Full wwPDB EM Validation Report

Jun 16, 2025 – 10:43 PM JST

PDB ID	:	7EY7 / pdb_00007ey7
EMDB ID	:	EMD-31321
Title	:	bacteriophage T7 tail complex
Authors	:	Liu, H.R.; Chen, W.Y.
Deposited on	:	2021-05-30
Resolution	:	4.30 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:

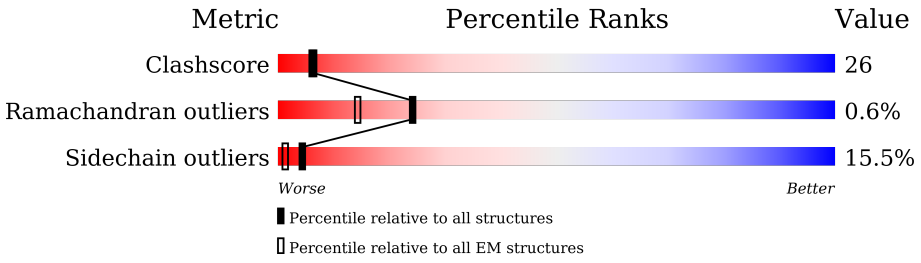
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.44

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 4.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 <=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	10% 8% 79%
1	b	553	8% 9% 79%
1	c	553	9% 8% 79%
1	d	553	10% 8% 79%
1	e	553	8% 9% 79%
1	f	553	9% 8% 79%
1	g	553	10% 7% 79%
1	h	553	8% 9% 79%

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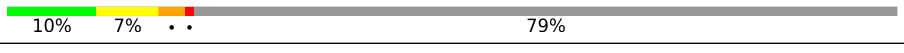
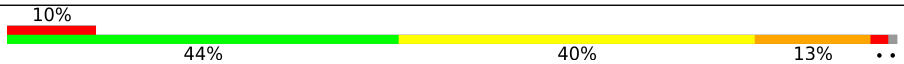
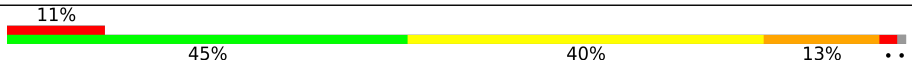
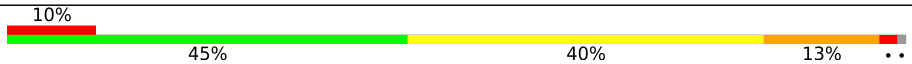
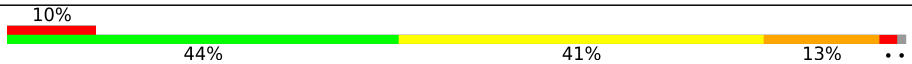
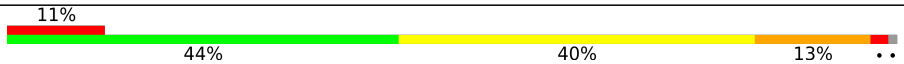
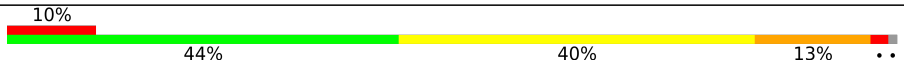
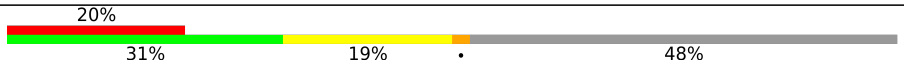
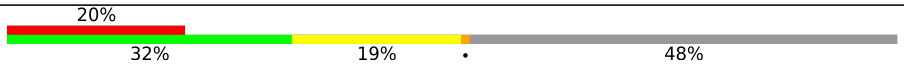
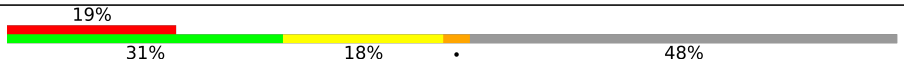
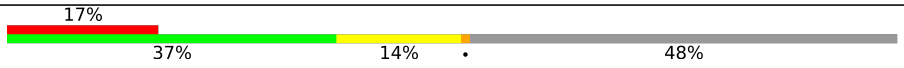
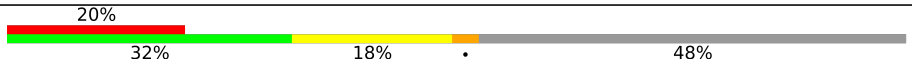
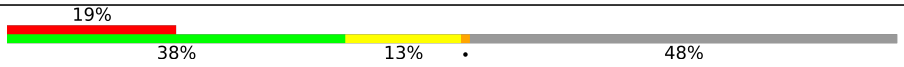
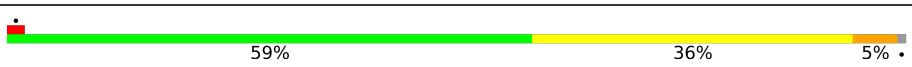
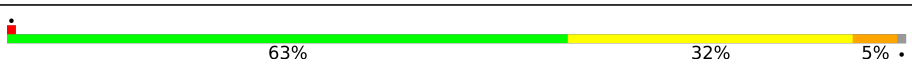
Mol	Chain	Length	Quality of chain
1	i	553	
1	j	553	
1	k	553	
1	l	553	
1	m	553	
1	n	553	
1	o	553	
1	p	553	
1	q	553	
1	r	553	
2	s	794	
2	t	794	
2	u	794	
2	v	794	
2	w	794	
2	x	794	
3	A	196	
3	B	196	
3	C	196	
3	D	196	
3	E	196	
3	F	196	
4	M	196	
4	N	196	
4	O	196	

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Mol	Chain	Length	Quality of chain
4	P	196	
4	Q	196	
4	R	196	
4	S	196	
4	T	196	
4	U	196	
4	V	196	
4	W	196	
4	X	196	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 77574 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	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	b	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	c	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	d	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	e	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	f	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	g	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	h	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	i	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	j	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	k	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	l	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	m	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	n	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	o	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	p	115	Total	C	N	O	S	0	0
			922	584	160	177	1		
1	q	115	Total	C	N	O	S	0	0
			922	584	160	177	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	r	115	Total	C	N	O	S	0	0
			922	584	160	177	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	s	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
2	t	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
2	u	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
2	v	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
2	w	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		
2	x	789	Total	C	N	O	S	0	0
			6289	3989	1083	1202	15		

- Molecule 3 is a protein called Internal virion protein gp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	102	Total	C	N	O	S	0	0
			787	475	146	160	6		
3	B	102	Total	C	N	O	S	0	0
			787	475	146	160	6		
3	C	102	Total	C	N	O	S	0	0
			787	475	146	160	6		
3	D	102	Total	C	N	O	S	0	0
			787	475	146	160	6		
3	E	102	Total	C	N	O	S	0	0
			787	475	146	160	6		
3	F	102	Total	C	N	O	S	0	0
			787	475	146	160	6		

- Molecule 4 is a protein called Tail tubular protein gp11.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	195	Total	C	N	O	S	0	0
			1553	965	263	316	9		
4	N	193	Total	C	N	O	S	0	0
			1534	954	258	314	8		

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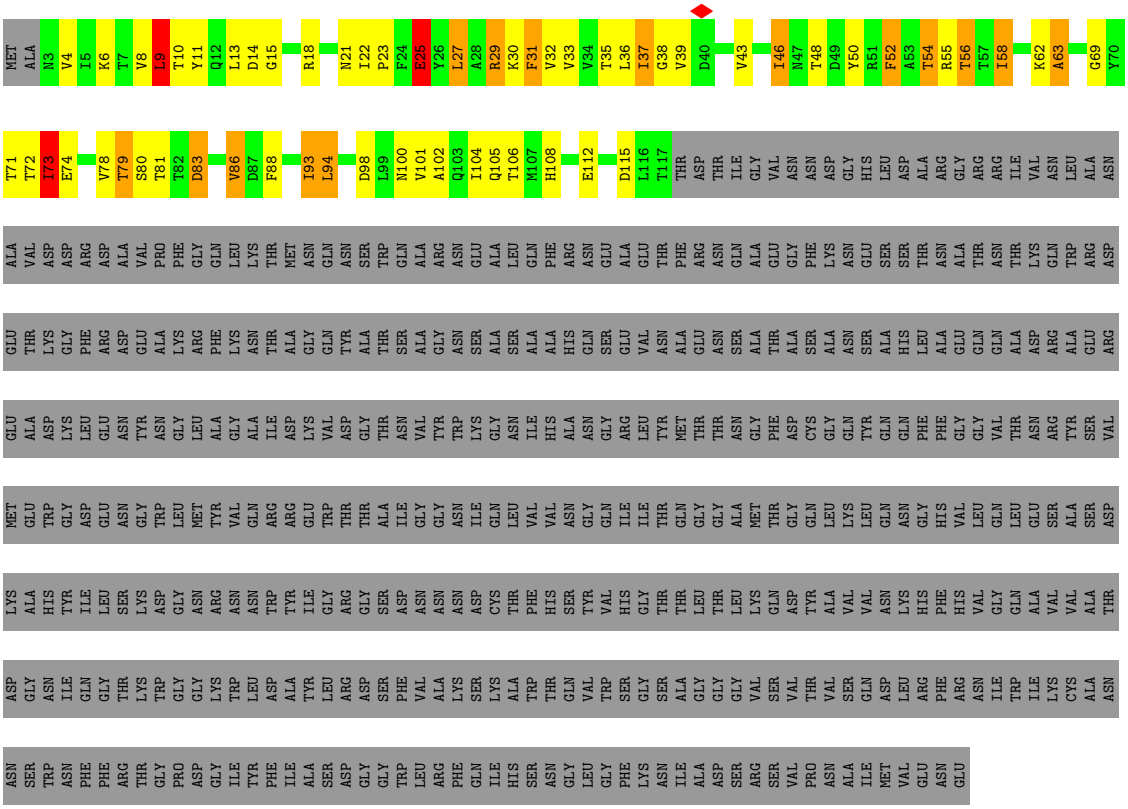
Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	195	Total	C	N	O	S	0	0
			1553	965	263	316	9		
4	P	193	Total	C	N	O	S	0	0
			1534	954	258	314	8		
4	Q	195	Total	C	N	O	S	0	0
			1553	965	263	316	9		
4	R	193	Total	C	N	O	S	0	0
			1534	954	258	314	8		
4	S	195	Total	C	N	O	S	0	0
			1553	965	263	316	9		
4	T	193	Total	C	N	O	S	0	0
			1534	954	258	314	8		
4	U	195	Total	C	N	O	S	0	0
			1553	965	263	316	9		
4	V	193	Total	C	N	O	S	0	0
			1534	954	258	314	8		
4	W	195	Total	C	N	O	S	0	0
			1553	965	263	316	9		
4	X	193	Total	C	N	O	S	0	0
			1534	954	258	314	8		

3 Residue-property plots (i)

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

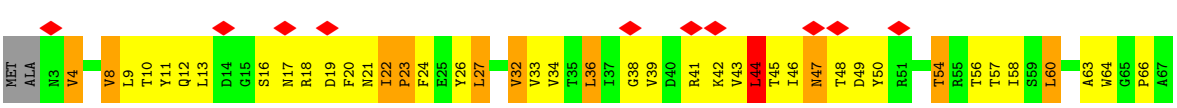
• Molecule 1: Tail fiber protein

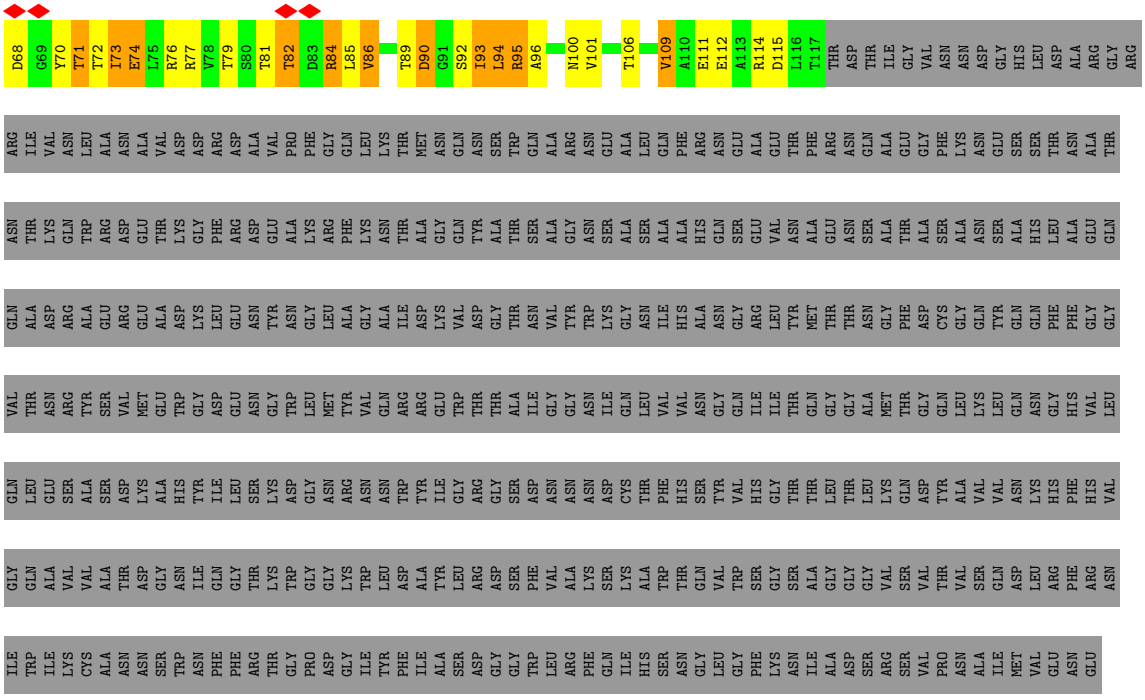
Chain a:



• Molecule 1: Tail fiber protein

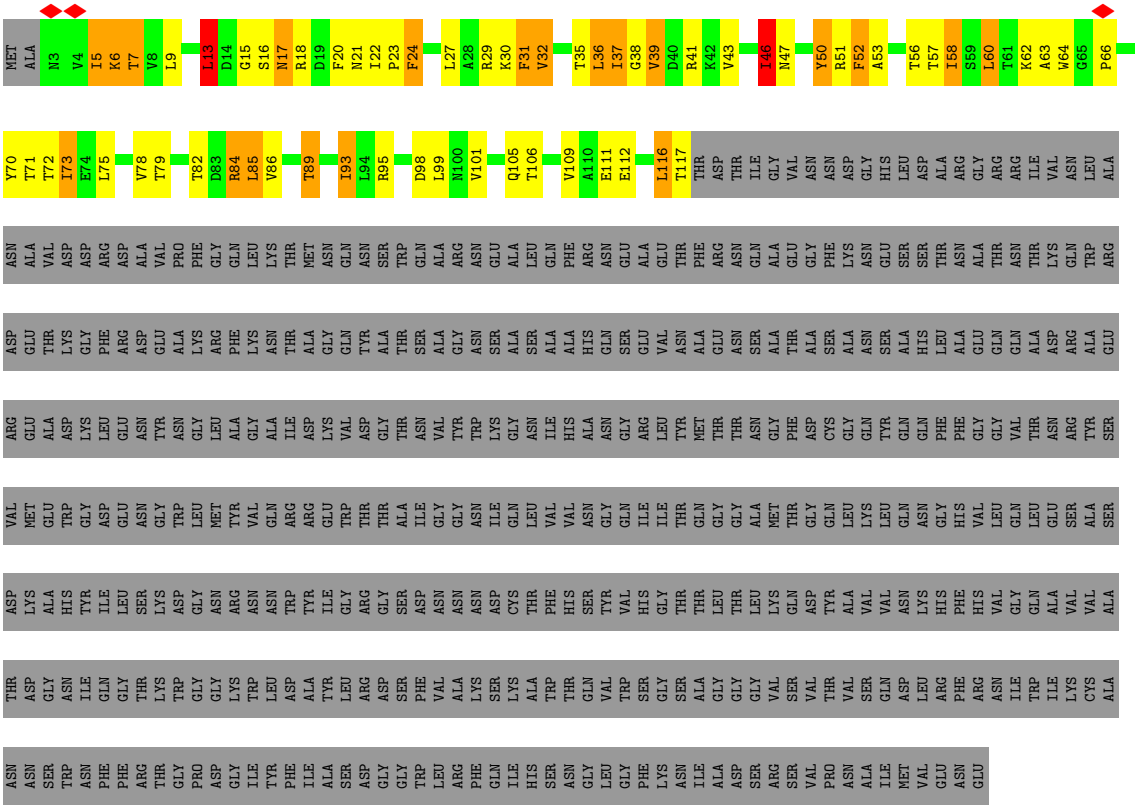
Chain b:





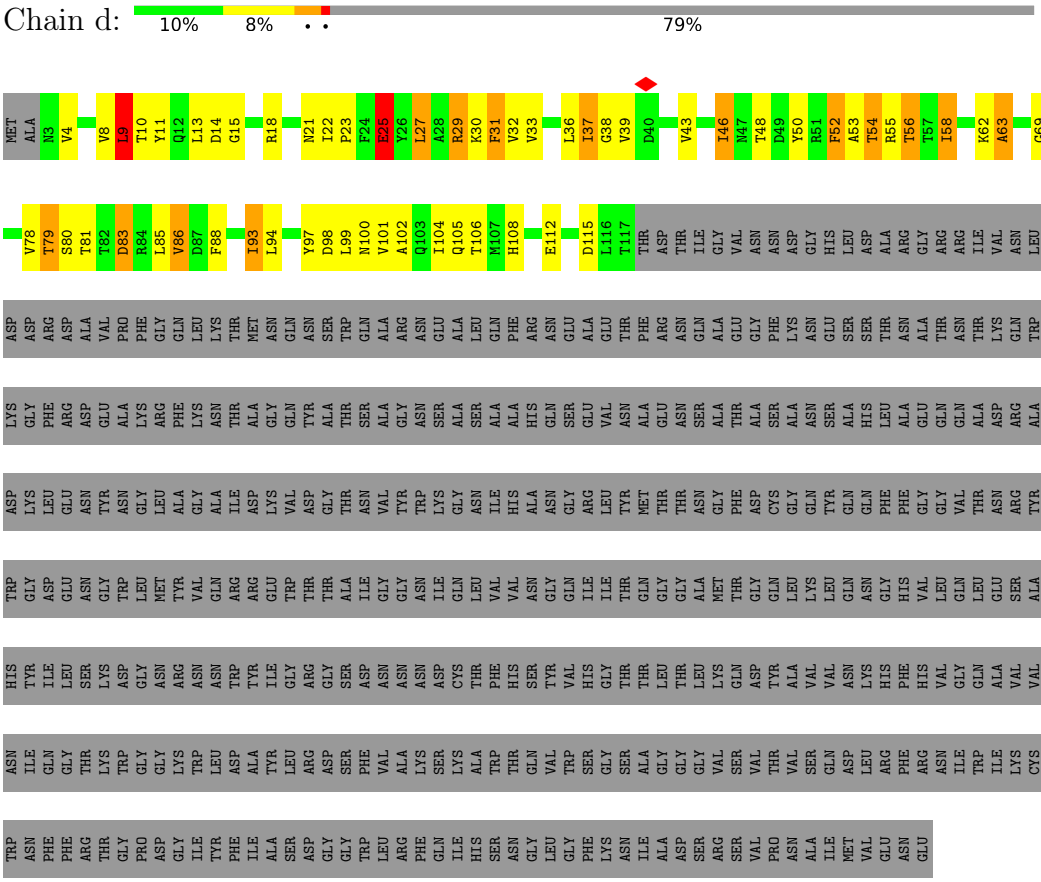
• Molecule 1: Tail fiber protein

Chain c:



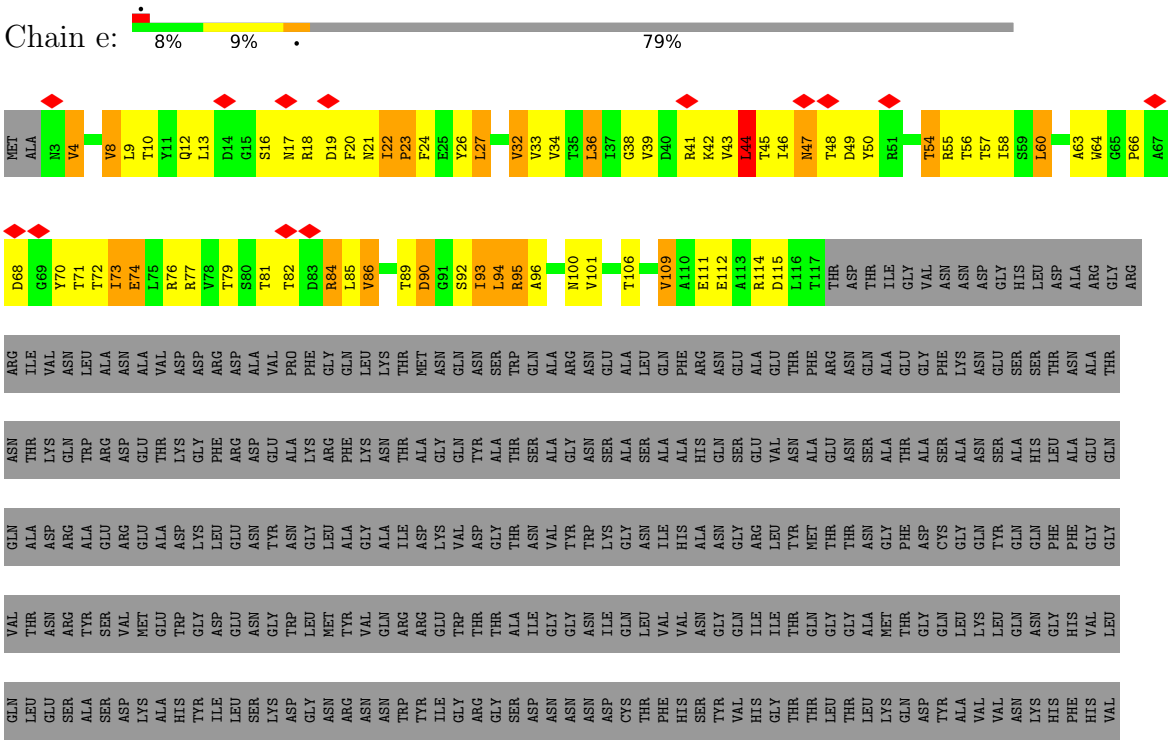
• Molecule 1: Tail fiber protein

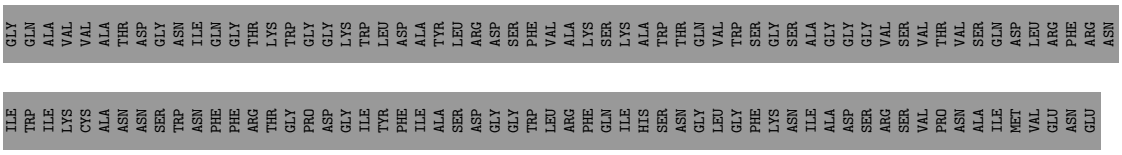
Chain d:



• Molecule 1: Tail fiber protein

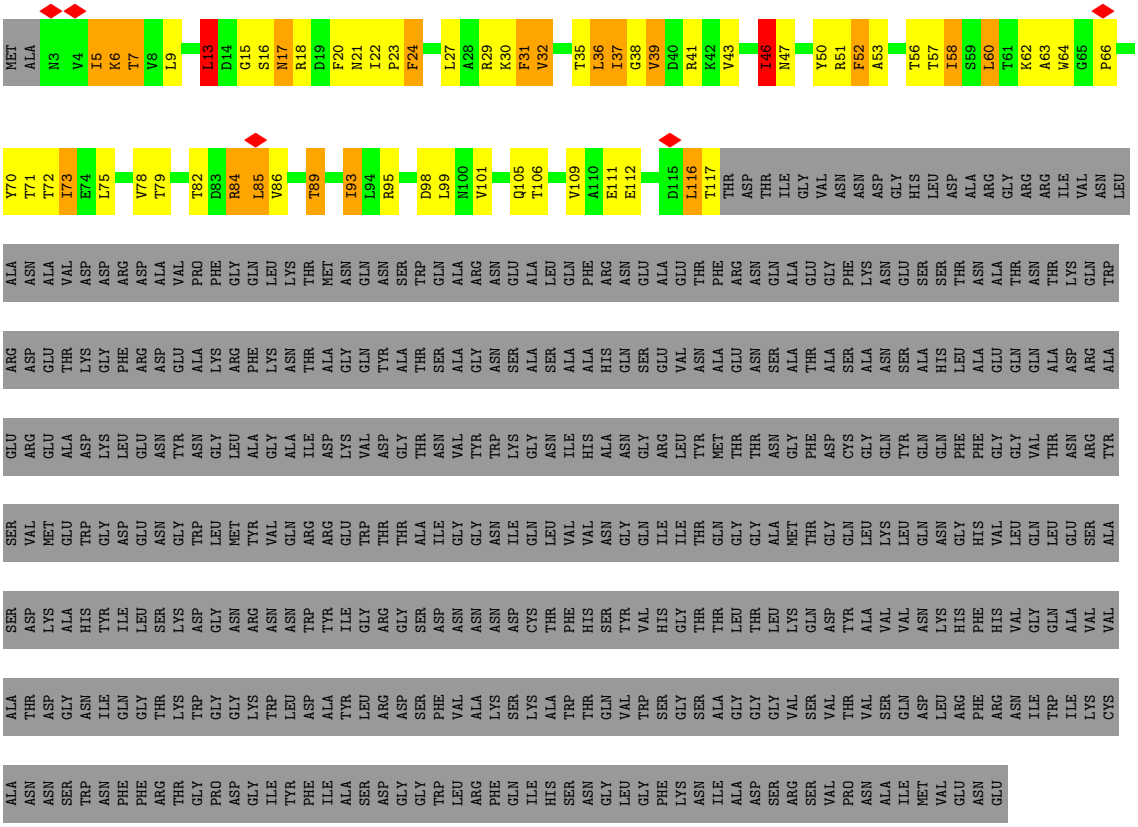
Chain e:





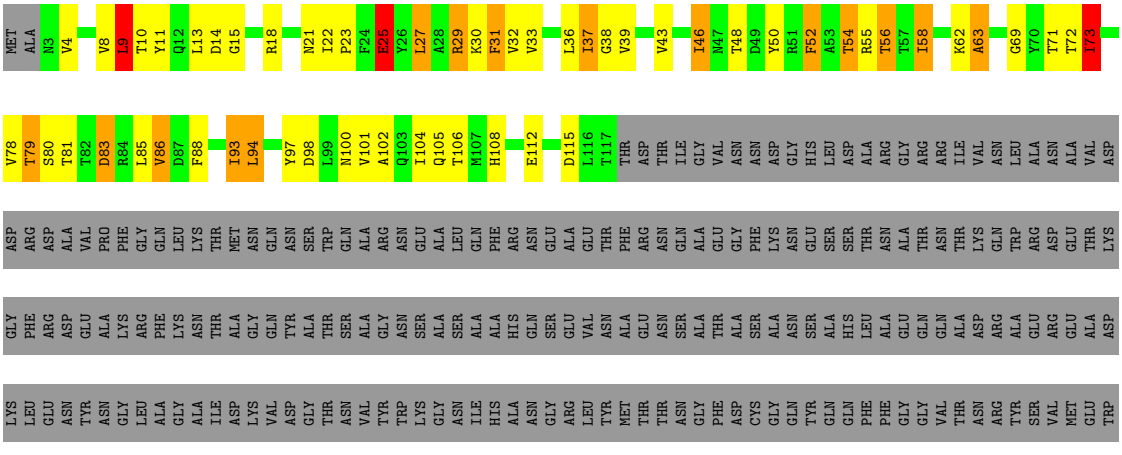
• Molecule 1: Tail fiber protein

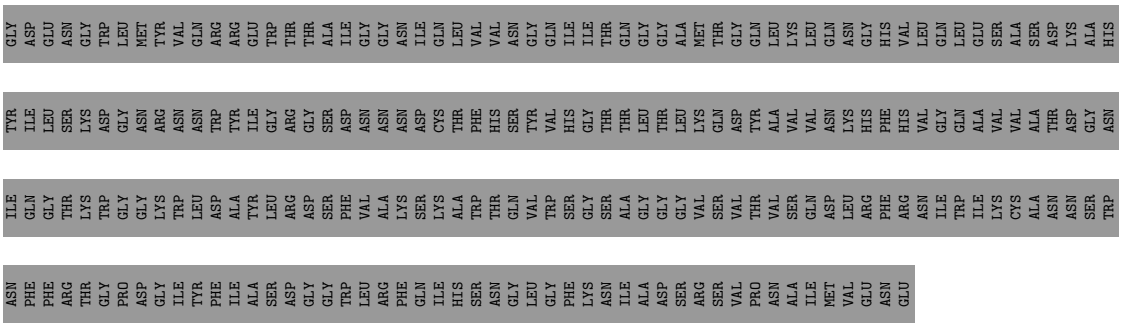
Chain f:



• Molecule 1: Tail fiber protein

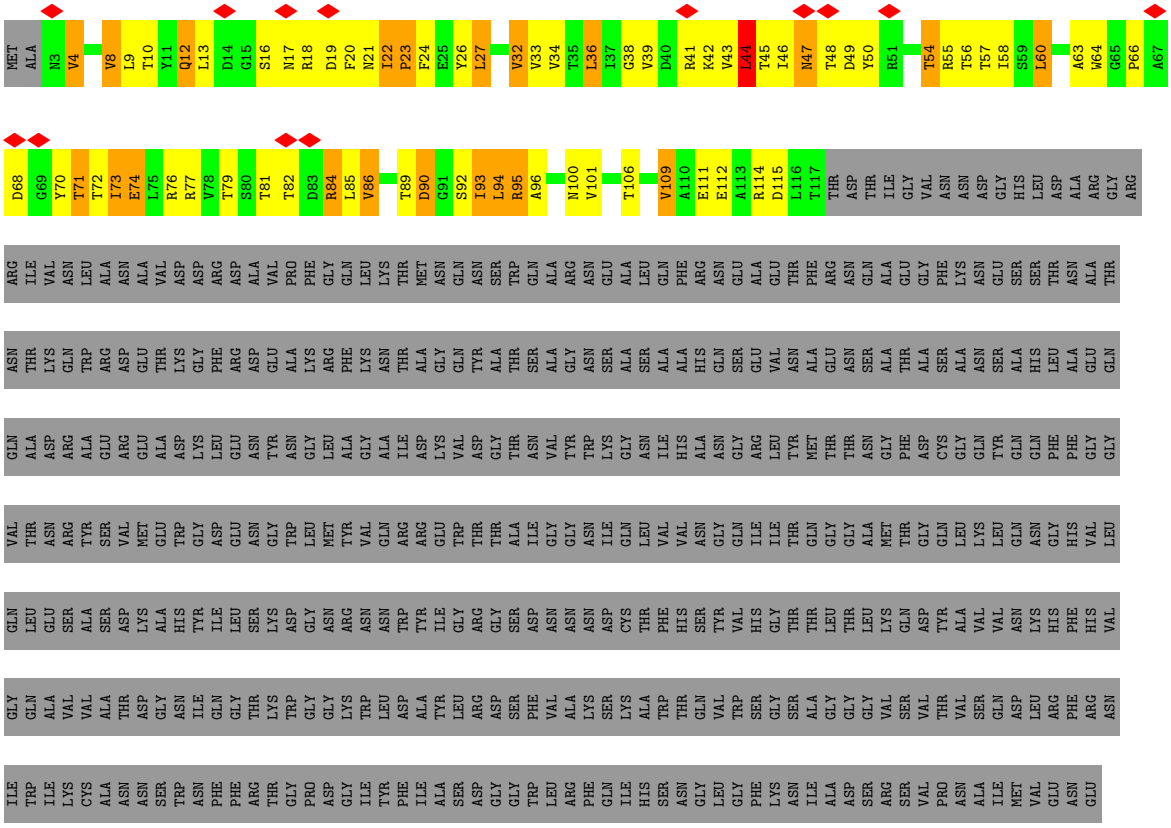
Chain g:





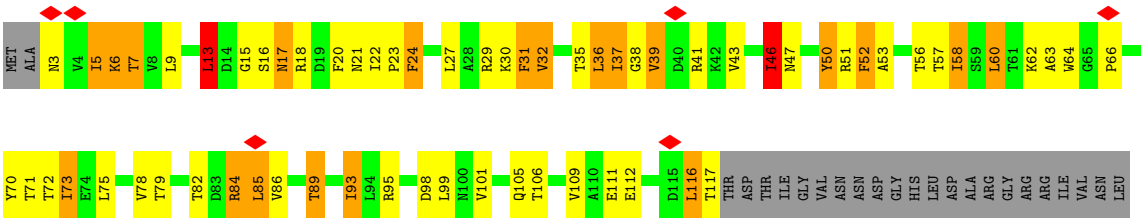
• Molecule 1: Tail fiber protein

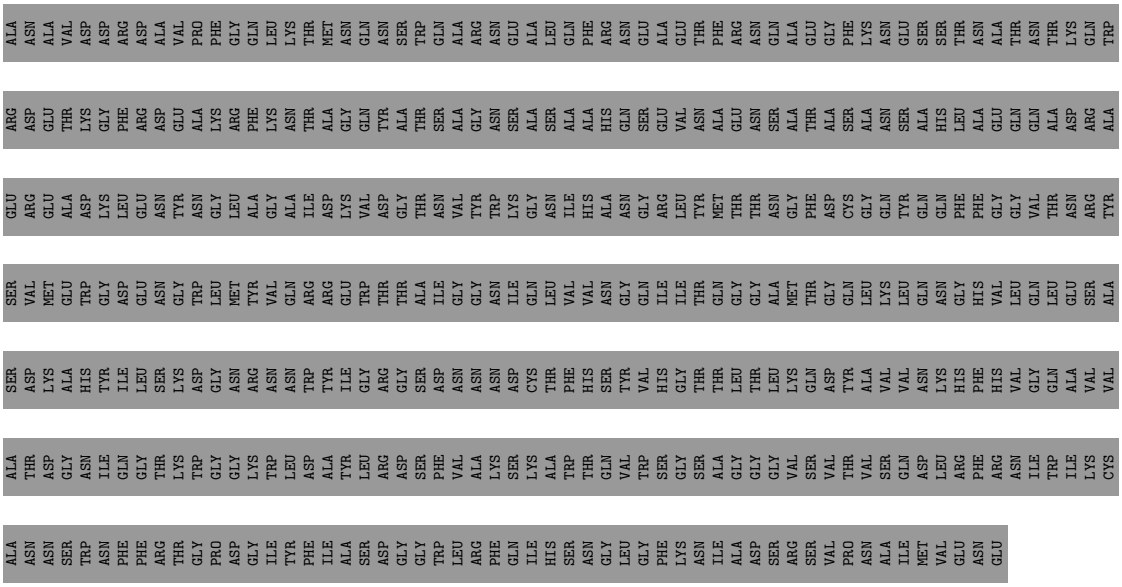
Chain h:



• Molecule 1: Tail fiber protein

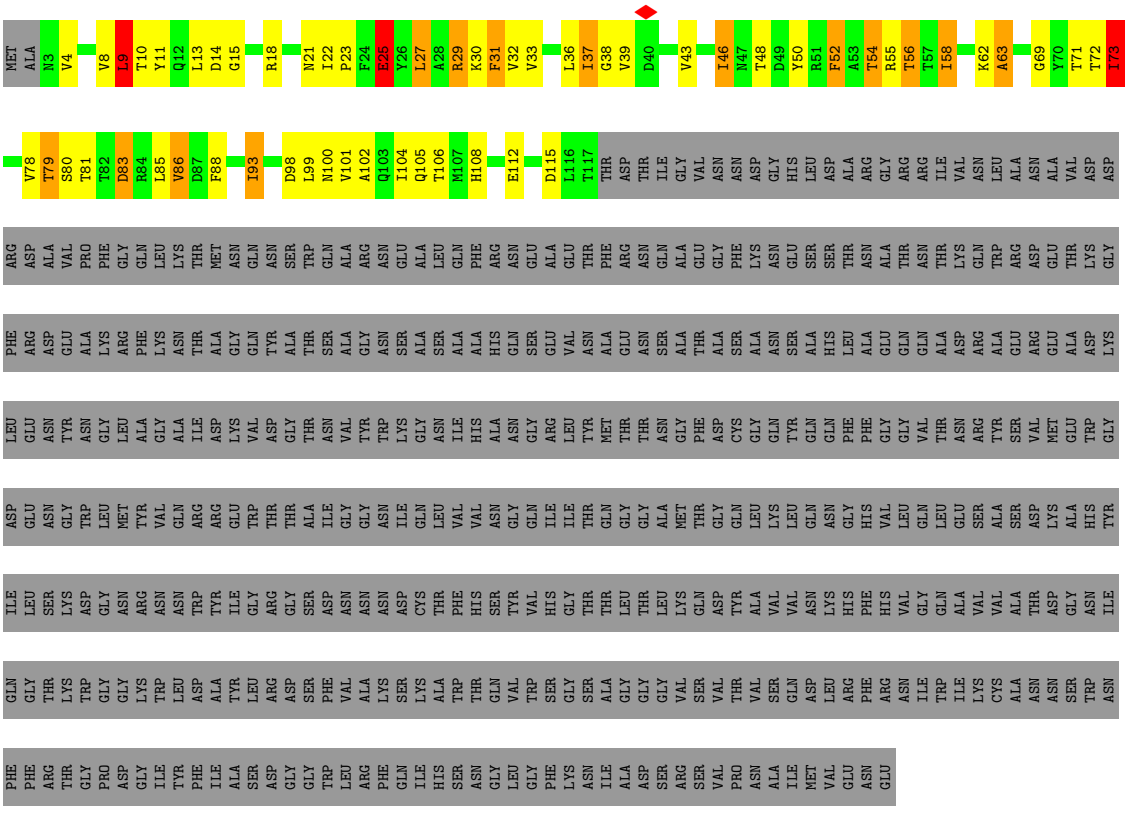
Chain i:





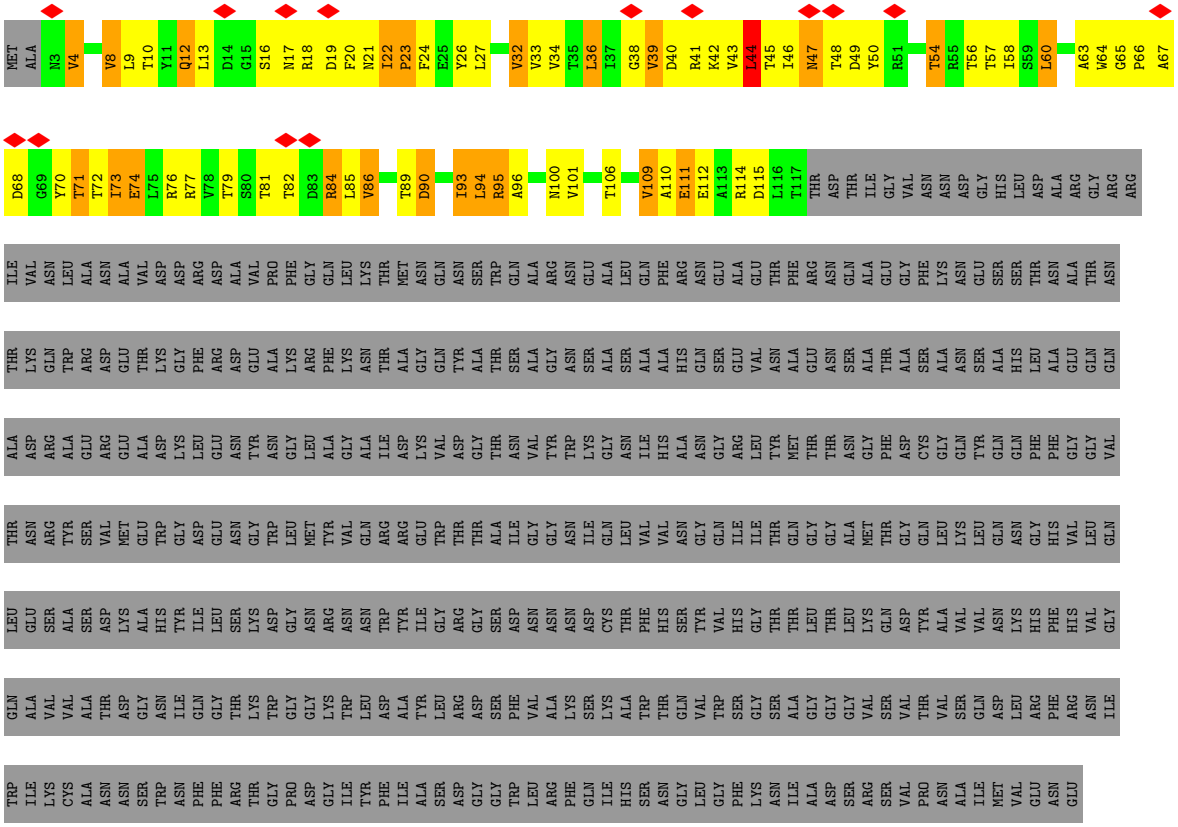
• Molecule 1: Tail fiber protein

Chain j:



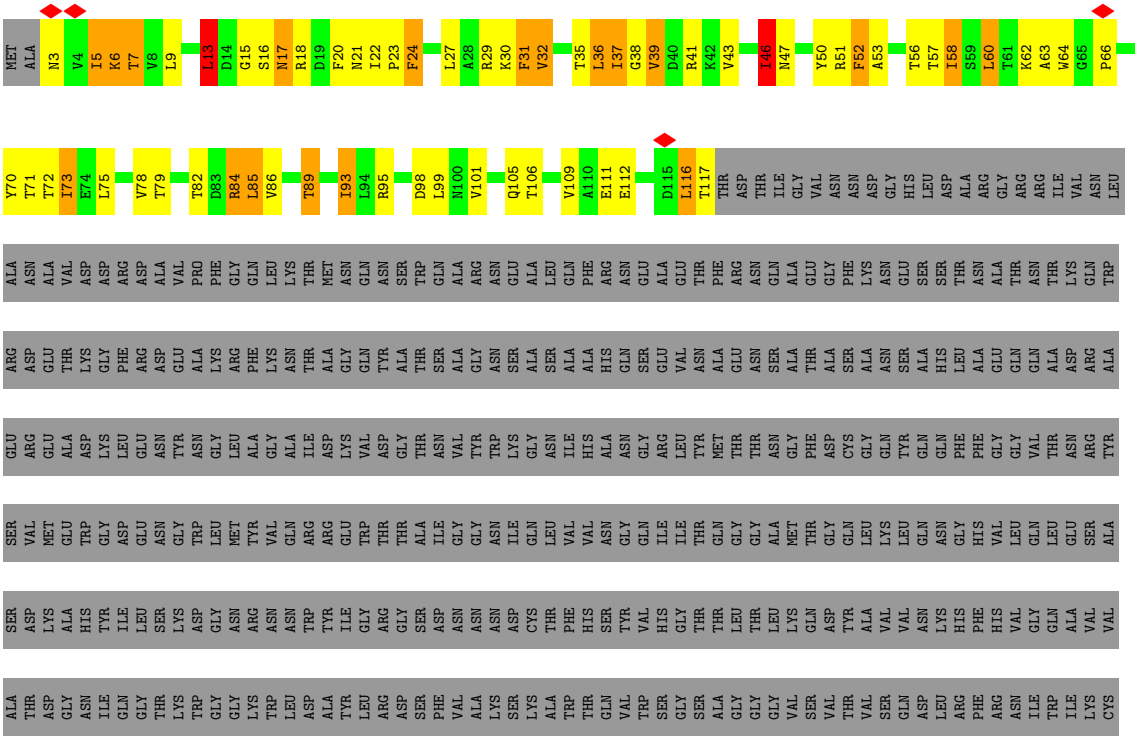
• Molecule 1: Tail fiber protein

Chain k:



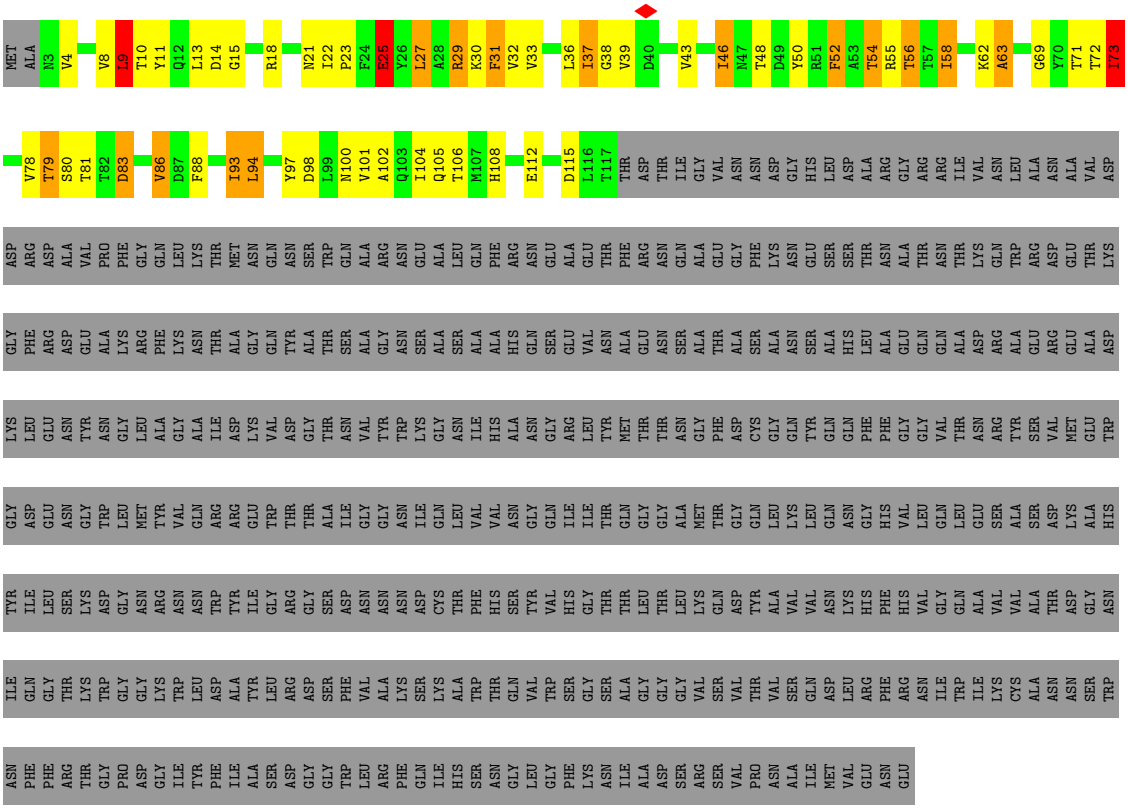
• Molecule 1: Tail fiber protein

Chain l:



