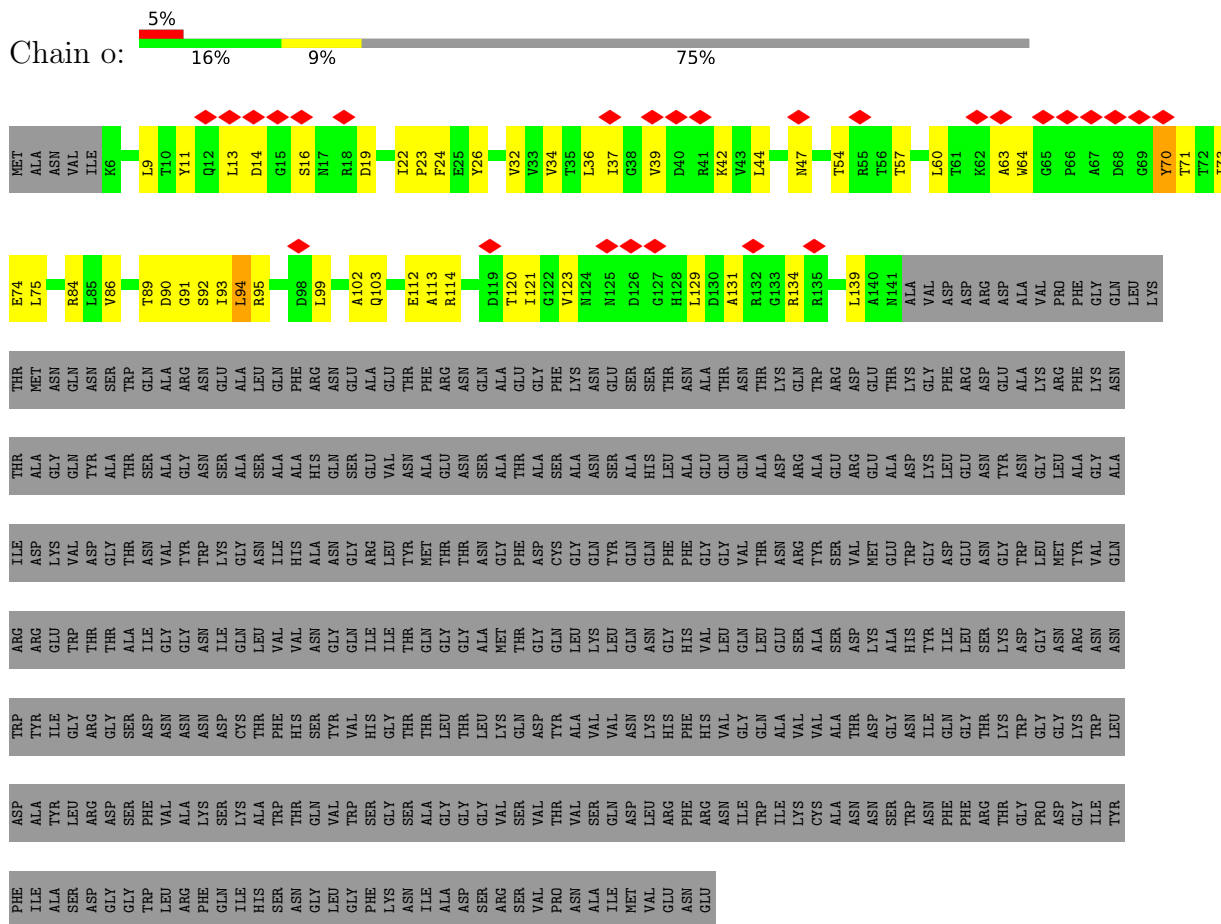
Chain k: 

Chain m: 16% 8% 75%

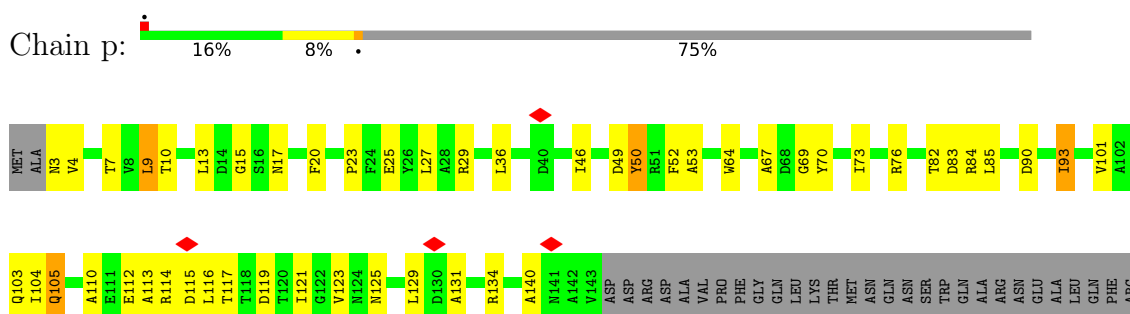


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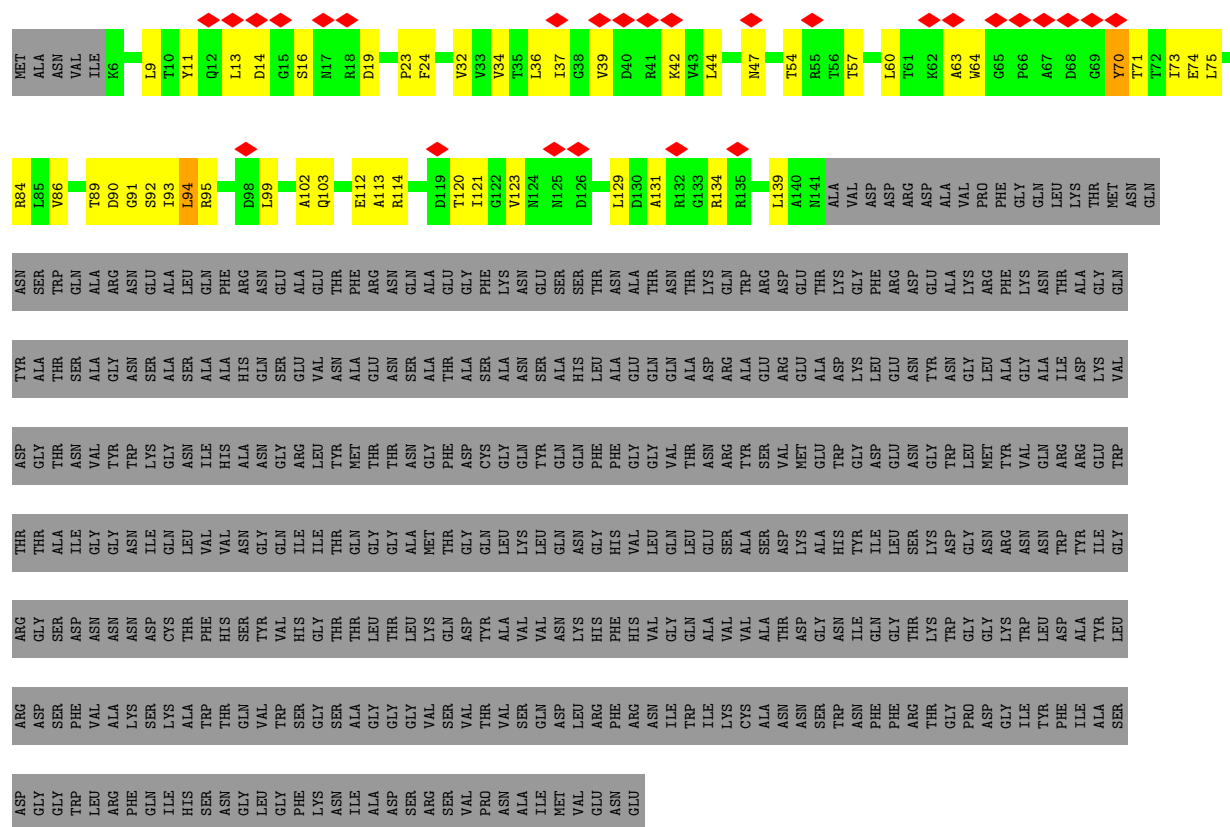
- Molecule 1: Tail fiber protein



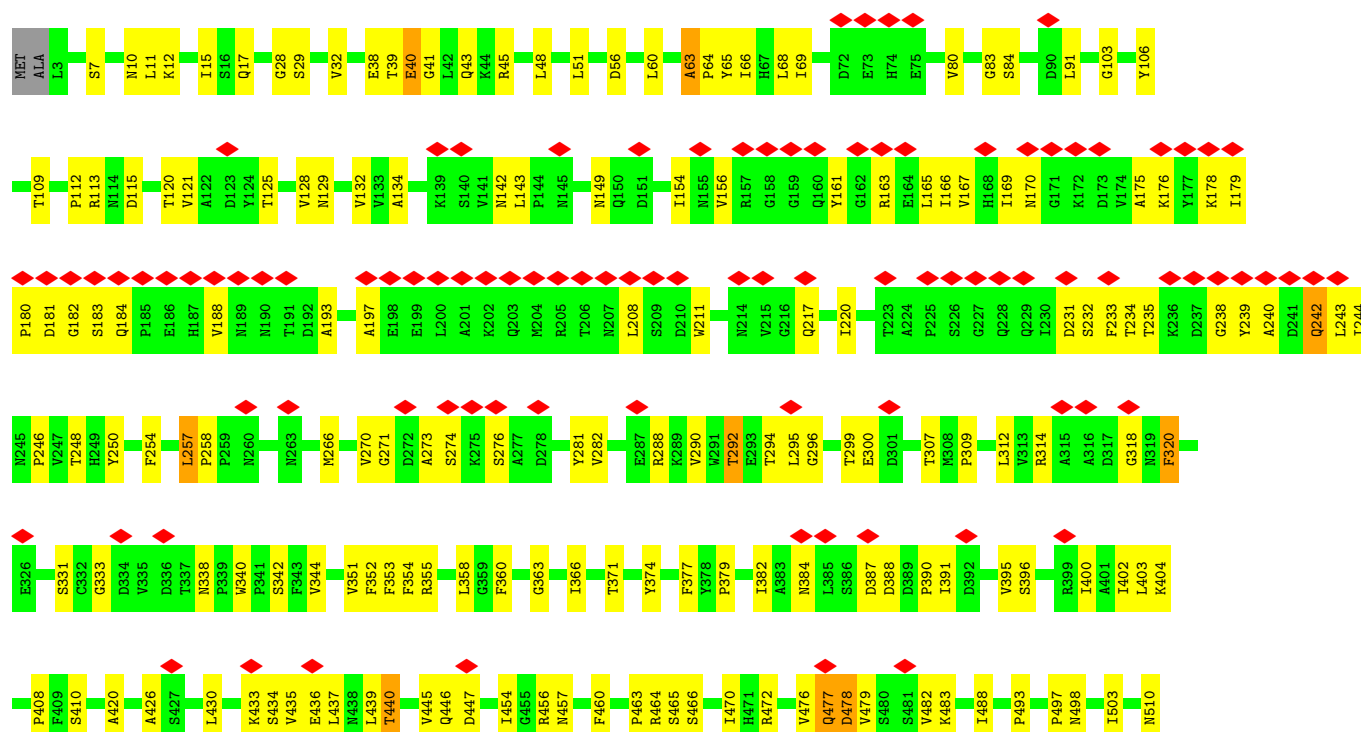
- Molecule 1: Tail fiber protein

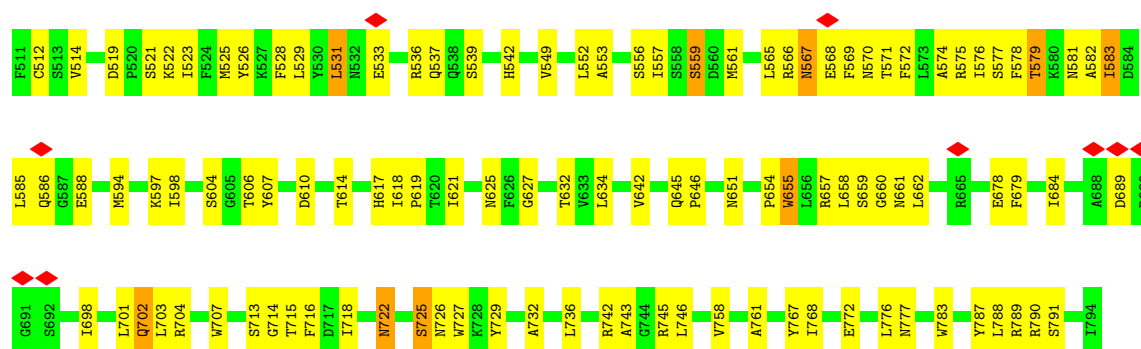




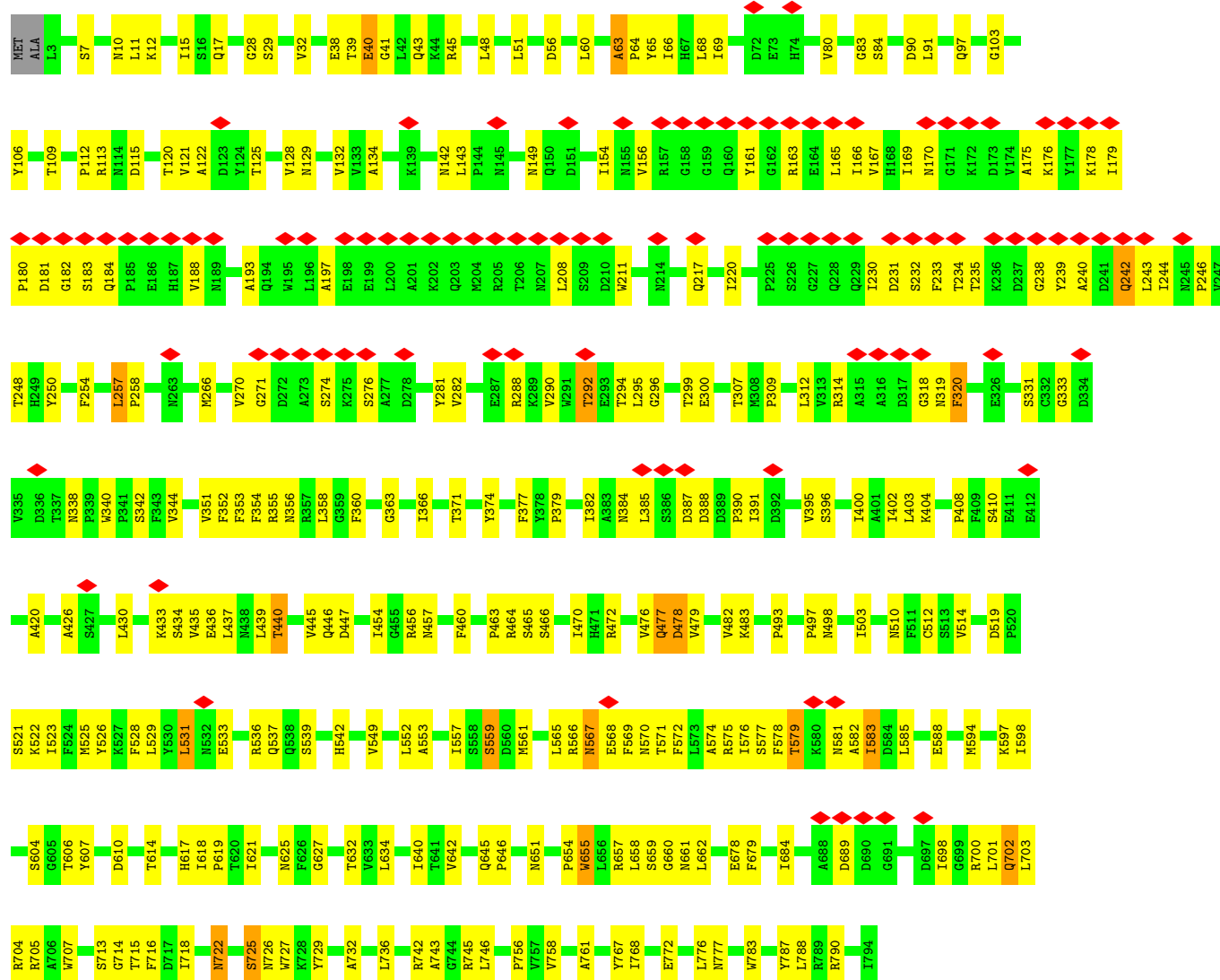


• Molecule 2: Tail tubular protein gp12



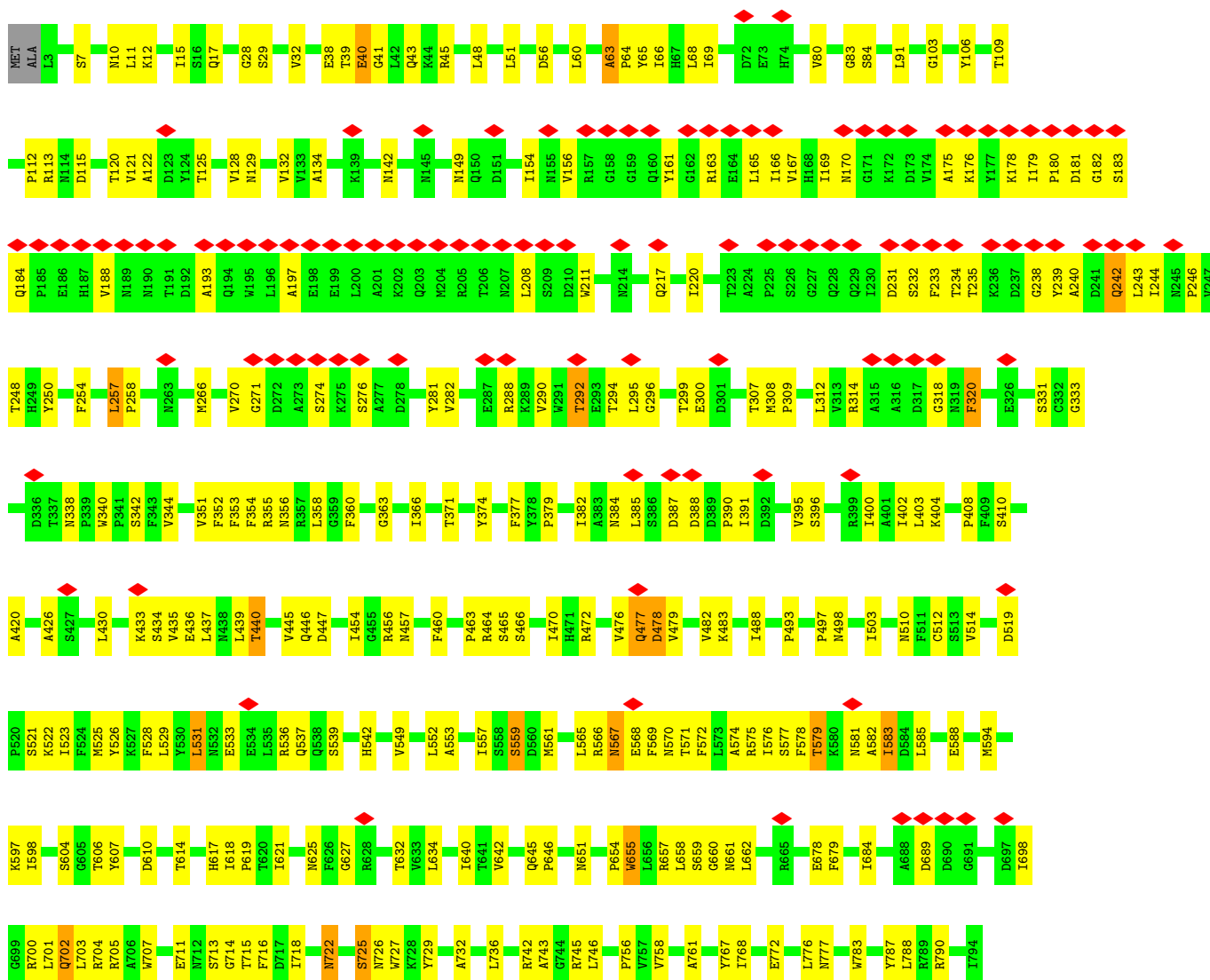


• Molecule 2: Tail tubular protein gp12

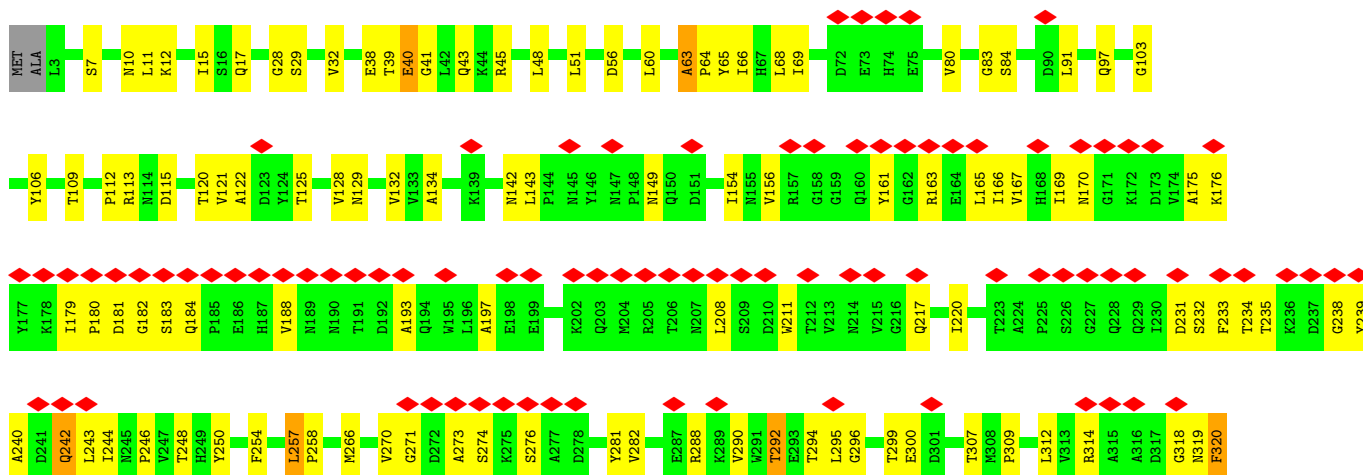


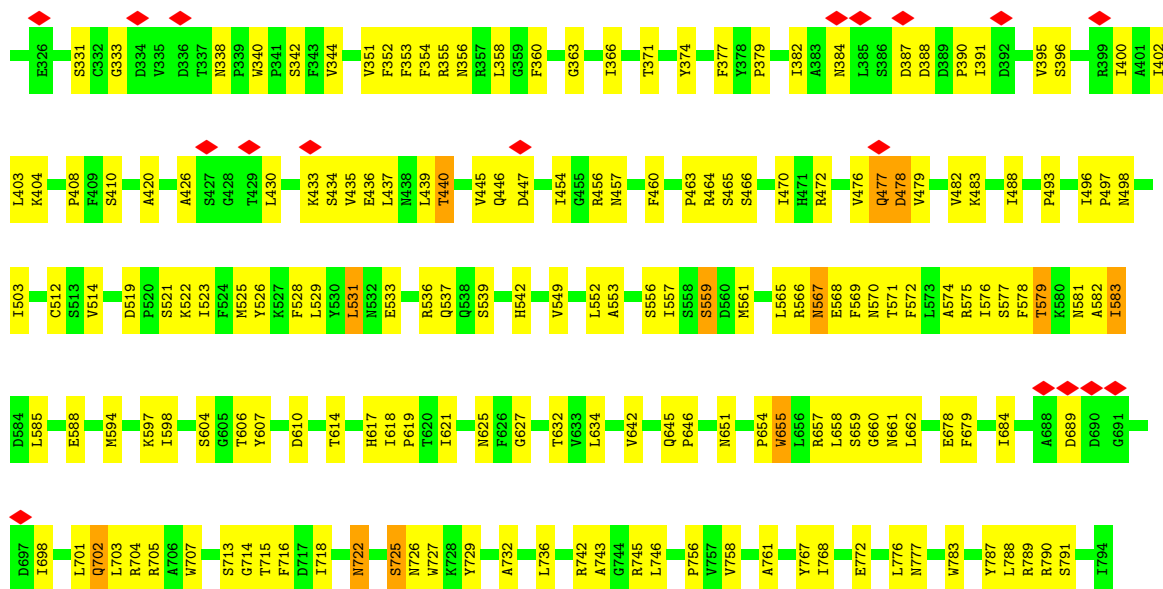
• Molecule 2: Tail tubular protein gp12



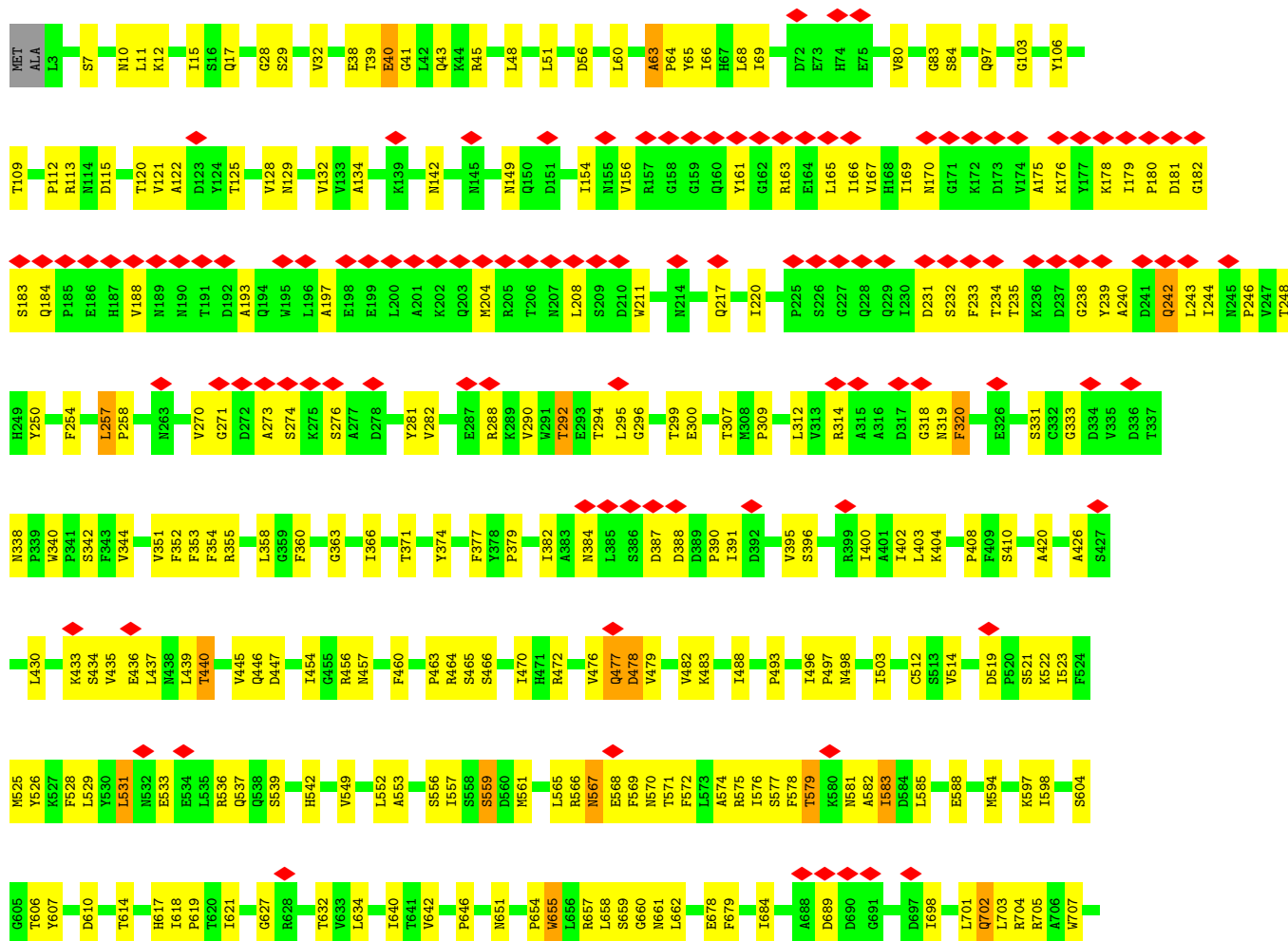


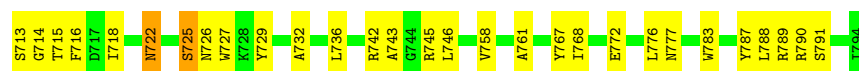
• Molecule 2: Tail tubular protein gp12



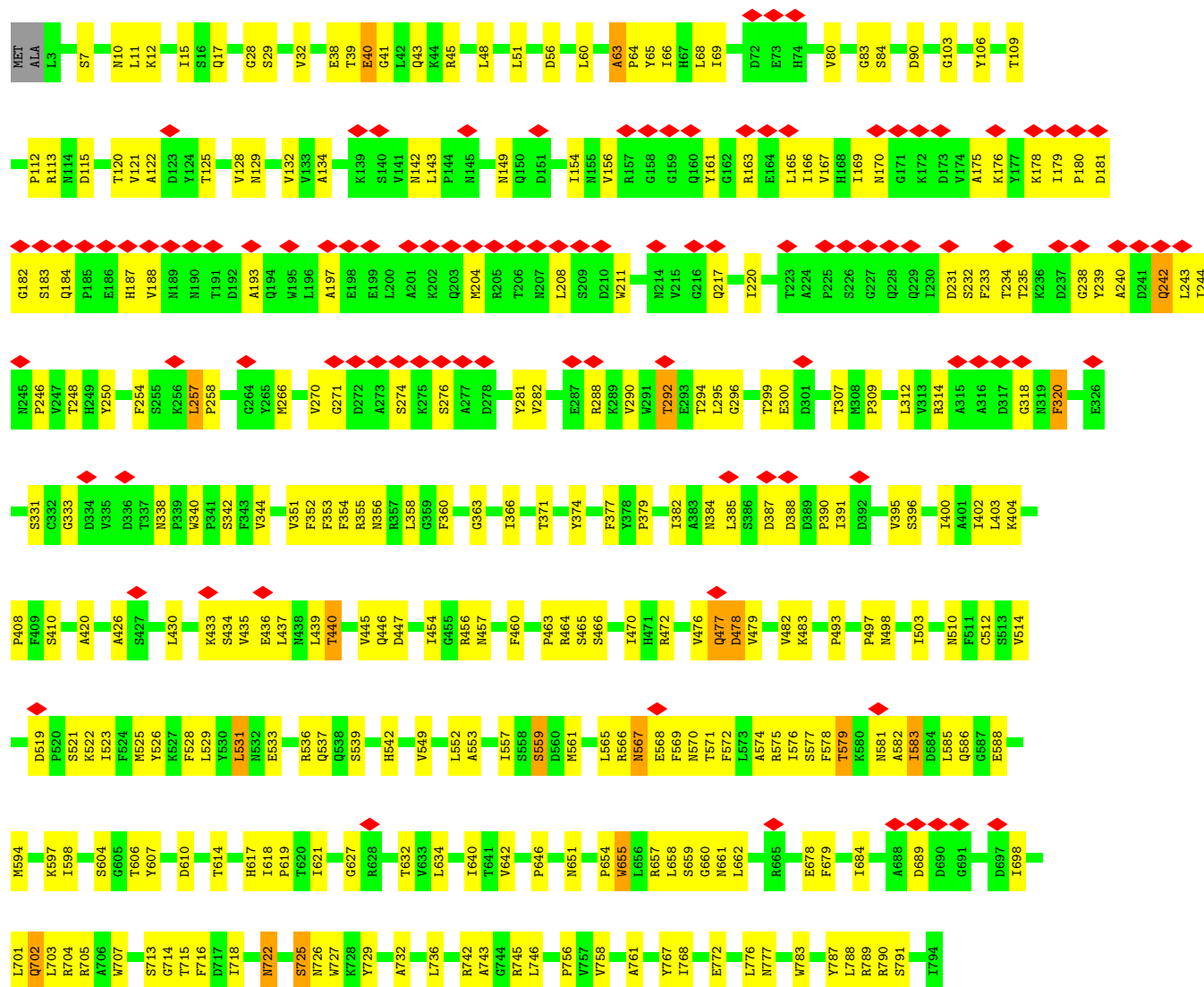


• Molecule 2: Tail tubular protein gp12

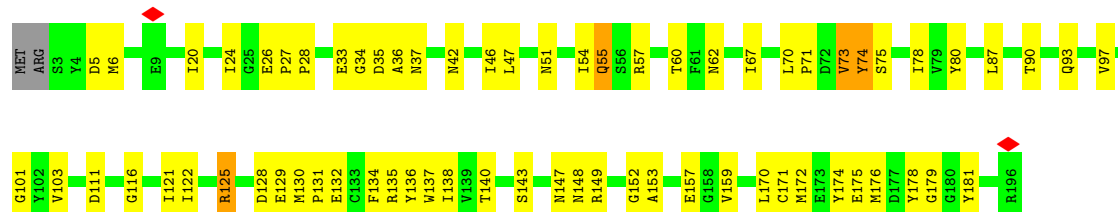




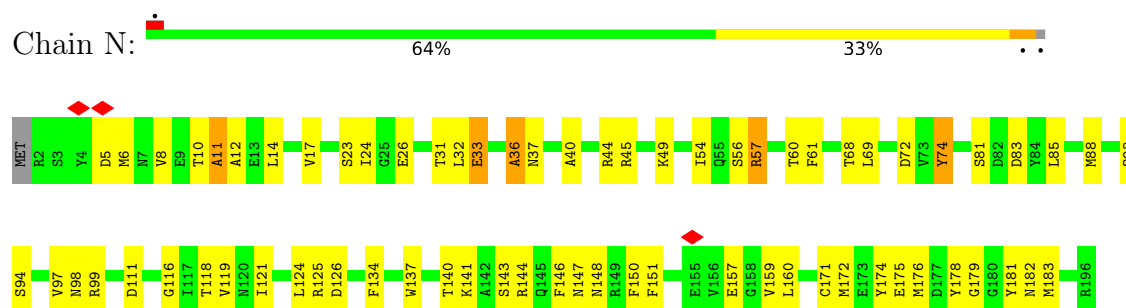
• Molecule 2: Tail tubular protein gp12



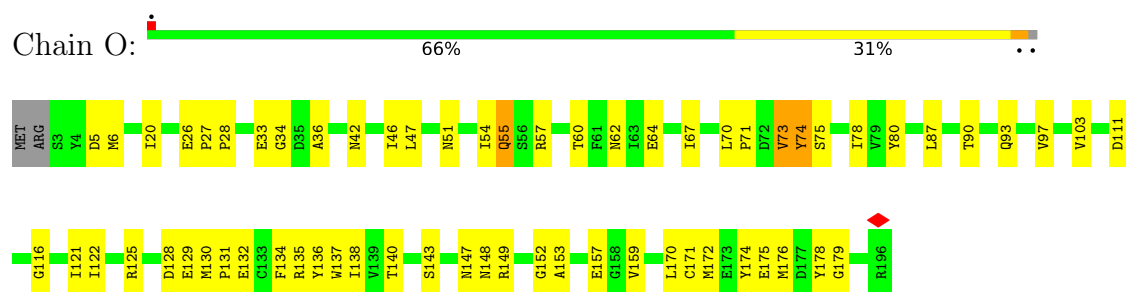
• Molecule 3: Tail tubular protein gp11



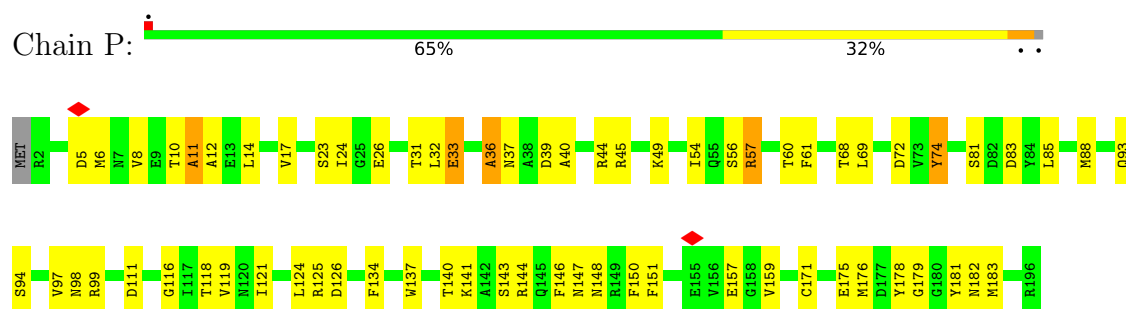
- Molecule 3: Tail tubular protein gp11



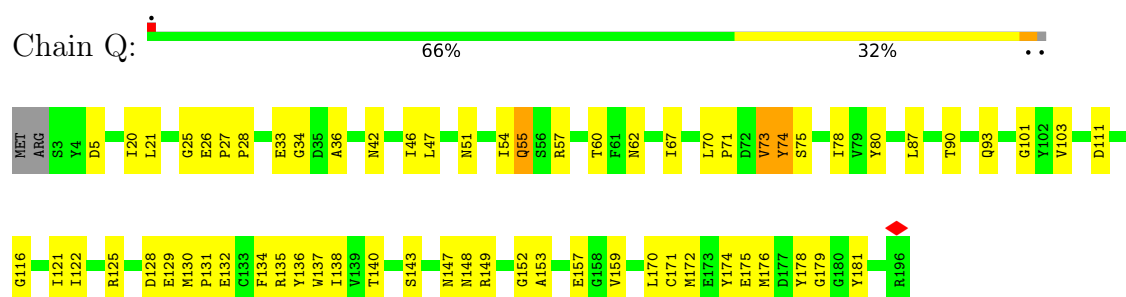
- Molecule 3: Tail tubular protein gp11



- Molecule 3: Tail tubular protein gp11

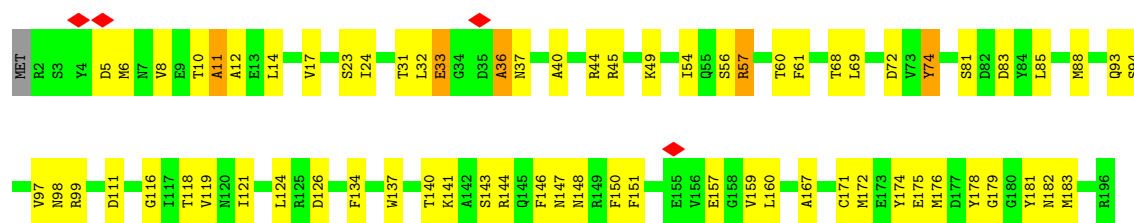


- Molecule 3: Tail tubular protein gp11

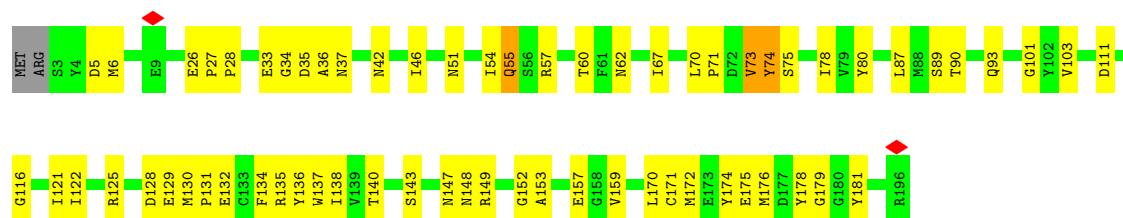


- Molecule 3: Tail tubular protein gp11

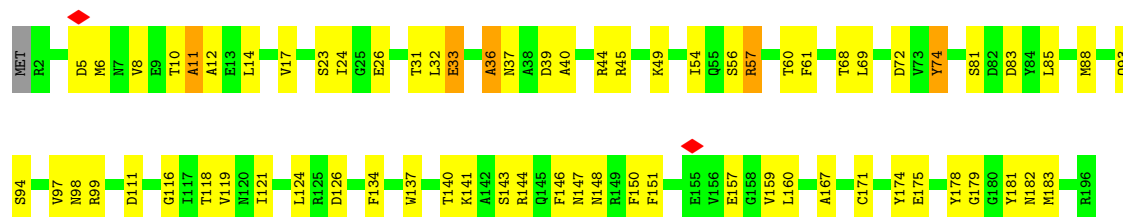




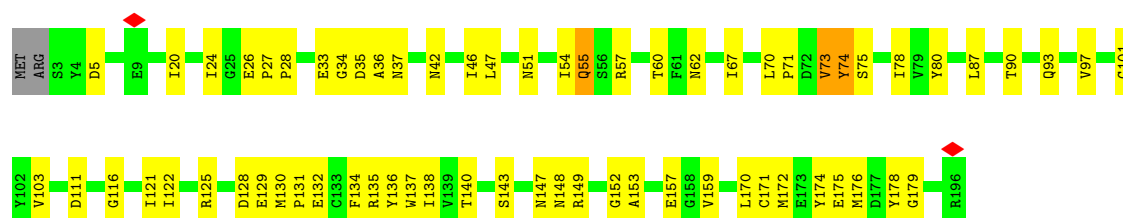
• Molecule 3: Tail tubular protein gp11



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• Molecule 3: Tail tubular protein gp11

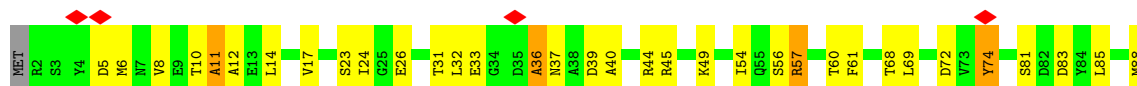




- Molecule 3: Tail tubular protein gp11



- Molecule 3: Tail tubular protein gp11



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	75068	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	64.905	Depositor
Minimum map value	-38.213	Depositor
Average map value	0.014	Depositor
Map value standard deviation	2.892	Depositor
Recommended contour level	9	Depositor
Map size (Å)	406.4, 406.4, 406.4	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.27, 1.27, 1.27	Depositor

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	1.14	2/1130 (0.2%)	1.29	13/1538 (0.8%)
1	b	0.84	0/1082	1.10	14/1471 (1.0%)
1	c	0.72	1/1095 (0.1%)	1.24	12/1489 (0.8%)
1	d	1.14	2/1130 (0.2%)	1.29	13/1538 (0.8%)
1	e	0.84	0/1082	1.10	15/1471 (1.0%)
1	f	0.72	1/1095 (0.1%)	1.24	12/1489 (0.8%)
1	g	1.14	2/1130 (0.2%)	1.29	13/1538 (0.8%)
1	h	0.84	0/1082	1.10	14/1471 (1.0%)
1	i	0.72	1/1095 (0.1%)	1.24	12/1489 (0.8%)
1	j	1.14	2/1130 (0.2%)	1.29	13/1538 (0.8%)
1	k	0.84	0/1082	1.10	14/1471 (1.0%)
1	l	0.72	1/1095 (0.1%)	1.24	12/1489 (0.8%)
1	m	1.14	2/1130 (0.2%)	1.29	13/1538 (0.8%)
1	n	0.84	0/1082	1.10	14/1471 (1.0%)
1	o	0.72	1/1095 (0.1%)	1.24	12/1489 (0.8%)
1	p	1.14	2/1130 (0.2%)	1.29	13/1538 (0.8%)
1	q	0.84	0/1082	1.10	15/1471 (1.0%)
1	r	0.72	1/1095 (0.1%)	1.24	12/1489 (0.8%)
2	s	0.92	3/6468 (0.0%)	1.23	71/8797 (0.8%)
2	t	0.91	3/6468 (0.0%)	1.23	72/8797 (0.8%)
2	u	0.91	4/6468 (0.1%)	1.23	71/8797 (0.8%)
2	v	0.92	3/6468 (0.0%)	1.23	71/8797 (0.8%)
2	w	0.91	3/6468 (0.0%)	1.23	71/8797 (0.8%)
2	x	0.92	3/6468 (0.0%)	1.23	73/8797 (0.8%)
3	M	1.00	1/1573 (0.1%)	1.14	16/2129 (0.8%)
3	N	0.94	0/1584	1.12	12/2143 (0.6%)
3	O	1.00	0/1573	1.14	15/2129 (0.7%)
3	P	0.94	0/1584	1.12	11/2143 (0.5%)
3	Q	1.01	1/1573 (0.1%)	1.13	14/2129 (0.7%)
3	R	0.94	0/1584	1.12	12/2143 (0.6%)
3	S	1.00	2/1573 (0.1%)	1.13	15/2129 (0.7%)
3	T	0.94	0/1584	1.11	12/2143 (0.6%)
3	U	1.00	1/1573 (0.1%)	1.14	14/2129 (0.7%)
3	V	0.94	0/1584	1.11	12/2143 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	W	1.00	1/1573 (0.1%)	1.13	14/2129 (0.7%)
3	X	0.94	0/1584	1.11	12/2143 (0.6%)
All	All	0.93	43/77592 (0.1%)	1.20	824/105402 (0.8%)

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	j	9	LEU	CA-C	-6.33	1.45	1.52
1	p	9	LEU	CA-C	-6.27	1.45	1.52
1	d	9	LEU	CA-C	-6.13	1.45	1.52
1	m	9	LEU	CA-C	-6.12	1.45	1.52
2	x	577	SER	C-O	-6.10	1.17	1.24
1	g	9	LEU	CA-C	-6.09	1.45	1.52
2	s	577	SER	C-O	-6.08	1.17	1.24
2	w	577	SER	C-O	-6.05	1.17	1.24
1	a	9	LEU	CA-C	-6.05	1.45	1.52
2	v	577	SER	C-O	-6.04	1.17	1.24
2	u	577	SER	C-O	-6.01	1.17	1.24
2	t	577	SER	C-O	-6.01	1.17	1.24
2	u	577	SER	CA-C	-5.67	1.45	1.52
2	s	577	SER	CA-C	-5.66	1.45	1.52
2	x	577	SER	CA-C	-5.66	1.45	1.52
2	t	577	SER	CA-C	-5.65	1.45	1.52
2	v	577	SER	CA-C	-5.63	1.45	1.52
2	w	577	SER	CA-C	-5.62	1.45	1.52
1	i	120	THR	CA-C	-5.56	1.50	1.53
1	l	120	THR	CA-C	-5.52	1.50	1.53
1	r	120	THR	CA-C	-5.48	1.50	1.53
3	Q	101	GLY	C-O	-5.43	1.20	1.24
1	p	49	ASP	CA-C	-5.43	1.48	1.52
1	c	120	THR	CA-C	-5.43	1.50	1.53
1	d	49	ASP	CA-C	-5.40	1.48	1.52
1	o	120	THR	CA-C	-5.39	1.50	1.53
1	a	49	ASP	CA-C	-5.38	1.48	1.52
1	j	49	ASP	CA-C	-5.38	1.48	1.52
1	f	120	THR	CA-C	-5.26	1.50	1.53
2	x	579	THR	CA-C	-5.26	1.46	1.52
1	m	49	ASP	CA-C	-5.25	1.48	1.52
2	s	579	THR	CA-C	-5.25	1.46	1.52
1	g	49	ASP	CA-C	-5.24	1.48	1.52
2	t	579	THR	CA-C	-5.18	1.46	1.52
2	w	579	THR	CA-C	-5.18	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	v	579	THR	CA-C	-5.18	1.46	1.52
2	u	579	THR	CA-C	-5.17	1.46	1.52
3	U	101	GLY	C-O	-5.11	1.20	1.24
3	M	101	GLY	C-O	-5.04	1.20	1.24
3	S	101	GLY	C-O	-5.04	1.20	1.24
3	S	89	SER	CA-C	-5.03	1.46	1.52
3	W	89	SER	CA-C	-5.02	1.46	1.52
2	u	711	GLU	C-O	-5.00	1.18	1.23