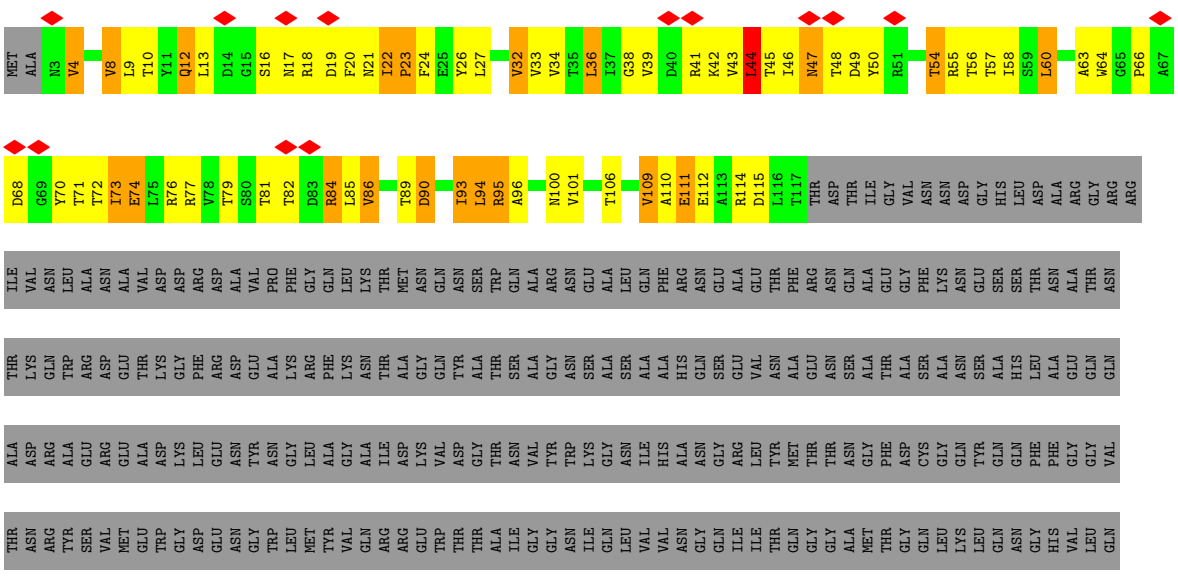
• Molecule 1: Tail fiber protein

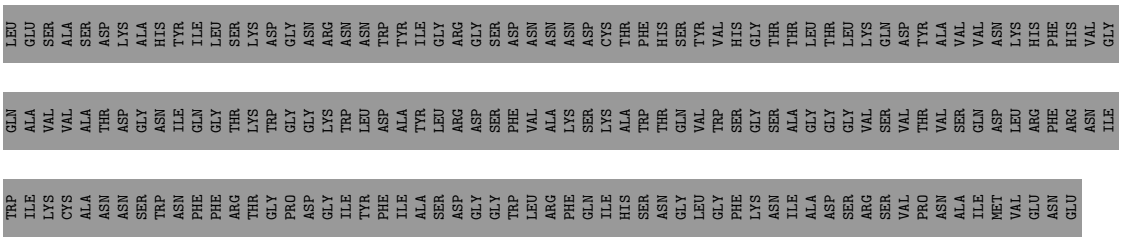
Chain m:



• Molecule 1: Tail fiber protein

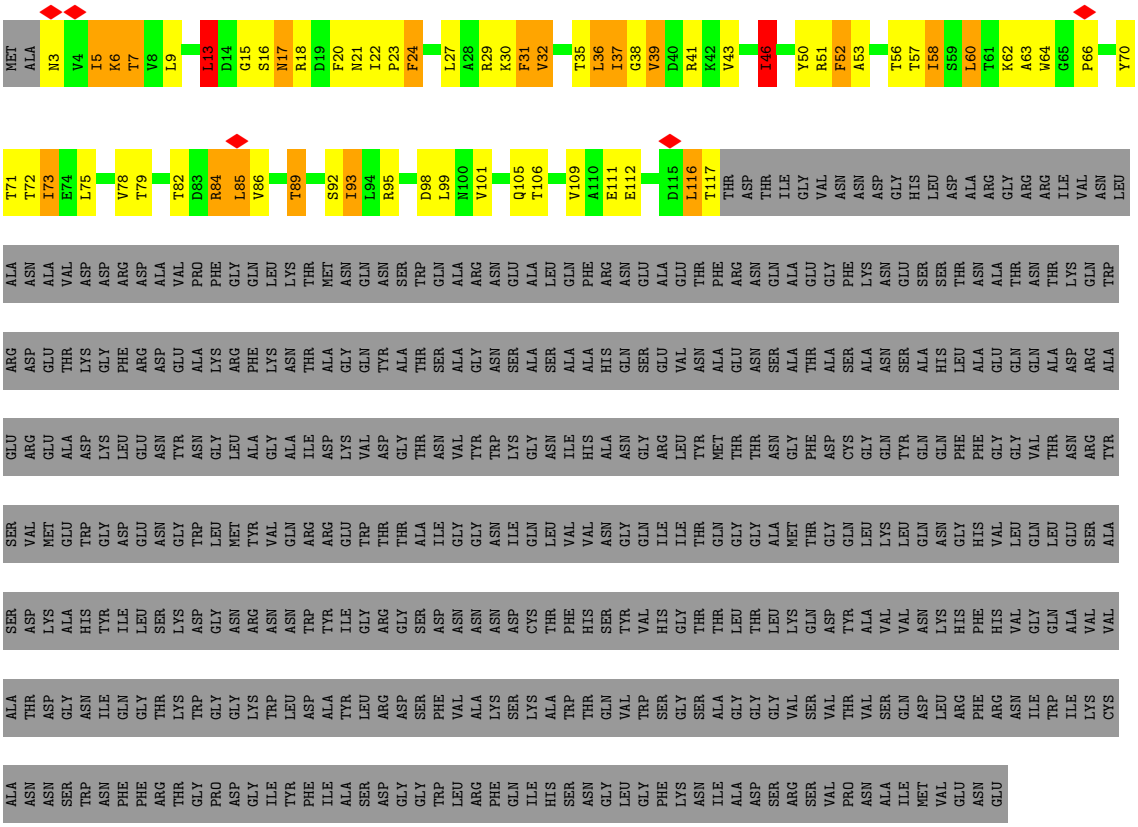
Chain n:





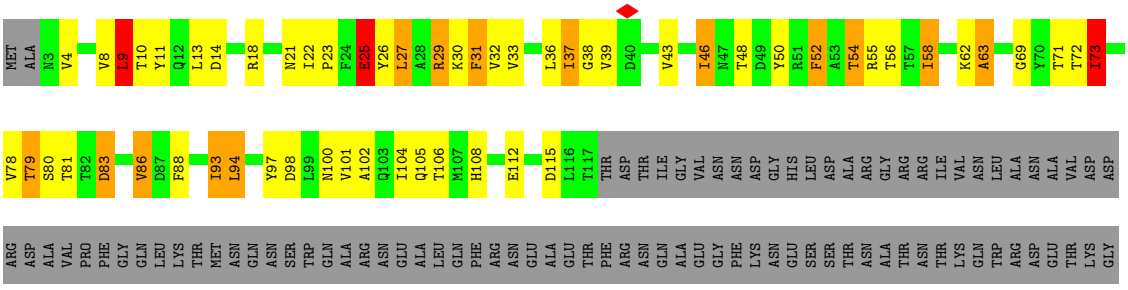
• Molecule 1: Tail fiber protein

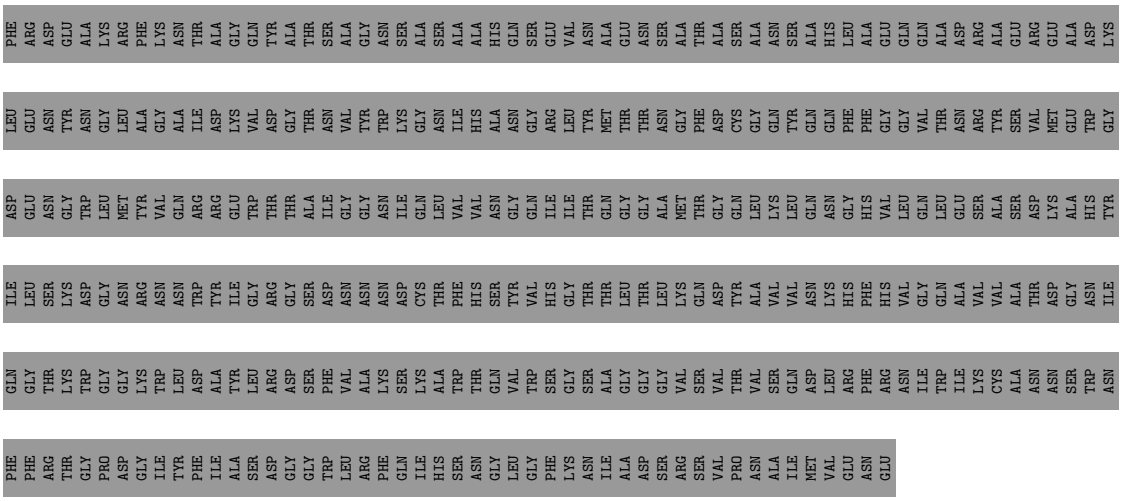
Chain o:



• Molecule 1: Tail fiber protein

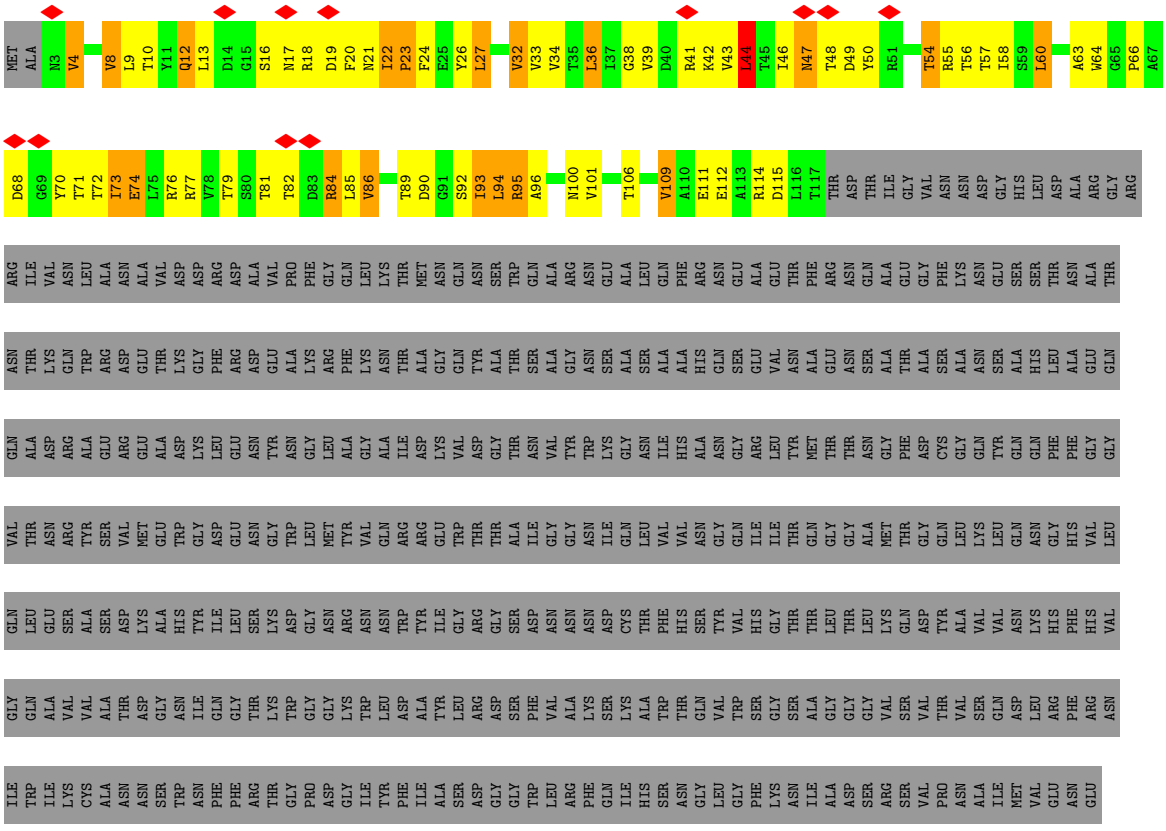
Chain p:





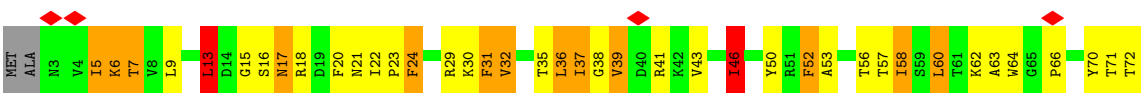
• Molecule 1: Tail fiber protein

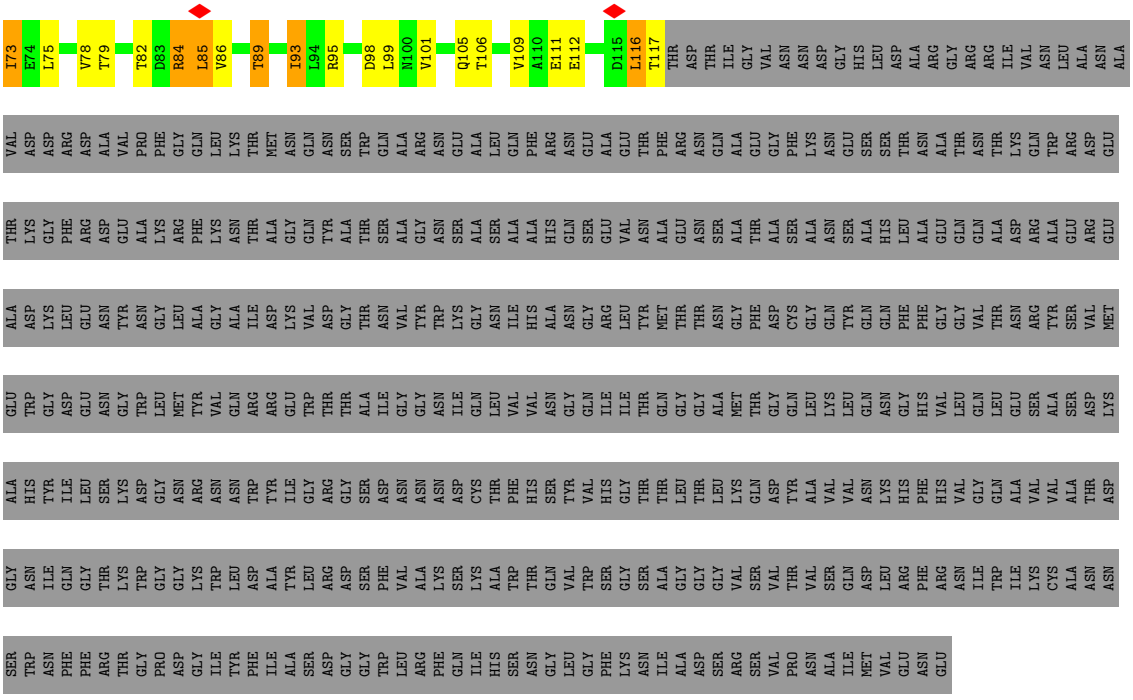
Chain q:



• Molecule 1: Tail fiber protein

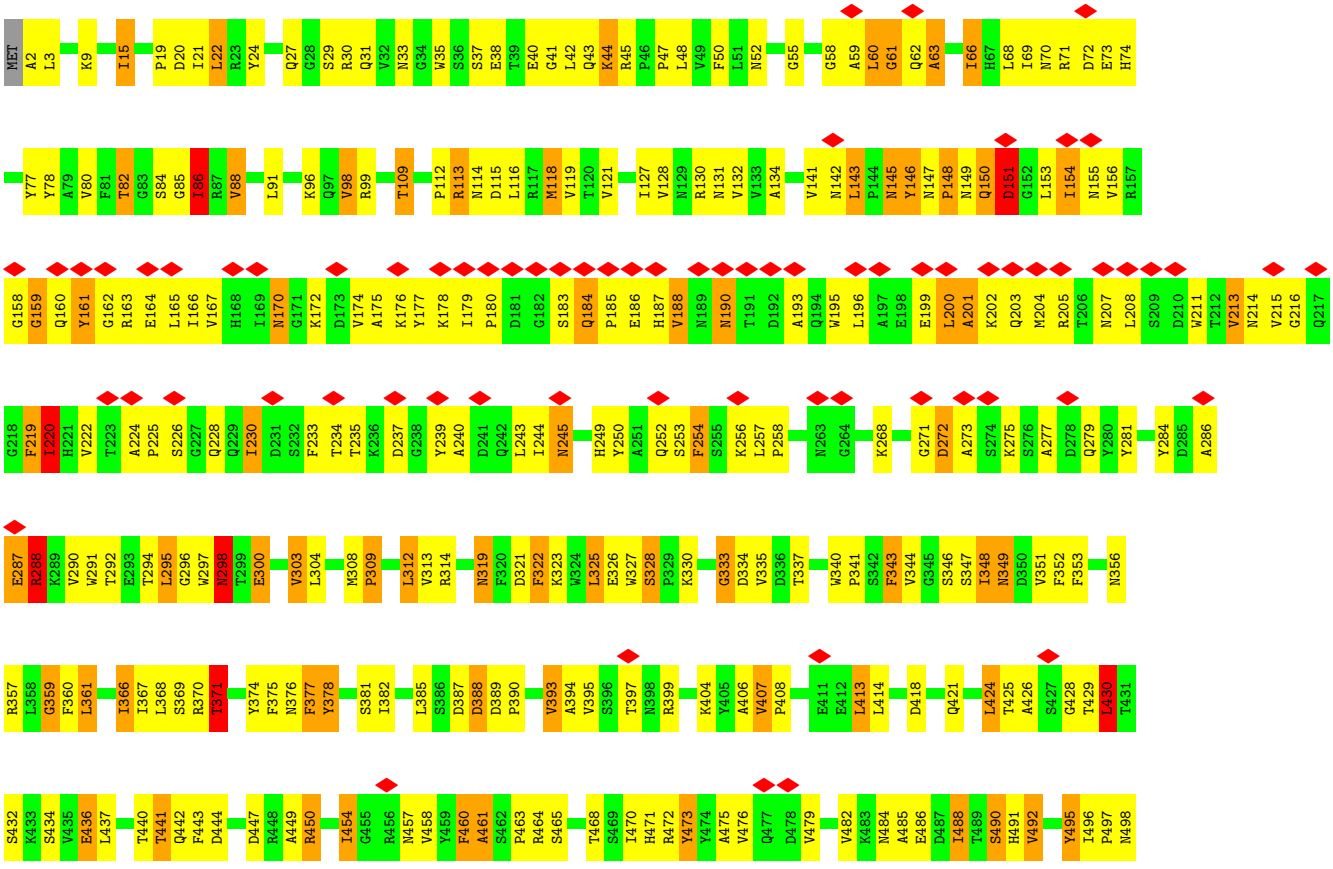
Chain r:

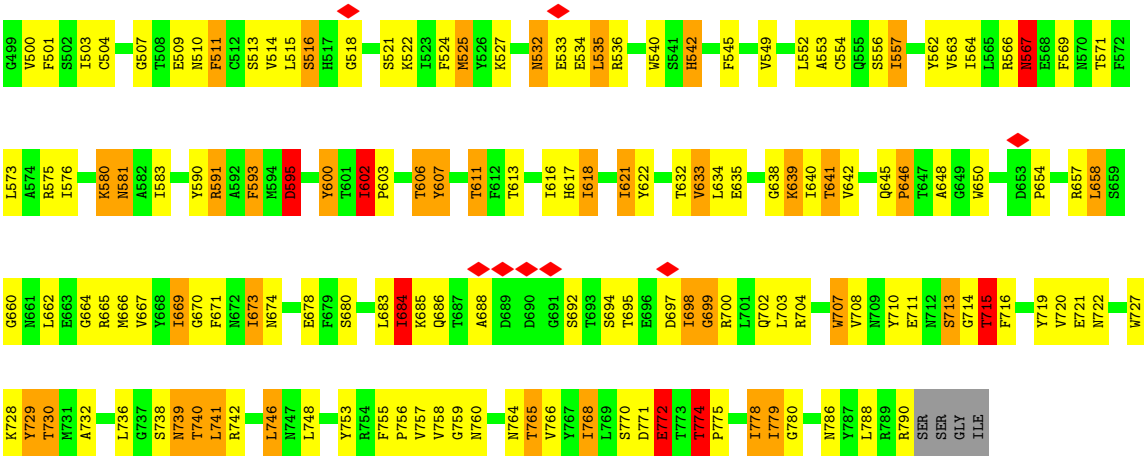




• Molecule 2: Tail tubular protein gp12

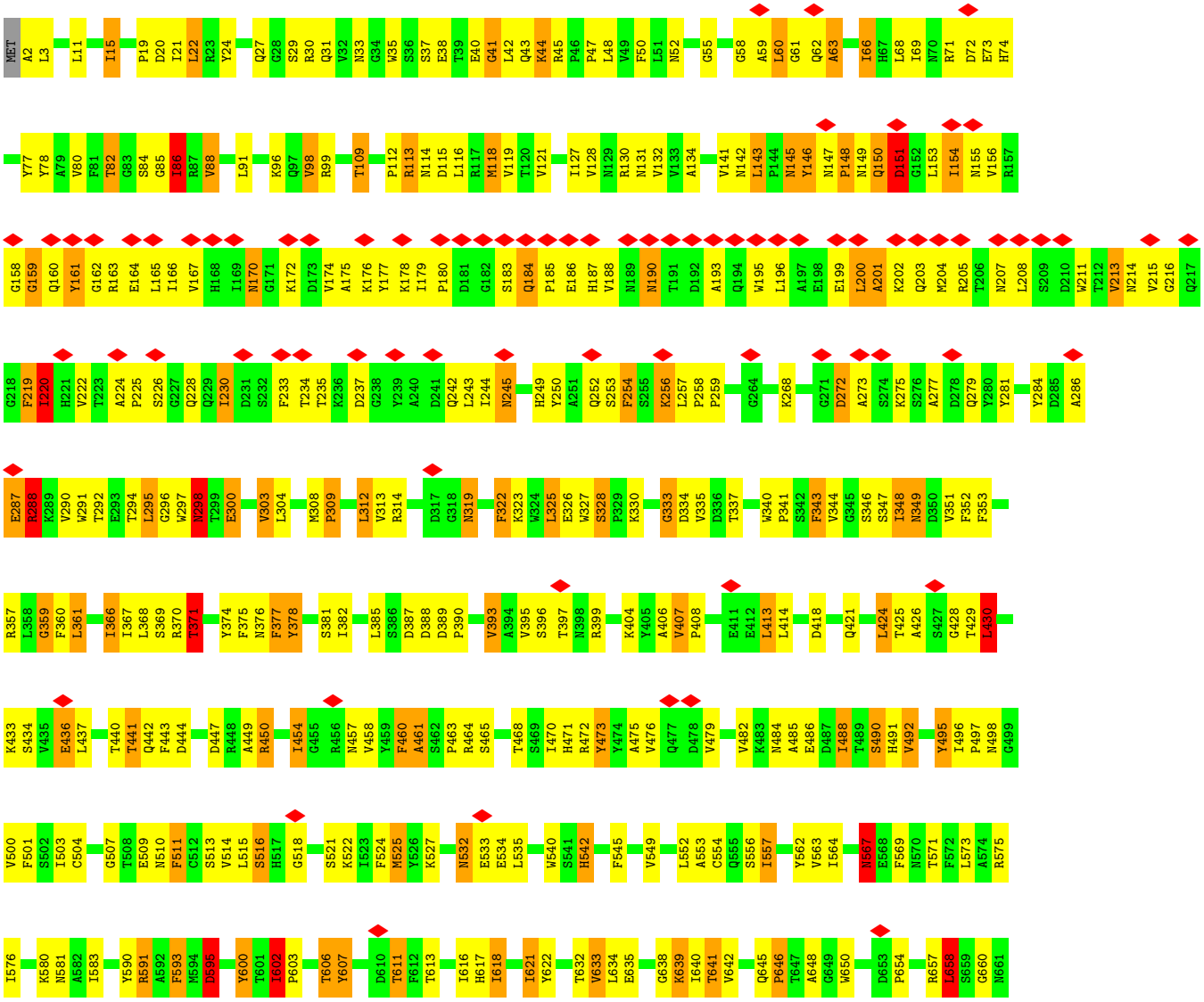
Chain s:

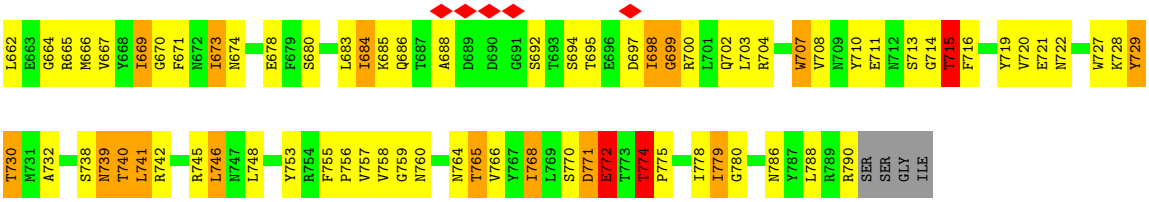




• Molecule 2: Tail tubular protein gp12

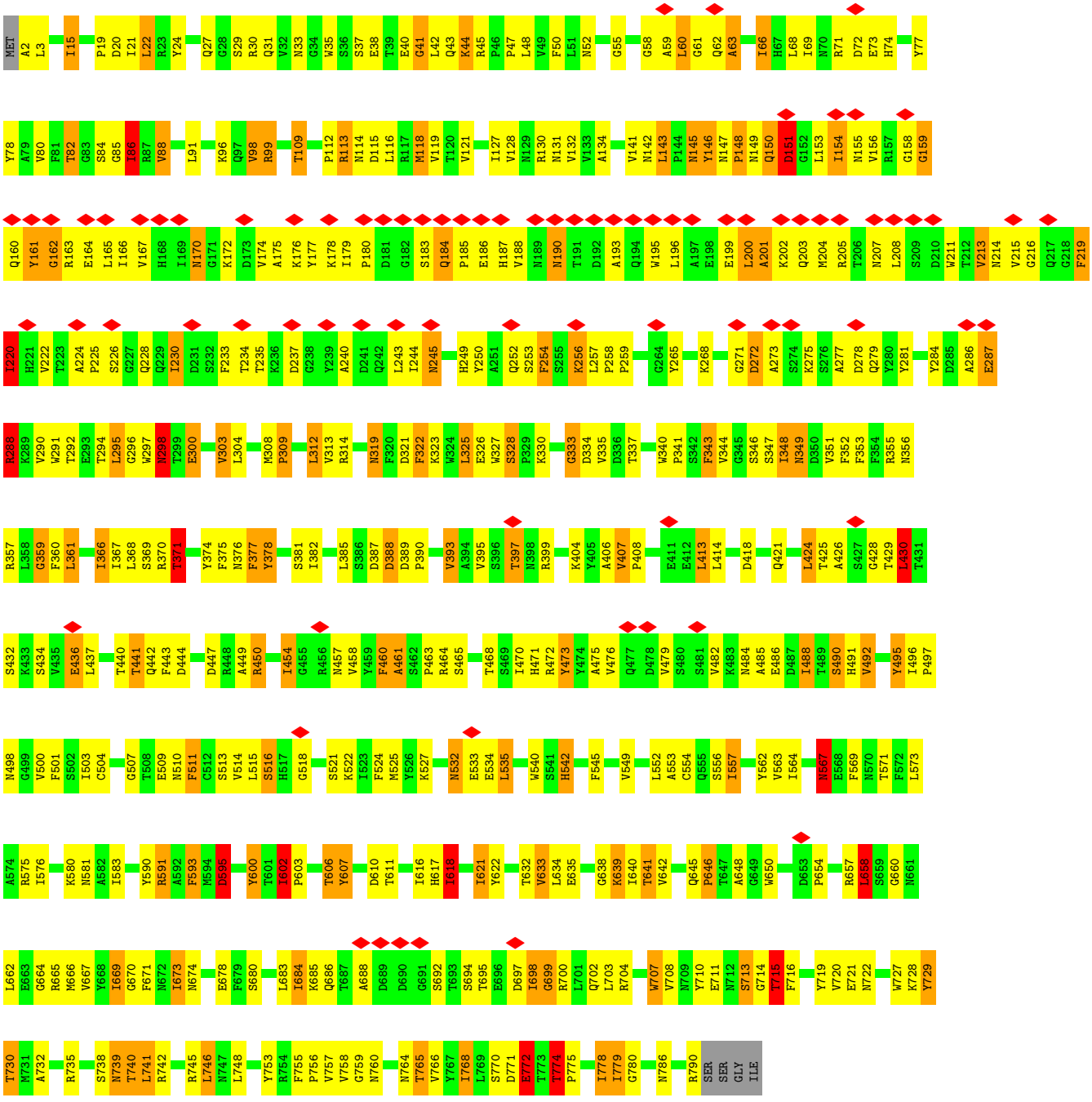
Chain t:





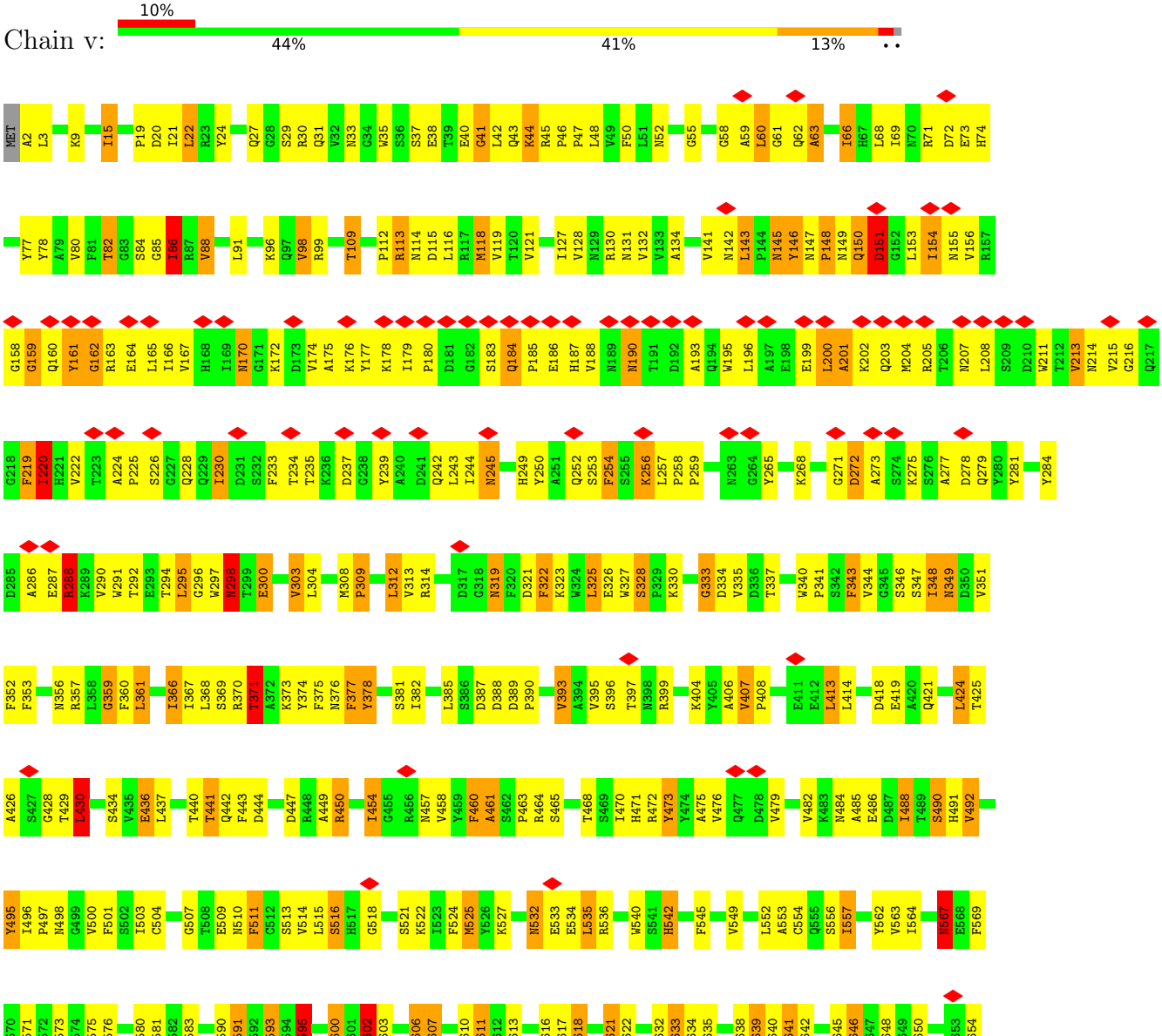
• Molecule 2: Tail tubular protein gp12

Chain u:



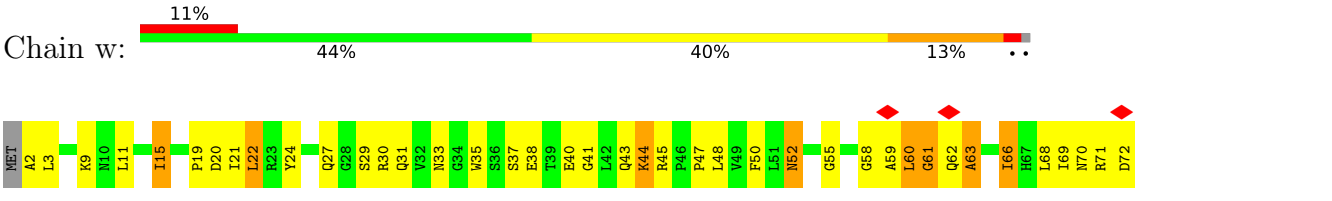
• Molecule 2: Tail tubular protein gp12

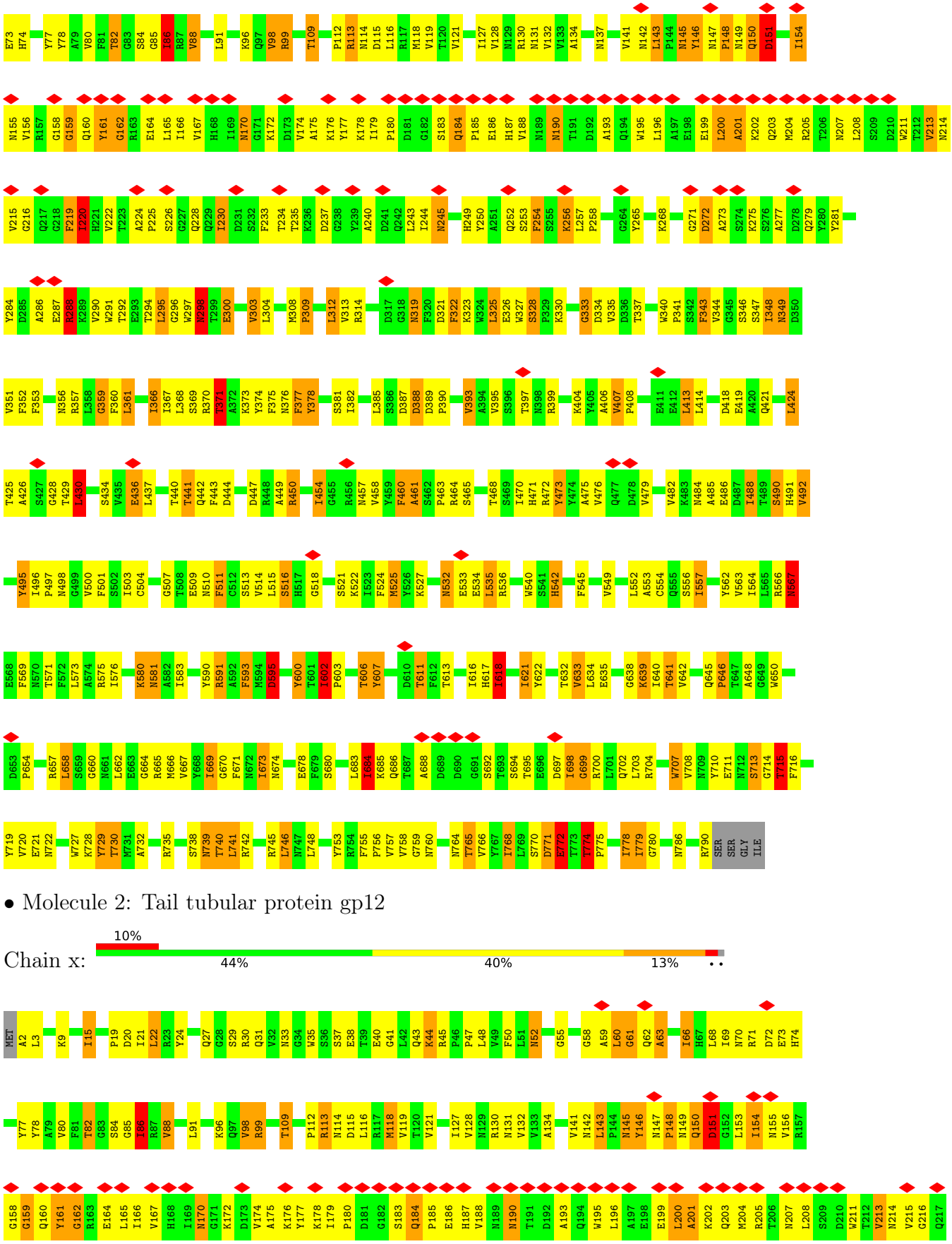
Chain v:



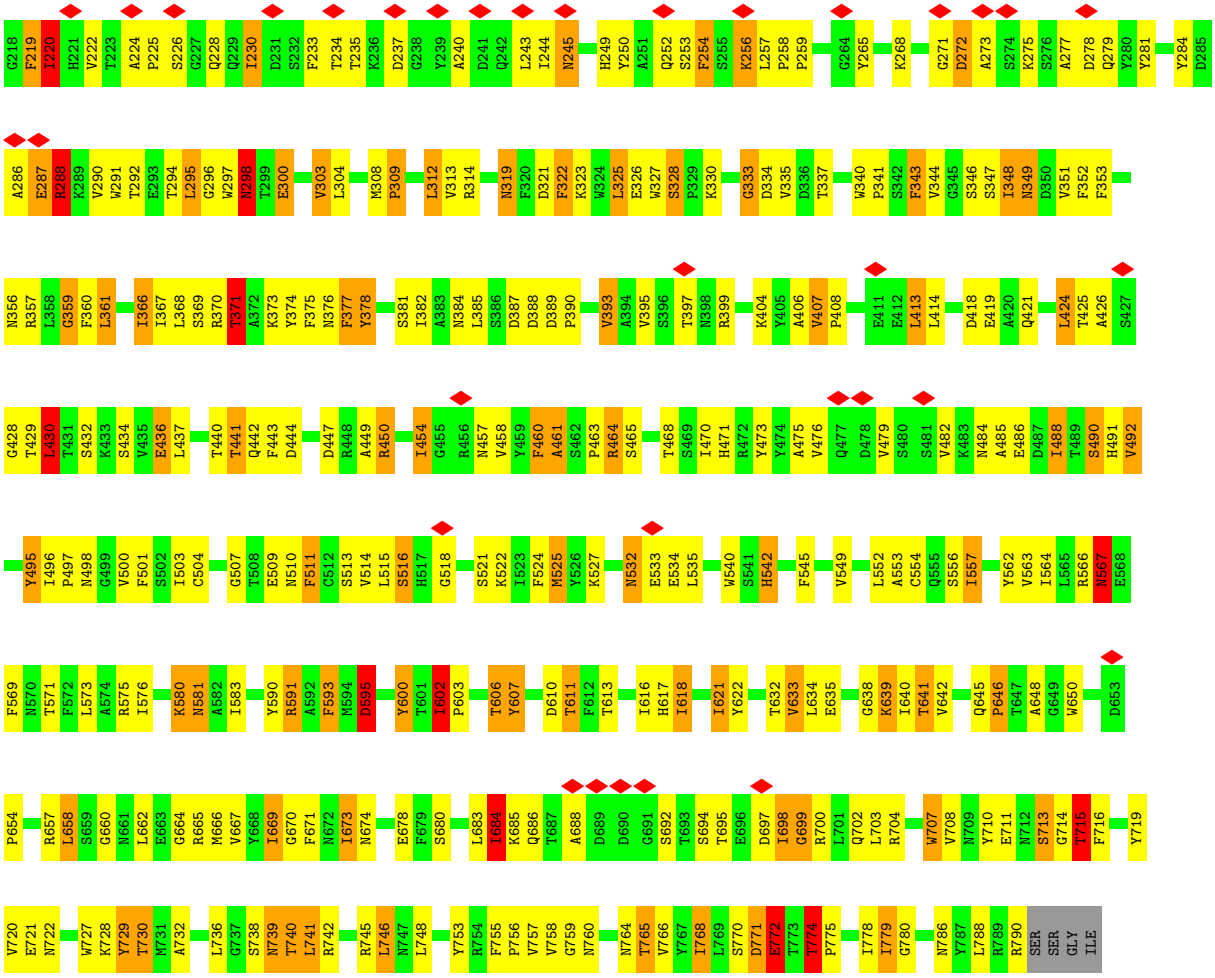
• Molecule 2: Tail tubular protein gp12

Chain w:

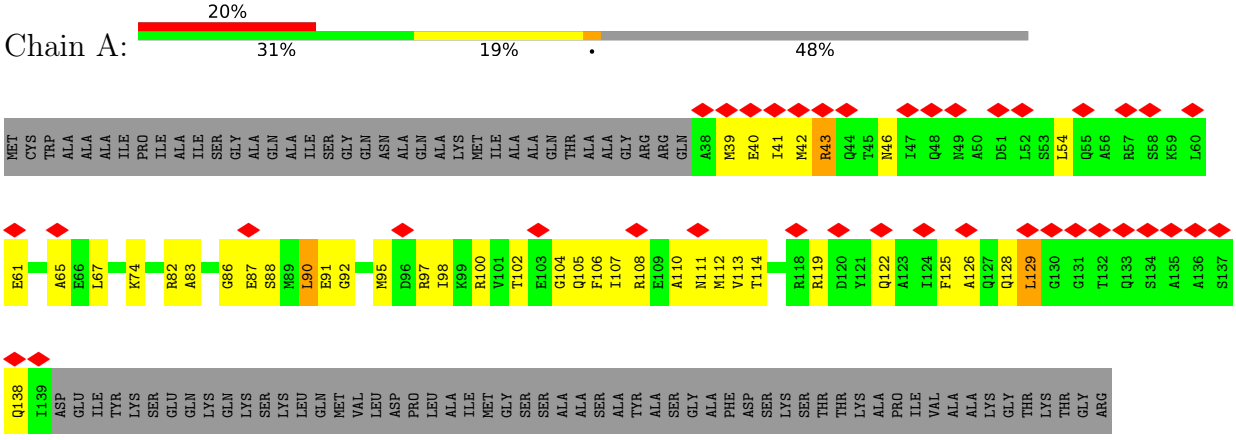




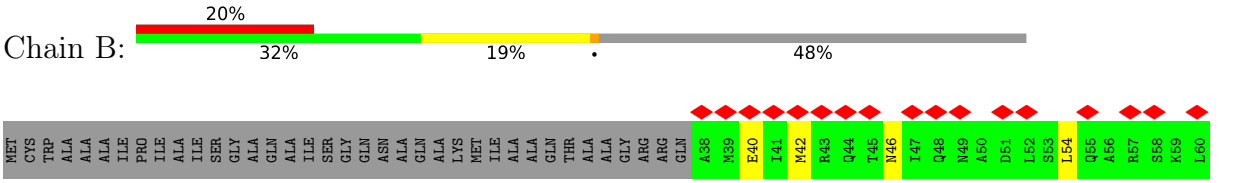
• Molecule 2: Tail tubular protein gp12

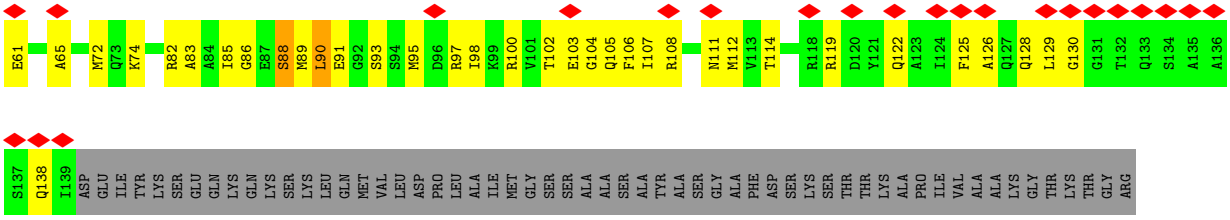


• Molecule 3: Internal virion protein gp14

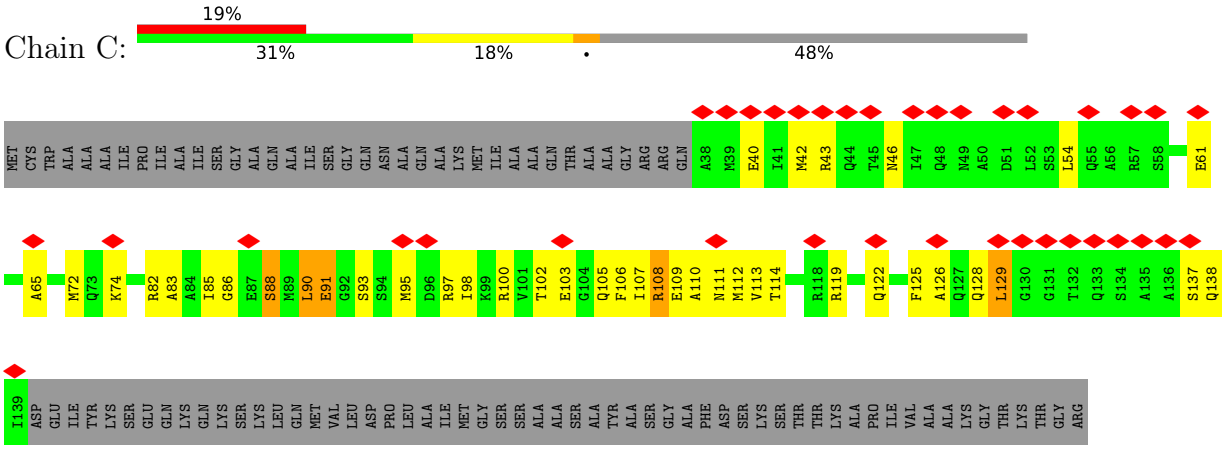


• Molecule 3: Internal virion protein gp14

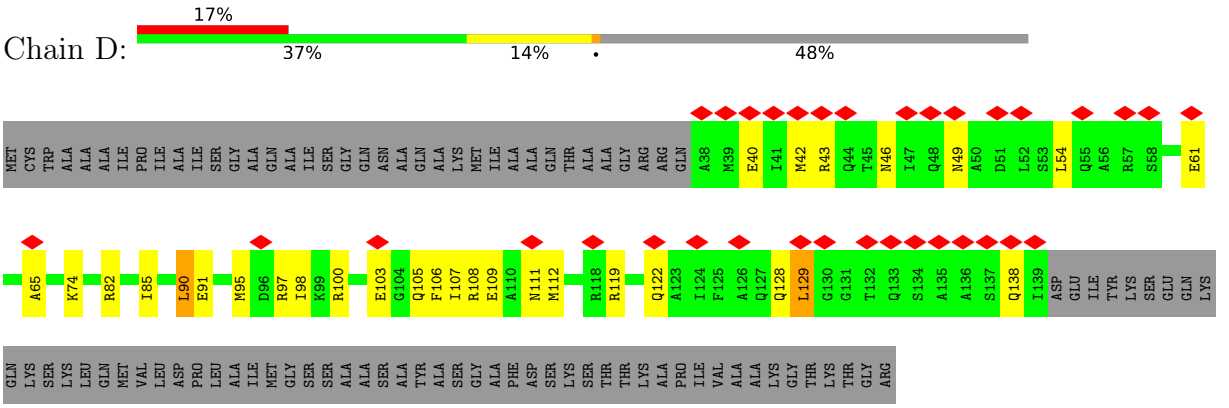




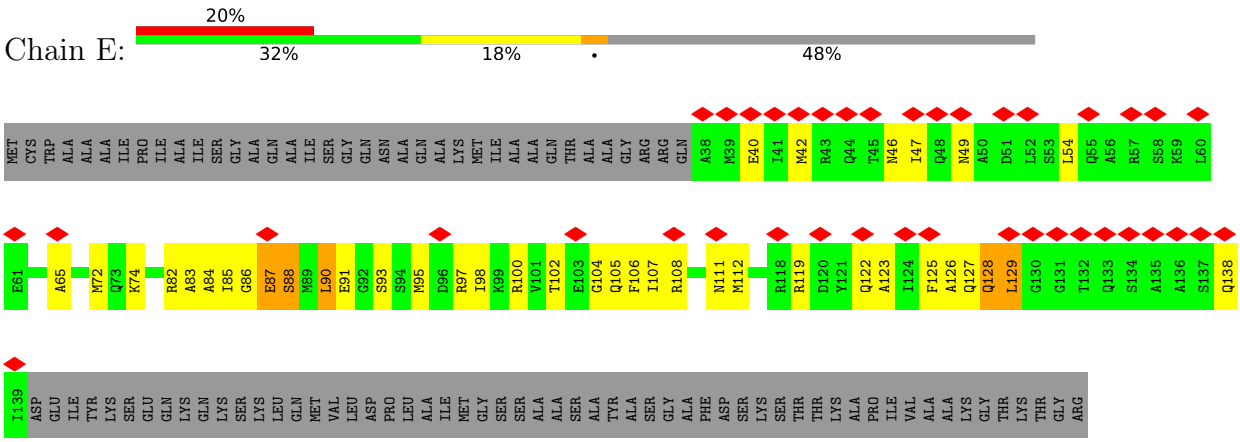
• Molecule 3: Internal virion protein gp14