All (824) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	d	69	GLY	N-CA-C	-15.06	89.05	112.84
1	j	69	GLY	N-CA-C	-15.00	89.14	112.84
1	p	69	GLY	N-CA-C	-14.99	89.15	112.84
1	a	69	GLY	N-CA-C	-14.99	89.16	112.84
1	m	69	GLY	N-CA-C	-14.97	89.18	112.84
1	g	69	GLY	N-CA-C	-14.97	89.19	112.84
1	c	14	ASP	N-CA-C	12.06	124.50	111.36
1	f	14	ASP	N-CA-C	12.04	124.48	111.36
1	l	14	ASP	N-CA-C	12.02	124.46	111.36
1	i	14	ASP	N-CA-C	11.99	124.43	111.36
1	r	14	ASP	N-CA-C	11.97	124.41	111.36
1	o	14	ASP	N-CA-C	11.94	124.37	111.36
1	o	54	THR	N-CA-C	-11.32	92.28	109.14
1	c	54	THR	N-CA-C	-11.31	92.29	109.14
1	r	54	THR	N-CA-C	-11.28	92.33	109.14
1	i	54	THR	N-CA-C	-11.28	92.33	109.14
1	f	54	THR	N-CA-C	-11.27	92.35	109.14
1	l	54	THR	N-CA-C	-11.26	92.36	109.14
2	v	404	LYS	N-CA-C	11.15	123.51	111.36
2	w	404	LYS	N-CA-C	11.13	123.49	111.36
2	t	404	LYS	N-CA-C	11.08	123.43	111.36
2	x	404	LYS	N-CA-C	11.08	123.43	111.36
2	s	404	LYS	N-CA-C	11.04	123.40	111.36
2	u	404	LYS	N-CA-C	11.03	123.39	111.36
1	b	119	ASP	N-CA-C	10.94	122.78	111.07
1	e	119	ASP	N-CA-C	10.89	122.72	111.07
1	k	119	ASP	N-CA-C	10.89	122.72	111.07
1	n	119	ASP	N-CA-C	10.88	122.72	111.07
1	h	119	ASP	N-CA-C	10.86	122.69	111.07
1	q	119	ASP	N-CA-C	10.86	122.69	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	s	659	SER	N-CA-C	10.56	122.79	111.28
2	w	659	SER	N-CA-C	10.53	122.75	111.28
2	t	659	SER	N-CA-C	10.52	122.74	111.28
2	u	659	SER	N-CA-C	10.51	122.74	111.28
2	x	659	SER	N-CA-C	10.47	122.69	111.28
2	v	659	SER	N-CA-C	10.46	122.68	111.28
2	u	498	ASN	N-CA-C	10.27	122.47	111.28
2	v	498	ASN	N-CA-C	10.26	122.46	111.28
2	t	498	ASN	N-CA-C	10.24	122.44	111.28
2	w	498	ASN	N-CA-C	10.24	122.44	111.28
2	x	498	ASN	N-CA-C	10.24	122.44	111.28
2	s	498	ASN	N-CA-C	10.21	122.42	111.28
3	N	116	GLY	N-CA-C	10.02	123.51	112.29
3	T	116	GLY	N-CA-C	10.01	123.50	112.29
3	R	116	GLY	N-CA-C	9.99	123.48	112.29
3	V	116	GLY	N-CA-C	9.95	123.44	112.29
3	P	116	GLY	N-CA-C	9.92	123.40	112.29
3	X	116	GLY	N-CA-C	9.91	123.39	112.29
1	o	39	VAL	N-CA-C	-9.27	101.16	110.62
1	i	39	VAL	N-CA-C	-9.26	101.18	110.62
1	l	39	VAL	N-CA-C	-9.25	101.18	110.62
1	r	39	VAL	N-CA-C	-9.25	101.19	110.62
1	f	39	VAL	N-CA-C	-9.25	101.19	110.62
1	c	39	VAL	N-CA-C	-9.22	101.21	110.62
2	u	12	LYS	N-CA-C	9.17	121.27	111.28
2	x	12	LYS	N-CA-C	9.16	121.27	111.28
2	t	12	LYS	N-CA-C	9.15	121.25	111.28
2	s	12	LYS	N-CA-C	9.14	121.24	111.28
2	w	12	LYS	N-CA-C	9.14	121.24	111.28
2	v	12	LYS	N-CA-C	9.12	121.22	111.28
2	w	83	GLY	N-CA-C	-9.01	103.21	114.92
2	x	83	GLY	N-CA-C	-8.99	103.23	114.92
2	u	83	GLY	N-CA-C	-8.98	103.25	114.92
2	v	83	GLY	N-CA-C	-8.96	103.28	114.92
2	t	83	GLY	N-CA-C	-8.95	103.28	114.92
2	s	83	GLY	N-CA-C	-8.94	103.30	114.92
2	t	447	ASP	N-CA-C	8.90	122.86	112.72
2	w	447	ASP	N-CA-C	8.87	122.83	112.72
2	s	447	ASP	N-CA-C	8.86	122.83	112.72
2	u	447	ASP	N-CA-C	8.85	122.81	112.72
2	x	447	ASP	N-CA-C	8.83	122.79	112.72
2	v	447	ASP	N-CA-C	8.82	122.77	112.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	b	27	LEU	N-CA-C	-8.54	97.89	110.52
1	q	27	LEU	N-CA-C	-8.52	97.91	110.52
1	e	27	LEU	N-CA-C	-8.52	97.91	110.52
1	i	71	THR	N-CA-C	8.51	121.25	108.31
1	l	71	THR	N-CA-C	8.51	121.25	108.31
1	f	71	THR	N-CA-C	8.49	121.22	108.31
1	c	71	THR	N-CA-C	8.49	121.22	108.31
1	h	27	LEU	N-CA-C	-8.48	97.97	110.52
1	k	27	LEU	N-CA-C	-8.48	97.97	110.52
1	r	71	THR	N-CA-C	8.47	121.19	108.31
1	n	27	LEU	N-CA-C	-8.47	97.98	110.52
1	o	71	THR	N-CA-C	8.44	121.14	108.31
1	n	22	ILE	N-CA-C	8.35	115.81	107.55
1	b	22	ILE	N-CA-C	8.34	115.81	107.55
1	q	22	ILE	N-CA-C	8.29	115.76	107.55
1	e	22	ILE	N-CA-C	8.29	115.75	107.55
1	k	22	ILE	N-CA-C	8.28	115.75	107.55
1	h	22	ILE	N-CA-C	8.28	115.75	107.55
2	x	440	THR	N-CA-C	8.15	120.96	111.02
2	t	440	THR	N-CA-C	8.14	120.95	111.02
2	v	726	ASN	N-CA-C	8.14	122.63	111.39
2	w	440	THR	N-CA-C	8.14	120.95	111.02
2	w	726	ASN	N-CA-C	8.13	122.61	111.39
2	s	726	ASN	N-CA-C	8.13	122.60	111.39
2	x	726	ASN	N-CA-C	8.12	122.60	111.39
2	t	726	ASN	N-CA-C	8.12	122.60	111.39
2	u	726	ASN	N-CA-C	8.11	122.59	111.39
2	v	440	THR	N-CA-C	8.11	120.92	111.02
2	u	440	THR	N-CA-C	8.06	120.85	111.02
2	s	440	THR	N-CA-C	8.05	120.85	111.02
1	a	90	ASP	N-CA-C	7.95	119.95	111.28
1	j	90	ASP	N-CA-C	7.95	119.94	111.28
1	p	90	ASP	N-CA-C	7.93	119.92	111.28
2	u	41	GLY	N-CA-C	7.92	122.24	112.73
1	g	90	ASP	N-CA-C	7.91	119.91	111.28
1	m	90	ASP	N-CA-C	7.91	119.90	111.28
2	v	41	GLY	N-CA-C	7.91	122.22	112.73
2	x	41	GLY	N-CA-C	7.90	122.21	112.73
1	d	90	ASP	N-CA-C	7.89	119.89	111.28
2	w	41	GLY	N-CA-C	7.88	122.18	112.73
2	t	41	GLY	N-CA-C	7.87	122.17	112.73
1	l	131	ALA	N-CA-C	-7.86	97.78	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	x	606	THR	N-CA-C	7.84	119.83	111.28
1	f	131	ALA	N-CA-C	-7.84	97.82	110.20
2	s	41	GLY	N-CA-C	7.83	122.13	112.73
2	s	651	ASN	N-CA-C	-7.83	104.21	114.31
2	v	606	THR	N-CA-C	7.83	119.81	111.28
2	x	655	TRP	N-CA-C	7.83	121.58	110.23
2	s	655	TRP	N-CA-C	7.82	121.57	110.23
2	w	655	TRP	N-CA-C	7.82	121.57	110.23
1	r	131	ALA	N-CA-C	-7.82	97.84	110.20
2	u	606	THR	N-CA-C	7.82	119.80	111.28
2	w	651	ASN	N-CA-C	-7.82	104.22	114.31
1	o	131	ALA	N-CA-C	-7.82	97.85	110.20
2	t	606	THR	N-CA-C	7.82	119.80	111.28
2	w	606	THR	N-CA-C	7.81	119.79	111.28
2	u	651	ASN	N-CA-C	-7.81	104.24	114.31
2	s	606	THR	N-CA-C	7.81	119.79	111.28
2	t	655	TRP	N-CA-C	7.80	121.55	110.23
2	v	655	TRP	N-CA-C	7.80	121.55	110.23
1	c	131	ALA	N-CA-C	-7.80	97.87	110.20
2	x	651	ASN	N-CA-C	-7.80	104.25	114.31
2	u	655	TRP	N-CA-C	7.79	121.52	110.23
1	i	131	ALA	N-CA-C	-7.78	97.91	110.20
2	v	651	ASN	N-CA-C	-7.77	104.29	114.31
2	t	651	ASN	N-CA-C	-7.74	104.32	114.31
2	v	182	GLY	N-CA-C	7.69	124.92	114.92
2	t	182	GLY	N-CA-C	7.65	124.86	114.92
2	x	182	GLY	N-CA-C	7.64	124.86	114.92
2	s	182	GLY	N-CA-C	7.62	124.83	114.92
2	w	182	GLY	N-CA-C	7.62	124.83	114.92
2	s	478	ASP	N-CA-C	7.61	119.36	111.14
2	u	182	GLY	N-CA-C	7.61	124.81	114.92
2	w	478	ASP	N-CA-C	7.59	119.34	111.14
2	x	478	ASP	N-CA-C	7.59	119.34	111.14
2	u	478	ASP	N-CA-C	7.57	119.32	111.14
2	s	714	GLY	N-CA-C	7.57	125.19	111.03
2	u	714	GLY	N-CA-C	7.56	125.17	111.03
2	v	714	GLY	N-CA-C	7.55	125.15	111.03
2	t	478	ASP	N-CA-C	7.54	119.29	111.14
2	v	478	ASP	N-CA-C	7.54	119.29	111.14
2	t	714	GLY	N-CA-C	7.53	125.11	111.03
2	x	714	GLY	N-CA-C	7.52	125.09	111.03
2	t	295	LEU	N-CA-C	7.51	121.28	112.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	u	295	LEU	N-CA-C	7.50	121.27	112.72
2	s	295	LEU	N-CA-C	7.49	121.26	112.72
2	w	714	GLY	N-CA-C	7.49	125.03	111.03
2	v	295	LEU	N-CA-C	7.48	121.25	112.72
3	W	57	ARG	N-CA-C	-7.47	98.97	110.10
3	O	116	GLY	N-CA-C	7.46	125.52	112.83
2	x	295	LEU	N-CA-C	7.46	121.22	112.72
2	w	295	LEU	N-CA-C	7.46	121.22	112.72
3	M	116	GLY	N-CA-C	7.45	125.50	112.83
3	W	116	GLY	N-CA-C	7.45	125.50	112.83
3	S	116	GLY	N-CA-C	7.45	125.50	112.83
3	S	57	ARG	N-CA-C	-7.45	99.01	110.10
3	Q	57	ARG	N-CA-C	-7.43	99.03	110.10
3	Q	116	GLY	N-CA-C	7.42	125.45	112.83
3	M	57	ARG	N-CA-C	-7.42	99.05	110.10
3	U	116	GLY	N-CA-C	7.42	125.44	112.83
3	U	57	ARG	N-CA-C	-7.40	99.07	110.10
3	O	57	ARG	N-CA-C	-7.40	99.08	110.10
2	x	627	GLY	N-CA-C	7.36	122.19	112.77
2	w	627	GLY	N-CA-C	7.35	122.18	112.77
1	j	46	ILE	N-CA-C	7.34	120.22	111.05
2	t	627	GLY	N-CA-C	7.34	122.16	112.77
2	u	627	GLY	N-CA-C	7.33	122.16	112.77
1	d	46	ILE	N-CA-C	7.30	120.18	111.05
1	g	46	ILE	N-CA-C	7.30	120.17	111.05
2	s	627	GLY	N-CA-C	7.30	122.11	112.77
2	s	239	TYR	N-CA-C	-7.29	98.62	108.24
2	w	239	TYR	N-CA-C	-7.29	98.62	108.24
1	p	46	ILE	N-CA-C	7.28	120.15	111.05
2	x	239	TYR	N-CA-C	-7.28	98.63	108.24
1	a	46	ILE	N-CA-C	7.28	120.15	111.05
2	u	239	TYR	N-CA-C	-7.28	98.64	108.24
2	u	464	ARG	N-CA-C	-7.26	101.17	110.53
2	v	627	GLY	N-CA-C	7.26	122.06	112.77
2	t	239	TYR	N-CA-C	-7.26	98.66	108.24
2	v	239	TYR	N-CA-C	-7.25	98.67	108.24
1	m	46	ILE	N-CA-C	7.25	120.11	111.05
2	s	464	ARG	N-CA-C	-7.20	101.25	110.53
2	x	725	SER	N-CA-C	7.20	122.25	112.68
2	t	464	ARG	N-CA-C	-7.18	101.27	110.53
2	w	464	ARG	N-CA-C	-7.18	101.27	110.53
2	x	464	ARG	N-CA-C	-7.17	101.28	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	t	725	SER	N-CA-C	7.16	122.20	112.68
2	v	464	ARG	N-CA-C	-7.16	101.30	110.53
2	w	725	SER	N-CA-C	7.14	122.17	112.68
2	v	725	SER	N-CA-C	7.12	122.15	112.68
2	s	725	SER	N-CA-C	7.12	122.15	112.68
2	u	725	SER	N-CA-C	7.10	122.12	112.68
3	U	73	VAL	N-CA-C	7.08	117.22	110.42
1	n	54	THR	N-CA-C	-7.07	98.67	109.41
3	O	73	VAL	N-CA-C	7.05	117.19	110.42
1	h	54	THR	N-CA-C	-7.05	98.69	109.41
1	k	54	THR	N-CA-C	-7.04	98.71	109.41
2	w	559	SER	N-CA-C	-7.04	103.80	112.88
2	x	559	SER	N-CA-C	-7.04	103.80	112.88
2	u	559	SER	N-CA-C	-7.03	103.81	112.88
3	S	73	VAL	N-CA-C	7.03	117.17	110.42
2	s	559	SER	N-CA-C	-7.03	103.82	112.88
2	v	559	SER	N-CA-C	-7.02	103.82	112.88
3	Q	73	VAL	N-CA-C	7.01	117.15	110.42
1	e	54	THR	N-CA-C	-7.00	98.77	109.41
2	t	559	SER	N-CA-C	-7.00	103.85	112.88
3	M	73	VAL	N-CA-C	7.00	117.14	110.42
3	W	73	VAL	N-CA-C	7.00	117.14	110.42
1	j	67	ALA	N-CA-C	6.99	118.90	111.28
1	q	54	THR	N-CA-C	-6.99	98.79	109.41
1	m	67	ALA	N-CA-C	6.98	118.89	111.28
1	b	54	THR	N-CA-C	-6.98	98.80	109.41
2	w	583	ILE	N-CA-C	-6.98	97.80	107.99
1	g	67	ALA	N-CA-C	6.98	118.89	111.28
1	p	67	ALA	N-CA-C	6.98	118.89	111.28
2	x	583	ILE	N-CA-C	-6.97	97.81	107.99
2	s	583	ILE	N-CA-C	-6.96	97.82	107.99
2	t	583	ILE	N-CA-C	-6.94	97.86	107.99
2	u	583	ILE	N-CA-C	-6.93	97.88	107.99
2	v	583	ILE	N-CA-C	-6.92	97.89	107.99
1	d	67	ALA	N-CA-C	6.91	118.81	111.28
1	a	67	ALA	N-CA-C	6.90	118.80	111.28
1	i	71	THR	CB-CA-C	-6.89	108.61	116.54
1	f	71	THR	CB-CA-C	-6.88	108.62	116.54
1	c	71	THR	CB-CA-C	-6.88	108.63	116.54
2	t	45	ARG	CA-C-N	-6.85	113.33	120.38
2	t	45	ARG	C-N-CA	-6.85	113.33	120.38
1	r	71	THR	CB-CA-C	-6.83	108.68	116.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	w	45	ARG	CA-C-N	-6.83	113.35	120.38
2	w	45	ARG	C-N-CA	-6.83	113.35	120.38
1	a	17	ASN	N-CA-C	-6.82	99.80	109.96
1	p	17	ASN	N-CA-C	-6.82	99.80	109.96
1	o	71	THR	CB-CA-C	-6.82	108.70	116.54
1	l	71	THR	CB-CA-C	-6.82	108.70	116.54
2	s	45	ARG	CA-C-N	-6.82	113.36	120.38
2	s	45	ARG	C-N-CA	-6.82	113.36	120.38
1	d	17	ASN	N-CA-C	-6.81	99.81	109.96
2	v	45	ARG	CA-C-N	-6.81	113.37	120.38
2	v	45	ARG	C-N-CA	-6.81	113.37	120.38
1	m	17	ASN	N-CA-C	-6.80	99.83	109.96
1	j	17	ASN	N-CA-C	-6.80	99.83	109.96
2	t	503	ILE	N-CA-C	-6.80	97.82	107.75
2	u	503	ILE	N-CA-C	-6.80	97.83	107.75
2	u	45	ARG	CA-C-N	-6.79	113.38	120.38
2	u	45	ARG	C-N-CA	-6.79	113.38	120.38
2	x	45	ARG	CA-C-N	-6.79	113.39	120.38
2	x	45	ARG	C-N-CA	-6.79	113.39	120.38
1	g	17	ASN	N-CA-C	-6.78	99.86	109.96
2	x	503	ILE	N-CA-C	-6.77	97.87	107.75
2	s	503	ILE	N-CA-C	-6.76	97.87	107.75
2	w	503	ILE	N-CA-C	-6.75	97.89	107.75
2	v	567	ASN	CA-C-N	6.75	133.85	121.70
2	v	567	ASN	C-N-CA	6.75	133.85	121.70
3	N	126	ASP	N-CA-C	6.75	120.50	110.52
2	v	503	ILE	N-CA-C	-6.73	97.92	107.75
2	t	567	ASN	CA-C-N	6.71	133.78	121.70
2	t	567	ASN	C-N-CA	6.71	133.78	121.70
3	V	126	ASP	N-CA-C	6.71	120.46	110.52
2	s	567	ASN	CA-C-N	6.71	133.78	121.70
2	s	567	ASN	C-N-CA	6.71	133.78	121.70
2	x	567	ASN	CA-C-N	6.70	133.75	121.70
2	x	567	ASN	C-N-CA	6.70	133.75	121.70
2	u	567	ASN	CA-C-N	6.69	133.75	121.70
2	u	567	ASN	C-N-CA	6.69	133.75	121.70
2	w	567	ASN	CA-C-N	6.68	133.73	121.70
2	w	567	ASN	C-N-CA	6.68	133.73	121.70
3	X	126	ASP	N-CA-C	6.68	120.41	110.52
3	N	57	ARG	N-CA-C	-6.67	100.16	110.10
3	P	57	ARG	N-CA-C	-6.67	100.16	110.10
3	R	126	ASP	N-CA-C	6.65	120.36	110.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	U	60	THR	N-CA-C	6.65	118.53	111.28
3	T	57	ARG	N-CA-C	-6.64	100.21	110.10
3	P	126	ASP	N-CA-C	6.64	120.34	110.52
1	q	14	ASP	N-CA-C	-6.63	99.38	109.85
1	h	14	ASP	N-CA-C	-6.62	99.39	109.85
1	k	14	ASP	N-CA-C	-6.62	99.39	109.85
1	b	14	ASP	N-CA-C	-6.62	99.39	109.85
1	n	14	ASP	N-CA-C	-6.62	99.39	109.85
3	T	126	ASP	N-CA-C	6.61	120.31	110.52
3	V	57	ARG	N-CA-C	-6.61	100.25	110.10
2	s	238	GLY	N-CA-C	-6.61	106.11	115.30
3	O	60	THR	N-CA-C	6.61	118.48	111.28
3	R	57	ARG	N-CA-C	-6.60	100.27	110.10
1	e	14	ASP	N-CA-C	-6.59	99.44	109.85
3	S	60	THR	N-CA-C	6.58	118.46	111.28
3	X	57	ARG	N-CA-C	-6.58	100.30	110.10
3	Q	60	THR	N-CA-C	6.58	118.45	111.28
2	w	238	GLY	N-CA-C	-6.56	106.18	115.30
2	s	299	THR	N-CA-C	6.56	119.93	109.24
2	u	299	THR	N-CA-C	6.56	119.93	109.24
3	W	60	THR	N-CA-C	6.55	118.42	111.28
2	t	238	GLY	N-CA-C	-6.55	106.19	115.30
2	u	238	GLY	N-CA-C	-6.55	106.19	115.30
3	M	60	THR	N-CA-C	6.54	118.41	111.28
2	x	238	GLY	N-CA-C	-6.54	106.21	115.30
2	x	299	THR	N-CA-C	6.54	119.89	109.24
2	v	299	THR	N-CA-C	6.54	119.89	109.24
2	v	238	GLY	N-CA-C	-6.53	106.22	115.30
2	t	299	THR	N-CA-C	6.52	119.87	109.24
2	w	299	THR	N-CA-C	6.51	119.84	109.24
3	O	70	LEU	CA-C-N	-6.50	113.25	120.14
3	O	70	LEU	C-N-CA	-6.50	113.25	120.14
1	g	140	ALA	CB-CA-C	-6.49	109.10	116.63
1	p	140	ALA	CB-CA-C	-6.48	109.11	116.63
1	a	140	ALA	CB-CA-C	-6.48	109.12	116.63
2	s	320	PHE	N-CA-C	6.48	119.08	110.53
1	d	140	ALA	CB-CA-C	-6.47	109.12	116.63
1	m	140	ALA	CB-CA-C	-6.44	109.16	116.63
2	x	320	PHE	N-CA-C	6.44	119.03	110.53
2	t	320	PHE	N-CA-C	6.43	119.02	110.53
2	w	320	PHE	N-CA-C	6.43	119.01	110.53
1	j	140	ALA	CB-CA-C	-6.42	109.18	116.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	w	604	SER	N-CA-C	6.42	118.27	111.28
2	u	604	SER	N-CA-C	6.37	118.23	111.28
2	v	320	PHE	N-CA-C	6.36	118.93	110.53
2	s	604	SER	N-CA-C	6.36	118.21	111.28
2	u	320	PHE	N-CA-C	6.35	118.92	110.53
2	t	294	THR	N-CA-C	6.35	117.81	108.86
3	U	73	VAL	CB-CA-C	-6.35	103.84	111.97
2	v	604	SER	N-CA-C	6.35	118.20	111.28
2	t	220	ILE	N-CA-C	-6.34	98.38	107.77
2	t	604	SER	N-CA-C	6.34	118.19	111.28
2	v	294	THR	N-CA-C	6.34	117.80	108.86
1	l	70	TYR	N-CA-C	6.34	120.62	113.01
2	w	220	ILE	N-CA-C	-6.34	98.39	107.77
3	Q	73	VAL	CB-CA-C	-6.34	103.86	111.97
2	u	294	THR	N-CA-C	6.33	117.79	108.86
2	x	220	ILE	N-CA-C	-6.33	98.40	107.77
2	x	604	SER	N-CA-C	6.33	118.18	111.28
3	M	70	LEU	CA-C-N	-6.33	113.43	120.14
3	M	70	LEU	C-N-CA	-6.33	113.43	120.14
2	s	294	THR	N-CA-C	6.33	117.78	108.86
2	v	220	ILE	N-CA-C	-6.33	98.41	107.77
2	u	220	ILE	N-CA-C	-6.32	98.41	107.77
2	t	716	PHE	N-CA-C	6.31	119.83	110.48
2	s	220	ILE	N-CA-C	-6.31	98.43	107.77
1	n	125	ASN	N-CA-C	-6.31	101.77	110.35
1	f	70	TYR	N-CA-C	6.31	120.58	113.01
1	r	70	TYR	N-CA-C	6.30	120.57	113.01
3	O	73	VAL	CB-CA-C	-6.30	103.90	111.97
2	s	716	PHE	N-CA-C	6.29	119.79	110.48
1	i	70	TYR	N-CA-C	6.29	120.56	113.01
3	W	73	VAL	CB-CA-C	-6.29	103.92	111.97
3	S	73	VAL	CB-CA-C	-6.29	103.92	111.97
2	t	436	GLU	N-CA-C	6.29	120.98	113.12
1	c	70	TYR	N-CA-C	6.28	120.55	113.01
2	s	436	GLU	N-CA-C	6.28	120.97	113.12
1	h	125	ASN	N-CA-C	-6.28	101.81	110.35
1	o	70	TYR	N-CA-C	6.28	120.54	113.01
2	x	294	THR	N-CA-C	6.28	117.71	108.86
2	w	436	GLU	N-CA-C	6.28	120.97	113.12
2	v	716	PHE	N-CA-C	6.27	119.76	110.48
3	M	73	VAL	CB-CA-C	-6.27	103.95	111.97
1	e	125	ASN	N-CA-C	-6.26	101.84	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	v	436	GLU	N-CA-C	6.25	120.94	113.12
3	W	33	GLU	N-CA-C	6.25	118.10	111.28
2	w	294	THR	N-CA-C	6.25	117.67	108.86
1	b	125	ASN	N-CA-C	-6.25	101.85	110.35
1	k	125	ASN	N-CA-C	-6.25	101.85	110.35
2	u	436	GLU	N-CA-C	6.25	120.93	113.12
1	q	125	ASN	N-CA-C	-6.24	101.86	110.35
2	w	716	PHE	N-CA-C	6.24	119.72	110.48
2	u	549	VAL	N-CA-C	6.24	116.23	107.37
2	x	436	GLU	N-CA-C	6.24	120.92	113.12
2	u	716	PHE	N-CA-C	6.23	119.71	110.48
2	x	716	PHE	N-CA-C	6.23	119.70	110.48
3	Q	33	GLU	N-CA-C	6.22	118.07	111.28
2	x	549	VAL	N-CA-C	6.22	116.20	107.37
2	t	549	VAL	N-CA-C	6.21	116.18	107.37
2	v	549	VAL	N-CA-C	6.19	116.16	107.37
3	S	33	GLU	N-CA-C	6.14	117.98	111.28
2	s	549	VAL	N-CA-C	6.14	116.09	107.37
2	w	549	VAL	N-CA-C	6.14	116.09	107.37
3	M	33	GLU	N-CA-C	6.12	117.95	111.28
3	Q	70	LEU	CA-C-N	-6.11	113.67	120.14
3	Q	70	LEU	C-N-CA	-6.11	113.67	120.14
3	O	33	GLU	N-CA-C	6.09	117.92	111.28
3	U	33	GLU	N-CA-C	6.08	117.91	111.28
1	k	129	LEU	N-CA-C	-6.07	102.36	110.55
3	R	11	ALA	CA-C-N	-6.06	110.90	120.60
3	R	11	ALA	C-N-CA	-6.06	110.90	120.60
1	b	129	LEU	N-CA-C	-6.06	102.37	110.55
1	n	129	LEU	N-CA-C	-6.06	102.37	110.55
1	e	120	THR	N-CA-C	6.06	123.70	110.80
1	n	120	THR	N-CA-C	6.06	123.70	110.80
1	h	120	THR	N-CA-C	6.05	123.69	110.80
1	e	129	LEU	N-CA-C	-6.05	102.38	110.55
1	b	120	THR	N-CA-C	6.04	123.66	110.80
1	q	120	THR	N-CA-C	6.04	123.66	110.80
1	k	120	THR	N-CA-C	6.04	123.66	110.80
1	h	129	LEU	N-CA-C	-6.02	102.42	110.55
3	N	11	ALA	CA-C-N	-6.01	110.98	120.60
3	N	11	ALA	C-N-CA	-6.01	110.98	120.60
3	V	11	ALA	CA-C-N	-6.01	110.98	120.60
3	V	11	ALA	C-N-CA	-6.01	110.98	120.60
1	q	129	LEU	N-CA-C	-6.01	102.44	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	b	30	LYS	N-CA-C	-6.00	105.67	112.87
2	v	331	SER	N-CA-C	6.00	117.82	111.28
1	q	56	THR	N-CA-C	6.00	120.30	112.92
1	e	56	THR	N-CA-C	5.99	120.29	112.92
2	x	40	GLU	N-CA-C	-5.99	99.14	108.90
1	q	30	LYS	N-CA-C	-5.98	105.69	112.87
3	X	11	ALA	CA-C-N	-5.98	111.03	120.60
3	X	11	ALA	C-N-CA	-5.98	111.03	120.60
3	P	11	ALA	CA-C-N	-5.98	111.03	120.60
3	P	11	ALA	C-N-CA	-5.98	111.03	120.60
2	u	40	GLU	N-CA-C	-5.97	99.16	108.90
2	v	40	GLU	N-CA-C	-5.97	99.16	108.90
3	T	11	ALA	CA-C-N	-5.97	111.04	120.60
3	T	11	ALA	C-N-CA	-5.97	111.04	120.60
1	k	56	THR	N-CA-C	5.97	120.27	112.92
2	s	331	SER	N-CA-C	5.97	117.79	111.28
2	t	331	SER	N-CA-C	5.97	117.79	111.28
3	U	70	LEU	CA-C-N	-5.97	113.81	120.14
3	U	70	LEU	C-N-CA	-5.97	113.81	120.14
2	u	331	SER	N-CA-C	5.97	117.78	111.28
1	k	30	LYS	N-CA-C	-5.97	105.71	112.87
2	x	331	SER	N-CA-C	5.96	117.78	111.28
1	h	30	LYS	N-CA-C	-5.96	105.72	112.87
2	s	40	GLU	N-CA-C	-5.96	99.18	108.90
2	t	40	GLU	N-CA-C	-5.96	99.18	108.90
2	w	40	GLU	N-CA-C	-5.96	99.18	108.90
1	n	30	LYS	N-CA-C	-5.95	105.73	112.87
3	N	74	TYR	N-CA-C	5.94	117.84	111.36
1	b	56	THR	N-CA-C	5.94	120.23	112.92
1	e	30	LYS	N-CA-C	-5.93	105.76	112.87
1	a	50	TYR	N-CA-C	5.91	119.16	109.76
1	h	56	THR	N-CA-C	5.91	120.19	112.92
1	j	50	TYR	N-CA-C	5.91	119.16	109.76
1	p	50	TYR	N-CA-C	5.91	119.15	109.76
1	d	50	TYR	N-CA-C	5.90	119.15	109.76
3	R	74	TYR	N-CA-C	5.90	117.79	111.36
1	m	50	TYR	N-CA-C	5.90	119.14	109.76
3	P	74	TYR	N-CA-C	5.90	117.79	111.36
1	n	56	THR	N-CA-C	5.90	120.17	112.92
1	g	50	TYR	N-CA-C	5.89	119.13	109.76
2	w	331	SER	N-CA-C	5.89	117.70	111.28
3	P	119	VAL	N-CA-C	5.88	116.65	108.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	119	VAL	N-CA-C	5.85	116.59	108.23
2	t	342	SER	N-CA-C	5.84	117.65	111.28
3	T	119	VAL	N-CA-C	5.84	116.58	108.23
3	T	74	TYR	N-CA-C	5.84	117.72	111.36
2	x	342	SER	N-CA-C	5.83	117.64	111.28
1	a	93	ILE	N-CA-C	-5.83	102.06	109.58
3	V	74	TYR	N-CA-C	5.83	117.71	111.36
2	v	477	GLN	N-CA-C	5.82	117.29	111.07
2	v	702	GLN	N-CA-C	-5.81	99.71	109.07
2	s	342	SER	N-CA-C	5.81	117.61	111.28
3	X	74	TYR	N-CA-C	5.80	117.69	111.36
1	p	93	ILE	N-CA-C	-5.80	102.10	109.58
3	X	119	VAL	N-CA-C	5.80	116.52	108.23
1	g	93	ILE	N-CA-C	-5.79	102.10	109.58
1	m	93	ILE	N-CA-C	-5.79	102.10	109.58
2	s	702	GLN	N-CA-C	-5.79	99.75	109.07
3	V	119	VAL	N-CA-C	5.78	116.50	108.23
3	R	119	VAL	N-CA-C	5.77	116.49	108.23
2	t	702	GLN	N-CA-C	-5.77	99.78	109.07
2	x	702	GLN	N-CA-C	-5.77	99.78	109.07
1	d	93	ILE	N-CA-C	-5.77	102.14	109.58
2	w	702	GLN	N-CA-C	-5.76	99.80	109.07
2	u	702	GLN	N-CA-C	-5.75	99.81	109.07
2	v	342	SER	N-CA-C	5.75	117.55	111.28
2	t	183	SER	N-CA-C	-5.75	97.63	107.23
2	u	183	SER	N-CA-C	-5.75	97.63	107.23
2	w	342	SER	N-CA-C	5.75	117.55	111.28
2	s	183	SER	N-CA-C	-5.75	97.63	107.23
1	j	93	ILE	N-CA-C	-5.75	102.17	109.58
3	S	122	ILE	N-CA-C	-5.74	99.61	107.99
2	t	477	GLN	N-CA-C	5.74	117.21	111.07
2	x	183	SER	N-CA-C	-5.74	97.64	107.23
2	u	342	SER	N-CA-C	5.74	117.53	111.28
2	u	477	GLN	N-CA-C	5.73	117.20	111.07
2	w	477	GLN	N-CA-C	5.73	117.20	111.07
3	U	122	ILE	N-CA-C	-5.72	99.63	107.99
2	w	183	SER	N-CA-C	-5.72	97.68	107.23
3	O	122	ILE	N-CA-C	-5.72	99.64	107.99
2	v	183	SER	N-CA-C	-5.72	97.68	107.23
3	S	70	LEU	CA-C-N	-5.72	114.08	120.14
3	S	70	LEU	C-N-CA	-5.72	114.08	120.14
3	M	174	TYR	N-CA-C	5.72	118.28	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	O	174	TYR	N-CA-C	5.72	118.28	111.71
3	W	122	ILE	N-CA-C	-5.72	99.64	107.99
2	w	113	ARG	N-CA-C	-5.71	105.14	111.36
2	v	257	LEU	CA-C-N	-5.70	114.51	120.38
2	v	257	LEU	C-N-CA	-5.70	114.51	120.38
2	x	257	LEU	CA-C-N	-5.68	114.53	120.38
2	x	257	LEU	C-N-CA	-5.68	114.53	120.38
2	x	477	GLN	N-CA-C	5.68	117.15	111.07
1	j	140	ALA	N-CA-C	5.68	117.68	108.08
3	M	122	ILE	N-CA-C	-5.67	99.70	107.99
2	u	523	ILE	N-CA-C	-5.67	98.27	107.28
3	U	174	TYR	N-CA-C	5.67	118.23	111.71
1	p	140	ALA	N-CA-C	5.66	117.65	108.08
2	t	523	ILE	N-CA-C	-5.66	98.28	107.28
1	a	140	ALA	N-CA-C	5.66	117.64	108.08
1	d	140	ALA	N-CA-C	5.65	117.63	108.08
2	s	477	GLN	N-CA-C	5.65	117.12	111.07
2	u	113	ARG	N-CA-C	-5.65	105.20	111.36
2	t	193	ALA	N-CA-C	5.65	117.52	111.36
1	m	123	VAL	N-CA-C	5.65	116.86	109.58
3	Q	122	ILE	N-CA-C	-5.64	99.75	107.99
2	x	113	ARG	N-CA-C	-5.64	105.21	111.36
3	Q	174	TYR	N-CA-C	5.64	118.20	111.71
1	m	140	ALA	N-CA-C	5.64	117.61	108.08
1	d	123	VAL	N-CA-C	5.64	116.86	109.58
1	g	140	ALA	N-CA-C	5.64	117.61	108.08
2	u	193	ALA	N-CA-C	5.63	117.50	111.36
2	s	113	ARG	N-CA-C	-5.62	105.23	111.36
2	x	523	ILE	N-CA-C	-5.62	98.34	107.28
2	x	193	ALA	N-CA-C	5.62	117.48	111.36
3	W	174	TYR	N-CA-C	5.62	118.17	111.71
2	u	257	LEU	CA-C-N	-5.61	114.60	120.38
2	u	257	LEU	C-N-CA	-5.61	114.60	120.38
2	v	193	ALA	N-CA-C	5.61	117.48	111.36
2	t	257	LEU	CA-C-N	-5.61	114.60	120.38
2	t	257	LEU	C-N-CA	-5.61	114.60	120.38
2	v	522	LYS	N-CA-C	5.61	118.78	110.48
2	s	193	ALA	N-CA-C	5.61	117.47	111.36
2	t	113	ARG	N-CA-C	-5.61	105.25	111.36
2	w	743	ALA	N-CA-C	5.61	117.39	111.28
3	S	174	TYR	N-CA-C	5.61	118.16	111.71
1	j	123	VAL	N-CA-C	5.60	116.81	109.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	s	523	ILE	N-CA-C	-5.60	98.37	107.28
2	v	113	ARG	N-CA-C	-5.60	105.25	111.36
2	w	523	ILE	N-CA-C	-5.60	98.37	107.28
2	w	522	LYS	N-CA-C	5.60	118.77	110.48
1	g	123	VAL	N-CA-C	5.59	116.80	109.58
2	v	523	ILE	N-CA-C	-5.59	98.39	107.28
2	w	257	LEU	CA-C-N	-5.58	114.63	120.38
2	w	257	LEU	C-N-CA	-5.58	114.63	120.38
1	a	123	VAL	N-CA-C	5.58	116.78	109.58
2	w	193	ALA	N-CA-C	5.58	117.44	111.36
1	p	123	VAL	N-CA-C	5.58	116.78	109.58
2	t	522	LYS	N-CA-C	5.58	118.74	110.48
2	x	522	LYS	N-CA-C	5.57	118.72	110.48
2	v	743	ALA	N-CA-C	5.57	117.35	111.28
2	x	743	ALA	N-CA-C	5.56	117.34	111.28
2	u	434	SER	N-CA-C	5.56	117.34	111.28
2	w	498	ASN	CA-C-N	-5.55	115.99	120.98
2	w	498	ASN	C-N-CA	-5.55	115.99	120.98
2	u	522	LYS	N-CA-C	5.55	118.69	110.48
2	w	434	SER	N-CA-C	5.55	117.33	111.28
2	t	743	ALA	N-CA-C	5.54	117.32	111.28
2	s	743	ALA	N-CA-C	5.54	117.31	111.28
2	s	522	LYS	N-CA-C	5.53	118.67	110.48
2	v	434	SER	N-CA-C	5.53	117.31	111.28
2	x	498	ASN	CA-C-N	-5.53	116.00	120.98
2	x	498	ASN	C-N-CA	-5.53	116.00	120.98
2	w	689	ASP	N-CA-C	-5.53	105.25	111.28
2	s	434	SER	N-CA-C	5.53	117.30	111.28
2	u	743	ALA	N-CA-C	5.52	117.30	111.28
2	w	184	GLN	N-CA-C	5.52	121.00	113.16
2	w	129	ASN	N-CA-C	-5.52	100.68	109.96
2	x	129	ASN	N-CA-C	-5.52	100.69	109.96
2	x	434	SER	N-CA-C	5.52	117.30	111.28
3	S	74	TYR	N-CA-C	5.52	117.38	111.36
2	s	257	LEU	CA-C-N	-5.51	114.70	120.38
2	s	257	LEU	C-N-CA	-5.51	114.70	120.38
2	v	129	ASN	N-CA-C	-5.51	100.71	109.96
2	v	498	ASN	CA-C-N	-5.51	116.02	120.98
2	v	498	ASN	C-N-CA	-5.51	116.02	120.98
2	u	689	ASP	N-CA-C	-5.51	105.28	111.28
2	s	689	ASP	N-CA-C	-5.50	105.28	111.28
2	t	434	SER	N-CA-C	5.50	117.27	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	s	498	ASN	CA-C-N	-5.50	116.03	120.98
2	s	498	ASN	C-N-CA	-5.50	116.03	120.98
2	x	646	PRO	N-CA-C	-5.50	102.64	111.38
1	k	16	SER	N-CA-C	5.49	120.09	113.17
1	h	16	SER	N-CA-C	5.49	120.08	113.17
2	t	689	ASP	N-CA-C	-5.49	105.30	111.28
2	v	689	ASP	N-CA-C	-5.49	105.30	111.28
2	s	129	ASN	N-CA-C	-5.49	100.74	109.96
2	u	184	GLN	N-CA-C	5.49	120.95	113.16
1	a	117	THR	CB-CA-C	-5.48	101.70	110.79
2	w	242	GLN	N-CA-C	5.48	117.25	111.28
2	u	646	PRO	N-CA-C	-5.48	102.67	111.38
1	q	16	SER	N-CA-C	5.47	120.07	113.17
2	t	184	GLN	N-CA-C	5.47	120.93	113.16
2	t	498	ASN	CA-C-N	-5.47	116.05	120.98
2	t	498	ASN	C-N-CA	-5.47	116.05	120.98
3	O	74	TYR	N-CA-C	5.47	117.32	111.36
3	Q	74	TYR	N-CA-C	5.47	117.32	111.36
1	p	117	THR	CB-CA-C	-5.47	101.72	110.79
2	u	242	GLN	N-CA-C	5.46	117.23	111.28
2	w	646	PRO	N-CA-C	-5.46	102.69	111.38
2	w	410	SER	CB-CA-C	-5.46	110.30	116.63
2	u	129	ASN	N-CA-C	-5.46	100.79	109.96
2	v	410	SER	CB-CA-C	-5.46	110.30	116.63
2	x	242	GLN	N-CA-C	5.46	117.23	111.28
3	W	70	LEU	CA-C-N	-5.46	114.35	120.14
3	W	70	LEU	C-N-CA	-5.46	114.35	120.14
2	t	242	GLN	N-CA-C	5.46	117.23	111.28
2	x	184	GLN	N-CA-C	5.46	120.91	113.16
1	m	117	THR	CB-CA-C	-5.45	101.74	110.79
2	s	646	PRO	N-CA-C	-5.45	102.71	111.38
2	x	689	ASP	N-CA-C	-5.45	105.34	111.28
1	j	117	THR	CB-CA-C	-5.45	101.74	110.79
2	s	184	GLN	N-CA-C	5.45	120.90	113.16
2	x	410	SER	CB-CA-C	-5.45	110.31	116.63
1	e	16	SER	N-CA-C	5.45	120.04	113.17
2	t	646	PRO	N-CA-C	-5.45	102.72	111.38
1	b	16	SER	N-CA-C	5.45	120.03	113.17
2	v	184	GLN	N-CA-C	5.45	120.89	113.16
3	W	55	GLN	N-CA-C	-5.44	105.38	112.23
1	n	16	SER	N-CA-C	5.43	120.02	113.17
2	t	129	ASN	N-CA-C	-5.43	100.84	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	s	410	SER	CB-CA-C	-5.42	110.34	116.63
3	M	74	TYR	N-CA-C	5.42	117.27	111.36
3	V	111	ASP	N-CA-C	-5.42	106.66	113.28
2	x	63	ALA	CA-C-N	-5.42	115.00	120.31
2	x	63	ALA	C-N-CA	-5.42	115.00	120.31
2	t	63	ALA	CA-C-N	-5.42	115.00	120.31
2	t	63	ALA	C-N-CA	-5.42	115.00	120.31
2	w	63	ALA	CA-C-N	-5.42	115.00	120.31
2	w	63	ALA	C-N-CA	-5.42	115.00	120.31
1	d	117	THR	CB-CA-C	-5.42	101.80	110.79
1	g	117	THR	CB-CA-C	-5.41	101.80	110.79
2	u	149	ASN	N-CA-C	5.40	117.87	111.33
3	W	74	TYR	N-CA-C	5.40	117.25	111.36
2	u	63	ALA	CA-C-N	-5.40	115.02	120.31
2	u	63	ALA	C-N-CA	-5.40	115.02	120.31
2	u	521	SER	N-CA-C	5.40	117.17	111.28
3	U	74	TYR	N-CA-C	5.40	117.25	111.36
2	w	521	SER	N-CA-C	5.40	117.17	111.28
2	s	242	GLN	N-CA-C	5.39	117.16	111.28
2	v	646	PRO	N-CA-C	-5.39	102.80	111.38
2	s	149	ASN	N-CA-C	5.39	117.85	111.33
2	v	521	SER	N-CA-C	5.39	117.16	111.28
2	v	242	GLN	N-CA-C	5.39	117.16	111.28
2	u	410	SER	CB-CA-C	-5.39	110.38	116.63
2	s	63	ALA	CA-C-N	-5.38	115.03	120.31
2	s	63	ALA	C-N-CA	-5.38	115.03	120.31
2	t	410	SER	CB-CA-C	-5.38	110.39	116.63
2	t	521	SER	N-CA-C	5.38	117.15	111.28
2	v	149	ASN	N-CA-C	5.38	117.84	111.33
3	X	111	ASP	N-CA-C	-5.38	106.72	113.28
3	P	60	THR	N-CA-C	5.37	117.14	111.28
3	N	60	THR	N-CA-C	5.37	117.14	111.28
3	R	111	ASP	N-CA-C	-5.37	106.73	113.28
3	M	55	GLN	N-CA-C	-5.37	105.47	112.23
3	R	60	THR	N-CA-C	5.37	117.13	111.28
2	u	498	ASN	CA-C-N	-5.36	116.15	120.98
2	u	498	ASN	C-N-CA	-5.36	116.15	120.98
2	x	149	ASN	N-CA-C	5.36	117.82	111.33
3	N	111	ASP	N-CA-C	-5.36	106.74	113.28
3	O	55	GLN	N-CA-C	-5.36	105.47	112.23
2	s	531	LEU	N-CA-C	-5.36	100.96	109.59
2	u	531	LEU	N-CA-C	-5.36	100.96	109.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	v	63	ALA	CA-C-N	-5.36	115.06	120.31
2	v	63	ALA	C-N-CA	-5.36	115.06	120.31
3	X	60	THR	N-CA-C	5.36	117.12	111.28
2	w	531	LEU	N-CA-C	-5.35	100.98	109.59
2	x	531	LEU	N-CA-C	-5.34	100.99	109.59
2	v	531	LEU	N-CA-C	-5.34	101.00	109.59
2	x	521	SER	N-CA-C	5.33	117.09	111.28
3	U	55	GLN	N-CA-C	-5.33	105.51	112.23
2	t	531	LEU	N-CA-C	-5.33	101.01	109.59
1	i	57	THR	N-CA-C	5.33	117.20	108.52
2	t	149	ASN	N-CA-C	5.32	117.77	111.33
2	s	521	SER	N-CA-C	5.32	117.08	111.28
3	T	60	THR	N-CA-C	5.32	117.08	111.28
3	P	111	ASP	N-CA-C	-5.31	106.80	113.28
1	g	114	ARG	N-CA-C	-5.30	105.67	111.82
1	m	114	ARG	N-CA-C	-5.30	105.67	111.82
2	w	149	ASN	N-CA-C	5.30	117.75	111.33
3	S	55	GLN	N-CA-C	-5.30	105.55	112.23
3	O	90	THR	N-CA-C	5.30	118.21	111.69
3	V	33	GLU	N-CA-C	5.30	117.91	110.23
1	j	105	GLN	N-CA-C	5.29	117.13	111.36
1	o	57	THR	N-CA-C	5.29	117.15	108.52
1	e	118	THR	N-CA-C	-5.29	105.51	111.28
1	f	19	ASP	N-CA-C	5.29	117.35	109.25
1	i	123	VAL	N-CA-C	5.29	115.74	108.12
1	r	57	THR	N-CA-C	5.29	117.15	108.52
1	o	19	ASP	N-CA-C	5.29	117.35	109.25
1	l	57	THR	N-CA-C	5.28	117.13	108.52
2	x	121	VAL	N-CA-C	-5.28	100.75	108.99
3	Q	55	GLN	N-CA-C	-5.28	105.58	112.23
1	d	114	ARG	N-CA-C	-5.28	105.70	111.82
1	g	105	GLN	N-CA-C	5.28	117.11	111.36
1	l	19	ASP	N-CA-C	5.28	117.32	109.25
3	V	60	THR	N-CA-C	5.28	117.03	111.28
1	c	19	ASP	N-CA-C	5.28	117.32	109.25
1	r	19	ASP	N-CA-C	5.28	117.32	109.25
1	c	57	THR	N-CA-C	5.27	117.12	108.52
1	p	105	GLN	N-CA-C	5.27	117.11	111.36
2	x	103	GLY	N-CA-C	5.27	118.86	112.48
1	f	57	THR	N-CA-C	5.27	117.11	108.52
1	j	114	ARG	N-CA-C	-5.27	105.71	111.82
1	p	114	ARG	N-CA-C	-5.27	105.71	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	w	103	GLY	N-CA-C	5.27	118.86	112.48
1	a	114	ARG	N-CA-C	-5.26	105.71	111.82
1	i	19	ASP	N-CA-C	5.26	117.31	109.25
2	t	121	VAL	N-CA-C	-5.26	100.78	108.99
1	c	123	VAL	N-CA-C	5.26	115.69	108.12
2	u	103	GLY	N-CA-C	5.26	118.84	112.48
1	h	118	THR	N-CA-C	-5.25	105.56	111.28
1	o	94	LEU	N-CA-C	-5.25	103.60	110.53
1	a	105	GLN	N-CA-C	5.24	117.08	111.36
1	q	118	THR	N-CA-C	-5.24	105.56	111.28
2	w	121	VAL	N-CA-C	-5.24	100.81	108.99
3	W	90	THR	N-CA-C	5.24	118.14	111.69
3	X	33	GLU	N-CA-C	5.24	117.83	110.23
1	f	123	VAL	N-CA-C	5.24	115.67	108.12
1	d	105	GLN	N-CA-C	5.24	117.07	111.36
1	m	105	GLN	N-CA-C	5.24	117.07	111.36
2	t	292	THR	N-CA-C	5.24	117.82	109.02
1	l	123	VAL	N-CA-C	5.24	115.66	108.12
3	P	33	GLU	N-CA-C	5.24	117.82	110.23
1	r	123	VAL	N-CA-C	5.23	115.66	108.12
2	s	84	SER	N-CA-C	-5.23	106.85	114.12
3	N	33	GLU	N-CA-C	5.23	117.82	110.23
2	v	121	VAL	N-CA-C	-5.23	100.83	108.99
3	R	33	GLU	N-CA-C	5.23	117.81	110.23
3	M	90	THR	N-CA-C	5.23	118.12	111.69
1	o	123	VAL	N-CA-C	5.22	115.64	108.12
1	b	118	THR	N-CA-C	-5.22	105.59	111.28
1	k	118	THR	N-CA-C	-5.22	105.59	111.28
1	n	118	THR	N-CA-C	-5.22	105.59	111.28
2	s	103	GLY	N-CA-C	5.22	118.80	112.48
3	T	111	ASP	N-CA-C	-5.22	106.91	113.28
3	Q	90	THR	N-CA-C	5.22	118.11	111.69
2	t	103	GLY	N-CA-C	5.21	118.79	112.48
2	u	121	VAL	N-CA-C	-5.21	100.86	108.99
3	T	33	GLU	N-CA-C	5.21	117.79	110.23
2	s	292	THR	N-CA-C	5.21	117.77	109.02
2	v	103	GLY	N-CA-C	5.21	118.78	112.48
2	w	292	THR	N-CA-C	5.21	117.77	109.02
2	s	121	VAL	N-CA-C	-5.20	100.87	108.99
2	w	84	SER	N-CA-C	-5.20	106.89	114.12
3	O	111	ASP	N-CA-C	-5.20	106.62	113.17
1	i	94	LEU	N-CA-C	-5.20	103.67	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	r	94	LEU	N-CA-C	-5.20	103.67	110.53
2	v	84	SER	N-CA-C	-5.19	106.90	114.12
3	U	90	THR	N-CA-C	5.18	118.07	111.69
2	u	292	THR	N-CA-C	5.18	117.73	109.02
2	u	84	SER	N-CA-C	-5.18	106.92	114.12
2	t	84	SER	N-CA-C	-5.17	106.93	114.12
1	f	94	LEU	N-CA-C	-5.17	103.71	110.53
1	e	28	ALA	CB-CA-C	-5.16	110.64	116.63
2	v	292	THR	N-CA-C	5.16	117.69	109.02
2	x	292	THR	N-CA-C	5.16	117.69	109.02
3	S	111	ASP	N-CA-C	-5.16	106.67	113.17
3	M	111	ASP	N-CA-C	-5.16	106.67	113.17
3	R	174	TYR	N-CA-C	5.16	116.90	111.28
2	w	274	SER	N-CA-C	-5.15	105.22	112.12
2	v	274	SER	N-CA-C	-5.15	105.22	112.12
1	c	94	LEU	N-CA-C	-5.15	103.73	110.53
2	s	274	SER	N-CA-C	-5.15	105.22	112.12
3	W	111	ASP	N-CA-C	-5.14	106.69	113.17
3	U	111	ASP	N-CA-C	-5.14	106.69	113.17
2	x	84	SER	N-CA-C	-5.14	106.98	114.12
2	x	274	SER	N-CA-C	-5.14	105.23	112.12
1	b	28	ALA	CB-CA-C	-5.14	110.67	116.63
1	r	16	SER	N-CA-C	-5.14	98.33	107.98
1	l	94	LEU	N-CA-C	-5.13	103.75	110.53
2	t	274	SER	N-CA-C	-5.13	105.24	112.12
1	k	28	ALA	CB-CA-C	-5.13	110.68	116.63
1	c	16	SER	N-CA-C	-5.13	98.34	107.98
1	i	16	SER	N-CA-C	-5.12	98.34	107.98
1	n	28	ALA	CB-CA-C	-5.12	110.69	116.63
1	f	16	SER	N-CA-C	-5.12	98.35	107.98
3	X	36	ALA	N-CA-C	-5.12	106.17	112.72
1	q	28	ALA	CB-CA-C	-5.12	110.69	116.63
1	h	121	ILE	CB-CA-C	-5.11	105.42	111.97
1	o	16	SER	N-CA-C	-5.11	98.38	107.98
1	h	28	ALA	CB-CA-C	-5.11	110.71	116.63
3	V	174	TYR	N-CA-C	5.11	116.85	111.28
2	x	722	ASN	N-CA-C	-5.10	101.95	109.86
1	l	16	SER	N-CA-C	-5.10	98.39	107.98
2	x	65	TYR	N-CA-C	-5.09	100.43	108.73
2	v	722	ASN	N-CA-C	-5.09	101.97	109.86
3	S	90	THR	N-CA-C	5.09	117.95	111.69
2	t	333	GLY	N-CA-C	5.08	125.23	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	36	ALA	N-CA-C	-5.08	106.21	112.72
1	k	121	ILE	CB-CA-C	-5.08	105.47	111.97
2	u	274	SER	N-CA-C	-5.08	105.31	112.12
2	v	333	GLY	N-CA-C	5.08	125.22	113.18
2	x	333	GLY	N-CA-C	5.08	125.22	113.18
3	T	36	ALA	N-CA-C	-5.08	106.22	112.72
1	q	121	ILE	CB-CA-C	-5.08	105.47	111.97
2	u	333	GLY	N-CA-C	5.08	125.21	113.18
3	N	174	TYR	N-CA-C	5.07	116.81	111.28
3	V	36	ALA	N-CA-C	-5.07	106.23	112.72
1	e	121	ILE	CB-CA-C	-5.07	105.48	111.97
2	s	65	TYR	N-CA-C	-5.07	100.47	108.73
1	n	121	ILE	CB-CA-C	-5.07	105.48	111.97
2	s	333	GLY	N-CA-C	5.07	125.18	113.18
3	N	36	ALA	N-CA-C	-5.06	106.24	112.72
3	X	174	TYR	N-CA-C	5.06	116.79	111.28
1	b	121	ILE	CB-CA-C	-5.05	105.50	111.97
3	T	174	TYR	N-CA-C	5.05	116.78	111.28
2	t	65	TYR	N-CA-C	-5.05	100.50	108.73
3	R	36	ALA	N-CA-C	-5.05	106.26	112.72
2	t	722	ASN	N-CA-C	-5.04	102.05	109.86
2	w	333	GLY	N-CA-C	5.04	125.12	113.18
3	Q	111	ASP	N-CA-C	-5.04	106.83	113.17
2	w	722	ASN	N-CA-C	-5.03	102.06	109.86
2	u	722	ASN	N-CA-C	-5.03	102.06	109.86
2	x	187	HIS	N-CA-C	5.02	116.84	111.36
2	s	722	ASN	N-CA-C	-5.02	102.08	109.86
2	w	65	TYR	N-CA-C	-5.02	100.54	108.73
2	v	65	TYR	N-CA-C	-5.02	100.55	108.73
1	q	133	GLY	N-CA-C	-5.02	101.69	111.02
3	O	6	MET	N-CA-C	5.02	117.41	107.98
2	t	90	ASP	N-CA-C	-5.01	103.91	110.53
2	u	65	TYR	N-CA-C	-5.01	100.56	108.73
3	S	6	MET	N-CA-C	5.01	117.41	107.98
3	M	6	MET	N-CA-C	5.01	117.40	107.98
1	e	133	GLY	N-CA-C	-5.01	101.70	111.02
2	x	90	ASP	N-CA-C	-5.01	103.92	110.53
3	M	125	ARG	N-CA-C	-5.00	101.76	109.52

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	1115	0	1122	59	0
1	b	1067	0	1071	72	0
1	c	1080	0	1082	52	0
1	d	1115	0	1122	55	0
1	e	1067	0	1071	73	0
1	f	1080	0	1082	51	0
1	g	1115	0	1122	58	0
1	h	1067	0	1071	72	0
1	i	1080	0	1082	54	0
1	j	1115	0	1122	56	0
1	k	1067	0	1071	73	0
1	l	1080	0	1082	51	0
1	m	1115	0	1122	56	0
1	n	1067	0	1071	74	0
1	o	1080	0	1082	50	0
1	p	1115	0	1122	57	0
1	q	1067	0	1071	73	0
1	r	1080	0	1082	49	0
2	s	6308	0	6070	292	0
2	t	6308	0	6070	300	0
2	u	6308	0	6070	298	0
2	v	6308	0	6070	293	0
2	w	6308	0	6070	288	0
2	x	6308	0	6070	289	0
3	M	1546	0	1460	78	0
3	N	1557	0	1473	104	0
3	O	1546	0	1460	72	0
3	P	1557	0	1473	102	0
3	Q	1546	0	1460	72	0
3	R	1557	0	1473	105	0
3	S	1546	0	1460	73	0
3	T	1557	0	1473	104	0
3	U	1546	0	1460	76	0
3	V	1557	0	1473	103	0
3	W	1546	0	1460	75	0
3	X	1557	0	1473	109	0
All	All	76038	0	73668	2755	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 18.