• Molecule 3: Internal virion protein gp14

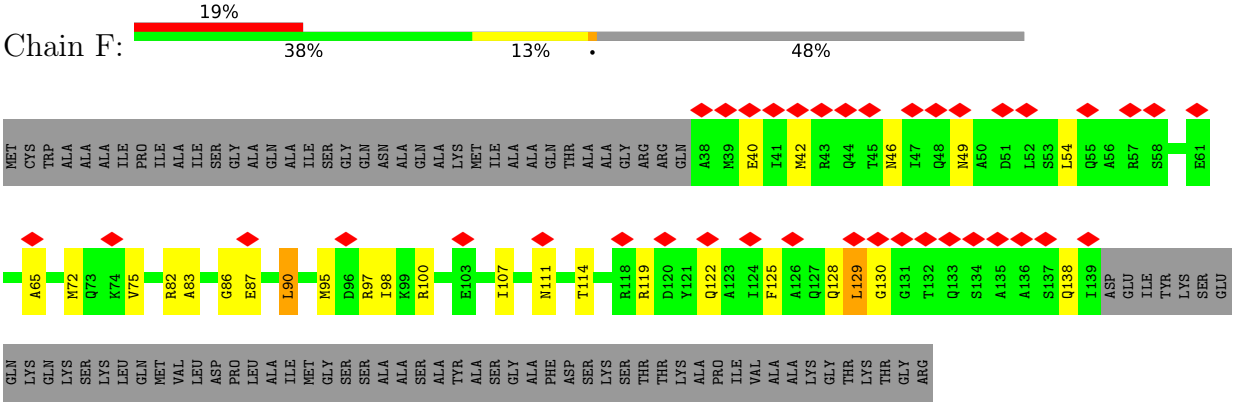


• Molecule 3: Internal virion protein gp14



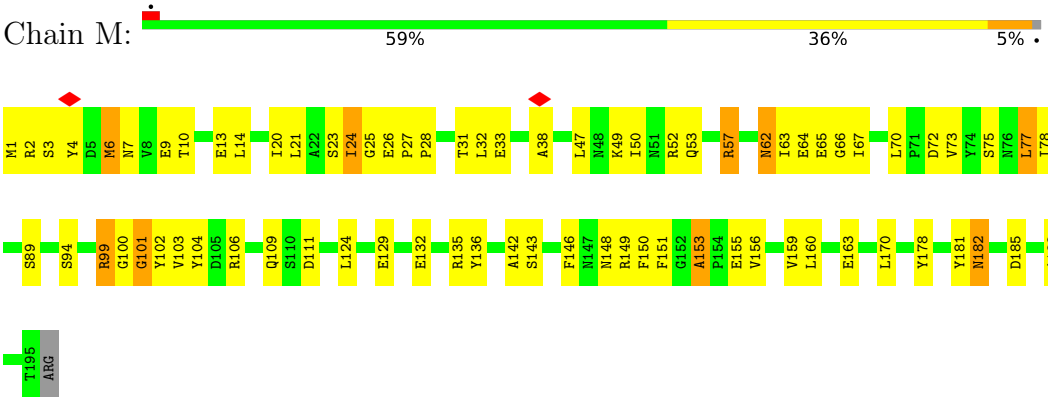
• Molecule 3: Internal virion protein gp14

Chain F:



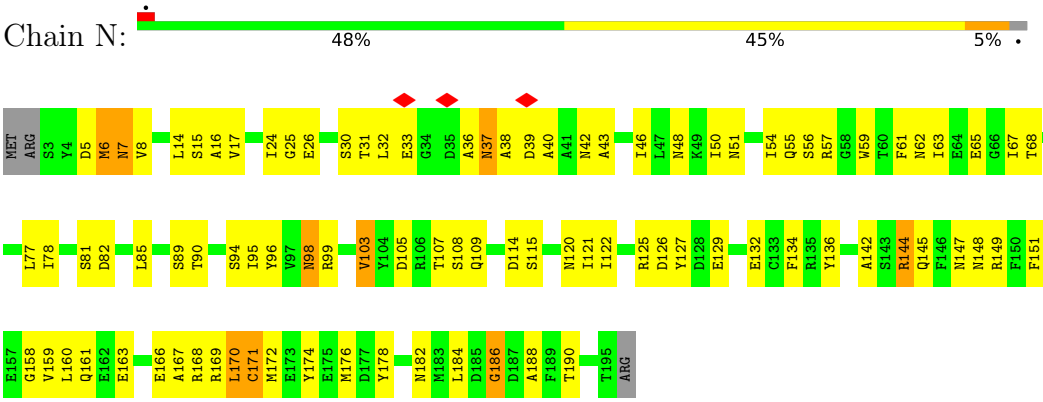
• Molecule 4: Tail tubular protein gp11

Chain M:



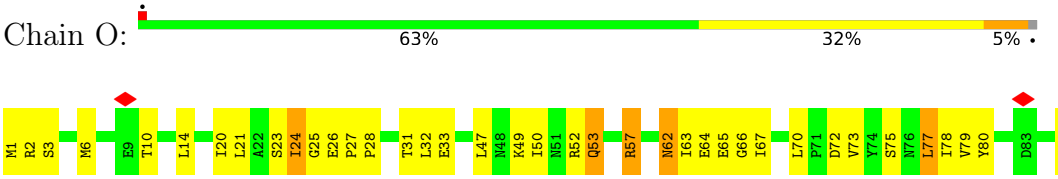
• Molecule 4: Tail tubular protein gp11

Chain N:



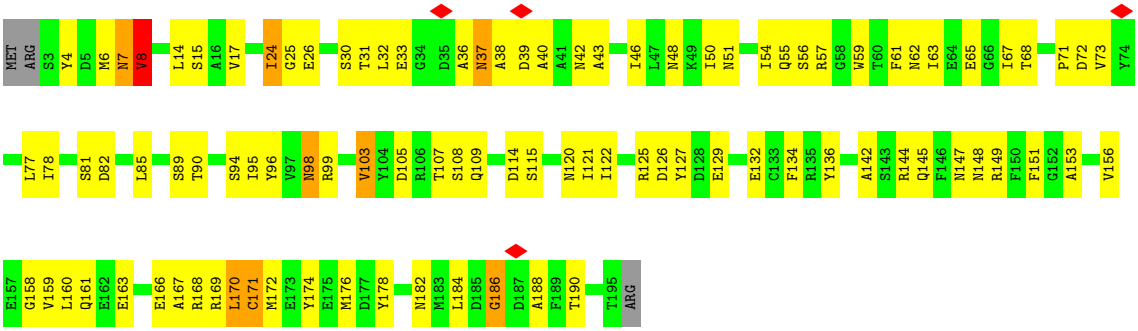
• Molecule 4: Tail tubular protein gp11

Chain O:



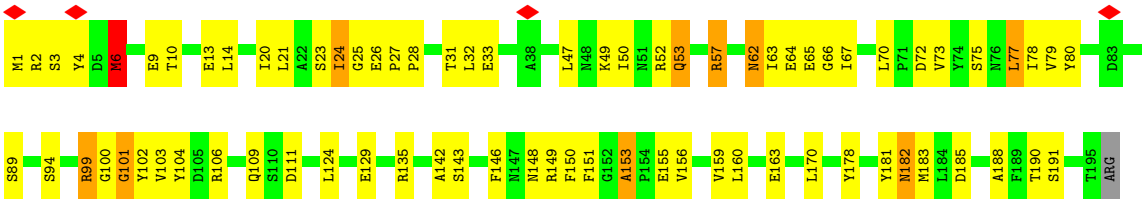
• Molecule 4: Tail tubular protein gp11

Chain P:



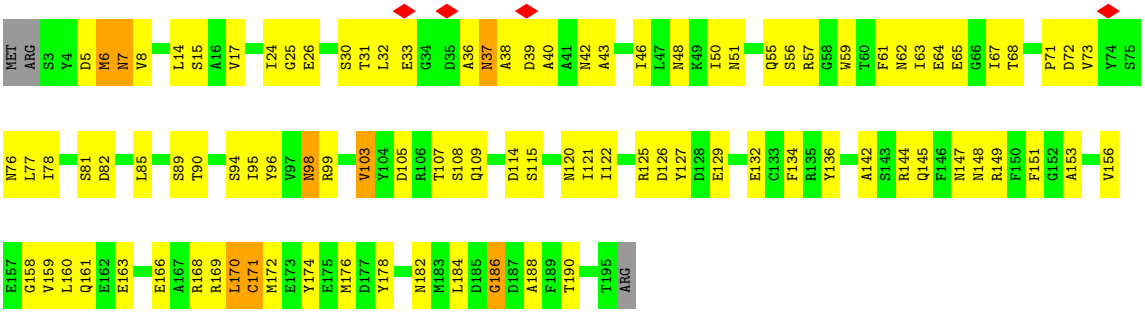
• Molecule 4: Tail tubular protein gp11

Chain Q:



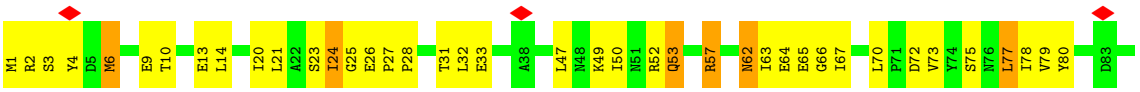
• Molecule 4: Tail tubular protein gp11

Chain R:



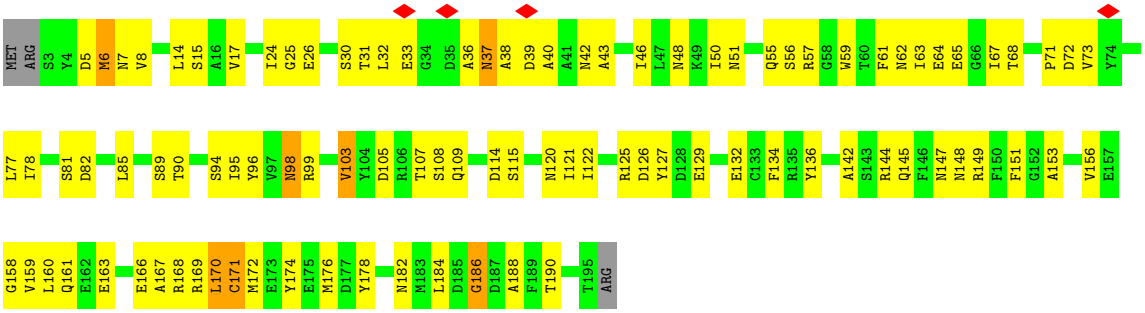
• Molecule 4: Tail tubular protein gp11

Chain S:



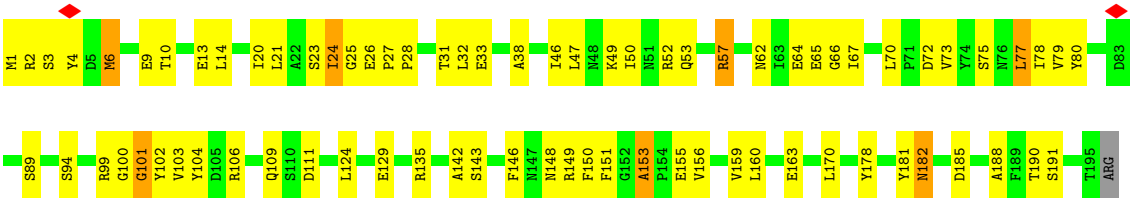
• Molecule 4: Tail tubular protein gp11

Chain T:



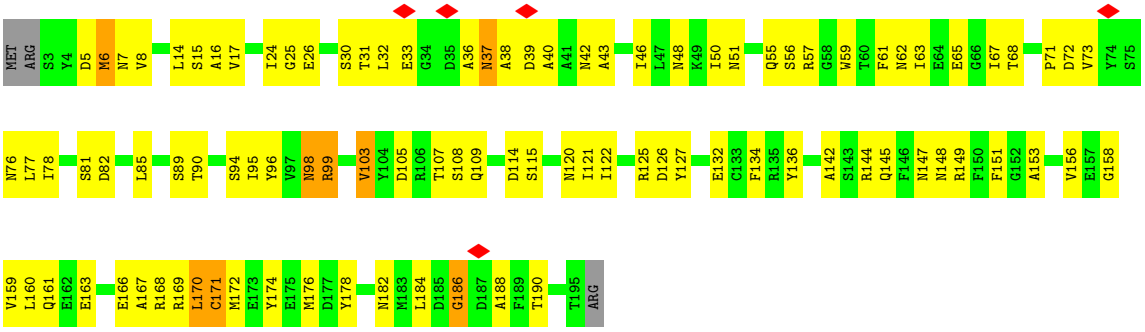
• Molecule 4: Tail tubular protein gp11

Chain U:



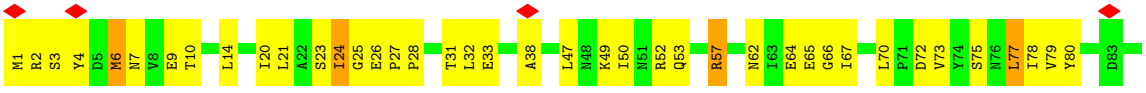
• Molecule 4: Tail tubular protein gp11

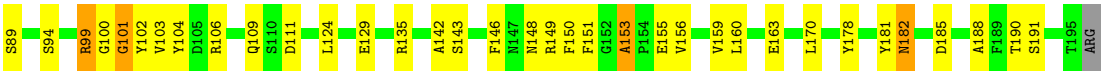
Chain V:



• Molecule 4: Tail tubular protein gp11

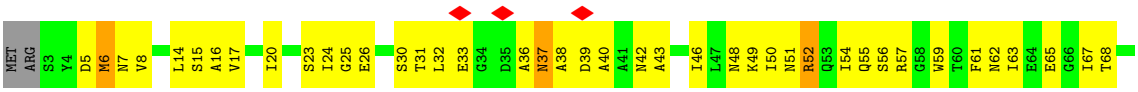
Chain W:

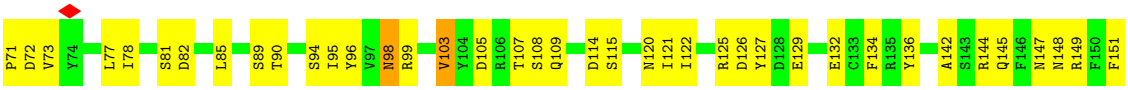




• Molecule 4: Tail tubular protein gp11

Chain X:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	59985	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 ($e^-/Å^2$)	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	43.195	Depositor
Minimum map value	-27.980	Depositor
Average map value	0.013	Depositor
Map value standard deviation	2.048	Depositor
Recommended contour level	8	Depositor
Map size (Å)	508.0, 508.0, 508.0	wwPDB
Map dimensions	400, 400, 400	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	1.23	3/936 (0.3%)	1.47	20/1274 (1.6%)
1	b	1.21	1/936 (0.1%)	1.63	31/1274 (2.4%)
1	c	1.13	2/936 (0.2%)	1.51	19/1274 (1.5%)
1	d	1.22	3/936 (0.3%)	1.45	20/1274 (1.6%)
1	e	1.22	1/936 (0.1%)	1.63	29/1274 (2.3%)
1	f	1.14	2/936 (0.2%)	1.51	19/1274 (1.5%)
1	g	1.23	3/936 (0.3%)	1.47	20/1274 (1.6%)
1	h	1.22	1/936 (0.1%)	1.63	31/1274 (2.4%)
1	i	1.14	2/936 (0.2%)	1.51	20/1274 (1.6%)
1	j	1.22	4/936 (0.4%)	1.45	20/1274 (1.6%)
1	k	1.21	1/936 (0.1%)	1.63	31/1274 (2.4%)
1	l	1.14	2/936 (0.2%)	1.51	19/1274 (1.5%)
1	m	1.23	3/936 (0.3%)	1.46	20/1274 (1.6%)
1	n	1.22	1/936 (0.1%)	1.63	30/1274 (2.4%)
1	o	1.14	2/936 (0.2%)	1.54	21/1274 (1.6%)
1	p	1.23	4/936 (0.4%)	1.46	19/1274 (1.5%)
1	q	1.22	1/936 (0.1%)	1.63	30/1274 (2.4%)
1	r	1.13	3/936 (0.3%)	1.54	21/1274 (1.6%)
2	s	1.20	20/6449 (0.3%)	1.55	152/8772 (1.7%)
2	t	1.20	21/6449 (0.3%)	1.55	151/8772 (1.7%)
2	u	1.20	20/6449 (0.3%)	1.55	155/8772 (1.8%)
2	v	1.20	21/6449 (0.3%)	1.55	152/8772 (1.7%)
2	w	1.20	21/6449 (0.3%)	1.55	155/8772 (1.8%)
2	x	1.20	22/6449 (0.3%)	1.56	154/8772 (1.8%)
3	A	0.37	0/790	0.68	2/1056 (0.2%)
3	B	0.33	0/790	0.62	2/1056 (0.2%)
3	C	0.38	0/790	0.68	2/1056 (0.2%)
3	D	0.36	0/790	0.63	1/1056 (0.1%)
3	E	0.40	0/790	0.75	3/1056 (0.3%)
3	F	0.38	0/790	0.67	1/1056 (0.1%)
4	M	0.72	1/1580 (0.1%)	1.08	15/2139 (0.7%)
4	N	0.61	0/1561	0.96	8/2115 (0.4%)
4	O	0.72	1/1580 (0.1%)	1.05	12/2139 (0.6%)
4	P	0.60	0/1561	0.96	9/2115 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
4	Q	0.72	1/1580 (0.1%)	1.08	15/2139 (0.7%)
4	R	0.61	0/1561	0.96	9/2115 (0.4%)
4	S	0.73	1/1580 (0.1%)	1.07	13/2139 (0.6%)
4	T	0.61	0/1561	0.96	9/2115 (0.4%)
4	U	0.72	1/1580 (0.1%)	1.07	14/2139 (0.7%)
4	V	0.60	0/1561	0.95	8/2115 (0.4%)
4	W	0.72	1/1580 (0.1%)	1.07	15/2139 (0.7%)
4	X	0.60	0/1561	0.96	8/2115 (0.4%)
All	All	1.06	170/79128 (0.2%)	1.40	1485/107424 (1.4%)

All (170) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Q	99	ARG	CA-C	-6.99	1.46	1.53
4	O	99	ARG	CA-C	-6.98	1.46	1.53
4	M	99	ARG	CA-C	-6.97	1.46	1.53
4	S	99	ARG	CA-C	-6.97	1.46	1.53
4	U	99	ARG	CA-C	-6.97	1.46	1.53
4	W	99	ARG	CA-C	-6.95	1.46	1.53
2	t	753	TYR	CA-C	-6.79	1.44	1.52
2	t	71	ARG	CA-C	-6.79	1.44	1.52
2	v	753	TYR	CA-C	-6.79	1.44	1.52
2	s	71	ARG	CA-C	-6.76	1.44	1.52
2	v	71	ARG	CA-C	-6.76	1.44	1.52
2	u	71	ARG	CA-C	-6.75	1.44	1.52
2	x	71	ARG	CA-C	-6.74	1.44	1.52
2	w	71	ARG	CA-C	-6.74	1.44	1.52
2	t	720	VAL	CA-C	-6.74	1.44	1.52
2	u	753	TYR	CA-C	-6.72	1.44	1.52
2	x	753	TYR	CA-C	-6.72	1.44	1.52
2	s	753	TYR	CA-C	-6.71	1.44	1.52
2	u	720	VAL	CA-C	-6.70	1.44	1.52
2	w	753	TYR	CA-C	-6.70	1.44	1.52
2	v	720	VAL	CA-C	-6.70	1.44	1.52
2	x	720	VAL	CA-C	-6.69	1.44	1.52
2	s	720	VAL	CA-C	-6.61	1.44	1.52
2	w	720	VAL	CA-C	-6.60	1.44	1.52
1	f	84	ARG	CA-C	-6.60	1.44	1.52
1	r	84	ARG	CA-C	-6.56	1.44	1.52
1	i	84	ARG	CA-C	-6.54	1.44	1.52
1	o	84	ARG	CA-C	-6.52	1.44	1.52
1	l	84	ARG	CA-C	-6.50	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	x	684	ILE	CA-C	-6.47	1.45	1.52
1	c	84	ARG	CA-C	-6.46	1.44	1.52
2	u	684	ILE	CA-C	-6.42	1.45	1.52
2	t	684	ILE	CA-C	-6.41	1.45	1.52
2	w	684	ILE	CA-C	-6.41	1.45	1.52
2	v	684	ILE	CA-C	-6.39	1.45	1.52
2	s	684	ILE	CA-C	-6.27	1.46	1.52
1	f	105	GLN	CA-C	-6.12	1.45	1.52
1	c	105	GLN	CA-C	-6.09	1.45	1.52
1	l	105	GLN	CA-C	-6.09	1.45	1.52
1	i	105	GLN	CA-C	-6.09	1.45	1.52
1	o	105	GLN	CA-C	-6.06	1.45	1.52
1	r	105	GLN	CA-C	-6.03	1.45	1.52
2	t	719	TYR	CA-C	-5.88	1.45	1.52
2	u	719	TYR	CA-C	-5.87	1.45	1.52
2	s	719	TYR	CA-C	-5.86	1.45	1.52
2	v	719	TYR	CA-C	-5.84	1.45	1.52
2	x	719	TYR	CA-C	-5.84	1.45	1.52
2	w	719	TYR	CA-C	-5.82	1.45	1.52
2	x	774	THR	CA-C	-5.80	1.46	1.52
2	u	774	THR	CA-C	-5.77	1.46	1.52
2	s	774	THR	CA-C	-5.74	1.46	1.52
2	t	774	THR	CA-C	-5.74	1.46	1.52
2	v	774	THR	CA-C	-5.73	1.46	1.52
2	w	774	THR	CA-C	-5.71	1.46	1.52
2	w	424	LEU	CA-C	-5.71	1.45	1.52
2	v	424	LEU	CA-C	-5.69	1.45	1.52
2	s	424	LEU	CA-C	-5.66	1.45	1.52
2	w	450	ARG	CA-C	-5.66	1.45	1.52
2	s	450	ARG	CA-C	-5.65	1.45	1.52
2	v	450	ARG	CA-C	-5.65	1.45	1.52
2	u	450	ARG	CA-C	-5.65	1.45	1.52
2	x	450	ARG	CA-C	-5.65	1.45	1.52
2	u	473	TYR	CA-C	-5.64	1.45	1.52
2	s	63	ALA	C-O	-5.64	1.21	1.23
2	t	450	ARG	CA-C	-5.64	1.45	1.52
2	u	424	LEU	CA-C	-5.62	1.46	1.52
2	v	473	TYR	CA-C	-5.62	1.45	1.52
2	t	424	LEU	CA-C	-5.62	1.46	1.52
2	x	424	LEU	CA-C	-5.61	1.46	1.52
2	x	554	CYS	CA-C	-5.61	1.46	1.52
1	g	14	ASP	CA-C	-5.60	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	s	554	CYS	CA-C	-5.60	1.46	1.52
2	t	473	TYR	CA-C	-5.59	1.45	1.52
2	w	473	TYR	CA-C	-5.59	1.45	1.52
2	s	473	TYR	CA-C	-5.58	1.45	1.52
2	x	473	TYR	CA-C	-5.58	1.45	1.52
2	u	554	CYS	CA-C	-5.58	1.46	1.52
1	e	16	SER	CA-C	-5.57	1.46	1.52
2	u	63	ALA	C-O	-5.57	1.21	1.23
2	u	770	SER	CA-C	-5.57	1.45	1.52
2	t	770	SER	CA-C	-5.56	1.45	1.52
2	w	770	SER	CA-C	-5.56	1.45	1.52
1	a	14	ASP	CA-C	-5.55	1.45	1.52
2	s	770	SER	CA-C	-5.54	1.45	1.52
2	v	770	SER	CA-C	-5.54	1.45	1.52
1	d	14	ASP	CA-C	-5.54	1.45	1.52
2	u	31	GLN	CA-C	-5.53	1.45	1.52
2	x	31	GLN	CA-C	-5.53	1.45	1.52
1	p	14	ASP	CA-C	-5.53	1.45	1.52
2	t	325	LEU	CA-C	-5.53	1.45	1.52
2	t	63	ALA	C-O	-5.52	1.21	1.23
2	w	63	ALA	C-O	-5.52	1.21	1.23
2	t	31	GLN	CA-C	-5.52	1.45	1.52
2	v	325	LEU	CA-C	-5.52	1.45	1.52
2	v	31	GLN	CA-C	-5.51	1.45	1.52
1	j	14	ASP	CA-C	-5.51	1.45	1.52
2	w	567	ASN	CA-C	-5.50	1.45	1.53
2	v	554	CYS	CA-C	-5.50	1.46	1.52
2	x	63	ALA	C-O	-5.50	1.21	1.23
2	w	325	LEU	CA-C	-5.50	1.45	1.52
2	x	325	LEU	CA-C	-5.50	1.45	1.52
1	g	9	LEU	CA-C	-5.49	1.46	1.52
2	t	567	ASN	CA-C	-5.49	1.45	1.53
2	u	325	LEU	CA-C	-5.49	1.45	1.52
2	v	567	ASN	CA-C	-5.49	1.45	1.53
1	p	9	LEU	CA-C	-5.49	1.46	1.52
2	s	45	ARG	CA-C	-5.49	1.47	1.53
2	u	567	ASN	CA-C	-5.49	1.45	1.53
2	t	554	CYS	CA-C	-5.49	1.46	1.52
2	w	554	CYS	CA-C	-5.49	1.46	1.52
1	m	14	ASP	CA-C	-5.48	1.46	1.52
2	s	567	ASN	CA-C	-5.48	1.45	1.53
1	j	9	LEU	CA-C	-5.48	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	s	325	LEU	CA-C	-5.48	1.45	1.52
2	v	63	ALA	C-O	-5.48	1.21	1.23
2	x	567	ASN	CA-C	-5.47	1.45	1.53
2	x	770	SER	CA-C	-5.47	1.46	1.52
2	x	45	ARG	CA-C	-5.47	1.47	1.53
1	d	9	LEU	CA-C	-5.46	1.46	1.52
2	u	45	ARG	CA-C	-5.46	1.47	1.53
2	v	45	ARG	CA-C	-5.46	1.47	1.53
1	q	16	SER	CA-C	-5.45	1.46	1.52
2	w	31	GLN	CA-C	-5.43	1.45	1.52
2	s	31	GLN	CA-C	-5.42	1.45	1.52
2	t	45	ARG	CA-C	-5.42	1.47	1.53
1	m	9	LEU	CA-C	-5.42	1.46	1.52
1	h	16	SER	CA-C	-5.37	1.46	1.52
2	w	45	ARG	CA-C	-5.37	1.47	1.53
1	a	9	LEU	CA-C	-5.37	1.46	1.52
1	b	16	SER	CA-C	-5.37	1.46	1.52
1	n	16	SER	CA-C	-5.35	1.46	1.52
1	k	16	SER	CA-C	-5.31	1.46	1.52
2	w	490	SER	CA-C	-5.31	1.45	1.52
2	s	490	SER	CA-C	-5.29	1.46	1.52
2	t	490	SER	CA-C	-5.29	1.46	1.52
2	u	490	SER	CA-C	-5.29	1.46	1.52
2	x	490	SER	CA-C	-5.29	1.46	1.52
2	v	490	SER	CA-C	-5.28	1.46	1.52
2	t	82	THR	CA-C	-5.24	1.46	1.53
2	w	82	THR	CA-C	-5.24	1.46	1.53
2	v	82	THR	CA-C	-5.23	1.46	1.53
2	u	82	THR	CA-C	-5.20	1.46	1.53
2	x	82	THR	CA-C	-5.20	1.46	1.53
2	u	275	LYS	CA-C	-5.16	1.46	1.52
2	s	82	THR	CA-C	-5.15	1.46	1.53
2	v	275	LYS	CA-C	-5.13	1.46	1.52
2	x	275	LYS	CA-C	-5.12	1.46	1.52
1	g	29	ARG	CA-C	-5.12	1.46	1.52
2	s	715	THR	CA-C	-5.12	1.46	1.52
2	t	715	THR	CA-C	-5.12	1.46	1.52
2	w	715	THR	CA-C	-5.12	1.46	1.52
2	s	275	LYS	CA-C	-5.11	1.46	1.52
2	x	771	ASP	N-CA	-5.11	1.41	1.46
1	j	29	ARG	CA-C	-5.11	1.46	1.52
2	u	715	THR	CA-C	-5.10	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	a	29	ARG	CA-C	-5.10	1.46	1.52
1	d	29	ARG	CA-C	-5.09	1.46	1.52
2	w	275	LYS	CA-C	-5.07	1.46	1.52
2	t	275	LYS	CA-C	-5.06	1.46	1.52
1	j	73	ILE	CA-C	-5.06	1.46	1.52
2	x	492	VAL	CA-C	-5.06	1.47	1.52
2	v	715	THR	CA-C	-5.05	1.46	1.52
2	x	715	THR	CA-C	-5.05	1.46	1.52
1	p	29	ARG	CA-C	-5.05	1.46	1.52
2	w	771	ASP	N-CA	-5.04	1.41	1.46
1	r	52	PHE	CA-C	-5.04	1.47	1.53
2	v	771	ASP	N-CA	-5.04	1.41	1.46
1	p	73	ILE	CA-C	-5.02	1.46	1.52
1	m	29	ARG	CA-C	-5.01	1.46	1.52
2	t	771	ASP	N-CA	-5.00	1.41	1.46