All (2755) 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:m:27:LEU:CD1	3:R:6:MET:HE3	1.43	1.49
1:p:27:LEU:CD1	3:P:6:MET:HE3	1.43	1.48
1:a:27:LEU:CD1	3:N:6:MET:HE3	1.43	1.47
1:d:27:LEU:CD1	3:X:6:MET:HE3	1.44	1.43
1:j:27:LEU:CD1	3:T:6:MET:HE3	1.48	1.43
1:g:27:LEU:CD1	3:V:6:MET:HE3	1.48	1.40
2:w:234:THR:HB	2:x:217:GLN:NE2	1.44	1.33
2:s:234:THR:HB	2:t:217:GLN:NE2	1.45	1.31
2:t:234:THR:HB	2:u:217:GLN:NE2	1.42	1.30
2:v:234:THR:HB	2:w:217:GLN:NE2	1.44	1.29
2:s:217:GLN:NE2	2:x:234:THR:HB	1.48	1.29
2:u:234:THR:HB	2:v:217:GLN:NE2	1.49	1.25
2:w:181:ASP:OD2	2:x:188:VAL:HB	1.38	1.22
2:t:181:ASP:OD2	2:u:188:VAL:HB	1.35	1.22
1:b:86:VAL:HG22	3:N:31:THR:CG2	1.72	1.19
2:v:181:ASP:OD2	2:w:188:VAL:HB	1.36	1.19
2:s:181:ASP:OD2	2:t:188:VAL:HB	1.39	1.19
2:s:188:VAL:HB	2:x:181:ASP:OD2	1.40	1.19
2:u:181:ASP:OD2	2:v:188:VAL:HB	1.43	1.19
1:n:86:VAL:HG22	3:R:31:THR:CG2	1.73	1.18
1:e:86:VAL:HG22	3:X:31:THR:CG2	1.74	1.18
1:l:90:ASP:HB3	2:t:715:THR:HG22	1.26	1.17
1:q:86:VAL:HG22	3:P:31:THR:CG2	1.74	1.17
1:b:94:LEU:HD13	2:w:736:LEU:HD21	1.28	1.14
1:h:86:VAL:HG22	3:V:31:THR:CG2	1.77	1.14
1:o:90:ASP:HB3	2:s:715:THR:HG22	1.30	1.14
1:k:86:VAL:HG22	3:T:31:THR:CG2	1.77	1.13
1:i:90:ASP:HB3	2:u:715:THR:HG22	1.27	1.12
1:r:90:ASP:HB3	2:x:715:THR:HG22	1.27	1.12
1:q:94:LEU:HD13	2:x:736:LEU:HD21	1.30	1.10
1:n:94:LEU:HD13	2:s:736:LEU:HD21	1.29	1.10
1:e:94:LEU:HD13	2:v:736:LEU:HD21	1.29	1.09
1:c:90:ASP:HB3	2:w:715:THR:HG22	1.26	1.09
1:f:90:ASP:HB3	2:v:715:THR:HG22	1.29	1.09
1:h:94:LEU:HD13	2:u:736:LEU:HD21	1.30	1.09
1:p:27:LEU:HD11	3:P:6:MET:CE	1.83	1.09
1:a:27:LEU:HD11	3:N:6:MET:CE	1.83	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:k:94:LEU:HD13	2:t:736:LEU:HD21	1.29	1.08
1:m:27:LEU:HD11	3:R:6:MET:CE	1.83	1.08
1:d:27:LEU:HD11	3:X:6:MET:CE	1.83	1.07
3:P:97:VAL:HG21	3:Q:125:ARG:HH22	1.20	1.06
3:V:97:VAL:HG21	3:W:125:ARG:HH22	1.19	1.06
3:M:125:ARG:HH22	3:X:97:VAL:HG21	1.18	1.06
3:R:97:VAL:HG21	3:S:125:ARG:HH22	1.21	1.06
3:T:97:VAL:HG21	3:U:125:ARG:HH22	1.22	1.05
1:g:27:LEU:HD11	3:V:6:MET:CE	1.87	1.05
1:h:86:VAL:HG22	3:V:31:THR:HG21	1.09	1.04
1:n:86:VAL:HG22	3:R:31:THR:HG21	1.04	1.03
3:N:97:VAL:HG21	3:O:125:ARG:HH22	1.21	1.03
1:k:86:VAL:HG22	3:T:31:THR:HG21	1.08	1.03
1:q:86:VAL:HG22	3:P:31:THR:HG21	1.04	1.03
1:e:86:VAL:HG22	3:X:31:THR:HG21	1.06	1.03
1:j:27:LEU:HD11	3:T:6:MET:HE3	1.03	1.02
2:t:234:THR:HB	2:u:217:GLN:HE21	1.02	1.02
1:j:27:LEU:HD11	3:T:6:MET:CE	1.87	1.02
2:s:39:THR:CG2	2:x:493:PRO:HG3	1.89	1.02
1:g:27:LEU:HD11	3:V:6:MET:HE3	1.03	1.02
2:u:493:PRO:HG3	2:v:39:THR:CG2	1.90	1.02
1:k:62:LYS:HG3	3:T:72:ASP:OD1	1.60	1.01
1:n:62:LYS:HG3	3:R:72:ASP:OD1	1.61	1.01
1:h:62:LYS:HG3	3:V:72:ASP:OD1	1.60	1.01
1:c:90:ASP:CB	2:w:715:THR:HG22	1.91	1.01
2:u:493:PRO:CG	2:v:39:THR:HG21	1.90	1.01
1:p:27:LEU:CD1	3:P:6:MET:CE	2.39	1.00
2:s:39:THR:HG21	2:x:493:PRO:CG	1.89	1.00
2:w:698:ILE:HD13	2:x:707:TRP:HH2	1.26	1.00
1:a:27:LEU:CD1	3:N:6:MET:CE	2.39	1.00
1:d:27:LEU:HD11	3:X:6:MET:HE3	1.00	1.00
2:s:493:PRO:HG3	2:t:39:THR:HG21	1.01	1.00
1:j:10:THR:HG21	3:S:74:TYR:CE2	1.96	1.00
2:u:493:PRO:HG3	2:v:39:THR:HG21	1.00	0.99
2:v:493:PRO:HG3	2:w:39:THR:CG2	1.92	0.99
2:s:707:TRP:HH2	2:x:698:ILE:HD13	1.27	0.99
2:v:493:PRO:HG3	2:w:39:THR:HG21	1.01	0.99
1:m:27:LEU:CD1	3:R:6:MET:CE	2.40	0.99
2:t:493:PRO:CG	2:u:39:THR:HG21	1.92	0.99
1:l:90:ASP:CB	2:t:715:THR:HG22	1.92	0.99
1:q:62:LYS:HG3	3:P:72:ASP:OD1	1.62	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:493:PRO:HG3	2:u:39:THR:CG2	1.91	0.99
2:w:493:PRO:HG3	2:x:39:THR:CG2	1.92	0.99
1:b:86:VAL:HG22	3:N:31:THR:HG21	1.02	0.99
2:t:234:THR:CB	2:u:217:GLN:HE21	1.76	0.99
1:p:27:LEU:HD11	3:P:6:MET:HE3	1.01	0.99
2:s:493:PRO:HG3	2:t:39:THR:CG2	1.92	0.99
2:t:493:PRO:HG3	2:u:39:THR:HG21	1.01	0.99
1:r:90:ASP:CB	2:x:715:THR:HG22	1.93	0.98
2:s:493:PRO:CG	2:t:39:THR:HG21	1.93	0.98
1:g:10:THR:HG21	3:U:74:TYR:CE2	1.97	0.98
2:w:493:PRO:CG	2:x:39:THR:HG21	1.92	0.98
1:a:27:LEU:HD11	3:N:6:MET:HE3	1.02	0.98
1:f:90:ASP:CB	2:v:715:THR:HG22	1.93	0.98
2:v:698:ILE:HD13	2:w:707:TRP:HH2	1.28	0.98
2:v:493:PRO:CG	2:w:39:THR:HG21	1.92	0.98
1:i:90:ASP:CB	2:u:715:THR:HG22	1.92	0.98
2:w:493:PRO:HG3	2:x:39:THR:HG21	1.01	0.98
1:m:27:LEU:HD11	3:R:6:MET:HE3	1.00	0.98
2:t:120:THR:HG23	2:t:125:THR:HG22	1.47	0.97
2:u:698:ILE:HD13	2:v:707:TRP:HH2	1.28	0.97
2:v:120:THR:HG23	2:v:125:THR:HG22	1.47	0.97
2:v:234:THR:CB	2:w:217:GLN:HE21	1.77	0.97
2:s:39:THR:HG21	2:x:493:PRO:HG3	0.99	0.97
1:e:62:LYS:HG3	3:X:72:ASP:OD1	1.65	0.96
2:s:120:THR:HG23	2:s:125:THR:HG22	1.47	0.96
2:s:456:ARG:HH11	2:x:482:VAL:HG11	1.30	0.96
1:d:27:LEU:CD1	3:X:6:MET:CE	2.41	0.96
1:m:10:THR:HG21	3:Q:74:TYR:CE2	2.00	0.96
1:o:90:ASP:CB	2:s:715:THR:HG22	1.93	0.96
2:u:120:THR:HG23	2:u:125:THR:HG22	1.47	0.96
3:M:5:ASP:HB3	3:N:10:THR:OG1	1.66	0.96
2:w:120:THR:HG23	2:w:125:THR:HG22	1.47	0.96
1:e:94:LEU:HD13	2:v:736:LEU:CD2	1.96	0.96
1:b:86:VAL:CG2	3:N:31:THR:HG21	1.96	0.96
2:x:120:THR:HG23	2:x:125:THR:HG22	1.47	0.96
1:n:94:LEU:HD13	2:s:736:LEU:CD2	1.96	0.95
3:Q:5:ASP:HB3	3:R:10:THR:OG1	1.66	0.95
1:p:10:THR:HG21	3:O:74:TYR:CE2	2.01	0.95
2:s:234:THR:CB	2:t:217:GLN:HE21	1.78	0.95
3:S:5:ASP:HB3	3:T:10:THR:OG1	1.66	0.95
1:a:10:THR:HG21	3:M:74:TYR:CE2	2.02	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:5:ASP:HB3	3:P:10:THR:OG1	1.66	0.95
1:d:10:THR:HG21	3:W:74:TYR:CE2	2.00	0.95
2:s:400:ILE:HD11	2:t:120:THR:HG22	1.48	0.95
2:v:482:VAL:HG11	2:w:456:ARG:HH11	1.32	0.95
2:t:698:ILE:HD13	2:u:707:TRP:HH2	1.26	0.95
3:U:5:ASP:HB3	3:V:10:THR:OG1	1.66	0.95
1:h:94:LEU:HD13	2:u:736:LEU:CD2	1.97	0.95
2:v:400:ILE:HD11	2:w:120:THR:HG22	1.49	0.95
1:k:94:LEU:HD13	2:t:736:LEU:CD2	1.97	0.95
1:n:86:VAL:CG2	3:R:31:THR:HG21	1.97	0.94
1:q:86:VAL:CG2	3:P:31:THR:HG21	1.97	0.94
2:s:698:ILE:HD13	2:t:707:TRP:HH2	1.28	0.94
2:t:400:ILE:HD11	2:u:120:THR:HG22	1.49	0.94
2:t:482:VAL:HG11	2:u:456:ARG:HH11	1.31	0.94
2:w:234:THR:CB	2:x:217:GLN:HE21	1.78	0.94
3:W:5:ASP:HB3	3:X:10:THR:OG1	1.66	0.94
2:t:234:THR:CB	2:u:217:GLN:NE2	2.30	0.94
2:w:400:ILE:HD11	2:x:120:THR:HG22	1.49	0.94
1:b:94:LEU:HD13	2:w:736:LEU:CD2	1.96	0.94
1:b:62:LYS:HG3	3:N:72:ASP:OD1	1.67	0.94
1:q:94:LEU:HD13	2:x:736:LEU:CD2	1.98	0.94
2:u:729:TYR:HE1	3:V:37:ASN:HA	1.33	0.94
2:u:482:VAL:HG11	2:v:456:ARG:HH11	1.32	0.93
2:w:482:VAL:HG11	2:x:456:ARG:HH11	1.32	0.92
2:u:234:THR:CB	2:v:217:GLN:HE21	1.83	0.92
2:s:234:THR:CB	2:t:217:GLN:NE2	2.33	0.92
1:j:27:LEU:CD1	3:T:6:MET:CE	2.45	0.92
2:s:120:THR:HG22	2:x:400:ILE:HD11	1.52	0.91
1:j:10:THR:O	3:S:73:VAL:HG23	1.69	0.91
2:u:400:ILE:HD11	2:v:120:THR:HG22	1.52	0.91
2:v:400:ILE:HD11	2:w:120:THR:CG2	2.01	0.91
2:t:729:TYR:HE1	3:T:37:ASN:HA	1.33	0.91
1:g:10:THR:O	3:U:73:VAL:HG23	1.70	0.91
2:s:217:GLN:HE21	2:x:234:THR:CB	1.81	0.91
2:v:234:THR:CB	2:w:217:GLN:NE2	2.32	0.90
2:s:482:VAL:HG11	2:t:456:ARG:HH11	1.33	0.90
2:u:234:THR:HB	2:v:217:GLN:HE21	1.08	0.90
1:e:86:VAL:CG2	3:X:31:THR:HG21	1.99	0.90
2:v:161:TYR:HB2	2:w:188:VAL:HG11	1.54	0.90
2:s:729:TYR:HE1	3:R:37:ASN:HA	1.37	0.90
2:s:400:ILE:HD11	2:t:120:THR:CG2	2.01	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:729:TYR:HE1	3:X:37:ASN:HA	1.37	0.89
2:s:120:THR:CG2	2:x:400:ILE:HD11	2.03	0.89
2:v:234:THR:HB	2:w:217:GLN:HE21	1.02	0.89
1:g:27:LEU:CD1	3:V:6:MET:CE	2.45	0.89
2:w:234:THR:CB	2:x:217:GLN:NE2	2.32	0.89
1:k:86:VAL:CG2	3:T:31:THR:HG21	2.01	0.89
1:d:76:ARG:NH2	1:d:115:ASP:HB3	1.89	0.88
1:j:76:ARG:NH2	1:j:115:ASP:HB3	1.89	0.88
2:u:400:ILE:HD11	2:v:120:THR:CG2	2.03	0.88
2:w:400:ILE:HD11	2:x:120:THR:CG2	2.02	0.88
1:a:27:LEU:HD12	3:N:6:MET:HE3	1.52	0.88
1:d:10:THR:O	3:W:73:VAL:HG23	1.73	0.88
1:m:10:THR:O	3:Q:73:VAL:HG23	1.73	0.88
2:t:400:ILE:HD11	2:u:120:THR:CG2	2.02	0.88
1:a:76:ARG:NH2	1:a:115:ASP:HB3	1.89	0.88
1:p:76:ARG:NH2	1:p:115:ASP:HB3	1.89	0.88
2:u:234:THR:CB	2:v:217:GLN:NE2	2.36	0.88
2:s:161:TYR:HB2	2:t:188:VAL:HG11	1.55	0.88
2:x:729:TYR:HE1	3:P:37:ASN:HA	1.39	0.88
1:k:62:LYS:CG	3:T:72:ASP:OD1	2.22	0.87
1:b:86:VAL:HA	3:N:31:THR:HG22	1.55	0.87
1:d:104:ILE:HD13	3:X:8:VAL:HG21	1.56	0.87
1:g:76:ARG:NH2	1:g:115:ASP:HB3	1.89	0.87
2:s:396:SER:HB2	2:t:353:PHE:O	1.74	0.87
2:v:396:SER:HB2	2:w:353:PHE:O	1.73	0.87
1:p:27:LEU:HD12	3:P:6:MET:HE3	1.53	0.87
2:t:482:VAL:CG1	2:u:456:ARG:HD2	2.05	0.87
1:m:76:ARG:NH2	1:m:115:ASP:HB3	1.89	0.87
2:s:456:ARG:HD2	2:x:482:VAL:CG1	2.04	0.87
2:w:482:VAL:CG1	2:x:456:ARG:HD2	2.05	0.87
2:v:482:VAL:CG1	2:w:456:ARG:HD2	2.05	0.86
1:n:62:LYS:CG	3:R:72:ASP:OD1	2.23	0.86
1:n:86:VAL:HA	3:R:31:THR:HG22	1.57	0.86
1:d:104:ILE:HD13	3:X:8:VAL:CG2	2.05	0.86
2:w:729:TYR:HE1	3:N:37:ASN:HA	1.41	0.86
1:g:104:ILE:HD13	3:V:8:VAL:CG2	2.06	0.86
1:q:86:VAL:HA	3:P:31:THR:HG22	1.57	0.86
2:s:234:THR:HB	2:t:217:GLN:HE21	1.02	0.86
2:t:161:TYR:HB2	2:u:188:VAL:HG11	1.58	0.86
2:t:396:SER:HB2	2:u:353:PHE:O	1.74	0.86
2:s:482:VAL:CG1	2:t:456:ARG:HD2	2.06	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:28:PRO:HB3	3:X:45:ARG:HH12	1.40	0.86
1:h:62:LYS:CG	3:V:72:ASP:OD1	2.23	0.86
1:h:86:VAL:CG2	3:V:31:THR:HG21	2.02	0.86
1:m:104:ILE:HD13	3:R:8:VAL:HG21	1.58	0.86
2:u:482:VAL:CG1	2:v:456:ARG:HD2	2.05	0.86
1:a:10:THR:O	3:M:73:VAL:HG23	1.76	0.85
1:p:10:THR:O	3:O:73:VAL:HG23	1.75	0.85
2:t:466:SER:OG	2:u:579:THR:HG23	1.76	0.85
2:w:234:THR:HB	2:x:217:GLN:HE21	1.03	0.85
1:m:27:LEU:HD12	3:R:6:MET:HE3	1.53	0.85
2:s:217:GLN:HE21	2:x:234:THR:HB	1.08	0.85
2:u:396:SER:HB2	2:v:353:PHE:O	1.76	0.85
1:q:62:LYS:CG	3:P:72:ASP:OD1	2.24	0.85
2:s:466:SER:OG	2:t:579:THR:HG23	1.76	0.85
1:j:104:ILE:HD13	3:T:8:VAL:CG2	2.07	0.85
1:g:104:ILE:HD13	3:V:8:VAL:HG21	1.59	0.85
2:s:353:PHE:O	2:x:396:SER:HB2	1.75	0.85
2:w:466:SER:OG	2:x:579:THR:HG23	1.76	0.85
2:v:466:SER:OG	2:w:579:THR:HG23	1.76	0.84
2:w:161:TYR:HB2	2:x:188:VAL:HG11	1.59	0.84
3:V:45:ARG:HH12	3:W:28:PRO:HB3	1.42	0.84
2:u:466:SER:OG	2:v:579:THR:HG23	1.77	0.84
3:P:88:MET:HG2	3:Q:178:TYR:HD1	1.41	0.84
3:R:88:MET:HG2	3:S:178:TYR:HD1	1.42	0.84
2:s:217:GLN:NE2	2:x:234:THR:CB	2.35	0.84
2:w:396:SER:HB2	2:x:353:PHE:O	1.75	0.84
1:m:104:ILE:HD13	3:R:8:VAL:CG2	2.06	0.84
1:d:104:ILE:CD1	3:X:8:VAL:HG21	2.07	0.84
1:j:27:LEU:HD12	3:T:6:MET:HE3	1.58	0.84
2:w:698:ILE:CD1	2:x:707:TRP:HH2	1.91	0.84
1:d:27:LEU:HD12	3:X:6:MET:HE3	1.57	0.84
1:g:27:LEU:HD12	3:V:6:MET:HE3	1.59	0.83
2:s:579:THR:HG23	2:x:466:SER:OG	1.77	0.83
3:M:178:TYR:HD1	3:X:88:MET:HG2	1.40	0.83
3:P:45:ARG:HH12	3:Q:28:PRO:HB3	1.43	0.83
1:j:104:ILE:HD13	3:T:8:VAL:HG21	1.60	0.83
3:M:178:TYR:CE1	3:X:94:SER:OG	2.30	0.83
1:a:104:ILE:HD13	3:N:8:VAL:HG21	1.59	0.83
1:o:90:ASP:C	2:s:715:THR:CG2	2.52	0.83
1:p:104:ILE:HD13	3:P:8:VAL:CG2	2.07	0.82
1:p:104:ILE:HD13	3:P:8:VAL:HG21	1.58	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:533:GLU:OE2	2:x:476:VAL:HG23	1.79	0.82
2:v:698:ILE:CD1	2:w:707:TRP:HH2	1.92	0.82
1:i:90:ASP:C	2:u:715:THR:CG2	2.52	0.82
3:P:94:SER:OG	3:Q:178:TYR:CE1	2.33	0.82
1:e:86:VAL:HA	3:X:31:THR:HG22	1.61	0.82
1:g:104:ILE:CD1	3:V:8:VAL:HG21	2.09	0.82
2:s:188:VAL:HG11	2:x:161:TYR:HB2	1.61	0.82
2:v:181:ASP:OD2	2:w:188:VAL:CB	2.26	0.82
2:s:707:TRP:HH2	2:x:698:ILE:CD1	1.93	0.82
2:u:161:TYR:HB2	2:v:188:VAL:HG11	1.62	0.82
3:V:88:MET:HG2	3:W:178:TYR:HD1	1.43	0.82
3:V:94:SER:OG	3:W:178:TYR:CE1	2.31	0.82
1:f:90:ASP:C	2:v:715:THR:CG2	2.53	0.81
1:a:104:ILE:HD13	3:N:8:VAL:CG2	2.09	0.81
3:R:94:SER:OG	3:S:178:TYR:CE1	2.33	0.81
3:T:45:ARG:HH12	3:U:28:PRO:HB3	1.45	0.81
1:b:62:LYS:CG	3:N:72:ASP:OD1	2.27	0.81
1:k:86:VAL:HA	3:T:31:THR:HG22	1.60	0.81
2:t:698:ILE:CD1	2:u:707:TRP:HH2	1.91	0.81
1:c:90:ASP:C	2:w:715:THR:CG2	2.54	0.81
2:w:698:ILE:HD13	2:x:707:TRP:CH2	2.15	0.81
3:N:94:SER:OG	3:O:178:TYR:CE1	2.33	0.81
3:T:88:MET:HG2	3:U:178:TYR:HD1	1.45	0.81
2:s:707:TRP:CH2	2:x:698:ILE:HD13	2.16	0.81
3:R:45:ARG:HH12	3:S:28:PRO:HB3	1.43	0.81
1:i:90:ASP:C	2:u:715:THR:HG21	2.05	0.81
3:M:129:GLU:CG	3:X:98:ASN:O	2.29	0.81
1:j:104:ILE:CD1	3:T:8:VAL:HG21	2.11	0.81
3:N:88:MET:HG2	3:O:178:TYR:HD1	1.43	0.81
1:l:90:ASP:C	2:t:715:THR:CG2	2.54	0.81
3:N:45:ARG:HH12	3:O:28:PRO:HB3	1.45	0.81
1:h:86:VAL:HA	3:V:31:THR:HG22	1.63	0.80
1:m:104:ILE:CD1	3:R:8:VAL:HG21	2.10	0.80
3:T:94:SER:OG	3:U:178:TYR:CE1	2.34	0.80
3:M:125:ARG:NH2	3:X:97:VAL:HG21	1.96	0.80
1:l:90:ASP:C	2:t:715:THR:HG21	2.07	0.80
2:u:476:VAL:HG23	2:v:533:GLU:OE2	1.81	0.80
1:e:62:LYS:CG	3:X:72:ASP:OD1	2.28	0.80
1:j:10:THR:HG21	3:S:74:TYR:CD2	2.16	0.80
2:u:698:ILE:CD1	2:v:707:TRP:HH2	1.94	0.80
2:w:181:ASP:OD2	2:x:188:VAL:CB	2.27	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:93:GLN:HE22	3:N:181:TYR:HE1	1.29	0.80
1:b:48:THR:HG22	3:N:83:ASP:HB2	1.62	0.80
1:p:104:ILE:CD1	3:P:8:VAL:HG21	2.11	0.80
2:s:698:ILE:CD1	2:t:707:TRP:HH2	1.93	0.80
1:i:91:GLY:N	2:u:715:THR:CG2	2.45	0.80
1:c:90:ASP:C	2:w:715:THR:HG21	2.07	0.80
3:W:93:GLN:HE22	3:X:181:TYR:HE1	1.30	0.80
1:a:104:ILE:CD1	3:N:8:VAL:HG21	2.12	0.79
1:o:90:ASP:C	2:s:715:THR:HG21	2.07	0.79
3:N:11:ALA:HB3	3:N:14:LEU:HB3	1.65	0.79
2:w:476:VAL:HG23	2:x:533:GLU:OE2	1.82	0.79
3:O:93:GLN:HE22	3:P:181:TYR:HE1	1.29	0.79
3:X:11:ALA:HB3	3:X:14:LEU:HB3	1.64	0.79
1:f:90:ASP:C	2:v:715:THR:HG21	2.07	0.79
3:P:11:ALA:HB3	3:P:14:LEU:HB3	1.65	0.79
3:S:93:GLN:HE22	3:T:181:TYR:HE1	1.29	0.79
3:U:93:GLN:HE22	3:V:181:TYR:HE1	1.29	0.79
3:V:11:ALA:HB3	3:V:14:LEU:HB3	1.64	0.79
2:s:188:VAL:CB	2:x:181:ASP:OD2	2.28	0.79
2:t:698:ILE:HD13	2:u:707:TRP:CH2	2.15	0.79
2:v:698:ILE:HD13	2:w:707:TRP:CH2	2.17	0.79
3:Q:93:GLN:HE22	3:R:181:TYR:HE1	1.29	0.79
3:T:11:ALA:HB3	3:T:14:LEU:HB3	1.65	0.79
3:R:11:ALA:HB3	3:R:14:LEU:HB3	1.65	0.79
1:r:90:ASP:C	2:x:715:THR:HG21	2.08	0.79
2:s:181:ASP:OD2	2:t:188:VAL:CB	2.29	0.79
2:u:698:ILE:HD13	2:v:707:TRP:CH2	2.17	0.79
2:t:181:ASP:OD2	2:u:188:VAL:CB	2.24	0.78
2:t:479:VAL:HG22	2:u:477:GLN:O	1.83	0.78
2:t:476:VAL:HG23	2:u:533:GLU:OE2	1.81	0.78
1:o:91:GLY:N	2:s:715:THR:CG2	2.46	0.78
1:r:90:ASP:C	2:x:715:THR:CG2	2.55	0.78
3:P:98:ASN:O	3:Q:129:GLU:CG	2.32	0.78
1:e:48:THR:HG22	3:X:83:ASP:HB2	1.66	0.78
3:V:98:ASN:O	3:W:129:GLU:CG	2.31	0.78
2:u:479:VAL:HG22	2:v:477:GLN:O	1.84	0.78
2:v:476:VAL:HG23	2:w:533:GLU:OE2	1.83	0.78
3:R:97:VAL:HG21	3:S:125:ARG:NH2	1.99	0.78
2:v:479:VAL:HG22	2:w:477:GLN:O	1.84	0.78
3:V:97:VAL:HG21	3:W:125:ARG:NH2	1.98	0.78
1:f:91:GLY:N	2:v:715:THR:CG2	2.46	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:u:722:ASN:HD22	3:W:27:PRO:HG3	1.47	0.78
1:p:93:ILE:HG12	2:x:742:ARG:NH1	2.00	0.77
2:v:722:ASN:HD22	3:M:27:PRO:HG3	1.49	0.77
2:s:476:VAL:HG23	2:t:533:GLU:OE2	1.84	0.77
2:u:790:ARG:NH1	3:W:152:GLY:HA3	2.00	0.77
2:v:234:THR:HB	2:w:217:GLN:HE22	1.50	0.77
1:a:93:ILE:HG12	2:w:742:ARG:NH1	2.00	0.77
3:N:98:ASN:O	3:O:129:GLU:CG	2.33	0.77
1:g:10:THR:HG21	3:U:74:TYR:CD2	2.20	0.77
1:g:10:THR:HG21	3:U:74:TYR:HE2	1.48	0.77
1:l:91:GLY:N	2:t:715:THR:CG2	2.48	0.77
2:s:433:LYS:HG2	2:t:387:ASP:OD2	1.85	0.77
2:v:790:ARG:NH1	3:M:152:GLY:HA3	2.00	0.77
3:R:98:ASN:O	3:S:129:GLU:CG	2.32	0.77
1:q:48:THR:HG22	3:P:83:ASP:HB2	1.66	0.77
3:X:68:THR:HG22	3:X:118:THR:HG22	1.67	0.76
2:s:217:GLN:HE22	2:x:234:THR:HB	1.49	0.76
2:u:181:ASP:OD2	2:v:188:VAL:CB	2.31	0.76
2:u:722:ASN:HD22	3:W:27:PRO:CG	1.98	0.76
3:V:68:THR:HG22	3:V:118:THR:HG22	1.67	0.76
1:g:93:ILE:HG12	2:u:742:ARG:NH1	2.00	0.76
1:c:91:GLY:N	2:w:715:THR:CG2	2.48	0.76
1:k:48:THR:HG22	3:T:83:ASP:HB2	1.67	0.76
1:n:48:THR:HG22	3:R:83:ASP:HB2	1.68	0.76
2:s:477:GLN:O	2:x:479:VAL:HG22	1.83	0.76
1:r:91:GLY:N	2:x:715:THR:CG2	2.49	0.76
2:w:698:ILE:HG23	2:x:707:TRP:CZ2	2.20	0.76
1:j:93:ILE:HG12	2:t:742:ARG:NH1	2.00	0.76
2:s:479:VAL:HG22	2:t:477:GLN:O	1.84	0.76
2:t:698:ILE:HG23	2:u:707:TRP:CZ2	2.21	0.76
3:T:68:THR:HG22	3:T:118:THR:HG22	1.66	0.76
2:s:456:ARG:NH1	2:x:482:VAL:HG11	2.01	0.76
3:N:68:THR:HG22	3:N:118:THR:HG22	1.67	0.76
1:e:8:VAL:HG22	1:e:76:ARG:HB2	1.68	0.76
2:w:479:VAL:HG22	2:x:477:GLN:O	1.84	0.76
1:h:8:VAL:HG22	1:h:76:ARG:HB2	1.68	0.75
2:s:698:ILE:HD13	2:t:707:TRP:CH2	2.17	0.75
1:o:93:ILE:HG12	2:s:746:LEU:HD23	1.68	0.75
3:T:98:ASN:O	3:U:129:GLU:CG	2.34	0.75
1:n:8:VAL:HG22	1:n:76:ARG:HB2	1.68	0.75
1:q:8:VAL:HG22	1:q:76:ARG:HB2	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:465:SER:HB2	2:t:559:SER:HB3	1.69	0.75
2:s:477:GLN:HG2	2:x:478:ASP:HB2	1.69	0.75
2:t:433:LYS:HG2	2:u:387:ASP:OD2	1.85	0.75
2:t:790:ARG:NH1	3:U:152:GLY:HA3	2.01	0.75
1:j:10:THR:HG21	3:S:74:TYR:HE2	1.49	0.75
1:k:93:ILE:HG21	2:t:732:ALA:H	1.51	0.75
1:m:10:THR:HG21	3:Q:74:TYR:CD2	2.20	0.75
2:s:698:ILE:HG23	2:t:707:TRP:CZ2	2.22	0.75
2:t:478:ASP:HB2	2:u:477:GLN:HG2	1.69	0.75
2:w:234:THR:HB	2:x:217:GLN:HE22	1.47	0.75
1:h:48:THR:HG22	3:V:83:ASP:HB2	1.69	0.75
1:q:38:GLY:HA2	1:q:71:THR:H	1.52	0.75
2:s:234:THR:HB	2:t:217:GLN:HE22	1.50	0.75
2:v:433:LYS:HG2	2:w:387:ASP:OD2	1.85	0.75
2:w:433:LYS:HG2	2:x:387:ASP:OD2	1.86	0.75
1:n:38:GLY:HA2	1:n:71:THR:H	1.52	0.75
3:N:97:VAL:HG21	3:O:125:ARG:NH2	1.99	0.75
1:b:38:GLY:HA2	1:b:71:THR:H	1.52	0.75
1:k:38:GLY:HA2	1:k:71:THR:H	1.52	0.75
1:q:93:ILE:HG21	2:x:732:ALA:H	1.51	0.75
1:j:85:LEU:H	1:j:105:GLN:HE22	1.33	0.75
1:m:85:LEU:H	1:m:105:GLN:HE22	1.33	0.75
2:t:722:ASN:HD22	3:U:27:PRO:CG	2.00	0.75
2:u:234:THR:HB	2:v:217:GLN:HE22	1.50	0.75
2:w:722:ASN:HD22	3:O:27:PRO:HG3	1.52	0.75
1:a:10:THR:HG21	3:M:74:TYR:CD2	2.21	0.74
1:h:38:GLY:HA2	1:h:71:THR:H	1.52	0.74
3:M:178:TYR:CD1	3:X:88:MET:HG2	2.22	0.74
3:T:93:GLN:NE2	3:U:179:GLY:O	2.20	0.74
1:b:8:VAL:HG22	1:b:76:ARG:HB2	1.67	0.74
2:t:377:PHE:O	2:t:390:PRO:HG3	1.88	0.74
2:t:722:ASN:HD22	3:U:27:PRO:HG3	1.50	0.74
2:u:729:TYR:CE1	3:V:37:ASN:HA	2.18	0.74
3:P:68:THR:HG22	3:P:118:THR:HG22	1.67	0.74
3:R:68:THR:HG22	3:R:118:THR:HG22	1.66	0.74
1:e:38:GLY:HA2	1:e:71:THR:H	1.52	0.74
1:k:8:VAL:HG22	1:k:76:ARG:HB2	1.67	0.74
2:u:482:VAL:HG11	2:v:456:ARG:NH1	2.02	0.74
2:w:482:VAL:HG13	2:x:456:ARG:HD2	1.70	0.74
3:P:97:VAL:HG21	3:Q:125:ARG:NH2	1.98	0.74
2:t:482:VAL:HG11	2:u:456:ARG:NH1	2.02	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:u:758:VAL:HG11	3:V:150:PHE:HE1	1.52	0.74
3:T:97:VAL:HG21	3:U:125:ARG:NH2	2.00	0.74
1:h:93:ILE:HG21	2:u:732:ALA:H	1.51	0.74
2:s:387:ASP:OD2	2:x:433:LYS:HG2	1.87	0.74
2:u:698:ILE:HG23	2:v:707:TRP:CZ2	2.23	0.74
2:s:377:PHE:O	2:s:390:PRO:HG3	1.88	0.74
2:t:234:THR:HB	2:u:217:GLN:HE22	1.46	0.74
2:s:456:ARG:HD2	2:x:482:VAL:HG13	1.68	0.74
2:w:465:SER:HB2	2:x:559:SER:HB3	1.70	0.74
1:p:10:THR:HG21	3:O:74:TYR:CD2	2.22	0.74
2:u:377:PHE:O	2:u:390:PRO:HG3	1.88	0.74
2:v:698:ILE:HG23	2:w:707:TRP:CZ2	2.22	0.74
3:R:93:GLN:NE2	3:S:179:GLY:O	2.20	0.74
2:w:478:ASP:HB2	2:x:477:GLN:HG2	1.70	0.74
1:b:93:ILE:HG21	2:w:732:ALA:H	1.52	0.73
2:u:478:ASP:HB2	2:v:477:GLN:HG2	1.70	0.73
2:v:478:ASP:HB2	2:w:477:GLN:HG2	1.69	0.73
2:v:482:VAL:HG11	2:w:456:ARG:NH1	2.03	0.73
2:w:790:ARG:NH1	3:O:152:GLY:HA3	2.03	0.73
3:M:125:ARG:HH22	3:X:97:VAL:CG2	1.99	0.73
3:M:179:GLY:O	3:X:93:GLN:NE2	2.21	0.73
2:s:729:TYR:CE1	3:R:37:ASN:HA	2.23	0.73
2:u:161:TYR:HB3	2:u:181:ASP:HB3	1.70	0.73
2:u:482:VAL:HG13	2:v:456:ARG:HD2	1.69	0.73
2:v:465:SER:HB2	2:w:559:SER:HB3	1.69	0.73
3:N:93:GLN:NE2	3:O:179:GLY:O	2.20	0.73
2:t:729:TYR:CE1	3:T:37:ASN:HA	2.18	0.73
2:w:377:PHE:O	2:w:390:PRO:HG3	1.87	0.73
2:s:707:TRP:CZ2	2:x:698:ILE:HG23	2.23	0.73
1:i:93:ILE:HG12	2:u:746:LEU:HD23	1.69	0.73
1:m:10:THR:HG21	3:Q:74:TYR:HE2	1.52	0.73
2:s:478:ASP:HB2	2:t:477:GLN:HG2	1.70	0.73
2:x:377:PHE:O	2:x:390:PRO:HG3	1.87	0.73
1:d:85:LEU:H	1:d:105:GLN:HE22	1.34	0.73
1:f:93:ILE:HG12	2:v:746:LEU:HD23	1.69	0.73
2:s:790:ARG:NH1	3:S:152:GLY:HA3	2.03	0.73
1:p:85:LEU:H	1:p:105:GLN:HE22	1.33	0.73
2:t:465:SER:HB2	2:u:559:SER:HB3	1.70	0.73
2:v:377:PHE:O	2:v:390:PRO:HG3	1.88	0.73
2:x:729:TYR:CE1	3:P:37:ASN:HA	2.24	0.73
1:g:85:LEU:H	1:g:105:GLN:HE22	1.33	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:161:TYR:HB3	2:t:181:ASP:HB3	1.70	0.73
1:a:85:LEU:H	1:a:105:GLN:HE22	1.33	0.72
2:t:482:VAL:HG13	2:u:456:ARG:HD2	1.69	0.72
2:w:482:VAL:HG11	2:x:456:ARG:NH1	2.03	0.72
1:p:10:THR:HG21	3:O:74:TYR:HE2	1.53	0.72
2:x:722:ASN:HD22	3:Q:27:PRO:HG3	1.53	0.72
3:N:97:VAL:CG2	3:O:125:ARG:HH22	2.02	0.72
2:v:161:TYR:HB3	2:v:181:ASP:HB3	1.70	0.72
1:d:10:THR:HG21	3:W:74:TYR:CD2	2.23	0.72
1:n:93:ILE:HG21	2:s:732:ALA:H	1.55	0.72
2:s:559:SER:HB3	2:x:465:SER:HB2	1.72	0.72
2:s:722:ASN:HD22	3:S:27:PRO:HG3	1.52	0.72
2:u:727:TRP:HB3	3:V:36:ALA:O	1.90	0.72
3:N:88:MET:HG2	3:O:178:TYR:CD1	2.25	0.72
1:c:93:ILE:HG12	2:w:746:LEU:HD23	1.72	0.72
1:m:121:ILE:HG12	1:o:129:LEU:HD23	1.72	0.72
2:u:433:LYS:HG2	2:v:387:ASP:OD2	1.89	0.72
3:V:88:MET:HG2	3:W:178:TYR:CD1	2.24	0.72
1:e:93:ILE:HG21	2:v:732:ALA:H	1.54	0.72
2:t:758:VAL:HG11	3:T:150:PHE:HE1	1.53	0.72
2:v:482:VAL:HG13	2:w:456:ARG:HD2	1.70	0.72
3:P:93:GLN:NE2	3:Q:179:GLY:O	2.21	0.72
2:v:722:ASN:HD22	3:M:27:PRO:CG	2.03	0.72
1:j:121:ILE:HG12	1:l:129:LEU:HD23	1.72	0.72
1:g:121:ILE:HG12	1:i:129:LEU:HD23	1.72	0.71
1:d:93:ILE:HG12	2:v:742:ARG:NH1	2.05	0.71
2:v:729:TYR:CE1	3:X:37:ASN:HA	2.22	0.71
3:M:148:ASN:HD21	3:M:157:GLU:HG3	1.55	0.71
3:O:148:ASN:HD21	3:O:157:GLU:HG3	1.55	0.71
3:V:93:GLN:NE2	3:W:179:GLY:O	2.21	0.71
1:p:121:ILE:HG12	1:r:129:LEU:HD23	1.72	0.71
1:r:93:ILE:HG12	2:x:746:LEU:HD23	1.73	0.71
2:w:722:ASN:HD22	3:O:27:PRO:CG	2.04	0.71
2:x:722:ASN:HD22	3:Q:27:PRO:CG	2.03	0.71
1:l:93:ILE:HG12	2:t:746:LEU:HD23	1.72	0.71
2:u:377:PHE:O	2:u:390:PRO:HB3	1.91	0.71
2:v:758:VAL:HG11	3:X:150:PHE:HE1	1.56	0.71
2:s:161:TYR:HB3	2:s:181:ASP:HB3	1.70	0.71
2:s:377:PHE:O	2:s:390:PRO:HB3	1.91	0.71
2:x:377:PHE:O	2:x:390:PRO:HB3	1.91	0.71
3:W:148:ASN:HD21	3:W:157:GLU:HG3	1.56	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:97:VAL:CG2	3:W:125:ARG:HH22	2.01	0.71
2:s:722:ASN:HD22	3:S:27:PRO:CG	2.03	0.71
2:x:790:ARG:NH1	3:Q:152:GLY:HA3	2.06	0.71
3:Q:148:ASN:HD21	3:Q:157:GLU:HG3	1.56	0.71
3:S:148:ASN:HD21	3:S:157:GLU:HG3	1.56	0.71
3:U:148:ASN:HD21	3:U:157:GLU:HG3	1.55	0.71
2:w:161:TYR:HB3	2:w:181:ASP:HB3	1.70	0.71
3:M:28:PRO:CB	3:X:45:ARG:HH12	2.04	0.71
1:d:10:THR:HG21	3:W:74:TYR:HE2	1.51	0.70
1:d:121:ILE:HG12	1:f:129:LEU:HD23	1.72	0.70
1:m:93:ILE:HG12	2:s:742:ARG:NH1	2.05	0.70
2:w:377:PHE:O	2:w:390:PRO:HB3	1.91	0.70
2:x:758:VAL:HG11	3:P:150:PHE:HE1	1.55	0.70
3:R:88:MET:HG2	3:S:178:TYR:CD1	2.24	0.70
1:g:110:ALA:HB1	1:h:109:VAL:HG12	1.73	0.70
2:w:729:TYR:CE1	3:N:37:ASN:HA	2.26	0.70
1:g:125:ASN:ND2	3:U:75:SER:O	2.25	0.70
2:s:482:VAL:HG13	2:t:456:ARG:HD2	1.71	0.70
2:t:338:ASN:HD21	2:t:379:PRO:HD2	1.57	0.70
2:u:338:ASN:HD21	2:u:379:PRO:HD2	1.57	0.70
2:u:465:SER:HB2	2:v:559:SER:HB3	1.71	0.70
1:a:121:ILE:HG12	1:c:129:LEU:HD23	1.72	0.70
2:t:377:PHE:O	2:t:390:PRO:HB3	1.91	0.70
2:x:161:TYR:HB3	2:x:181:ASP:HB3	1.70	0.70
1:a:10:THR:HG21	3:M:74:TYR:HE2	1.53	0.70
2:v:338:ASN:HD21	2:v:379:PRO:HD2	1.57	0.70
1:a:110:ALA:HB1	1:b:109:VAL:HG12	1.73	0.70
2:w:338:ASN:HD21	2:w:379:PRO:HD2	1.57	0.70
3:U:5:ASP:CB	3:V:10:THR:OG1	2.40	0.70
2:x:66:ILE:HB	2:x:80:VAL:HG23	1.73	0.70
3:P:88:MET:HG2	3:Q:178:TYR:CD1	2.23	0.70
1:d:125:ASN:ND2	3:W:75:SER:O	2.25	0.70
2:s:594:MET:HB2	2:s:597:LYS:HD3	1.74	0.70
2:v:377:PHE:O	2:v:390:PRO:HB3	1.91	0.70
2:t:594:MET:HB2	2:t:597:LYS:HD3	1.74	0.69
2:w:66:ILE:HB	2:w:80:VAL:HG23	1.73	0.69
2:s:377:PHE:O	2:s:390:PRO:CB	2.40	0.69
3:O:5:ASP:CB	3:P:10:THR:OG1	2.40	0.69
3:U:175:GLU:HA	3:U:178:TYR:HB3	1.74	0.69
2:s:66:ILE:HB	2:s:80:VAL:HG23	1.73	0.69
2:t:66:ILE:HB	2:t:80:VAL:HG23	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:377:PHE:O	2:t:390:PRO:CB	2.40	0.69
2:t:727:TRP:HB3	3:T:36:ALA:O	1.92	0.69
2:u:377:PHE:O	2:u:390:PRO:CB	2.40	0.69
3:T:88:MET:HG2	3:U:178:TYR:CD1	2.26	0.69
1:m:110:ALA:HB1	1:n:109:VAL:HG12	1.73	0.69
2:s:240:ALA:HB3	2:s:242:GLN:HG2	1.74	0.69
2:w:567:ASN:HB3	2:w:569:PHE:H	1.58	0.69
2:w:758:VAL:HG11	3:N:150:PHE:HE1	1.57	0.69
3:V:45:ARG:HH12	3:W:28:PRO:CB	2.06	0.69
2:v:66:ILE:HB	2:v:80:VAL:HG23	1.73	0.69
2:v:727:TRP:HB3	3:X:36:ALA:O	1.92	0.69
2:x:240:ALA:HB3	2:x:242:GLN:HG2	1.74	0.69
2:x:594:MET:HB2	2:x:597:LYS:HD3	1.74	0.69
1:p:110:ALA:HB1	1:q:109:VAL:HG12	1.73	0.69
2:u:594:MET:HB2	2:u:597:LYS:HD3	1.74	0.69
1:j:110:ALA:HB1	1:k:109:VAL:HG12	1.73	0.69
2:x:338:ASN:HD21	2:x:379:PRO:HD2	1.57	0.69
2:x:567:ASN:HB3	2:x:569:PHE:H	1.57	0.69
3:M:175:GLU:HA	3:M:178:TYR:HB3	1.74	0.69
1:d:110:ALA:HB1	1:e:109:VAL:HG12	1.73	0.69
2:s:482:VAL:HG11	2:t:456:ARG:NH1	2.05	0.69
2:v:377:PHE:O	2:v:390:PRO:CB	2.41	0.69
2:x:377:PHE:O	2:x:390:PRO:CB	2.40	0.69
3:M:5:ASP:CB	3:N:10:THR:OG1	2.40	0.69
3:O:175:GLU:HA	3:O:178:TYR:HB3	1.74	0.69
3:P:175:GLU:HA	3:P:178:TYR:HB3	1.75	0.69
3:Q:5:ASP:CB	3:R:10:THR:OG1	2.40	0.69
2:s:338:ASN:HD21	2:s:379:PRO:HD2	1.57	0.69
2:s:758:VAL:HG11	3:R:150:PHE:HE1	1.56	0.69
2:u:66:ILE:HB	2:u:80:VAL:HG23	1.73	0.69
2:v:567:ASN:HB3	2:v:569:PHE:H	1.58	0.69
3:R:175:GLU:HA	3:R:178:TYR:HB3	1.74	0.69
3:N:175:GLU:HA	3:N:178:TYR:HB3	1.74	0.69
2:t:240:ALA:HB3	2:t:242:GLN:HG2	1.74	0.68
2:w:377:PHE:O	2:w:390:PRO:CB	2.41	0.68
3:Q:175:GLU:HA	3:Q:178:TYR:HB3	1.74	0.68
3:S:175:GLU:HA	3:S:178:TYR:HB3	1.74	0.68
2:t:567:ASN:HB3	2:t:569:PHE:H	1.58	0.68
2:v:240:ALA:HB3	2:v:242:GLN:HG2	1.74	0.68
3:W:5:ASP:CB	3:X:10:THR:OG1	2.40	0.68
3:V:175:GLU:HA	3:V:178:TYR:HB3	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:86:VAL:CG2	3:N:31:THR:CG2	2.64	0.68
2:w:240:ALA:HB3	2:w:242:GLN:HG2	1.74	0.68
2:w:594:MET:HB2	2:w:597:LYS:HD3	1.74	0.68
3:R:97:VAL:CG2	3:S:125:ARG:HH22	2.01	0.68
1:n:60:LEU:HD11	1:n:73:ILE:HD11	1.76	0.68
2:u:567:ASN:HB3	2:u:569:PHE:H	1.57	0.68
3:W:175:GLU:HA	3:W:178:TYR:HB3	1.74	0.68
1:b:60:LEU:HD11	1:b:73:ILE:HD11	1.76	0.68
1:p:125:ASN:ND2	3:O:75:SER:O	2.27	0.68
2:v:594:MET:HB2	2:v:597:LYS:HD3	1.74	0.68
3:P:45:ARG:HH12	3:Q:28:PRO:CB	2.07	0.68
3:T:97:VAL:CG2	3:U:125:ARG:HH22	2.03	0.68
2:s:567:ASN:HB3	2:s:569:PHE:H	1.58	0.68
2:u:240:ALA:HB3	2:u:242:GLN:HG2	1.74	0.68
3:P:97:VAL:CG2	3:Q:125:ARG:HH22	2.00	0.68
3:R:45:ARG:HH12	3:S:28:PRO:CB	2.07	0.68
3:X:175:GLU:HA	3:X:178:TYR:HB3	1.75	0.68
1:k:60:LEU:HD11	1:k:73:ILE:HD11	1.76	0.67
1:e:49:ASP:OD1	1:e:49:ASP:N	2.27	0.67
1:q:60:LEU:HD11	1:q:73:ILE:HD11	1.76	0.67
3:T:175:GLU:HA	3:T:178:TYR:HB3	1.75	0.67
1:n:49:ASP:OD1	1:n:49:ASP:N	2.27	0.67
3:T:45:ARG:HH12	3:U:28:PRO:CB	2.08	0.67
3:M:132:GLU:HG2	3:X:56:SER:OG	1.95	0.67
1:e:60:LEU:HD11	1:e:73:ILE:HD11	1.76	0.67
3:M:28:PRO:HB3	3:X:45:ARG:NH1	2.09	0.67
3:N:45:ARG:HH12	3:O:28:PRO:CB	2.08	0.67
1:j:131:ALA:O	1:j:134:ARG:HG2	1.95	0.67
1:b:94:LEU:CD1	2:w:736:LEU:HD21	2.17	0.67
1:d:131:ALA:O	1:d:134:ARG:HG2	1.95	0.67
1:h:60:LEU:HD11	1:h:73:ILE:HD11	1.76	0.67
2:u:614:THR:HG23	2:u:658:LEU:HB2	1.77	0.66
3:S:5:ASP:CB	3:T:10:THR:OG1	2.40	0.66
1:m:131:ALA:O	1:m:134:ARG:HG2	1.95	0.66
1:o:90:ASP:C	2:s:715:THR:HG22	2.20	0.66
1:g:36:LEU:HD12	1:g:70:TYR:HB3	1.77	0.66
3:V:56:SER:OG	3:W:132:GLU:HG2	1.95	0.66
1:a:131:ALA:O	1:a:134:ARG:HG2	1.95	0.66
1:g:131:ALA:O	1:g:134:ARG:HG2	1.95	0.66
1:j:36:LEU:HD12	1:j:70:TYR:HB3	1.77	0.66
2:x:281:TYR:CD2	2:x:296:GLY:HA2	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:d:104:ILE:CD1	3:X:8:VAL:CG2	2.72	0.66
1:n:86:VAL:CG2	3:R:31:THR:CG2	2.64	0.66
1:p:131:ALA:O	1:p:134:ARG:HG2	1.95	0.66
2:s:281:TYR:CD2	2:s:296:GLY:HA2	2.31	0.66
3:N:94:SER:OG	3:O:178:TYR:CD1	2.49	0.66
1:l:90:ASP:HB3	2:t:715:THR:CG2	2.15	0.66
2:w:281:TYR:CD2	2:w:296:GLY:HA2	2.31	0.65
1:b:67:ALA:HB3	3:N:74:TYR:OH	1.96	0.65
1:b:49:ASP:N	1:b:49:ASP:OD1	2.27	0.65
2:v:614:THR:HG23	2:v:658:LEU:HB2	1.77	0.65
2:w:614:THR:HG23	2:w:658:LEU:HB2	1.77	0.65
1:d:36:LEU:HD12	1:d:70:TYR:HB3	1.77	0.65
1:i:9:LEU:HD21	1:i:23:PRO:HD2	1.79	0.65
1:j:125:ASN:ND2	3:S:75:SER:O	2.29	0.65
1:i:90:ASP:C	2:u:715:THR:HG22	2.21	0.65
1:m:36:LEU:HD12	1:m:70:TYR:HB3	1.78	0.65
1:m:125:ASN:ND2	3:Q:75:SER:O	2.29	0.65
2:v:281:TYR:CD2	2:v:296:GLY:HA2	2.31	0.65
1:e:94:LEU:CD1	2:v:736:LEU:HD21	2.17	0.65
2:t:281:TYR:CD2	2:t:296:GLY:HA2	2.31	0.65
2:u:156:VAL:HG21	2:u:197:ALA:HB2	1.79	0.65
1:g:101:VAL:HG22	3:V:6:MET:HE1	1.78	0.65
1:i:90:ASP:HB3	2:u:715:THR:CG2	2.16	0.65
1:j:101:VAL:HG22	3:T:6:MET:HE1	1.79	0.65
1:p:36:LEU:HD12	1:p:70:TYR:HB3	1.77	0.65
1:r:90:ASP:HB3	2:x:715:THR:CG2	2.16	0.65
2:u:281:TYR:CD2	2:u:296:GLY:HA2	2.31	0.65
3:R:94:SER:OG	3:S:178:TYR:CD1	2.48	0.65
3:V:45:ARG:NH1	3:W:28:PRO:HB3	2.11	0.65
1:k:49:ASP:OD1	1:k:49:ASP:N	2.27	0.65
1:n:94:LEU:HB2	2:s:736:LEU:CD2	2.27	0.65
2:v:161:TYR:CB	2:w:188:VAL:HG11	2.27	0.65
2:x:614:THR:HG23	2:x:658:LEU:HB2	1.77	0.65
1:f:9:LEU:HD21	1:f:23:PRO:HD2	1.79	0.65
1:k:94:LEU:CD1	2:t:736:LEU:HD21	2.18	0.65
1:l:9:LEU:HD21	1:l:23:PRO:HD2	1.79	0.65
2:t:614:THR:HG23	2:t:658:LEU:HB2	1.77	0.65
1:e:94:LEU:HB2	2:v:736:LEU:CD2	2.27	0.65
1:f:90:ASP:C	2:v:715:THR:HG22	2.20	0.65
2:s:614:THR:HG23	2:s:658:LEU:HB2	1.77	0.65
3:T:56:SER:OG	3:U:132:GLU:HG2	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:q:94:LEU:CD1	2:x:736:LEU:HD21	2.18	0.64
2:x:727:TRP:HB3	3:P:36:ALA:O	1.97	0.64
3:N:56:SER:OG	3:O:132:GLU:HG2	1.97	0.64
1:a:36:LEU:HD12	1:a:70:TYR:HB3	1.77	0.64
2:v:156:VAL:HG21	2:v:197:ALA:HB2	1.79	0.64
1:m:104:ILE:CD1	3:R:8:VAL:CG2	2.74	0.64
2:s:156:VAL:HG21	2:s:197:ALA:HB2	1.79	0.64
2:x:156:VAL:HG21	2:x:197:ALA:HB2	1.79	0.64
3:P:45:ARG:NH1	3:Q:28:PRO:HB3	2.12	0.64
2:t:698:ILE:HG23	2:u:707:TRP:HZ2	1.62	0.64
2:w:156:VAL:HG21	2:w:197:ALA:HB2	1.79	0.64
3:P:56:SER:OG	3:Q:132:GLU:HG2	1.97	0.64
3:V:94:SER:OG	3:W:178:TYR:CD1	2.48	0.64
1:b:62:LYS:HE2	3:N:72:ASP:OD1	1.98	0.64
3:Q:54:ILE:HG13	3:Q:138:ILE:HG12	1.80	0.64
3:R:56:SER:OG	3:S:132:GLU:HG2	1.98	0.64
3:T:94:SER:OG	3:U:178:TYR:CD1	2.50	0.64
1:a:29:ARG:NE	3:N:5:ASP:HB3	2.11	0.64
1:d:13:LEU:HG	1:d:64:TRP:O	1.98	0.64
1:p:29:ARG:NE	3:P:5:ASP:HB3	2.11	0.64
2:s:727:TRP:HB3	3:R:36:ALA:O	1.97	0.64
3:S:54:ILE:HG13	3:S:138:ILE:HG12	1.80	0.64
1:c:90:ASP:C	2:w:715:THR:HG22	2.23	0.64
1:r:9:LEU:HD21	1:r:23:PRO:HD2	1.79	0.64
1:a:125:ASN:ND2	3:M:75:SER:O	2.31	0.63
1:c:9:LEU:HD21	1:c:23:PRO:HD2	1.79	0.63
1:m:101:VAL:HG22	3:R:6:MET:HE1	1.79	0.63
3:O:54:ILE:HG13	3:O:138:ILE:HG12	1.79	0.63
1:o:9:LEU:HD21	1:o:23:PRO:HD2	1.79	0.63
1:g:104:ILE:HD13	3:V:8:VAL:HG23	1.81	0.63
3:W:54:ILE:HG13	3:W:138:ILE:HG12	1.80	0.63
2:t:156:VAL:HG21	2:t:197:ALA:HB2	1.79	0.63
3:M:178:TYR:CD1	3:X:94:SER:OG	2.46	0.63
1:c:90:ASP:HB3	2:w:715:THR:CG2	2.15	0.63
1:j:13:LEU:HG	1:j:64:TRP:O	1.98	0.63
1:j:84:ARG:NH2	1:l:103:GLN:OE1	2.32	0.63
1:m:29:ARG:NE	3:R:5:ASP:HB3	2.12	0.63
1:o:90:ASP:HB3	2:s:715:THR:CG2	2.19	0.63
1:p:13:LEU:HG	1:p:64:TRP:O	1.98	0.63
3:R:45:ARG:NH1	3:S:28:PRO:HB3	2.13	0.63
1:m:13:LEU:HG	1:m:64:TRP:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:q:86:VAL:CG2	3:p:31:THR:CG2	2.65	0.63
1:m:84:ARG:NH2	1:o:103:GLN:OE1	2.32	0.63
1:p:84:ARG:NH2	1:r:103:GLN:OE1	2.32	0.63
2:w:377:PHE:O	2:w:390:PRO:CG	2.47	0.63
3:n:45:ARG:NH1	3:o:28:PRO:HB3	2.13	0.63
1:l:90:ASP:C	2:t:715:THR:HG22	2.23	0.63
2:s:163:ARG:O	2:s:179:ILE:HG13	1.99	0.63
2:t:377:PHE:O	2:t:390:PRO:CG	2.47	0.63
2:w:727:TRP:HB3	3:n:36:ALA:O	1.98	0.63
1:g:13:LEU:HG	1:g:64:TRP:O	1.98	0.63
1:g:84:ARG:NH2	1:i:103:GLN:OE1	2.32	0.63
1:p:101:VAL:HG22	3:p:6:MET:HE1	1.81	0.63
2:s:632:THR:HG22	2:s:642:VAL:HG22	1.81	0.62
2:s:698:ILE:HG23	2:t:707:TRP:HZ2	1.64	0.62
2:x:377:PHE:O	2:x:390:PRO:CG	2.47	0.62
1:b:94:LEU:HB2	2:w:736:LEU:CD2	2.29	0.62
1:r:90:ASP:C	2:x:715:THR:HG22	2.24	0.62
1:d:84:ARG:NH2	1:f:103:GLN:OE1	2.32	0.62
2:s:270:VAL:HG11	2:t:290:VAL:HG11	1.81	0.62
2:s:377:PHE:O	2:s:390:PRO:CG	2.47	0.62
2:t:632:THR:HG22	2:t:642:VAL:HG22	1.82	0.62
2:u:377:PHE:O	2:u:390:PRO:CG	2.47	0.62
1:l:90:ASP:CB	2:t:715:THR:CG2	2.75	0.62
1:n:94:LEU:CD1	2:s:736:LEU:HD21	2.17	0.62
1:n:107:MET:HE1	1:o:84:ARG:HG2	1.82	0.62
1:q:107:MET:HE1	1:r:84:ARG:HG2	1.82	0.62
2:t:163:ARG:O	2:t:179:ILE:HG13	1.99	0.62
2:u:632:THR:HG22	2:u:642:VAL:HG22	1.82	0.62
2:x:163:ARG:O	2:x:179:ILE:HG13	1.99	0.62
1:a:13:LEU:HG	1:a:64:TRP:O	1.98	0.62
1:a:84:ARG:NH2	1:c:103:GLN:OE1	2.32	0.62
1:h:94:LEU:CD1	2:u:736:LEU:HD21	2.19	0.62
2:s:40:GLU:HB2	2:s:43:GLN:HE21	1.65	0.62
2:v:40:GLU:HB2	2:v:43:GLN:HE21	1.65	0.62
3:m:129:GLU:HG3	3:x:98:ASN:O	1.98	0.62
2:v:163:ARG:O	2:v:179:ILE:HG13	1.99	0.62
2:v:377:PHE:O	2:v:390:PRO:CG	2.47	0.62
3:v:98:ASN:O	3:w:129:GLU:HG3	1.99	0.62
1:q:94:LEU:HB2	2:x:736:LEU:CD2	2.30	0.62
2:w:40:GLU:HB2	2:w:43:GLN:HE21	1.65	0.62
2:x:632:THR:HG22	2:x:642:VAL:HG22	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:j:104:ILE:HD13	3:T:8:VAL:HG23	1.81	0.62
2:s:440:THR:HG21	2:s:483:LYS:HE2	1.81	0.62
2:w:698:ILE:CD1	2:x:7:SER:HB3	2.30	0.62
2:x:40:GLU:HB2	2:x:43:GLN:HE21	1.65	0.62
3:M:54:ILE:HG13	3:M:138:ILE:HG12	1.80	0.62
3:U:54:ILE:HG13	3:U:138:ILE:HG12	1.80	0.62
1:k:86:VAL:CG2	3:T:31:THR:CG2	2.68	0.61
1:k:107:MET:HE1	1:l:84:ARG:HG2	1.82	0.61
1:n:94:LEU:HB2	2:s:736:LEU:HD22	1.82	0.61
1:q:49:ASP:OD1	1:q:49:ASP:N	2.27	0.61
2:v:440:THR:HG21	2:v:483:LYS:HE2	1.82	0.61
3:T:45:ARG:NH1	3:U:28:PRO:HB3	2.13	0.61
1:d:101:VAL:HG22	3:X:6:MET:HE1	1.80	0.61
2:v:632:THR:HG22	2:v:642:VAL:HG22	1.82	0.61
2:w:632:THR:HG22	2:w:642:VAL:HG22	1.82	0.61
3:P:94:SER:OG	3:Q:178:TYR:CD1	2.49	0.61
1:b:107:MET:HE1	1:c:84:ARG:HG2	1.82	0.61
1:e:86:VAL:HG22	3:X:31:THR:HG22	1.78	0.61
2:s:120:THR:HG21	2:x:400:ILE:HD11	1.82	0.61
2:u:698:ILE:HG23	2:v:707:TRP:HZ2	1.63	0.61
2:t:440:THR:HG21	2:t:483:LYS:HE2	1.82	0.61
2:t:702:GLN:HB3	2:t:704:ARG:HH21	1.66	0.61
2:w:270:VAL:HG11	2:x:290:VAL:HG11	1.82	0.61
1:e:94:LEU:HB2	2:v:736:LEU:HD22	1.83	0.61
2:u:163:ARG:O	2:u:179:ILE:HG13	1.99	0.61
2:u:355:ARG:HG3	2:u:430:LEU:CD1	2.31	0.61
2:u:702:GLN:HB3	2:u:704:ARG:HH21	1.65	0.61
2:w:698:ILE:HG23	2:x:707:TRP:HZ2	1.62	0.61
2:t:355:ARG:HG3	2:t:430:LEU:CD1	2.31	0.61
1:p:104:ILE:CD1	3:P:8:VAL:CG2	2.76	0.61
2:s:698:ILE:CD1	2:t:7:SER:HB3	2.30	0.61
2:u:40:GLU:HB2	2:u:43:GLN:HE21	1.65	0.61
2:v:270:VAL:HG11	2:w:290:VAL:HG11	1.82	0.61
1:h:107:MET:HE1	1:i:84:ARG:HG2	1.82	0.61
2:t:40:GLU:HB2	2:t:43:GLN:HE21	1.65	0.61
2:w:440:THR:HG21	2:w:483:LYS:HE2	1.82	0.61
3:P:10:THR:HG22	3:P:11:ALA:N	2.16	0.61
1:e:107:MET:HE1	1:f:84:ARG:HG2	1.82	0.61
1:f:90:ASP:HB3	2:v:715:THR:CG2	2.18	0.61
2:s:702:GLN:HB3	2:s:704:ARG:HH21	1.65	0.61
2:s:707:TRP:HZ2	2:x:698:ILE:HG23	1.63	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:w:355:ARG:HG3	2:w:430:LEU:CD1	2.31	0.61
2:x:355:ARG:HG3	2:x:430:LEU:CD1	2.31	0.61
1:i:90:ASP:CB	2:u:715:THR:CG2	2.75	0.60
1:m:104:ILE:HD13	3:R:8:VAL:HG23	1.82	0.60
1:m:110:ALA:CB	1:n:109:VAL:HG12	2.31	0.60
2:s:161:TYR:CB	2:t:188:VAL:HG11	2.28	0.60
2:s:355:ARG:HG3	2:s:430:LEU:CD1	2.31	0.60
2:t:698:ILE:CD1	2:u:7:SER:HB3	2.31	0.60
2:v:355:ARG:HG3	2:v:430:LEU:CD1	2.31	0.60
2:v:698:ILE:CD1	2:w:7:SER:HB3	2.31	0.60
3:V:148:ASN:HD21	3:V:157:GLU:HG3	1.66	0.60
1:g:110:ALA:CB	1:h:109:VAL:HG12	2.31	0.60
1:j:29:ARG:NE	3:T:5:ASP:HB3	2.15	0.60
1:j:76:ARG:HH21	1:j:115:ASP:HB3	1.65	0.60
2:t:109:THR:HG21	2:t:115:ASP:HB2	1.83	0.60
2:u:440:THR:HG21	2:u:483:LYS:HE2	1.82	0.60
3:N:10:THR:HG22	3:N:11:ALA:N	2.16	0.60
2:t:106:TYR:CE1	2:t:132:VAL:HG11	2.37	0.60
3:P:98:ASN:O	3:Q:129:GLU:HG3	2.01	0.60
3:R:98:ASN:O	3:S:129:GLU:HG3	2.02	0.60
3:T:10:THR:HG22	3:T:11:ALA:N	2.15	0.60
1:d:76:ARG:HH21	1:d:115:ASP:HB3	1.65	0.60
1:k:67:ALA:HB3	3:T:74:TYR:OH	2.02	0.60
2:v:400:ILE:HD11	2:w:120:THR:HG21	1.81	0.60
2:w:163:ARG:O	2:w:179:ILE:HG13	1.99	0.60
2:w:400:ILE:HD11	2:x:120:THR:HG21	1.83	0.60
1:h:49:ASP:OD1	1:h:49:ASP:N	2.27	0.60
1:j:110:ALA:CB	1:k:109:VAL:HG12	2.31	0.60
1:k:62:LYS:HE2	3:T:72:ASP:OD1	2.02	0.60
2:u:106:TYR:CE1	2:u:132:VAL:HG11	2.37	0.60
2:w:109:THR:HG21	2:w:115:ASP:HB2	1.84	0.60
1:a:101:VAL:HG22	3:N:6:MET:HE1	1.83	0.60
1:h:94:LEU:HB2	2:u:736:LEU:CD2	2.32	0.60
1:k:94:LEU:HB2	2:t:736:LEU:CD2	2.30	0.60
2:s:106:TYR:CE1	2:s:132:VAL:HG11	2.37	0.60
1:a:110:ALA:CB	1:b:109:VAL:HG12	2.31	0.60
2:t:270:VAL:HG11	2:u:290:VAL:HG11	1.83	0.60
2:u:698:ILE:CD1	2:v:7:SER:HB3	2.32	0.60
2:v:109:THR:HG21	2:v:115:ASP:HB2	1.84	0.60
2:v:698:ILE:HG23	2:w:707:TRP:HZ2	1.64	0.60
3:M:178:TYR:CZ	3:X:94:SER:OG	2.54	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:T:148:ASN:HD21	3:T:157:GLU:HG3	1.66	0.60
1:d:110:ALA:CB	1:e:109:VAL:HG12	2.31	0.60
1:g:104:ILE:CD1	3:V:8:VAL:CG2	2.73	0.60
1:i:91:GLY:N	2:u:715:THR:HG21	2.14	0.60
2:v:702:GLN:HB3	2:v:704:ARG:HH21	1.66	0.60
3:P:11:ALA:HB3	3:P:14:LEU:CB	2.32	0.60
1:b:94:LEU:HB2	2:w:736:LEU:HD22	1.84	0.60
1:g:76:ARG:HH21	1:g:115:ASP:HB3	1.65	0.60
2:t:161:TYR:CB	2:u:188:VAL:HG11	2.30	0.60
2:x:106:TYR:CE1	2:x:132:VAL:HG11	2.37	0.60
2:x:109:THR:HG21	2:x:115:ASP:HB2	1.83	0.60
3:T:98:ASN:O	3:U:129:GLU:HG3	2.02	0.60
3:X:148:ASN:HD21	3:X:157:GLU:HG3	1.66	0.60
1:n:67:ALA:HB3	3:R:74:TYR:OH	2.02	0.60
2:x:440:THR:HG21	2:x:483:LYS:HE2	1.82	0.60
2:x:702:GLN:HB3	2:x:704:ARG:HH21	1.66	0.60
3:N:148:ASN:HD21	3:N:157:GLU:HG3	1.66	0.60
3:R:11:ALA:HB3	3:R:14:LEU:CB	2.32	0.60
3:X:10:THR:HG22	3:X:11:ALA:N	2.16	0.60
1:p:110:ALA:CB	1:q:109:VAL:HG12	2.31	0.59
2:u:788:LEU:HG	3:W:153:ALA:HA	1.84	0.59
2:w:340:TRP:HB3	2:w:344:VAL:HG11	1.84	0.59
2:w:702:GLN:HB3	2:w:704:ARG:HH21	1.65	0.59
3:N:11:ALA:HB3	3:N:14:LEU:CB	2.32	0.59
3:P:148:ASN:HD21	3:P:157:GLU:HG3	1.67	0.59
2:u:391:ILE:HG21	2:u:435:VAL:HG11	1.84	0.59
2:v:106:TYR:CE1	2:v:132:VAL:HG11	2.37	0.59
2:v:161:TYR:HB2	2:w:188:VAL:CG1	2.30	0.59
1:e:86:VAL:CG2	3:X:31:THR:CG2	2.66	0.59
2:s:109:THR:HG21	2:s:115:ASP:HB2	1.83	0.59
2:u:109:THR:HG21	2:u:115:ASP:HB2	1.84	0.59
2:u:758:VAL:HG11	3:V:150:PHE:CE1	2.35	0.59
3:M:134:PHE:CE1	3:M:171:CYS:HB3	2.38	0.59
3:T:11:ALA:HB3	3:T:14:LEU:CB	2.32	0.59
1:d:104:ILE:HD13	3:X:8:VAL:HG23	1.81	0.59
1:k:94:LEU:HB2	2:t:736:LEU:HD22	1.85	0.59
2:s:533:GLU:OE2	2:x:476:VAL:CG2	2.51	0.59
2:v:391:ILE:HG21	2:v:435:VAL:HG11	1.84	0.59
2:w:106:TYR:CE1	2:w:132:VAL:HG11	2.37	0.59
2:w:454:ILE:HD11	2:w:512:CYS:HB2	1.85	0.59
1:e:67:ALA:HB3	3:X:74:TYR:OH	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:91:GLY:N	2:v:715:THR:HG21	2.17	0.59
1:m:76:ARG:HH21	1:m:115:ASP:HB3	1.65	0.59
2:s:7:SER:HB3	2:x:698:ILE:CD1	2.32	0.59
2:s:400:ILE:HD11	2:t:120:THR:HG21	1.82	0.59
2:u:454:ILE:HD11	2:u:512:CYS:HB2	1.85	0.59
2:w:69:ILE:HG23	2:w:120:THR:HG21	1.85	0.59
3:R:10:THR:HG22	3:R:11:ALA:N	2.16	0.59
3:R:148:ASN:HD21	3:R:157:GLU:HG3	1.66	0.59
3:W:134:PHE:CE1	3:W:171:CYS:HB3	2.38	0.59
1:q:62:LYS:HE2	3:P:72:ASP:OD1	2.03	0.59
2:s:69:ILE:HG23	2:s:120:THR:HG21	1.85	0.59
2:t:69:ILE:HG23	2:t:120:THR:HG21	1.85	0.59
2:v:698:ILE:CD1	2:w:707:TRP:CH2	2.82	0.59
2:w:161:TYR:CB	2:x:188:VAL:HG11	2.31	0.59
2:x:340:TRP:HB3	2:x:344:VAL:HG11	1.84	0.59
2:x:391:ILE:HG21	2:x:435:VAL:HG11	1.84	0.59
3:N:98:ASN:O	3:O:129:GLU:HG3	2.02	0.59
3:S:134:PHE:CE1	3:S:171:CYS:HB3	2.38	0.59
2:s:300:GLU:HB2	2:s:340:TRP:HZ2	1.68	0.59
2:t:454:ILE:HD11	2:t:512:CYS:HB2	1.85	0.59
2:v:69:ILE:HG23	2:v:120:THR:HG21	1.85	0.59
2:v:340:TRP:HB3	2:v:344:VAL:HG11	1.84	0.59
3:Q:134:PHE:CE1	3:Q:171:CYS:HB3	2.38	0.59
1:n:62:LYS:HE2	3:R:72:ASP:OD1	2.03	0.59
2:w:391:ILE:HG21	2:w:435:VAL:HG11	1.84	0.59
3:U:134:PHE:CE1	3:U:171:CYS:HB3	2.38	0.59
3:V:11:ALA:HB3	3:V:14:LEU:CB	2.32	0.59
1:g:76:ARG:HH22	1:g:115:ASP:HB3	1.68	0.59
1:o:90:ASP:CB	2:s:715:THR:CG2	2.77	0.59
1:q:94:LEU:HB2	2:x:736:LEU:HD22	1.85	0.59
2:s:454:ILE:HD11	2:s:512:CYS:HB2	1.85	0.59
2:v:300:GLU:HB2	2:v:340:TRP:HZ2	1.68	0.59
1:g:29:ARG:NE	3:V:5:ASP:HB3	2.17	0.58
1:h:114:ARG:NH1	1:i:112:GLU:OE2	2.36	0.58
2:t:391:ILE:HG21	2:t:435:VAL:HG11	1.84	0.58
2:u:300:GLU:HB2	2:u:340:TRP:HZ2	1.68	0.58
2:x:69:ILE:HG23	2:x:120:THR:HG21	1.85	0.58
2:v:790:ARG:HH12	3:M:152:GLY:HA3	1.67	0.58
1:b:114:ARG:NH1	1:c:112:GLU:OE2	2.37	0.58
1:p:104:ILE:HD13	3:P:8:VAL:HG23	1.84	0.58
1:q:67:ALA:HB3	3:P:74:TYR:OH	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:340:TRP:HB3	2:s:344:VAL:HG11	1.84	0.58
2:u:69:ILE:HG23	2:u:120:THR:HG21	1.85	0.58
2:w:698:ILE:CD1	2:x:707:TRP:CH2	2.81	0.58
3:O:134:PHE:CE1	3:O:171:CYS:HB3	2.38	0.58
3:V:10:THR:HG22	3:V:11:ALA:N	2.16	0.58
1:b:48:THR:CG2	3:N:83:ASP:HB2	2.31	0.58
1:k:114:ARG:NH1	1:l:112:GLU:OE2	2.37	0.58
3:O:71:PRO:HA	3:O:78:ILE:HG12	1.85	0.58
3:Q:71:PRO:HA	3:Q:78:ILE:HG12	1.85	0.58
3:V:94:SER:OG	3:W:178:TYR:CZ	2.56	0.58
1:a:103:GLN:HG3	1:b:102:ALA:HB1	1.86	0.58
1:j:103:GLN:HG3	1:k:102:ALA:HB1	1.86	0.58
1:n:86:VAL:HG22	3:R:31:THR:HG22	1.80	0.58
1:q:114:ARG:NH1	1:r:112:GLU:OE2	2.37	0.58
2:s:290:VAL:HG11	2:x:270:VAL:HG11	1.86	0.58
2:t:300:GLU:HB2	2:t:340:TRP:HZ2	1.68	0.58
2:t:702:GLN:HE21	3:U:26:GLU:HG2	1.69	0.58
2:x:300:GLU:HB2	2:x:340:TRP:HZ2	1.68	0.58
1:a:29:ARG:CZ	3:N:5:ASP:HB3	2.33	0.58
1:d:29:ARG:NE	3:X:5:ASP:HB3	2.18	0.58
1:g:103:GLN:HG3	1:h:102:ALA:HB1	1.86	0.58
1:n:114:ARG:NH1	1:o:112:GLU:OE2	2.37	0.58
2:t:758:VAL:HG11	3:T:150:PHE:CE1	2.37	0.58
1:h:94:LEU:HB2	2:u:736:LEU:HD22	1.86	0.58
1:m:103:GLN:HG3	1:n:102:ALA:HB1	1.86	0.58
1:p:103:GLN:HG3	1:q:102:ALA:HB1	1.86	0.58
2:u:340:TRP:HB3	2:u:344:VAL:HG11	1.84	0.58
2:x:454:ILE:HD11	2:x:512:CYS:HB2	1.85	0.58
3:W:71:PRO:HA	3:W:78:ILE:HG12	1.85	0.58
1:d:103:GLN:HG3	1:e:102:ALA:HB1	1.86	0.58
1:e:114:ARG:NH1	1:f:112:GLU:OE2	2.37	0.58
2:t:788:LEU:HG	3:U:153:ALA:HA	1.84	0.58
2:v:454:ILE:HD11	2:v:512:CYS:HB2	1.85	0.58
2:x:312:LEU:HD22	2:x:320:PHE:HB3	1.85	0.58
2:s:312:LEU:HD22	2:s:320:PHE:HB3	1.85	0.58
2:u:312:LEU:HD22	2:u:320:PHE:HB3	1.85	0.58
3:U:71:PRO:HA	3:U:78:ILE:HG12	1.85	0.58
1:f:90:ASP:CB	2:v:715:THR:CG2	2.77	0.58
1:h:22:ILE:HG22	1:h:75:LEU:HD12	1.86	0.58
2:t:312:LEU:HD22	2:t:320:PHE:HB3	1.85	0.58
2:w:300:GLU:HB2	2:w:340:TRP:HZ2	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:22:ILE:HG22	1:b:75:LEU:HD12	1.86	0.57
1:p:76:ARG:HH21	1:p:115:ASP:HB3	1.65	0.57
2:t:400:ILE:HD11	2:u:120:THR:HG21	1.83	0.57
1:c:37:ILE:HG13	1:c:74:GLU:HB2	1.86	0.57
1:p:29:ARG:CZ	3:P:5:ASP:HB3	2.34	0.57
1:r:86:VAL:HG21	1:r:102:ALA:HB2	1.87	0.57
2:v:312:LEU:HD22	2:v:320:PHE:HB3	1.85	0.57
2:w:312:LEU:HD22	2:w:320:PHE:HB3	1.85	0.57
1:e:22:ILE:HG22	1:e:75:LEU:HD12	1.87	0.57
2:u:270:VAL:HG11	2:v:290:VAL:HG11	1.84	0.57
1:k:22:ILE:HG22	1:k:75:LEU:HD12	1.87	0.57
1:o:24:PHE:HE2	1:o:32:VAL:HG22	1.70	0.57
2:s:391:ILE:HG21	2:s:435:VAL:HG11	1.84	0.57
2:t:340:TRP:HB3	2:t:344:VAL:HG11	1.84	0.57
2:u:66:ILE:HG23	2:u:553:ALA:HB3	1.87	0.57
2:u:790:ARG:HH12	3:W:152:GLY:HA3	1.69	0.57
2:w:38:GLU:HG2	2:w:529:LEU:HD22	1.86	0.57
1:f:86:VAL:HG21	1:f:102:ALA:HB2	1.87	0.57
1:i:86:VAL:HG21	1:i:102:ALA:HB2	1.87	0.57
2:x:38:GLU:HG2	2:x:529:LEU:HD22	1.86	0.57
1:a:104:ILE:CD1	3:N:8:VAL:CG2	2.77	0.57
1:c:86:VAL:HG21	1:c:102:ALA:HB2	1.87	0.57
1:n:22:ILE:HG22	1:n:75:LEU:HD12	1.87	0.57
1:r:37:ILE:HG13	1:r:74:GLU:HB2	1.86	0.57
2:s:38:GLU:HG2	2:s:529:LEU:HD22	1.86	0.57
2:u:38:GLU:HG2	2:u:529:LEU:HD22	1.86	0.57
1:o:90:ASP:CA	2:s:715:THR:HG22	2.35	0.57
1:q:48:THR:CG2	3:P:83:ASP:HB2	2.35	0.57
1:f:24:PHE:HE2	1:f:32:VAL:HG22	1.70	0.57
1:o:37:ILE:HG13	1:o:74:GLU:HB2	1.86	0.57
1:p:76:ARG:HH22	1:p:115:ASP:HB3	1.68	0.57
1:q:22:ILE:HG22	1:q:75:LEU:HD12	1.87	0.57
2:t:66:ILE:HG23	2:t:553:ALA:HB3	1.87	0.57
3:S:71:PRO:HA	3:S:78:ILE:HG12	1.85	0.57
1:b:67:ALA:CB	3:N:74:TYR:OH	2.52	0.57
1:i:24:PHE:HE2	1:i:32:VAL:HG22	1.70	0.57
1:i:90:ASP:CA	2:u:715:THR:HG22	2.34	0.57
2:v:439:LEU:HD12	2:w:408:PRO:HB2	1.87	0.57
2:w:476:VAL:CG2	2:x:533:GLU:OE2	2.53	0.57
3:M:71:PRO:HA	3:M:78:ILE:HG12	1.85	0.57
3:N:99:ARG:HH21	3:N:99:ARG:HB3	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:c:91:GLY:HA2	1:c:92:SER:C	2.30	0.57
1:f:90:ASP:CA	2:v:715:THR:HG22	2.35	0.57
1:i:37:ILE:HG13	1:i:74:GLU:HB2	1.86	0.57
1:l:24:PHE:HE2	1:l:32:VAL:HG22	1.70	0.57
1:l:90:ASP:CA	2:t:715:THR:HG22	2.35	0.57
2:w:614:THR:HG21	2:w:662:LEU:HB2	1.87	0.57
2:x:788:LEU:HG	3:Q:153:ALA:HA	1.85	0.57
3:X:11:ALA:HB3	3:X:14:LEU:CB	2.32	0.57
1:f:37:ILE:HG13	1:f:74:GLU:HB2	1.86	0.56
1:l:37:ILE:HG13	1:l:74:GLU:HB2	1.86	0.56
1:l:60:LEU:HD13	1:l:63:ALA:HA	1.87	0.56
1:l:86:VAL:HG21	1:l:102:ALA:HB2	1.87	0.56
2:t:476:VAL:CG2	2:u:533:GLU:OE2	2.52	0.56
2:v:66:ILE:HG23	2:v:553:ALA:HB3	1.87	0.56
1:a:76:ARG:HH21	1:a:115:ASP:HB3	1.66	0.56
1:c:90:ASP:CB	2:w:715:THR:CG2	2.74	0.56
1:o:86:VAL:HG21	1:o:102:ALA:HB2	1.87	0.56
1:r:91:GLY:HA2	1:r:92:SER:C	2.30	0.56
2:u:476:VAL:CG2	2:v:533:GLU:OE2	2.52	0.56
2:v:250:TYR:CE2	2:w:288:ARG:HG2	2.40	0.56
1:c:24:PHE:HE2	1:c:32:VAL:HG22	1.70	0.56
1:j:76:ARG:HH22	1:j:115:ASP:HB3	1.68	0.56
1:r:24:PHE:HE2	1:r:32:VAL:HG22	1.70	0.56
2:s:66:ILE:HG23	2:s:553:ALA:HB3	1.86	0.56
2:s:477:GLN:HA	2:x:479:VAL:HG22	1.87	0.56
2:s:614:THR:HG21	2:s:662:LEU:HB2	1.87	0.56
2:s:618:ILE:HG13	2:s:654:PRO:O	2.06	0.56
2:t:38:GLU:HG2	2:t:529:LEU:HD22	1.86	0.56
2:t:618:ILE:HG13	2:t:654:PRO:O	2.06	0.56
2:u:400:ILE:HD11	2:v:120:THR:HG21	1.83	0.56
2:v:38:GLU:HG2	2:v:529:LEU:HD22	1.86	0.56
1:f:60:LEU:HD13	1:f:63:ALA:HA	1.87	0.56
2:s:250:TYR:CE2	2:t:288:ARG:HG2	2.40	0.56
2:v:788:LEU:HG	3:M:153:ALA:HA	1.87	0.56
2:w:48:LEU:HD23	2:w:576:ILE:HG13	1.87	0.56
2:w:790:ARG:HH12	3:O:152:GLY:HA3	1.71	0.56
2:s:48:LEU:HD23	2:s:576:ILE:HG13	1.87	0.56
2:v:614:THR:HG21	2:v:662:LEU:HB2	1.87	0.56
2:x:48:LEU:HD23	2:x:576:ILE:HG13	1.88	0.56
1:e:48:THR:CG2	3:X:83:ASP:HB2	2.36	0.56
1:e:62:LYS:HE2	3:X:72:ASP:OD1	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:n:48:THR:CG2	3:R:83:ASP:HB2	2.36	0.56
2:x:758:VAL:HG11	3:P:150:PHE:CE1	2.38	0.56
3:M:80:TYR:HE1	3:M:87:LEU:HB2	1.70	0.56
3:S:80:TYR:HE1	3:S:87:LEU:HB2	1.70	0.56
1:j:113:ALA:CB	1:k:113:ALA:HB1	2.36	0.56
1:o:91:GLY:HA2	1:o:92:SER:C	2.30	0.56
2:t:614:THR:HG21	2:t:662:LEU:HB2	1.87	0.56
2:v:618:ILE:HG13	2:v:654:PRO:O	2.06	0.56
3:N:94:SER:OG	3:O:178:TYR:CZ	2.58	0.56
1:a:104:ILE:HD13	3:N:8:VAL:HG23	1.86	0.56
1:c:90:ASP:CA	2:w:715:THR:HG22	2.35	0.56
1:f:91:GLY:HA2	1:f:92:SER:C	2.30	0.56
2:t:439:LEU:HD12	2:u:408:PRO:HB2	1.88	0.56
2:w:618:ILE:HG13	2:w:654:PRO:O	2.06	0.56
1:a:113:ALA:CB	1:b:113:ALA:HB1	2.36	0.56
2:t:479:VAL:HG22	2:u:477:GLN:HA	1.88	0.56
2:u:614:THR:HG21	2:u:662:LEU:HB2	1.87	0.56
2:v:48:LEU:HD23	2:v:576:ILE:HG13	1.88	0.56
2:w:439:LEU:HD12	2:x:408:PRO:HB2	1.88	0.56
3:Q:80:TYR:HE1	3:Q:87:LEU:HB2	1.70	0.56
1:m:29:ARG:CZ	3:R:5:ASP:HB3	2.36	0.56
3:O:80:TYR:HE1	3:O:87:LEU:HB2	1.70	0.56
3:P:32:LEU:HD13	3:P:40:ALA:HB1	1.88	0.56
3:Q:134:PHE:HE1	3:Q:171:CYS:HB3	1.71	0.56
3:W:80:TYR:HE1	3:W:87:LEU:HB2	1.70	0.56
1:d:113:ALA:CB	1:e:113:ALA:HB1	2.36	0.55
1:j:104:ILE:CD1	3:T:8:VAL:CG2	2.74	0.55
1:k:86:VAL:HG22	3:T:31:THR:HG22	1.83	0.55
2:w:66:ILE:HG23	2:w:553:ALA:HB3	1.87	0.55
2:x:618:ILE:HG13	2:x:654:PRO:O	2.06	0.55
1:h:67:ALA:HB3	3:V:74:TYR:OH	2.07	0.55
1:l:91:GLY:HA2	1:l:92:SER:C	2.30	0.55
2:t:583:ILE:CG2	2:t:588:GLU:HB3	2.37	0.55
2:u:618:ILE:HG13	2:u:654:PRO:O	2.06	0.55
2:v:526:TYR:HA	2:v:539:SER:O	2.07	0.55
3:T:94:SER:OG	3:U:178:TYR:CZ	2.59	0.55
1:i:60:LEU:HD13	1:i:63:ALA:HA	1.87	0.55
1:i:91:GLY:HA2	1:i:92:SER:C	2.30	0.55
2:s:678:GLU:HG2	2:s:767:TYR:HB3	1.88	0.55
2:s:707:TRP:CH2	2:x:698:ILE:CD1	2.82	0.55
2:s:758:VAL:HG11	3:R:150:PHE:CE1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:678:GLU:HG2	2:v:767:TYR:HB3	1.88	0.55
2:w:526:TYR:HA	2:w:539:SER:O	2.07	0.55
1:c:60:LEU:HD13	1:c:63:ALA:HA	1.87	0.55
1:h:62:LYS:HE2	3:V:72:ASP:OD1	2.07	0.55
1:p:113:ALA:CB	1:q:113:ALA:HB1	2.36	0.55
1:r:90:ASP:CB	2:x:715:THR:CG2	2.76	0.55
2:x:66:ILE:HG23	2:x:553:ALA:HB3	1.86	0.55
2:s:439:LEU:HD12	2:t:408:PRO:HB2	1.87	0.55
2:u:678:GLU:HG2	2:u:767:TYR:HB3	1.88	0.55
2:v:476:VAL:CG2	2:w:533:GLU:OE2	2.54	0.55
2:x:614:THR:HG21	2:x:662:LEU:HB2	1.88	0.55
1:h:79:THR:OG1	1:h:112:GLU:OE2	2.25	0.55
1:l:91:GLY:N	2:t:715:THR:HG21	2.16	0.55
2:s:788:LEU:HG	3:S:153:ALA:HA	1.87	0.55
2:w:161:TYR:HB2	2:x:188:VAL:CG1	2.35	0.55
2:w:583:ILE:CG2	2:w:588:GLU:HB3	2.37	0.55
1:j:29:ARG:CZ	3:T:5:ASP:HB3	2.37	0.55
2:t:250:TYR:CE2	2:u:288:ARG:HG2	2.42	0.55
2:t:678:GLU:HG2	2:t:767:TYR:HB3	1.88	0.55
2:u:526:TYR:HA	2:u:539:SER:O	2.07	0.55
2:w:788:LEU:HG	3:O:153:ALA:HA	1.87	0.55
3:P:94:SER:OG	3:Q:178:TYR:CZ	2.57	0.55
1:o:60:LEU:HD13	1:o:63:ALA:HA	1.87	0.55
2:s:457:ASN:HB3	2:s:472:ARG:HG3	1.89	0.55
2:w:338:ASN:ND2	2:w:379:PRO:HD2	2.22	0.55
2:x:17:GLN:HB2	2:x:493:PRO:HD2	1.89	0.55
2:x:678:GLU:HG2	2:x:767:TYR:HB3	1.88	0.55
3:M:134:PHE:HE1	3:M:171:CYS:HB3	1.71	0.55
3:T:32:LEU:HD13	3:T:40:ALA:HB1	1.88	0.55
3:U:80:TYR:HE1	3:U:87:LEU:HB2	1.70	0.55
1:b:86:VAL:CA	3:N:31:THR:HG22	2.35	0.55
1:g:113:ALA:CB	1:h:113:ALA:HB1	2.36	0.55
1:h:24:PHE:HE1	1:h:32:VAL:HG22	1.72	0.55
1:r:60:LEU:HD13	1:r:63:ALA:HA	1.87	0.55
2:x:526:TYR:HA	2:x:539:SER:O	2.06	0.55
3:M:170:LEU:HG	3:X:57:ARG:HG2	1.89	0.55
3:O:137:TRP:HA	3:O:140:THR:HG22	1.89	0.55
3:O:140:THR:HA	3:O:143:SER:HB3	1.89	0.55
1:e:127:GLY:O	1:f:134:ARG:HD2	2.07	0.55
1:q:79:THR:OG1	1:q:112:GLU:OE2	2.25	0.55
1:r:91:GLY:N	2:x:715:THR:HG21	2.17	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:583:ILE:CG2	2:s:588:GLU:HB3	2.37	0.55
2:t:48:LEU:HD23	2:t:576:ILE:HG13	1.87	0.55
2:t:698:ILE:CD1	2:u:707:TRP:CH2	2.81	0.55
2:u:48:LEU:HD23	2:u:576:ILE:HG13	1.88	0.55
2:u:583:ILE:CG2	2:u:588:GLU:HB3	2.37	0.55
3:M:129:GLU:OE1	3:X:98:ASN:O	2.25	0.55
3:S:140:THR:HA	3:S:143:SER:HB3	1.90	0.55
1:m:76:ARG:HH22	1:m:115:ASP:HB3	1.68	0.54
2:s:408:PRO:HB2	2:x:439:LEU:HD12	1.88	0.54
2:s:476:VAL:CG2	2:t:533:GLU:OE2	2.55	0.54
2:s:698:ILE:CD1	2:t:707:TRP:CH2	2.83	0.54
2:u:60:LEU:HG	2:u:80:VAL:HG11	1.89	0.54
2:v:583:ILE:CG2	2:v:588:GLU:HB3	2.37	0.54
3:M:129:GLU:HA	3:X:98:ASN:HD21	1.71	0.54
3:O:134:PHE:HE1	3:O:171:CYS:HB3	1.71	0.54
2:s:17:GLN:HB2	2:s:493:PRO:HD2	1.89	0.54
2:t:457:ASN:HB3	2:t:472:ARG:HG3	1.89	0.54
3:R:32:LEU:HD13	3:R:40:ALA:HB1	1.88	0.54
1:b:24:PHE:HE1	1:b:32:VAL:HG22	1.72	0.54
1:e:24:PHE:HE1	1:e:32:VAL:HG22	1.72	0.54
1:k:127:GLY:O	1:l:134:ARG:HD2	2.07	0.54
1:m:113:ALA:CB	1:n:113:ALA:HB1	2.36	0.54
1:o:91:GLY:N	2:s:715:THR:HG21	2.16	0.54
2:t:526:TYR:HA	2:t:539:SER:O	2.07	0.54
2:u:17:GLN:HB2	2:u:493:PRO:HD2	1.89	0.54
2:v:338:ASN:ND2	2:v:379:PRO:HD2	2.22	0.54
2:w:17:GLN:HB2	2:w:493:PRO:HD2	1.89	0.54
2:w:678:GLU:HG2	2:w:767:TYR:HB3	1.88	0.54
2:w:698:ILE:HD11	2:x:7:SER:HB3	1.89	0.54
2:x:583:ILE:CG2	2:x:588:GLU:HB3	2.37	0.54
3:N:175:GLU:O	3:N:179:GLY:N	2.30	0.54
3:V:32:LEU:HD13	3:V:40:ALA:HB1	1.88	0.54
1:b:127:GLY:O	1:c:134:ARG:HD2	2.07	0.54
2:s:254:PHE:O	2:s:257:LEU:HB2	2.07	0.54
2:u:254:PHE:O	2:u:257:LEU:HB2	2.07	0.54
2:u:439:LEU:HD12	2:v:408:PRO:HB2	1.89	0.54
2:v:60:LEU:HG	2:v:80:VAL:HG11	1.89	0.54
2:v:758:VAL:HG11	3:X:150:PHE:CE1	2.38	0.54
3:U:137:TRP:HA	3:U:140:THR:HG22	1.89	0.54
3:W:134:PHE:HE1	3:W:171:CYS:HB3	1.71	0.54
1:h:86:VAL:HG22	3:V:31:THR:HG22	1.81	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:k:24:PHE:HE1	1:k:32:VAL:HG22	1.72	0.54
1:q:24:PHE:HE1	1:q:32:VAL:HG22	1.72	0.54
2:x:254:PHE:O	2:x:257:LEU:HB2	2.07	0.54
3:M:140:THR:HA	3:M:143:SER:HB3	1.89	0.54
3:Q:140:THR:HA	3:Q:143:SER:HB3	1.90	0.54
3:W:137:TRP:HA	3:W:140:THR:HG22	1.89	0.54
1:a:93:ILE:HG12	2:w:742:ARG:HH12	1.71	0.54
2:s:161:TYR:HB2	2:t:188:VAL:CG1	2.31	0.54
2:s:526:TYR:HA	2:s:539:SER:O	2.07	0.54
2:t:254:PHE:O	2:t:257:LEU:HB2	2.07	0.54
3:R:99:ARG:HA	3:S:129:GLU:OE1	2.07	0.54
3:X:32:LEU:HD13	3:X:40:ALA:HB1	1.88	0.54
1:g:29:ARG:CZ	3:V:5:ASP:HB3	2.38	0.54
1:g:112:GLU:O	1:g:115:ASP:HB2	2.08	0.54
1:r:90:ASP:CA	2:x:715:THR:HG22	2.37	0.54
2:u:355:ARG:HG3	2:u:430:LEU:HD12	1.90	0.54
2:v:355:ARG:HG3	2:v:430:LEU:HD12	1.90	0.54
2:w:355:ARG:HG3	2:w:430:LEU:HD12	1.90	0.54
2:x:457:ASN:HB3	2:x:472:ARG:HG3	1.89	0.54
3:U:140:THR:HA	3:U:143:SER:HB3	1.90	0.54
3:W:140:THR:HA	3:W:143:SER:HB3	1.89	0.54
1:k:48:THR:CG2	3:T:83:ASP:HB2	2.36	0.54
2:t:17:GLN:HB2	2:t:493:PRO:HD2	1.89	0.54
2:w:254:PHE:O	2:w:257:LEU:HB2	2.07	0.54
2:x:701:LEU:HD12	2:x:761:ALA:HB2	1.90	0.54
3:M:137:TRP:HA	3:M:140:THR:HG22	1.88	0.54
3:Q:137:TRP:HA	3:Q:140:THR:HG22	1.89	0.54
1:k:79:THR:OG1	1:k:112:GLU:OE2	2.25	0.54
1:m:112:GLU:O	1:m:115:ASP:HB2	2.08	0.54
1:n:127:GLY:O	1:o:134:ARG:HD2	2.07	0.54
2:s:479:VAL:HG22	2:t:477:GLN:HA	1.90	0.54
2:v:457:ASN:HB3	2:v:472:ARG:HG3	1.89	0.54
2:w:479:VAL:HG22	2:x:477:GLN:HA	1.89	0.54
3:N:32:LEU:HD13	3:N:40:ALA:HB1	1.88	0.54
3:R:17:VAL:HG11	3:R:32:LEU:HD11	1.90	0.54
1:a:76:ARG:HH22	1:a:115:ASP:HB3	1.68	0.54
1:b:90:ASP:CG	3:M:34:GLY:O	2.51	0.54
1:e:90:ASP:CG	3:W:34:GLY:O	2.51	0.54
1:j:112:GLU:O	1:j:115:ASP:HB2	2.08	0.54
2:s:702:GLN:HE21	3:S:26:GLU:HG2	1.73	0.54
3:U:134:PHE:HE1	3:U:171:CYS:HB3	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:79:THR:OG1	1:b:112:GLU:OE2	2.25	0.53
1:g:93:ILE:HG12	2:u:742:ARG:HH12	1.72	0.53
1:p:93:ILE:HG12	2:x:742:ARG:HH12	1.72	0.53
1:q:127:GLY:O	1:r:134:ARG:HD2	2.07	0.53
2:t:400:ILE:CD1	2:u:120:THR:HG22	2.33	0.53
2:u:698:ILE:CD1	2:v:707:TRP:CH2	2.83	0.53
2:w:11:LEU:HD21	2:w:679:PHE:HE1	1.73	0.53
3:P:57:ARG:HG2	3:Q:170:LEU:HG	1.90	0.53
3:S:137:TRP:HA	3:S:140:THR:HG22	1.89	0.53
1:c:92:SER:O	1:c:92:SER:OG	2.26	0.53
1:h:127:GLY:O	1:i:134:ARG:HD2	2.07	0.53
1:p:112:GLU:O	1:p:115:ASP:HB2	2.08	0.53
2:v:17:GLN:HB2	2:v:493:PRO:HD2	1.89	0.53
2:v:479:VAL:HG22	2:w:477:GLN:HA	1.89	0.53
3:X:17:VAL:HG11	3:X:32:LEU:HD11	1.91	0.53
1:n:24:PHE:HE1	1:n:32:VAL:HG22	1.72	0.53
2:s:338:ASN:ND2	2:s:379:PRO:HD2	2.22	0.53
2:t:338:ASN:ND2	2:t:379:PRO:HD2	2.22	0.53
2:v:254:PHE:O	2:v:257:LEU:HB2	2.07	0.53
2:v:698:ILE:HD11	2:w:7:SER:HB3	1.90	0.53
2:w:250:TYR:CE2	2:x:288:ARG:HG2	2.43	0.53
2:x:11:LEU:HD21	2:x:679:PHE:HE1	1.73	0.53
1:j:10:THR:CG2	3:S:74:TYR:CD2	2.88	0.53
1:m:9:LEU:HD11	1:m:23:PRO:HD2	1.91	0.53
2:s:698:ILE:HD11	2:t:7:SER:HB3	1.90	0.53
2:u:702:GLN:HE21	3:W:26:GLU:HG2	1.73	0.53
3:P:17:VAL:HG11	3:P:32:LEU:HD11	1.91	0.53
3:S:134:PHE:HE1	3:S:171:CYS:HB3	1.72	0.53
3:V:17:VAL:HG11	3:V:32:LEU:HD11	1.91	0.53
2:s:188:VAL:HG11	2:x:161:TYR:CB	2.35	0.53
2:t:11:LEU:HD21	2:t:679:PHE:HE1	1.73	0.53
2:t:60:LEU:HG	2:t:80:VAL:HG11	1.89	0.53
2:u:479:VAL:HG22	2:v:477:GLN:HA	1.89	0.53
2:x:585:LEU:HD11	2:x:597:LYS:HB3	1.91	0.53
3:V:57:ARG:HG2	3:W:170:LEU:HG	1.91	0.53
1:d:9:LEU:HD11	1:d:23:PRO:HD2	1.91	0.53
1:d:112:GLU:O	1:d:115:ASP:HB2	2.08	0.53
1:h:48:THR:CG2	3:V:83:ASP:HB2	2.38	0.53
2:u:713:SER:HB3	2:u:777:ASN:H	1.74	0.53
2:w:60:LEU:HG	2:w:80:VAL:HG11	1.89	0.53
2:x:60:LEU:HG	2:x:80:VAL:HG11	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:17:VAL:HG11	3:N:32:LEU:HD11	1.90	0.53
3:N:99:ARG:HA	3:O:129:GLU:OE1	2.08	0.53
3:U:42:ASN:O	3:U:46:ILE:HG12	2.09	0.53
2:s:270:VAL:CG1	2:t:290:VAL:HG11	2.39	0.53
2:t:585:LEU:HD11	2:t:597:LYS:HB3	1.91	0.53
2:u:457:ASN:HB3	2:u:472:ARG:HG3	1.89	0.53
2:u:701:LEU:HD12	2:u:761:ALA:HB2	1.91	0.53
2:v:11:LEU:HD21	2:v:679:PHE:HE1	1.73	0.53
2:s:585:LEU:HD11	2:s:597:LYS:HB3	1.91	0.53
2:t:355:ARG:HG3	2:t:430:LEU:HD12	1.90	0.53
2:v:426:ALA:HB2	2:v:430:LEU:HD23	1.91	0.53
2:w:701:LEU:HD12	2:w:761:ALA:HB2	1.90	0.53
3:S:42:ASN:O	3:S:46:ILE:HG12	2.09	0.53
3:V:137:TRP:HA	3:V:140:THR:HG22	1.91	0.53
1:e:90:ASP:OD1	3:W:34:GLY:O	2.26	0.53
2:s:11:LEU:HD21	2:s:679:PHE:HE1	1.73	0.53
2:s:701:LEU:HD12	2:s:761:ALA:HB2	1.91	0.53
2:v:531:LEU:HB2	2:v:536:ARG:HD3	1.91	0.53
2:v:701:LEU:HD12	2:v:761:ALA:HB2	1.90	0.53
2:v:713:SER:HB3	2:v:777:ASN:H	1.74	0.53
2:w:457:ASN:HB3	2:w:472:ARG:HG3	1.89	0.53
2:w:531:LEU:HB2	2:w:536:ARG:HD3	1.91	0.53
3:R:94:SER:OG	3:S:178:TYR:CZ	2.58	0.53
3:T:17:VAL:HG11	3:T:32:LEU:HD11	1.91	0.53
2:s:426:ALA:HB2	2:s:430:LEU:HD23	1.91	0.53
2:s:477:GLN:CG	2:x:478:ASP:HB2	2.38	0.53
2:t:698:ILE:HD11	2:u:7:SER:HB3	1.89	0.53
2:u:698:ILE:HD11	2:v:7:SER:HB3	1.91	0.53
3:R:57:ARG:HG2	3:S:170:LEU:HG	1.91	0.53
1:a:9:LEU:HD11	1:a:23:PRO:HD2	1.91	0.52
2:s:525:MET:HE1	2:s:561:MET:HE1	1.91	0.52
2:t:165:LEU:HD21	2:t:243:LEU:HD12	1.91	0.52
2:u:531:LEU:HB2	2:u:536:ARG:HD3	1.91	0.52
2:u:585:LEU:HD11	2:u:597:LYS:HB3	1.91	0.52
2:x:355:ARG:HG3	2:x:430:LEU:HD12	1.90	0.52
3:M:129:GLU:OE1	3:X:99:ARG:HA	2.07	0.52
3:P:98:ASN:O	3:Q:129:GLU:OE1	2.27	0.52
3:Q:42:ASN:O	3:Q:46:ILE:HG12	2.09	0.52
1:a:112:GLU:O	1:a:115:ASP:HB2	2.08	0.52
2:s:165:LEU:HD21	2:s:243:LEU:HD12	1.92	0.52
2:s:713:SER:HB3	2:s:777:ASN:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:366:ILE:HD11	2:t:403:LEU:HD13	1.92	0.52
2:t:426:ALA:HB2	2:t:430:LEU:HD23	1.91	0.52
2:u:338:ASN:ND2	2:u:379:PRO:HD2	2.22	0.52
2:w:585:LEU:HD11	2:w:597:LYS:HB3	1.91	0.52
3:P:99:ARG:HA	3:Q:129:GLU:OE1	2.09	0.52
3:T:137:TRP:HA	3:T:140:THR:HG22	1.91	0.52
3:W:42:ASN:O	3:W:46:ILE:HG12	2.09	0.52
1:c:89:THR:O	1:c:92:SER:OG	2.28	0.52
1:j:9:LEU:HD11	1:j:23:PRO:HD2	1.91	0.52
2:t:282:VAL:HG23	2:t:292:THR:O	2.10	0.52
2:v:585:LEU:HD11	2:v:597:LYS:HB3	1.91	0.52
3:O:42:ASN:O	3:O:46:ILE:HG12	2.09	0.52
3:P:98:ASN:HD21	3:Q:129:GLU:HA	1.74	0.52
3:U:67:ILE:HD11	3:U:121:ILE:HD12	1.92	0.52
3:V:98:ASN:O	3:W:129:GLU:OE1	2.28	0.52
1:h:86:VAL:CG2	3:V:31:THR:CG2	2.68	0.52
2:s:790:ARG:HH12	3:S:152:GLY:HA3	1.71	0.52
2:u:11:LEU:HD21	2:u:679:PHE:HE1	1.73	0.52
2:w:758:VAL:HG11	3:N:150:PHE:CE1	2.40	0.52
3:R:98:ASN:HD21	3:S:129:GLU:HA	1.74	0.52
3:X:137:TRP:HA	3:X:140:THR:HG22	1.91	0.52
1:p:9:LEU:HD11	1:p:23:PRO:HD2	1.91	0.52
2:s:7:SER:HB3	2:x:698:ILE:HD11	1.90	0.52
2:s:60:LEU:HG	2:s:80:VAL:HG11	1.89	0.52
2:u:161:TYR:HB2	2:v:188:VAL:CG1	2.38	0.52
2:u:165:LEU:HD21	2:u:243:LEU:HD12	1.92	0.52
2:v:282:VAL:HG23	2:v:292:THR:O	2.10	0.52
2:w:282:VAL:HG23	2:w:292:THR:O	2.10	0.52
2:x:525:MET:HE1	2:x:561:MET:HE1	1.92	0.52
2:x:531:LEU:HB2	2:x:536:ARG:HD3	1.91	0.52
3:M:42:ASN:O	3:M:46:ILE:HG12	2.09	0.52
1:d:29:ARG:CZ	3:X:5:ASP:HB3	2.39	0.52
1:f:89:THR:O	1:f:92:SER:OG	2.28	0.52
1:h:90:ASP:CG	3:U:34:GLY:O	2.52	0.52
1:h:131:ALA:HA	1:h:134:ARG:HH21	1.75	0.52
2:t:525:MET:HE1	2:t:561:MET:HE1	1.91	0.52
2:t:790:ARG:HH12	3:U:152:GLY:HA3	1.71	0.52
2:w:525:MET:HE1	2:w:561:MET:HE1	1.91	0.52
2:s:594:MET:HE1	2:s:634:LEU:HB2	1.91	0.52
2:t:531:LEU:HB2	2:t:536:ARG:HD3	1.91	0.52
2:t:701:LEU:HD12	2:t:761:ALA:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:718:ILE:HG23	2:v:768:ILE:HG12	1.92	0.52
2:x:338:ASN:ND2	2:x:379:PRO:HD2	2.22	0.52
3:P:148:ASN:ND2	3:Q:159:VAL:HG11	2.24	0.52
3:P:175:GLU:O	3:P:179:GLY:N	2.31	0.52
3:R:137:TRP:HA	3:R:140:THR:HG22	1.91	0.52
1:b:86:VAL:HG22	3:N:31:THR:HG22	1.80	0.52
1:f:92:SER:OG	1:f:92:SER:O	2.26	0.52
2:t:713:SER:HB3	2:t:777:ASN:H	1.74	0.52
2:u:366:ILE:HD11	2:u:403:LEU:HD13	1.92	0.52
2:w:718:ILE:HG23	2:w:768:ILE:HG12	1.92	0.52
2:x:282:VAL:HG23	2:x:292:THR:O	2.10	0.52
2:x:426:ALA:HB2	2:x:430:LEU:HD23	1.91	0.52
3:V:98:ASN:HD21	3:W:129:GLU:HA	1.74	0.52
1:r:89:THR:O	1:r:92:SER:OG	2.28	0.52
2:v:165:LEU:HD21	2:v:243:LEU:HD12	1.92	0.52
2:w:400:ILE:CD1	2:x:120:THR:HG22	2.33	0.52
2:x:713:SER:HB3	2:x:777:ASN:H	1.74	0.52
1:j:93:ILE:HG12	2:t:742:ARG:HH12	1.71	0.52
1:k:38:GLY:CA	1:k:71:THR:H	2.23	0.52
2:s:400:ILE:CD1	2:t:120:THR:HG22	2.32	0.52
2:t:617:HIS:CD2	2:t:654:PRO:HB2	2.45	0.52
2:u:426:ALA:HB2	2:u:430:LEU:HD23	1.91	0.52
3:R:175:GLU:O	3:R:179:GLY:N	2.31	0.52
1:c:91:GLY:N	2:w:715:THR:HG21	2.17	0.51
1:e:131:ALA:HA	1:e:134:ARG:HH21	1.75	0.51
2:s:531:LEU:HB2	2:s:536:ARG:HD3	1.91	0.51
2:u:161:TYR:CB	2:v:188:VAL:HG11	2.36	0.51
3:N:57:ARG:HG2	3:O:170:LEU:HG	1.92	0.51
3:N:98:ASN:O	3:O:129:GLU:OE1	2.29	0.51
3:T:99:ARG:HA	3:U:129:GLU:OE1	2.09	0.51
3:U:67:ILE:HD11	3:U:121:ILE:CD1	2.40	0.51
1:h:38:GLY:CA	1:h:71:THR:H	2.23	0.51
1:k:131:ALA:HA	1:k:134:ARG:HH21	1.75	0.51
2:v:420:ALA:HB1	2:v:439:LEU:HD21	1.93	0.51
2:v:594:MET:HE1	2:v:634:LEU:HB2	1.92	0.51
2:x:165:LEU:HD21	2:x:243:LEU:HD12	1.92	0.51
1:g:9:LEU:HD11	1:g:23:PRO:HD2	1.91	0.51
1:n:38:GLY:CA	1:n:71:THR:H	2.23	0.51
2:u:617:HIS:CD2	2:u:654:PRO:HB2	2.46	0.51
2:w:713:SER:HB3	2:w:777:ASN:H	1.74	0.51
2:x:420:ALA:HB1	2:x:439:LEU:HD21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:137:TRP:HA	3:N:140:THR:HG22	1.91	0.51
1:d:76:ARG:HH22	1:d:115:ASP:HB3	1.68	0.51
1:e:11:TYR:HD2	1:e:75:LEU:HD21	1.76	0.51
2:s:420:ALA:HB1	2:s:439:LEU:HD21	1.93	0.51
2:s:617:HIS:CD2	2:s:654:PRO:HB2	2.45	0.51
2:u:718:ILE:HG23	2:u:768:ILE:HG12	1.92	0.51
3:R:134:PHE:CE1	3:R:171:CYS:HB3	2.45	0.51
3:T:175:GLU:O	3:T:179:GLY:N	2.31	0.51
2:s:366:ILE:HD11	2:s:403:LEU:HD13	1.92	0.51
2:t:702:GLN:NE2	3:U:26:GLU:HG2	2.25	0.51
2:u:282:VAL:HG23	2:u:292:THR:O	2.10	0.51
2:u:420:ALA:HB1	2:u:439:LEU:HD21	1.93	0.51
2:v:617:HIS:CD2	2:v:654:PRO:HB2	2.46	0.51
2:w:594:MET:HE1	2:w:634:LEU:HB2	1.92	0.51
2:x:594:MET:HE1	2:x:634:LEU:HB2	1.92	0.51
2:x:718:ILE:HG23	2:x:768:ILE:HG12	1.92	0.51
3:N:134:PHE:CE1	3:N:171:CYS:HB3	2.45	0.51
3:P:137:TRP:HA	3:P:140:THR:HG22	1.91	0.51
1:b:48:THR:HA	3:N:81:SER:CB	2.41	0.51
1:g:10:THR:CG2	3:U:74:TYR:CD2	2.91	0.51
1:i:89:THR:O	1:i:92:SER:OG	2.28	0.51
1:j:25:GLU:CD	1:k:84:ARG:HH22	2.19	0.51
1:k:48:THR:HA	3:T:81:SER:CB	2.41	0.51
1:n:48:THR:HA	3:R:81:SER:CB	2.41	0.51
2:s:282:VAL:HG23	2:s:292:THR:O	2.10	0.51
2:w:420:ALA:HB1	2:w:439:LEU:HD21	1.93	0.51
2:w:426:ALA:HB2	2:w:430:LEU:HD23	1.92	0.51
2:x:366:ILE:HD11	2:x:403:LEU:HD13	1.92	0.51
3:N:148:ASN:ND2	3:O:159:VAL:HG11	2.26	0.51
1:a:10:THR:CG2	3:M:74:TYR:CD2	2.93	0.51
1:n:67:ALA:CB	3:R:74:TYR:OH	2.59	0.51
1:q:38:GLY:CA	1:q:71:THR:H	2.23	0.51
2:t:420:ALA:HB1	2:t:439:LEU:HD21	1.93	0.51
2:w:165:LEU:HD21	2:w:243:LEU:HD12	1.91	0.51
2:w:366:ILE:HD11	2:w:403:LEU:HD13	1.91	0.51
2:w:478:ASP:HB2	2:x:477:GLN:CG	2.39	0.51
2:w:567:ASN:H	2:w:568:GLU:HA	1.76	0.51
2:w:617:HIS:CD2	2:w:654:PRO:HB2	2.46	0.51
3:R:98:ASN:O	3:S:129:GLU:OE1	2.28	0.51
3:T:99:ARG:HH21	3:T:99:ARG:HB3	1.76	0.51
3:T:134:PHE:CE1	3:T:171:CYS:HB3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:24:PHE:CE1	1:b:32:VAL:HG22	2.46	0.51
1:h:24:PHE:CE1	1:h:32:VAL:HG22	2.46	0.51
1:k:62:LYS:HE2	3:T:72:ASP:HA	1.92	0.51
1:m:25:GLU:CD	1:n:84:ARG:HH22	2.19	0.51
1:o:89:THR:O	1:o:92:SER:OG	2.28	0.51
2:s:288:ARG:HG2	2:x:250:TYR:CE2	2.45	0.51
2:t:594:MET:HE1	2:t:634:LEU:HB2	1.92	0.51
1:b:11:TYR:HD2	1:b:75:LEU:HD21	1.76	0.51
1:e:38:GLY:CA	1:e:71:THR:H	2.23	0.51
1:h:11:TYR:HD2	1:h:75:LEU:HD21	1.76	0.51
1:n:62:LYS:HE2	3:R:72:ASP:HA	1.92	0.51
2:s:478:ASP:HB2	2:t:477:GLN:CG	2.40	0.51
2:t:478:ASP:HB2	2:u:477:GLN:CG	2.39	0.51
2:u:250:TYR:CE2	2:v:288:ARG:HG2	2.46	0.51
2:u:525:MET:HE1	2:u:561:MET:HE1	1.91	0.51
2:v:525:MET:HE1	2:v:561:MET:HE1	1.91	0.51
2:x:567:ASN:H	2:x:568:GLU:HA	1.76	0.51
2:x:617:HIS:CD2	2:x:654:PRO:HB2	2.46	0.51
3:X:134:PHE:CE1	3:X:171:CYS:HB3	2.46	0.51
1:g:25:GLU:CD	1:h:84:ARG:HH22	2.19	0.51
1:k:67:ALA:CB	3:T:74:TYR:OH	2.59	0.51
1:k:90:ASP:CG	3:S:34:GLY:O	2.53	0.51
1:n:11:TYR:HD2	1:n:75:LEU:HD21	1.76	0.51
1:q:131:ALA:HA	1:q:134:ARG:HH21	1.75	0.51
2:v:270:VAL:CG1	2:w:290:VAL:HG11	2.40	0.51
2:w:702:GLN:HE21	3:O:26:GLU:HG2	1.76	0.51
3:P:10:THR:HG22	3:P:11:ALA:H	1.77	0.51
3:P:134:PHE:CE1	3:P:171:CYS:HB3	2.46	0.51
1:b:38:GLY:CA	1:b:71:THR:H	2.23	0.50
1:e:67:ALA:CB	3:X:74:TYR:OH	2.59	0.50
1:k:24:PHE:CE1	1:k:32:VAL:HG22	2.46	0.50
1:q:24:PHE:CE1	1:q:32:VAL:HG22	2.46	0.50
3:N:10:THR:HG22	3:N:11:ALA:H	1.76	0.50
3:P:85:LEU:HD11	3:P:124:LEU:HD23	1.94	0.50
3:T:148:ASN:ND2	3:U:159:VAL:HG11	2.26	0.50
1:d:93:ILE:HG12	2:v:742:ARG:HH12	1.76	0.50
1:e:79:THR:OG1	1:e:112:GLU:OE2	2.25	0.50
1:k:11:TYR:HD2	1:k:75:LEU:HD21	1.76	0.50
1:l:89:THR:O	1:l:92:SER:OG	2.28	0.50
1:q:11:TYR:HD2	1:q:75:LEU:HD21	1.75	0.50
2:v:567:ASN:H	2:v:568:GLU:HA	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:85:LEU:HD11	3:N:124:LEU:HD23	1.93	0.50
3:R:85:LEU:HD11	3:R:124:LEU:HD23	1.94	0.50
3:T:98:ASN:O	3:U:129:GLU:OE1	2.29	0.50
1:e:24:PHE:CE1	1:e:32:VAL:HG22	2.46	0.50
1:n:131:ALA:HA	1:n:134:ARG:HH21	1.75	0.50
2:s:355:ARG:HG3	2:s:430:LEU:HD12	1.90	0.50
2:u:594:MET:HE1	2:u:634:LEU:HB2	1.92	0.50
2:v:366:ILE:HD11	2:v:403:LEU:HD13	1.92	0.50
3:N:61:PHE:HE1	3:N:134:PHE:HE2	1.59	0.50
3:P:61:PHE:HE1	3:P:134:PHE:HE2	1.59	0.50
3:T:57:ARG:HG2	3:U:170:LEU:HG	1.93	0.50
3:T:85:LEU:HD11	3:T:124:LEU:HD23	1.94	0.50
3:V:134:PHE:CE1	3:V:171:CYS:HB3	2.46	0.50
1:n:79:THR:OG1	1:n:112:GLU:OE2	2.25	0.50
1:q:90:ASP:CG	3:O:34:GLY:O	2.54	0.50
2:s:567:ASN:H	2:s:568:GLU:HA	1.76	0.50
3:V:148:ASN:ND2	3:W:159:VAL:HG11	2.26	0.50
1:b:90:ASP:OD1	3:M:34:GLY:O	2.29	0.50
1:b:131:ALA:HA	1:b:134:ARG:HH21	1.75	0.50
1:p:25:GLU:CD	1:q:84:ARG:HH22	2.19	0.50
2:s:142:ASN:ND2	2:s:296:GLY:O	2.45	0.50
2:s:718:ILE:HG23	2:s:768:ILE:HG12	1.92	0.50
2:t:718:ILE:HG23	2:t:768:ILE:HG12	1.92	0.50
3:N:98:ASN:HD21	3:O:129:GLU:HA	1.75	0.50
3:W:67:ILE:HD11	3:W:121:ILE:CD1	2.42	0.50
1:d:25:GLU:CD	1:e:84:ARG:HH22	2.19	0.50
3:V:85:LEU:HD11	3:V:124:LEU:HD23	1.93	0.50
3:X:10:THR:HG22	3:X:11:ALA:H	1.76	0.50
3:X:175:GLU:O	3:X:179:GLY:N	2.31	0.50
1:h:22:ILE:HG22	1:h:75:LEU:CD1	2.42	0.50
1:k:22:ILE:HG22	1:k:75:LEU:CD1	2.42	0.50
1:q:67:ALA:CB	3:P:74:TYR:OH	2.60	0.50
2:t:167:VAL:HG13	2:t:175:ALA:HB3	1.94	0.50
2:v:598:ILE:HG21	2:v:621:ILE:HG22	1.94	0.50
2:x:257:LEU:HD12	2:x:258:PRO:HD2	1.94	0.50
3:P:11:ALA:O	3:P:12:ALA:C	2.52	0.50
3:Q:67:ILE:HD11	3:Q:121:ILE:CD1	2.41	0.50
3:R:61:PHE:HE1	3:R:134:PHE:HE2	1.59	0.50
3:R:99:ARG:HB3	3:R:99:ARG:HH21	1.77	0.50
3:T:98:ASN:HD21	3:U:129:GLU:HA	1.76	0.50
1:a:25:GLU:CD	1:b:84:ARG:HH22	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:136:ILE:HG13	1:i:139:LEU:HD11	1.94	0.50
2:v:167:VAL:HG13	2:v:175:ALA:HB3	1.94	0.50
3:R:148:ASN:ND2	3:S:159:VAL:HG11	2.26	0.50
3:V:175:GLU:O	3:V:179:GLY:N	2.31	0.50
3:W:128:ASP:O	3:W:135:ARG:NH2	2.43	0.50
1:e:22:ILE:HG22	1:e:75:LEU:CD1	2.42	0.50
2:s:598:ILE:HG21	2:s:621:ILE:HG22	1.94	0.50
2:t:567:ASN:H	2:t:568:GLU:HA	1.76	0.50
2:v:142:ASN:ND2	2:v:296:GLY:O	2.45	0.50
2:x:142:ASN:ND2	2:x:296:GLY:O	2.45	0.50
3:V:99:ARG:HA	3:W:129:GLU:OE1	2.12	0.50
1:h:62:LYS:HE2	3:V:72:ASP:HA	1.93	0.49
1:h:90:ASP:OD1	3:U:34:GLY:O	2.29	0.49
1:k:136:ILE:HG13	1:l:139:LEU:HD11	1.94	0.49
1:n:24:PHE:CE1	1:n:32:VAL:HG22	2.46	0.49
1:o:92:SER:OG	1:o:92:SER:O	2.26	0.49
2:t:48:LEU:HD22	2:t:574:ALA:HB3	1.94	0.49
2:t:598:ILE:HG21	2:t:621:ILE:HG22	1.94	0.49
2:t:722:ASN:ND2	3:U:27:PRO:HG3	2.24	0.49
2:u:48:LEU:HD22	2:u:574:ALA:HB3	1.94	0.49
2:v:478:ASP:HB2	2:w:477:GLN:CG	2.39	0.49
2:w:598:ILE:HG21	2:w:621:ILE:HG22	1.94	0.49
2:x:598:ILE:HG21	2:x:621:ILE:HG22	1.94	0.49
3:R:10:THR:HG22	3:R:11:ALA:H	1.77	0.49
1:h:48:THR:HA	3:V:81:SER:CB	2.42	0.49
1:n:22:ILE:HG22	1:n:75:LEU:CD1	2.42	0.49
1:n:86:VAL:CA	3:R:31:THR:HG22	2.36	0.49
1:q:48:THR:HA	3:P:81:SER:CB	2.41	0.49
2:s:167:VAL:HG13	2:s:175:ALA:HB3	1.94	0.49
2:u:142:ASN:ND2	2:u:296:GLY:O	2.45	0.49
2:u:567:ASN:H	2:u:568:GLU:HA	1.76	0.49
2:v:704:ARG:NH1	3:X:150:PHE:O	2.43	0.49
2:x:702:GLN:HE21	3:Q:26:GLU:HG2	1.76	0.49
1:k:86:VAL:CA	3:T:31:THR:HG22	2.39	0.49
2:s:257:LEU:HD12	2:s:258:PRO:HD2	1.94	0.49
2:v:552:LEU:HD21	2:v:566:ARG:HH12	1.78	0.49
2:x:248:THR:HG23	2:x:250:TYR:H	1.78	0.49
3:X:61:PHE:HE1	3:X:134:PHE:HE2	1.59	0.49
3:X:85:LEU:HD11	3:X:124:LEU:HD23	1.93	0.49
1:h:29:ARG:C	1:h:31:PHE:N	2.70	0.49
1:k:90:ASP:OD1	3:S:34:GLY:O	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:92:SER:OG	1:l:92:SER:O	2.26	0.49
2:s:396:SER:HB3	2:t:355:ARG:O	2.12	0.49
2:t:270:VAL:CG1	2:u:290:VAL:HG11	2.42	0.49
2:u:167:VAL:HG13	2:u:175:ALA:HB3	1.94	0.49
2:u:598:ILE:HG21	2:u:621:ILE:HG22	1.94	0.49
2:w:552:LEU:HD21	2:w:566:ARG:HH12	1.78	0.49
2:x:552:LEU:HD21	2:x:566:ARG:HH12	1.78	0.49
3:M:159:VAL:HG11	3:X:148:ASN:ND2	2.27	0.49
1:p:10:THR:CG2	3:O:74:TYR:CD2	2.94	0.49
2:t:248:THR:HG23	2:t:250:TYR:H	1.78	0.49
2:t:371:THR:HG22	2:t:388:ASP:HB3	1.94	0.49
2:v:248:THR:HG23	2:v:250:TYR:H	1.78	0.49
2:v:276:SER:N	2:w:384:ASN:OD1	2.46	0.49
3:P:49:LYS:HE3	3:Q:136:TYR:HE1	1.78	0.49
3:Q:67:ILE:HD11	3:Q:121:ILE:HD12	1.94	0.49
1:q:22:ILE:HG22	1:q:75:LEU:CD1	2.42	0.49
2:t:161:TYR:HB2	2:u:188:VAL:CG1	2.34	0.49
2:w:142:ASN:ND2	2:w:296:GLY:O	2.45	0.49
2:w:166:ILE:HA	2:w:175:ALA:O	2.13	0.49
2:w:270:VAL:CG1	2:x:290:VAL:HG11	2.41	0.49
1:m:10:THR:CG2	3:Q:74:TYR:CD2	2.92	0.49
1:n:86:VAL:HG13	3:R:31:THR:CG2	2.43	0.49
2:t:704:ARG:HH11	3:T:150:PHE:HA	1.77	0.49
2:v:48:LEU:HD22	2:v:574:ALA:HB3	1.94	0.49
2:w:248:THR:HG23	2:w:250:TYR:H	1.78	0.49
2:s:552:LEU:HD21	2:s:566:ARG:HH12	1.78	0.49
2:t:142:ASN:ND2	2:t:296:GLY:O	2.45	0.49
2:u:248:THR:HG23	2:u:250:TYR:H	1.78	0.49
2:u:257:LEU:HD12	2:u:258:PRO:HD2	1.94	0.49
2:u:704:ARG:HH11	3:V:150:PHE:HA	1.77	0.49
2:w:167:VAL:HG13	2:w:175:ALA:HB3	1.94	0.49
2:w:257:LEU:HD12	2:w:258:PRO:HD2	1.94	0.49
2:x:790:ARG:HH12	3:Q:152:GLY:HA3	1.74	0.49
3:T:61:PHE:HE1	3:T:134:PHE:HE2	1.59	0.49
1:b:22:ILE:HG22	1:b:75:LEU:CD1	2.42	0.49
1:o:36:LEU:HA	1:o:73:ILE:HA	1.95	0.49
2:u:352:PHE:HE2	2:u:354:PHE:HB2	1.78	0.49
2:w:15:ILE:HA	2:w:28:GLY:O	2.13	0.49
2:x:15:ILE:HA	2:x:28:GLY:O	2.13	0.49
3:S:67:ILE:HD11	3:S:121:ILE:CD1	2.43	0.49
3:W:67:ILE:HD11	3:W:121:ILE:HD12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:d:27:LEU:HD12	3:X:6:MET:HG3	1.95	0.49
3:S:67:ILE:HD11	3:S:121:ILE:HD12	1.95	0.49
1:b:136:ILE:HG13	1:c:139:LEU:HD11	1.94	0.48
1:f:99:LEU:H	1:f:99:LEU:HD12	1.78	0.48
1:j:13:LEU:HD13	1:j:13:LEU:HA	1.70	0.48
1:l:36:LEU:HA	1:l:73:ILE:HA	1.95	0.48
1:q:62:LYS:HE2	3:P:72:ASP:HA	1.94	0.48
2:w:371:THR:HG22	2:w:388:ASP:HB3	1.94	0.48
3:M:128:ASP:O	3:M:135:ARG:NH2	2.43	0.48
1:h:121:ILE:H	1:h:121:ILE:HG13	1.37	0.48
2:t:257:LEU:HD12	2:t:258:PRO:HD2	1.94	0.48
2:v:257:LEU:HD12	2:v:258:PRO:HD2	1.94	0.48
2:v:352:PHE:HE2	2:v:354:PHE:HB2	1.78	0.48
2:x:48:LEU:HD22	2:x:574:ALA:HB3	1.94	0.48
2:x:371:THR:HG22	2:x:388:ASP:HB3	1.94	0.48
3:N:11:ALA:O	3:N:12:ALA:C	2.52	0.48
3:N:140:THR:HA	3:N:143:SER:HB3	1.95	0.48
3:O:128:ASP:O	3:O:135:ARG:NH2	2.43	0.48
3:R:11:ALA:O	3:R:12:ALA:C	2.52	0.48
3:R:140:THR:HA	3:R:143:SER:HB3	1.95	0.48
3:T:10:THR:HG22	3:T:11:ALA:H	1.76	0.48
3:T:140:THR:HA	3:T:143:SER:HB3	1.96	0.48
3:V:61:PHE:HE1	3:V:134:PHE:HE2	1.59	0.48
3:V:140:THR:HA	3:V:143:SER:HB3	1.95	0.48
1:c:95:ARG:O	1:c:99:LEU:HD12	2.14	0.48
1:l:93:ILE:HG22	1:l:94:LEU:O	2.14	0.48
1:o:99:LEU:H	1:o:99:LEU:HD12	1.78	0.48
2:s:166:ILE:HA	2:s:175:ALA:O	2.13	0.48
2:s:276:SER:N	2:t:384:ASN:OD1	2.46	0.48
2:u:371:THR:HG22	2:u:388:ASP:HB3	1.95	0.48
2:u:552:LEU:HD21	2:u:566:ARG:HH12	1.78	0.48
2:u:702:GLN:NE2	3:W:26:GLU:HG2	2.28	0.48
2:v:702:GLN:HE21	3:M:26:GLU:HG2	1.77	0.48
2:w:48:LEU:HD22	2:w:574:ALA:HB3	1.94	0.48
2:x:166:ILE:HA	2:x:175:ALA:O	2.13	0.48
3:P:140:THR:HA	3:P:143:SER:HB3	1.95	0.48
3:X:172:MET:HB2	3:X:172:MET:HE2	1.65	0.48
1:c:99:LEU:HD12	1:c:99:LEU:H	1.78	0.48
1:f:95:ARG:O	1:f:99:LEU:HD12	2.14	0.48
1:q:136:ILE:HG13	1:r:139:LEU:HD11	1.94	0.48
2:s:371:THR:HG22	2:s:388:ASP:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:478:ASP:CB	2:u:477:GLN:HG2	2.42	0.48
2:u:478:ASP:HB2	2:v:477:GLN:CG	2.40	0.48
2:v:276:SER:HB3	2:w:384:ASN:CB	2.43	0.48
2:x:352:PHE:HE2	2:x:354:PHE:HB2	1.78	0.48
3:N:148:ASN:ND2	3:N:157:GLU:HG3	2.28	0.48
3:R:49:LYS:HE3	3:S:136:TYR:HE1	1.78	0.48
3:X:140:THR:HA	3:X:143:SER:HB3	1.95	0.48
1:c:9:LEU:HD21	1:c:23:PRO:CD	2.44	0.48
1:f:9:LEU:HD21	1:f:23:PRO:CD	2.44	0.48
1:k:121:ILE:H	1:k:121:ILE:HG13	1.37	0.48
2:s:48:LEU:HD22	2:s:574:ALA:HB3	1.94	0.48
2:u:578:PHE:CD1	2:u:578:PHE:N	2.82	0.48
2:u:722:ASN:ND2	3:W:27:PRO:HG3	2.22	0.48
2:v:15:ILE:HA	2:v:28:GLY:O	2.13	0.48
2:v:704:ARG:HH11	3:X:150:PHE:HA	1.78	0.48
1:c:36:LEU:HD21	1:c:64:TRP:CD1	2.49	0.48
1:d:10:THR:CG2	3:W:74:TYR:CD2	2.95	0.48
1:e:48:THR:HA	3:X:81:SER:CB	2.44	0.48
2:u:478:ASP:CB	2:v:477:GLN:HG2	2.43	0.48
2:v:396:SER:HB3	2:w:355:ARG:O	2.13	0.48
2:v:578:PHE:CD1	2:v:578:PHE:N	2.82	0.48
2:x:338:ASN:HD22	2:x:338:ASN:HA	1.41	0.48
1:b:45:THR:OG1	1:b:48:THR:OG1	2.31	0.48
1:e:20:PHE:CE2	1:e:73:ILE:HD12	2.49	0.48
1:f:36:LEU:HA	1:f:73:ILE:HA	1.95	0.48
1:r:95:ARG:O	1:r:99:LEU:HD12	2.14	0.48
1:r:99:LEU:HD12	1:r:99:LEU:H	1.79	0.48
2:t:352:PHE:HE2	2:t:354:PHE:HB2	1.78	0.48
2:t:466:SER:OG	2:u:579:THR:CG2	2.57	0.48
2:u:338:ASN:HD22	2:u:338:ASN:HA	1.42	0.48
2:v:400:ILE:CD1	2:w:120:THR:HG22	2.32	0.48
2:w:352:PHE:HE2	2:w:354:PHE:HB2	1.78	0.48
2:x:167:VAL:HG13	2:x:175:ALA:HB3	1.94	0.48
1:e:136:ILE:HG13	1:f:139:LEU:HD11	1.94	0.48
1:i:93:ILE:HG22	1:i:94:LEU:O	2.14	0.48
1:i:99:LEU:H	1:i:99:LEU:HD12	1.79	0.48
1:r:36:LEU:HA	1:r:73:ILE:HA	1.95	0.48
2:s:477:GLN:HA	2:x:479:VAL:CG2	2.43	0.48
2:v:352:PHE:CE2	2:v:354:PHE:HB2	2.49	0.48
2:v:355:ARG:HG3	2:v:430:LEU:HD11	1.96	0.48
2:x:128:VAL:HG13	2:x:309:PRO:HG3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:x:352:PHE:CE2	2:x:354:PHE:HB2	2.49	0.48
3:V:10:THR:HG22	3:V:11:ALA:H	1.76	0.48
1:c:93:ILE:HG22	1:c:94:LEU:O	2.14	0.48
1:e:86:VAL:CA	3:X:31:THR:HG22	2.40	0.48
1:n:136:ILE:HG13	1:o:139:LEU:HD11	1.94	0.48
1:o:36:LEU:HD21	1:o:64:TRP:CD1	2.49	0.48
1:r:93:ILE:HG22	1:r:94:LEU:O	2.14	0.48
2:s:15:ILE:HA	2:s:28:GLY:O	2.13	0.48
2:s:248:THR:HG23	2:s:250:TYR:H	1.78	0.48
2:t:352:PHE:CE2	2:t:354:PHE:HB2	2.49	0.48
2:t:479:VAL:CG2	2:u:477:GLN:HA	2.44	0.48
2:u:352:PHE:CE2	2:u:354:PHE:HB2	2.49	0.48
2:u:355:ARG:HG3	2:u:430:LEU:HD11	1.96	0.48
2:w:128:VAL:HG13	2:w:309:PRO:HG3	1.96	0.48
2:w:355:ARG:HG3	2:w:430:LEU:HD11	1.96	0.48
1:b:62:LYS:HE2	3:N:72:ASP:HA	1.96	0.48
1:c:36:LEU:HA	1:c:73:ILE:HA	1.95	0.48
1:c:92:SER:O	1:c:93:ILE:C	2.57	0.48
1:i:95:ARG:O	1:i:99:LEU:HD12	2.14	0.48
1:l:36:LEU:HD21	1:l:64:TRP:CD1	2.49	0.48
1:l:99:LEU:H	1:l:99:LEU:HD12	1.78	0.48
1:n:45:THR:OG1	1:n:48:THR:OG1	2.31	0.48
1:o:93:ILE:HG22	1:o:94:LEU:O	2.14	0.48
1:r:36:LEU:HD21	1:r:64:TRP:CD1	2.49	0.48
1:r:92:SER:OG	1:r:92:SER:O	2.26	0.48
2:t:396:SER:HB3	2:u:355:ARG:O	2.14	0.48
2:v:10:ASN:HD22	2:v:10:ASN:HA	1.48	0.48
2:w:352:PHE:CE2	2:w:354:PHE:HB2	2.49	0.48
2:w:578:PHE:CD1	2:w:578:PHE:N	2.82	0.48
1:a:134:ARG:HG3	1:c:129:LEU:HD22	1.96	0.47
1:e:29:ARG:C	1:e:31:PHE:N	2.70	0.47
1:f:36:LEU:HD21	1:f:64:TRP:CD1	2.49	0.47
1:h:45:THR:OG1	1:h:48:THR:OG1	2.31	0.47
1:i:92:SER:OG	1:i:92:SER:O	2.26	0.47
1:n:101:VAL:HG11	3:R:33:GLU:OE1	2.14	0.47
1:q:86:VAL:HG22	3:P:31:THR:HG22	1.81	0.47
2:s:68:LEU:HD21	2:s:557:ILE:HG12	1.96	0.47
2:s:91:LEU:HD13	2:s:91:LEU:HA	1.56	0.47
2:s:352:PHE:CE2	2:s:354:PHE:HB2	2.49	0.47
2:t:166:ILE:HA	2:t:175:ALA:O	2.13	0.47
2:t:552:LEU:HD21	2:t:566:ARG:HH12	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:175:GLU:O	3:M:179:GLY:N	2.30	0.47
1:f:93:ILE:HG22	1:f:94:LEU:O	2.14	0.47
1:i:36:LEU:HD21	1:i:64:TRP:CD1	2.49	0.47
1:i:36:LEU:HA	1:i:73:ILE:HA	1.95	0.47
1:i:92:SER:O	1:i:93:ILE:C	2.57	0.47
1:n:90:ASP:CG	3:Q:34:GLY:O	2.56	0.47
1:o:95:ARG:O	1:o:99:LEU:HD12	2.14	0.47
1:p:134:ARG:HG3	1:r:129:LEU:HD22	1.96	0.47
2:u:56:ASP:O	2:u:571:THR:HG22	2.14	0.47
2:u:166:ILE:HA	2:u:175:ALA:O	2.13	0.47
2:w:655:TRP:HB2	2:w:657:ARG:HH11	1.79	0.47
1:g:134:ARG:HG3	1:i:129:LEU:HD22	1.96	0.47
1:m:134:ARG:HG3	1:o:129:LEU:HD22	1.96	0.47
2:s:276:SER:HB3	2:t:384:ASN:CB	2.44	0.47
2:s:352:PHE:HE2	2:s:354:PHE:HB2	1.78	0.47
2:v:166:ILE:HA	2:v:175:ALA:O	2.13	0.47
2:x:382:ILE:HD13	2:x:382:ILE:HA	1.60	0.47
3:P:148:ASN:ND2	3:P:157:GLU:HG3	2.29	0.47
1:b:20:PHE:CE2	1:b:73:ILE:HD12	2.49	0.47
1:d:134:ARG:HG3	1:f:129:LEU:HD22	1.96	0.47
1:l:95:ARG:O	1:l:99:LEU:HD12	2.14	0.47
2:s:56:ASP:O	2:s:571:THR:HG22	2.14	0.47
2:u:15:ILE:HA	2:u:28:GLY:O	2.13	0.47
2:v:128:VAL:HG13	2:v:309:PRO:HG3	1.96	0.47
2:v:371:THR:HG22	2:v:388:ASP:HB3	1.94	0.47
2:w:396:SER:HB3	2:x:355:ARG:O	2.14	0.47
2:x:56:ASP:O	2:x:571:THR:HG22	2.14	0.47
3:N:49:LYS:HE3	3:O:136:TYR:HE1	1.79	0.47
1:q:86:VAL:HG13	3:P:31:THR:CG2	2.44	0.47
1:r:92:SER:O	1:r:93:ILE:C	2.57	0.47
2:s:128:VAL:HG13	2:s:309:PRO:HG3	1.96	0.47
2:v:276:SER:HB3	2:w:384:ASN:HB3	1.96	0.47
2:x:607:TYR:CE1	2:x:661:ASN:HB3	2.50	0.47
2:x:655:TRP:HB2	2:x:657:ARG:HH11	1.79	0.47
3:M:67:ILE:HD11	3:M:121:ILE:CD1	2.44	0.47
3:P:98:ASN:O	3:Q:129:GLU:HG2	2.12	0.47
1:e:38:GLY:HA3	1:e:70:TYR:HA	1.96	0.47
1:e:121:ILE:H	1:e:121:ILE:HG13	1.37	0.47
1:n:20:PHE:CE2	1:n:73:ILE:HD12	2.49	0.47
2:s:276:SER:HB3	2:t:384:ASN:HB3	1.97	0.47
2:s:456:ARG:HH11	2:x:482:VAL:CG1	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:395:VAL:HG23	2:v:437:LEU:HG	1.97	0.47
2:x:355:ARG:HG3	2:x:430:LEU:HD11	1.96	0.47
3:Q:170:LEU:HD13	3:Q:170:LEU:HA	1.70	0.47
3:W:175:GLU:O	3:W:179:GLY:N	2.31	0.47
1:a:9:LEU:CD1	1:a:23:PRO:HD2	2.45	0.47
1:j:9:LEU:CD1	1:j:23:PRO:HD2	2.45	0.47
1:j:134:ARG:HG3	1:l:129:LEU:HD22	1.96	0.47
1:k:38:GLY:HA3	1:k:70:TYR:HA	1.96	0.47
1:l:92:SER:O	1:l:93:ILE:C	2.57	0.47
1:q:20:PHE:CE2	1:q:73:ILE:HD12	2.49	0.47
2:s:290:VAL:HG11	2:x:270:VAL:CG1	2.44	0.47
2:s:578:PHE:N	2:s:578:PHE:CD1	2.82	0.47
2:s:607:TYR:CE1	2:s:661:ASN:HB3	2.50	0.47
2:t:15:ILE:HA	2:t:28:GLY:O	2.13	0.47
2:t:68:LEU:HD21	2:t:557:ILE:HG12	1.96	0.47
2:t:276:SER:HB3	2:u:384:ASN:CB	2.45	0.47
2:t:276:SER:HB3	2:u:384:ASN:HB3	1.96	0.47
2:t:355:ARG:HG3	2:t:430:LEU:HD11	1.96	0.47
2:t:704:ARG:HD2	3:T:150:PHE:HA	1.96	0.47
2:u:166:ILE:HG12	2:u:176:LYS:HG3	1.97	0.47
2:u:270:VAL:CG1	2:v:290:VAL:HG11	2.43	0.47
2:u:704:ARG:HD2	3:V:150:PHE:HA	1.95	0.47
2:v:478:ASP:CB	2:w:477:GLN:HG2	2.42	0.47
2:w:607:TYR:CE1	2:w:661:ASN:HB3	2.50	0.47
2:x:395:VAL:HG23	2:x:437:LEU:HG	1.97	0.47
3:V:49:LYS:HE3	3:W:136:TYR:HE1	1.80	0.47
3:V:148:ASN:ND2	3:V:157:GLU:HG3	2.28	0.47
3:X:148:ASN:ND2	3:X:157:GLU:HG3	2.28	0.47
1:m:93:ILE:HG12	2:s:742:ARG:HH12	1.77	0.47
2:t:166:ILE:HG12	2:t:176:LYS:HG3	1.97	0.47
2:x:578:PHE:CD1	2:x:578:PHE:N	2.82	0.47
1:e:62:LYS:HE2	3:X:72:ASP:HA	1.96	0.47
1:g:9:LEU:CD1	1:g:23:PRO:HD2	2.45	0.47
1:k:20:PHE:CE2	1:k:73:ILE:HD12	2.49	0.47
1:m:9:LEU:CD1	1:m:23:PRO:HD2	2.45	0.47
1:p:29:ARG:HB2	3:P:5:ASP:CB	2.45	0.47
1:p:116:LEU:HD21	1:r:114:ARG:NE	2.30	0.47
1:r:9:LEU:HD21	1:r:23:PRO:CD	2.44	0.47
2:u:128:VAL:HG13	2:u:309:PRO:HG3	1.96	0.47
1:b:38:GLY:HA3	1:b:70:TYR:HA	1.96	0.47
1:d:116:LEU:HD21	1:f:114:ARG:NE	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:20:PHE:CE2	1:h:73:ILE:HD12	2.49	0.47
1:n:90:ASP:OD1	3:Q:34:GLY:O	2.33	0.47
1:q:90:ASP:OD1	3:O:34:GLY:O	2.32	0.47
2:s:395:VAL:HG23	2:s:437:LEU:HG	1.97	0.47
2:t:655:TRP:HB2	2:t:657:ARG:HH11	1.79	0.47
2:w:68:LEU:HD21	2:w:557:ILE:HG12	1.96	0.47
2:w:395:VAL:HG23	2:w:437:LEU:HG	1.97	0.47
2:x:68:LEU:HD21	2:x:557:ILE:HG12	1.96	0.47
3:M:129:GLU:HG2	3:X:98:ASN:O	2.10	0.47
3:T:49:LYS:HE3	3:U:136:TYR:HE1	1.80	0.47
1:d:9:LEU:CD1	1:d:23:PRO:HD2	2.45	0.46
1:n:38:GLY:HA3	1:n:70:TYR:HA	1.96	0.46
2:s:188:VAL:CG1	2:x:161:TYR:HB2	2.37	0.46
2:s:704:ARG:HH11	3:R:150:PHE:HA	1.80	0.46
2:s:722:ASN:ND2	3:S:27:PRO:HG3	2.27	0.46
2:t:56:ASP:O	2:t:571:THR:HG22	2.14	0.46
2:t:128:VAL:HG13	2:t:309:PRO:HG3	1.96	0.46
2:v:479:VAL:CG2	2:w:477:GLN:HA	2.45	0.46
2:v:607:TYR:CE1	2:v:661:ASN:HB3	2.50	0.46
2:w:479:VAL:CG2	2:x:477:GLN:HA	2.45	0.46
3:P:147:ASN:ND2	3:P:151:PHE:O	2.49	0.46
1:a:116:LEU:HD21	1:c:114:ARG:NE	2.30	0.46
1:j:116:LEU:HA	1:j:116:LEU:HD13	1.66	0.46
1:m:116:LEU:HD21	1:o:114:ARG:NE	2.30	0.46
1:n:121:ILE:H	1:n:121:ILE:HG13	1.37	0.46
2:s:579:THR:CG2	2:x:466:SER:OG	2.57	0.46
2:t:607:TYR:CE1	2:t:661:ASN:HB3	2.50	0.46
2:u:68:LEU:HD21	2:u:557:ILE:HG12	1.96	0.46
2:v:56:ASP:O	2:v:571:THR:HG22	2.14	0.46
2:v:528:PHE:HA	2:v:537:GLN:O	2.15	0.46
2:v:655:TRP:HB2	2:v:657:ARG:HH11	1.79	0.46
2:w:56:ASP:O	2:w:571:THR:HG22	2.14	0.46
3:M:67:ILE:HD11	3:M:121:ILE:HD12	1.98	0.46
1:a:7:THR:OG1	1:a:115:ASP:OD1	2.34	0.46
1:f:92:SER:O	1:f:93:ILE:C	2.57	0.46
1:j:116:LEU:HD21	1:l:114:ARG:NE	2.30	0.46
1:n:114:ARG:HA	1:o:113:ALA:HB1	1.98	0.46
2:s:528:PHE:HA	2:s:537:GLN:O	2.15	0.46
2:s:702:GLN:NE2	3:S:26:GLU:HG2	2.29	0.46
2:u:134:ALA:HA	2:u:307:THR:HB	1.98	0.46
2:u:395:VAL:HG23	2:u:437:LEU:HG	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:u:396:SER:HB3	2:v:355:ARG:O	2.16	0.46
2:u:528:PHE:HA	2:u:537:GLN:O	2.16	0.46
2:w:276:SER:HB3	2:x:384:ASN:CB	2.46	0.46
3:R:88:MET:CG	3:S:178:TYR:HD1	2.23	0.46
3:S:175:GLU:O	3:S:179:GLY:N	2.30	0.46
1:g:116:LEU:HD21	1:i:114:ARG:NE	2.30	0.46
1:k:114:ARG:HA	1:l:113:ALA:HB1	1.98	0.46
2:s:655:TRP:HB2	2:s:657:ARG:HH11	1.79	0.46
2:t:528:PHE:HA	2:t:537:GLN:O	2.15	0.46
2:u:607:TYR:CE1	2:u:661:ASN:HB3	2.50	0.46
2:v:68:LEU:HD21	2:v:557:ILE:HG12	1.96	0.46
2:v:166:ILE:HG12	2:v:176:LYS:HG3	1.97	0.46
2:v:266:MET:HE2	2:v:266:MET:HB3	1.83	0.46
3:M:136:TYR:HE1	3:X:49:LYS:HE3	1.80	0.46
1:h:38:GLY:HA3	1:h:70:TYR:HA	1.96	0.46
1:m:29:ARG:HB2	3:R:5:ASP:CB	2.46	0.46
1:n:29:ARG:C	1:n:31:PHE:N	2.70	0.46
1:q:101:VAL:HG11	3:P:33:GLU:OE1	2.15	0.46
2:t:91:LEU:HA	2:t:91:LEU:HD13	1.56	0.46
2:t:165:LEU:HD13	2:t:244:ILE:HD13	1.97	0.46
2:t:276:SER:N	2:u:384:ASN:OD1	2.48	0.46
2:u:466:SER:OG	2:v:579:THR:CG2	2.57	0.46
2:x:235:THR:HB	2:x:246:PRO:HD3	1.98	0.46
3:N:147:ASN:ND2	3:N:151:PHE:O	2.49	0.46
3:R:172:MET:HE2	3:R:172:MET:HB2	1.65	0.46
3:T:148:ASN:ND2	3:T:157:GLU:HG3	2.29	0.46
3:W:170:LEU:HD13	3:W:170:LEU:HA	1.71	0.46
3:X:11:ALA:O	3:X:12:ALA:C	2.52	0.46
3:X:147:ASN:ND2	3:X:151:PHE:O	2.49	0.46
1:c:11:TYR:HD1	1:c:11:TYR:HA	1.63	0.46
1:k:101:VAL:HG11	3:T:33:GLU:OE1	2.16	0.46
2:s:165:LEU:HD13	2:s:244:ILE:HD13	1.97	0.46