All (1485) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	i	39	VAL	N-CA-C	-12.72	101.57	111.62
1	l	39	VAL	N-CA-C	-12.71	101.58	111.62
1	o	39	VAL	N-CA-C	-12.71	101.58	111.62
1	r	39	VAL	N-CA-C	-12.68	101.60	111.62
1	c	39	VAL	N-CA-C	-12.66	101.62	111.62
1	f	39	VAL	N-CA-C	-12.66	101.62	111.62
2	s	580	LYS	N-CA-C	12.32	124.25	111.07
2	t	580	LYS	N-CA-C	12.31	124.24	111.07
2	v	580	LYS	N-CA-C	12.31	124.24	111.07
2	x	580	LYS	N-CA-C	12.29	124.22	111.07
2	w	580	LYS	N-CA-C	12.27	124.19	111.07
2	u	580	LYS	N-CA-C	12.25	124.18	111.07
2	s	447	ASP	N-CA-C	11.59	123.91	111.28
2	v	447	ASP	N-CA-C	11.59	123.91	111.28
2	u	447	ASP	N-CA-C	11.56	123.88	111.28
2	t	447	ASP	N-CA-C	11.55	123.87	111.28
2	w	447	ASP	N-CA-C	11.55	123.87	111.28
2	x	447	ASP	N-CA-C	11.48	123.80	111.28
2	x	382	ILE	N-CA-C	11.31	122.14	110.72
2	v	382	ILE	N-CA-C	11.30	122.13	110.72
2	w	382	ILE	N-CA-C	11.29	122.12	110.72
2	u	382	ILE	N-CA-C	11.28	122.11	110.72
2	t	382	ILE	N-CA-C	11.26	122.09	110.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	s	382	ILE	N-CA-C	11.24	122.07	110.72
2	x	569	PHE	N-CA-C	11.23	123.27	111.14
2	s	569	PHE	N-CA-C	11.22	123.26	111.14
2	u	569	PHE	N-CA-C	11.20	123.23	111.14
2	v	569	PHE	N-CA-C	11.19	123.22	111.14
2	t	569	PHE	N-CA-C	11.18	123.22	111.14
2	u	786	ASN	N-CA-C	11.16	123.19	111.14
2	w	569	PHE	N-CA-C	11.15	123.18	111.14
2	v	786	ASN	N-CA-C	11.14	123.17	111.14
2	s	786	ASN	N-CA-C	11.13	123.16	111.14
2	t	786	ASN	N-CA-C	11.12	123.15	111.14
2	w	786	ASN	N-CA-C	11.12	123.15	111.14
2	x	786	ASN	N-CA-C	11.11	123.13	111.14
2	x	298	ASN	N-CA-C	10.83	125.90	112.47
2	w	298	ASN	N-CA-C	10.82	125.89	112.47
2	s	298	ASN	N-CA-C	10.81	125.87	112.47
2	v	298	ASN	N-CA-C	10.81	125.87	112.47
2	s	498	ASN	N-CA-C	10.79	123.04	111.28
2	t	298	ASN	N-CA-C	10.78	125.83	112.47
2	u	298	ASN	N-CA-C	10.77	125.83	112.47
2	t	498	ASN	N-CA-C	10.72	122.96	111.28
2	v	498	ASN	N-CA-C	10.72	122.96	111.28
2	u	498	ASN	N-CA-C	10.71	122.95	111.28
2	x	498	ASN	N-CA-C	10.68	122.92	111.28
2	w	498	ASN	N-CA-C	10.66	122.90	111.28
2	t	74	HIS	N-CA-C	10.27	122.56	111.36
2	v	74	HIS	N-CA-C	10.27	122.55	111.36
2	x	74	HIS	N-CA-C	10.25	122.53	111.36
2	s	74	HIS	N-CA-C	10.24	122.52	111.36
2	u	74	HIS	N-CA-C	10.23	122.52	111.36
2	w	74	HIS	N-CA-C	10.22	122.50	111.36
4	R	188	ALA	N-CA-C	10.16	122.36	111.28
4	X	188	ALA	N-CA-C	10.14	122.33	111.28
4	V	188	ALA	N-CA-C	10.13	122.33	111.28
4	N	188	ALA	N-CA-C	10.11	122.30	111.28
4	T	188	ALA	N-CA-C	10.11	122.30	111.28
4	P	188	ALA	N-CA-C	10.10	122.29	111.28
4	Q	100	GLY	N-CA-C	-9.77	99.04	112.13
4	O	100	GLY	N-CA-C	-9.77	99.04	112.13
2	w	349	ASN	N-CA-C	9.76	122.00	111.36
4	S	100	GLY	N-CA-C	-9.76	99.06	112.13
4	W	100	GLY	N-CA-C	-9.74	99.07	112.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	M	100	GLY	N-CA-C	-9.73	99.09	112.13
2	s	349	ASN	N-CA-C	9.73	121.97	111.36
2	v	349	ASN	N-CA-C	9.70	121.94	111.36
2	u	349	ASN	N-CA-C	9.70	121.93	111.36
2	t	349	ASN	N-CA-C	9.69	121.92	111.36
4	U	100	GLY	N-CA-C	-9.69	99.15	112.13
2	x	349	ASN	N-CA-C	9.67	121.90	111.36
4	R	98	ASN	N-CA-C	9.53	122.87	109.15
4	T	98	ASN	N-CA-C	9.53	122.87	109.15
2	t	252	GLN	N-CA-C	9.51	121.72	111.36
2	s	252	GLN	N-CA-C	9.48	121.69	111.36
2	u	252	GLN	N-CA-C	9.47	121.68	111.36
2	x	286	ALA	N-CA-C	9.46	121.67	111.36
1	r	52	PHE	N-CA-C	-9.46	97.53	110.68
2	v	252	GLN	N-CA-C	9.45	121.66	111.36
2	v	286	ALA	N-CA-C	9.45	121.66	111.36
2	w	286	ALA	N-CA-C	9.45	121.66	111.36
2	u	286	ALA	N-CA-C	9.43	121.64	111.36
2	w	252	GLN	N-CA-C	9.43	121.64	111.36
2	x	252	GLN	N-CA-C	9.43	121.64	111.36
2	s	286	ALA	N-CA-C	9.43	121.64	111.36
2	t	492	VAL	CA-C-N	-9.41	111.08	120.31
2	t	492	VAL	C-N-CA	-9.41	111.08	120.31
2	t	286	ALA	N-CA-C	9.41	121.61	111.36
2	u	492	VAL	CA-C-N	-9.40	111.09	120.31
2	u	492	VAL	C-N-CA	-9.40	111.09	120.31
2	w	492	VAL	CA-C-N	-9.38	111.12	120.31
2	w	492	VAL	C-N-CA	-9.38	111.12	120.31
2	x	492	VAL	CA-C-N	-9.37	111.12	120.31
2	x	492	VAL	C-N-CA	-9.37	111.12	120.31
2	v	492	VAL	CA-C-N	-9.37	111.13	120.31
2	v	492	VAL	C-N-CA	-9.37	111.13	120.31
2	s	492	VAL	CA-C-N	-9.35	111.15	120.31
2	s	492	VAL	C-N-CA	-9.35	111.15	120.31
2	u	30	ARG	N-CA-C	9.31	124.30	111.74
2	s	30	ARG	N-CA-C	9.30	124.29	111.74
1	l	24	PHE	N-CA-C	9.30	122.52	110.53
1	c	24	PHE	N-CA-C	9.27	122.48	110.53
1	i	24	PHE	N-CA-C	9.27	122.48	110.53
2	v	30	ARG	N-CA-C	9.27	124.25	111.74
2	t	30	ARG	N-CA-C	9.26	124.24	111.74
2	x	30	ARG	N-CA-C	9.26	124.23	111.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	r	24	PHE	N-CA-C	9.25	122.46	110.53
2	w	30	ARG	N-CA-C	9.24	124.22	111.74
1	f	24	PHE	N-CA-C	9.24	122.45	110.53
1	o	24	PHE	N-CA-C	9.23	122.44	110.53
2	x	149	ASN	N-CA-C	9.22	121.34	111.28
2	w	149	ASN	N-CA-C	9.19	121.30	111.28
2	v	149	ASN	N-CA-C	9.17	121.28	111.28
2	t	115	ASP	N-CA-C	9.17	121.35	111.36
2	u	149	ASN	N-CA-C	9.16	121.27	111.28
2	s	115	ASP	N-CA-C	9.13	121.31	111.36
2	w	115	ASP	N-CA-C	9.13	121.31	111.36
2	t	149	ASN	N-CA-C	9.13	121.23	111.28
2	v	115	ASP	N-CA-C	9.12	121.31	111.36
2	x	115	ASP	N-CA-C	9.12	121.30	111.36
2	s	149	ASN	N-CA-C	9.11	121.22	111.28
2	u	115	ASP	N-CA-C	9.08	121.25	111.36
4	X	98	ASN	N-CA-C	9.07	122.22	109.15
4	N	98	ASN	N-CA-C	9.00	122.11	109.15
3	C	88	SER	N-CA-C	8.99	123.51	112.54
2	s	557	ILE	N-CA-C	-8.97	97.87	109.80
2	u	557	ILE	N-CA-C	-8.95	97.89	109.80
2	w	557	ILE	N-CA-C	-8.95	97.89	109.80
2	t	557	ILE	N-CA-C	-8.94	97.91	109.80
1	k	60	LEU	N-CA-C	-8.94	98.48	110.55
2	x	557	ILE	N-CA-C	-8.94	97.91	109.80
2	v	557	ILE	N-CA-C	-8.92	97.93	109.80
1	q	60	LEU	N-CA-C	-8.91	98.52	110.55
2	u	522	LYS	N-CA-C	8.91	123.42	108.90
2	v	522	LYS	N-CA-C	8.90	123.42	108.90
2	s	522	LYS	N-CA-C	8.90	123.41	108.90
2	t	522	LYS	N-CA-C	8.90	123.41	108.90
2	w	522	LYS	N-CA-C	8.90	123.41	108.90
2	x	522	LYS	N-CA-C	8.89	123.39	108.90
1	n	60	LEU	N-CA-C	-8.88	98.56	110.55
1	e	60	LEU	N-CA-C	-8.88	98.56	110.55
1	b	60	LEU	N-CA-C	-8.88	98.57	110.55
1	p	115	ASP	N-CA-C	8.86	121.02	111.36
2	s	20	ASP	N-CA-C	8.86	120.94	111.28
2	w	20	ASP	N-CA-C	8.85	120.92	111.28
1	h	60	LEU	N-CA-C	-8.84	98.62	110.55
1	j	115	ASP	N-CA-C	8.82	120.98	111.36
1	m	115	ASP	N-CA-C	8.81	120.97	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	t	20	ASP	N-CA-C	8.81	120.88	111.28
1	g	115	ASP	N-CA-C	8.80	120.95	111.36
1	r	46	ILE	N-CA-C	8.80	118.87	110.42
1	d	115	ASP	N-CA-C	8.80	120.95	111.36
1	a	115	ASP	N-CA-C	8.77	120.92	111.36
2	v	20	ASP	N-CA-C	8.77	120.84	111.28
2	x	20	ASP	N-CA-C	8.77	120.84	111.28
3	B	88	SER	N-CA-C	8.75	121.77	111.71
1	i	56	THR	N-CA-C	8.74	120.89	111.36
1	o	56	THR	N-CA-C	8.74	120.89	111.36
2	u	20	ASP	N-CA-C	8.74	120.81	111.28
2	t	618	ILE	N-CA-CB	8.73	116.00	110.50
1	f	56	THR	N-CA-C	8.71	120.86	111.36
2	u	618	ILE	N-CA-CB	8.71	115.99	110.50
1	c	56	THR	N-CA-C	8.71	120.85	111.36
2	s	618	ILE	N-CA-CB	8.71	115.99	110.50
2	v	618	ILE	N-CA-CB	8.71	115.99	110.50
1	l	56	THR	N-CA-C	8.71	120.85	111.36
1	r	56	THR	N-CA-C	8.70	120.84	111.36
2	w	618	ILE	N-CA-CB	8.68	115.97	110.50
4	W	188	ALA	N-CA-C	-8.68	102.62	113.55
4	U	188	ALA	N-CA-C	-8.67	102.63	113.55
4	M	188	ALA	N-CA-C	-8.66	102.64	113.55
4	S	188	ALA	N-CA-C	-8.65	102.65	113.55
4	V	98	ASN	N-CA-C	8.65	121.61	109.15
4	Q	188	ALA	N-CA-C	-8.64	102.66	113.55
2	x	618	ILE	N-CA-CB	8.61	115.93	110.50
4	O	188	ALA	N-CA-C	-8.61	102.71	113.55
1	k	48	THR	N-CA-C	8.60	120.43	111.14
4	P	98	ASN	N-CA-C	8.60	121.53	109.15
1	q	48	THR	N-CA-C	8.58	120.41	111.14
1	b	48	THR	N-CA-C	8.56	120.39	111.14
1	e	48	THR	N-CA-C	8.56	120.38	111.14
1	n	48	THR	N-CA-C	8.54	120.36	111.14
1	h	48	THR	N-CA-C	8.53	120.35	111.14
2	t	404	LYS	N-CA-C	8.50	120.32	111.14
2	u	404	LYS	N-CA-C	8.49	120.31	111.14
2	x	404	LYS	N-CA-C	8.48	120.30	111.14
2	v	404	LYS	N-CA-C	8.47	120.29	111.14
2	s	404	LYS	N-CA-C	8.47	120.28	111.14
2	w	404	LYS	N-CA-C	8.46	120.28	111.14
2	s	219	PHE	N-CA-C	8.42	120.90	108.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	w	219	PHE	N-CA-C	8.39	120.85	108.60
2	u	219	PHE	N-CA-C	8.39	120.85	108.60
3	E	88	SER	N-CA-C	8.39	123.56	113.16
1	c	31	PHE	N-CA-C	8.39	120.42	111.28
2	v	219	PHE	N-CA-C	8.39	120.84	108.60
2	x	219	PHE	N-CA-C	8.38	120.83	108.60
2	t	219	PHE	N-CA-C	8.38	120.83	108.60
1	o	31	PHE	N-CA-C	8.38	120.41	111.28
1	i	31	PHE	N-CA-C	8.37	120.41	111.28
1	f	31	PHE	N-CA-C	8.34	120.38	111.28
1	l	31	PHE	N-CA-C	8.34	120.38	111.28
1	r	31	PHE	N-CA-C	8.34	120.37	111.28
3	E	93	SER	N-CA-C	-8.26	102.28	111.28
1	b	84	ARG	N-CA-C	-8.22	98.11	110.28
1	n	84	ARG	N-CA-C	-8.19	98.16	110.28
1	h	84	ARG	N-CA-C	-8.19	98.17	110.28
1	q	84	ARG	N-CA-C	-8.18	98.17	110.28
2	u	343	PHE	N-CA-C	-8.18	102.87	113.17
2	s	343	PHE	N-CA-C	-8.17	102.88	113.17
1	k	84	ARG	N-CA-C	-8.15	98.21	110.28
2	x	113	ARG	N-CA-C	8.15	119.79	111.07
1	e	84	ARG	N-CA-C	-8.15	98.22	110.28
2	t	343	PHE	N-CA-C	-8.15	102.90	113.17
2	x	450	ARG	CA-C-N	-8.15	111.96	120.03
2	x	450	ARG	C-N-CA	-8.15	111.96	120.03
2	w	343	PHE	N-CA-C	-8.14	102.91	113.17
2	v	450	ARG	CA-C-N	-8.14	111.97	120.03
2	v	450	ARG	C-N-CA	-8.14	111.97	120.03
2	v	343	PHE	N-CA-C	-8.13	102.92	113.17
2	x	343	PHE	N-CA-C	-8.12	102.94	113.17
2	u	96	LYS	N-CA-C	-8.12	97.78	109.96
2	t	96	LYS	N-CA-C	-8.12	97.79	109.96
2	v	96	LYS	N-CA-C	-8.10	97.80	109.96
2	s	96	LYS	N-CA-C	-8.10	97.82	109.96
2	t	113	ARG	N-CA-C	8.09	119.73	111.07
2	t	450	ARG	CA-C-N	-8.09	112.02	120.03
2	t	450	ARG	C-N-CA	-8.09	112.02	120.03
2	w	96	LYS	N-CA-C	-8.09	97.82	109.96
4	U	62	ASN	N-CA-C	8.09	120.18	111.36
2	s	450	ARG	CA-C-N	-8.09	112.02	120.03
2	s	450	ARG	C-N-CA	-8.09	112.02	120.03
2	x	96	LYS	N-CA-C	-8.09	97.83	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	S	62	ASN	N-CA-C	8.09	120.17	111.36
2	v	113	ARG	N-CA-C	8.07	119.71	111.07
2	w	113	ARG	N-CA-C	8.07	119.70	111.07
2	t	60	LEU	N-CA-C	-8.06	103.17	113.16
2	u	450	ARG	CA-C-N	-8.05	112.06	120.03
2	u	450	ARG	C-N-CA	-8.05	112.06	120.03
4	W	62	ASN	N-CA-C	8.05	120.14	111.36
2	w	60	LEU	N-CA-C	-8.05	103.18	113.16
2	w	450	ARG	CA-C-N	-8.05	112.06	120.03
2	w	450	ARG	C-N-CA	-8.05	112.06	120.03
2	x	60	LEU	N-CA-C	-8.04	103.19	113.16
2	u	113	ARG	N-CA-C	8.04	119.67	111.07
4	M	62	ASN	N-CA-C	8.04	120.12	111.36
4	O	62	ASN	N-CA-C	8.03	120.12	111.36
2	u	60	LEU	N-CA-C	-8.03	103.20	113.16
4	Q	62	ASN	N-CA-C	8.03	120.11	111.36
2	t	516	SER	N-CA-C	8.02	121.35	109.24
2	x	516	SER	N-CA-C	8.01	121.33	109.24
2	s	60	LEU	N-CA-C	-8.01	103.23	113.16
2	s	113	ARG	N-CA-C	8.01	119.64	111.07
2	v	60	LEU	N-CA-C	-8.00	103.24	113.16
2	u	516	SER	N-CA-C	7.99	121.31	109.24
2	s	516	SER	N-CA-C	7.99	121.30	109.24
1	f	52	PHE	N-CA-C	-7.97	98.34	110.70
1	o	52	PHE	N-CA-C	-7.96	98.36	110.70
2	s	507	GLY	N-CA-C	7.96	122.96	112.77
2	w	516	SER	N-CA-C	7.95	121.24	109.24
2	w	333	GLY	N-CA-C	7.95	122.35	111.54
2	x	333	GLY	N-CA-C	7.95	122.34	111.54
2	u	333	GLY	N-CA-C	7.94	122.34	111.54
2	v	516	SER	N-CA-C	7.94	121.23	109.24
2	u	507	GLY	N-CA-C	7.93	122.93	112.77
2	t	333	GLY	N-CA-C	7.93	122.33	111.54
2	v	333	GLY	N-CA-C	7.93	122.33	111.54
2	w	507	GLY	N-CA-C	7.92	122.91	112.77
2	s	333	GLY	N-CA-C	7.92	122.31	111.54
4	R	186	GLY	N-CA-C	7.91	122.22	112.73
2	t	507	GLY	N-CA-C	7.91	122.89	112.77
2	x	507	GLY	N-CA-C	7.91	122.89	112.77
2	v	507	GLY	N-CA-C	7.90	122.88	112.77
1	i	52	PHE	N-CA-C	-7.88	98.48	110.70
4	N	186	GLY	N-CA-C	7.84	122.14	112.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	X	186	GLY	N-CA-C	7.83	122.13	112.73
2	u	150	GLN	N-CA-C	7.83	119.81	111.28
1	l	52	PHE	N-CA-C	-7.83	98.57	110.70
4	T	186	GLY	N-CA-C	7.83	122.12	112.73
4	P	186	GLY	N-CA-C	7.82	122.12	112.73
2	t	150	GLN	N-CA-C	7.81	119.79	111.28
1	c	52	PHE	N-CA-C	-7.80	98.61	110.70
4	T	99	ARG	N-CA-C	-7.79	96.52	109.46
1	e	54	THR	N-CA-C	7.79	121.00	109.24
2	x	150	GLN	N-CA-C	7.79	119.77	111.28
2	u	84	SER	N-CA-C	7.78	119.84	111.36
2	w	150	GLN	N-CA-C	7.78	119.77	111.28
4	R	99	ARG	N-CA-C	-7.78	96.56	109.24
2	v	150	GLN	N-CA-C	7.77	119.75	111.28
1	k	54	THR	N-CA-C	7.77	120.97	109.24
2	v	84	SER	N-CA-C	7.77	119.83	111.36
2	s	84	SER	N-CA-C	7.76	119.82	111.36
4	V	186	GLY	N-CA-C	7.76	122.04	112.73
1	h	54	THR	N-CA-C	7.76	120.95	109.24
2	x	84	SER	N-CA-C	7.75	119.81	111.36
2	s	150	GLN	N-CA-C	7.74	119.72	111.28
2	w	84	SER	N-CA-C	7.74	119.79	111.36
1	q	54	THR	N-CA-C	7.73	120.92	109.24
4	V	99	ARG	N-CA-C	-7.73	96.12	108.73
1	b	54	THR	N-CA-C	7.72	120.90	109.24
2	u	740	THR	N-CA-C	7.71	119.69	111.28
1	n	54	THR	N-CA-C	7.71	120.88	109.24
2	t	84	SER	N-CA-C	7.70	119.75	111.36
2	x	740	THR	N-CA-C	7.70	119.67	111.28
2	s	740	THR	N-CA-C	7.68	119.66	111.28
2	v	740	THR	N-CA-C	7.68	119.66	111.28
2	w	740	THR	N-CA-C	7.68	119.65	111.28
2	w	45	ARG	CA-C-N	-7.68	112.47	120.38
2	w	45	ARG	C-N-CA	-7.68	112.47	120.38
2	t	45	ARG	CA-C-N	-7.67	112.48	120.38
2	t	45	ARG	C-N-CA	-7.67	112.48	120.38
2	x	45	ARG	CA-C-N	-7.67	112.48	120.38
2	x	45	ARG	C-N-CA	-7.67	112.48	120.38
2	t	740	THR	N-CA-C	7.66	119.63	111.28
2	s	45	ARG	CA-C-N	-7.65	112.50	120.38
2	s	45	ARG	C-N-CA	-7.65	112.50	120.38
2	u	45	ARG	CA-C-N	-7.63	112.52	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	u	45	ARG	C-N-CA	-7.63	112.52	120.38
4	Q	153	ALA	N-CA-C	7.62	120.45	109.48
4	O	153	ALA	N-CA-C	7.62	120.45	109.48
2	w	377	PHE	N-CA-C	7.61	119.57	111.28
2	x	377	PHE	N-CA-C	7.60	119.57	111.28
2	v	377	PHE	N-CA-C	7.60	119.56	111.28
2	u	518	GLY	N-CA-C	7.60	122.49	112.77
4	S	153	ALA	N-CA-C	7.60	120.42	109.48
2	x	488	ILE	N-CA-C	-7.59	105.91	113.20
4	U	153	ALA	N-CA-C	7.59	120.41	109.48
2	s	377	PHE	N-CA-C	7.59	119.55	111.28
2	t	377	PHE	N-CA-C	7.58	119.55	111.28
2	s	518	GLY	N-CA-C	7.58	122.48	112.77
4	M	153	ALA	N-CA-C	7.58	120.40	109.48
2	u	377	PHE	N-CA-C	7.58	119.54	111.28
2	v	45	ARG	CA-C-N	-7.58	112.57	120.38
2	v	45	ARG	C-N-CA	-7.58	112.57	120.38
4	W	153	ALA	N-CA-C	7.57	120.38	109.48
2	w	518	GLY	N-CA-C	7.57	122.45	112.77
2	v	518	GLY	N-CA-C	7.56	122.45	112.77
2	t	518	GLY	N-CA-C	7.56	122.44	112.77
1	n	22	ILE	CA-C-N	-7.56	110.39	119.84
1	n	22	ILE	C-N-CA	-7.56	110.39	119.84
2	s	488	ILE	N-CA-C	-7.56	105.95	113.20
1	r	85	LEU	N-CA-C	-7.55	103.17	112.38
2	x	518	GLY	N-CA-C	7.55	122.43	112.77
2	t	488	ILE	N-CA-C	-7.55	105.95	113.20
2	w	488	ILE	N-CA-C	-7.53	105.97	113.20
1	f	85	LEU	N-CA-C	-7.53	103.20	112.38
2	u	488	ILE	N-CA-C	-7.52	105.98	113.20
2	v	488	ILE	N-CA-C	-7.52	105.98	113.20
4	S	64	GLU	N-CA-C	-7.52	99.35	110.48
4	W	64	GLU	N-CA-C	-7.51	99.37	110.48
2	x	159	GLY	N-CA-C	7.51	122.38	112.77
1	b	22	ILE	CA-C-N	-7.50	110.46	119.84
1	b	22	ILE	C-N-CA	-7.50	110.46	119.84
1	k	66	PRO	N-CA-C	-7.50	104.09	113.84
2	s	159	GLY	N-CA-C	7.50	122.37	112.77
1	o	85	LEU	N-CA-C	-7.50	103.23	112.38
1	c	85	LEU	N-CA-C	-7.50	103.23	112.38
1	k	22	ILE	CA-C-N	-7.50	110.47	119.84
1	k	22	ILE	C-N-CA	-7.50	110.47	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	O	64	GLU	N-CA-C	-7.49	99.39	110.48
4	Q	64	GLU	N-CA-C	-7.49	99.39	110.48
4	M	64	GLU	N-CA-C	-7.49	99.39	110.48
1	e	22	ILE	CA-C-N	-7.49	110.48	119.84
1	e	22	ILE	C-N-CA	-7.49	110.48	119.84
1	i	85	LEU	N-CA-C	-7.48	103.25	112.38
1	q	22	ILE	CA-C-N	-7.48	110.49	119.84
1	q	22	ILE	C-N-CA	-7.48	110.49	119.84
1	h	22	ILE	CA-C-N	-7.48	110.49	119.84
1	h	22	ILE	C-N-CA	-7.48	110.49	119.84
2	t	159	GLY	N-CA-C	7.48	122.34	112.77
2	v	159	GLY	N-CA-C	7.48	122.34	112.77
2	w	159	GLY	N-CA-C	7.48	122.34	112.77
4	U	64	GLU	N-CA-C	-7.48	99.42	110.48
1	e	66	PRO	N-CA-C	-7.47	104.12	113.84
1	h	66	PRO	N-CA-C	-7.47	104.13	113.84
1	l	85	LEU	N-CA-C	-7.46	103.27	112.38
4	P	7	ASN	N-CA-C	-7.45	104.70	114.31
2	u	159	GLY	N-CA-C	7.45	122.30	112.77
1	n	66	PRO	N-CA-C	-7.45	104.16	113.84
1	b	66	PRO	N-CA-C	-7.43	104.18	113.84
1	b	82	THR	N-CA-C	7.40	119.35	111.28
2	s	670	GLY	N-CA-C	7.40	124.96	110.83
2	v	670	GLY	N-CA-C	7.40	124.96	110.83
1	q	66	PRO	N-CA-C	-7.39	104.23	113.84
2	t	567	ASN	N-CA-C	-7.39	101.00	110.53
1	q	82	THR	N-CA-C	7.39	119.33	111.28
2	w	670	GLY	N-CA-C	7.39	124.94	110.83
1	n	82	THR	N-CA-C	7.39	119.33	111.28
2	u	670	GLY	N-CA-C	7.39	124.94	110.83
2	s	567	ASN	N-CA-C	-7.38	101.01	110.53
2	u	567	ASN	N-CA-C	-7.38	101.01	110.53
1	k	82	THR	N-CA-C	7.37	119.31	111.28
2	x	567	ASN	N-CA-C	-7.37	101.02	110.53
2	x	670	GLY	N-CA-C	7.37	124.91	110.83
2	t	670	GLY	N-CA-C	7.37	124.90	110.83
2	v	567	ASN	N-CA-C	-7.36	101.04	110.53
1	e	82	THR	N-CA-C	7.35	119.29	111.28
1	h	82	THR	N-CA-C	7.34	119.29	111.28
2	w	567	ASN	N-CA-C	-7.34	101.06	110.53
2	w	556	SER	N-CA-C	7.28	120.28	108.41
1	n	111	GLU	N-CA-C	-7.25	103.37	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	x	556	SER	N-CA-C	7.25	120.23	108.41
2	s	556	SER	N-CA-C	7.25	120.22	108.41
2	u	556	SER	N-CA-C	7.24	120.22	108.41
2	x	158	GLY	N-CA-C	7.24	119.83	111.36
2	t	556	SER	N-CA-C	7.24	120.21	108.41
2	v	556	SER	N-CA-C	7.24	120.20	108.41
1	k	111	GLU	N-CA-C	-7.23	103.40	111.28
2	x	772	GLU	N-CA-C	7.23	120.13	110.88
2	w	772	GLU	N-CA-C	7.22	120.12	110.88
2	u	772	GLU	N-CA-C	7.21	120.11	110.88
2	s	158	GLY	N-CA-C	7.21	119.80	111.36
2	s	772	GLU	N-CA-C	7.21	120.11	110.88
1	o	21	ASN	N-CA-C	7.20	120.94	110.28
1	l	21	ASN	N-CA-C	7.20	120.94	110.28
1	q	111	GLU	N-CA-C	-7.20	103.43	111.28
2	u	158	GLY	N-CA-C	7.20	119.78	111.36
1	b	111	GLU	N-CA-C	-7.20	103.43	111.28
1	h	111	GLU	N-CA-C	-7.20	103.43	111.28
2	t	158	GLY	N-CA-C	7.19	119.78	111.36
2	v	158	GLY	N-CA-C	7.19	119.77	111.36
1	o	93	ILE	N-CA-C	-7.18	100.32	109.30
1	c	21	ASN	N-CA-C	7.18	120.90	110.28
1	e	111	GLU	N-CA-C	-7.18	103.46	111.28
2	x	44	LYS	N-CA-C	-7.17	100.38	110.50
1	i	21	ASN	N-CA-C	7.17	120.90	110.28
2	v	772	GLU	N-CA-C	7.17	120.06	110.88
2	t	772	GLU	N-CA-C	7.17	120.06	110.88
1	r	21	ASN	N-CA-C	7.16	120.88	110.28
2	t	346	SER	N-CA-C	7.16	120.21	110.55
2	u	193	ALA	N-CA-C	7.16	118.73	111.07
2	w	158	GLY	N-CA-C	7.16	119.73	111.36
2	t	44	LYS	N-CA-C	-7.15	100.42	110.50
2	u	44	LYS	N-CA-C	-7.15	100.42	110.50
2	w	193	ALA	N-CA-C	7.15	118.72	111.07
1	f	21	ASN	N-CA-C	7.14	120.85	110.28
2	t	193	ALA	N-CA-C	7.14	118.71	111.07
1	k	95	ARG	N-CA-C	-7.14	99.59	110.30
2	u	346	SER	N-CA-C	7.14	120.19	110.55
2	v	44	LYS	N-CA-C	-7.14	100.44	110.50
2	s	346	SER	N-CA-C	7.13	120.18	110.55
2	w	44	LYS	N-CA-C	-7.13	100.44	110.50
1	g	31	PHE	N-CA-C	7.13	119.05	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	x	346	SER	N-CA-C	7.13	120.18	110.55
2	v	193	ALA	N-CA-C	7.13	118.70	111.07
2	w	346	SER	N-CA-C	7.13	120.17	110.55
2	v	346	SER	N-CA-C	7.12	120.17	110.55
1	j	31	PHE	N-CA-C	7.12	119.05	111.28
1	n	95	ARG	N-CA-C	-7.12	99.62	110.30
2	x	193	ALA	N-CA-C	7.11	118.68	111.07
2	s	44	LYS	N-CA-C	-7.11	100.48	110.50
1	q	95	ARG	N-CA-C	-7.11	99.64	110.30
4	R	37	ASN	N-CA-C	-7.10	101.59	111.39
4	Q	6	MET	N-CA-C	7.09	119.09	111.36
2	v	184	GLN	CA-C-N	-7.09	111.24	119.32
2	v	184	GLN	C-N-CA	-7.09	111.24	119.32
1	p	31	PHE	N-CA-C	7.08	119.00	111.28
2	u	184	GLN	CA-C-N	-7.08	111.24	119.32
2	u	184	GLN	C-N-CA	-7.08	111.24	119.32
1	e	95	ARG	N-CA-C	-7.08	99.67	110.30
2	s	389	ASP	CA-C-N	-7.08	113.02	120.03
2	s	389	ASP	C-N-CA	-7.08	113.02	120.03
1	a	52	PHE	N-CA-C	-7.08	99.80	110.28
1	d	31	PHE	N-CA-C	7.08	119.00	111.28
4	X	37	ASN	N-CA-C	-7.08	101.62	111.39
1	d	52	PHE	N-CA-C	-7.08	99.80	110.28
1	m	52	PHE	N-CA-C	-7.08	99.80	110.28
1	m	31	PHE	N-CA-C	7.08	118.99	111.28
2	v	388	ASP	N-CA-C	-7.07	104.66	112.72
4	N	37	ASN	N-CA-C	-7.07	101.63	111.39
1	p	52	PHE	N-CA-C	-7.07	99.81	110.28
1	b	95	ARG	N-CA-C	-7.07	99.70	110.30
4	P	37	ASN	N-CA-C	-7.06	101.64	111.39
4	M	9	GLU	N-CA-C	-7.06	97.55	108.42
2	t	389	ASP	CA-C-N	-7.06	113.04	120.03
2	t	389	ASP	C-N-CA	-7.06	113.04	120.03
2	w	389	ASP	CA-C-N	-7.06	113.04	120.03
2	w	389	ASP	C-N-CA	-7.06	113.04	120.03
1	a	31	PHE	N-CA-C	7.06	118.97	111.28
2	s	193	ALA	N-CA-C	7.06	118.62	111.07
2	v	389	ASP	CA-C-N	-7.06	113.04	120.03
2	v	389	ASP	C-N-CA	-7.06	113.04	120.03
4	P	99	ARG	N-CA-C	-7.06	97.23	108.73
1	h	95	ARG	N-CA-C	-7.05	99.72	110.30
4	T	37	ASN	N-CA-C	-7.05	101.66	111.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	g	52	PHE	N-CA-C	-7.05	99.85	110.28
2	x	184	GLN	CA-C-N	-7.05	111.29	119.32
2	x	184	GLN	C-N-CA	-7.05	111.29	119.32
4	M	57	ARG	N-CA-C	-7.04	99.46	109.96
2	w	184	GLN	CA-C-N	-7.04	111.29	119.32
2	w	184	GLN	C-N-CA	-7.04	111.29	119.32
4	V	37	ASN	N-CA-C	-7.04	101.67	111.39
1	j	52	PHE	N-CA-C	-7.04	99.86	110.28
4	O	57	ARG	N-CA-C	-7.04	99.47	109.96
2	x	389	ASP	CA-C-N	-7.04	113.06	120.03
2	x	389	ASP	C-N-CA	-7.04	113.06	120.03
2	u	389	ASP	CA-C-N	-7.04	113.06	120.03
2	u	389	ASP	C-N-CA	-7.04	113.06	120.03
2	s	184	GLN	CA-C-N	-7.03	111.31	119.32
2	s	184	GLN	C-N-CA	-7.03	111.31	119.32
4	Q	9	GLU	N-CA-C	-7.03	97.60	108.42
4	S	57	ARG	N-CA-C	-7.02	99.50	109.96
2	t	184	GLN	CA-C-N	-7.02	111.32	119.32
2	t	184	GLN	C-N-CA	-7.02	111.32	119.32
1	o	82	THR	N-CA-C	7.01	118.92	111.28
4	U	57	ARG	N-CA-C	-7.01	99.51	109.96
1	l	82	THR	N-CA-C	7.00	118.91	111.28
1	e	20	PHE	N-CA-C	-6.98	97.52	108.90
4	W	57	ARG	N-CA-C	-6.98	99.56	109.96
1	f	82	THR	N-CA-C	6.97	118.88	111.28
1	k	20	PHE	N-CA-C	-6.97	97.53	108.90
1	n	20	PHE	N-CA-C	-6.97	97.54	108.90
2	t	132	VAL	N-CA-C	6.97	118.90	108.23
1	i	82	THR	N-CA-C	6.97	118.87	111.28
4	Q	57	ARG	N-CA-C	-6.96	99.59	109.96
1	b	20	PHE	N-CA-C	-6.95	97.57	108.90
2	t	388	ASP	N-CA-C	-6.95	104.80	112.72
1	c	82	THR	N-CA-C	6.95	118.85	111.28
1	q	18	ARG	N-CA-C	-6.95	103.71	111.28
1	h	20	PHE	N-CA-C	-6.94	97.59	108.90
1	n	18	ARG	N-CA-C	-6.93	103.72	111.28
1	q	20	PHE	N-CA-C	-6.93	97.60	108.90
2	x	388	ASP	N-CA-C	-6.93	104.82	112.72
2	u	132	VAL	N-CA-C	6.93	118.83	108.23
4	N	99	ARG	N-CA-C	-6.93	97.44	108.73
2	s	132	VAL	N-CA-C	6.92	118.82	108.23
2	x	132	VAL	N-CA-C	6.92	118.81	108.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	v	132	VAL	N-CA-C	6.91	118.81	108.23
1	e	18	ARG	N-CA-C	-6.91	103.75	111.28
2	w	132	VAL	N-CA-C	6.91	118.81	108.23
1	r	82	THR	N-CA-C	6.89	118.79	111.28
1	h	18	ARG	N-CA-C	-6.88	103.78	111.28
1	k	18	ARG	N-CA-C	-6.87	103.79	111.28
2	t	273	ALA	N-CA-C	6.87	118.77	111.28
1	d	48	THR	N-CA-C	6.87	118.42	111.07
1	b	18	ARG	N-CA-C	-6.87	103.80	111.28
2	x	273	ALA	N-CA-C	6.86	118.76	111.28
2	u	43	GLN	N-CA-C	-6.84	98.91	109.52
2	w	43	GLN	N-CA-C	-6.84	98.91	109.52
2	v	273	ALA	N-CA-C	6.84	118.73	111.28
2	u	436	GLU	N-CA-C	6.83	121.09	111.52
2	w	436	GLU	N-CA-C	6.83	121.08	111.52
2	v	43	GLN	N-CA-C	-6.83	98.94	109.52
2	x	43	GLN	N-CA-C	-6.82	98.94	109.52
1	j	46	ILE	N-CA-C	6.82	116.97	110.42
2	t	43	GLN	N-CA-C	-6.82	98.95	109.52
4	X	99	ARG	N-CA-C	-6.82	97.62	108.73
2	t	436	GLU	N-CA-C	6.81	121.05	111.52
2	w	328	SER	N-CA-C	6.81	119.47	110.08
2	s	273	ALA	N-CA-C	6.80	118.70	111.28
2	v	436	GLU	N-CA-C	6.80	121.05	111.52
2	s	43	GLN	N-CA-C	-6.80	98.97	109.52
2	u	273	ALA	N-CA-C	6.80	118.69	111.28
1	p	46	ILE	N-CA-C	6.80	116.94	110.42
2	w	273	ALA	N-CA-C	6.79	118.68	111.28
2	x	38	GLU	N-CA-C	6.79	118.34	111.07
2	s	436	GLU	N-CA-C	6.79	121.02	111.52
2	x	436	GLU	N-CA-C	6.78	121.02	111.52
1	m	48	THR	N-CA-C	6.78	118.32	111.07
1	g	46	ILE	N-CA-C	6.78	116.92	110.42
2	v	38	GLU	N-CA-C	6.77	118.31	111.07
2	w	38	GLU	N-CA-C	6.77	118.31	111.07
1	m	46	ILE	N-CA-C	6.76	116.92	110.42
2	u	328	SER	N-CA-C	6.76	119.42	110.08
2	s	755	PHE	CA-C-N	-6.76	112.49	120.13
2	s	755	PHE	C-N-CA	-6.76	112.49	120.13
2	u	755	PHE	CA-C-N	-6.76	112.49	120.13
2	u	755	PHE	C-N-CA	-6.76	112.49	120.13
4	W	9	GLU	N-CA-C	-6.76	98.01	108.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	g	48	THR	N-CA-C	6.76	118.30	111.07
2	u	774	THR	CA-C-N	-6.76	112.80	119.76
2	u	774	THR	C-N-CA	-6.76	112.80	119.76
2	t	38	GLU	N-CA-C	6.75	118.30	111.07
2	x	328	SER	N-CA-C	6.75	119.39	110.08
2	s	328	SER	N-CA-C	6.74	119.39	110.08
1	j	48	THR	N-CA-C	6.74	118.28	111.07
2	t	699	GLY	N-CA-C	6.73	118.34	111.95
1	a	48	THR	N-CA-C	6.73	118.27	111.07
2	v	328	SER	N-CA-C	6.73	119.37	110.08
2	u	38	GLU	N-CA-C	6.73	118.27	111.07
1	p	48	THR	N-CA-C	6.72	118.27	111.07
2	t	755	PHE	CA-C-N	-6.72	112.53	120.13
2	t	755	PHE	C-N-CA	-6.72	112.53	120.13
2	s	38	GLU	N-CA-C	6.72	118.26	111.07
2	u	699	GLY	N-CA-C	6.72	118.33	111.95
2	v	699	GLY	N-CA-C	6.72	118.33	111.95
2	v	774	THR	CA-C-N	-6.72	112.84	119.76
2	v	774	THR	C-N-CA	-6.72	112.84	119.76
2	t	774	THR	CA-C-N	-6.71	112.85	119.76
2	t	774	THR	C-N-CA	-6.71	112.85	119.76
2	t	328	SER	N-CA-C	6.71	119.33	110.08
2	x	755	PHE	CA-C-N	-6.71	112.55	120.13
2	x	755	PHE	C-N-CA	-6.71	112.55	120.13
2	u	622	TYR	N-CA-C	-6.70	101.50	110.55
2	v	755	PHE	CA-C-N	-6.70	112.56	120.13
2	v	755	PHE	C-N-CA	-6.70	112.56	120.13
1	d	46	ILE	N-CA-C	6.70	116.85	110.42
2	w	755	PHE	CA-C-N	-6.70	112.56	120.13
2	w	755	PHE	C-N-CA	-6.70	112.56	120.13
2	s	774	THR	CA-C-N	-6.70	112.86	119.76
2	s	774	THR	C-N-CA	-6.70	112.86	119.76
2	x	774	THR	CA-C-N	-6.70	112.86	119.76
2	x	774	THR	C-N-CA	-6.70	112.86	119.76
2	t	622	TYR	N-CA-C	-6.69	101.52	110.55
2	w	774	THR	CA-C-N	-6.68	112.88	119.76
2	w	774	THR	C-N-CA	-6.68	112.88	119.76
2	x	622	TYR	N-CA-C	-6.68	101.53	110.55
1	a	46	ILE	N-CA-C	6.68	116.83	110.42
2	s	622	TYR	N-CA-C	-6.68	101.53	110.55
2	w	699	GLY	N-CA-C	6.67	118.29	111.95
2	w	622	TYR	N-CA-C	-6.67	101.55	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	v	622	TYR	N-CA-C	-6.66	101.56	110.55
2	u	713	SER	N-CA-C	6.64	119.26	109.24
2	v	254	PHE	N-CA-C	-6.63	104.05	111.28
2	s	699	GLY	N-CA-C	6.63	118.25	111.95
2	s	713	SER	N-CA-C	6.63	119.25	109.24
3	D	85	ILE	N-CA-C	6.63	117.13	110.23
2	s	319	ASN	N-CA-C	-6.63	99.38	109.85
2	t	319	ASN	N-CA-C	-6.62	99.39	109.85
2	w	319	ASN	N-CA-C	-6.62	99.39	109.85
2	x	699	GLY	N-CA-C	6.62	118.24	111.95
2	u	319	ASN	N-CA-C	-6.62	99.40	109.85
2	v	319	ASN	N-CA-C	-6.62	99.39	109.85
2	x	254	PHE	N-CA-C	-6.62	104.07	111.28
2	x	319	ASN	N-CA-C	-6.61	99.40	109.85
2	w	713	SER	N-CA-C	6.60	119.20	109.24
2	t	713	SER	N-CA-C	6.59	119.19	109.24
2	w	254	PHE	N-CA-C	-6.59	104.10	111.28
4	U	9	GLU	N-CA-C	-6.58	96.77	110.80
2	v	713	SER	N-CA-C	6.58	119.18	109.24
2	t	254	PHE	N-CA-C	-6.58	104.11	111.28
2	u	254	PHE	N-CA-C	-6.58	104.11	111.28
2	x	713	SER	N-CA-C	6.58	119.17	109.24
3	F	87	GLU	N-CA-C	6.57	121.47	113.38
2	s	201	ALA	N-CA-C	6.57	118.52	111.36
2	s	254	PHE	N-CA-C	-6.57	104.12	111.28
2	w	602	ILE	CA-C-N	-6.56	113.88	120.31
2	w	602	ILE	C-N-CA	-6.56	113.88	120.31
2	u	201	ALA	N-CA-C	6.56	118.51	111.36
2	x	660	GLY	N-CA-C	-6.55	103.14	111.72
2	v	201	ALA	N-CA-C	6.55	118.50	111.36
2	s	660	GLY	N-CA-C	-6.54	103.15	111.72
2	x	375	PHE	N-CA-C	6.54	121.42	113.17
2	w	201	ALA	N-CA-C	6.54	118.49	111.36
2	t	660	GLY	N-CA-C	-6.54	103.16	111.72
2	v	602	ILE	CA-C-N	-6.53	113.91	120.31
2	v	602	ILE	C-N-CA	-6.53	113.91	120.31
2	v	660	GLY	N-CA-C	-6.53	103.17	111.72
2	u	660	GLY	N-CA-C	-6.52	103.18	111.72
2	x	201	ALA	N-CA-C	6.52	118.47	111.36
2	t	602	ILE	CA-C-N	-6.52	113.92	120.31
2	t	602	ILE	C-N-CA	-6.52	113.92	120.31
2	v	375	PHE	N-CA-C	6.52	121.38	113.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	t	201	ALA	N-CA-C	6.51	118.46	111.36
2	u	602	ILE	CA-C-N	-6.51	113.93	120.31
2	u	602	ILE	C-N-CA	-6.51	113.93	120.31
2	w	660	GLY	N-CA-C	-6.51	103.19	111.72
2	x	602	ILE	CA-C-N	-6.51	113.93	120.31
2	x	602	ILE	C-N-CA	-6.51	113.93	120.31
1	k	63	ALA	N-CA-C	-6.50	98.62	108.96
2	u	375	PHE	N-CA-C	6.50	121.36	113.17
2	w	375	PHE	N-CA-C	6.50	121.35	113.17
1	e	63	ALA	N-CA-C	-6.49	98.63	108.96
2	t	375	PHE	N-CA-C	6.49	121.35	113.17
1	q	63	ALA	N-CA-C	-6.49	98.64	108.96
2	v	366	ILE	N-CA-C	-6.49	97.60	107.73
1	b	63	ALA	N-CA-C	-6.49	98.64	108.96
1	h	63	ALA	N-CA-C	-6.49	98.64	108.96
1	n	63	ALA	N-CA-C	-6.49	98.64	108.96
2	s	375	PHE	N-CA-C	6.48	121.34	113.17
2	s	602	ILE	CA-C-N	-6.48	113.96	120.31
2	s	602	ILE	C-N-CA	-6.48	113.96	120.31
2	t	366	ILE	N-CA-C	-6.48	97.62	107.73
2	w	366	ILE	N-CA-C	-6.48	97.62	107.73
2	x	118	MET	N-CA-C	6.48	119.02	109.24
2	s	366	ILE	N-CA-C	-6.47	97.63	107.73
2	u	366	ILE	N-CA-C	-6.47	97.63	107.73
2	s	118	MET	N-CA-C	6.47	119.01	109.24
2	v	27	GLN	N-CA-C	-6.47	99.51	109.14
2	x	366	ILE	N-CA-C	-6.46	97.65	107.73
1	i	5	ILE	N-CA-C	-6.46	101.21	109.80
2	u	27	GLN	N-CA-C	-6.45	99.53	109.14
1	k	4	VAL	N-CA-C	6.45	118.38	109.80
2	t	118	MET	N-CA-C	6.45	118.98	109.24
1	l	5	ILE	N-CA-C	-6.44	101.23	109.80
2	s	27	GLN	N-CA-C	-6.44	99.55	109.14
2	t	27	GLN	N-CA-C	-6.44	99.55	109.14
1	e	4	VAL	N-CA-C	6.43	118.36	109.80
1	f	5	ILE	N-CA-C	-6.43	101.24	109.80
1	o	5	ILE	N-CA-C	-6.43	101.25	109.80
2	u	118	MET	N-CA-C	6.43	118.95	109.24
2	w	118	MET	N-CA-C	6.43	118.94	109.24
1	c	5	ILE	N-CA-C	-6.42	101.25	109.80
1	n	4	VAL	N-CA-C	6.42	118.35	109.80
2	w	27	GLN	N-CA-C	-6.42	99.57	109.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	v	118	MET	N-CA-C	6.41	118.92	109.24
2	x	27	GLN	N-CA-C	-6.41	99.58	109.14
1	q	4	VAL	N-CA-C	6.41	118.32	109.80
1	r	5	ILE	N-CA-C	-6.40	101.29	109.80
1	b	4	VAL	N-CA-C	6.40	118.31	109.80
1	n	93	ILE	N-CA-C	-6.39	101.34	109.58
1	k	93	ILE	N-CA-C	-6.38	101.34	109.58
2	s	461	ALA	N-CA-C	6.38	119.30	108.90
2	x	461	ALA	N-CA-C	6.38	119.30	108.90
2	t	461	ALA	N-CA-C	6.36	119.27	108.90
2	u	461	ALA	N-CA-C	6.36	119.27	108.90
1	b	93	ILE	N-CA-C	-6.35	101.39	109.58
1	h	4	VAL	N-CA-C	6.35	118.24	109.80
1	e	93	ILE	N-CA-C	-6.35	101.39	109.58
1	h	93	ILE	N-CA-C	-6.34	101.41	109.58
2	v	461	ALA	N-CA-C	6.34	119.23	108.90
1	q	19	ASP	N-CA-C	6.33	119.06	108.73
1	h	68	ASP	N-CA-C	-6.32	104.44	111.71
1	n	19	ASP	N-CA-C	6.32	119.04	108.73
1	r	13	LEU	N-CA-C	6.32	119.53	110.24
2	w	461	ALA	N-CA-C	6.32	119.20	108.90
1	b	19	ASP	N-CA-C	6.32	119.03	108.73
1	b	68	ASP	N-CA-C	-6.31	104.45	111.71
2	v	430	LEU	N-CA-C	-6.31	100.50	109.96
1	k	68	ASP	N-CA-C	-6.31	104.46	111.71
4	S	9	GLU	N-CA-C	-6.31	98.71	108.42
1	e	19	ASP	N-CA-C	6.31	119.01	108.73
1	k	19	ASP	N-CA-C	6.30	119.00	108.73
2	s	430	LEU	N-CA-C	-6.30	100.51	109.96
2	t	444	ASP	N-CA-C	6.30	119.05	110.55
1	h	19	ASP	N-CA-C	6.30	118.99	108.73
2	s	444	ASP	N-CA-C	6.30	119.05	110.55
2	x	430	LEU	N-CA-C	-6.30	100.52	109.96
2	w	430	LEU	N-CA-C	-6.29	100.52	109.96
1	q	93	ILE	N-CA-C	-6.29	101.46	109.58
1	c	13	LEU	N-CA-C	6.29	119.48	110.24
1	o	13	LEU	N-CA-C	6.28	119.48	110.24
1	e	68	ASP	N-CA-C	-6.28	104.49	111.71
2	w	444	ASP	N-CA-C	6.28	119.02	110.55
4	R	65	GLU	N-CA-C	6.27	118.12	111.28
2	v	444	ASP	N-CA-C	6.27	119.02	110.55
2	u	430	LEU	N-CA-C	-6.27	100.55	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	u	454	ILE	N-CA-C	-6.27	98.17	107.51
2	u	602	ILE	CB-CA-C	6.27	117.89	110.68
2	x	602	ILE	CB-CA-C	6.27	117.89	110.68
1	i	13	LEU	N-CA-C	6.27	119.45	110.24
1	n	68	ASP	N-CA-C	-6.27	104.50	111.71
2	t	430	LEU	N-CA-C	-6.27	100.56	109.96