2:u:479:VAL:CG2	2:v:477:GLN:HA	2.46	0.46
2:u:655:TRP:HB2	2:u:657:ARG:HH11	1.79	0.46
3:R:147:ASN:ND2	3:R:151:PHE:O	2.49	0.46
3:V:54:ILE:HD11	3:V:141:LYS:HD3	1.98	0.46
3:V:147:ASN:ND2	3:V:151:PHE:O	2.49	0.46
1:a:3:ASN:HA	1:a:4:VAL:HA	1.69	0.46
1:b:29:ARG:C	1:b:31:PHE:N	2.70	0.46
1:k:86:VAL:HG13	3:T:31:THR:CG2	2.46	0.46
2:v:91:LEU:HD13	2:v:91:LEU:HA	1.57	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:382:ILE:HD13	2:v:382:ILE:HA	1.60	0.46
2:w:276:SER:HB3	2:x:384:ASN:HB3	1.98	0.46
2:w:276:SER:N	2:x:384:ASN:OD1	2.48	0.46
3:T:11:ALA:O	3:T:12:ALA:C	2.52	0.46
1:e:114:ARG:HA	1:f:113:ALA:HB1	1.97	0.46
1:h:86:VAL:CA	3:V:31:THR:HG22	2.41	0.46
1:m:7:THR:OG1	1:m:115:ASP:OD1	2.34	0.46
1:o:93:ILE:HG23	2:s:745:ARG:O	2.15	0.46
1:q:11:TYR:CD2	1:q:75:LEU:HD21	2.51	0.46
2:s:355:ARG:HG3	2:s:430:LEU:HD11	1.96	0.46
2:s:478:ASP:CB	2:t:477:GLN:HG2	2.43	0.46
2:t:578:PHE:N	2:t:578:PHE:CD1	2.82	0.46
2:u:594:MET:O	2:u:597:LYS:HG2	2.16	0.46
2:u:722:ASN:ND2	3:W:27:PRO:CG	2.75	0.46
2:v:134:ALA:HA	2:v:307:THR:HB	1.98	0.46
2:w:235:THR:HB	2:w:246:PRO:HD3	1.98	0.46
2:x:166:ILE:HG12	2:x:176:LYS:HG3	1.97	0.46
1:k:11:TYR:CD2	1:k:75:LEU:HD21	2.51	0.46
1:p:9:LEU:CD1	1:p:23:PRO:HD2	2.45	0.46
1:q:136:ILE:H	1:r:139:LEU:HD11	1.81	0.46
2:s:477:GLN:HG2	2:x:478:ASP:CB	2.41	0.46
2:w:466:SER:OG	2:x:579:THR:CG2	2.57	0.46
3:M:172:MET:HE3	3:M:172:MET:HB2	1.56	0.46
3:T:134:PHE:HE1	3:T:171:CYS:HB3	1.81	0.46
3:T:147:ASN:ND2	3:T:151:PHE:O	2.49	0.46
1:b:11:TYR:CD2	1:b:75:LEU:HD21	2.51	0.46
1:b:136:ILE:H	1:c:139:LEU:HD11	1.81	0.46
1:h:136:ILE:H	1:i:139:LEU:HD11	1.81	0.46
1:i:42:LYS:HG3	1:i:70:TYR:CE1	2.51	0.46
1:i:47:ASN:OD1	2:u:610:ASP:HB2	2.16	0.46
1:j:116:LEU:HD21	1:l:114:ARG:CZ	2.46	0.46
1:o:42:LYS:HG3	1:o:70:TYR:CE1	2.51	0.46
1:o:92:SER:O	1:o:93:ILE:C	2.57	0.46
2:t:235:THR:HB	2:t:246:PRO:HD3	1.98	0.46
2:t:594:MET:O	2:t:597:LYS:HG2	2.16	0.46
2:u:165:LEU:HD13	2:u:244:ILE:HD13	1.97	0.46
2:v:594:MET:O	2:v:597:LYS:HG2	2.16	0.46
2:w:165:LEU:HD13	2:w:244:ILE:HD13	1.97	0.46
2:w:166:ILE:HG12	2:w:176:LYS:HG3	1.97	0.46
2:w:528:PHE:HA	2:w:537:GLN:O	2.15	0.46
2:x:165:LEU:HD13	2:x:244:ILE:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:98:ASN:O	3:S:129:GLU:HG2	2.12	0.46
3:T:54:ILE:HD11	3:T:141:LYS:HD3	1.98	0.46
3:T:98:ASN:O	3:U:129:GLU:HG2	2.14	0.46
3:X:54:ILE:HD11	3:X:141:LYS:HD3	1.98	0.46
1:b:114:ARG:HA	1:c:113:ALA:HB1	1.98	0.45
1:b:121:ILE:H	1:b:121:ILE:HG13	1.37	0.45
1:e:136:ILE:H	1:f:139:LEU:HD11	1.81	0.45
1:q:29:ARG:C	1:q:31:PHE:N	2.70	0.45
1:r:11:TYR:HD1	1:r:11:TYR:HA	1.63	0.45
2:s:166:ILE:HG12	2:s:176:LYS:HG3	1.97	0.45
2:s:466:SER:OG	2:t:579:THR:CG2	2.57	0.45
2:v:645:GLN:HE21	2:v:645:GLN:HB2	1.50	0.45
3:S:130:MET:HG3	3:S:131:PRO:HD2	1.97	0.45
3:V:134:PHE:HE1	3:V:171:CYS:HB3	1.81	0.45
1:e:45:THR:OG1	1:e:48:THR:OG1	2.31	0.45
1:o:13:LEU:HD23	1:o:13:LEU:HA	1.72	0.45
1:p:27:LEU:HD12	3:P:6:MET:HG3	1.99	0.45
1:q:38:GLY:HA3	1:q:70:TYR:HA	1.96	0.45
1:q:121:ILE:H	1:q:121:ILE:HG13	1.37	0.45
2:t:266:MET:HE2	2:t:266:MET:HB3	1.83	0.45
2:t:395:VAL:HG23	2:t:437:LEU:HG	1.97	0.45
2:v:565:LEU:HB2	2:v:572:PHE:HD1	1.82	0.45
2:v:705:ARG:CZ	3:X:26:GLU:HG2	2.47	0.45
3:N:98:ASN:O	3:O:129:GLU:HG2	2.13	0.45
3:R:61:PHE:CE1	3:R:134:PHE:HE2	2.34	0.45
1:c:71:THR:HB	1:c:72:THR:H	1.54	0.45
1:d:116:LEU:HD21	1:f:114:ARG:CZ	2.46	0.45
1:f:42:LYS:HG3	1:f:70:TYR:CE1	2.51	0.45
1:f:93:ILE:HG23	2:v:745:ARG:O	2.16	0.45
1:h:11:TYR:CD2	1:h:75:LEU:HD21	2.51	0.45
1:i:34:VAL:HG22	1:i:75:LEU:HB3	1.98	0.45
1:k:29:ARG:C	1:k:31:PHE:N	2.70	0.45
1:k:136:ILE:H	1:l:139:LEU:HD11	1.81	0.45
1:m:116:LEU:HD21	1:o:114:ARG:CZ	2.46	0.45
2:u:235:THR:HB	2:u:246:PRO:HD3	1.98	0.45
2:w:594:MET:O	2:w:597:LYS:HG2	2.16	0.45
2:x:528:PHE:HA	2:x:537:GLN:O	2.16	0.45
3:Q:130:MET:HG3	3:Q:131:PRO:HD2	1.98	0.45
3:S:172:MET:HB2	3:S:172:MET:HE3	1.56	0.45
1:a:29:ARG:HB2	3:N:5:ASP:CB	2.46	0.45
1:e:90:ASP:OD2	3:W:34:GLY:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:42:LYS:HG3	1:l:70:TYR:CE1	2.51	0.45
1:o:9:LEU:HD21	1:o:23:PRO:CD	2.44	0.45
1:r:42:LYS:HG3	1:r:70:TYR:CE1	2.51	0.45
2:s:257:LEU:HD12	2:s:257:LEU:HA	1.81	0.45
2:s:594:MET:O	2:s:597:LYS:HG2	2.16	0.45
2:u:510:ASN:HD22	2:u:510:ASN:HA	1.50	0.45
2:u:565:LEU:HB2	2:u:572:PHE:HD1	1.82	0.45
2:w:725:SER:HB3	2:w:727:TRP:CE2	2.52	0.45
2:x:722:ASN:ND2	3:Q:27:PRO:HG3	2.28	0.45
3:N:134:PHE:HE1	3:N:171:CYS:HB3	1.81	0.45
3:P:134:PHE:HE1	3:P:171:CYS:HB3	1.82	0.45
3:W:172:MET:HE3	3:W:172:MET:HB2	1.56	0.45
1:c:34:VAL:HG22	1:c:75:LEU:HB3	1.98	0.45
1:g:13:LEU:HD13	1:g:13:LEU:HA	1.69	0.45
1:h:67:ALA:CB	3:V:74:TYR:OH	2.64	0.45
1:h:114:ARG:HA	1:i:113:ALA:HB1	1.98	0.45
1:l:34:VAL:HG22	1:l:75:LEU:HB3	1.98	0.45
1:q:45:THR:OG1	1:q:48:THR:OG1	2.31	0.45
2:t:10:ASN:HD22	2:t:10:ASN:HA	1.48	0.45
2:v:235:THR:HB	2:v:246:PRO:HD3	1.98	0.45
2:x:10:ASN:HD22	2:x:10:ASN:HA	1.48	0.45
3:M:130:MET:HG3	3:M:131:PRO:HD2	1.98	0.45
3:O:148:ASN:CG	3:P:159:VAL:HG11	2.42	0.45
3:P:61:PHE:CE1	3:P:134:PHE:HE2	2.34	0.45
3:R:148:ASN:ND2	3:R:157:GLU:HG3	2.29	0.45
1:f:13:LEU:HD23	1:f:13:LEU:HA	1.72	0.45
1:k:135:ARG:HE	1:k:135:ARG:HB2	1.56	0.45
1:q:114:ARG:HA	1:r:113:ALA:HB1	1.98	0.45
1:r:34:VAL:HG22	1:r:75:LEU:HB3	1.98	0.45
2:t:746:LEU:HD23	2:t:746:LEU:HA	1.66	0.45
2:u:382:ILE:HA	2:u:382:ILE:HD13	1.60	0.45
2:v:725:SER:HB3	2:v:727:TRP:CE2	2.52	0.45
3:Q:148:ASN:CG	3:R:159:VAL:HG11	2.42	0.45
3:V:11:ALA:O	3:V:12:ALA:C	2.52	0.45
1:p:7:THR:OG1	1:p:115:ASP:OD1	2.34	0.45
1:p:53:ALA:HB1	3:N:99:ARG:NH1	2.32	0.45
2:s:479:VAL:CG2	2:t:477:GLN:HA	2.47	0.45
2:v:338:ASN:HD22	2:v:338:ASN:HA	1.42	0.45
2:w:565:LEU:HB2	2:w:572:PHE:HD1	1.81	0.45
2:x:445:VAL:HG22	2:x:460:PHE:CD2	2.52	0.45
2:x:594:MET:O	2:x:597:LYS:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:61:PHE:CE1	3:N:134:PHE:HE2	2.34	0.45
3:O:130:MET:HG3	3:O:131:PRO:HD2	1.98	0.45
3:S:148:ASN:CG	3:T:159:VAL:HG11	2.42	0.45
3:T:61:PHE:CE1	3:T:134:PHE:HE2	2.34	0.45
3:W:148:ASN:CG	3:X:159:VAL:HG11	2.42	0.45
1:c:22:ILE:HA	1:c:23:PRO:HD3	1.81	0.45
1:e:11:TYR:CD2	1:e:75:LEU:HD21	2.51	0.45
1:g:7:THR:OG1	1:g:115:ASP:OD1	2.34	0.45
1:h:90:ASP:OD2	3:U:34:GLY:C	2.60	0.45
1:h:90:ASP:OD2	3:U:34:GLY:O	2.35	0.45
2:s:235:THR:HB	2:s:246:PRO:HD3	1.98	0.45
2:s:384:ASN:HB3	2:x:276:SER:HB3	1.99	0.45
2:s:445:VAL:HG22	2:s:460:PHE:CD2	2.52	0.45
2:t:134:ALA:HA	2:t:307:THR:HB	1.98	0.45
2:t:178:LYS:HE3	2:t:178:LYS:HB3	1.85	0.45
2:w:338:ASN:HD22	2:w:338:ASN:HA	1.42	0.45
2:x:134:ALA:HA	2:x:307:THR:HB	1.98	0.45
2:x:725:SER:HB3	2:x:727:TRP:CE2	2.52	0.45
3:R:54:ILE:HD11	3:R:141:LYS:HD3	1.98	0.45
3:S:170:LEU:HD13	3:S:170:LEU:HA	1.71	0.45
3:X:24:ILE:HG21	3:X:146:PHE:HE2	1.82	0.45
1:a:27:LEU:HD12	3:N:6:MET:HG3	1.99	0.45
1:f:34:VAL:HG22	1:f:75:LEU:HB3	1.98	0.45
1:g:116:LEU:HD21	1:i:114:ARG:CZ	2.46	0.45
1:k:48:THR:HA	3:T:81:SER:HB3	1.98	0.45
1:m:27:LEU:HD12	3:R:6:MET:HG3	1.98	0.45
1:p:116:LEU:HD21	1:r:114:ARG:CZ	2.46	0.45
2:s:698:ILE:HD11	2:t:7:SER:CB	2.47	0.45
2:t:788:LEU:HG	3:U:153:ALA:CA	2.47	0.45
2:u:10:ASN:HD22	2:u:10:ASN:HA	1.47	0.45
2:u:165:LEU:HD23	2:u:165:LEU:HA	1.68	0.45
2:u:704:ARG:NH1	3:V:150:PHE:O	2.45	0.45
3:M:78:ILE:HB	3:M:103:VAL:HG22	1.99	0.45
3:M:148:ASN:CG	3:N:159:VAL:HG11	2.42	0.45
3:N:24:ILE:HG21	3:N:146:PHE:HE2	1.82	0.45
3:U:148:ASN:CG	3:V:159:VAL:HG11	2.42	0.45
3:W:130:MET:HG3	3:W:131:PRO:HD2	1.98	0.45
1:b:86:VAL:HG13	3:N:31:THR:CG2	2.47	0.45
1:b:90:ASP:OD2	3:M:34:GLY:C	2.61	0.45
1:b:90:ASP:OD2	3:M:34:GLY:O	2.35	0.45
1:c:42:LYS:HG3	1:c:70:TYR:CE1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:n:11:TYR:CD2	1:n:75:LEU:HD21	2.51	0.45
1:r:13:LEU:HA	1:r:13:LEU:HD23	1.72	0.45
2:s:134:ALA:HA	2:s:307:THR:HB	1.98	0.45
2:u:91:LEU:HA	2:u:91:LEU:HD13	1.56	0.45
2:v:702:GLN:NE2	3:M:26:GLU:HG2	2.32	0.45
2:w:698:ILE:HD11	2:x:7:SER:CB	2.47	0.45
2:x:178:LYS:HE3	2:x:178:LYS:HB3	1.85	0.45
3:N:54:ILE:HD11	3:N:141:LYS:HD3	1.98	0.45
3:P:54:ILE:HD11	3:P:141:LYS:HD3	1.98	0.45
3:X:61:PHE:CE1	3:X:134:PHE:HE2	2.34	0.45
1:d:119:ASP:O	1:f:129:LEU:HD11	2.17	0.44
1:i:47:ASN:CG	2:u:610:ASP:HB2	2.43	0.44
1:l:71:THR:HB	1:l:72:THR:H	1.54	0.44
1:n:136:ILE:H	1:o:139:LEU:HD11	1.81	0.44
2:t:619:PRO:HD3	2:t:654:PRO:HB3	1.99	0.44
2:u:619:PRO:HD3	2:u:654:PRO:HB3	1.99	0.44
2:v:722:ASN:ND2	3:M:27:PRO:HG3	2.25	0.44
3:V:98:ASN:O	3:W:129:GLU:HG2	2.12	0.44
3:X:176:MET:HE3	3:X:176:MET:HB3	1.82	0.44
1:b:129:LEU:HD13	1:c:121:ILE:HD11	2.00	0.44
1:c:13:LEU:HD23	1:c:13:LEU:HA	1.72	0.44
1:g:119:ASP:O	1:i:129:LEU:HD11	2.17	0.44
1:i:9:LEU:HD21	1:i:23:PRO:CD	2.44	0.44
1:m:82:THR:OG1	1:m:83:ASP:N	2.51	0.44
2:t:445:VAL:HG22	2:t:460:PHE:CD2	2.52	0.44
2:u:725:SER:HB3	2:u:727:TRP:CE2	2.52	0.44
2:u:756:PRO:HG3	3:V:39:ASP:CG	2.42	0.44
2:v:594:MET:HB2	2:v:597:LYS:CD	2.46	0.44
2:w:446:GLN:HB3	2:w:463:PRO:HG3	2.00	0.44
2:x:746:LEU:HD23	2:x:746:LEU:HA	1.66	0.44
3:P:32:LEU:HD12	3:P:44:ARG:HD2	2.00	0.44
3:S:78:ILE:HB	3:S:103:VAL:HG22	1.99	0.44
3:W:78:ILE:HB	3:W:103:VAL:HG22	1.99	0.44
1:a:116:LEU:HD21	1:c:114:ARG:CZ	2.46	0.44
1:j:82:THR:OG1	1:j:83:ASP:N	2.50	0.44
1:n:48:THR:HA	3:R:81:SER:HB3	1.98	0.44
1:p:82:THR:OG1	1:p:83:ASP:N	2.51	0.44
2:t:565:LEU:HB2	2:t:572:PHE:HD1	1.82	0.44
2:t:698:ILE:HD11	2:u:7:SER:CB	2.48	0.44
2:v:165:LEU:HD13	2:v:244:ILE:HD13	1.97	0.44
2:w:169:ILE:HA	2:w:232:SER:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:67:ILE:HD11	3:O:121:ILE:HD12	1.98	0.44
1:e:135:ARG:HE	1:e:135:ARG:HB2	1.56	0.44
1:h:86:VAL:HG13	3:V:31:THR:CG2	2.47	0.44
2:s:384:ASN:OD1	2:x:276:SER:N	2.49	0.44
2:s:704:ARG:HD2	3:R:150:PHE:HA	2.00	0.44
2:u:266:MET:HE2	2:u:266:MET:HB3	1.83	0.44
2:u:276:SER:N	2:v:384:ASN:OD1	2.51	0.44
2:u:446:GLN:HB3	2:u:463:PRO:HG3	2.00	0.44
2:v:704:ARG:HD2	3:X:150:PHE:HA	1.99	0.44
2:v:713:SER:HB2	2:v:776:LEU:HA	2.00	0.44
2:w:134:ALA:HA	2:w:307:THR:HB	1.98	0.44
3:N:32:LEU:HD12	3:N:44:ARG:HD2	2.00	0.44
3:X:32:LEU:HD12	3:X:44:ARG:HD2	2.00	0.44
1:a:119:ASP:O	1:c:129:LEU:HD11	2.17	0.44
1:c:47:ASN:OD1	2:w:610:ASP:HB2	2.18	0.44
1:g:53:ALA:HB1	3:T:99:ARG:NH1	2.32	0.44
1:k:90:ASP:OD2	3:S:34:GLY:O	2.35	0.44
2:s:384:ASN:CB	2:x:276:SER:HB3	2.47	0.44
2:s:565:LEU:HB2	2:s:572:PHE:HD1	1.82	0.44
2:t:446:GLN:HB3	2:t:463:PRO:HG3	2.00	0.44
2:u:178:LYS:HE3	2:u:178:LYS:HB3	1.85	0.44
2:v:446:GLN:HB3	2:v:463:PRO:HG3	2.00	0.44
2:x:169:ILE:HA	2:x:232:SER:O	2.18	0.44
2:x:586:GLN:HE21	2:x:586:GLN:HB3	1.63	0.44
3:O:175:GLU:O	3:O:179:GLY:N	2.31	0.44
3:R:134:PHE:HE1	3:R:171:CYS:HB3	1.81	0.44
3:U:78:ILE:HB	3:U:103:VAL:HG22	1.99	0.44
3:V:24:ILE:HG21	3:V:146:PHE:HE2	1.82	0.44
3:V:32:LEU:HD12	3:V:44:ARG:HD2	2.00	0.44
3:V:61:PHE:CE1	3:V:134:PHE:HE2	2.34	0.44
1:e:94:LEU:CD1	2:v:736:LEU:CD2	2.84	0.44
1:h:24:PHE:HE1	1:h:32:VAL:CG2	2.31	0.44
1:i:92:SER:HA	2:u:640:ILE:HD12	1.99	0.44
1:l:9:LEU:HD21	1:l:23:PRO:CD	2.44	0.44
1:q:129:LEU:HD13	1:r:121:ILE:HD11	2.00	0.44
2:s:270:VAL:HG12	2:s:271:GLY:N	2.33	0.44
2:s:355:ARG:O	2:x:396:SER:HB3	2.17	0.44
2:s:725:SER:HB3	2:s:727:TRP:CE2	2.52	0.44
2:t:552:LEU:HD23	2:t:552:LEU:HA	1.84	0.44
2:u:713:SER:HB2	2:u:776:LEU:HA	2.00	0.44
2:v:169:ILE:HA	2:v:232:SER:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:466:SER:OG	2:w:579:THR:CG2	2.57	0.44
2:w:270:VAL:HG12	2:w:271:GLY:N	2.33	0.44
2:x:446:GLN:HB3	2:x:463:PRO:HG3	2.00	0.44
2:x:704:ARG:HD2	3:P:150:PHE:HA	1.99	0.44
3:Q:128:ASP:O	3:Q:135:ARG:NH2	2.44	0.44
3:R:24:ILE:HG21	3:R:146:PHE:HE2	1.81	0.44
1:d:29:ARG:HB2	3:X:5:ASP:CB	2.48	0.44
1:k:90:ASP:OD2	3:S:34:GLY:C	2.61	0.44
1:p:36:LEU:HD22	1:p:73:ILE:HG13	2.00	0.44
1:q:29:ARG:C	1:q:31:PHE:H	2.26	0.44
2:s:273:ALA:HB3	2:t:254:PHE:CE1	2.53	0.44
2:s:619:PRO:HD3	2:s:654:PRO:HB3	1.99	0.44
2:t:701:LEU:HD23	2:t:787:TYR:HB2	2.00	0.44
2:u:701:LEU:HD23	2:u:787:TYR:HB2	2.00	0.44
2:w:445:VAL:HG22	2:w:460:PHE:CD2	2.53	0.44
2:x:314:ARG:HG2	2:x:318:GLY:HA2	2.00	0.44
3:T:24:ILE:HG21	3:T:146:PHE:HE2	1.82	0.44
1:a:82:THR:OG1	1:a:83:ASP:N	2.51	0.44
1:h:48:THR:HA	3:V:81:SER:HB3	2.00	0.44
1:j:3:ASN:HA	1:j:4:VAL:HA	1.69	0.44
1:n:15:GLY:HA2	1:n:65:GLY:HA3	2.00	0.44
2:s:178:LYS:HE3	2:s:178:LYS:HB3	1.85	0.44
2:t:48:LEU:HD22	2:t:574:ALA:CB	2.48	0.44
2:t:143:LEU:HD13	2:t:143:LEU:HA	1.88	0.44
2:v:48:LEU:HD22	2:v:574:ALA:CB	2.48	0.44
2:v:270:VAL:HG12	2:v:271:GLY:N	2.33	0.44
2:w:178:LYS:HE3	2:w:178:LYS:HB3	1.85	0.44
2:w:722:ASN:ND2	3:O:27:PRO:HG3	2.28	0.44
3:M:176:MET:HE3	3:M:176:MET:HB3	1.91	0.44
3:R:32:LEU:HD12	3:R:44:ARG:HD2	2.00	0.44
1:d:82:THR:OG1	1:d:83:ASP:N	2.51	0.44
1:g:27:LEU:HD12	3:V:6:MET:HG3	1.98	0.44
1:j:36:LEU:HD22	1:j:73:ILE:HG13	2.00	0.44
1:k:45:THR:OG1	1:k:48:THR:OG1	2.31	0.44
2:s:208:LEU:HB3	2:s:211:TRP:HB2	2.00	0.44
2:s:314:ARG:HG2	2:s:318:GLY:HA2	2.00	0.44
2:s:446:GLN:HB3	2:s:463:PRO:HG3	2.00	0.44
2:s:477:GLN:CA	2:x:479:VAL:HG22	2.48	0.44
2:t:314:ARG:HG2	2:t:318:GLY:HA2	2.00	0.44
2:t:482:VAL:CG1	2:u:456:ARG:HH11	2.16	0.44
2:u:645:GLN:HE21	2:u:645:GLN:HB2	1.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:619:PRO:HD3	2:v:654:PRO:HB3	1.99	0.44
2:w:314:ARG:HG2	2:w:318:GLY:HA2	2.00	0.44
2:x:619:PRO:HD3	2:x:654:PRO:HB3	1.99	0.44
1:e:24:PHE:HE1	1:e:32:VAL:CG2	2.31	0.43
1:j:119:ASP:O	1:l:129:LEU:HD11	2.17	0.43
1:k:24:PHE:HE1	1:k:32:VAL:CG2	2.31	0.43
1:k:129:LEU:HD13	1:l:121:ILE:HD11	2.00	0.43
1:o:34:VAL:HG22	1:o:75:LEU:HB3	1.98	0.43
2:s:169:ILE:HA	2:s:232:SER:O	2.18	0.43
2:w:619:PRO:HD3	2:w:654:PRO:HB3	1.99	0.43
2:w:713:SER:HB2	2:w:776:LEU:HA	2.00	0.43
2:x:704:ARG:HH11	3:P:150:PHE:HA	1.83	0.43
3:P:24:ILE:HG21	3:P:146:PHE:HE2	1.82	0.43
3:Q:78:ILE:HB	3:Q:103:VAL:HG22	1.99	0.43
1:e:125:ASN:O	1:e:126:ASP:HB2	2.18	0.43
1:h:22:ILE:HD13	1:h:22:ILE:HG21	1.74	0.43
1:j:53:ALA:HB1	3:R:99:ARG:NH1	2.33	0.43
1:m:3:ASN:HA	1:m:4:VAL:HA	1.69	0.43
1:n:24:PHE:HE1	1:n:32:VAL:CG2	2.31	0.43
1:n:29:ARG:C	1:n:31:PHE:H	2.26	0.43
1:p:119:ASP:O	1:r:129:LEU:HD11	2.17	0.43
1:q:15:GLY:HA2	1:q:65:GLY:HA3	2.00	0.43
2:t:169:ILE:HA	2:t:232:SER:O	2.18	0.43
2:t:645:GLN:HE21	2:t:645:GLN:HB2	1.50	0.43
2:t:725:SER:HB3	2:t:727:TRP:CE2	2.52	0.43
2:u:169:ILE:HA	2:u:232:SER:O	2.18	0.43
2:w:581:ASN:O	2:w:581:ASN:ND2	2.51	0.43
2:x:208:LEU:HB3	2:x:211:TRP:HB2	2.00	0.43
3:T:32:LEU:HD12	3:T:44:ARG:HD2	2.00	0.43
3:U:130:MET:HG3	3:U:131:PRO:HD2	1.98	0.43
1:e:90:ASP:OD2	3:W:34:GLY:O	2.36	0.43
1:e:129:LEU:HD13	1:f:121:ILE:HD11	2.00	0.43
1:h:125:ASN:O	1:h:126:ASP:HB2	2.18	0.43
1:j:7:THR:OG1	1:j:115:ASP:OD1	2.34	0.43
1:k:15:GLY:HA2	1:k:65:GLY:HA3	2.00	0.43
2:s:482:VAL:CG1	2:t:456:ARG:HH11	2.19	0.43
2:t:594:MET:HB2	2:t:597:LYS:CD	2.47	0.43
2:u:581:ASN:ND2	2:u:581:ASN:O	2.51	0.43
2:v:581:ASN:O	2:v:581:ASN:ND2	2.52	0.43
2:w:48:LEU:HD22	2:w:574:ALA:CB	2.48	0.43
2:w:63:ALA:O	2:w:112:PRO:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:w:395:VAL:HB	2:w:403:LEU:HD11	2.01	0.43
2:w:705:ARG:CZ	3:N:26:GLU:HG2	2.48	0.43
2:x:270:VAL:HG12	2:x:271:GLY:N	2.33	0.43
2:x:565:LEU:HB2	2:x:572:PHE:HD1	1.82	0.43
3:M:129:GLU:CD	3:X:98:ASN:O	2.60	0.43
3:X:99:ARG:HB3	3:X:99:ARG:HH21	1.82	0.43
1:h:134:ARG:HE	1:h:134:ARG:HB2	1.57	0.43
1:n:129:LEU:HD13	1:o:121:ILE:HD11	2.00	0.43
1:p:13:LEU:HD13	1:p:13:LEU:HA	1.69	0.43
1:q:48:THR:HA	3:P:81:SER:HB3	1.99	0.43
1:q:86:VAL:CA	3:P:31:THR:HG22	2.36	0.43
2:s:400:ILE:HG23	2:t:122:ALA:HB2	2.00	0.43
2:s:625:ASN:OD1	2:s:625:ASN:N	2.51	0.43
2:u:314:ARG:HG2	2:u:318:GLY:HA2	2.00	0.43
2:w:257:LEU:HD12	2:w:257:LEU:HA	1.81	0.43
2:w:702:GLN:NE2	3:O:26:GLU:HG2	2.32	0.43
2:x:48:LEU:HD22	2:x:574:ALA:CB	2.48	0.43
2:x:63:ALA:O	2:x:112:PRO:HG2	2.18	0.43
3:U:176:MET:HE3	3:U:176:MET:HB3	1.91	0.43
1:b:24:PHE:HE1	1:b:32:VAL:CG2	2.31	0.43
1:b:48:THR:HA	3:N:81:SER:HB3	2.00	0.43
1:f:11:TYR:HD1	1:f:11:TYR:HA	1.63	0.43
1:l:92:SER:HA	2:t:640:ILE:HD12	2.01	0.43
1:q:125:ASN:O	1:q:126:ASP:HB2	2.18	0.43
2:t:208:LEU:HB3	2:t:211:TRP:HB2	2.00	0.43
2:t:248:THR:HG21	2:u:288:ARG:O	2.18	0.43
2:t:713:SER:HB2	2:t:776:LEU:HA	2.00	0.43
2:u:208:LEU:HB3	2:u:211:TRP:HB2	2.00	0.43
2:v:208:LEU:HB3	2:v:211:TRP:HB2	2.00	0.43
3:U:54:ILE:HD12	3:U:137:TRP:CZ3	2.53	0.43
3:W:54:ILE:HD12	3:W:137:TRP:CZ3	2.53	0.43
1:b:101:VAL:HG11	3:N:33:GLU:OE1	2.17	0.43
1:d:7:THR:OG1	1:d:115:ASP:OD1	2.34	0.43
1:d:36:LEU:HD22	1:d:73:ILE:HG13	2.00	0.43
1:k:11:TYR:O	1:k:72:THR:HA	2.19	0.43
1:o:90:ASP:O	2:s:715:THR:HG21	2.19	0.43
2:t:395:VAL:HB	2:t:403:LEU:HD11	2.01	0.43
2:t:579:THR:HG21	2:t:582:ALA:HB2	2.01	0.43
2:u:445:VAL:HG22	2:u:460:PHE:CD2	2.52	0.43
2:v:445:VAL:HG22	2:v:460:PHE:CD2	2.52	0.43
2:v:701:LEU:HD23	2:v:787:TYR:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:w:165:LEU:HD23	2:w:165:LEU:HA	1.68	0.43
2:w:579:THR:HG21	2:w:582:ALA:HB2	2.01	0.43
2:w:617:HIS:O	2:w:621:ILE:HG13	2.19	0.43
2:x:701:LEU:HD11	2:x:783:TRP:CZ3	2.54	0.43
2:x:713:SER:HB2	2:x:776:LEU:HA	2.00	0.43
3:M:24:ILE:HD13	3:M:24:ILE:HG21	1.85	0.43
3:N:144:ARG:O	3:N:148:ASN:N	2.51	0.43
3:S:54:ILE:HD12	3:S:137:TRP:CZ3	2.54	0.43
1:b:15:GLY:HA2	1:b:65:GLY:HA3	2.00	0.43
1:e:15:GLY:HA2	1:e:65:GLY:HA3	2.00	0.43
1:g:82:THR:OG1	1:g:83:ASP:N	2.51	0.43
2:s:395:VAL:HB	2:s:403:LEU:HD11	2.01	0.43
2:s:510:ASN:HD22	2:s:510:ASN:HA	1.50	0.43
2:t:63:ALA:O	2:t:112:PRO:HG2	2.18	0.43
2:u:63:ALA:O	2:u:112:PRO:HG2	2.18	0.43
2:u:270:VAL:HG12	2:u:271:GLY:N	2.33	0.43
2:v:314:ARG:HG2	2:v:318:GLY:HA2	2.00	0.43
2:v:698:ILE:HD11	2:w:7:SER:CB	2.48	0.43
2:w:701:LEU:HD23	2:w:787:TYR:HB2	2.00	0.43
3:M:54:ILE:HD12	3:M:137:TRP:CZ3	2.53	0.43
3:O:54:ILE:HD12	3:O:137:TRP:CZ3	2.54	0.43
3:Q:54:ILE:HD12	3:Q:137:TRP:CZ3	2.53	0.43
1:e:22:ILE:HD13	1:e:22:ILE:HG21	1.74	0.43
1:h:129:LEU:HD13	1:i:121:ILE:HD11	2.00	0.43
1:l:47:ASN:OD1	2:t:610:ASP:HB2	2.19	0.43
1:m:119:ASP:O	1:o:129:LEU:HD11	2.17	0.43
2:s:48:LEU:HD22	2:s:574:ALA:CB	2.48	0.43
2:s:701:LEU:HD11	2:s:783:TRP:CZ3	2.54	0.43
2:t:510:ASN:HD22	2:t:510:ASN:HA	1.50	0.43
2:t:698:ILE:H	2:t:698:ILE:HG12	1.62	0.43
2:t:701:LEU:HD11	2:t:783:TRP:CZ3	2.54	0.43
2:u:48:LEU:HD22	2:u:574:ALA:CB	2.48	0.43
2:u:400:ILE:CD1	2:v:120:THR:HG22	2.35	0.43
2:v:395:VAL:HB	2:v:403:LEU:HD11	2.01	0.43
2:w:704:ARG:HH11	3:N:150:PHE:HA	1.83	0.43
2:x:617:HIS:O	2:x:621:ILE:HG13	2.19	0.43
2:x:702:GLN:NE2	3:Q:26:GLU:HG2	2.33	0.43
3:M:178:TYR:HD1	3:X:88:MET:CG	2.21	0.43
3:Q:175:GLU:O	3:Q:179:GLY:N	2.31	0.43
3:V:176:MET:HE3	3:V:176:MET:HB3	1.82	0.43
1:c:93:ILE:HG23	2:w:745:ARG:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:101:VAL:HG11	3:V:33:GLU:OE1	2.18	0.43
1:r:44:LEU:HD12	1:r:44:LEU:HA	1.78	0.43
2:s:497:PRO:HG3	2:s:519:ASP:H	1.84	0.43
2:u:276:SER:HB3	2:v:384:ASN:CB	2.49	0.43
2:u:356:ASN:HD22	2:u:356:ASN:HA	1.67	0.43
2:w:400:ILE:HG23	2:x:122:ALA:HB2	2.01	0.43
2:w:704:ARG:NH1	3:N:150:PHE:O	2.48	0.43
2:x:356:ASN:HD22	2:x:356:ASN:HA	1.67	0.43
3:M:170:LEU:HD13	3:M:170:LEU:HA	1.71	0.43
3:O:78:ILE:HB	3:O:103:VAL:HG22	1.99	0.43
3:P:144:ARG:O	3:P:148:ASN:N	2.51	0.43
3:S:55:GLN:O	3:S:62:ASN:ND2	2.52	0.43
1:a:36:LEU:HD22	1:a:73:ILE:HG13	2.00	0.43
1:b:125:ASN:O	1:b:126:ASP:HB2	2.18	0.43
1:g:36:LEU:HD22	1:g:73:ILE:HG13	2.00	0.43
1:h:11:TYR:O	1:h:72:THR:HA	2.18	0.43
1:h:94:LEU:HD13	2:u:736:LEU:HD23	1.96	0.43
1:l:47:ASN:CG	2:t:610:ASP:HB2	2.44	0.43
2:s:10:ASN:HD22	2:s:10:ASN:HA	1.48	0.43
2:s:579:THR:HG21	2:s:582:ALA:HB2	2.01	0.43
2:s:701:LEU:HD23	2:s:787:TYR:HB2	2.00	0.43
2:s:713:SER:HB2	2:s:776:LEU:HA	2.00	0.43
2:t:106:TYR:HE1	2:t:132:VAL:HG11	1.84	0.43
2:t:400:ILE:HG23	2:u:122:ALA:HB2	2.01	0.43
2:t:581:ASN:O	2:t:581:ASN:ND2	2.52	0.43
2:t:625:ASN:OD1	2:t:625:ASN:N	2.51	0.43
2:t:702:GLN:NE2	3:U:26:GLU:CG	2.82	0.43
2:u:552:LEU:HD23	2:u:552:LEU:HA	1.84	0.43
2:w:497:PRO:HG3	2:w:519:ASP:H	1.84	0.43
2:w:704:ARG:HD2	3:N:150:PHE:HA	2.01	0.43
2:x:128:VAL:HG21	2:x:351:VAL:HG23	2.01	0.43
2:x:266:MET:HE2	2:x:266:MET:HB3	1.83	0.43
2:x:395:VAL:HB	2:x:403:LEU:HD11	2.01	0.43
2:x:701:LEU:HD23	2:x:787:TYR:HB2	2.00	0.43
3:Q:55:GLN:O	3:Q:62:ASN:ND2	2.52	0.43
1:e:11:TYR:O	1:e:72:THR:HA	2.19	0.42
1:h:29:ARG:C	1:h:31:PHE:H	2.26	0.42
1:n:11:TYR:O	1:n:72:THR:HA	2.19	0.42
1:p:3:ASN:HA	1:p:4:VAL:HA	1.69	0.42
2:s:63:ALA:O	2:s:112:PRO:HG2	2.18	0.42
2:s:143:LEU:HD13	2:s:143:LEU:HA	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:266:MET:HE2	2:s:266:MET:HB3	1.83	0.42
2:t:270:VAL:HG12	2:t:271:GLY:N	2.33	0.42
2:u:701:LEU:HD11	2:u:783:TRP:CZ3	2.54	0.42
2:v:250:TYR:CD2	2:w:288:ARG:HG2	2.54	0.42
2:v:701:LEU:HD11	2:v:783:TRP:CZ3	2.54	0.42
2:w:478:ASP:CB	2:x:477:GLN:HG2	2.42	0.42
2:w:701:LEU:HD11	2:w:783:TRP:CZ3	2.54	0.42
2:x:581:ASN:ND2	2:x:581:ASN:O	2.52	0.42
3:M:132:GLU:CG	3:X:56:SER:OG	2.64	0.42
3:O:67:ILE:HD11	3:O:121:ILE:HG13	2.01	0.42
3:Q:172:MET:HB2	3:Q:172:MET:HE3	1.56	0.42
3:R:176:MET:HE3	3:R:176:MET:HB3	1.82	0.42
3:R:182:ASN:HD22	3:R:183:MET:N	2.17	0.42
1:a:29:ARG:NH2	3:N:5:ASP:HB3	2.34	0.42
1:k:29:ARG:C	1:k:31:PHE:H	2.26	0.42
1:n:60:LEU:HD11	1:n:73:ILE:CD1	2.48	0.42
2:s:7:SER:CB	2:x:698:ILE:HD11	2.49	0.42
2:u:395:VAL:HB	2:u:403:LEU:HD11	2.01	0.42
2:u:497:PRO:HG3	2:u:519:ASP:H	1.84	0.42
2:u:705:ARG:CZ	3:V:26:GLU:HG2	2.48	0.42
2:v:63:ALA:O	2:v:112:PRO:HG2	2.18	0.42
2:v:356:ASN:HD22	2:v:356:ASN:HA	1.67	0.42
2:v:617:HIS:O	2:v:621:ILE:HG13	2.19	0.42
3:N:176:MET:HE3	3:N:176:MET:HB3	1.82	0.42
3:N:182:ASN:HD22	3:N:183:MET:N	2.17	0.42
3:O:170:LEU:HD13	3:O:170:LEU:HA	1.71	0.42
3:O:176:MET:HE3	3:O:176:MET:HB3	1.91	0.42
1:e:30:LYS:HG2	1:e:31:PHE:CD1	2.54	0.42
1:m:36:LEU:HD22	1:m:73:ILE:HG13	2.00	0.42
1:n:125:ASN:O	1:n:126:ASP:HB2	2.18	0.42
2:s:120:THR:HG22	2:x:400:ILE:CD1	2.35	0.42
2:s:581:ASN:O	2:s:581:ASN:ND2	2.52	0.42
2:s:645:GLN:HE21	2:s:645:GLN:HB2	1.50	0.42
2:t:479:VAL:HG22	2:u:477:GLN:C	2.44	0.42
2:v:248:THR:HG21	2:w:288:ARG:O	2.18	0.42
2:v:400:ILE:HG23	2:w:122:ALA:HB2	2.02	0.42
2:x:358:LEU:HB2	2:x:374:TYR:HB3	2.02	0.42
2:x:510:ASN:HD22	2:x:510:ASN:HA	1.50	0.42
2:x:758:VAL:HG12	3:Q:25:GLY:O	2.19	0.42
3:U:128:ASP:O	3:U:135:ARG:NH2	2.43	0.42
3:X:134:PHE:HE1	3:X:171:CYS:HB3	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:30:LYS:HG2	1:b:31:PHE:CD1	2.54	0.42
1:c:42:LYS:HE3	1:c:42:LYS:HB3	1.86	0.42
1:h:30:LYS:HG2	1:h:31:PHE:CD1	2.54	0.42
1:l:13:LEU:HD23	1:l:13:LEU:HA	1.72	0.42
1:o:44:LEU:HD12	1:o:44:LEU:HA	1.78	0.42
1:q:11:TYR:O	1:q:72:THR:HA	2.19	0.42
1:r:47:ASN:CG	2:x:610:ASP:HB2	2.44	0.42
1:r:92:SER:HA	2:x:640:ILE:HD12	2.00	0.42
2:t:51:LEU:HD21	2:t:575:ARG:NH1	2.34	0.42
2:v:579:THR:HG21	2:v:582:ALA:HB2	2.01	0.42
2:w:128:VAL:HG21	2:w:351:VAL:HG23	2.02	0.42
2:x:579:THR:HG21	2:x:582:ALA:HB2	2.01	0.42
3:O:55:GLN:O	3:O:62:ASN:ND2	2.52	0.42
3:O:172:MET:HB2	3:O:172:MET:HE3	1.56	0.42
1:j:27:LEU:HD12	3:T:6:MET:HG3	2.00	0.42
1:m:13:LEU:HD13	1:m:13:LEU:HA	1.69	0.42
1:o:47:ASN:CG	2:s:610:ASP:HB2	2.45	0.42
1:q:24:PHE:HE1	1:q:32:VAL:CG2	2.31	0.42
1:q:60:LEU:HD11	1:q:73:ILE:CD1	2.48	0.42
2:s:715:THR:HB	2:s:772:GLU:HG2	2.01	0.42
2:u:308:MET:HE2	2:u:308:MET:HB3	1.97	0.42
2:u:715:THR:HB	2:u:772:GLU:HG2	2.01	0.42
2:v:497:PRO:HG3	2:v:519:ASP:H	1.84	0.42
2:w:248:THR:HG21	2:x:288:ARG:O	2.20	0.42
3:M:55:GLN:O	3:M:62:ASN:ND2	2.52	0.42
3:M:181:TYR:HE1	3:X:93:GLN:HE22	1.68	0.42
3:P:61:PHE:HE1	3:P:134:PHE:CE2	2.38	0.42
3:T:182:ASN:HD22	3:T:183:MET:N	2.17	0.42
3:U:55:GLN:O	3:U:62:ASN:ND2	2.52	0.42
1:b:11:TYR:O	1:b:72:THR:HA	2.19	0.42
1:c:47:ASN:CG	2:w:610:ASP:HB2	2.43	0.42
1:f:47:ASN:CG	2:v:610:ASP:HB2	2.45	0.42
1:h:15:GLY:HA2	1:h:65:GLY:HA3	2.00	0.42
1:q:22:ILE:HG21	1:q:22:ILE:HD13	1.74	0.42
1:q:90:ASP:OD2	3:O:34:GLY:O	2.37	0.42
2:t:470:ILE:HG12	2:t:514:VAL:HG21	2.02	0.42
2:t:617:HIS:O	2:t:621:ILE:HG13	2.19	0.42
2:u:470:ILE:HG12	2:u:514:VAL:HG21	2.02	0.42
2:u:617:HIS:O	2:u:621:ILE:HG13	2.19	0.42
2:v:51:LEU:HD21	2:v:575:ARG:NH1	2.35	0.42
2:v:363:GLY:HA2	2:v:402:ILE:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:w:51:LEU:HD21	2:w:575:ARG:NH1	2.34	0.42
2:w:358:LEU:HB2	2:w:374:TYR:HB3	2.02	0.42
2:x:240:ALA:C	2:x:242:GLN:N	2.78	0.42
3:N:172:MET:HB2	3:N:172:MET:HE2	1.65	0.42
3:O:67:ILE:HD11	3:O:121:ILE:CG1	2.50	0.42
3:P:98:ASN:O	3:Q:129:GLU:CD	2.63	0.42
3:S:128:ASP:O	3:S:135:ARG:NH2	2.43	0.42
3:V:56:SER:OG	3:W:132:GLU:CG	2.66	0.42
3:X:144:ARG:O	3:X:148:ASN:N	2.51	0.42
1:g:50:TYR:HE2	1:g:52:PHE:HE1	1.68	0.42
1:i:44:LEU:HA	1:i:44:LEU:HD12	1.78	0.42
1:i:91:GLY:N	2:u:715:THR:HG22	2.31	0.42
1:k:30:LYS:HG2	1:k:31:PHE:CD1	2.54	0.42
1:m:116:LEU:HD13	1:m:116:LEU:HA	1.66	0.42
2:u:698:ILE:HD11	2:v:7:SER:CB	2.49	0.42
2:v:625:ASN:OD1	2:v:625:ASN:N	2.51	0.42
2:w:208:LEU:HB3	2:w:211:TRP:HB2	2.00	0.42
2:w:470:ILE:HG12	2:w:514:VAL:HG21	2.02	0.42
2:w:565:LEU:HB2	2:w:572:PHE:CD1	2.55	0.42
2:w:715:THR:HB	2:w:772:GLU:HG2	2.01	0.42
2:x:51:LEU:HD21	2:x:575:ARG:NH1	2.34	0.42
1:b:116:LEU:O	1:b:120:THR:HG23	2.20	0.42
1:d:3:ASN:HA	1:d:4:VAL:HA	1.69	0.42
2:s:128:VAL:HG21	2:s:351:VAL:HG23	2.01	0.42
2:s:358:LEU:HB2	2:s:374:TYR:HB3	2.01	0.42
2:s:382:ILE:HD13	2:s:382:ILE:HA	1.60	0.42
2:t:756:PRO:HG3	3:T:39:ASP:CG	2.44	0.42
2:v:128:VAL:HG21	2:v:351:VAL:HG23	2.01	0.42
2:w:703:LEU:O	2:w:758:VAL:HA	2.20	0.42
3:O:51:ASN:O	3:O:55:GLN:HG3	2.20	0.42
3:Q:51:ASN:O	3:Q:55:GLN:HG3	2.19	0.42
3:W:55:GLN:O	3:W:62:ASN:ND2	2.52	0.42
3:X:61:PHE:HE1	3:X:134:PHE:CE2	2.38	0.42
3:X:182:ASN:HD22	3:X:183:MET:N	2.17	0.42
1:n:94:LEU:CD1	2:s:736:LEU:CD2	2.84	0.42
1:q:30:LYS:HG2	1:q:31:PHE:CD1	2.54	0.42
2:s:60:LEU:O	2:s:64:PRO:HG3	2.20	0.42
2:t:15:ILE:HG23	2:t:29:SER:O	2.20	0.42
2:t:479:VAL:HG22	2:u:477:GLN:CA	2.49	0.42
2:t:565:LEU:HB2	2:t:572:PHE:CD1	2.55	0.42
2:t:715:THR:HB	2:t:772:GLU:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:u:15:ILE:HG23	2:u:29:SER:O	2.20	0.42
2:x:497:PRO:HG3	2:x:519:ASP:H	1.84	0.42
3:S:51:ASN:O	3:S:55:GLN:HG3	2.20	0.42
3:S:147:ASN:O	3:S:147:ASN:ND2	2.53	0.42
1:d:50:TYR:HE2	1:d:52:PHE:HE1	1.68	0.42
1:k:125:ASN:O	1:k:126:ASP:HB2	2.18	0.42
1:o:42:LYS:HE3	1:o:42:LYS:HB3	1.86	0.42
1:r:47:ASN:OD1	2:x:610:ASP:HB2	2.20	0.42
2:s:617:HIS:O	2:s:621:ILE:HG13	2.19	0.42
2:t:363:GLY:HA2	2:t:402:ILE:HG23	2.02	0.42
2:u:358:LEU:HB2	2:u:374:TYR:HB3	2.02	0.42
2:v:470:ILE:HG12	2:v:514:VAL:HG21	2.02	0.42
2:v:756:PRO:HG3	3:X:39:ASP:CG	2.45	0.42
2:w:15:ILE:HG23	2:w:29:SER:O	2.20	0.42
2:w:363:GLY:HA2	2:w:402:ILE:HG23	2.02	0.42
2:x:684:ILE:H	2:x:684:ILE:HD12	1.85	0.42
3:O:149:ARG:HG2	3:P:23:SER:HA	2.02	0.42
3:P:176:MET:HE3	3:P:176:MET:HB3	1.82	0.42
3:Q:147:ASN:O	3:Q:147:ASN:ND2	2.53	0.42
3:R:93:GLN:HE22	3:S:181:TYR:HE1	1.68	0.42
3:R:144:ARG:O	3:R:148:ASN:N	2.51	0.42
3:U:170:LEU:HA	3:U:170:LEU:HD13	1.70	0.42
3:V:182:ASN:HD22	3:V:183:MET:N	2.17	0.42
1:a:107:MET:HE2	1:a:107:MET:HB2	1.98	0.41
1:d:27:LEU:HD12	1:d:27:LEU:HA	1.87	0.41
1:i:71:THR:HB	1:i:72:THR:H	1.54	0.41
1:j:50:TYR:HE2	1:j:52:PHE:HE1	1.68	0.41
1:n:49:ASP:O	1:n:61:THR:OG1	2.35	0.41
2:s:240:ALA:C	2:s:242:GLN:N	2.78	0.41
2:s:248:THR:HG21	2:t:288:ARG:O	2.20	0.41
2:s:614:THR:HG22	2:s:660:GLY:O	2.20	0.41
2:s:703:LEU:O	2:s:758:VAL:HA	2.20	0.41
2:t:240:ALA:C	2:t:242:GLN:H	2.28	0.41
2:t:700:ARG:HH12	3:U:24:ILE:HD13	1.85	0.41
2:u:60:LEU:O	2:u:64:PRO:HG3	2.20	0.41
2:u:240:ALA:C	2:u:242:GLN:N	2.78	0.41
2:u:579:THR:HG21	2:u:582:ALA:HB2	2.01	0.41
2:v:32:VAL:HG13	2:v:542:HIS:CE1	2.55	0.41
2:v:273:ALA:HB3	2:w:254:PHE:CE1	2.54	0.41
2:v:565:LEU:HB2	2:v:572:PHE:CD1	2.55	0.41
2:v:703:LEU:O	2:v:758:VAL:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:715:THR:HB	2:v:772:GLU:HG2	2.01	0.41
2:w:382:ILE:HD13	2:w:382:ILE:HA	1.60	0.41
2:w:594:MET:HB2	2:w:597:LYS:CD	2.46	0.41
2:w:746:LEU:HD23	2:w:746:LEU:HA	1.66	0.41
3:M:51:ASN:O	3:M:55:GLN:HG3	2.20	0.41
3:P:182:ASN:HD22	3:P:183:MET:N	2.17	0.41
3:W:147:ASN:ND2	3:W:147:ASN:O	2.53	0.41
1:b:29:ARG:C	1:b:31:PHE:H	2.26	0.41
1:i:46:ILE:O	1:i:47:ASN:C	2.62	0.41
1:k:116:LEU:O	1:k:120:THR:HG23	2.20	0.41
2:s:466:SER:HG	2:t:579:THR:HG23	1.83	0.41
2:s:565:LEU:HB2	2:s:572:PHE:CD1	2.55	0.41
2:v:165:LEU:HA	2:v:165:LEU:HD23	1.68	0.41
2:w:240:ALA:C	2:w:242:GLN:N	2.78	0.41
2:w:789:ARG:NE	2:w:791:SER:O	2.53	0.41
2:x:470:ILE:HG12	2:x:514:VAL:HG21	2.02	0.41
2:x:565:LEU:HB2	2:x:572:PHE:CD1	2.55	0.41
2:x:705:ARG:CZ	3:P:26:GLU:HG2	2.50	0.41
2:x:789:ARG:NE	2:x:791:SER:O	2.53	0.41
3:O:147:ASN:ND2	3:O:147:ASN:O	2.53	0.41
3:P:93:GLN:HE22	3:Q:181:TYR:HE1	1.68	0.41
3:V:98:ASN:O	3:W:129:GLU:CD	2.63	0.41
3:W:51:ASN:O	3:W:55:GLN:HG3	2.20	0.41
1:b:18:ARG:HE	1:b:63:ALA:HB2	1.86	0.41
1:j:112:GLU:HA	1:j:115:ASP:OD1	2.21	0.41
1:m:50:TYR:HE2	1:m:52:PHE:HE1	1.68	0.41
1:o:11:TYR:HD1	1:o:11:TYR:HA	1.64	0.41
2:t:56:ASP:HA	2:t:570:ASN:HA	2.03	0.41
2:t:240:ALA:C	2:t:242:GLN:N	2.78	0.41
2:t:497:PRO:HG3	2:t:519:ASP:H	1.84	0.41
2:u:128:VAL:HG21	2:u:351:VAL:HG23	2.01	0.41
2:u:240:ALA:C	2:u:242:GLN:H	2.28	0.41
2:u:276:SER:HB3	2:v:384:ASN:HB3	2.01	0.41
2:u:565:LEU:HB2	2:u:572:PHE:CD1	2.55	0.41
2:v:56:ASP:HA	2:v:570:ASN:HA	2.03	0.41
2:v:60:LEU:O	2:v:64:PRO:HG3	2.20	0.41
2:v:143:LEU:HD13	2:v:143:LEU:HA	1.88	0.41
2:v:552:LEU:HD23	2:v:552:LEU:HA	1.84	0.41
2:x:15:ILE:HG23	2:x:29:SER:O	2.20	0.41
2:x:60:LEU:O	2:x:64:PRO:HG3	2.20	0.41
2:x:715:THR:HB	2:x:772:GLU:HG2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:149:ARG:HG2	3:N:23:SER:HA	2.02	0.41
3:U:51:ASN:O	3:U:55:GLN:HG3	2.20	0.41
1:a:13:LEU:HD13	1:a:20:PHE:HZ	1.86	0.41
1:e:29:ARG:C	1:e:31:PHE:H	2.26	0.41
1:e:86:VAL:HG13	3:X:31:THR:CG2	2.49	0.41
1:h:116:LEU:O	1:h:120:THR:HG23	2.20	0.41
1:i:93:ILE:HG23	2:u:745:ARG:O	2.20	0.41
1:m:13:LEU:HD13	1:m:20:PHE:HZ	1.86	0.41
2:s:56:ASP:HA	2:s:570:ASN:HA	2.02	0.41
2:s:435:VAL:H	2:s:435:VAL:HG12	1.66	0.41
2:s:746:LEU:HD23	2:s:746:LEU:HA	1.66	0.41
2:t:703:LEU:O	2:t:758:VAL:HA	2.20	0.41
2:u:51:LEU:HD21	2:u:575:ARG:NH1	2.35	0.41
2:w:32:VAL:HG13	2:w:542:HIS:CE1	2.55	0.41
2:w:56:ASP:HA	2:w:570:ASN:HA	2.02	0.41
2:x:56:ASP:HA	2:x:570:ASN:HA	2.02	0.41
3:T:61:PHE:HE1	3:T:134:PHE:CE2	2.38	0.41
1:c:92:SER:HA	2:w:640:ILE:HD12	2.02	0.41
1:d:129:LEU:HG	1:e:134:ARG:HB3	2.03	0.41
1:e:18:ARG:HE	1:e:63:ALA:HB2	1.86	0.41
1:i:22:ILE:HA	1:i:23:PRO:HD3	1.81	0.41
1:k:18:ARG:HE	1:k:63:ALA:HB2	1.86	0.41
1:n:18:ARG:HE	1:n:63:ALA:HB2	1.85	0.41
1:n:30:LYS:HG2	1:n:31:PHE:CD1	2.54	0.41
2:s:288:ARG:O	2:x:248:THR:HG21	2.20	0.41
2:s:363:GLY:HA2	2:s:402:ILE:HG23	2.02	0.41
2:s:470:ILE:HG12	2:s:514:VAL:HG21	2.02	0.41
2:t:60:LEU:O	2:t:64:PRO:HG3	2.20	0.41
2:t:170:ASN:ND2	2:t:231:ASP:H	2.19	0.41
2:u:56:ASP:HA	2:u:570:ASN:HA	2.03	0.41
2:u:106:TYR:HE1	2:u:132:VAL:HG11	1.84	0.41
2:u:244:ILE:HD13	2:u:244:ILE:HG21	1.81	0.41
2:u:351:VAL:HG22	2:u:360:PHE:CE1	2.56	0.41
2:v:15:ILE:HG23	2:v:29:SER:O	2.20	0.41
2:v:154:ILE:HG12	2:v:233:PHE:CZ	2.56	0.41
2:v:351:VAL:HG22	2:v:360:PHE:CE1	2.56	0.41
2:v:479:VAL:HG22	2:w:477:GLN:C	2.45	0.41
2:w:684:ILE:H	2:w:684:ILE:HD12	1.86	0.41
2:x:351:VAL:HG22	2:x:360:PHE:CE1	2.55	0.41
3:N:69:LEU:HD11	3:N:121:ILE:HD11	2.03	0.41
3:Q:20:ILE:HD11	3:Q:47:LEU:HD13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:98:ASN:O	3:S:129:GLU:CD	2.64	0.41
3:U:175:GLU:O	3:U:179:GLY:N	2.31	0.41
3:W:97:VAL:CG2	3:X:125:ARG:HH12	2.34	0.41
1:a:129:LEU:HG	1:b:134:ARG:HB3	2.03	0.41
1:j:13:LEU:HD13	1:j:20:PHE:HZ	1.86	0.41
1:m:13:LEU:CD1	1:m:20:PHE:HZ	2.34	0.41
1:n:94:LEU:HD13	2:s:736:LEU:HD23	1.94	0.41
1:p:29:ARG:NH2	3:P:5:ASP:HB3	2.35	0.41
1:q:90:ASP:OD2	3:O:34:GLY:C	2.63	0.41
1:q:93:ILE:H	1:q:93:ILE:HG12	1.55	0.41
1:q:94:LEU:HD12	1:q:94:LEU:HA	1.87	0.41
2:s:586:GLN:HE21	2:s:586:GLN:HB3	1.63	0.41
2:s:684:ILE:H	2:s:684:ILE:HD12	1.86	0.41
2:t:32:VAL:HG13	2:t:542:HIS:CE1	2.55	0.41
2:t:351:VAL:HG22	2:t:360:PHE:CE1	2.56	0.41
2:t:358:LEU:HB2	2:t:374:TYR:HB3	2.02	0.41
2:t:684:ILE:HD12	2:t:684:ILE:H	1.86	0.41
2:u:363:GLY:HA2	2:u:402:ILE:HG23	2.02	0.41
2:v:789:ARG:NE	2:v:791:SER:O	2.53	0.41
2:w:60:LEU:O	2:w:64:PRO:HG3	2.20	0.41
2:w:479:VAL:HG22	2:x:477:GLN:CA	2.50	0.41
2:w:614:THR:HG22	2:w:660:GLY:O	2.20	0.41
2:x:154:ILE:HG12	2:x:233:PHE:CZ	2.56	0.41
2:x:698:ILE:H	2:x:698:ILE:HG12	1.63	0.41
2:x:703:LEU:O	2:x:758:VAL:HA	2.20	0.41
3:P:69:LEU:HD11	3:P:121:ILE:HD11	2.03	0.41
3:T:88:MET:CG	3:U:178:TYR:HD1	2.25	0.41
3:T:144:ARG:O	3:T:148:ASN:N	2.51	0.41
3:V:144:ARG:O	3:V:148:ASN:N	2.51	0.41
1:a:50:TYR:HE2	1:a:52:PHE:HE1	1.68	0.41
1:e:116:LEU:O	1:e:120:THR:HG23	2.20	0.41
1:f:47:ASN:OD1	2:v:610:ASP:HB2	2.21	0.41
1:f:90:ASP:O	2:v:715:THR:HG21	2.19	0.41
1:i:90:ASP:O	2:u:715:THR:HG21	2.20	0.41
1:j:29:ARG:NH2	3:T:5:ASP:HB3	2.35	0.41
1:m:112:GLU:HA	1:m:115:ASP:OD1	2.21	0.41
1:n:116:LEU:O	1:n:120:THR:HG23	2.20	0.41
2:s:15:ILE:HG23	2:s:29:SER:O	2.20	0.41
2:s:51:LEU:HD21	2:s:575:ARG:NH1	2.35	0.41
2:t:356:ASN:HD22	2:t:356:ASN:HA	1.67	0.41
2:u:154:ILE:HG12	2:u:233:PHE:CZ	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:u:594:MET:HB2	2:u:597:LYS:CD	2.46	0.41
2:v:704:ARG:HA	2:v:704:ARG:HD3	1.79	0.41
2:w:273:ALA:HB3	2:x:254:PHE:CE1	2.55	0.41
2:x:32:VAL:HG13	2:x:542:HIS:CE1	2.55	0.41
3:N:61:PHE:HE1	3:N:134:PHE:CE2	2.38	0.41
3:O:20:ILE:HD11	3:O:47:LEU:HD13	2.03	0.41
3:T:56:SER:OG	3:U:132:GLU:CG	2.67	0.41
3:U:147:ASN:O	3:U:147:ASN:ND2	2.53	0.41
3:X:69:LEU:HD11	3:X:121:ILE:HD11	2.03	0.41
1:a:13:LEU:CD1	1:a:20:PHE:HZ	2.34	0.41
1:e:48:THR:HA	3:X:81:SER:HB3	2.02	0.41
1:g:129:LEU:HG	1:h:134:ARG:HB3	2.03	0.41
1:h:18:ARG:HE	1:h:63:ALA:HB2	1.85	0.41
1:l:42:LYS:HE3	1:l:42:LYS:HB3	1.86	0.41
1:n:94:LEU:HD12	1:n:94:LEU:HA	1.87	0.41
1:q:18:ARG:HE	1:q:63:ALA:HB2	1.85	0.41
2:s:170:ASN:ND2	2:s:231:ASP:H	2.19	0.41
2:t:128:VAL:HG21	2:t:351:VAL:HG23	2.01	0.41
2:u:32:VAL:HG13	2:u:542:HIS:CE1	2.55	0.41
2:u:170:ASN:ND2	2:u:231:ASP:H	2.19	0.41
2:u:703:LEU:O	2:u:758:VAL:HA	2.20	0.41
2:u:788:LEU:HG	3:W:153:ALA:CA	2.48	0.41
2:w:351:VAL:HG22	2:w:360:PHE:CE1	2.56	0.41
2:w:698:ILE:HG23	2:x:707:TRP:CH2	2.55	0.41
2:x:165:LEU:HD23	2:x:165:LEU:HA	1.68	0.41
2:x:614:THR:HG22	2:x:660:GLY:O	2.20	0.41
2:x:756:PRO:HG3	3:P:39:ASP:CG	2.45	0.41
3:M:97:VAL:CG2	3:N:125:ARG:HH12	2.34	0.41
3:M:147:ASN:O	3:M:147:ASN:ND2	2.53	0.41
3:O:97:VAL:CG2	3:P:125:ARG:HH12	2.34	0.41
3:Q:149:ARG:HG2	3:R:23:SER:HA	2.02	0.41
3:W:149:ARG:HG2	3:X:23:SER:HA	2.03	0.41
1:a:53:ALA:HB1	3:X:99:ARG:NH1	2.36	0.41
1:f:46:ILE:O	1:f:47:ASN:C	2.62	0.41
1:g:13:LEU:CD1	1:g:20:PHE:HZ	2.34	0.41
1:g:112:GLU:HA	1:g:115:ASP:OD1	2.21	0.41
1:g:131:ALA:O	1:g:132:ARG:C	2.64	0.41
1:k:60:LEU:HD11	1:k:73:ILE:CD1	2.48	0.41
1:k:94:LEU:HD13	2:t:736:LEU:HD23	1.97	0.41
1:n:10:THR:HB	1:n:74:GLU:OE1	2.21	0.41
1:p:129:LEU:HG	1:q:134:ARG:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:r:93:ILE:HG23	2:x:745:ARG:O	2.21	0.41
2:s:154:ILE:HG12	2:s:233:PHE:CZ	2.56	0.41
2:s:250:TYR:CD2	2:t:288:ARG:HG2	2.54	0.41
2:s:351:VAL:HG22	2:s:360:PHE:CE1	2.56	0.41
2:s:477:GLN:C	2:x:479:VAL:HG22	2.44	0.41
2:s:556:SER:HA	2:s:561:MET:HA	2.03	0.41
2:t:154:ILE:HG12	2:t:233:PHE:CZ	2.56	0.41
2:t:382:ILE:HD13	2:t:382:ILE:HA	1.60	0.41
2:t:385:LEU:HD21	2:t:433:LYS:HE3	2.03	0.41
2:u:385:LEU:HD21	2:u:433:LYS:HE3	2.03	0.41
2:u:400:ILE:HG23	2:v:122:ALA:HB2	2.03	0.41
2:u:470:ILE:HG22	2:u:488:ILE:HD11	2.03	0.41
2:u:479:VAL:HG22	2:v:477:GLN:C	2.45	0.41
2:u:614:THR:HG22	2:u:660:GLY:O	2.21	0.41
2:u:684:ILE:H	2:u:684:ILE:HD12	1.86	0.41
2:u:704:ARG:HA	2:u:704:ARG:HD3	1.79	0.41
2:v:170:ASN:ND2	2:v:231:ASP:H	2.19	0.41
2:v:470:ILE:HG22	2:v:488:ILE:HD11	2.03	0.41
2:v:496:ILE:H	2:v:496:ILE:HG12	1.76	0.41
2:v:556:SER:HA	2:v:561:MET:HA	2.03	0.41
2:v:614:THR:HG22	2:v:660:GLY:O	2.21	0.41
2:v:684:ILE:H	2:v:684:ILE:HD12	1.86	0.41
2:v:722:ASN:ND2	3:M:27:PRO:CG	2.80	0.41
2:w:10:ASN:HD22	2:w:10:ASN:HA	1.48	0.41
2:w:154:ILE:HG12	2:w:233:PHE:CZ	2.56	0.41
2:w:240:ALA:C	2:w:242:GLN:H	2.28	0.41
2:w:496:ILE:H	2:w:496:ILE:HG12	1.76	0.41
2:x:204:MET:HE3	2:x:204:MET:HB2	1.88	0.41
2:x:240:ALA:C	2:x:242:GLN:H	2.28	0.41
2:x:363:GLY:HA2	2:x:402:ILE:HG23	2.02	0.41
3:M:20:ILE:HD11	3:M:47:LEU:HD13	2.03	0.41
3:Q:121:ILE:HD13	3:Q:121:ILE:HG21	1.78	0.41
3:V:69:LEU:HD11	3:V:121:ILE:HD11	2.03	0.41
3:W:20:ILE:HD11	3:W:47:LEU:HD13	2.03	0.41
1:d:53:ALA:HB1	3:V:99:ARG:NH1	2.36	0.41
1:h:10:THR:HB	1:h:74:GLU:OE1	2.21	0.41
1:i:44:LEU:HG	1:i:49:ASP:HB3	2.04	0.41
1:k:22:ILE:HD13	1:k:22:ILE:HG21	1.74	0.41
1:l:93:ILE:HG23	2:t:745:ARG:O	2.20	0.41
1:q:13:LEU:HD22	1:q:73:ILE:HG13	2.03	0.41
2:s:698:ILE:HG23	2:t:707:TRP:CH2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:789:ARG:NE	2:s:791:SER:O	2.54	0.41
2:t:704:ARG:HA	2:t:704:ARG:HD3	1.79	0.41
3:O:64:GLU:OE1	3:O:67:ILE:HD13	2.21	0.41
3:R:144:ARG:HB2	3:R:160:LEU:HD12	2.03	0.41
3:S:176:MET:HE3	3:S:176:MET:HB3	1.91	0.41
3:W:176:MET:HE3	3:W:176:MET:HB3	1.91	0.41
1:a:18:ARG:O	1:a:59:SER:HA	2.21	0.40
1:b:10:THR:HB	1:b:74:GLU:OE1	2.21	0.40
1:d:112:GLU:HA	1:d:115:ASP:OD1	2.21	0.40
1:g:18:ARG:O	1:g:59:SER:HA	2.21	0.40
1:m:129:LEU:HG	1:n:134:ARG:HB3	2.03	0.40
1:m:131:ALA:O	1:m:132:ARG:C	2.64	0.40
1:o:22:ILE:HD11	1:o:26:TYR:CE2	2.57	0.40
1:q:116:LEU:O	1:q:120:THR:HG23	2.20	0.40
2:s:240:ALA:C	2:s:242:GLN:H	2.28	0.40
2:s:470:ILE:HG22	2:s:488:ILE:HD11	2.03	0.40
2:u:479:VAL:HG22	2:v:477:GLN:CA	2.50	0.40
2:w:204:MET:HE3	2:w:204:MET:HB2	1.88	0.40
2:w:479:VAL:HG22	2:x:477:GLN:C	2.46	0.40
2:x:170:ASN:ND2	2:x:231:ASP:H	2.19	0.40
2:x:385:LEU:HD21	2:x:433:LYS:HE3	2.03	0.40
3:R:56:SER:OG	3:S:132:GLU:CG	2.67	0.40
3:S:35:ASP:O	3:S:37:ASN:N	2.54	0.40
3:T:69:LEU:HD11	3:T:121:ILE:HD11	2.03	0.40
3:T:137:TRP:CD1	3:T:167:ALA:HB3	2.57	0.40
3:U:20:ILE:HD11	3:U:47:LEU:HD13	2.02	0.40
3:U:97:VAL:CG2	3:V:125:ARG:HH12	2.34	0.40
3:U:149:ARG:HG2	3:V:23:SER:HA	2.03	0.40
3:U:172:MET:HE3	3:U:172:MET:HB2	1.56	0.40
1:e:10:THR:HB	1:e:74:GLU:OE1	2.21	0.40
1:g:29:ARG:HB2	3:V:5:ASP:CB	2.52	0.40
1:j:129:LEU:HG	1:k:134:ARG:HB3	2.03	0.40
1:l:22:ILE:HD11	1:l:26:TYR:CE2	2.57	0.40
1:n:22:ILE:HG21	1:n:22:ILE:HD13	1.74	0.40
1:o:94:LEU:HD23	1:o:94:LEU:HA	1.87	0.40
1:p:50:TYR:HE2	1:p:52:PHE:HE1	1.68	0.40
2:s:32:VAL:HG13	2:s:542:HIS:CE1	2.55	0.40
2:s:552:LEU:HD23	2:s:552:LEU:HA	1.83	0.40
2:t:169:ILE:HG23	2:t:230:ILE:HG23	2.03	0.40
2:t:705:ARG:CZ	3:T:26:GLU:HG2	2.51	0.40
2:v:358:LEU:HB2	2:v:374:TYR:HB3	2.01	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:454:ILE:HG21	2:v:528:PHE:HZ	1.87	0.40
2:w:97:GLN:O	2:w:319:ASN:HB3	2.22	0.40
3:S:149:ARG:HG2	3:T:23:SER:HA	2.02	0.40
1:a:107:MET:SD	1:b:109:VAL:HG21	2.61	0.40
1:b:60:LEU:HD11	1:b:73:ILE:CD1	2.48	0.40
1:c:22:ILE:HD11	1:c:26:TYR:CE2	2.57	0.40
1:g:29:ARG:NH2	3:V:5:ASP:HB3	2.36	0.40
1:l:90:ASP:O	2:t:715:THR:HG21	2.21	0.40
2:s:704:ARG:NH1	3:R:150:PHE:O	2.49	0.40
2:t:704:ARG:NH1	3:T:150:PHE:O	2.49	0.40
2:w:170:ASN:ND2	2:w:231:ASP:H	2.19	0.40
2:w:556:SER:HA	2:w:561:MET:HA	2.03	0.40
3:M:35:ASP:O	3:M:37:ASN:N	2.55	0.40
3:M:129:GLU:HA	3:X:98:ASN:ND2	2.35	0.40
3:N:144:ARG:HB2	3:N:160:LEU:HD12	2.03	0.40
3:R:69:LEU:HD11	3:R:121:ILE:HD11	2.03	0.40
1:a:116:LEU:HD21	1:c:114:ARG:NH2	2.37	0.40
1:e:13:LEU:HB3	1:e:71:THR:HA	2.04	0.40
1:f:91:GLY:N	2:v:715:THR:HG22	2.31	0.40
1:j:107:MET:SD	1:k:109:VAL:HG21	2.61	0.40
1:l:94:LEU:HD23	1:l:94:LEU:HA	1.87	0.40
1:p:13:LEU:HD13	1:p:20:PHE:HZ	1.86	0.40
1:p:13:LEU:CD1	1:p:20:PHE:HZ	2.34	0.40
1:p:112:GLU:HA	1:p:115:ASP:OD1	2.21	0.40
1:p:116:LEU:HD21	1:r:114:ARG:NH2	2.37	0.40
2:s:243:LEU:HD22	2:s:243:LEU:HA	1.93	0.40
2:u:625:ASN:OD1	2:u:625:ASN:N	2.51	0.40
2:u:700:ARG:HH12	3:W:24:ILE:HD13	1.87	0.40
2:v:97:GLN:O	2:v:319:ASN:HB3	2.22	0.40
2:v:240:ALA:C	2:v:242:GLN:N	2.78	0.40
3:Q:21:LEU:HD23	3:Q:21:LEU:HA	1.89	0.40
3:R:137:TRP:CD1	3:R:167:ALA:HB3	2.57	0.40
3:T:144:ARG:HB2	3:T:160:LEU:HD12	2.03	0.40
3:U:35:ASP:O	3:U:37:ASN:N	2.55	0.40
3:X:144:ARG:HB2	3:X:160:LEU:HD12	2.04	0.40
1:a:112:GLU:HA	1:a:115:ASP:OD1	2.21	0.40
1:b:13:LEU:HB3	1:b:71:THR:HA	2.04	0.40
1:d:13:LEU:HA	1:d:13:LEU:HD13	1.69	0.40
1:d:18:ARG:O	1:d:59:SER:HA	2.21	0.40
1:e:13:LEU:HD22	1:e:73:ILE:HG13	2.03	0.40
1:f:22:ILE:HD11	1:f:26:TYR:CE2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:44:LEU:HG	1:f:49:ASP:HB3	2.04	0.40
1:g:13:LEU:HD13	1:g:20:PHE:HZ	1.86	0.40
1:g:116:LEU:HD21	1:i:114:ARG:NH2	2.37	0.40
1:i:25:GLU:O	1:i:77:ARG:NH1	2.55	0.40
1:n:13:LEU:HD22	1:n:73:ILE:HG13	2.03	0.40
2:t:97:GLN:O	2:t:319:ASN:HB3	2.22	0.40
2:t:614:THR:HG22	2:t:660:GLY:O	2.21	0.40
2:u:454:ILE:HG21	2:u:528:PHE:HZ	1.86	0.40
2:w:470:ILE:HG22	2:w:488:ILE:HD11	2.03	0.40
2:x:143:LEU:HD13	2:x:143:LEU:HA	1.88	0.40
3:Q:176:MET:HE3	3:Q:176:MET:HB3	1.91	0.40
3:X:54:ILE:HG23	3:X:137:TRP:CZ3	2.57	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 PDB entries followed by that with respect to all EM entries.

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	139/553 (25%)	127 (91%)	11 (8%)	1 (1%)	18	47
1	b	132/553 (24%)	121 (92%)	9 (7%)	2 (2%)	8	30
1	c	134/553 (24%)	126 (94%)	8 (6%)	0	100	100
1	d	139/553 (25%)	127 (91%)	11 (8%)	1 (1%)	18	47
1	e	132/553 (24%)	121 (92%)	9 (7%)	2 (2%)	8	30
1	f	134/553 (24%)	126 (94%)	8 (6%)	0	100	100
1	g	139/553 (25%)	127 (91%)	11 (8%)	1 (1%)	18	47
1	h	132/553 (24%)	121 (92%)	9 (7%)	2 (2%)	8	30
1	i	134/553 (24%)	126 (94%)	8 (6%)	0	100	100
1	j	139/553 (25%)	127 (91%)	11 (8%)	1 (1%)	18	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	k	132/553 (24%)	121 (92%)	9 (7%)	2 (2%)	8	30
1	l	134/553 (24%)	126 (94%)	8 (6%)	0	100	100
1	m	139/553 (25%)	127 (91%)	11 (8%)	1 (1%)	18	47
1	n	132/553 (24%)	121 (92%)	9 (7%)	2 (2%)	8	30
1	o	134/553 (24%)	126 (94%)	8 (6%)	0	100	100
1	p	139/553 (25%)	127 (91%)	11 (8%)	1 (1%)	18	47
1	q	132/553 (24%)	121 (92%)	9 (7%)	2 (2%)	8	30
1	r	134/553 (24%)	126 (94%)	8 (6%)	0	100	100
2	s	790/794 (100%)	759 (96%)	30 (4%)	1 (0%)	48	78
2	t	790/794 (100%)	759 (96%)	30 (4%)	1 (0%)	48	78
2	u	790/794 (100%)	759 (96%)	30 (4%)	1 (0%)	48	78
2	v	790/794 (100%)	759 (96%)	30 (4%)	1 (0%)	48	78
2	w	790/794 (100%)	759 (96%)	30 (4%)	1 (0%)	48	78
2	x	790/794 (100%)	759 (96%)	30 (4%)	1 (0%)	48	78
3	M	192/196 (98%)	183 (95%)	8 (4%)	1 (0%)	24	54
3	N	193/196 (98%)	181 (94%)	12 (6%)	0	100	100
3	O	192/196 (98%)	184 (96%)	7 (4%)	1 (0%)	24	54
3	P	193/196 (98%)	182 (94%)	11 (6%)	0	100	100
3	Q	192/196 (98%)	184 (96%)	7 (4%)	1 (0%)	24	54
3	R	193/196 (98%)	182 (94%)	11 (6%)	0	100	100
3	S	192/196 (98%)	184 (96%)	7 (4%)	1 (0%)	24	54
3	T	193/196 (98%)	182 (94%)	11 (6%)	0	100	100
3	U	192/196 (98%)	184 (96%)	7 (4%)	1 (0%)	24	54
3	V	193/196 (98%)	181 (94%)	12 (6%)	0	100	100
3	W	192/196 (98%)	183 (95%)	8 (4%)	1 (0%)	24	54
3	X	193/196 (98%)	182 (94%)	11 (6%)	0	100	100
All	All	9480/17070 (56%)	8990 (95%)	460 (5%)	30 (0%)	37	65