1	q	68	ASP	N-CA-C	-6.26	104.51	111.71
2	s	511	PHE	N-CA-C	6.26	119.76	107.98
2	t	602	ILE	CB-CA-C	6.26	117.88	110.68
2	x	511	PHE	N-CA-C	6.26	119.75	107.98
4	V	65	GLU	N-CA-C	6.26	118.10	111.28
2	v	602	ILE	CB-CA-C	6.25	117.87	110.68
2	t	511	PHE	N-CA-C	6.25	119.73	107.98
1	m	69	GLY	N-CA-C	-6.25	106.00	115.00
2	v	511	PHE	N-CA-C	6.25	119.73	107.98
2	x	444	ASP	N-CA-C	6.25	118.99	110.55
1	p	69	GLY	N-CA-C	-6.24	106.01	115.00
2	u	511	PHE	N-CA-C	6.24	119.72	107.98
2	s	454	ILE	N-CA-C	-6.24	98.21	107.51
2	w	511	PHE	N-CA-C	6.24	119.71	107.98
4	P	65	GLU	N-CA-C	6.24	118.08	111.28
4	T	72	ASP	N-CA-C	-6.24	100.80	110.10
1	f	13	LEU	N-CA-C	6.24	119.41	110.24
1	j	69	GLY	N-CA-C	-6.24	106.02	115.00
4	N	65	GLU	N-CA-C	6.24	118.08	111.28
4	V	72	ASP	N-CA-C	-6.24	100.81	110.10
2	t	454	ILE	N-CA-C	-6.23	98.22	107.51
2	u	444	ASP	N-CA-C	6.23	118.97	110.55
4	X	65	GLU	N-CA-C	6.23	118.07	111.28
2	w	454	ILE	N-CA-C	-6.23	98.23	107.51
2	s	602	ILE	CB-CA-C	6.22	117.84	110.68
1	l	13	LEU	N-CA-C	6.22	119.39	110.24
1	l	17	ASN	N-CA-C	6.22	119.70	108.69
1	a	69	GLY	N-CA-C	-6.22	106.04	115.00
4	T	65	GLU	N-CA-C	6.22	118.06	111.28
1	g	69	GLY	N-CA-C	-6.22	106.05	115.00
2	v	454	ILE	N-CA-C	-6.21	98.25	107.51
1	i	17	ASN	N-CA-C	6.21	119.69	108.69
1	d	69	GLY	N-CA-C	-6.21	106.06	115.00
2	w	602	ILE	CB-CA-C	6.21	117.82	110.68
4	N	72	ASP	N-CA-C	-6.21	100.85	110.10
4	R	72	ASP	N-CA-C	-6.21	100.85	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	x	454	ILE	N-CA-C	-6.20	98.27	107.51
4	P	72	ASP	N-CA-C	-6.20	100.86	110.10
1	o	17	ASN	N-CA-C	6.19	119.65	108.69
1	f	17	ASN	N-CA-C	6.19	119.65	108.69
4	X	72	ASP	N-CA-C	-6.19	100.88	110.10
1	c	17	ASN	N-CA-C	6.18	119.64	108.69
2	u	146	TYR	N-CA-C	-6.18	100.89	110.10
2	w	61	GLY	N-CA-C	6.18	121.96	112.51
2	w	146	TYR	N-CA-C	-6.17	100.90	110.10
2	s	61	GLY	N-CA-C	6.17	121.95	112.51
2	t	146	TYR	N-CA-C	-6.17	100.91	110.10
1	p	79	THR	N-CA-C	-6.16	100.92	110.10
2	x	146	TYR	N-CA-C	-6.16	100.92	110.10
1	m	79	THR	N-CA-C	-6.16	100.92	110.10
2	v	146	TYR	N-CA-C	-6.16	100.92	110.10
2	t	61	GLY	N-CA-C	6.16	121.93	112.51
1	r	17	ASN	N-CA-C	6.16	119.59	108.69
2	s	146	TYR	N-CA-C	-6.16	100.93	110.10
2	u	61	GLY	N-CA-C	6.16	121.93	112.51
2	x	61	GLY	N-CA-C	6.16	121.93	112.51
1	d	79	THR	N-CA-C	-6.15	100.93	110.10
1	a	79	THR	N-CA-C	-6.15	100.94	110.10
1	g	79	THR	N-CA-C	-6.15	100.94	110.10
1	j	79	THR	N-CA-C	-6.14	100.96	110.10
2	v	61	GLY	N-CA-C	6.13	121.89	112.51
3	B	93	SER	N-CA-C	-6.11	104.62	111.28
3	E	87	GLU	N-CA-C	6.11	117.74	111.14
2	w	388	ASP	N-CA-C	-6.09	105.43	112.92
2	u	759	GLY	N-CA-C	6.08	118.78	110.69
2	s	759	GLY	N-CA-C	6.08	118.78	110.69
2	t	759	GLY	N-CA-C	6.08	118.78	110.69
2	x	759	GLY	N-CA-C	6.08	118.77	110.69
1	k	115	ASP	N-CA-C	6.07	117.98	111.36
2	v	759	GLY	N-CA-C	6.07	118.77	110.69
2	w	759	GLY	N-CA-C	6.07	118.76	110.69
1	j	93	ILE	N-CA-C	-6.07	98.27	107.73
1	n	41	ARG	N-CA-C	-6.06	101.07	110.10
2	u	388	ASP	N-CA-C	-6.05	105.48	112.92
2	s	352	PHE	N-CA-C	6.04	119.39	108.69
1	b	41	ARG	N-CA-C	-6.04	101.10	110.10
1	k	41	ARG	N-CA-C	-6.04	101.10	110.10
4	O	67	ILE	N-CA-C	-6.04	99.99	108.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	x	352	PHE	N-CA-C	6.03	119.37	108.69
2	x	465	SER	N-CA-C	6.03	117.52	111.07
4	Q	67	ILE	N-CA-C	-6.03	100.00	108.80
2	s	465	SER	N-CA-C	6.02	117.52	111.07
2	t	371	THR	N-CA-C	6.02	117.84	111.28
4	M	67	ILE	N-CA-C	-6.02	100.01	108.80
1	e	115	ASP	N-CA-C	6.01	117.92	111.36
1	q	115	ASP	N-CA-C	6.01	117.91	111.36
2	s	388	ASP	N-CA-C	-6.01	105.53	112.92
4	S	67	ILE	N-CA-C	-6.01	100.02	108.80
2	v	352	PHE	N-CA-C	6.01	119.33	108.69
2	v	371	THR	N-CA-C	6.01	117.83	111.28
2	w	371	THR	N-CA-C	6.01	117.83	111.28
2	t	465	SER	N-CA-C	6.01	117.50	111.07
2	w	352	PHE	N-CA-C	6.01	119.32	108.69
2	w	465	SER	N-CA-C	6.01	117.50	111.07
2	t	352	PHE	N-CA-C	6.00	119.32	108.69
1	d	93	ILE	N-CA-C	-6.00	98.36	107.73
1	b	115	ASP	N-CA-C	6.00	117.90	111.36
2	u	371	THR	N-CA-C	6.00	117.82	111.28
2	x	371	THR	N-CA-C	6.00	117.82	111.28
1	h	115	ASP	N-CA-C	5.99	117.89	111.36
2	u	352	PHE	N-CA-C	5.99	119.30	108.69
4	W	67	ILE	N-CA-C	-5.99	100.05	108.80
2	v	465	SER	N-CA-C	5.99	117.48	111.07
2	t	434	SER	N-CA-C	5.99	120.60	112.88
4	U	67	ILE	N-CA-C	-5.99	100.06	108.80
1	e	41	ARG	N-CA-C	-5.98	101.19	110.10
1	b	21	ASN	N-CA-C	5.98	118.40	109.25
1	q	41	ARG	N-CA-C	-5.98	101.19	110.10
2	w	288	ARG	N-CA-C	-5.98	99.45	109.07
1	h	21	ASN	N-CA-C	5.97	118.39	109.25
1	n	115	ASP	N-CA-C	5.97	117.87	111.36
2	v	434	SER	N-CA-C	5.97	120.58	112.88
1	h	41	ARG	N-CA-C	-5.97	101.21	110.10
1	n	21	ASN	N-CA-C	5.97	118.38	109.25
2	s	288	ARG	N-CA-C	-5.97	99.46	109.07
2	u	40	GLU	N-CA-C	-5.97	102.65	110.53
2	t	40	GLU	N-CA-C	-5.96	102.66	110.53
2	x	434	SER	N-CA-C	5.96	120.57	112.88
2	s	40	GLU	N-CA-C	-5.96	102.67	110.53
2	u	465	SER	N-CA-C	5.96	117.44	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	w	434	SER	N-CA-C	5.96	120.56	112.88
1	q	21	ASN	N-CA-C	5.95	118.36	109.25
2	u	288	ARG	N-CA-C	-5.95	99.49	109.07
4	S	102	TYR	N-CA-C	5.95	118.89	110.50
2	v	288	ARG	N-CA-C	-5.94	99.50	109.07
2	s	371	THR	N-CA-C	5.94	117.76	111.28
2	t	288	ARG	N-CA-C	-5.94	99.50	109.07
2	u	434	SER	N-CA-C	5.94	120.54	112.88
1	m	100	ASN	N-CA-C	5.94	117.83	111.36
2	v	40	GLU	N-CA-C	-5.94	102.69	110.53
4	O	102	TYR	N-CA-C	5.94	118.87	110.50
4	Q	102	TYR	N-CA-C	5.93	118.87	110.50
1	a	100	ASN	N-CA-C	5.93	117.83	111.36
1	k	21	ASN	N-CA-C	5.93	118.32	109.25
2	s	434	SER	N-CA-C	5.93	120.53	112.88
2	x	288	ARG	N-CA-C	-5.93	99.53	109.07
1	g	100	ASN	N-CA-C	5.92	117.82	111.36
2	x	245	ASN	CA-C-N	-5.92	113.84	119.76
2	x	245	ASN	C-N-CA	-5.92	113.84	119.76
2	u	245	ASN	CA-C-N	-5.92	113.84	119.76
2	u	245	ASN	C-N-CA	-5.92	113.84	119.76
4	M	102	TYR	N-CA-C	5.92	118.85	110.50
2	w	245	ASN	CA-C-N	-5.92	113.84	119.76
2	w	245	ASN	C-N-CA	-5.92	113.84	119.76
2	s	722	ASN	N-CA-C	-5.92	100.35	109.52
2	w	715	THR	CB-CA-C	-5.92	100.67	109.90
2	v	722	ASN	N-CA-C	-5.91	100.36	109.52
2	x	722	ASN	N-CA-C	-5.91	100.36	109.52
1	e	21	ASN	N-CA-C	5.91	118.29	109.25
2	t	722	ASN	N-CA-C	-5.91	100.36	109.52
2	x	40	GLU	N-CA-C	-5.91	102.73	110.53
4	W	102	TYR	N-CA-C	5.91	118.83	110.50
2	s	245	ASN	CA-C-N	-5.91	113.85	119.76
2	s	245	ASN	C-N-CA	-5.91	113.85	119.76
2	u	715	THR	CB-CA-C	-5.91	100.68	109.90
4	U	102	TYR	N-CA-C	5.91	118.83	110.50
2	v	131	ASN	N-CA-C	5.91	117.80	111.36
2	x	715	THR	CB-CA-C	-5.90	100.69	109.90
2	s	715	THR	CB-CA-C	-5.90	100.69	109.90
2	v	715	THR	CB-CA-C	-5.90	100.70	109.90
1	p	100	ASN	N-CA-C	5.90	117.79	111.36
2	t	738	SER	N-CA-C	-5.90	102.59	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	w	40	GLU	N-CA-C	-5.90	102.75	110.53
2	t	245	ASN	CA-C-N	-5.90	113.86	119.76
2	t	245	ASN	C-N-CA	-5.90	113.86	119.76
2	v	738	SER	N-CA-C	-5.89	102.59	110.55
2	w	722	ASN	N-CA-C	-5.89	100.39	109.52
2	t	162	GLY	N-CA-C	5.88	120.95	113.24
2	t	715	THR	CB-CA-C	-5.88	100.72	109.90
2	u	162	GLY	N-CA-C	5.88	120.95	113.24
2	s	162	GLY	N-CA-C	5.88	120.95	113.24
2	u	131	ASN	N-CA-C	5.88	117.77	111.36
2	x	131	ASN	N-CA-C	5.88	117.77	111.36
4	Q	191	SER	N-CA-C	-5.88	104.95	111.71
1	q	26	TYR	N-CA-C	5.88	118.10	108.52
2	v	162	GLY	N-CA-C	5.88	120.94	113.24
2	v	245	ASN	CA-C-N	-5.88	113.89	119.76
2	v	245	ASN	C-N-CA	-5.88	113.89	119.76
2	w	162	GLY	N-CA-C	5.88	120.94	113.24
2	x	738	SER	N-CA-C	-5.88	102.62	110.55
1	n	36	LEU	N-CA-C	5.87	118.78	108.56
2	x	162	GLY	N-CA-C	5.87	120.94	113.24
2	w	738	SER	N-CA-C	-5.87	102.62	110.55
1	d	100	ASN	N-CA-C	5.87	117.76	111.36
1	k	36	LEU	N-CA-C	5.87	118.77	108.56
2	t	131	ASN	N-CA-C	5.87	117.75	111.36
2	w	131	ASN	N-CA-C	5.86	117.75	111.36
2	u	722	ASN	N-CA-C	-5.86	100.44	109.52
4	O	191	SER	N-CA-C	-5.86	104.97	111.71
1	h	26	TYR	N-CA-C	5.85	118.06	108.52
1	k	26	TYR	N-CA-C	5.85	118.06	108.52
2	u	738	SER	N-CA-C	-5.85	102.65	110.55
2	s	738	SER	N-CA-C	-5.85	102.66	110.55
1	h	36	LEU	N-CA-C	5.84	118.73	108.56
1	e	36	LEU	N-CA-C	5.84	118.73	108.56
1	b	36	LEU	N-CA-C	5.84	118.72	108.56
1	j	100	ASN	N-CA-C	5.84	117.72	111.36
1	n	26	TYR	N-CA-C	5.84	118.03	108.52
2	s	131	ASN	N-CA-C	5.84	117.72	111.36
1	q	36	LEU	N-CA-C	5.83	118.71	108.56
1	g	93	ILE	N-CA-C	-5.83	98.23	107.15
4	W	191	SER	N-CA-C	-5.83	105.01	111.71
1	b	26	TYR	N-CA-C	5.82	118.01	108.52
1	m	93	ILE	N-CA-C	-5.82	98.25	107.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	t	58	GLY	N-CA-C	5.82	120.22	112.77
1	p	93	ILE	N-CA-C	-5.81	98.26	107.15
2	v	58	GLY	N-CA-C	5.81	120.20	112.77
4	S	191	SER	N-CA-C	-5.80	105.03	111.71
1	e	26	TYR	N-CA-C	5.80	117.98	108.52
2	s	58	GLY	N-CA-C	5.80	120.20	112.77
2	w	58	GLY	N-CA-C	5.79	120.19	112.77
2	x	58	GLY	N-CA-C	5.79	120.18	112.77
4	U	191	SER	N-CA-C	-5.79	105.06	111.71
4	M	191	SER	N-CA-C	-5.78	105.07	111.71
2	u	58	GLY	N-CA-C	5.77	120.15	112.77
1	a	93	ILE	N-CA-C	-5.76	98.34	107.15
1	c	18	ARG	N-CA-C	-5.76	104.93	112.41
1	i	18	ARG	N-CA-C	-5.76	104.93	112.41
1	r	18	ARG	N-CA-C	-5.74	104.94	112.41
1	d	36	LEU	N-CA-C	-5.74	100.43	109.50
1	m	36	LEU	N-CA-C	-5.74	100.43	109.50
1	r	73	ILE	CB-CA-C	-5.74	103.95	111.81
1	d	25	GLU	N-CA-C	5.74	118.30	110.55
3	A	87	GLU	N-CA-C	5.74	120.44	113.38
1	p	36	LEU	N-CA-C	-5.73	100.44	109.50
2	w	658	LEU	N-CA-C	-5.73	100.64	109.52
1	m	25	GLU	N-CA-C	5.73	118.28	110.55
2	s	374	TYR	N-CA-C	5.73	117.52	111.28
1	o	18	ARG	N-CA-C	-5.72	104.97	112.41
1	a	25	GLU	N-CA-C	5.72	118.27	110.55
1	p	25	GLU	N-CA-C	5.72	118.27	110.55
2	v	22	LEU	N-CA-C	5.72	117.59	111.36
1	j	25	GLU	N-CA-C	5.72	118.27	110.55
1	i	73	ILE	CB-CA-C	-5.71	103.98	111.81
1	q	112	GLU	N-CA-C	-5.71	105.05	111.28
2	t	658	LEU	N-CA-C	-5.71	100.67	109.52
1	f	73	ILE	CB-CA-C	-5.71	103.99	111.81
1	a	36	LEU	N-CA-C	-5.71	100.49	109.50
1	o	73	ILE	CB-CA-C	-5.71	103.99	111.81
2	s	658	LEU	N-CA-C	-5.70	100.68	109.52
2	v	658	LEU	N-CA-C	-5.70	100.68	109.52
1	f	18	ARG	N-CA-C	-5.70	105.00	112.41
1	j	36	LEU	N-CA-C	-5.70	100.49	109.50
1	g	25	GLU	N-CA-C	5.70	118.24	110.55
2	v	374	TYR	N-CA-C	5.69	117.48	111.28
2	x	374	TYR	N-CA-C	5.69	117.48	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	b	112	GLU	N-CA-C	-5.69	105.08	111.28
1	l	18	ARG	N-CA-C	-5.69	105.01	112.41
2	w	374	TYR	N-CA-C	5.69	117.48	111.28
2	s	684	ILE	CB-CA-C	-5.69	102.86	111.33
2	u	658	LEU	N-CA-C	-5.69	100.71	109.52
1	g	36	LEU	N-CA-C	-5.68	100.53	109.50
2	t	684	ILE	CB-CA-C	-5.68	102.87	111.33
1	c	73	ILE	CB-CA-C	-5.68	104.03	111.81
2	u	374	TYR	N-CA-C	5.68	117.47	111.28
2	s	22	LEU	N-CA-C	5.67	117.55	111.36
1	e	112	GLU	N-CA-C	-5.67	105.10	111.28
2	x	658	LEU	N-CA-C	-5.67	100.73	109.52
1	l	73	ILE	CB-CA-C	-5.67	104.04	111.81
1	k	112	GLU	N-CA-C	-5.67	105.10	111.28
2	t	374	TYR	N-CA-C	5.66	117.45	111.28
2	u	22	LEU	N-CA-C	5.66	117.53	111.36
2	x	22	LEU	N-CA-C	5.66	117.53	111.36
1	b	32	VAL	N-CA-C	5.66	116.36	108.89
1	n	112	GLU	N-CA-C	-5.65	105.12	111.28
2	v	148	PRO	N-CA-C	-5.65	105.83	113.40
2	x	684	ILE	CB-CA-C	-5.65	102.91	111.33
1	d	78	VAL	CB-CA-C	-5.65	102.02	111.29
2	t	22	LEU	N-CA-C	5.65	117.52	111.36
2	v	684	ILE	CB-CA-C	-5.64	102.92	111.33
2	w	22	LEU	N-CA-C	5.64	117.51	111.36
1	h	112	GLU	N-CA-C	-5.64	105.13	111.28
2	u	684	ILE	CB-CA-C	-5.64	102.93	111.33
2	w	684	ILE	CB-CA-C	-5.64	102.93	111.33
2	u	148	PRO	N-CA-C	-5.63	105.85	113.40
1	q	32	VAL	N-CA-C	5.63	116.32	108.89
1	e	32	VAL	N-CA-C	5.63	116.32	108.89
2	w	148	PRO	N-CA-C	-5.63	105.86	113.40
1	k	32	VAL	N-CA-C	5.62	116.31	108.89
1	n	32	VAL	N-CA-C	5.62	116.31	108.89
2	s	382	ILE	CB-CA-C	-5.62	104.47	112.22
2	w	382	ILE	CB-CA-C	-5.61	104.47	112.22
2	v	382	ILE	CB-CA-C	-5.61	104.47	112.22
2	u	382	ILE	CB-CA-C	-5.61	104.48	112.22
1	a	78	VAL	CB-CA-C	-5.61	102.09	111.29
1	r	93	ILE	N-CA-C	-5.60	101.44	108.84
2	x	382	ILE	CB-CA-C	-5.60	104.49	112.22
2	t	382	ILE	CB-CA-C	-5.60	104.49	112.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	x	646	PRO	N-CA-C	-5.60	102.40	111.19
2	s	646	PRO	N-CA-C	-5.60	102.40	111.19
2	u	646	PRO	N-CA-C	-5.60	102.40	111.19
2	v	646	PRO	N-CA-C	-5.60	102.40	111.19
2	x	464	ARG	N-CA-C	-5.60	101.01	108.34
1	h	32	VAL	N-CA-C	5.59	116.27	108.89
1	j	78	VAL	CB-CA-C	-5.59	102.12	111.29
2	w	646	PRO	N-CA-C	-5.59	102.41	111.19
2	x	148	PRO	N-CA-C	-5.59	105.91	113.40
2	t	148	PRO	N-CA-C	-5.59	105.91	113.40
2	t	646	PRO	N-CA-C	-5.59	102.42	111.19
1	o	93	ILE	N-CA-CB	5.59	117.18	110.31
2	s	148	PRO	N-CA-C	-5.59	105.91	113.40
2	w	464	ARG	N-CA-C	-5.58	101.02	108.34
1	g	78	VAL	CB-CA-C	-5.58	102.14	111.29
3	A	92	GLY	N-CA-C	5.58	120.48	111.38
1	p	78	VAL	CB-CA-C	-5.58	102.14	111.29
1	m	78	VAL	CB-CA-C	-5.58	102.14	111.29
2	u	464	ARG	N-CA-C	-5.58	101.03	108.34
2	v	464	ARG	N-CA-C	-5.58	101.04	108.34
1	f	93	ILE	N-CA-C	-5.57	101.49	108.84
2	u	666	MET	N-CA-C	-5.57	99.30	108.49
2	s	464	ARG	N-CA-C	-5.57	101.05	108.34
2	v	666	MET	N-CA-C	-5.57	99.31	108.49
1	l	93	ILE	N-CA-C	-5.56	101.50	108.84
2	w	666	MET	N-CA-C	-5.55	99.33	108.49
2	t	666	MET	N-CA-C	-5.55	99.33	108.49
1	q	70	TYR	N-CA-C	-5.55	98.68	108.23
2	x	298	ASN	CA-C-N	-5.55	115.17	123.00
2	x	298	ASN	C-N-CA	-5.55	115.17	123.00
1	c	93	ILE	N-CA-C	-5.55	101.52	108.84
2	x	666	MET	N-CA-C	-5.54	99.34	108.49
1	i	93	ILE	N-CA-C	-5.54	101.53	108.84
1	k	70	TYR	N-CA-C	-5.54	98.70	108.23
2	v	425	THR	N-CA-C	5.54	117.42	108.34
2	t	595	ASP	N-CA-C	5.53	117.39	111.36
2	x	425	THR	N-CA-C	5.53	117.41	108.34
2	s	666	MET	N-CA-C	-5.53	99.37	108.49
2	t	425	THR	N-CA-C	5.53	117.41	108.34
2	u	533	GLU	N-CA-C	-5.53	105.22	112.41
2	w	595	ASP	N-CA-C	5.53	117.39	111.36
2	u	298	ASN	CA-C-N	-5.53	115.20	123.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	u	298	ASN	C-N-CA	-5.53	115.20	123.00
2	t	464	ARG	N-CA-C	-5.52	101.11	108.34
1	b	70	TYR	N-CA-C	-5.52	98.74	108.23
1	h	70	TYR	N-CA-C	-5.52	98.74	108.23
2	t	298	ASN	CA-C-N	-5.52	115.22	123.00
2	t	298	ASN	C-N-CA	-5.52	115.22	123.00
2	u	595	ASP	N-CA-C	5.51	117.37	111.36
2	w	298	ASN	CA-C-N	-5.51	115.22	123.00
2	w	298	ASN	C-N-CA	-5.51	115.22	123.00
2	s	298	ASN	CA-C-N	-5.51	115.23	123.00
2	s	298	ASN	C-N-CA	-5.51	115.23	123.00
2	w	425	THR	N-CA-C	5.51	117.37	108.34
2	x	595	ASP	N-CA-C	5.51	117.36	111.36
1	a	54	THR	N-CA-C	-5.50	102.74	110.50
1	e	70	TYR	N-CA-C	-5.50	98.77	108.23
1	p	54	THR	N-CA-C	-5.50	102.74	110.50
2	s	425	THR	N-CA-C	5.50	117.36	108.34
2	u	425	THR	N-CA-C	5.50	117.36	108.34
2	v	595	ASP	N-CA-C	5.50	117.35	111.36
2	x	716	PHE	N-CA-C	-5.50	99.72	109.06
1	d	48	THR	CB-CA-C	-5.49	102.25	110.88
1	g	54	THR	N-CA-C	-5.49	102.76	110.50
1	m	54	THR	N-CA-C	-5.49	102.76	110.50
2	t	533	GLU	N-CA-C	-5.49	105.28	112.41
1	d	54	THR	N-CA-C	-5.48	102.77	110.50
1	j	54	THR	N-CA-C	-5.48	102.77	110.50
4	Q	101	GLY	N-CA-C	-5.48	106.16	112.73
2	v	298	ASN	CA-C-N	-5.48	115.28	123.00
2	v	298	ASN	C-N-CA	-5.48	115.28	123.00
2	t	716	PHE	N-CA-C	-5.48	99.75	109.06
2	u	309	PRO	CB-CA-C	-5.48	104.69	111.64
2	w	716	PHE	N-CA-C	-5.48	99.75	109.06
2	x	533	GLU	N-CA-C	-5.47	105.29	112.41
2	s	595	ASP	N-CA-C	5.47	117.33	111.36
2	v	533	GLU	N-CA-C	-5.47	105.30	112.41
2	w	533	GLU	N-CA-C	-5.47	105.30	112.41
2	x	309	PRO	CB-CA-C	-5.47	104.69	111.64
2	s	533	GLU	N-CA-C	-5.47	105.30	112.41
2	w	309	PRO	CB-CA-C	-5.47	104.70	111.64
1	n	70	TYR	N-CA-C	-5.46	98.83	108.23
2	t	309	PRO	CB-CA-C	-5.46	104.71	111.64
1	h	47	ASN	N-CA-C	5.46	117.31	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	s	716	PHE	N-CA-C	-5.46	99.78	109.06
2	v	716	PHE	N-CA-C	-5.46	99.78	109.06
4	U	101	GLY	N-CA-C	-5.45	106.19	112.73
2	u	716	PHE	N-CA-C	-5.45	99.79	109.06
2	s	309	PRO	CB-CA-C	-5.45	104.72	111.64
4	W	7	ASN	N-CA-C	-5.44	101.80	109.96
1	b	47	ASN	N-CA-C	5.43	117.28	111.36
4	O	101	GLY	N-CA-C	-5.43	106.21	112.73
4	W	101	GLY	N-CA-C	-5.43	106.22	112.73
1	p	48	THR	CB-CA-C	-5.43	102.36	110.88
2	v	309	PRO	CB-CA-C	-5.43	104.75	111.64
1	m	48	THR	CB-CA-C	-5.43	102.36	110.88
1	r	53	ALA	N-CA-C	5.42	117.19	111.28
1	a	48	THR	CB-CA-C	-5.42	102.37	110.88
1	g	48	THR	CB-CA-C	-5.42	102.37	110.88
1	j	48	THR	CB-CA-C	-5.42	102.37	110.88
2	s	33	ASN	N-CA-C	5.42	118.91	111.54
1	k	47	ASN	N-CA-C	5.41	117.26	111.36
4	S	101	GLY	N-CA-C	-5.41	106.24	112.73
2	w	33	ASN	N-CA-C	5.41	118.90	111.54
2	x	33	ASN	N-CA-C	5.41	118.89	111.54
2	t	145	ASN	N-CA-C	-5.40	99.30	110.80
2	w	37	SER	N-CA-C	5.40	118.23	109.86
4	M	101	GLY	N-CA-C	-5.40	106.25	112.73
2	u	33	ASN	N-CA-C	5.40	118.88	111.54
2	w	680	SER	N-CA-C	5.40	122.30	110.80
1	e	47	ASN	N-CA-C	5.39	117.24	111.36
2	t	37	SER	N-CA-C	5.39	118.21	109.86
2	x	37	SER	N-CA-C	5.39	118.21	109.86
1	q	47	ASN	N-CA-C	5.39	117.23	111.36
2	s	145	ASN	N-CA-C	-5.39	99.33	110.80
2	x	145	ASN	N-CA-C	-5.39	99.33	110.80
1	l	101	VAL	CB-CA-C	-5.38	104.87	112.14
2	v	37	SER	N-CA-C	5.38	118.21	109.86
2	u	680	SER	N-CA-C	5.38	122.27	110.80
2	u	145	ASN	N-CA-C	-5.37	99.36	110.80
2	w	145	ASN	N-CA-C	-5.37	99.36	110.80
1	i	101	VAL	CB-CA-C	-5.37	104.89	112.14
2	t	33	ASN	N-CA-C	5.37	118.84	111.54
2	u	86	ILE	CB-CA-C	-5.37	105.43	111.23
2	v	680	SER	N-CA-C	5.37	122.24	110.80
1	j	71	THR	N-CA-C	5.37	120.49	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	n	47	ASN	N-CA-C	5.37	117.21	111.36
2	s	680	SER	N-CA-C	5.37	122.24	110.80
2	x	680	SER	N-CA-C	5.36	122.23	110.80
1	q	17	ASN	N-CA-C	-5.36	99.20	108.69
2	s	37	SER	N-CA-C	5.36	118.17	109.86
2	u	37	SER	N-CA-C	5.36	118.17	109.86
2	w	764	ASN	N-CA-C	5.36	117.70	109.07
1	e	44	LEU	N-CA-C	-5.36	102.95	110.50
2	v	145	ASN	N-CA-C	-5.36	99.39	110.80
1	c	101	VAL	CB-CA-C	-5.36	104.91	112.14
1	f	101	VAL	CB-CA-C	-5.36	104.91	112.14
2	v	33	ASN	N-CA-C	5.36	118.82	111.54
1	a	71	THR	N-CA-C	5.35	120.47	113.30
2	s	764	ASN	N-CA-C	5.35	117.69	109.07
2	t	680	SER	N-CA-C	5.35	122.20	110.80
2	w	86	ILE	CB-CA-C	-5.34	105.46	111.23
2	s	739	ASN	N-CA-C	-5.34	105.86	112.38
2	v	739	ASN	N-CA-C	-5.34	105.86	112.38
2	x	86	ILE	CB-CA-C	-5.34	105.47	111.23
1	r	101	VAL	CB-CA-C	-5.33	104.94	112.14
2	x	764	ASN	N-CA-C	5.33	117.66	109.07
1	p	71	THR	N-CA-C	5.33	120.44	113.30
2	t	408	PRO	CB-CA-C	-5.33	104.58	113.06
2	u	739	ASN	N-CA-C	-5.33	105.88	112.38
2	v	764	ASN	N-CA-C	5.33	117.65	109.07
2	w	151	ASP	N-CA-C	5.33	117.93	109.24
2	v	41	GLY	N-CA-C	-5.33	104.99	112.13
2	s	408	PRO	CB-CA-C	-5.33	104.59	113.06
2	t	739	ASN	N-CA-C	-5.33	105.88	112.38
2	x	322	PHE	N-CA-C	-5.33	102.40	110.28
2	s	532	ASN	CB-CA-C	-5.32	110.42	116.54
2	t	86	ILE	CB-CA-C	-5.32	105.48	111.23
2	u	41	GLY	N-CA-C	-5.32	105.00	112.13
2	u	216	GLY	N-CA-C	-5.32	102.99	111.18
2	s	216	GLY	N-CA-C	-5.32	102.99	111.18
2	x	151	ASP	N-CA-C	5.32	117.91	109.24
1	n	17	ASN	N-CA-C	-5.32	99.28	108.69
2	x	41	GLY	N-CA-C	-5.32	105.01	112.13
2	w	216	GLY	N-CA-C	-5.31	103.00	111.18
2	s	86	ILE	CB-CA-C	-5.31	105.49	111.23
2	t	41	GLY	N-CA-C	-5.31	105.01	112.13
2	s	151	ASP	N-CA-C	5.31	117.89	109.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	d	71	THR	N-CA-C	5.31	120.41	113.30
2	t	764	ASN	N-CA-C	5.31	117.61	109.07
2	w	41	GLY	N-CA-C	-5.31	105.02	112.13
2	t	216	GLY	N-CA-C	-5.31	103.01	111.18
2	v	216	GLY	N-CA-C	-5.31	103.01	111.18
2	w	532	ASN	CB-CA-C	-5.30	110.44	116.54
1	o	101	VAL	CB-CA-C	-5.30	104.98	112.14
2	v	86	ILE	CB-CA-C	-5.30	105.50	111.23
2	u	764	ASN	N-CA-C	5.30	117.61	109.07
2	w	739	ASN	N-CA-C	-5.30	105.91	112.38
2	x	408	PRO	CB-CA-C	-5.30	104.64	113.06
3	C	93	SER	N-CA-C	-5.30	105.50	111.28
2	v	532	ASN	CB-CA-C	-5.30	110.45	116.54
1	m	71	THR	N-CA-C	5.29	120.39	113.30
2	u	322	PHE	N-CA-C	-5.29	102.44	110.28
2	u	532	ASN	CB-CA-C	-5.29	110.45	116.54
2	x	216	GLY	N-CA-C	-5.29	103.03	111.18
2	x	739	ASN	N-CA-C	-5.29	105.92	112.38
1	g	71	THR	N-CA-C	5.29	120.39	113.30
1	g	83	ASP	N-CA-C	5.29	118.03	109.40
1	e	17	ASN	N-CA-C	-5.29	99.33	108.69
1	k	44	LEU	N-CA-C	-5.29	103.04	110.50
1	b	17	ASN	N-CA-C	-5.29	99.33	108.69
1	k	17	ASN	N-CA-C	-5.29	99.33	108.69
2	t	151	ASP	N-CA-C	5.29	117.86	109.24
2	t	532	ASN	CB-CA-C	-5.29	110.46	116.54
1	h	44	LEU	N-CA-C	-5.29	103.05	110.50
2	s	322	PHE	N-CA-C	-5.28	102.46	110.28
1	n	44	LEU	N-CA-C	-5.28	103.06	110.50
2	w	408	PRO	CB-CA-C	-5.28	104.67	113.06
2	w	230	ILE	N-CA-C	-5.28	100.01	107.98
2	x	532	ASN	CB-CA-C	-5.28	110.47	116.54
2	v	408	PRO	CB-CA-C	-5.28	104.67	113.06
1	h	17	ASN	N-CA-C	-5.27	99.36	108.69
2	u	408	PRO	CB-CA-C	-5.27	104.68	113.06
1	b	44	LEU	N-CA-C	-5.27	103.07	110.50
2	v	322	PHE	N-CA-C	-5.27	102.48	110.28
1	m	102	ALA	N-CA-C	5.27	117.02	111.28
2	t	24	TYR	CA-C-N	-5.27	115.15	120.21
2	t	24	TYR	C-N-CA	-5.27	115.15	120.21
2	t	230	ILE	N-CA-C	-5.27	100.03	107.98
2	u	24	TYR	CA-C-N	-5.27	115.15	120.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	u	24	TYR	C-N-CA	-5.27	115.15	120.21
2	v	151	ASP	N-CA-C	5.27	117.83	109.24
2	w	322	PHE	N-CA-C	-5.27	102.48	110.28
1	j	83	ASP	N-CA-C	5.26	117.98	109.40
2	u	230	ILE	N-CA-C	-5.26	100.03	107.98
1	q	44	LEU	N-CA-C	-5.26	103.08	110.50
2	s	230	ILE	N-CA-C	-5.26	100.04	107.98
2	u	710	TYR	N-CA-C	5.26	118.06	110.28
2	v	24	TYR	CA-C-N	-5.26	115.16	120.21
2	v	24	TYR	C-N-CA	-5.26	115.16	120.21
2	v	710	TYR	N-CA-C	5.26	118.06	110.28
2	u	151	ASP	N-CA-C	5.26	117.81	109.24
2	x	710	TYR	N-CA-C	5.26	118.06	110.28
2	s	24	TYR	CA-C-N	-5.25	115.17	120.21
2	s	24	TYR	C-N-CA	-5.25	115.17	120.21
1	d	102	ALA	N-CA-C	5.25	117.01	111.28
1	g	102	ALA	N-CA-C	5.25	117.01	111.28
1	r	46	ILE	CB-CA-C	-5.25	105.25	111.97
2	v	230	ILE	N-CA-C	-5.25	100.05	107.98
1	c	47	ASN	N-CA-C	5.25	117.75	111.71
1	j	102	ALA	N-CA-C	5.25	117.00	111.28
4	S	135	ARG	N-CA-C	-5.25	105.56	111.28
2	x	230	ILE	N-CA-C	-5.25	100.05	107.98
1	m	83	ASP	N-CA-C	5.25	117.95	109.40
2	u	294	THR	N-CA-C	-5.25	101.39	109.52
2	w	450	ARG	N-CA-C	-5.25	99.08	109.10
2	w	24	TYR	CA-C-N	-5.25	115.17	120.21
2	w	24	TYR	C-N-CA	-5.25	115.17	120.21
1	j	73	ILE	N-CA-C	-5.24	100.77	108.11
2	t	322	PHE	N-CA-C	-5.24	102.52	110.28
2	w	710	TYR	N-CA-C	5.24	118.04	110.28
2	x	294	THR	N-CA-C	-5.24	101.39	109.52
2	u	450	ARG	N-CA-C	-5.24	99.09	109.10
2	t	294	THR	N-CA-C	-5.24	101.40	109.52
1	p	83	ASP	N-CA-C	5.24	117.94	109.40
2	t	450	ARG	N-CA-C	-5.24	99.10	109.10
2	v	450	ARG	N-CA-C	-5.24	99.09	109.10
2	x	24	TYR	CA-C-N	-5.24	115.18	120.21
2	x	24	TYR	C-N-CA	-5.24	115.18	120.21
2	x	59	ALA	N-CA-C	5.24	117.07	111.36
2	s	710	TYR	N-CA-C	5.23	118.03	110.28
2	w	294	THR	N-CA-C	-5.23	101.42	109.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	v	294	THR	N-CA-C	-5.23	101.42	109.52
1	a	83	ASP	N-CA-C	5.23	117.92	109.40
2	s	510	ASN	N-CA-C	5.22	121.08	113.40
2	v	535	LEU	N-CA-C	-5.22	104.44	111.54
2	x	450	ARG	N-CA-C	-5.22	99.12	109.10
4	W	135	ARG	N-CA-C	-5.22	105.59	111.28
1	l	47	ASN	N-CA-C	5.22	117.72	111.71
1	a	102	ALA	N-CA-C	5.22	116.97	111.28
2	s	294	THR	N-CA-C	-5.22	101.43	109.52
2	t	510	ASN	N-CA-C	5.22	121.07	113.40
1	a	73	ILE	N-CA-C	-5.21	100.81	108.11
2	s	450	ARG	N-CA-C	-5.21	99.14	109.10
2	x	510	ASN	N-CA-C	5.21	121.06	113.40
1	d	83	ASP	N-CA-C	5.21	117.89	109.40
1	d	73	ILE	N-CA-C	-5.21	100.82	108.11
1	o	92	SER	CA-C-N	-5.21	113.90	120.98
1	o	92	SER	C-N-CA	-5.21	113.90	120.98
2	u	510	ASN	N-CA-C	5.21	121.05	113.40
2	s	720	VAL	CB-CA-C	-5.20	103.08	110.83
4	M	7	ASN	N-CA-C	-5.20	102.16	109.96
1	g	73	ILE	N-CA-C	-5.20	100.83	108.11
2	x	535	LEU	N-CA-C	-5.20	104.47	111.54
2	v	510	ASN	N-CA-C	5.20	121.04	113.40
2	w	535	LEU	N-CA-C	-5.20	104.47	111.54
2	s	535	LEU	N-CA-C	-5.20	104.47	111.54
1	g	80	SER	N-CA-C	5.20	118.02	109.76
1	p	80	SER	N-CA-C	5.20	118.02	109.76
2	u	59	ALA	N-CA-C	5.20	117.02	111.36
2	w	510	ASN	N-CA-C	5.20	121.04	113.40
1	p	102	ALA	N-CA-C	5.19	116.93	111.28
4	O	135	ARG	N-CA-C	-5.19	105.62	111.28
2	t	59	ALA	N-CA-C	5.19	117.01	111.36
2	v	720	VAL	CB-CA-C	-5.19	103.10	110.83
2	s	82	THR	N-CA-C	-5.18	103.84	110.53
2	t	720	VAL	CB-CA-C	-5.18	103.11	110.83
2	w	720	VAL	CB-CA-C	-5.18	103.11	110.83
2	s	59	ALA	N-CA-C	5.18	117.01	111.36
2	s	674	ASN	N-CA-C	5.18	116.96	108.52
2	t	535	LEU	N-CA-C	-5.18	104.50	111.54
2	w	59	ALA	N-CA-C	5.18	117.01	111.36
2	x	720	VAL	CB-CA-C	-5.18	103.11	110.83
2	x	82	THR	N-CA-C	-5.18	103.85	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	v	85	GLY	N-CA-C	5.18	120.72	110.83
1	i	50	TYR	N-CA-C	5.17	117.54	109.52
1	m	80	SER	N-CA-C	5.17	117.99	109.76
2	t	710	TYR	N-CA-C	5.17	117.94	110.28
2	u	720	VAL	CB-CA-C	-5.17	103.12	110.83
4	M	135	ARG	N-CA-C	-5.17	105.64	111.28
4	S	182	ASN	N-CA-C	-5.17	102.03	110.20
4	Q	135	ARG	N-CA-C	-5.17	105.65	111.28
2	t	85	GLY	N-CA-C	5.17	120.70	110.83
4	R	109	GLN	N-CA-C	-5.17	106.93	113.23
4	V	109	GLN	N-CA-C	-5.17	106.93	113.23
2	s	85	GLY	N-CA-C	5.16	120.69	110.83
2	u	535	LEU	N-CA-C	-5.16	104.52	111.54
4	X	109	GLN	N-CA-C	-5.16	106.93	113.23
2	t	82	THR	N-CA-C	-5.16	103.87	110.53
2	u	674	ASN	N-CA-C	5.16	116.93	108.52
2	v	82	THR	N-CA-C	-5.16	103.87	110.53
2	x	674	ASN	N-CA-C	5.16	116.93	108.52
2	v	674	ASN	N-CA-C	5.16	116.93	108.52
4	N	109	GLN	N-CA-C	-5.16	106.94	113.23
1	p	73	ILE	N-CA-C	-5.16	100.89	108.11
2	u	82	THR	N-CA-C	-5.16	103.88	110.53
2	v	59	ALA	N-CA-C	5.16	116.98	111.36
2	w	82	THR	N-CA-C	-5.16	103.88	110.53
2	w	85	GLY	N-CA-C	5.16	120.68	110.83
1	j	80	SER	N-CA-C	5.15	117.95	109.76
4	P	109	GLN	N-CA-C	-5.15	106.94	113.23
2	s	226	SER	N-CA-C	5.15	116.89	111.28
2	x	671	PHE	N-CA-C	-5.15	101.30	109.59
1	m	73	ILE	N-CA-C	-5.15	100.91	108.11
2	w	674	ASN	N-CA-C	5.14	116.90	108.52
4	W	182	ASN	N-CA-C	-5.14	102.07	110.20
2	v	671	PHE	N-CA-C	-5.14	101.31	109.59
2	x	85	GLY	N-CA-C	5.14	120.65	110.83
2	u	85	GLY	N-CA-C	5.14	120.64	110.83
1	a	80	SER	N-CA-C	5.14	117.93	109.76
2	s	671	PHE	N-CA-C	-5.14	101.32	109.59
2	t	226	SER	N-CA-C	5.14	116.88	111.28
1	d	80	SER	N-CA-C	5.13	117.92	109.76
2	v	226	SER	N-CA-C	5.13	116.88	111.28
2	w	671	PHE	N-CA-C	-5.13	101.32	109.59
2	w	226	SER	N-CA-C	5.13	116.87	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	U	135	ARG	N-CA-C	-5.13	105.69	111.28
2	s	475	ALA	N-CA-C	-5.13	102.46	110.10
2	u	671	PHE	N-CA-C	-5.13	101.33	109.59
1	e	85	LEU	N-CA-C	-5.13	105.69	111.28
1	n	85	LEU	N-CA-C	-5.13	105.69	111.28
2	t	674	ASN	N-CA-C	5.13	116.88	108.52
2	w	729	TYR	CB-CA-C	-5.13	104.31	111.85
2	x	226	SER	N-CA-C	5.13	116.87	111.28
1	l	85	LEU	CA-C-N	-5.12	116.43	123.14
1	l	85	LEU	C-N-CA	-5.12	116.43	123.14
2	t	220	ILE	CB-CA-C	5.12	117.81	110.33
4	Q	182	ASN	N-CA-C	-5.12	102.10	110.20
2	x	220	ILE	CB-CA-C	5.12	117.81	110.33
2	w	707	TRP	N-CA-C	5.12	117.59	109.50
4	O	182	ASN	N-CA-C	-5.12	102.11	110.20
4	M	182	ASN	N-CA-C	-5.12	102.12	110.20
4	T	109	GLN	N-CA-C	-5.12	106.99	113.23
4	U	182	ASN	N-CA-C	-5.12	102.12	110.20
2	t	671	PHE	N-CA-C	-5.11	101.36	109.59
2	u	226	SER	N-CA-C	5.11	116.85	111.28
1	c	85	LEU	CA-C-N	-5.11	116.45	123.14
1	c	85	LEU	C-N-CA	-5.11	116.45	123.14
2	s	220	ILE	CB-CA-C	5.11	117.79	110.33
2	x	707	TRP	N-CA-C	5.11	117.57	109.50
4	Q	149	ARG	N-CA-C	5.11	116.93	111.36
1	f	85	LEU	CA-C-N	-5.11	116.45	123.14
1	f	85	LEU	C-N-CA	-5.11	116.45	123.14
1	b	16	SER	N-CA-C	5.10	116.71	108.34
1	k	85	LEU	N-CA-C	-5.10	105.72	111.28
1	j	15	GLY	N-CA-C	5.10	118.85	112.73
2	u	475	ALA	N-CA-C	-5.10	102.50	110.10
2	w	475	ALA	N-CA-C	-5.10	102.50	110.10
2	u	220	ILE	CB-CA-C	5.10	117.77	110.33
2	w	220	ILE	CB-CA-C	5.10	117.77	110.33
4	W	149	ARG	N-CA-C	5.10	116.92	111.36
2	v	475	ALA	N-CA-C	-5.09	102.51	110.10
1	d	15	GLY	N-CA-C	5.09	118.84	112.73
1	h	85	LEU	N-CA-C	-5.09	105.73	111.28
2	s	729	TYR	CB-CA-C	-5.09	104.36	111.85
1	n	16	SER	N-CA-C	5.09	116.68	108.34
2	t	729	TYR	CB-CA-C	-5.09	104.37	111.85
2	v	707	TRP	N-CA-C	5.09	117.54	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	u	707	TRP	N-CA-C	5.08	117.53	109.50
2	s	707	TRP	N-CA-C	5.08	117.53	109.50
2	t	707	TRP	N-CA-C	5.08	117.53	109.50
1	o	85	LEU	CA-C-N	-5.08	116.49	123.14
1	o	85	LEU	C-N-CA	-5.08	116.49	123.14
2	x	475	ALA	N-CA-C	-5.08	102.53	110.10
2	u	729	TYR	CB-CA-C	-5.08	104.39	111.85
2	v	220	ILE	CB-CA-C	5.08	117.74	110.33
2	x	729	TYR	CB-CA-C	-5.08	104.39	111.85
2	v	729	TYR	CB-CA-C	-5.08	104.39	111.85
2	x	321	ASP	N-CA-C	5.07	116.79	108.52
1	i	85	LEU	CA-C-N	-5.07	116.50	123.14
1	i	85	LEU	C-N-CA	-5.07	116.50	123.14
1	l	41	ARG	N-CA-C	5.07	117.78	110.28
1	q	85	LEU	N-CA-C	-5.07	105.75	111.28
2	v	780	GLY	N-CA-C	5.07	120.26	111.14
2	s	321	ASP	N-CA-C	5.06	116.77	108.52
1	f	41	ARG	N-CA-C	5.06	117.77	110.28
1	g	15	GLY	N-CA-C	5.06	118.80	112.73
1	a	15	GLY	N-CA-C	5.06	118.80	112.73
2	t	359	GLY	N-CA-C	5.06	119.45	110.80
1	b	85	LEU	N-CA-C	-5.06	105.77	111.28
1	m	15	GLY	N-CA-C	5.05	118.80	112.73
1	r	85	LEU	CA-C-N	-5.05	116.52	123.14
1	r	85	LEU	C-N-CA	-5.05	116.52	123.14
2	s	780	GLY	N-CA-C	5.05	120.24	111.14
1	h	16	SER	N-CA-C	5.05	116.62	108.34
1	k	16	SER	N-CA-C	5.05	116.62	108.34
2	v	321	ASP	N-CA-C	5.05	116.75	108.52
1	o	41	ARG	N-CA-C	5.05	117.75	110.28
2	x	359	GLY	N-CA-C	5.05	119.43	110.80
2	x	780	GLY	N-CA-C	5.05	120.23	111.14
2	w	780	GLY	N-CA-C	5.05	120.22	111.14
1	r	41	ARG	N-CA-C	5.04	117.75	110.28
2	t	361	LEU	N-CA-C	-5.04	100.51	108.73
2	s	359	GLY	N-CA-C	5.04	119.42	110.80
2	v	113	ARG	CB-CA-C	-5.04	102.97	110.88
2	w	99	ARG	CA-C-N	-5.04	116.96	123.16
2	w	99	ARG	C-N-CA	-5.04	116.96	123.16
1	k	71	THR	N-CA-C	5.04	116.85	111.36
1	q	16	SER	N-CA-C	5.04	116.60	108.34
2	w	113	ARG	CB-CA-C	-5.04	102.97	110.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	x	361	LEU	N-CA-C	-5.04	100.52	108.73
2	t	475	ALA	N-CA-C	-5.04	102.60	110.10
1	h	71	THR	N-CA-C	5.03	116.85	111.36
2	w	778	ILE	N-CA-C	5.03	114.82	107.37
4	M	149	ARG	N-CA-C	5.03	116.84	111.36
2	u	359	GLY	N-CA-C	5.03	119.40	110.80
2	u	99	ARG	CA-C-N	-5.03	116.97	123.16
2	u	99	ARG	C-N-CA	-5.03	116.97	123.16
2	u	321	ASP	N-CA-C	5.03	116.72	108.52
2	w	361	LEU	N-CA-C	-5.03	100.54	108.73
1	b	71	THR	N-CA-C	5.02	116.83	111.36
2	v	359	GLY	N-CA-C	5.02	119.39	110.80
2	x	113	ARG	CB-CA-C	-5.02	103.00	110.88
2	s	113	ARG	CB-CA-C	-5.02	103.00	110.88
2	t	113	ARG	CB-CA-C	-5.02	103.00	110.88
2	v	361	LEU	N-CA-C	-5.02	100.55	108.73
2	u	113	ARG	CB-CA-C	-5.02	103.00	110.88
2	u	778	ILE	N-CA-C	5.02	114.80	107.37
2	t	780	GLY	N-CA-C	5.02	120.17	111.14
2	s	361	LEU	N-CA-C	-5.02	100.55	108.73
2	w	359	GLY	N-CA-C	5.02	119.38	110.80
1	i	47	ASN	N-CA-C	5.01	117.48	111.71
2	u	361	LEU	N-CA-C	-5.01	100.56	108.73
2	w	321	ASP	N-CA-C	5.01	116.69	108.52
2	u	780	GLY	N-CA-C	5.01	120.16	111.14
1	c	50	TYR	N-CA-C	5.01	117.28	109.52
1	i	41	ARG	N-CA-C	5.01	117.69	110.28
2	x	99	ARG	CA-C-N	-5.01	117.00	123.16
2	x	99	ARG	C-N-CA	-5.01	117.00	123.16
4	U	149	ARG	N-CA-C	5.01	116.82	111.36
2	s	778	ILE	N-CA-C	5.01	114.78	107.37
4	R	64	GLU	N-CA-C	-5.01	101.01	109.07
1	f	47	ASN	N-CA-C	5.00	117.46	111.71
4	T	64	GLU	N-CA-C	-5.00	101.02	109.07

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	922	0	931	41	0
1	b	922	0	931	37	0
1	c	922	0	931	80	0
1	d	922	0	931	44	0
1	e	922	0	931	36	0
1	f	922	0	931	79	0
1	g	922	0	931	40	0
1	h	922	0	931	37	0
1	i	922	0	931	81	0
1	j	922	0	931	41	0
1	k	922	0	931	36	0
1	l	922	0	931	80	0
1	m	922	0	931	41	0
1	n	922	0	931	35	0
1	o	922	0	931	69	0
1	p	922	0	931	45	0
1	q	922	0	931	35	0
1	r	922	0	931	83	0
2	s	6289	0	6051	405	0
2	t	6289	0	6051	404	0
2	u	6289	0	6051	399	0
2	v	6289	0	6051	410	0
2	w	6289	0	6051	399	0
2	x	6289	0	6051	412	0
3	A	787	0	784	83	0
3	B	787	0	784	64	0
3	C	787	0	784	75	0
3	D	787	0	784	66	0
3	E	787	0	784	70	0
3	F	787	0	784	47	0
4	M	1553	0	1472	86	0
4	N	1534	0	1447	106	0
4	O	1553	0	1472	89	0
4	P	1534	0	1447	107	0
4	Q	1553	0	1472	84	0
4	R	1534	0	1447	103	0
4	S	1553	0	1472	82	0
4	T	1534	0	1447	100	0
4	U	1553	0	1472	82	0
4	V	1534	0	1447	103	0
4	W	1553	0	1472	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	X	1534	0	1447	110	0
All	All	77574	0	75282	3909	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 26.