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	29	ARG
1	b	120	THR

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Mol	Chain	Res	Type
1	e	29	ARG
1	e	120	THR
1	h	29	ARG
1	h	120	THR
1	k	29	ARG
1	k	120	THR
1	n	29	ARG
1	n	120	THR
1	q	29	ARG
1	q	120	THR
3	M	36	ALA
3	O	36	ALA
3	Q	36	ALA
3	S	36	ALA
3	U	36	ALA
3	W	36	ALA
1	a	15	GLY
1	d	15	GLY
1	g	15	GLY
1	j	15	GLY
1	m	15	GLY
1	p	15	GLY
2	s	180	PRO
2	t	180	PRO
2	u	180	PRO
2	v	180	PRO
2	w	180	PRO
2	x	180	PRO

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

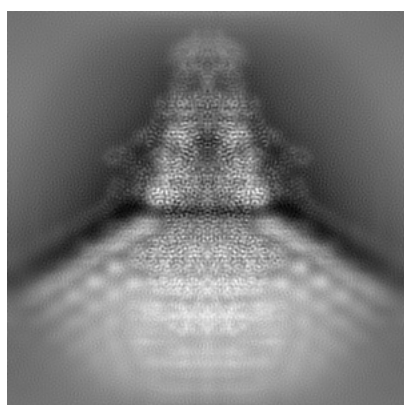
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31319. These allow visual inspection of the internal detail of the map and identification of artifacts.

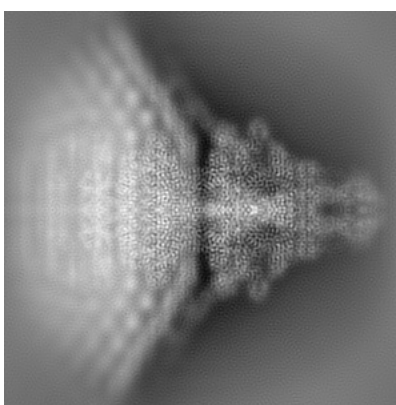
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

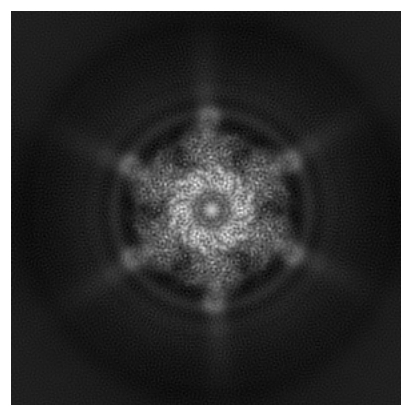
6.1.1 Primary map



X



Y

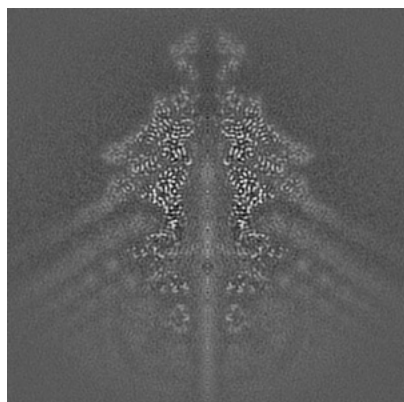


Z

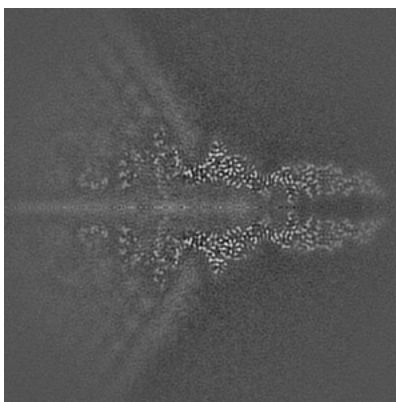
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

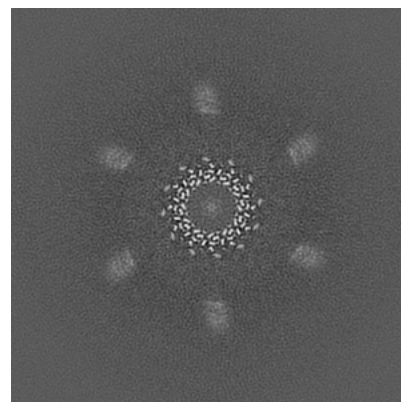
6.2.1 Primary map



X Index: 160



Y Index: 160

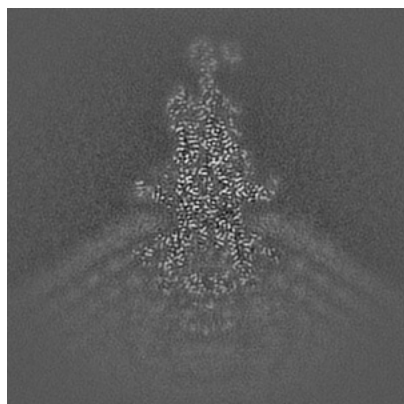


Z Index: 160

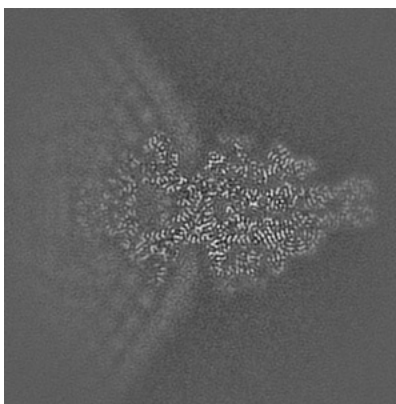
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

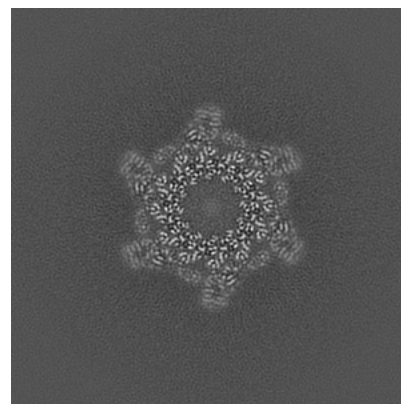
6.3.1 Primary map



X Index: 183



Y Index: 181

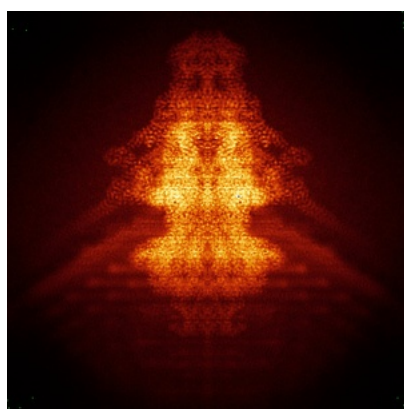


Z Index: 174

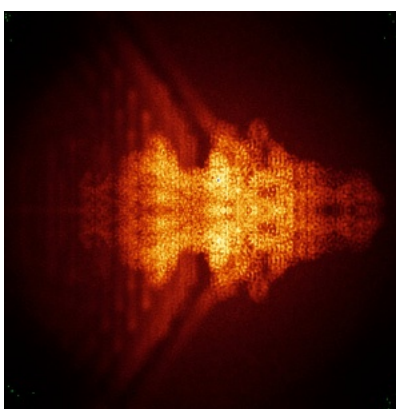
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

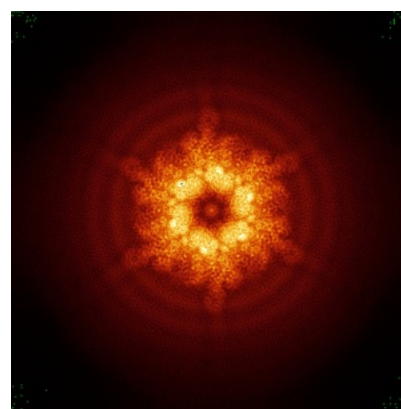
6.4.1 Primary map



X



Y

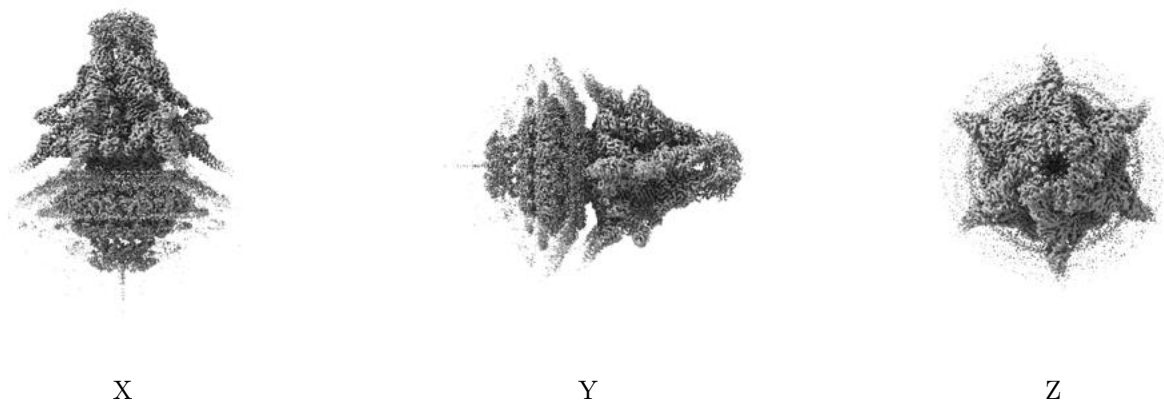


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 9.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

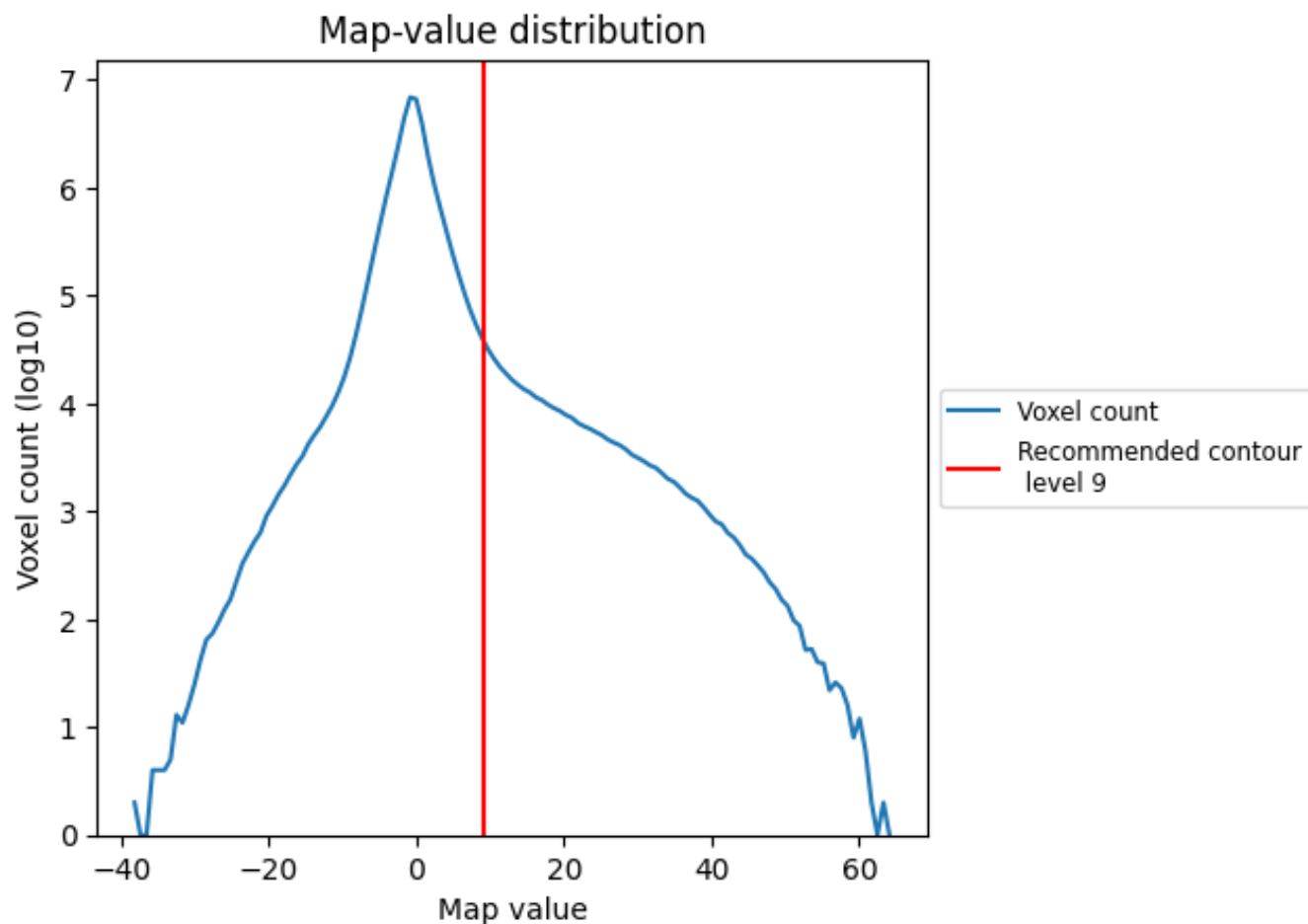
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

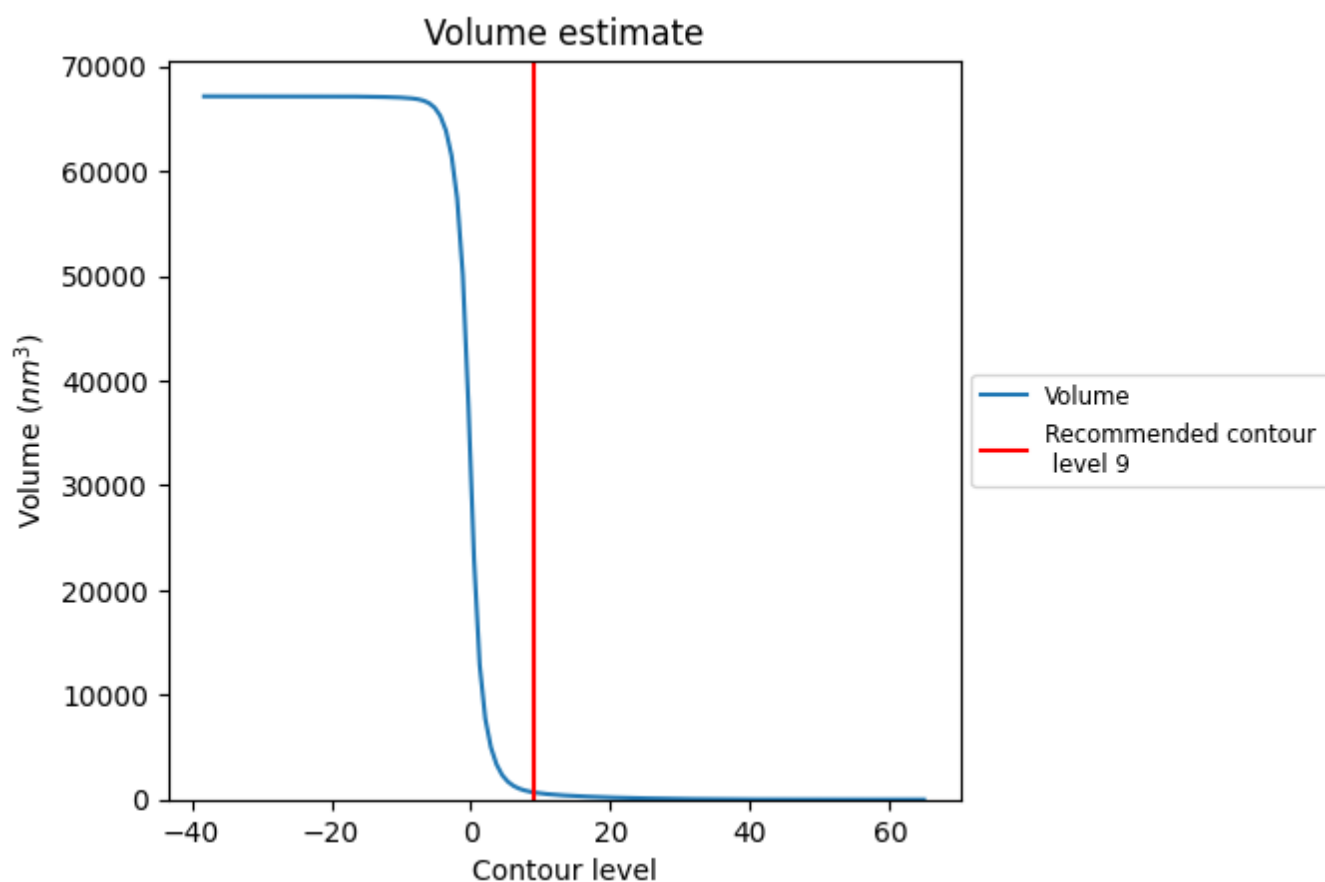
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

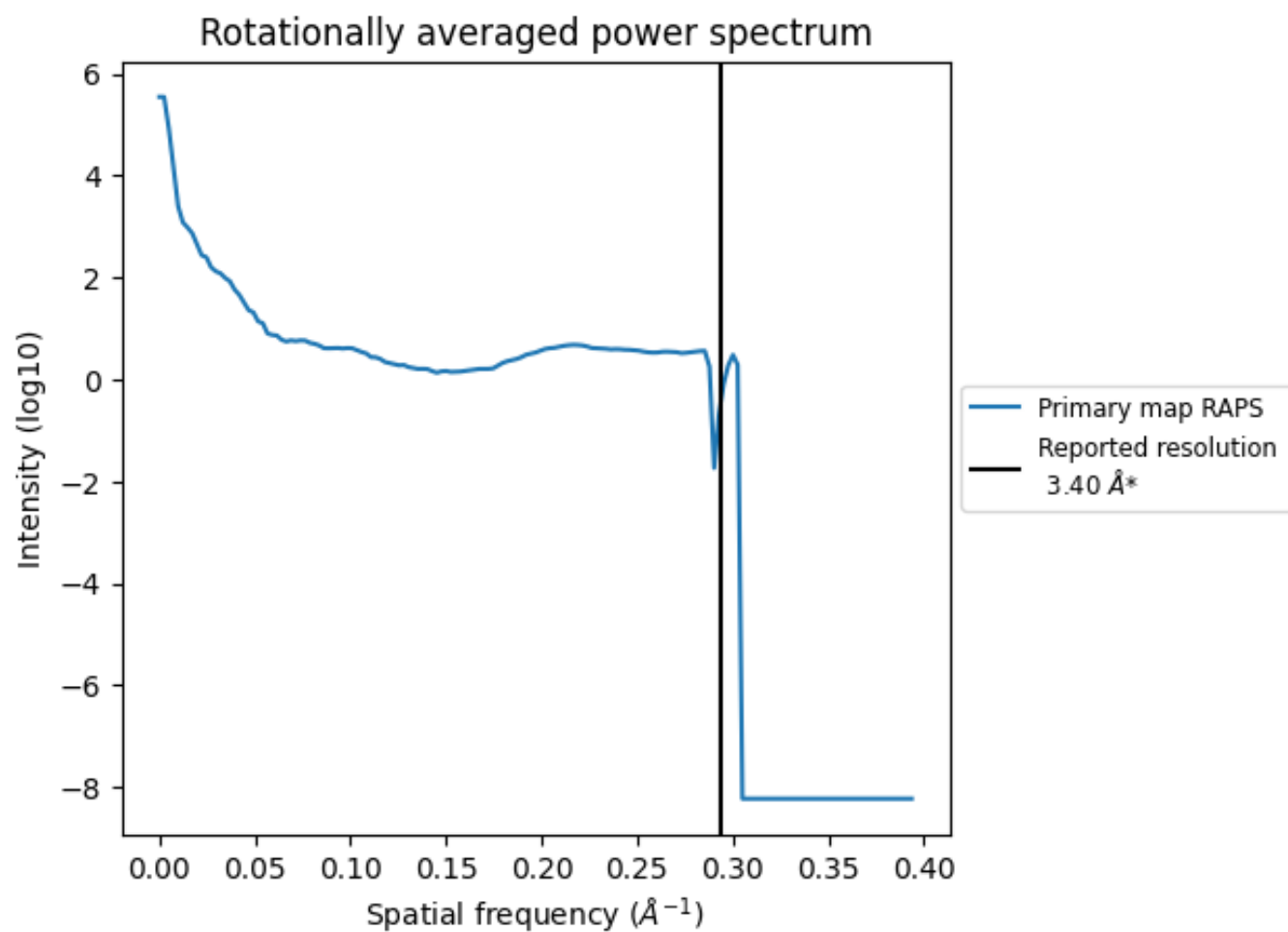
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 690 nm³; this corresponds to an approximate mass of 624 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

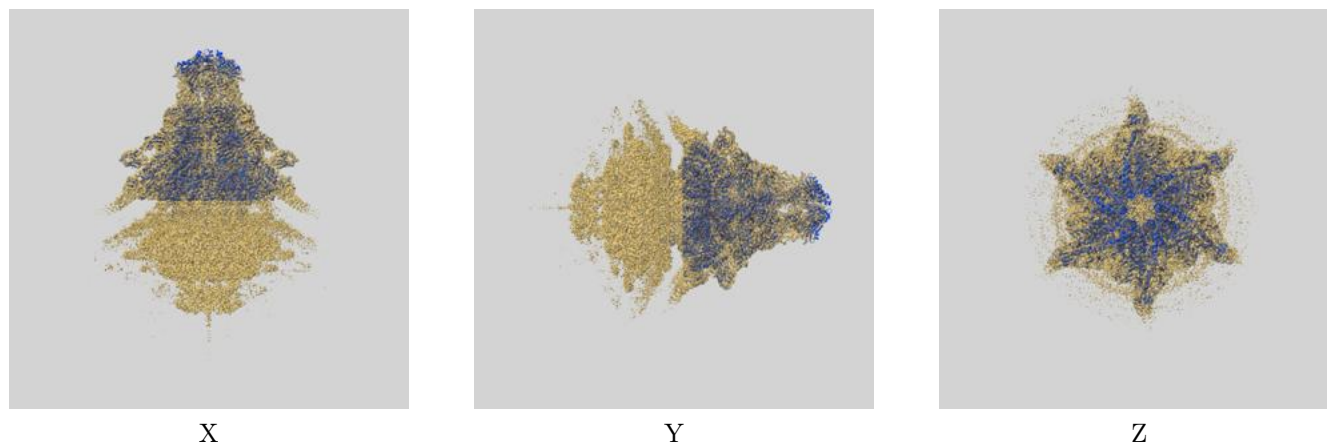
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

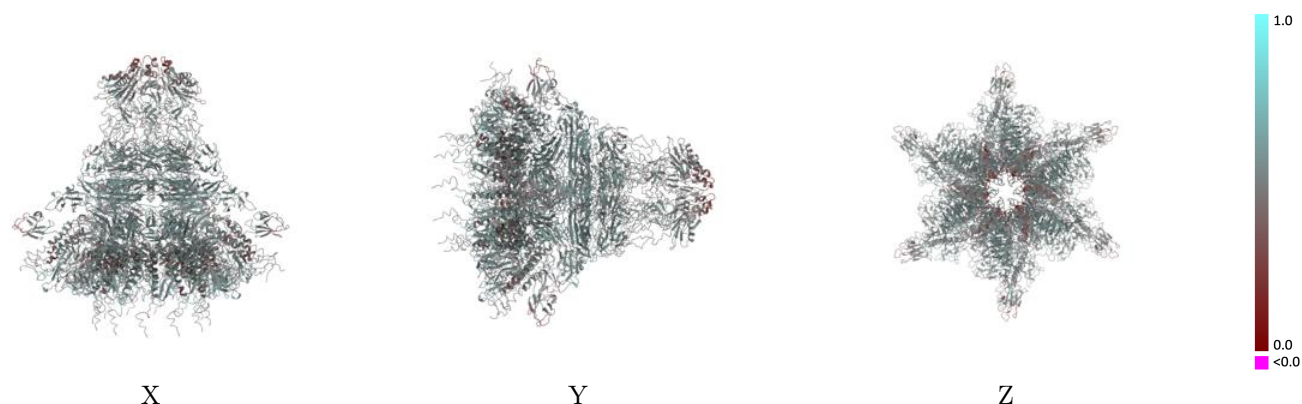
This section contains information regarding the fit between EMDB map EMD-31319 and PDB model 7EY9. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



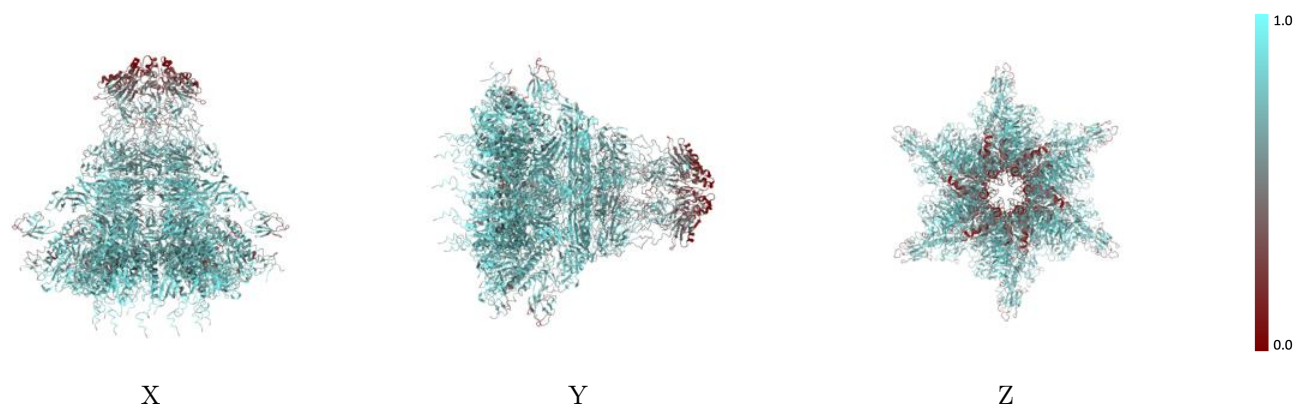
The images above show the 3D surface view of the map at the recommended contour level 9.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



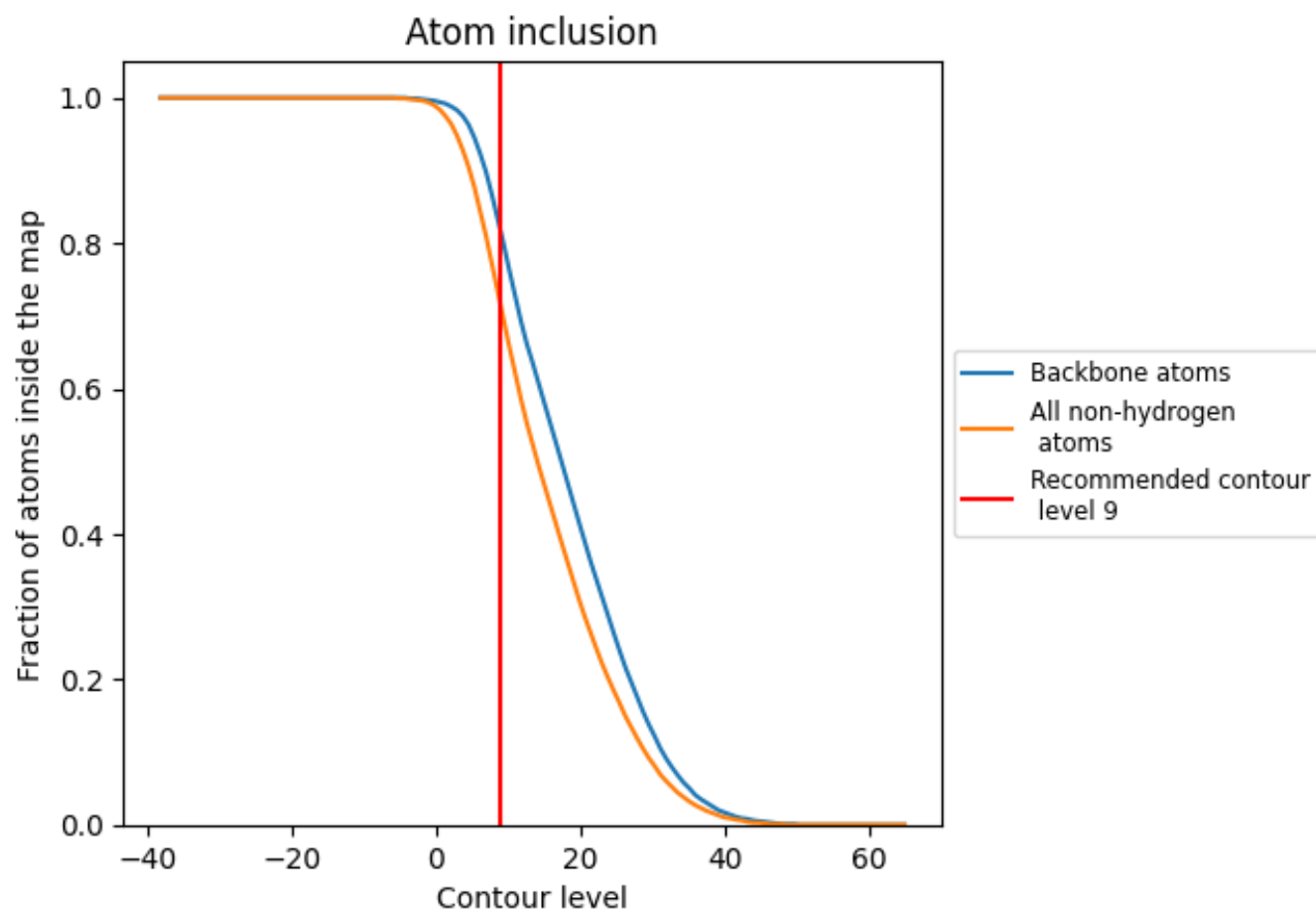
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 71% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7110	 0.5060
M	 0.7970	 0.5080
N	 0.7710	 0.5080
O	 0.7960	 0.5080
P	 0.7680	 0.5050
Q	 0.7990	 0.5040
R	 0.7720	 0.5060
S	 0.7990	 0.5070
T	 0.7730	 0.5070
U	 0.7950	 0.5070
V	 0.7700	 0.5070
W	 0.7960	 0.5060
X	 0.7700	 0.5060
a	 0.7760	 0.5280
b	 0.7260	 0.5080
c	 0.6300	 0.4610
d	 0.7680	 0.5180
e	 0.7240	 0.5020
f	 0.6060	 0.4490
g	 0.7730	 0.5200
h	 0.7340	 0.5010
i	 0.6140	 0.4520
j	 0.7650	 0.5260
k	 0.7230	 0.5050
l	 0.6330	 0.4610
m	 0.7550	 0.5200
n	 0.7240	 0.5030
o	 0.6200	 0.4510
p	 0.7680	 0.5210
q	 0.7360	 0.5010
r	 0.6150	 0.4460
s	 0.6840	 0.5190
t	 0.6780	 0.5100
u	 0.6750	 0.5080
v	 0.6840	 0.5150



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Chain	Atom inclusion	Q-score
w	 0.6760	 0.5090
x	 0.6750	 0.5090