All (3909) 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)
2:v:396:SER:HB2	3:A:91:GLU:CD	1.51	1.34
2:t:19:PRO:HG2	2:u:711:GLU:CD	1.57	1.28
2:s:711:GLU:CD	2:x:19:PRO:HG2	1.58	1.27
2:u:19:PRO:HG2	2:v:711:GLU:CD	1.59	1.27
2:v:19:PRO:HG2	2:w:711:GLU:CD	1.59	1.27
1:h:101:VAL:HG21	4:V:33:GLU:OE2	1.32	1.27
1:b:101:VAL:HG21	4:N:33:GLU:OE2	1.33	1.26
2:s:19:PRO:HG2	2:t:711:GLU:CD	1.60	1.26
1:i:116:LEU:O	1:i:116:LEU:HD23	1.33	1.26
1:e:101:VAL:HG21	4:X:33:GLU:OE2	1.34	1.25
1:q:101:VAL:HG21	4:P:33:GLU:OE2	1.33	1.25
1:l:116:LEU:O	1:l:116:LEU:HD23	1.33	1.25
2:s:150:GLN:CD	2:s:224:ALA:HB1	1.62	1.25
2:s:185:PRO:CD	3:E:42:MET:HE1	1.67	1.25
1:f:116:LEU:O	1:f:116:LEU:HD23	1.33	1.24
2:t:150:GLN:CD	2:t:224:ALA:HB1	1.62	1.24
2:w:19:PRO:HG2	2:x:711:GLU:CD	1.60	1.24
2:s:185:PRO:HD3	3:E:42:MET:CE	1.64	1.24
1:c:116:LEU:HD23	1:c:116:LEU:O	1.33	1.24
1:n:101:VAL:HG21	4:R:33:GLU:OE2	1.34	1.24
2:x:150:GLN:CD	2:x:224:ALA:HB1	1.62	1.24
2:u:150:GLN:CD	2:u:224:ALA:HB1	1.62	1.23
2:w:150:GLN:CD	2:w:224:ALA:HB1	1.62	1.22
1:c:31:PHE:HB3	1:c:78:VAL:O	1.39	1.22
1:r:116:LEU:O	1:r:116:LEU:HD23	1.33	1.22
2:v:150:GLN:CD	2:v:224:ALA:HB1	1.62	1.22
2:x:185:PRO:HD3	3:F:42:MET:CE	1.68	1.22
1:k:101:VAL:HG21	4:T:33:GLU:OE2	1.33	1.22
1:o:116:LEU:O	1:o:116:LEU:HD23	1.33	1.22
1:f:93:ILE:HB	2:v:638:GLY:O	1.40	1.21
1:i:93:ILE:HB	2:u:638:GLY:O	1.39	1.20
2:w:86:ILE:O	2:w:98:VAL:HG11	1.40	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:x:86:ILE:O	2:x:98:VAL:HG11	1.40	1.20
2:t:418:ASP:OD2	2:u:73:GLU:HG3	1.41	1.20
1:l:93:ILE:HB	2:t:638:GLY:O	1.41	1.20
2:x:185:PRO:CD	3:F:42:MET:HE1	1.71	1.20
1:o:31:PHE:HB3	1:o:78:VAL:O	1.39	1.19
2:u:86:ILE:O	2:u:98:VAL:HG11	1.40	1.19
1:c:93:ILE:HB	2:w:638:GLY:O	1.40	1.19
1:i:31:PHE:HB3	1:i:78:VAL:O	1.40	1.19
2:t:86:ILE:O	2:t:98:VAL:HG11	1.40	1.19
2:w:176:LYS:NZ	2:w:178:LYS:HE3	1.57	1.19
1:f:31:PHE:HB3	1:f:78:VAL:O	1.39	1.19
2:v:418:ASP:OD2	2:w:73:GLU:HG3	1.43	1.19
1:f:93:ILE:CD1	2:v:746:LEU:HA	1.72	1.18
2:v:86:ILE:O	2:v:98:VAL:HG11	1.40	1.18
2:v:176:LYS:NZ	2:v:178:LYS:HE3	1.57	1.18
1:l:31:PHE:HB3	1:l:78:VAL:O	1.39	1.18
1:r:31:PHE:HB3	1:r:78:VAL:O	1.39	1.18
2:t:176:LYS:NZ	2:t:178:LYS:HE3	1.57	1.18
2:s:176:LYS:NZ	2:s:178:LYS:HE3	1.57	1.18
2:u:143:LEU:HD13	2:u:146:TYR:HB2	1.19	1.18
1:i:93:ILE:CD1	2:u:746:LEU:HA	1.74	1.18
1:l:93:ILE:CD1	2:t:746:LEU:HA	1.73	1.18
2:s:86:ILE:O	2:s:98:VAL:HG11	1.40	1.18
2:s:418:ASP:OD2	2:t:73:GLU:HG3	1.44	1.18
2:x:176:LYS:NZ	2:x:178:LYS:HE3	1.57	1.18
1:p:97:TYR:CD1	4:O:6:MET:HE1	1.79	1.18
2:w:164:GLU:HB2	2:w:178:LYS:HG2	1.27	1.17
2:u:176:LYS:NZ	2:u:178:LYS:HE3	1.57	1.17
2:s:73:GLU:HG3	2:x:418:ASP:OD2	1.41	1.17
1:c:93:ILE:CD1	2:w:746:LEU:HA	1.73	1.16
1:r:93:ILE:CD1	2:x:746:LEU:HA	1.72	1.16
2:u:19:PRO:HG2	2:v:711:GLU:OE1	1.45	1.16
1:c:93:ILE:CG1	2:w:638:GLY:HA3	1.76	1.16
1:i:93:ILE:CG1	2:u:638:GLY:HA3	1.74	1.16
2:u:418:ASP:OD2	2:v:73:GLU:HG3	1.42	1.16
2:w:727:TRP:HB3	4:N:36:ALA:HB1	1.25	1.16
2:s:711:GLU:OE1	2:x:19:PRO:HG2	1.46	1.16
2:u:357:ARG:HB3	2:u:371:THR:HA	1.28	1.16
2:w:418:ASP:OD2	2:x:73:GLU:HG3	1.43	1.16
1:f:89:THR:HG21	2:v:640:ILE:O	1.44	1.16
2:t:143:LEU:HD13	2:t:146:TYR:HB2	1.19	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:164:GLU:HB2	2:v:178:LYS:HG2	1.27	1.16
2:v:357:ARG:HB3	2:v:371:THR:HA	1.28	1.16
1:f:93:ILE:CG1	2:v:638:GLY:HA3	1.76	1.15
2:t:19:PRO:HG2	2:u:711:GLU:OE1	1.45	1.15
2:v:22:LEU:HD21	2:w:779:ILE:CG1	1.77	1.15
1:r:93:ILE:HB	2:x:638:GLY:O	1.42	1.15
2:u:22:LEU:HD21	2:v:779:ILE:CG1	1.76	1.15
2:t:185:PRO:HD3	3:D:42:MET:CE	1.76	1.15
2:s:22:LEU:HD21	2:t:779:ILE:HG12	1.17	1.15
2:u:22:LEU:HD21	2:v:779:ILE:HG12	1.16	1.15
1:p:97:TYR:CE1	4:O:6:MET:HE1	1.82	1.14
2:t:22:LEU:HD21	2:u:779:ILE:HG12	1.15	1.14
1:i:89:THR:HG21	2:u:640:ILE:O	1.45	1.14
2:s:143:LEU:HD13	2:s:146:TYR:HB2	1.19	1.14
2:u:714:GLY:HA3	2:u:774:THR:HG21	1.15	1.14
2:w:22:LEU:HD21	2:x:779:ILE:CG1	1.77	1.14
3:A:39:MET:SD	3:A:43:ARG:NH2	2.20	1.14
2:v:714:GLY:HA3	2:v:774:THR:HG21	1.15	1.14
1:l:93:ILE:CG1	2:t:638:GLY:HA3	1.76	1.14
1:r:89:THR:HG21	2:x:640:ILE:O	1.47	1.14
2:s:779:ILE:CG1	2:x:22:LEU:HD21	1.77	1.14
2:w:19:PRO:HG2	2:x:711:GLU:OE1	1.47	1.14
2:t:357:ARG:HB3	2:t:371:THR:HA	1.28	1.14
2:x:164:GLU:HB2	2:x:178:LYS:HG2	1.27	1.14
2:v:143:LEU:HD13	2:v:146:TYR:HB2	1.19	1.13
2:v:727:TRP:HB3	4:X:36:ALA:HB1	1.25	1.13
1:c:89:THR:HG21	2:w:640:ILE:O	1.46	1.13
2:s:19:PRO:HG2	2:t:711:GLU:OE1	1.46	1.13
2:t:22:LEU:HD21	2:u:779:ILE:CG1	1.76	1.13
2:v:22:LEU:HD21	2:w:779:ILE:HG12	1.16	1.13
2:v:19:PRO:HG2	2:w:711:GLU:OE1	1.45	1.13
1:r:93:ILE:CG1	2:x:638:GLY:HA3	1.79	1.12
2:s:22:LEU:HD21	2:t:779:ILE:CG1	1.77	1.13
2:w:357:ARG:HB3	2:w:371:THR:HA	1.28	1.12
1:l:89:THR:HG21	2:t:640:ILE:O	1.47	1.12
2:t:185:PRO:CD	3:D:42:MET:HE1	1.78	1.12
2:u:164:GLU:HB2	2:u:178:LYS:HG2	1.27	1.12
2:u:727:TRP:HB3	4:V:36:ALA:HB1	1.26	1.12
2:x:727:TRP:HB3	4:P:36:ALA:HB1	1.25	1.12
2:s:357:ARG:HB3	2:s:371:THR:HA	1.28	1.11
2:t:714:GLY:HA3	2:t:774:THR:HG21	1.15	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:o:89:THR:HG21	2:s:640:ILE:O	1.46	1.11
2:t:727:TRP:HB3	4:T:36:ALA:HB1	1.26	1.11
1:i:93:ILE:HD12	2:u:746:LEU:HA	1.14	1.11
2:w:714:GLY:HA3	2:w:774:THR:HG21	1.15	1.11
3:B:126:ALA:HA	3:B:129:LEU:CD2	1.78	1.11
2:s:714:GLY:CA	2:s:774:THR:HG21	1.81	1.11
2:t:19:PRO:CG	2:u:711:GLU:CD	2.24	1.11
2:t:714:GLY:CA	2:t:774:THR:HG21	1.81	1.11
2:x:357:ARG:HB3	2:x:371:THR:HA	1.28	1.11
2:s:164:GLU:HB2	2:s:178:LYS:HG2	1.27	1.10
2:t:164:GLU:HB2	2:t:178:LYS:HG2	1.27	1.10
2:w:143:LEU:HD13	2:w:146:TYR:HB2	1.19	1.10
2:s:779:ILE:HG12	2:x:22:LEU:HD21	1.16	1.10
2:u:714:GLY:CA	2:u:774:THR:HG21	1.81	1.10
3:A:39:MET:O	3:A:43:ARG:HG3	1.49	1.10
2:x:143:LEU:HD13	2:x:146:TYR:HB2	1.19	1.10
2:x:714:GLY:CA	2:x:774:THR:HG21	1.81	1.10
1:l:93:ILE:HD12	2:t:746:LEU:HA	1.13	1.09
2:v:714:GLY:CA	2:v:774:THR:HG21	1.81	1.09
2:w:714:GLY:CA	2:w:774:THR:HG21	1.81	1.09
2:s:19:PRO:CG	2:t:711:GLU:CD	2.26	1.09
2:s:714:GLY:HA3	2:s:774:THR:HG21	1.15	1.09
2:x:714:GLY:HA3	2:x:774:THR:HG21	1.15	1.09
2:w:22:LEU:HD21	2:x:779:ILE:HG12	1.17	1.08
2:s:727:TRP:HB3	4:R:36:ALA:HB1	1.27	1.08
2:v:19:PRO:CG	2:w:711:GLU:CD	2.25	1.08
2:s:711:GLU:CD	2:x:19:PRO:CG	2.25	1.07
2:u:19:PRO:CG	2:v:711:GLU:CD	2.25	1.07
2:u:758:VAL:HG12	4:W:25:GLY:O	1.55	1.07
2:w:19:PRO:CG	2:x:711:GLU:CD	2.27	1.07
1:r:93:ILE:HD12	2:x:746:LEU:HA	1.13	1.07
1:c:93:ILE:HD12	2:w:746:LEU:HA	1.13	1.06
2:v:758:VAL:HG12	4:M:25:GLY:O	1.55	1.06
1:f:93:ILE:HD12	2:v:746:LEU:HA	1.13	1.06
2:s:185:PRO:CD	3:E:42:MET:CE	2.29	1.06
2:u:22:LEU:CD2	2:v:779:ILE:HG12	1.86	1.06
2:w:758:VAL:HG12	4:O:25:GLY:O	1.55	1.06
1:i:93:ILE:HG13	2:u:638:GLY:HA3	1.35	1.05
2:t:22:LEU:CD2	2:u:779:ILE:HG12	1.86	1.05
2:s:164:GLU:CB	2:s:178:LYS:HG2	1.86	1.05
4:P:57:ARG:HG3	4:Q:170:LEU:HD11	1.35	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:T:57:ARG:HG3	4:U:170:LEU:HD11	1.37	1.05
2:v:22:LEU:CD2	2:w:779:ILE:HG12	1.87	1.05
2:x:164:GLU:CB	2:x:178:LYS:HG2	1.87	1.05
1:c:93:ILE:HG13	2:w:638:GLY:HA3	1.36	1.04
2:s:779:ILE:HG12	2:x:22:LEU:CD2	1.86	1.04
2:v:150:GLN:HB3	2:v:224:ALA:CB	1.88	1.04
4:R:57:ARG:HG3	4:S:170:LEU:HD11	1.39	1.04
1:r:93:ILE:HG13	2:x:638:GLY:HA3	1.39	1.04
2:s:185:PRO:HD3	3:E:42:MET:HE3	1.36	1.04
2:t:164:GLU:CB	2:t:178:LYS:HG2	1.86	1.04
1:l:93:ILE:HG13	2:t:638:GLY:HA3	1.36	1.04
2:u:150:GLN:HB3	2:u:224:ALA:CB	1.88	1.04
2:u:164:GLU:CB	2:u:178:LYS:HG2	1.86	1.04
2:v:728:LYS:H	4:X:36:ALA:HB2	1.20	1.04
2:w:176:LYS:HZ1	2:w:178:LYS:HE3	1.09	1.04
2:t:758:VAL:HG12	4:U:25:GLY:O	1.57	1.04
2:v:164:GLU:CB	2:v:178:LYS:HG2	1.86	1.04
4:V:57:ARG:HG3	4:W:170:LEU:HD11	1.37	1.04
2:s:22:LEU:CD2	2:t:779:ILE:HG12	1.87	1.03
2:s:150:GLN:CD	2:s:224:ALA:CB	2.32	1.03
2:w:164:GLU:CB	2:w:178:LYS:HG2	1.86	1.03
2:t:150:GLN:HB3	2:t:224:ALA:CB	1.88	1.03
2:u:728:LYS:H	4:V:36:ALA:HB2	1.20	1.03
2:w:22:LEU:CD2	2:x:779:ILE:HG12	1.88	1.03
2:w:728:LYS:H	4:N:36:ALA:HB2	1.20	1.03
2:s:150:GLN:HB3	2:s:224:ALA:CB	1.88	1.03
2:s:758:VAL:HG12	4:S:25:GLY:O	1.57	1.03
2:t:150:GLN:CD	2:t:224:ALA:CB	2.32	1.03
2:s:728:LYS:H	4:R:36:ALA:HB2	1.23	1.02
2:t:185:PRO:CD	3:D:42:MET:CE	2.37	1.02
3:A:40:GLU:HA	3:A:43:ARG:HD2	1.42	1.02
4:N:57:ARG:HG3	4:O:170:LEU:HD11	1.36	1.02
2:x:150:GLN:CD	2:x:224:ALA:CB	2.32	1.02
4:M:170:LEU:HD11	4:X:57:ARG:HG3	1.36	1.02
2:x:150:GLN:HB3	2:x:224:ALA:CB	1.88	1.02
2:x:758:VAL:HG12	4:Q:25:GLY:O	1.57	1.02
2:t:728:LYS:H	4:T:36:ALA:HB2	1.24	1.02
2:u:150:GLN:CD	2:u:224:ALA:CB	2.32	1.02
2:v:150:GLN:CD	2:v:224:ALA:CB	2.32	1.02
2:w:388:ASP:OD2	3:A:82:ARG:HB2	1.60	1.02
2:w:150:GLN:HB3	2:w:224:ALA:CB	1.88	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:x:728:LYS:H	4:P:36:ALA:HB2	1.22	1.01
2:w:150:GLN:CD	2:w:224:ALA:CB	2.32	1.01
1:f:93:ILE:HG13	2:v:638:GLY:HA3	1.37	1.00
2:u:500:VAL:HG23	2:u:500:VAL:O	1.62	0.99
2:x:185:PRO:HD3	3:F:42:MET:HE3	1.42	0.98
2:v:500:VAL:HG23	2:v:500:VAL:O	1.62	0.98
2:x:185:PRO:CD	3:F:42:MET:CE	2.35	0.98
2:s:500:VAL:HG23	2:s:500:VAL:O	1.62	0.97
2:x:348:ILE:H	2:x:348:ILE:HD12	1.30	0.97
2:t:185:PRO:HD3	3:D:42:MET:HE3	1.42	0.97
3:D:105:GLN:HA	3:D:108:ARG:NH2	1.79	0.97
2:s:348:ILE:H	2:s:348:ILE:HD12	1.30	0.97
3:E:108:ARG:NH1	3:F:72:MET:SD	2.38	0.97
2:w:348:ILE:H	2:w:348:ILE:HD12	1.30	0.97
2:x:176:LYS:HZ1	2:x:178:LYS:HE3	1.23	0.96
3:A:119:ARG:O	3:A:122:GLN:HG2	1.65	0.96
1:i:93:ILE:HG12	2:u:638:GLY:HA3	1.45	0.96
2:t:348:ILE:H	2:t:348:ILE:HD12	1.30	0.96
2:v:348:ILE:HD12	2:v:348:ILE:H	1.30	0.96
2:u:348:ILE:H	2:u:348:ILE:HD12	1.30	0.95
2:w:500:VAL:O	2:w:500:VAL:HG23	1.62	0.95
2:s:150:GLN:HB3	2:s:224:ALA:HB2	1.49	0.95
2:x:150:GLN:HB3	2:x:224:ALA:HB2	1.49	0.95
2:u:150:GLN:HB3	2:u:224:ALA:HB2	1.49	0.94
1:f:93:ILE:HG12	2:v:638:GLY:HA3	1.45	0.94
1:l:93:ILE:HG12	2:t:638:GLY:HA3	1.48	0.94
2:t:500:VAL:O	2:t:500:VAL:HG23	1.62	0.94
2:v:272:ASP:C	2:v:272:ASP:OD1	2.10	0.94
2:x:500:VAL:HG23	2:x:500:VAL:O	1.62	0.94
1:d:9:LEU:HD21	4:W:72:ASP:OD2	1.68	0.94
3:C:88:SER:HB2	3:C:90:LEU:HD13	1.48	0.94
1:f:116:LEU:O	1:f:116:LEU:CD2	2.16	0.94
3:C:119:ARG:O	3:C:122:GLN:HG2	1.65	0.94
1:i:116:LEU:O	1:i:116:LEU:CD2	2.16	0.93
2:v:150:GLN:HB3	2:v:224:ALA:HB2	1.49	0.93
1:g:9:LEU:HD21	4:U:72:ASP:OD2	1.68	0.93
1:c:93:ILE:HG12	2:w:638:GLY:HA3	1.47	0.93
1:l:116:LEU:O	1:l:116:LEU:CD2	2.16	0.93
1:o:116:LEU:O	1:o:116:LEU:CD2	2.16	0.93
2:t:176:LYS:HZ1	2:t:178:LYS:HE3	1.14	0.93
1:p:9:LEU:HD21	4:O:72:ASP:OD2	1.68	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:c:116:LEU:O	1:c:116:LEU:CD2	2.16	0.93
1:r:93:ILE:HG12	2:x:638:GLY:HA3	1.49	0.93
2:w:272:ASP:C	2:w:272:ASP:OD1	2.10	0.93
1:m:9:LEU:HD21	4:Q:72:ASP:OD2	1.68	0.93
2:t:150:GLN:HB3	2:t:224:ALA:HB2	1.49	0.93
1:p:97:TYR:CD1	4:O:6:MET:CE	2.51	0.92
2:t:272:ASP:OD1	2:t:272:ASP:C	2.10	0.92
2:u:272:ASP:C	2:u:272:ASP:OD1	2.10	0.92
2:x:150:GLN:CG	2:x:224:ALA:HB1	1.99	0.92
2:t:150:GLN:CG	2:t:224:ALA:HB1	1.99	0.92
2:w:150:GLN:HB3	2:w:224:ALA:HB2	1.49	0.92
2:x:185:PRO:HD3	3:F:42:MET:HE1	1.32	0.92
4:M:2:ARG:HH11	4:M:124:LEU:HD21	1.34	0.92
2:u:150:GLN:CG	2:u:224:ALA:HB1	1.99	0.92
2:u:728:LYS:H	4:V:36:ALA:CB	1.82	0.92
1:r:116:LEU:O	1:r:116:LEU:CD2	2.16	0.92
2:u:370:ARG:HD3	2:u:376:ASN:HB2	1.52	0.92
3:B:126:ALA:HA	3:B:129:LEU:HD21	1.49	0.92
3:C:137:SER:HB3	3:D:43:ARG:HH22	1.32	0.92
4:W:2:ARG:HH11	4:W:124:LEU:HD21	1.34	0.92
2:w:150:GLN:CG	2:w:224:ALA:HB1	1.99	0.92
2:s:150:GLN:CG	2:s:224:ALA:HB1	1.99	0.92
2:t:370:ARG:HD3	2:t:376:ASN:HB2	1.52	0.92
3:B:108:ARG:NH1	3:C:72:MET:SD	2.43	0.92
3:B:129:LEU:HD12	3:B:130:GLY:N	1.84	0.92
1:a:9:LEU:HD21	4:M:72:ASP:OD2	1.69	0.91
4:O:2:ARG:HH11	4:O:124:LEU:HD21	1.34	0.91
1:i:93:ILE:HG13	2:u:638:GLY:CA	1.99	0.91
4:N:168:ARG:NH1	4:N:172:MET:CE	2.34	0.91
2:v:150:GLN:CG	2:v:224:ALA:HB1	1.99	0.91
2:v:728:LYS:H	4:X:36:ALA:CB	1.82	0.91
3:C:108:ARG:CZ	3:C:108:ARG:HB3	1.98	0.91
4:U:2:ARG:HH11	4:U:124:LEU:HD21	1.34	0.91
1:o:93:ILE:HD11	2:s:746:LEU:HD23	1.50	0.91
2:v:196:LEU:O	2:v:200:LEU:HD23	1.71	0.91
2:w:370:ARG:HD3	2:w:376:ASN:HB2	1.52	0.91
2:x:196:LEU:O	2:x:200:LEU:HD23	1.71	0.91
2:x:272:ASP:C	2:x:272:ASP:OD1	2.10	0.91
3:B:126:ALA:O	3:B:129:LEU:HG	1.68	0.91
4:R:168:ARG:NH1	4:R:172:MET:CE	2.34	0.91
4:V:168:ARG:NH1	4:V:172:MET:CE	2.34	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:272:ASP:C	2:s:272:ASP:OD1	2.10	0.91
2:v:728:LYS:N	4:X:36:ALA:HB2	1.85	0.91
2:w:254:PHE:HE2	3:A:65:ALA:CB	1.84	0.91
1:c:93:ILE:HG13	2:w:638:GLY:CA	2.01	0.91
2:t:184:GLN:HA	3:D:42:MET:HE1	1.52	0.91
2:w:196:LEU:O	2:w:200:LEU:HD23	1.71	0.91
2:x:370:ARG:HD3	2:x:376:ASN:HB2	1.52	0.91
1:j:9:LEU:HD21	4:S:72:ASP:OD2	1.70	0.91
2:t:437:LEU:HD13	3:C:90:LEU:HD12	1.52	0.91
4:T:168:ARG:NH1	4:T:172:MET:CE	2.34	0.91
2:s:254:PHE:HE2	3:E:65:ALA:CB	1.84	0.90
2:x:143:LEU:CD1	2:x:146:TYR:HB2	2.02	0.90
3:A:108:ARG:NH1	3:B:72:MET:SD	2.44	0.90
4:X:168:ARG:NH1	4:X:172:MET:CE	2.34	0.90
2:u:277:ALA:HA	3:B:100:ARG:CG	2.01	0.90
2:u:728:LYS:N	4:V:36:ALA:HB2	1.86	0.90
4:P:168:ARG:NH1	4:P:172:MET:CE	2.34	0.90
4:S:2:ARG:HH11	4:S:124:LEU:HD21	1.34	0.90
2:w:150:GLN:OE1	2:w:224:ALA:CB	2.20	0.90
2:w:277:ALA:HA	3:F:100:ARG:CG	2.00	0.90
2:s:143:LEU:CD1	2:s:146:TYR:HB2	2.02	0.90
2:u:143:LEU:CD1	2:u:146:TYR:HB2	2.02	0.90
2:x:150:GLN:OE1	2:x:224:ALA:CB	2.20	0.90
2:w:143:LEU:CD1	2:w:146:TYR:HB2	2.02	0.90
2:s:277:ALA:HA	3:D:100:ARG:CG	2.01	0.90
4:Q:2:ARG:HH11	4:Q:124:LEU:HD21	1.34	0.90
2:v:370:ARG:HD3	2:v:376:ASN:HB2	1.52	0.90
2:v:396:SER:HB2	3:A:91:GLU:OE2	1.72	0.90
4:X:55:GLN:HE22	4:X:125:ARG:HB2	1.37	0.90
2:w:176:LYS:HZ1	2:w:178:LYS:CE	1.85	0.89
2:v:277:ALA:HA	3:A:100:ARG:CG	2.02	0.89
2:w:728:LYS:N	4:N:36:ALA:HB2	1.86	0.89
2:t:196:LEU:O	2:t:200:LEU:HD23	1.71	0.89
2:v:150:GLN:OE1	2:v:224:ALA:CB	2.20	0.89
2:s:150:GLN:OE1	2:s:224:ALA:CB	2.20	0.89
1:f:93:ILE:HG13	2:v:638:GLY:CA	2.01	0.89
2:s:143:LEU:HD13	2:s:146:TYR:CB	2.03	0.89
2:u:196:LEU:O	2:u:200:LEU:HD23	1.71	0.89
2:u:758:VAL:CG1	4:W:25:GLY:O	2.20	0.89
2:v:758:VAL:CG1	4:M:25:GLY:O	2.20	0.89
4:V:55:GLN:HE22	4:V:125:ARG:HB2	1.37	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:254:PHE:HE2	3:B:65:ALA:CB	1.86	0.89
2:x:254:PHE:HE2	3:F:65:ALA:CB	1.86	0.89
2:v:143:LEU:CD1	2:v:146:TYR:HB2	2.02	0.89
2:w:758:VAL:CG1	4:O:25:GLY:O	2.20	0.89
1:l:93:ILE:HG13	2:t:638:GLY:CA	2.01	0.89
1:r:93:ILE:HG13	2:x:638:GLY:CA	2.03	0.89
2:w:728:LYS:H	4:N:36:ALA:CB	1.84	0.89
2:s:196:LEU:O	2:s:200:LEU:HD23	1.71	0.89
2:x:143:LEU:HD13	2:x:146:TYR:CB	2.03	0.89
2:t:143:LEU:HD13	2:t:146:TYR:CB	2.03	0.89
1:p:97:TYR:HD1	4:O:6:MET:CE	1.86	0.88
2:u:150:GLN:OE1	2:u:224:ALA:CB	2.20	0.88
2:v:143:LEU:HD13	2:v:146:TYR:CB	2.03	0.88
2:w:143:LEU:HD13	2:w:146:TYR:CB	2.03	0.88
2:t:150:GLN:OE1	2:t:224:ALA:CB	2.20	0.88
4:R:55:GLN:HE22	4:R:125:ARG:HB2	1.37	0.88
2:x:277:ALA:HA	3:E:100:ARG:CG	2.03	0.88
2:s:176:LYS:HZ1	2:s:178:LYS:HE3	1.34	0.88
2:s:370:ARG:HD3	2:s:376:ASN:HB2	1.52	0.88
4:P:55:GLN:HE22	4:P:125:ARG:HB2	1.37	0.87
2:t:183:SER:HB2	3:D:42:MET:HB2	1.54	0.87
2:x:758:VAL:CG1	4:Q:25:GLY:O	2.23	0.87
1:i:93:ILE:CG1	2:u:638:GLY:CA	2.52	0.87
2:v:727:TRP:HB3	4:X:36:ALA:CB	2.04	0.87
2:x:728:LYS:N	4:P:36:ALA:HB2	1.87	0.87
2:t:143:LEU:CD1	2:t:146:TYR:HB2	2.02	0.87
2:t:728:LYS:H	4:T:36:ALA:CB	1.86	0.87
2:u:254:PHE:HE2	3:C:65:ALA:CB	1.87	0.87
4:T:55:GLN:HE22	4:T:125:ARG:HB2	1.37	0.87
2:s:728:LYS:H	4:R:36:ALA:CB	1.86	0.87
2:w:727:TRP:HB3	4:N:36:ALA:CB	2.04	0.87
4:T:148:ASN:HD21	4:U:159:VAL:HG11	1.40	0.87
2:v:128:VAL:HG21	2:v:351:VAL:HG21	1.57	0.87
2:v:739:ASN:HD21	2:v:742:ARG:HH21	1.21	0.87
2:x:728:LYS:H	4:P:36:ALA:CB	1.85	0.87
2:s:758:VAL:CG1	4:S:25:GLY:O	2.23	0.87
2:t:758:VAL:CG1	4:U:25:GLY:O	2.22	0.87
2:u:143:LEU:HD13	2:u:146:TYR:CB	2.03	0.87
3:A:39:MET:O	3:A:43:ARG:CG	2.21	0.87
4:P:148:ASN:HD21	4:Q:159:VAL:HG11	1.40	0.86
1:c:93:ILE:CG1	2:w:638:GLY:CA	2.53	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:348:ILE:HD12	2:s:348:ILE:N	1.90	0.86
2:s:739:ASN:HD21	2:s:742:ARG:HH21	1.21	0.86
4:N:55:GLN:HE22	4:N:125:ARG:HB2	1.37	0.86
2:u:739:ASN:HD21	2:u:742:ARG:HH21	1.21	0.86
2:w:128:VAL:HG21	2:w:351:VAL:HG21	1.57	0.86
4:T:168:ARG:HH12	4:T:172:MET:CE	1.89	0.86
2:t:277:ALA:HA	3:C:100:ARG:CG	2.04	0.86
2:t:348:ILE:HD12	2:t:348:ILE:N	1.90	0.86
2:u:128:VAL:HG21	2:u:351:VAL:HG21	1.57	0.86
2:s:128:VAL:HG21	2:s:351:VAL:HG21	1.57	0.86
4:R:168:ARG:HH12	4:R:172:MET:CE	1.89	0.86
1:h:93:ILE:CG2	2:u:732:ALA:O	2.24	0.86
2:u:727:TRP:HB3	4:V:36:ALA:CB	2.06	0.86
2:t:727:TRP:HB3	4:T:36:ALA:CB	2.05	0.85
2:t:728:LYS:N	4:T:36:ALA:HB2	1.90	0.85
2:w:183:SER:HB2	3:A:42:MET:HB2	1.58	0.85
2:u:176:LYS:HZ3	2:u:178:LYS:HE3	1.39	0.85
2:w:348:ILE:HD12	2:w:348:ILE:N	1.90	0.85
2:w:739:ASN:HD21	2:w:742:ARG:HH21	1.21	0.85
4:N:168:ARG:HH12	4:N:172:MET:CE	1.89	0.85
4:V:148:ASN:HD21	4:W:159:VAL:HG11	1.41	0.85
2:w:388:ASP:OD2	3:A:82:ARG:CB	2.24	0.85
4:X:168:ARG:HH12	4:X:172:MET:CE	1.89	0.85
2:x:727:TRP:HB3	4:P:36:ALA:CB	2.04	0.85
1:c:116:LEU:HD23	1:c:116:LEU:C	1.99	0.85
2:t:128:VAL:HG21	2:t:351:VAL:HG21	1.57	0.85
4:N:168:ARG:NH1	4:N:172:MET:HE3	1.92	0.85
4:X:168:ARG:NH1	4:X:172:MET:HE3	1.92	0.85
2:v:728:LYS:N	4:X:36:ALA:CB	2.39	0.85
2:x:348:ILE:HD12	2:x:348:ILE:N	1.90	0.85
4:R:148:ASN:HD21	4:S:159:VAL:HG11	1.42	0.85
1:f:89:THR:CG2	2:v:640:ILE:O	2.24	0.85
1:i:89:THR:CG2	2:u:640:ILE:O	2.25	0.85
1:o:116:LEU:HD23	1:o:116:LEU:C	1.99	0.85
2:u:150:GLN:CB	2:u:224:ALA:CB	2.55	0.85
2:u:348:ILE:HD12	2:u:348:ILE:N	1.90	0.85
2:x:739:ASN:HD21	2:x:742:ARG:HH21	1.21	0.85
2:u:728:LYS:N	4:V:36:ALA:CB	2.40	0.85
2:v:348:ILE:HD12	2:v:348:ILE:N	1.90	0.85
4:N:148:ASN:HD21	4:O:159:VAL:HG11	1.40	0.85
4:T:168:ARG:NH1	4:T:172:MET:HE3	1.92	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:93:ILE:CG1	2:v:638:GLY:CA	2.53	0.85
2:w:150:GLN:CB	2:w:224:ALA:CB	2.55	0.85
4:P:94:SER:HB2	4:Q:178:TYR:CE1	2.12	0.85
4:V:168:ARG:HH12	4:V:172:MET:CE	1.89	0.85
1:e:93:ILE:CG2	2:v:732:ALA:O	2.24	0.84
1:o:93:ILE:HB	2:s:638:GLY:O	1.76	0.84
4:V:168:ARG:NH1	4:V:172:MET:HE3	1.92	0.84
1:r:116:LEU:HD23	1:r:116:LEU:C	1.99	0.84
2:s:728:LYS:N	4:R:36:ALA:HB2	1.90	0.84
2:t:739:ASN:HD21	2:t:742:ARG:HH21	1.21	0.84
2:x:128:VAL:HG21	2:x:351:VAL:HG21	1.57	0.84
3:E:49:ASN:OD1	3:E:128:GLN:HB2	1.78	0.84
4:P:94:SER:CB	4:Q:178:TYR:CE1	2.60	0.84
2:v:176:LYS:HZ3	2:v:178:LYS:HE3	1.38	0.84
1:k:93:ILE:CG2	2:t:732:ALA:O	2.26	0.84
2:x:150:GLN:CB	2:x:224:ALA:CB	2.55	0.84
4:P:168:ARG:HH12	4:P:172:MET:CE	1.89	0.84
2:t:150:GLN:CB	2:t:224:ALA:CB	2.55	0.84
1:r:93:ILE:CG1	2:x:638:GLY:CA	2.56	0.84
2:t:437:LEU:CD1	3:C:90:LEU:HD12	2.07	0.84
4:N:94:SER:HB2	4:O:178:TYR:CE1	2.13	0.84
2:u:768:ILE:HD13	2:u:778:ILE:HD11	1.59	0.84
1:n:93:ILE:CG2	2:s:732:ALA:O	2.26	0.84
2:v:150:GLN:CB	2:v:224:ALA:CB	2.55	0.84
4:R:168:ARG:NH1	4:R:172:MET:HE3	1.92	0.84
1:f:116:LEU:HD23	1:f:116:LEU:C	1.99	0.83
1:b:93:ILE:CG2	2:w:732:ALA:O	2.25	0.83
1:e:93:ILE:HG21	2:v:732:ALA:O	1.78	0.83
1:i:116:LEU:HD23	1:i:116:LEU:C	1.99	0.83
2:t:176:LYS:HZ1	2:t:178:LYS:CE	1.90	0.83
1:r:93:ILE:HD12	2:x:746:LEU:CA	2.05	0.83
4:P:168:ARG:NH1	4:P:172:MET:HE3	1.92	0.83
1:l:116:LEU:HD23	1:l:116:LEU:C	1.99	0.83
2:v:768:ILE:HD13	2:v:778:ILE:HD11	1.59	0.83
2:w:728:LYS:N	4:N:36:ALA:CB	2.40	0.83
1:h:93:ILE:HG21	2:u:732:ALA:O	1.78	0.83
2:s:150:GLN:CB	2:s:224:ALA:CB	2.55	0.83
1:c:89:THR:CG2	2:w:640:ILE:O	2.26	0.83
2:u:183:SER:HB2	3:C:42:MET:HB2	1.59	0.83
4:M:178:TYR:CE1	4:X:94:SER:HB2	2.13	0.83
4:N:94:SER:CB	4:O:178:TYR:CE1	2.62	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:89:THR:CG2	2:t:640:ILE:O	2.27	0.83
1:l:93:ILE:CG1	2:t:638:GLY:CA	2.54	0.83
1:o:89:THR:CG2	2:s:640:ILE:O	2.27	0.83
2:x:728:LYS:N	4:P:36:ALA:CB	2.42	0.83
4:M:159:VAL:HG11	4:X:148:ASN:HD21	1.42	0.83
1:d:93:ILE:HD11	2:v:739:ASN:OD1	1.79	0.82
2:t:768:ILE:HD13	2:t:778:ILE:HD11	1.59	0.82
2:w:768:ILE:HD13	2:w:778:ILE:HD11	1.59	0.82
2:t:150:GLN:CB	2:t:224:ALA:HB2	2.09	0.82
2:u:150:GLN:CB	2:u:224:ALA:HB2	2.09	0.82
2:u:277:ALA:HA	3:B:100:ARG:HG3	1.61	0.82
2:v:396:SER:CB	3:A:91:GLU:CD	2.47	0.82
2:s:768:ILE:HD13	2:s:778:ILE:HD11	1.59	0.82
2:x:768:ILE:HD13	2:x:778:ILE:HD11	1.59	0.82
4:M:178:TYR:CE1	4:X:94:SER:CB	2.62	0.82
1:j:93:ILE:HD11	2:t:739:ASN:OD1	1.79	0.82
2:s:183:SER:HB2	3:E:42:MET:HB2	1.61	0.82
2:t:130:ARG:O	2:t:347:SER:HB2	1.80	0.82
2:v:150:GLN:CB	2:v:224:ALA:HB2	2.09	0.82
2:v:396:SER:HB2	3:A:91:GLU:OE1	1.78	0.82
3:D:105:GLN:HA	3:D:108:ARG:HH21	1.43	0.82
1:b:93:ILE:HG21	2:w:732:ALA:O	1.79	0.82
2:s:150:GLN:CB	2:s:224:ALA:HB2	2.09	0.82
2:w:150:GLN:CB	2:w:224:ALA:HB2	2.09	0.82
2:v:130:ARG:O	2:v:347:SER:HB2	1.80	0.81
2:w:130:ARG:O	2:w:347:SER:HB2	1.80	0.81
1:d:11:TYR:CE2	4:W:70:LEU:O	2.32	0.81
1:a:11:TYR:CE2	4:M:70:LEU:O	2.34	0.81
2:s:727:TRP:HB3	4:R:36:ALA:CB	2.06	0.81
2:u:130:ARG:O	2:u:347:SER:HB2	1.80	0.81
2:v:176:LYS:HZ1	2:v:178:LYS:HE3	1.44	0.81
2:x:130:ARG:O	2:x:347:SER:HB2	1.80	0.81
2:x:150:GLN:CB	2:x:224:ALA:HB2	2.09	0.81
1:i:116:LEU:CD2	1:i:116:LEU:C	2.54	0.81
1:n:93:ILE:HG21	2:s:732:ALA:O	1.80	0.81
1:r:89:THR:CG2	2:x:640:ILE:O	2.28	0.81
2:t:254:PHE:HE2	3:D:65:ALA:CB	1.92	0.81
1:m:11:TYR:CE2	4:Q:70:LEU:O	2.32	0.81
1:q:93:ILE:CG2	2:x:732:ALA:O	2.28	0.81
2:v:163:ARG:HH21	3:A:129:LEU:HD13	1.46	0.81
2:s:728:LYS:N	4:R:36:ALA:CB	2.44	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:94:SER:HB2	4:W:178:TYR:CE1	2.15	0.81
1:o:52:PHE:HA	1:o:58:ILE:HG22	1.63	0.81
1:p:93:ILE:HD11	2:x:739:ASN:OD1	1.80	0.81
2:u:176:LYS:HZ1	2:u:178:LYS:HE3	1.43	0.81
4:P:94:SER:HB2	4:Q:178:TYR:CD1	2.16	0.81
1:c:9:LEU:HD21	1:c:23:PRO:HG3	1.63	0.81
1:i:52:PHE:HA	1:i:58:ILE:HG22	1.63	0.81
1:p:11:TYR:CE2	4:O:70:LEU:O	2.34	0.81
4:V:94:SER:CB	4:W:178:TYR:CE1	2.64	0.81
1:g:93:ILE:HD11	2:u:739:ASN:OD1	1.81	0.81
2:v:277:ALA:HA	3:A:100:ARG:HG3	1.63	0.81
2:w:183:SER:HB2	3:A:42:MET:CB	2.10	0.81
3:C:137:SER:HB3	3:D:43:ARG:NH2	1.94	0.81
2:w:277:ALA:HA	3:F:100:ARG:HG3	1.63	0.81
1:c:116:LEU:CD2	1:c:116:LEU:C	2.54	0.80
1:o:9:LEU:HD21	1:o:23:PRO:HG3	1.63	0.80
4:T:94:SER:HB2	4:U:178:TYR:CE1	2.16	0.80
1:q:93:ILE:HG21	2:x:732:ALA:O	1.82	0.80
2:v:86:ILE:O	2:v:98:VAL:CG1	2.28	0.80
4:R:94:SER:HB2	4:S:178:TYR:CE1	2.16	0.80
2:s:185:PRO:HD3	3:E:42:MET:HE1	1.34	0.80
1:a:93:ILE:HD11	2:w:739:ASN:OD1	1.79	0.80
1:o:116:LEU:CD2	1:o:116:LEU:C	2.54	0.80
4:T:94:SER:CB	4:U:178:TYR:CE1	2.65	0.80
1:g:11:TYR:CE2	4:U:70:LEU:O	2.34	0.80
1:k:93:ILE:HG21	2:t:732:ALA:O	1.80	0.80
1:l:93:ILE:HD12	2:t:746:LEU:CA	2.06	0.80
4:R:94:SER:CB	4:S:178:TYR:CE1	2.65	0.80
1:f:9:LEU:HD21	1:f:23:PRO:HG3	1.63	0.80
1:f:116:LEU:CD2	1:f:116:LEU:C	2.54	0.80
1:l:116:LEU:CD2	1:l:116:LEU:C	2.54	0.80
1:j:11:TYR:CE2	4:S:70:LEU:O	2.34	0.80
3:A:119:ARG:HD2	3:A:122:GLN:NE2	1.96	0.80
3:C:119:ARG:HD2	3:C:122:GLN:NE2	1.96	0.80
1:f:52:PHE:HA	1:f:58:ILE:HG22	1.64	0.80
2:t:86:ILE:O	2:t:98:VAL:CG1	2.28	0.80
2:t:728:LYS:N	4:T:36:ALA:CB	2.44	0.80
1:m:93:ILE:HD11	2:s:739:ASN:OD1	1.80	0.79
2:s:272:ASP:OD1	2:s:272:ASP:O	2.00	0.79
3:C:137:SER:CB	3:D:43:ARG:NH2	2.44	0.79
1:r:116:LEU:CD2	1:r:116:LEU:C	2.54	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:130:ARG:O	2:s:347:SER:HB2	1.80	0.79
2:x:277:ALA:HA	3:E:100:ARG:HG3	1.63	0.79
1:l:9:LEU:HD21	1:l:23:PRO:HG3	1.63	0.79
2:s:184:GLN:HA	3:E:42:MET:HE1	1.64	0.79
2:s:277:ALA:HA	3:D:100:ARG:HG3	1.63	0.79
2:w:176:LYS:CE	2:w:178:LYS:HE3	2.12	0.79
2:x:272:ASP:OD1	2:x:272:ASP:O	2.00	0.79
2:x:176:LYS:CE	2:x:178:LYS:HE3	2.13	0.79
1:c:93:ILE:HD12	2:w:746:LEU:CA	2.06	0.79
1:f:93:ILE:HD12	2:v:746:LEU:CA	2.05	0.79
1:l:52:PHE:HA	1:l:58:ILE:HG22	1.65	0.79
2:t:272:ASP:OD1	2:t:272:ASP:O	2.00	0.79
2:s:176:LYS:CE	2:s:178:LYS:HE3	2.12	0.79
4:M:178:TYR:CD1	4:X:94:SER:HB2	2.18	0.79
2:v:176:LYS:CE	2:v:178:LYS:HE3	2.12	0.79
2:v:272:ASP:OD1	2:v:272:ASP:O	2.00	0.79
4:N:94:SER:HB2	4:O:178:TYR:CD1	2.18	0.79
1:r:9:LEU:HD21	1:r:23:PRO:HG3	1.63	0.78
2:x:86:ILE:O	2:x:98:VAL:CG1	2.28	0.78
2:s:176:LYS:NZ	2:s:178:LYS:CE	2.45	0.78
2:w:142:ASN:HB3	2:w:295:LEU:HD11	1.66	0.78
1:i:9:LEU:HD21	1:i:23:PRO:HG3	1.63	0.78
2:v:145:ASN:OD1	2:v:145:ASN:O	2.02	0.78
2:v:183:SER:HB2	3:B:42:MET:HB2	1.65	0.78
1:c:52:PHE:HA	1:c:58:ILE:HG22	1.66	0.78
1:i:93:ILE:HD12	2:u:746:LEU:CA	2.06	0.78
1:l:93:ILE:CB	2:t:638:GLY:O	2.30	0.78
2:u:145:ASN:OD1	2:u:145:ASN:O	2.02	0.78
2:w:145:ASN:O	2:w:145:ASN:OD1	2.02	0.78
2:w:272:ASP:OD1	2:w:272:ASP:O	2.00	0.78
2:x:378:TYR:H	2:x:378:TYR:HD1	1.31	0.78
2:t:142:ASN:HB3	2:t:295:LEU:HD11	1.66	0.78
2:u:176:LYS:CE	2:u:178:LYS:HE3	2.12	0.78
2:x:142:ASN:HB3	2:x:295:LEU:HD11	1.66	0.78
1:i:95:ARG:HG3	2:u:639:LYS:HG3	1.65	0.78
2:v:176:LYS:NZ	2:v:178:LYS:CE	2.46	0.78
2:t:145:ASN:O	2:t:145:ASN:OD1	2.02	0.77
2:u:272:ASP:OD1	2:u:272:ASP:O	2.00	0.77
2:u:500:VAL:O	2:u:500:VAL:CG2	2.33	0.77
2:v:500:VAL:O	2:v:500:VAL:CG2	2.33	0.77
2:w:500:VAL:O	2:w:500:VAL:CG2	2.33	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:176:LYS:CE	2:t:178:LYS:HE3	2.12	0.77
2:t:277:ALA:HA	3:C:100:ARG:HG3	1.65	0.77
2:x:176:LYS:NZ	2:x:178:LYS:CE	2.45	0.77
2:u:142:ASN:HB3	2:u:295:LEU:HD11	1.66	0.77
2:s:145:ASN:OD1	2:s:145:ASN:O	2.02	0.77
2:t:500:VAL:O	2:t:500:VAL:CG2	2.33	0.77
1:f:36:LEU:HD22	1:f:73:ILE:HD13	1.67	0.77
2:x:145:ASN:OD1	2:x:145:ASN:O	2.02	0.77
1:c:93:ILE:CB	2:w:638:GLY:O	2.29	0.77
2:s:240:ALA:HB1	3:D:122:GLN:HG2	1.65	0.77
4:S:72:ASP:HB2	4:S:75:SER:HB2	1.67	0.77
4:V:94:SER:HB2	4:W:178:TYR:CD1	2.19	0.77
2:s:188:VAL:HG23	3:E:46:ASN:OD1	1.85	0.77
1:c:36:LEU:HD22	1:c:73:ILE:HD13	1.66	0.77
2:s:378:TYR:H	2:s:378:TYR:HD1	1.31	0.77
2:x:500:VAL:O	2:x:500:VAL:CG2	2.33	0.77
2:u:176:LYS:NZ	2:u:178:LYS:CE	2.45	0.76
1:c:95:ARG:HG3	2:w:639:LYS:HG3	1.68	0.76
2:u:378:TYR:HD1	2:u:378:TYR:H	1.32	0.76
2:w:378:TYR:HD1	2:w:378:TYR:H	1.32	0.76
2:s:176:LYS:HZ3	2:s:178:LYS:HE3	1.47	0.76
2:u:86:ILE:O	2:u:98:VAL:CG1	2.28	0.76
2:s:426:ALA:HB3	2:s:430:LEU:HD22	1.68	0.76
2:u:284:TYR:HB2	2:u:291:TRP:CZ2	2.21	0.76
2:v:160:GLN:HG3	3:B:54:LEU:HD11	1.68	0.76
2:w:177:TYR:CZ	2:w:179:ILE:HA	2.21	0.76
2:x:177:TYR:CZ	2:x:179:ILE:HA	2.21	0.76
4:U:72:ASP:HB2	4:U:75:SER:HB2	1.67	0.76
1:l:36:LEU:HD22	1:l:73:ILE:HD13	1.66	0.76
2:s:142:ASN:HB3	2:s:295:LEU:HD11	1.66	0.76
2:s:177:TYR:CZ	2:s:179:ILE:HA	2.21	0.76
2:t:177:TYR:CZ	2:t:179:ILE:HA	2.21	0.76
2:v:142:ASN:HB3	2:v:295:LEU:HD11	1.66	0.76
2:x:426:ALA:HB3	2:x:430:LEU:HD22	1.68	0.76
1:f:95:ARG:HG3	2:v:639:LYS:HG3	1.68	0.76
2:s:160:GLN:HG3	3:E:54:LEU:HD11	1.68	0.76
2:s:188:VAL:CG2	3:E:46:ASN:OD1	2.34	0.76
4:R:94:SER:HB2	4:S:178:TYR:CD1	2.20	0.76
4:S:2:ARG:HE	4:S:124:LEU:HD22	1.51	0.76
1:o:36:LEU:HD22	1:o:73:ILE:HD13	1.67	0.76
2:v:284:TYR:HB2	2:v:291:TRP:CZ2	2.21	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U:2:ARG:HE	4:U:124:LEU:HD22	1.51	0.76
2:s:432:SER:HB3	3:D:95:MET:HE1	1.69	0.75
2:v:127:ILE:HD11	2:v:312:LEU:HB2	1.69	0.75
2:t:426:ALA:HB3	2:t:430:LEU:HD22	1.68	0.75
4:Q:2:ARG:HE	4:Q:124:LEU:HD22	1.51	0.75
2:s:500:VAL:O	2:s:500:VAL:CG2	2.33	0.75
2:w:127:ILE:HD11	2:w:312:LEU:HB2	1.69	0.75
2:x:127:ILE:HD11	2:x:312:LEU:HB2	1.69	0.75
3:C:126:ALA:HA	3:C:129:LEU:HD23	1.68	0.75
2:v:177:TYR:CZ	2:v:179:ILE:HA	2.21	0.75
2:t:688:ALA:HB3	2:t:692:SER:HB3	1.68	0.75
2:w:284:TYR:HB2	2:w:291:TRP:CZ2	2.21	0.75
4:O:72:ASP:HB2	4:O:75:SER:HB2	1.67	0.75
2:u:688:ALA:HB3	2:u:692:SER:HB3	1.68	0.75
4:T:94:SER:HB2	4:U:178:TYR:CD1	2.21	0.75
1:j:13:LEU:HD13	1:j:73:ILE:HG13	1.69	0.75
2:s:127:ILE:HD11	2:s:312:LEU:HB2	1.69	0.75
2:t:378:TYR:HD1	2:t:378:TYR:H	1.31	0.75
2:w:426:ALA:HB3	2:w:430:LEU:HD22	1.68	0.75
2:x:284:TYR:HB2	2:x:291:TRP:CZ2	2.21	0.75
4:M:72:ASP:HB2	4:M:75:SER:HB2	1.67	0.75
4:T:57:ARG:HG3	4:U:170:LEU:CD1	2.17	0.75
4:W:2:ARG:HE	4:W:124:LEU:HD22	1.51	0.75
1:l:95:ARG:HG3	2:t:639:LYS:HG3	1.68	0.75
2:u:426:ALA:HB3	2:u:430:LEU:HD22	1.68	0.75
4:W:72:ASP:HB2	4:W:75:SER:HB2	1.67	0.75
2:s:284:TYR:HB2	2:s:291:TRP:CZ2	2.21	0.75
2:s:688:ALA:HB3	2:s:692:SER:HB3	1.68	0.75
4:O:2:ARG:HE	4:O:124:LEU:HD22	1.51	0.75
1:g:13:LEU:HD13	1:g:73:ILE:HG13	1.69	0.74
2:v:426:ALA:HB3	2:v:430:LEU:HD22	1.68	0.74
2:x:176:LYS:HZ1	2:x:178:LYS:CE	1.99	0.74
1:i:36:LEU:HD22	1:i:73:ILE:HD13	1.67	0.74
1:r:36:LEU:HD22	1:r:73:ILE:HD13	1.67	0.74
2:t:176:LYS:NZ	2:t:178:LYS:CE	2.46	0.74
2:u:177:TYR:CZ	2:u:179:ILE:HA	2.21	0.74
2:w:284:TYR:HB2	2:w:291:TRP:CH2	2.23	0.74
4:T:148:ASN:ND2	4:U:159:VAL:HG11	2.03	0.74
4:V:57:ARG:HG3	4:W:170:LEU:CD1	2.16	0.74
2:s:86:ILE:O	2:s:98:VAL:CG1	2.28	0.74
2:t:284:TYR:HB2	2:t:291:TRP:CZ2	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:u:127:ILE:HD11	2:u:312:LEU:HB2	1.69	0.74
2:v:378:TYR:H	2:v:378:TYR:HD1	1.31	0.74
2:x:183:SER:HB2	3:F:42:MET:HB2	1.69	0.74
4:M:2:ARG:HE	4:M:124:LEU:HD22	1.51	0.74
4:P:57:ARG:HG3	4:Q:170:LEU:CD1	2.14	0.74
2:v:284:TYR:HB2	2:v:291:TRP:CH2	2.23	0.74
2:w:714:GLY:N	2:w:774:THR:HG21	2.02	0.74
3:D:108:ARG:NH1	3:E:72:MET:SD	2.61	0.74
4:Q:72:ASP:HB2	4:Q:75:SER:HB2	1.67	0.74
1:r:95:ARG:HG3	2:x:639:LYS:HG3	1.70	0.74
2:t:714:GLY:N	2:t:774:THR:HG21	2.03	0.74
2:u:714:GLY:N	2:u:774:THR:HG21	2.03	0.74
2:x:160:GLN:HG3	3:F:54:LEU:HD11	1.70	0.74
4:O:3:SER:HB3	4:O:6:MET:HB2	1.69	0.74
1:m:13:LEU:HD13	1:m:73:ILE:HG13	1.69	0.74
1:p:13:LEU:HD13	1:p:73:ILE:HG13	1.69	0.74
2:t:127:ILE:HD11	2:t:312:LEU:HB2	1.69	0.74
2:t:284:TYR:HB2	2:t:291:TRP:CH2	2.23	0.74
2:v:714:GLY:N	2:v:774:THR:HG21	2.03	0.74
2:w:86:ILE:O	2:w:98:VAL:CG1	2.28	0.74
4:M:170:LEU:CD1	4:X:57:ARG:HG3	2.16	0.74
4:N:57:ARG:HG3	4:O:170:LEU:CD1	2.15	0.74
1:e:90:ASP:HB2	4:W:4:TYR:OH	1.87	0.74
1:r:93:ILE:CB	2:x:638:GLY:O	2.31	0.74
2:s:284:TYR:HB2	2:s:291:TRP:CH2	2.23	0.74
2:x:378:TYR:N	2:x:378:TYR:CD1	2.56	0.74
3:C:74:LYS:HA	3:C:106:PHE:CE2	2.22	0.74
2:s:600:TYR:HE2	2:s:603:PRO:HD3	1.53	0.73
2:s:185:PRO:N	3:E:42:MET:CE	2.52	0.73
2:u:163:ARG:HH21	3:B:129:LEU:HD13	1.51	0.73
2:x:600:TYR:HE2	2:x:603:PRO:HD3	1.53	0.73
2:x:688:ALA:HB3	2:x:692:SER:HB3	1.68	0.73
1:o:95:ARG:HG3	2:s:639:LYS:HG3	1.70	0.73
1:q:9:LEU:HB2	1:q:23:PRO:HG3	1.71	0.73
1:a:13:LEU:HD13	1:a:73:ILE:HG13	1.69	0.73
2:v:688:ALA:HB3	2:v:692:SER:HB3	1.68	0.73
2:x:284:TYR:HB2	2:x:291:TRP:CH2	2.23	0.73
1:b:9:LEU:HB2	1:b:23:PRO:HG3	1.71	0.73
1:b:90:ASP:HB2	4:M:4:TYR:OH	1.87	0.73
2:s:378:TYR:CD1	2:s:378:TYR:N	2.56	0.73
2:u:284:TYR:HB2	2:u:291:TRP:CH2	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:w:378:TYR:N	2:w:378:TYR:CD1	2.56	0.73
2:w:688:ALA:HB3	2:w:692:SER:HB3	1.68	0.73
2:x:254:PHE:HE2	3:F:65:ALA:HB2	1.53	0.73
1:d:13:LEU:HD13	1:d:73:ILE:HG13	1.69	0.73
1:e:9:LEU:HB2	1:e:23:PRO:HG3	1.71	0.73
2:u:366:ILE:HD13	2:u:424:LEU:HD11	1.71	0.73
2:u:378:TYR:N	2:u:378:TYR:CD1	2.56	0.73
2:w:600:TYR:HE2	2:w:603:PRO:HD3	1.53	0.73
2:x:370:ARG:HG3	2:x:376:ASN:O	1.89	0.73
4:V:17:VAL:HG21	4:V:32:LEU:HD21	1.71	0.73
4:V:148:ASN:ND2	4:W:159:VAL:HG11	2.04	0.73
1:n:90:ASP:HB2	4:Q:4:TYR:OH	1.89	0.73
2:s:277:ALA:HA	3:D:100:ARG:HG2	1.70	0.73
2:t:366:ILE:HD13	2:t:424:LEU:HD11	1.71	0.73
2:t:378:TYR:N	2:t:378:TYR:CD1	2.56	0.73
2:u:160:GLN:HG3	3:C:54:LEU:HD11	1.71	0.73
1:n:9:LEU:HB2	1:n:23:PRO:HG3	1.71	0.73
2:t:68:LEU:HD21	2:t:557:ILE:HG12	1.71	0.73
2:t:370:ARG:HG3	2:t:376:ASN:O	1.89	0.73
2:w:254:PHE:CE2	3:A:65:ALA:CB	2.71	0.73
2:x:714:GLY:N	2:x:774:THR:HG21	2.02	0.73
1:g:93:ILE:HD13	2:u:742:ARG:HG2	1.69	0.72
1:h:90:ASP:HB2	4:U:4:TYR:OH	1.87	0.72
2:s:68:LEU:HD21	2:s:557:ILE:HG12	1.71	0.72
2:s:366:ILE:HD13	2:s:424:LEU:HD11	1.71	0.72
2:s:370:ARG:HG3	2:s:376:ASN:O	1.89	0.72
2:t:22:LEU:HD21	2:u:779:ILE:HG13	1.70	0.72
2:u:369:SER:HB2	2:u:377:PHE:CE2	2.24	0.72
2:u:370:ARG:HG3	2:u:376:ASN:O	1.89	0.72
2:x:366:ILE:HD13	2:x:424:LEU:HD11	1.71	0.72
4:P:94:SER:HB3	4:Q:178:TYR:CE1	2.23	0.72
4:T:17:VAL:HG21	4:T:32:LEU:HD21	1.71	0.72
1:k:9:LEU:HB2	1:k:23:PRO:HG3	1.71	0.72
2:s:254:PHE:HE2	3:E:65:ALA:HB2	1.52	0.72
2:s:369:SER:HB2	2:s:377:PHE:CE2	2.24	0.72
2:s:443:PHE:CG	2:s:485:ALA:HB2	2.24	0.72
2:u:254:PHE:HE2	3:C:65:ALA:HB2	1.53	0.72
2:v:369:SER:HB2	2:v:377:PHE:CE2	2.24	0.72
2:v:378:TYR:N	2:v:378:TYR:CD1	2.56	0.72
2:x:443:PHE:CG	2:x:485:ALA:HB2	2.24	0.72
1:i:93:ILE:CB	2:u:638:GLY:O	2.28	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:k:101:VAL:CG2	4:T:33:GLU:OE2	2.27	0.72
2:s:22:LEU:HD21	2:t:779:ILE:HG13	1.71	0.72
2:s:714:GLY:N	2:s:774:THR:HG21	2.02	0.72
2:v:366:ILE:HD13	2:v:424:LEU:HD11	1.71	0.72
2:w:370:ARG:HG3	2:w:376:ASN:O	1.89	0.72
4:P:148:ASN:ND2	4:Q:159:VAL:HG11	2.04	0.72
2:u:68:LEU:HD21	2:u:557:ILE:HG12	1.71	0.72
2:v:370:ARG:HG3	2:v:376:ASN:O	1.89	0.72
2:w:366:ILE:HD13	2:w:424:LEU:HD11	1.71	0.72
2:x:184:GLN:HA	3:F:42:MET:HE1	1.71	0.72
3:A:42:MET:O	3:A:46:ASN:ND2	2.22	0.72
1:i:95:ARG:CG	2:u:639:LYS:HG3	2.19	0.72
1:p:26:TYR:CZ	4:P:7:ASN:HB2	2.23	0.72
2:w:22:LEU:HD21	2:x:779:ILE:HG13	1.72	0.72
2:w:277:ALA:HA	3:F:100:ARG:HG2	1.70	0.72
1:o:93:ILE:HG12	2:s:746:LEU:HA	1.69	0.72
2:v:68:LEU:HD21	2:v:557:ILE:HG12	1.71	0.72
2:v:600:TYR:HE2	2:v:603:PRO:HD3	1.53	0.72
4:R:148:ASN:ND2	4:S:159:VAL:HG11	2.05	0.72
1:a:93:ILE:HD13	2:w:742:ARG:HG2	1.70	0.72
1:h:9:LEU:HB2	1:h:23:PRO:HG3	1.71	0.72
2:s:381:SER:O	3:D:97:ARG:NH2	2.21	0.72
2:w:443:PHE:CG	2:w:485:ALA:HB2	2.24	0.72
2:x:225:PRO:HB2	2:x:228:GLN:O	1.90	0.72
2:x:369:SER:HB2	2:x:377:PHE:CE2	2.24	0.72
3:C:137:SER:CB	3:D:43:ARG:HH22	2.01	0.72
2:t:160:GLN:HG3	3:D:54:LEU:HD11	1.72	0.72
2:w:254:PHE:HE2	3:A:65:ALA:HB2	1.53	0.72
1:g:9:LEU:CD2	4:U:72:ASP:OD2	2.38	0.72
2:t:443:PHE:CG	2:t:485:ALA:HB2	2.24	0.72
2:u:200:LEU:HD22	2:u:200:LEU:N	2.05	0.72
2:u:600:TYR:HE2	2:u:603:PRO:HD3	1.53	0.72
2:w:348:ILE:H	2:w:348:ILE:CD1	2.03	0.72
2:s:143:LEU:HD12	2:s:297:TRP:HA	1.72	0.72
2:s:254:PHE:CZ	3:D:112:MET:SD	2.83	0.72
2:t:225:PRO:HB2	2:t:228:GLN:O	1.90	0.72
2:t:369:SER:HB2	2:t:377:PHE:CE2	2.24	0.72
2:x:254:PHE:CE2	3:F:65:ALA:CB	2.73	0.72
1:j:9:LEU:CD2	4:S:72:ASP:OD2	2.38	0.71
2:t:185:PRO:N	3:D:42:MET:CE	2.52	0.71
2:w:369:SER:HB2	2:w:377:PHE:CE2	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:94:SER:HB3	4:O:178:TYR:CE1	2.26	0.71
1:a:6:LYS:NZ	1:b:82:THR:HG21	2.05	0.71
2:t:143:LEU:HD12	2:t:297:TRP:HA	1.72	0.71
2:t:600:TYR:HE2	2:t:603:PRO:HD3	1.53	0.71
2:u:277:ALA:HA	3:B:100:ARG:HG2	1.71	0.71
4:N:17:VAL:HG21	4:N:32:LEU:HD21	1.70	0.71
4:P:17:VAL:HG21	4:P:32:LEU:HD21	1.71	0.71
4:X:17:VAL:HG21	4:X:32:LEU:HD21	1.71	0.71
1:d:9:LEU:CD2	4:W:72:ASP:OD2	2.37	0.71
1:j:93:ILE:HD13	2:t:742:ARG:HG2	1.71	0.71
1:m:9:LEU:CD2	4:Q:72:ASP:OD2	2.36	0.71
2:u:225:PRO:HB2	2:u:228:GLN:O	1.90	0.71
2:u:443:PHE:CG	2:u:485:ALA:HB2	2.24	0.71
2:x:200:LEU:HD22	2:x:200:LEU:N	2.05	0.71
2:x:348:ILE:H	2:x:348:ILE:CD1	2.03	0.71
4:M:159:VAL:HG11	4:X:148:ASN:ND2	2.05	0.71
4:N:148:ASN:ND2	4:O:159:VAL:HG11	2.04	0.71
4:V:98:ASN:HD21	4:W:129:GLU:HA	1.55	0.71
1:k:90:ASP:HB2	4:S:4:TYR:OH	1.90	0.71
2:t:200:LEU:N	2:t:200:LEU:HD22	2.05	0.71
2:t:277:ALA:HA	3:C:100:ARG:HG2	1.73	0.71
2:v:348:ILE:H	2:v:348:ILE:CD1	2.03	0.71
2:v:443:PHE:CG	2:v:485:ALA:HB2	2.24	0.71
2:w:68:LEU:HD21	2:w:557:ILE:HG12	1.71	0.71
2:x:68:LEU:HD21	2:x:557:ILE:HG12	1.71	0.71
2:v:225:PRO:HB2	2:v:228:GLN:O	1.90	0.71
2:v:727:TRP:CB	4:X:36:ALA:HB1	2.14	0.71
2:x:143:LEU:HD12	2:x:297:TRP:HA	1.72	0.71
4:R:17:VAL:HG21	4:R:32:LEU:HD21	1.71	0.71
2:s:225:PRO:HB2	2:s:228:GLN:O	1.90	0.71
2:v:254:PHE:HE2	3:B:65:ALA:HB2	1.55	0.71
2:w:225:PRO:HB2	2:w:228:GLN:O	1.90	0.71
3:D:90:LEU:HD13	3:D:95:MET:HG3	1.71	0.71
2:t:348:ILE:H	2:t:348:ILE:CD1	2.03	0.71
2:v:200:LEU:HD22	2:v:200:LEU:N	2.05	0.71
3:C:119:ARG:O	3:C:122:GLN:CG	2.39	0.71
2:u:22:LEU:HD21	2:v:779:ILE:HG13	1.70	0.71
2:w:160:GLN:HG3	3:A:54:LEU:HD11	1.73	0.71
3:A:119:ARG:O	3:A:122:GLN:CG	2.39	0.71
4:M:178:TYR:CE1	4:X:94:SER:HB3	2.25	0.71
2:s:348:ILE:H	2:s:348:ILE:CD1	2.02	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:779:ILE:HG13	2:x:22:LEU:HD21	1.71	0.71
2:t:396:SER:HB2	3:C:91:GLU:CD	2.16	0.71
1:d:93:ILE:HD13	2:v:742:ARG:HG2	1.71	0.70
1:m:93:ILE:HD13	2:s:742:ARG:HG2	1.73	0.70
2:s:253:SER:HB3	3:D:111:ASN:HB3	1.74	0.70
4:M:182:ASN:OD1	4:M:185:ASP:HB3	1.91	0.70
1:l:95:ARG:CG	2:t:639:LYS:HG3	2.21	0.70
2:u:143:LEU:HD12	2:u:297:TRP:HA	1.72	0.70
1:c:95:ARG:CG	2:w:639:LYS:HG3	2.21	0.70
1:p:9:LEU:CD2	4:O:72:ASP:OD2	2.38	0.70
2:w:200:LEU:HD22	2:w:200:LEU:N	2.05	0.70
4:P:98:ASN:HD21	4:Q:129:GLU:HA	1.56	0.70
4:W:99:ARG:O	4:X:129:GLU:HG3	1.91	0.70
1:f:95:ARG:CG	2:v:639:LYS:HG3	2.22	0.70
1:p:93:ILE:HD13	2:x:742:ARG:HG2	1.73	0.70
2:t:200:LEU:N	2:t:200:LEU:CD2	2.55	0.70
2:v:277:ALA:HA	3:A:100:ARG:HG2	1.72	0.70
2:w:200:LEU:N	2:w:200:LEU:CD2	2.55	0.70
2:x:253:SER:HB3	3:E:111:ASN:HB3	1.74	0.70
2:x:21:ILE:HG12	2:x:697:ASP:OD2	1.92	0.70
2:x:200:LEU:N	2:x:200:LEU:CD2	2.55	0.70
1:a:9:LEU:CD2	4:M:72:ASP:OD2	2.38	0.70
1:b:101:VAL:CG2	4:N:33:GLU:OE2	2.27	0.70
1:h:101:VAL:CG2	4:V:33:GLU:OE2	2.27	0.70
1:n:101:VAL:CG2	4:R:33:GLU:OE2	2.28	0.70
1:f:93:ILE:CB	2:v:638:GLY:O	2.29	0.70
1:o:36:LEU:HA	1:o:72:THR:O	1.92	0.70
2:s:200:LEU:N	2:s:200:LEU:CD2	2.55	0.70
2:t:303:VAL:HG22	2:t:378:TYR:OH	1.92	0.70
4:V:94:SER:HB3	4:W:178:TYR:CE1	2.27	0.70
2:s:21:ILE:HG12	2:s:697:ASP:OD2	1.92	0.70
2:v:303:VAL:HG22	2:v:378:TYR:OH	1.92	0.70
3:B:126:ALA:C	3:B:129:LEU:HG	2.17	0.70
4:S:99:ARG:O	4:T:129:GLU:HG3	1.91	0.70
1:r:46:ILE:CD1	2:x:610:ASP:HB3	2.21	0.69
2:s:200:LEU:N	2:s:200:LEU:HD22	2.05	0.69
4:R:37:ASN:HB3	4:R:40:ALA:HB3	1.74	0.69
2:u:303:VAL:HG22	2:u:378:TYR:OH	1.92	0.69
2:v:200:LEU:N	2:v:200:LEU:CD2	2.55	0.69
3:C:108:ARG:HB3	3:C:108:ARG:NH2	2.06	0.69
4:O:99:ARG:O	4:P:129:GLU:HG3	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:38:GLY:HA3	1:l:70:TYR:HA	1.74	0.69
2:u:200:LEU:N	2:u:200:LEU:CD2	2.55	0.69
2:v:143:LEU:HD12	2:v:297:TRP:HA	1.72	0.69
2:v:704:ARG:HD2	4:X:151:PHE:HA	1.74	0.69
2:w:143:LEU:HD12	2:w:297:TRP:HA	1.72	0.69
1:c:36:LEU:HA	1:c:72:THR:O	1.92	0.69
1:r:36:LEU:HA	1:r:72:THR:O	1.92	0.69
2:v:21:ILE:HG12	2:v:697:ASP:OD2	1.92	0.69
2:w:21:ILE:HG12	2:w:697:ASP:OD2	1.92	0.69
2:w:704:ARG:HD2	4:N:151:PHE:HA	1.74	0.69
4:M:31:THR:HG22	4:M:33:GLU:H	1.57	0.69
4:Q:99:ARG:O	4:R:129:GLU:HG3	1.91	0.69
4:W:31:THR:HG22	4:W:33:GLU:H	1.57	0.69
1:l:36:LEU:HA	1:l:72:THR:O	1.92	0.69
2:u:21:ILE:HG12	2:u:697:ASP:OD2	1.92	0.69
1:q:101:VAL:CG2	4:P:33:GLU:OE2	2.27	0.69
1:o:38:GLY:HA3	1:o:70:TYR:HA	1.75	0.69
2:t:253:SER:HB3	3:C:111:ASN:HB3	1.75	0.69
4:M:99:ARG:O	4:N:129:GLU:HG3	1.91	0.69
4:W:148:ASN:ND2	4:X:159:VAL:HG11	2.07	0.69
1:i:13:LEU:HD22	1:i:70:TYR:O	1.93	0.69
1:l:13:LEU:HD22	1:l:70:TYR:O	1.93	0.69
1:o:13:LEU:HD22	1:o:70:TYR:O	1.93	0.69
2:t:21:ILE:HG12	2:t:697:ASP:OD2	1.92	0.69
2:t:254:PHE:HE2	3:D:65:ALA:HB2	1.55	0.69
2:u:21:ILE:HG12	2:u:697:ASP:OD1	1.93	0.69
2:u:253:SER:HB3	3:B:111:ASN:HB3	1.74	0.69
2:x:303:VAL:HG22	2:x:378:TYR:OH	1.92	0.69
3:B:90:LEU:HD13	3:B:95:MET:HG3	1.75	0.69
4:M:148:ASN:ND2	4:N:159:VAL:HG11	2.07	0.69
4:P:37:ASN:HB3	4:P:40:ALA:HB3	1.74	0.69
4:S:6:MET:HA	4:S:6:MET:HE3	1.73	0.69
4:T:94:SER:HB3	4:U:178:TYR:CE1	2.28	0.69
4:U:31:THR:HG22	4:U:33:GLU:H	1.57	0.69
1:c:13:LEU:HD22	1:c:70:TYR:O	1.93	0.69
2:w:303:VAL:HG22	2:w:378:TYR:OH	1.92	0.69
4:T:37:ASN:HB3	4:T:40:ALA:HB3	1.74	0.69
1:i:36:LEU:HA	1:i:72:THR:O	1.92	0.69
1:r:7:THR:HG21	1:r:112:GLU:HA	1.75	0.69
2:s:254:PHE:CE2	3:E:65:ALA:CB	2.71	0.69
1:c:7:THR:HG21	1:c:112:GLU:HA	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:13:LEU:HD22	1:f:70:TYR:O	1.93	0.68
1:i:7:THR:HG21	1:i:112:GLU:HA	1.75	0.68
1:r:13:LEU:HD22	1:r:70:TYR:O	1.93	0.68
2:t:184:GLN:HA	3:D:42:MET:CE	2.22	0.68
2:v:254:PHE:CE2	3:B:65:ALA:CB	2.73	0.68
2:w:21:ILE:HG12	2:w:697:ASP:OD1	1.93	0.68
2:x:432:SER:HB3	3:E:95:MET:HE1	1.74	0.68
4:R:57:ARG:HG3	4:S:170:LEU:CD1	2.18	0.68
1:f:36:LEU:HA	1:f:72:THR:O	1.92	0.68
1:o:31:PHE:CB	1:o:78:VAL:O	2.32	0.68
2:v:21:ILE:HG12	2:v:697:ASP:CG	2.19	0.68
2:w:727:TRP:CB	4:N:36:ALA:HB1	2.14	0.68
4:R:89:SER:N	4:R:94:SER:OG	2.24	0.68
1:l:7:THR:HG21	1:l:112:GLU:HA	1.75	0.68
1:o:7:THR:HG21	1:o:112:GLU:HA	1.75	0.68
2:t:21:ILE:HG12	2:t:697:ASP:OD1	1.93	0.68
2:u:21:ILE:HG12	2:u:697:ASP:CG	2.19	0.68
2:u:240:ALA:HB1	3:B:122:GLN:HG2	1.75	0.68
2:w:281:TYR:HD1	2:w:333:GLY:HA3	1.58	0.68
2:x:21:ILE:HG12	2:x:697:ASP:OD1	1.93	0.68
2:v:21:ILE:HG12	2:v:697:ASP:OD1	1.93	0.68
2:w:21:ILE:HG12	2:w:697:ASP:CG	2.19	0.68
4:Q:182:ASN:OD1	4:Q:185:ASP:HB3	1.94	0.68
4:U:182:ASN:OD1	4:U:185:ASP:HB3	1.94	0.68
2:x:281:TYR:HD1	2:x:333:GLY:HA3	1.58	0.68
4:O:182:ASN:OD1	4:O:185:ASP:HB3	1.94	0.68
4:S:148:ASN:ND2	4:T:159:VAL:HG11	2.08	0.68
1:o:95:ARG:CG	2:s:639:LYS:HG3	2.23	0.68
1:r:95:ARG:CG	2:x:639:LYS:HG3	2.23	0.68
2:t:21:ILE:HG12	2:t:697:ASP:CG	2.19	0.68
2:v:714:GLY:N	2:v:774:THR:CG2	2.57	0.68
2:x:21:ILE:HG12	2:x:697:ASP:CG	2.19	0.68
4:R:98:ASN:HD21	4:S:129:GLU:HA	1.58	0.68
2:x:277:ALA:HA	3:E:100:ARG:HG2	1.75	0.68
4:Q:148:ASN:ND2	4:R:159:VAL:HG11	2.07	0.68
4:W:182:ASN:OD1	4:W:185:ASP:HB3	1.94	0.68
1:f:7:THR:HG21	1:f:112:GLU:HA	1.75	0.68
1:r:52:PHE:HA	1:r:58:ILE:HG22	1.76	0.68
2:s:21:ILE:HG12	2:s:697:ASP:CG	2.19	0.68
2:t:185:PRO:N	3:D:42:MET:HE1	2.09	0.68
2:u:714:GLY:N	2:u:774:THR:CG2	2.57	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:37:ASN:HB3	4:N:40:ALA:HB3	1.74	0.68
4:O:31:THR:HG22	4:O:33:GLU:H	1.57	0.68
4:Q:31:THR:HG22	4:Q:33:GLU:H	1.57	0.68
4:U:148:ASN:ND2	4:V:159:VAL:HG11	2.07	0.68
2:t:714:GLY:N	2:t:774:THR:CG2	2.57	0.68
2:v:253:SER:HB3	3:A:111:ASN:HB3	1.75	0.68
2:w:176:LYS:NZ	2:w:178:LYS:CE	2.46	0.68
2:w:201:ALA:HA	2:w:204:MET:HG2	1.76	0.68
2:x:714:GLY:N	2:x:774:THR:CG2	2.57	0.68
4:R:94:SER:HB3	4:S:178:TYR:CE1	2.28	0.68
2:s:303:VAL:HG22	2:s:378:TYR:OH	1.92	0.68
2:u:727:TRP:HH2	4:W:27:PRO:HB3	1.59	0.68
2:w:240:ALA:HB1	3:F:122:GLN:HG2	1.75	0.68
4:O:148:ASN:ND2	4:P:159:VAL:HG11	2.08	0.68
2:u:254:PHE:CE2	3:C:65:ALA:CB	2.74	0.67
2:v:201:ALA:HA	2:v:204:MET:HG2	1.76	0.67
2:w:714:GLY:N	2:w:774:THR:CG2	2.57	0.67
4:S:31:THR:HG22	4:S:33:GLU:H	1.57	0.67
1:c:38:GLY:HA3	1:c:70:TYR:HA	1.75	0.67
1:f:38:GLY:HA3	1:f:70:TYR:HA	1.75	0.67
2:t:254:PHE:CE2	3:D:65:ALA:CB	2.77	0.67
4:P:147:ASN:HD21	4:P:156:VAL:HG13	1.59	0.67
1:b:44:LEU:HB2	1:b:50:TYR:HD1	1.59	0.67
2:t:201:ALA:HA	2:t:204:MET:HG2	1.76	0.67
2:u:281:TYR:HD1	2:u:333:GLY:HA3	1.58	0.67
3:B:126:ALA:HA	3:B:129:LEU:HD23	1.73	0.67
4:V:89:SER:N	4:V:94:SER:OG	2.24	0.67
1:i:38:GLY:HA3	1:i:70:TYR:HA	1.75	0.67
2:v:281:TYR:HD1	2:v:333:GLY:HA3	1.58	0.67
2:x:128:VAL:HG22	2:x:309:PRO:HB3	1.77	0.67
2:x:201:ALA:HA	2:x:204:MET:HG2	1.76	0.67
4:S:182:ASN:OD1	4:S:185:ASP:HB3	1.94	0.67
2:x:704:ARG:HD2	4:P:151:PHE:HA	1.75	0.67
4:V:37:ASN:HB3	4:V:40:ALA:HB3	1.74	0.67
1:e:44:LEU:HB2	1:e:50:TYR:HD1	1.59	0.67
2:s:21:ILE:HG12	2:s:697:ASP:OD1	1.93	0.67
2:t:281:TYR:HD1	2:t:333:GLY:HA3	1.58	0.67
2:u:704:ARG:HD2	4:V:151:PHE:HA	1.75	0.67
2:v:268:LYS:HE2	2:v:279:GLN:HB3	1.77	0.67
2:x:240:ALA:HB1	3:E:122:GLN:HG2	1.76	0.67
4:N:147:ASN:HD21	4:N:156:VAL:HG13	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:37:ASN:HB3	4:X:40:ALA:HB3	1.74	0.67
2:w:128:VAL:HG22	2:w:309:PRO:HB3	1.77	0.67
4:X:147:ASN:HD21	4:X:156:VAL:HG13	1.59	0.67
1:r:38:GLY:HA3	1:r:70:TYR:HA	1.75	0.67
2:s:201:ALA:HA	2:s:204:MET:HG2	1.76	0.67
2:s:281:TYR:HD1	2:s:333:GLY:HA3	1.58	0.67
2:s:714:GLY:N	2:s:774:THR:CG2	2.57	0.67
2:t:254:PHE:CZ	3:C:112:MET:SD	2.88	0.67
4:N:98:ASN:HD21	4:O:129:GLU:HA	1.59	0.67
2:v:22:LEU:HD21	2:w:779:ILE:HG13	1.70	0.67
3:B:126:ALA:HA	3:B:129:LEU:CG	2.25	0.67
4:P:89:SER:N	4:P:94:SER:OG	2.24	0.67
1:d:106:THR:HG21	1:f:106:THR:HG22	1.77	0.67
2:s:727:TRP:CB	4:R:36:ALA:HB1	2.17	0.67
1:r:93:ILE:HD11	2:x:746:LEU:HA	1.76	0.66
2:x:177:TYR:OH	2:x:179:ILE:HA	1.96	0.66
4:T:98:ASN:HD21	4:U:129:GLU:HA	1.58	0.66
1:c:9:LEU:HD12	1:c:75:LEU:HB2	1.78	0.66
1:k:44:LEU:HB2	1:k:50:TYR:HD1	1.59	0.66
1:n:44:LEU:HB2	1:n:50:TYR:HD1	1.59	0.66
2:u:201:ALA:HA	2:u:204:MET:HG2	1.76	0.66
2:u:268:LYS:HE2	2:u:279:GLN:HB3	1.76	0.66
2:w:177:TYR:OH	2:w:179:ILE:HA	1.96	0.66
4:R:144:ARG:HE	4:R:161:GLN:HB3	1.59	0.66
4:R:147:ASN:HD21	4:R:156:VAL:HG13	1.59	0.66
4:T:89:SER:N	4:T:94:SER:OG	2.24	0.66
2:t:268:LYS:HE2	2:t:279:GLN:HB3	1.76	0.66
2:t:381:SER:O	3:C:97:ARG:NH2	2.28	0.66
2:w:204:MET:O	2:w:211:TRP:CZ3	2.49	0.66
2:x:288:ARG:HE	2:x:290:VAL:HG21	1.61	0.66
3:E:42:MET:O	3:E:46:ASN:ND2	2.26	0.66
1:f:9:LEU:HD12	1:f:75:LEU:HB2	1.78	0.66
2:s:128:VAL:HG22	2:s:309:PRO:HB3	1.77	0.66
2:s:177:TYR:OH	2:s:179:ILE:HA	1.96	0.66
2:v:239:TYR:HD2	3:A:129:LEU:HD22	1.61	0.66
2:v:727:TRP:HH2	4:M:27:PRO:HB3	1.60	0.66
2:x:199:GLU:O	2:x:203:GLN:HG3	1.96	0.66
2:s:199:GLU:O	2:s:203:GLN:HG3	1.95	0.66
2:t:177:TYR:OH	2:t:179:ILE:HA	1.96	0.66
3:E:90:LEU:HD13	3:E:95:MET:HG3	1.78	0.66
1:a:106:THR:HG21	1:c:106:THR:HG22	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:g:106:THR:HG21	1:i:106:THR:HG22	1.78	0.66
2:s:704:ARG:HD2	4:R:151:PHE:HA	1.77	0.66
2:t:288:ARG:HE	2:t:290:VAL:HG21	1.61	0.66
2:v:199:GLU:O	2:v:203:GLN:HG3	1.95	0.66
2:v:396:SER:CB	3:A:91:GLU:OE2	2.41	0.66
2:x:727:TRP:CB	4:P:36:ALA:HB1	2.15	0.66
1:f:31:PHE:CB	1:f:78:VAL:O	2.32	0.66
1:r:9:LEU:HD12	1:r:75:LEU:HB2	1.78	0.66
2:s:164:GLU:HB3	2:s:178:LYS:HG2	1.77	0.66
2:s:288:ARG:HE	2:s:290:VAL:HG21	1.61	0.66
2:t:164:GLU:HB3	2:t:178:LYS:HG2	1.77	0.66
2:v:66:ILE:HG13	2:v:553:ALA:HB2	1.78	0.66
2:v:128:VAL:HG22	2:v:309:PRO:HB3	1.77	0.66
2:v:176:LYS:HZ3	2:v:178:LYS:CE	2.06	0.66
2:w:164:GLU:HB3	2:w:178:LYS:HG2	1.77	0.66
2:x:176:LYS:HZ3	2:x:178:LYS:HE3	1.59	0.66
4:M:129:GLU:HA	4:X:98:ASN:HD21	1.60	0.66
4:T:147:ASN:HD21	4:T:156:VAL:HG13	1.59	0.66
4:V:147:ASN:HD21	4:V:156:VAL:HG13	1.59	0.66
2:s:185:PRO:N	3:E:42:MET:HE1	2.09	0.66
2:s:254:PHE:CE1	3:D:112:MET:SD	2.89	0.66
2:t:66:ILE:HG13	2:t:553:ALA:HB2	1.78	0.66
2:u:199:GLU:O	2:u:203:GLN:HG3	1.95	0.66
2:w:154:ILE:HD13	2:w:220:ILE:HG12	1.78	0.66
2:w:288:ARG:HE	2:w:290:VAL:HG21	1.61	0.66
1:q:44:LEU:HB2	1:q:50:TYR:HD1	1.59	0.66
2:u:288:ARG:HE	2:u:290:VAL:HG21	1.61	0.66
2:x:268:LYS:HE2	2:x:279:GLN:HB3	1.76	0.66
4:S:24:ILE:HG21	4:S:146:PHE:HD1	1.61	0.66
4:S:80:TYR:HB3	4:S:101:GLY:O	1.96	0.66
2:s:268:LYS:HE2	2:s:279:GLN:HB3	1.76	0.66
2:v:288:ARG:HE	2:v:290:VAL:HG21	1.61	0.66
2:x:204:MET:O	2:x:211:TRP:CZ3	2.49	0.66
3:A:40:GLU:HA	3:A:43:ARG:CD	2.23	0.66
1:l:9:LEU:HD12	1:l:75:LEU:HB2	1.78	0.65
2:v:204:MET:O	2:v:211:TRP:CZ3	2.49	0.65
2:v:154:ILE:HD13	2:v:220:ILE:HG12	1.78	0.65
2:v:177:TYR:OH	2:v:179:ILE:HA	1.96	0.65
2:t:199:GLU:O	2:t:203:GLN:HG3	1.96	0.65
2:u:177:TYR:OH	2:u:179:ILE:HA	1.96	0.65
2:u:432:SER:HB3	3:B:95:MET:HE1	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:x:154:ILE:HD13	2:x:220:ILE:HG12	1.78	0.65
2:x:164:GLU:HB3	2:x:178:LYS:HG2	1.77	0.65
4:W:80:TYR:HB3	4:W:101:GLY:O	1.96	0.65
1:p:106:THR:HG21	1:r:106:THR:HG22	1.77	0.65
2:s:204:MET:O	2:s:211:TRP:CZ3	2.49	0.65
2:v:63:ALA:HB1	2:v:113:ARG:NE	2.12	0.65
3:F:90:LEU:HB2	3:F:95:MET:HG3	1.77	0.65
4:U:24:ILE:HG21	4:U:146:PHE:HD1	1.61	0.65
1:o:9:LEU:HD12	1:o:75:LEU:HB2	1.77	0.65
1:r:31:PHE:CB	1:r:78:VAL:O	2.32	0.65
2:t:128:VAL:HG22	2:t:309:PRO:HB3	1.77	0.65
2:t:204:MET:O	2:t:211:TRP:CZ3	2.49	0.65
2:t:704:ARG:HD2	4:T:151:PHE:HA	1.77	0.65
2:u:727:TRP:CB	4:V:36:ALA:HB1	2.15	0.65
2:w:727:TRP:HH2	4:O:27:PRO:HB3	1.60	0.65
4:Q:80:TYR:HB3	4:Q:101:GLY:O	1.96	0.65
1:j:106:THR:HG21	1:l:106:THR:HG22	1.78	0.65
2:u:154:ILE:HD13	2:u:220:ILE:HG12	1.78	0.65
2:v:728:LYS:O	4:X:36:ALA:HB3	1.97	0.65
2:w:63:ALA:HB1	2:w:113:ARG:NE	2.12	0.65
2:w:199:GLU:O	2:w:203:GLN:HG3	1.95	0.65
2:x:185:PRO:N	3:F:42:MET:CE	2.60	0.65
1:h:44:LEU:HB2	1:h:50:TYR:HD1	1.59	0.65
2:s:284:TYR:HB2	2:s:291:TRP:CE2	2.31	0.65
2:u:128:VAL:HG22	2:u:309:PRO:HB3	1.77	0.65
2:u:204:MET:O	2:u:211:TRP:CZ3	2.49	0.65
4:M:80:TYR:HB3	4:M:101:GLY:O	1.96	0.65
4:Q:24:ILE:HG21	4:Q:146:PHE:HD1	1.61	0.65
1:f:46:ILE:HG22	1:f:52:PHE:HE2	1.62	0.65
2:t:727:TRP:HH2	4:U:27:PRO:HB3	1.62	0.65
2:u:164:GLU:HB3	2:u:178:LYS:HG2	1.77	0.65
2:w:66:ILE:HG13	2:w:553:ALA:HB2	1.78	0.65
2:x:284:TYR:HB2	2:x:291:TRP:CE2	2.31	0.65
4:O:80:TYR:HB3	4:O:101:GLY:O	1.96	0.65
4:P:94:SER:HB3	4:Q:178:TYR:HE1	1.60	0.65
4:U:106:ARG:O	4:U:109:GLN:NE2	2.30	0.65
1:m:106:THR:HG21	1:o:106:THR:HG22	1.78	0.65
2:s:211:TRP:HB3	2:s:225:PRO:HG3	1.79	0.65
2:u:63:ALA:HB1	2:u:113:ARG:NE	2.12	0.65
2:u:66:ILE:HG13	2:u:553:ALA:HB2	1.78	0.65
2:v:284:TYR:HB2	2:v:291:TRP:CE2	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:w:284:TYR:HB2	2:w:291:TRP:CE2	2.31	0.65
4:M:24:ILE:HG21	4:M:146:PHE:HD1	1.61	0.65
2:s:19:PRO:HG3	2:t:711:GLU:CD	2.21	0.65
2:u:685:LYS:HG2	2:u:695:THR:HG22	1.79	0.65
2:w:268:LYS:HE2	2:w:279:GLN:HB3	1.76	0.65
2:w:728:LYS:O	4:N:36:ALA:HB3	1.97	0.65
4:O:106:ARG:O	4:O:109:GLN:NE2	2.30	0.65
4:U:80:TYR:HB3	4:U:101:GLY:O	1.96	0.64
2:t:183:SER:O	3:D:42:MET:HE2	1.97	0.64
2:t:284:TYR:HB2	2:t:291:TRP:CE2	2.31	0.64
2:u:211:TRP:HB3	2:u:225:PRO:HG3	1.80	0.64
4:O:24:ILE:HG21	4:O:146:PHE:HD1	1.61	0.64
4:W:24:ILE:HG21	4:W:146:PHE:HD1	1.61	0.64
2:t:63:ALA:HB1	2:t:113:ARG:NE	2.12	0.64
2:v:685:LYS:HG2	2:v:695:THR:HG22	1.79	0.64
2:w:253:SER:HB3	3:F:111:ASN:HB3	1.78	0.64
2:x:63:ALA:HB1	2:x:113:ARG:NE	2.12	0.64
3:C:137:SER:OG	3:D:43:ARG:NH2	2.30	0.64
1:i:9:LEU:HD12	1:i:75:LEU:HB2	1.78	0.64
2:t:211:TRP:HB3	2:t:225:PRO:HG3	1.80	0.64
4:N:89:SER:N	4:N:94:SER:OG	2.24	0.64
1:o:46:ILE:HG22	1:o:52:PHE:HE2	1.62	0.64
2:s:66:ILE:HG13	2:s:553:ALA:HB2	1.78	0.64
2:t:727:TRP:CB	4:T:36:ALA:HB1	2.15	0.64
2:v:48:LEU:HG	2:v:576:ILE:HG12	1.80	0.64
2:x:211:TRP:HB3	2:x:225:PRO:HG3	1.79	0.64
2:x:685:LYS:HG2	2:x:695:THR:HG22	1.79	0.64
1:c:31:PHE:CB	1:c:78:VAL:O	2.32	0.64
1:m:23:PRO:HB2	4:Q:79:VAL:HG11	1.80	0.64
2:s:254:PHE:CE2	3:E:65:ALA:HB1	2.33	0.64
2:t:154:ILE:HD13	2:t:220:ILE:HG12	1.78	0.64
2:u:284:TYR:HB2	2:u:291:TRP:CE2	2.31	0.64
2:u:728:LYS:O	4:V:36:ALA:HB3	1.97	0.64
3:C:40:GLU:HA	3:C:43:ARG:HE	1.60	0.64
4:W:106:ARG:O	4:W:109:GLN:NE2	2.30	0.64
2:s:727:TRP:HH2	4:S:27:PRO:HB3	1.62	0.64
2:u:254:PHE:CZ	3:B:112:MET:SD	2.91	0.64
4:M:106:ARG:O	4:M:109:GLN:NE2	2.30	0.64
4:N:94:SER:HB3	4:O:178:TYR:HE1	1.62	0.64
4:X:89:SER:N	4:X:94:SER:OG	2.24	0.64
2:s:73:GLU:CG	2:x:418:ASP:OD2	2.34	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:154:ILE:HD13	2:s:220:ILE:HG12	1.78	0.64
2:x:66:ILE:HG13	2:x:553:ALA:HB2	1.78	0.64
2:s:63:ALA:HB1	2:s:113:ARG:NE	2.12	0.64
2:s:685:LYS:HG2	2:s:695:THR:HG22	1.79	0.64
2:v:211:TRP:HB3	2:v:225:PRO:HG3	1.79	0.64
2:x:728:LYS:O	4:P:36:ALA:HB3	1.98	0.64
4:Q:106:ARG:O	4:Q:109:GLN:NE2	2.30	0.64
1:p:97:TYR:HE1	4:O:6:MET:HE1	1.54	0.63
2:s:48:LEU:HG	2:s:576:ILE:HG12	1.80	0.63
2:x:370:ARG:HD3	2:x:376:ASN:CB	2.28	0.63
2:x:600:TYR:CE2	2:x:603:PRO:HD3	2.33	0.63
2:u:48:LEU:HG	2:u:576:ILE:HG12	1.80	0.63
2:u:150:GLN:CB	2:u:224:ALA:HB1	2.27	0.63
2:w:600:TYR:OH	2:w:602:ILE:HG12	1.99	0.63
2:x:727:TRP:HH2	4:Q:27:PRO:HB3	1.62	0.63
3:D:90:LEU:HD12	3:D:91:GLU:H	1.61	0.63
2:s:728:LYS:O	4:R:36:ALA:HB3	1.99	0.63
2:w:48:LEU:HG	2:w:576:ILE:HG12	1.80	0.63
2:w:211:TRP:HB3	2:w:225:PRO:HG3	1.79	0.63
2:w:254:PHE:CE2	3:A:65:ALA:HB1	2.33	0.63
1:c:93:ILE:HD11	2:w:746:LEU:HA	1.78	0.63
1:i:31:PHE:CB	1:i:78:VAL:O	2.32	0.63
2:v:254:PHE:CZ	3:A:112:MET:SD	2.92	0.63
3:A:40:GLU:OE2	3:F:138:GLN:NE2	2.31	0.63
2:s:600:TYR:CE2	2:s:603:PRO:HD3	2.33	0.63
2:w:150:GLN:CB	2:w:224:ALA:HB1	2.27	0.63
2:w:370:ARG:HD3	2:w:376:ASN:CB	2.28	0.63
3:A:138:GLN:NE2	3:B:40:GLU:OE2	2.31	0.63
4:O:6:MET:SD	4:P:6:MET:HG3	2.39	0.63
1:j:23:PRO:HB2	4:S:79:VAL:HG11	1.81	0.63
2:s:185:PRO:HD2	3:E:42:MET:HE1	1.75	0.63
2:v:164:GLU:HB3	2:v:178:LYS:HG2	1.77	0.63
2:w:685:LYS:HG2	2:w:695:THR:HG22	1.79	0.63
1:a:11:TYR:HE2	4:M:70:LEU:O	1.82	0.63
2:u:176:LYS:HZ3	2:u:178:LYS:CE	2.08	0.63
2:u:729:TYR:CE1	2:u:756:PRO:HD2	2.34	0.63
2:v:600:TYR:OH	2:v:602:ILE:HG12	1.99	0.63
2:s:176:LYS:HZ1	2:s:178:LYS:CE	2.10	0.63
2:s:370:ARG:HD3	2:s:376:ASN:CB	2.28	0.63
2:t:729:TYR:CE1	2:t:756:PRO:HD2	2.34	0.63
2:x:254:PHE:CZ	3:E:112:MET:SD	2.92	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:x:600:TYR:OH	2:x:602:ILE:HG12	1.99	0.63
3:C:119:ARG:HD2	3:C:122:GLN:HE22	1.63	0.63
4:W:2:ARG:HE	4:W:124:LEU:CD2	2.12	0.63
2:s:600:TYR:OH	2:s:602:ILE:HG12	1.99	0.62
2:v:729:TYR:CE1	2:v:756:PRO:HD2	2.34	0.62
2:w:600:TYR:CE2	2:w:603:PRO:HD3	2.33	0.62
2:u:348:ILE:H	2:u:348:ILE:CD1	2.03	0.62
2:x:48:LEU:HG	2:x:576:ILE:HG12	1.80	0.62
2:v:19:PRO:HG3	2:w:711:GLU:CD	2.20	0.62
4:S:106:ARG:O	4:S:109:GLN:NE2	2.30	0.62
2:t:150:GLN:CB	2:t:224:ALA:HB1	2.27	0.62
4:P:46:ILE:HD11	4:P:145:GLN:HG2	1.81	0.62
2:s:711:GLU:CD	2:x:19:PRO:HG3	2.21	0.62
2:t:48:LEU:HG	2:t:576:ILE:HG12	1.80	0.62
2:t:685:LYS:HG2	2:t:695:THR:HG22	1.79	0.62
2:s:184:GLN:HA	3:E:42:MET:CE	2.29	0.62
3:A:119:ARG:HD2	3:A:122:GLN:HE22	1.63	0.62
4:M:2:ARG:HE	4:M:124:LEU:CD2	2.12	0.62
4:S:2:ARG:HE	4:S:124:LEU:CD2	2.12	0.62
1:b:94:LEU:HD11	2:w:741:LEU:HD11	1.82	0.62
2:w:19:PRO:HG3	2:x:711:GLU:CD	2.22	0.62
2:w:359:GLY:C	2:w:360:PHE:HD1	2.08	0.62
3:C:40:GLU:CA	3:C:43:ARG:HH21	2.13	0.62
4:X:46:ILE:HD11	4:X:145:GLN:HG2	1.81	0.62
1:e:101:VAL:CG2	4:X:33:GLU:OE2	2.28	0.62
1:i:46:ILE:HG22	1:i:52:PHE:HE2	1.65	0.62
1:m:11:TYR:HE2	4:Q:70:LEU:O	1.80	0.62
2:t:600:TYR:CE2	2:t:603:PRO:HD3	2.33	0.62
4:R:94:SER:HB3	4:S:178:TYR:HE1	1.64	0.62
4:T:94:SER:HB3	4:U:178:TYR:HE1	1.64	0.62
4:V:46:ILE:HD11	4:V:145:GLN:HG2	1.81	0.62
1:e:94:LEU:HD11	2:v:741:LEU:HD11	1.81	0.62
2:s:461:ALA:HB2	2:s:503:ILE:HD11	1.81	0.62
2:t:254:PHE:CE1	3:C:112:MET:SD	2.92	0.62
2:v:600:TYR:CE2	2:v:603:PRO:HD3	2.33	0.62
4:R:46:ILE:HD11	4:R:145:GLN:HG2	1.81	0.62
2:u:600:TYR:OH	2:u:602:ILE:HG12	1.99	0.62
2:u:600:TYR:CE2	2:u:603:PRO:HD3	2.33	0.62
2:w:155:ASN:HB3	2:w:245:ASN:H	1.65	0.62
1:g:23:PRO:HB2	4:U:79:VAL:HG11	1.82	0.61
1:k:13:LEU:HD21	1:k:64:TRP:HB2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:95:ARG:HD2	2:t:639:LYS:CG	2.30	0.61
1:p:11:TYR:HE2	4:O:70:LEU:O	1.81	0.61
2:t:359:GLY:C	2:t:360:PHE:HD1	2.08	0.61
2:x:359:GLY:C	2:x:360:PHE:HD1	2.08	0.61
4:T:46:ILE:HD11	4:T:145:GLN:HG2	1.81	0.61
4:U:2:ARG:HE	4:U:124:LEU:CD2	2.12	0.61
1:h:44:LEU:HB3	1:h:49:ASP:HB3	1.82	0.61
2:s:729:TYR:CE1	2:s:756:PRO:HD2	2.34	0.61
2:t:600:TYR:OH	2:t:602:ILE:HG12	1.99	0.61
2:t:728:LYS:O	4:T:36:ALA:HB3	2.00	0.61
2:v:461:ALA:HB2	2:v:503:ILE:HD11	1.82	0.61
2:x:381:SER:O	3:E:97:ARG:NH2	2.32	0.61
2:x:421:GLN:HB2	2:x:441:THR:HG23	1.82	0.61
3:A:95:MET:O	3:A:98:ILE:HG22	2.00	0.61
4:Q:2:ARG:HE	4:Q:124:LEU:CD2	2.12	0.61
1:d:23:PRO:HB2	4:W:79:VAL:HG11	1.81	0.61
2:v:370:ARG:HD3	2:v:376:ASN:CB	2.28	0.61
2:w:421:GLN:HB2	2:w:441:THR:HG23	1.83	0.61
2:w:461:ALA:HB2	2:w:503:ILE:HD11	1.82	0.61
2:w:729:TYR:CE1	2:w:756:PRO:HD2	2.34	0.61
2:x:185:PRO:N	3:F:42:MET:HE1	2.15	0.61
3:A:40:GLU:HA	3:A:43:ARG:HH11	1.65	0.61
3:A:126:ALA:HA	3:A:129:LEU:HG	1.82	0.61
1:b:44:LEU:HB3	1:b:49:ASP:HB3	1.82	0.61
1:n:44:LEU:HB3	1:n:49:ASP:HB3	1.82	0.61
1:r:46:ILE:HD12	2:x:610:ASP:HB3	1.82	0.61
2:s:359:GLY:C	2:s:360:PHE:HD1	2.08	0.61
2:s:421:GLN:HB2	2:s:441:THR:HG23	1.83	0.61
4:W:2:ARG:NH1	4:W:124:LEU:HD21	2.13	0.61
1:k:94:LEU:HD11	2:t:741:LEU:HD11	1.82	0.61
1:n:13:LEU:HD21	1:n:64:TRP:HB2	1.82	0.61
2:t:421:GLN:HB2	2:t:441:THR:HG23	1.83	0.61
2:u:200:LEU:CD2	2:u:200:LEU:H	2.14	0.61
2:v:254:PHE:CE2	3:B:65:ALA:HB1	2.35	0.61
2:x:729:TYR:CE1	2:x:756:PRO:HD2	2.34	0.61
4:O:2:ARG:HE	4:O:124:LEU:CD2	2.12	0.61
4:R:134:PHE:CG	4:R:171:CYS:SG	2.94	0.61
2:t:370:ARG:HD3	2:t:376:ASN:CB	2.28	0.61
2:u:19:PRO:HG3	2:v:711:GLU:CD	2.20	0.61
2:u:421:GLN:HB2	2:u:441:THR:HG23	1.82	0.61
2:w:381:SER:O	3:F:97:ARG:NH2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:31:PHE:CB	1:l:78:VAL:O	2.32	0.61
1:n:94:LEU:HD11	2:s:741:LEU:HD11	1.83	0.61
1:q:94:LEU:HD11	2:x:741:LEU:HD11	1.83	0.61
2:v:421:GLN:HB2	2:v:441:THR:HG23	1.82	0.61
1:e:13:LEU:HD21	1:e:64:TRP:HB2	1.82	0.61
1:k:44:LEU:HB3	1:k:49:ASP:HB3	1.82	0.61
2:s:254:PHE:HZ	3:D:112:MET:SD	2.24	0.61
2:v:593:PHE:N	2:v:593:PHE:CD1	2.69	0.61
2:x:373:LYS:HE3	3:F:82:ARG:CZ	2.31	0.61
1:f:93:ILE:HG12	2:v:638:GLY:CA	2.25	0.61
1:h:13:LEU:HD21	1:h:64:TRP:HB2	1.82	0.61
2:t:200:LEU:CD2	2:t:200:LEU:H	2.14	0.61
2:v:155:ASN:HB3	2:v:245:ASN:H	1.65	0.61
2:x:150:GLN:CB	2:x:224:ALA:HB1	2.27	0.61
4:N:134:PHE:CG	4:N:171:CYS:SG	2.94	0.61
4:P:134:PHE:CG	4:P:171:CYS:SG	2.94	0.61
4:T:134:PHE:CG	4:T:171:CYS:SG	2.94	0.61
1:c:95:ARG:HD2	2:w:639:LYS:CG	2.31	0.61
1:r:95:ARG:HD2	2:x:639:LYS:CG	2.31	0.61
2:s:200:LEU:CD2	2:s:200:LEU:H	2.14	0.61
2:u:370:ARG:HD3	2:u:376:ASN:CB	2.28	0.61
2:v:359:GLY:C	2:v:360:PHE:HD1	2.08	0.61
4:M:178:TYR:HE1	4:X:94:SER:HB3	1.62	0.61
1:d:93:ILE:CD1	2:v:739:ASN:OD1	2.49	0.60
1:e:44:LEU:HB3	1:e:49:ASP:HB3	1.82	0.60
1:k:95:ARG:HD2	2:t:730:THR:HG23	1.82	0.60
2:s:190:ASN:HA	2:s:195:TRP:CZ3	2.36	0.60
2:w:190:ASN:HA	2:w:195:TRP:CZ3	2.36	0.60
2:x:190:ASN:HA	2:x:195:TRP:CZ3	2.36	0.60
2:x:461:ALA:HB2	2:x:503:ILE:HD11	1.82	0.60
1:o:9:LEU:HD11	1:o:23:PRO:HD2	1.84	0.60
2:s:150:GLN:CB	2:s:224:ALA:HB1	2.27	0.60
2:s:388:ASP:OD2	3:E:82:ARG:HB2	2.01	0.60
1:a:23:PRO:HB2	4:M:79:VAL:HG11	1.82	0.60
1:f:93:ILE:HD11	2:v:746:LEU:HA	1.77	0.60
1:i:95:ARG:HD2	2:u:639:LYS:CG	2.30	0.60
1:q:13:LEU:HD21	1:q:64:TRP:HB2	1.82	0.60
2:t:418:ASP:OD2	2:u:73:GLU:CG	2.34	0.60
2:t:461:ALA:HB2	2:t:503:ILE:HD11	1.82	0.60
2:x:155:ASN:HB3	2:x:245:ASN:H	1.65	0.60
2:x:254:PHE:CE2	3:F:65:ALA:HB1	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:119:ARG:C	3:A:122:GLN:HG2	2.26	0.60
4:N:46:ILE:HD11	4:N:145:GLN:HG2	1.81	0.60
1:q:44:LEU:HB3	1:q:49:ASP:HB3	1.82	0.60
2:u:359:GLY:C	2:u:360:PHE:HD1	2.08	0.60
2:u:593:PHE:N	2:u:593:PHE:CD1	2.69	0.60
2:v:200:LEU:CD2	2:v:200:LEU:H	2.14	0.60
2:x:200:LEU:CD2	2:x:200:LEU:H	2.14	0.60
3:B:138:GLN:NE2	3:C:40:GLU:OE2	2.34	0.60
3:C:119:ARG:C	3:C:122:GLN:HG2	2.27	0.60
3:E:128:GLN:O	3:E:129:LEU:C	2.44	0.60
4:X:134:PHE:CG	4:X:171:CYS:SG	2.94	0.60
1:b:95:ARG:HD2	2:w:730:THR:HG23	1.83	0.60
1:d:9:LEU:HG	4:W:72:ASP:CG	2.27	0.60
1:f:9:LEU:HD11	1:f:23:PRO:HD2	1.84	0.60
1:j:93:ILE:CD1	2:t:739:ASN:OD1	2.49	0.60
1:l:9:LEU:HD11	1:l:23:PRO:HD2	1.83	0.60
2:v:443:PHE:CD2	2:v:485:ALA:HB2	2.37	0.60
1:a:93:ILE:CD1	2:w:739:ASN:OD1	2.49	0.60
1:c:9:LEU:HD11	1:c:23:PRO:HD2	1.83	0.60
1:d:11:TYR:HE2	4:W:70:LEU:O	1.80	0.60
1:g:11:TYR:HE2	4:U:70:LEU:O	1.81	0.60
1:h:94:LEU:HD11	2:u:741:LEU:HD11	1.82	0.60
2:s:155:ASN:HB3	2:s:245:ASN:H	1.65	0.60
2:u:397:THR:O	3:B:89:MET:CE	2.49	0.60
2:u:461:ALA:HB2	2:u:503:ILE:HD11	1.82	0.60
2:w:443:PHE:CD2	2:w:485:ALA:HB2	2.37	0.60
1:a:9:LEU:HG	4:M:72:ASP:CG	2.27	0.60
2:s:600:TYR:CE2	2:s:602:ILE:HA	2.37	0.60
2:t:185:PRO:CD	3:D:42:MET:HE3	2.19	0.60
1:b:13:LEU:HD21	1:b:64:TRP:HB2	1.82	0.60
1:p:23:PRO:HB2	4:O:79:VAL:HG11	1.83	0.60
2:t:19:PRO:HG3	2:u:711:GLU:CD	2.20	0.60
2:t:190:ASN:HA	2:t:195:TRP:CZ3	2.36	0.60
2:v:190:ASN:HA	2:v:195:TRP:CZ3	2.36	0.60
2:x:600:TYR:CE2	2:x:602:ILE:HA	2.37	0.60
4:V:94:SER:HB3	4:W:178:TYR:HE1	1.63	0.60
2:s:369:SER:HB2	2:s:377:PHE:CZ	2.37	0.60
2:t:369:SER:HB2	2:t:377:PHE:CZ	2.37	0.60
2:t:593:PHE:N	2:t:593:PHE:CD1	2.69	0.60
2:t:600:TYR:CE2	2:t:602:ILE:HA	2.37	0.60
2:w:702:GLN:HE22	4:O:24:ILE:HD12	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:134:PHE:CG	4:V:171:CYS:SG	2.94	0.60
2:u:600:TYR:CE2	2:u:602:ILE:HA	2.37	0.60
1:a:6:LYS:HZ3	1:b:82:THR:HG21	1.65	0.59
2:u:443:PHE:CD2	2:u:485:ALA:HB2	2.37	0.59
2:w:369:SER:HB2	2:w:377:PHE:CZ	2.37	0.59
1:m:93:ILE:CD1	2:s:739:ASN:OD1	2.49	0.59
2:s:443:PHE:CD2	2:s:485:ALA:HB2	2.37	0.59
2:t:155:ASN:HB3	2:t:245:ASN:H	1.65	0.59
2:u:381:SER:O	3:B:97:ARG:NH2	2.31	0.59
1:i:95:ARG:CD	2:u:639:LYS:HG3	2.33	0.59
1:l:95:ARG:CD	2:t:639:LYS:HG3	2.32	0.59
1:o:95:ARG:HD2	2:s:639:LYS:CG	2.32	0.59
2:v:702:GLN:HE22	4:M:24:ILE:HD12	1.67	0.59
2:v:369:SER:HB2	2:v:377:PHE:CZ	2.37	0.59
2:w:200:LEU:CD2	2:w:200:LEU:H	2.14	0.59
2:x:443:PHE:CD2	2:x:485:ALA:HB2	2.37	0.59
1:h:95:ARG:HD2	2:u:730:THR:HG23	1.83	0.59
2:u:190:ASN:HA	2:u:195:TRP:CZ3	2.36	0.59
4:N:149:ARG:HD2	4:O:23:SER:HA	1.84	0.59
1:p:93:ILE:CD1	2:x:739:ASN:OD1	2.49	0.59
1:q:95:ARG:HD2	2:x:730:THR:HG23	1.84	0.59
2:s:714:GLY:H	2:s:774:THR:CG2	2.16	0.59
2:u:155:ASN:HB3	2:u:245:ASN:H	1.65	0.59
2:x:369:SER:HB2	2:x:377:PHE:CZ	2.37	0.59
4:M:23:SER:HA	4:X:149:ARG:HD2	1.84	0.59
1:n:95:ARG:HD2	2:s:730:THR:HG23	1.84	0.59
2:t:443:PHE:CD2	2:t:485:ALA:HB2	2.37	0.59
2:u:702:GLN:HE22	4:W:24:ILE:HD12	1.68	0.59
4:X:178:TYR:HD1	4:X:178:TYR:O	1.86	0.59
1:i:9:LEU:HD11	1:i:23:PRO:HD2	1.83	0.59
1:r:9:LEU:HD11	1:r:23:PRO:HD2	1.83	0.59
2:t:314:ARG:HG3	2:t:314:ARG:O	2.03	0.59
2:x:714:GLY:H	2:x:774:THR:CG2	2.16	0.59
2:u:254:PHE:CE2	3:C:65:ALA:HB1	2.37	0.59
2:u:278:ASP:OD2	3:B:108:ARG:CG	2.51	0.59
2:w:600:TYR:CE2	2:w:602:ILE:HA	2.37	0.59
1:f:95:ARG:HD2	2:v:639:LYS:CG	2.33	0.59
2:s:593:PHE:N	2:s:593:PHE:CD1	2.69	0.59
2:u:369:SER:HB2	2:u:377:PHE:CZ	2.37	0.59
3:C:40:GLU:HB2	3:C:43:ARG:HH21	1.68	0.59
4:V:168:ARG:HH12	4:V:172:MET:HE1	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:178:TYR:O	4:V:178:TYR:HD1	1.86	0.59
1:p:26:TYR:CE1	4:P:7:ASN:HB2	2.38	0.58
1:f:20:PHE:CE2	1:f:60:LEU:HG	2.39	0.58
1:i:38:GLY:H	1:i:70:TYR:HD1	1.52	0.58
1:l:20:PHE:CE2	1:l:60:LEU:HG	2.38	0.58
1:l:95:ARG:HD2	2:t:639:LYS:HG3	1.85	0.58
1:r:46:ILE:HD12	2:x:610:ASP:CB	2.33	0.58
2:u:739:ASN:HD21	2:u:742:ARG:NH2	1.99	0.58
4:S:6:MET:HA	4:S:6:MET:CE	2.33	0.58
1:e:95:ARG:HD2	2:v:730:THR:HG23	1.83	0.58
1:j:11:TYR:HE2	4:S:70:LEU:O	1.82	0.58
1:c:95:ARG:CD	2:w:639:LYS:HG3	2.33	0.58
1:g:9:LEU:HG	4:U:72:ASP:CG	2.28	0.58
1:g:93:ILE:CD1	2:u:739:ASN:OD1	2.50	0.58
1:l:38:GLY:H	1:l:70:TYR:HD1	1.52	0.58
1:o:20:PHE:CE2	1:o:60:LEU:HG	2.38	0.58
1:r:50:TYR:HB3	1:r:60:LEU:HB3	1.85	0.58
2:v:600:TYR:CE2	2:v:602:ILE:HA	2.37	0.58
2:w:183:SER:HB2	3:A:42:MET:HB3	1.85	0.58
2:w:418:ASP:OD2	2:x:73:GLU:CG	2.36	0.58
3:D:105:GLN:CA	3:D:108:ARG:HH21	2.16	0.58
1:f:38:GLY:H	1:f:70:TYR:HD1	1.52	0.58
1:i:20:PHE:CE2	1:i:60:LEU:HG	2.38	0.58
2:s:204:MET:HB2	2:s:213:VAL:HG21	1.85	0.58
2:s:314:ARG:HG3	2:s:314:ARG:O	2.03	0.58
2:s:702:GLN:HE22	4:S:24:ILE:HD12	1.68	0.58
2:t:15:ILE:HG12	2:t:495:TYR:CE2	2.39	0.58
4:R:178:TYR:HD1	4:R:178:TYR:O	1.86	0.58
1:j:9:LEU:HG	4:S:72:ASP:CG	2.28	0.58
1:r:20:PHE:CE2	1:r:60:LEU:HG	2.38	0.58
2:t:714:GLY:H	2:t:774:THR:CG2	2.16	0.58
2:w:727:TRP:CA	4:N:36:ALA:HB2	2.33	0.58
4:N:178:TYR:O	4:N:178:TYR:HD1	1.86	0.58
1:m:9:LEU:HG	4:Q:72:ASP:CG	2.28	0.58
1:p:9:LEU:HG	4:O:72:ASP:CG	2.29	0.58
2:s:15:ILE:HG12	2:s:495:TYR:CE2	2.39	0.58
2:v:15:ILE:HG12	2:v:495:TYR:CE2	2.39	0.58
4:M:2:ARG:NH1	4:M:124:LEU:HD21	2.13	0.58
4:P:149:ARG:HD2	4:Q:23:SER:HA	1.86	0.58
4:Q:182:ASN:OD1	4:Q:182:ASN:O	2.21	0.58
1:c:38:GLY:H	1:c:70:TYR:HD1	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:204:MET:HB2	2:t:213:VAL:HG21	1.85	0.58
2:w:179:ILE:HG23	2:w:190:ASN:HB2	1.86	0.58
2:x:204:MET:HB2	2:x:213:VAL:HG21	1.85	0.58
3:E:138:GLN:NE2	3:F:40:GLU:OE2	2.37	0.58
4:R:168:ARG:HH12	4:R:172:MET:HE1	1.68	0.58
4:S:182:ASN:OD1	4:S:182:ASN:O	2.22	0.58
4:T:149:ARG:HD2	4:U:23:SER:HA	1.86	0.58
4:U:182:ASN:OD1	4:U:182:ASN:O	2.21	0.58
1:r:95:ARG:HD2	2:x:639:LYS:HG3	1.86	0.58
2:u:15:ILE:HG12	2:u:495:TYR:CE2	2.39	0.58
2:v:179:ILE:HG23	2:v:190:ASN:HB2	1.86	0.58
2:v:278:ASP:OD2	3:A:108:ARG:CG	2.51	0.58
2:w:15:ILE:HG12	2:w:495:TYR:CE2	2.39	0.58
2:x:593:PHE:N	2:x:593:PHE:CD1	2.69	0.58
1:c:20:PHE:CE2	1:c:60:LEU:HG	2.39	0.58
1:o:38:GLY:H	1:o:70:TYR:HD1	1.52	0.58
2:t:702:GLN:HE22	4:U:24:ILE:HD12	1.68	0.58
2:u:314:ARG:HG3	2:u:314:ARG:O	2.03	0.58
2:v:314:ARG:HG3	2:v:314:ARG:O	2.03	0.58
2:v:727:TRP:CA	4:X:36:ALA:HB2	2.33	0.58
4:T:178:TYR:O	4:T:178:TYR:HD1	1.86	0.58
2:w:207:ASN:O	2:w:208:LEU:HG	2.04	0.57
2:w:714:GLY:H	2:w:774:THR:CG2	2.16	0.57
2:x:179:ILE:HG23	2:x:190:ASN:HB2	1.86	0.57
2:x:207:ASN:O	2:x:208:LEU:HG	2.04	0.57
4:P:178:TYR:O	4:P:178:TYR:HD1	1.86	0.57
4:S:3:SER:OG	4:S:6:MET:SD	2.62	0.57
1:n:114:ARG:NH1	1:o:109:VAL:HG23	2.19	0.57
1:r:22:ILE:HD11	1:r:58:ILE:HG23	1.87	0.57
1:r:38:GLY:H	1:r:70:TYR:HD1	1.52	0.57
1:r:95:ARG:CD	2:x:639:LYS:HG3	2.33	0.57
2:u:179:ILE:HG23	2:u:190:ASN:HB2	1.86	0.57
2:u:727:TRP:CH2	4:W:27:PRO:HB3	2.38	0.57
2:v:207:ASN:O	2:v:208:LEU:HG	2.04	0.57
2:v:714:GLY:H	2:v:774:THR:CG2	2.16	0.57
2:x:727:TRP:CA	4:P:36:ALA:HB2	2.34	0.57
4:V:149:ARG:HD2	4:W:23:SER:HA	1.86	0.57
1:o:22:ILE:HD11	1:o:58:ILE:HG23	1.87	0.57
2:s:207:ASN:O	2:s:208:LEU:HG	2.04	0.57
2:t:179:ILE:HG23	2:t:190:ASN:HB2	1.86	0.57
2:x:15:ILE:HG12	2:x:495:TYR:CE2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:128:GLN:HG3	3:D:129:LEU:HD22	1.85	0.57
4:M:182:ASN:OD1	4:M:182:ASN:O	2.22	0.57
1:f:95:ARG:CD	2:v:639:LYS:HG3	2.35	0.57
2:u:207:ASN:O	2:u:208:LEU:HG	2.04	0.57
2:u:254:PHE:CE1	3:B:112:MET:SD	2.98	0.57
2:u:524:PHE:CD2	2:u:542:HIS:HB2	2.40	0.57
2:x:524:PHE:CD2	2:x:542:HIS:HB2	2.40	0.57
4:P:7:ASN:O	4:P:8:VAL:C	2.46	0.57
4:Q:6:MET:HA	4:Q:6:MET:HE3	1.86	0.57
4:W:182:ASN:OD1	4:W:182:ASN:O	2.21	0.57
1:c:22:ILE:HD11	1:c:58:ILE:HG23	1.87	0.57
1:m:9:LEU:CG	4:Q:72:ASP:OD2	2.53	0.57
2:s:179:ILE:HG23	2:s:190:ASN:HB2	1.86	0.57
4:M:132:GLU:CD	4:X:52:ARG:HH12	2.12	0.57
4:M:132:GLU:OE2	4:X:52:ARG:NH1	2.38	0.57
2:s:524:PHE:CD2	2:s:542:HIS:HB2	2.40	0.57
2:t:284:TYR:HB2	2:t:291:TRP:CZ3	2.40	0.57
2:t:524:PHE:CD2	2:t:542:HIS:HB2	2.40	0.57
2:v:284:TYR:HB2	2:v:291:TRP:CZ3	2.40	0.57
2:v:739:ASN:HD21	2:v:742:ARG:NH2	1.99	0.57
2:w:204:MET:HB2	2:w:213:VAL:HG21	1.85	0.57
4:M:52:ARG:HH11	4:N:132:GLU:CD	2.12	0.57
1:e:114:ARG:NH1	1:f:109:VAL:HG23	2.20	0.57
1:i:95:ARG:HD2	2:u:639:LYS:HG3	1.87	0.57
1:l:22:ILE:HD11	1:l:58:ILE:HG23	1.86	0.57
1:p:97:TYR:CE1	4:O:6:MET:CE	2.73	0.57
2:s:284:TYR:HB2	2:s:291:TRP:CZ3	2.40	0.57
2:s:347:SER:OG	2:s:349:ASN:OD1	2.23	0.57
2:u:727:TRP:CA	4:V:36:ALA:HB2	2.35	0.57
2:v:254:PHE:CE1	3:A:112:MET:SD	2.98	0.57
2:w:314:ARG:O	2:w:314:ARG:HG3	2.03	0.57
2:w:593:PHE:N	2:w:593:PHE:CD1	2.69	0.57
3:C:138:GLN:NE2	3:D:40:GLU:OE2	2.38	0.57
4:O:182:ASN:OD1	4:O:182:ASN:O	2.21	0.57
1:f:22:ILE:HD11	1:f:58:ILE:HG23	1.87	0.57
2:t:19:PRO:CG	2:u:711:GLU:OE2	2.53	0.57
2:t:207:ASN:O	2:t:208:LEU:HG	2.04	0.57
2:v:381:SER:O	3:A:97:ARG:NH2	2.34	0.57
2:v:727:TRP:CD2	4:X:38:ALA:HB2	2.40	0.57
2:w:284:TYR:HB2	2:w:291:TRP:CZ3	2.40	0.57
2:x:314:ARG:HG3	2:x:314:ARG:O	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:x:702:GLN:HE22	4:Q:24:ILE:HD12	1.69	0.57
3:C:108:ARG:O	3:C:109:GLU:C	2.46	0.57
4:Q:52:ARG:HH11	4:R:132:GLU:CD	2.12	0.57
4:X:134:PHE:HA	4:X:171:CYS:SG	2.45	0.57
1:d:9:LEU:CD2	4:W:72:ASP:CG	2.78	0.57
1:i:95:ARG:NH1	2:u:635:GLU:OE2	2.38	0.57
2:s:91:LEU:HD21	2:s:562:TYR:CE1	2.40	0.57
2:v:201:ALA:HB2	2:v:220:ILE:HD12	1.86	0.57
3:B:88:SER:HB3	3:B:90:LEU:HG	1.87	0.57
4:X:85:LEU:HB2	4:X:122:ILE:HG13	1.86	0.57
1:c:95:ARG:HD2	2:w:639:LYS:HG3	1.87	0.57
1:i:22:ILE:HD11	1:i:58:ILE:HG23	1.86	0.57
2:s:201:ALA:HB2	2:s:220:ILE:HD12	1.86	0.57
2:w:739:ASN:HD21	2:w:742:ARG:NH2	1.99	0.57
2:t:727:TRP:CA	4:T:36:ALA:HB2	2.35	0.56
2:u:91:LEU:HD21	2:u:562:TYR:CE1	2.40	0.56
2:v:524:PHE:CD2	2:v:542:HIS:HB2	2.40	0.56
2:x:739:ASN:HD21	2:x:742:ARG:NH2	1.99	0.56
4:V:134:PHE:HA	4:V:171:CYS:SG	2.45	0.56
1:l:46:ILE:HG22	1:l:52:PHE:HE2	1.69	0.56
1:o:95:ARG:HD2	2:s:639:LYS:HG3	1.87	0.56
1:p:9:LEU:CD2	4:O:72:ASP:CG	2.78	0.56
1:q:114:ARG:NH1	1:r:109:VAL:HG23	2.20	0.56
2:t:201:ALA:HB2	2:t:220:ILE:HD12	1.87	0.56
2:t:309:PRO:HB2	2:t:327:TRP:HZ2	1.71	0.56
2:u:204:MET:HB2	2:u:213:VAL:HG21	1.86	0.56
2:v:91:LEU:HD21	2:v:562:TYR:CE1	2.40	0.56
2:x:284:TYR:HB2	2:x:291:TRP:CZ3	2.40	0.56
4:N:134:PHE:HA	4:N:171:CYS:SG	2.45	0.56
4:T:134:PHE:HA	4:T:171:CYS:SG	2.46	0.56
4:V:71:PRO:HA	4:V:78:ILE:HG12	1.87	0.56
4:W:52:ARG:HH11	4:X:132:GLU:CD	2.12	0.56
1:d:9:LEU:CG	4:W:72:ASP:OD2	2.53	0.56
1:h:114:ARG:NH1	1:i:109:VAL:HG23	2.20	0.56
1:j:9:LEU:CG	4:S:72:ASP:OD2	2.54	0.56
1:k:114:ARG:NH1	1:l:109:VAL:HG23	2.20	0.56
1:o:95:ARG:CD	2:s:639:LYS:HG3	2.35	0.56
2:t:91:LEU:HD21	2:t:562:TYR:CE1	2.40	0.56
2:t:714:GLY:H	2:t:774:THR:HG22	1.71	0.56
2:u:309:PRO:HB2	2:u:327:TRP:HZ2	1.71	0.56
2:u:714:GLY:H	2:u:774:THR:CG2	2.16	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:204:MET:HB2	2:v:213:VAL:HG21	1.85	0.56
2:v:727:TRP:CH2	4:M:27:PRO:HB3	2.39	0.56
2:w:309:PRO:HB2	2:w:327:TRP:HZ2	1.71	0.56
2:w:524:PHE:CD2	2:w:542:HIS:HB2	2.40	0.56
2:w:727:TRP:CD2	4:N:38:ALA:HB2	2.41	0.56
2:x:91:LEU:HD21	2:x:562:TYR:CE1	2.40	0.56
2:x:201:ALA:HB2	2:x:220:ILE:HD12	1.87	0.56
2:x:347:SER:OG	2:x:349:ASN:OD1	2.23	0.56
4:O:52:ARG:HH11	4:P:132:GLU:CD	2.12	0.56
4:P:85:LEU:HB2	4:P:122:ILE:HG13	1.86	0.56
4:R:85:LEU:HB2	4:R:122:ILE:HG13	1.86	0.56
4:U:6:MET:SD	4:V:6:MET:HB2	2.45	0.56
4:V:85:LEU:HB2	4:V:122:ILE:HG13	1.86	0.56
4:X:168:ARG:HH12	4:X:172:MET:HE1	1.68	0.56
1:a:9:LEU:CG	4:M:72:ASP:OD2	2.53	0.56
1:d:94:LEU:HD21	1:d:99:LEU:HD12	1.87	0.56
1:m:9:LEU:CD2	4:Q:72:ASP:CG	2.79	0.56
1:q:36:LEU:H	1:q:42:LYS:H	1.53	0.56
1:r:46:ILE:HD12	2:x:610:ASP:CG	2.30	0.56
2:s:309:PRO:HB2	2:s:327:TRP:HZ2	1.71	0.56
2:v:418:ASP:OD2	2:w:73:GLU:CG	2.35	0.56
2:x:714:GLY:CA	2:x:774:THR:CG2	2.72	0.56
2:s:714:GLY:H	2:s:774:THR:HG22	1.71	0.56
2:u:727:TRP:CD2	4:V:38:ALA:HB2	2.40	0.56
2:x:309:PRO:HB2	2:x:327:TRP:HZ2	1.71	0.56
4:R:71:PRO:HA	4:R:78:ILE:HG12	1.87	0.56
4:T:85:LEU:HB2	4:T:122:ILE:HG13	1.86	0.56
1:b:114:ARG:NH1	1:c:109:VAL:HG23	2.20	0.56
1:c:46:ILE:HG22	1:c:52:PHE:HE2	1.70	0.56
2:u:284:TYR:HB2	2:u:291:TRP:CZ3	2.40	0.56
2:w:91:LEU:HD21	2:w:562:TYR:CE1	2.40	0.56
4:P:71:PRO:HA	4:P:78:ILE:HG12	1.87	0.56
4:P:134:PHE:HA	4:P:171:CYS:SG	2.45	0.56
1:g:9:LEU:CD2	4:U:72:ASP:CG	2.79	0.56
2:v:721:GLU:HG3	2:v:765:THR:HG23	1.88	0.56
2:x:254:PHE:CE1	3:E:112:MET:SD	2.99	0.56
4:R:149:ARG:HD2	4:S:23:SER:HA	1.87	0.56
2:u:721:GLU:HG3	2:u:765:THR:HG23	1.88	0.56
2:v:278:ASP:OD2	3:A:108:ARG:HG3	2.06	0.56
2:w:347:SER:OG	2:w:349:ASN:OD1	2.23	0.56
2:w:727:TRP:CH2	4:O:27:PRO:HB3	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:x:714:GLY:H	2:x:774:THR:HG22	1.71	0.56
4:M:50:ILE:HD12	4:M:142:ALA:HA	1.88	0.56
4:O:50:ILE:HD12	4:O:142:ALA:HA	1.88	0.56
4:R:134:PHE:HA	4:R:171:CYS:SG	2.45	0.56
1:i:89:THR:HG21	2:u:641:THR:HA	1.87	0.56
2:u:714:GLY:H	2:u:774:THR:HG22	1.71	0.56
4:U:52:ARG:HH11	4:V:132:GLU:CD	2.12	0.56
1:b:36:LEU:H	1:b:42:LYS:H	1.53	0.56
1:e:36:LEU:H	1:e:42:LYS:H	1.53	0.56
1:o:93:ILE:CG1	2:s:746:LEU:HA	2.36	0.56
2:v:128:VAL:HG21	2:v:351:VAL:CG2	2.34	0.56
2:w:714:GLY:H	2:w:774:THR:HG22	1.71	0.56
1:a:9:LEU:CD2	4:M:72:ASP:CG	2.78	0.55
2:w:369:SER:O	2:w:370:ARG:C	2.49	0.55
4:N:85:LEU:HB2	4:N:122:ILE:HG13	1.86	0.55
4:R:168:ARG:HH11	4:R:172:MET:HE3	1.71	0.55
4:X:71:PRO:HA	4:X:78:ILE:HG12	1.87	0.55
1:i:93:ILE:HD11	2:u:746:LEU:HA	1.79	0.55
2:s:727:TRP:CA	4:R:36:ALA:HB2	2.36	0.55
2:u:278:ASP:OD2	3:B:108:ARG:HG3	2.05	0.55
2:v:309:PRO:HB2	2:v:327:TRP:HZ2	1.71	0.55
2:x:369:SER:O	2:x:370:ARG:C	2.49	0.55
3:A:40:GLU:HB2	3:A:43:ARG:NH1	2.22	0.55
4:P:168:ARG:HH12	4:P:172:MET:HE1	1.68	0.55
1:f:95:ARG:HD2	2:v:639:LYS:HG3	1.88	0.55
1:g:9:LEU:CG	4:U:72:ASP:OD2	2.54	0.55
2:s:714:GLY:CA	2:s:774:THR:CG2	2.72	0.55
2:v:347:SER:OG	2:v:349:ASN:OD1	2.23	0.55
4:M:104:TYR:HD1	4:M:111:ASP:HB3	1.72	0.55
4:U:104:TYR:HD1	4:U:111:ASP:HB3	1.71	0.55
1:l:93:ILE:HG12	2:t:638:GLY:CA	2.27	0.55
1:l:95:ARG:NH1	2:t:635:GLU:OE2	2.39	0.55
2:u:19:PRO:CG	2:v:711:GLU:OE2	2.55	0.55
4:S:2:ARG:NH1	4:S:124:LEU:HD21	2.13	0.55
4:S:52:ARG:HH11	4:T:132:GLU:CD	2.12	0.55
4:T:71:PRO:HA	4:T:78:ILE:HG12	1.87	0.55
1:f:89:THR:HG21	2:v:641:THR:HA	1.88	0.55
1:h:36:LEU:H	1:h:42:LYS:H	1.53	0.55
2:u:201:ALA:HB2	2:u:220:ILE:HD12	1.87	0.55
2:w:340:TRP:HE3	2:w:341:PRO:HD2	1.72	0.55
4:Q:50:ILE:HD12	4:Q:142:ALA:HA	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:104:TYR:HD1	4:W:111:ASP:HB3	1.71	0.55
1:j:9:LEU:CD2	4:S:72:ASP:CG	2.80	0.55
1:n:36:LEU:H	1:n:42:LYS:H	1.53	0.55
2:t:161:TYR:CE1	3:D:46:ASN:HB3	2.41	0.55
2:t:714:GLY:CA	2:t:774:THR:CG2	2.72	0.55
2:t:739:ASN:HD21	2:t:742:ARG:NH2	1.99	0.55
2:u:128:VAL:HG21	2:u:351:VAL:CG2	2.34	0.55
2:u:184:GLN:HB2	2:u:187:HIS:CG	2.42	0.55
2:u:341:PRO:HD3	2:u:378:TYR:CE2	2.42	0.55
2:u:437:LEU:H	2:u:437:LEU:HD12	1.72	0.55
2:w:201:ALA:HB2	2:w:220:ILE:HD12	1.87	0.55
3:E:105:GLN:HG2	3:E:108:ARG:NH2	2.22	0.55
4:S:104:TYR:HD1	4:S:111:ASP:HB3	1.72	0.55
4:T:178:TYR:HD1	4:T:178:TYR:C	2.15	0.55
4:W:50:ILE:HD12	4:W:142:ALA:HA	1.88	0.55
2:s:437:LEU:H	2:s:437:LEU:HD12	1.72	0.55
4:N:168:ARG:HH11	4:N:172:MET:HE3	1.71	0.55
4:O:2:ARG:NH1	4:O:124:LEU:HD21	2.13	0.55
4:O:104:TYR:HD1	4:O:111:ASP:HB3	1.71	0.55
2:t:340:TRP:HE3	2:t:341:PRO:HD2	1.72	0.55
2:u:347:SER:OG	2:u:349:ASN:OD1	2.23	0.55
2:v:369:SER:O	2:v:370:ARG:C	2.49	0.55
2:x:341:PRO:HD3	2:x:378:TYR:CE2	2.42	0.55
2:x:721:GLU:HG3	2:x:765:THR:HG23	1.88	0.55
2:x:727:TRP:CD2	4:P:38:ALA:HB2	2.42	0.55
4:N:71:PRO:HA	4:N:78:ILE:HG12	1.87	0.55
4:N:178:TYR:HD1	4:N:178:TYR:C	2.15	0.55
4:O:6:MET:HE3	4:P:6:MET:HE2	1.89	0.55
4:Q:104:TYR:HD1	4:Q:111:ASP:HB3	1.71	0.55
4:R:178:TYR:HD1	4:R:178:TYR:C	2.15	0.55
4:U:2:ARG:NH1	4:U:124:LEU:HD21	2.13	0.55
4:V:178:TYR:CD1	4:V:178:TYR:C	2.85	0.55
1:c:95:ARG:NH1	2:w:635:GLU:OE2	2.40	0.55
2:s:721:GLU:HG3	2:s:765:THR:HG23	1.88	0.55
2:v:184:GLN:HB2	2:v:187:HIS:CG	2.42	0.55
2:v:370:ARG:HG2	2:v:390:PRO:HD3	1.88	0.55
2:v:437:LEU:H	2:v:437:LEU:HD12	1.72	0.55
2:v:714:GLY:H	2:v:774:THR:HG22	1.71	0.55
2:x:340:TRP:HE3	2:x:341:PRO:HD2	1.72	0.55
3:B:105:GLN:HG2	3:B:108:ARG:NH2	2.22	0.55
1:d:9:LEU:HD21	4:W:72:ASP:CG	2.32	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:340:TRP:HE3	2:s:341:PRO:HD2	1.72	0.55
2:u:340:TRP:HE3	2:u:341:PRO:HD2	1.72	0.55
2:x:278:ASP:OD2	3:E:108:ARG:CG	2.54	0.55
4:V:178:TYR:HD1	4:V:178:TYR:C	2.14	0.55
1:i:93:ILE:HG12	2:u:638:GLY:CA	2.25	0.54
2:u:369:SER:O	2:u:370:ARG:C	2.49	0.54
2:v:340:TRP:HE3	2:v:341:PRO:HD2	1.72	0.54
2:w:721:GLU:HG3	2:w:765:THR:HG23	1.88	0.54
3:A:105:GLN:HG2	3:A:108:ARG:NH2	2.22	0.54
4:T:168:ARG:HH12	4:T:172:MET:HE1	1.68	0.54
4:X:178:TYR:CD1	4:X:178:TYR:C	2.85	0.54
1:f:95:ARG:NH1	2:v:635:GLU:OE2	2.41	0.54
1:l:93:ILE:HD11	2:t:746:LEU:HA	1.78	0.54
2:s:341:PRO:HD3	2:s:378:TYR:CE2	2.42	0.54
2:t:184:GLN:HB2	2:t:187:HIS:CG	2.42	0.54
2:t:254:PHE:HZ	3:C:112:MET:SD	2.30	0.54
2:t:341:PRO:HD3	2:t:378:TYR:CE2	2.42	0.54
2:t:347:SER:OG	2:t:349:ASN:OD1	2.23	0.54
2:w:437:LEU:HD12	2:w:437:LEU:H	1.72	0.54
3:A:40:GLU:CA	3:A:43:ARG:HH11	2.20	0.54
1:a:27:LEU:HD21	1:a:104:ILE:HG22	1.90	0.54
2:s:271:GLY:HA3	3:D:107:ILE:HG21	1.90	0.54
2:s:370:ARG:HG2	2:s:390:PRO:HD3	1.89	0.54
2:u:388:ASP:OD2	3:C:82:ARG:HB2	2.07	0.54
3:C:119:ARG:HH12	3:D:61:GLU:CD	2.16	0.54
4:X:134:PHE:CD2	4:X:171:CYS:SG	3.01	0.54
1:d:27:LEU:HD21	1:d:104:ILE:HG22	1.90	0.54
2:s:394:ALA:O	3:D:90:LEU:O	2.25	0.54
2:u:370:ARG:HG2	2:u:390:PRO:HD3	1.89	0.54
2:x:370:ARG:HG2	2:x:390:PRO:HD3	1.88	0.54
3:C:119:ARG:NH1	3:D:61:GLU:OE1	2.41	0.54
4:S:50:ILE:HD12	4:S:142:ALA:HA	1.88	0.54
1:g:9:LEU:HD21	4:U:72:ASP:CG	2.33	0.54
1:g:27:LEU:HD21	1:g:104:ILE:HG22	1.90	0.54
1:r:93:ILE:HG12	2:x:638:GLY:CA	2.29	0.54
2:s:184:GLN:HB2	2:s:187:HIS:CG	2.42	0.54
2:t:721:GLU:HG3	2:t:765:THR:HG23	1.88	0.54
2:u:190:ASN:HA	2:u:195:TRP:HZ3	1.73	0.54
2:x:254:PHE:HZ	3:E:112:MET:SD	2.31	0.54
2:x:278:ASP:OD2	3:E:108:ARG:HG3	2.08	0.54
4:Q:148:ASN:HD21	4:R:159:VAL:HG11	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:89:THR:HG21	2:t:641:THR:HA	1.89	0.54
2:s:204:MET:O	2:s:211:TRP:CH2	2.61	0.54
2:t:204:MET:O	2:t:211:TRP:CH2	2.61	0.54
2:t:370:ARG:HG2	2:t:390:PRO:HD3	1.89	0.54
2:w:184:GLN:HB2	2:w:187:HIS:CG	2.42	0.54
4:V:134:PHE:CD2	4:V:171:CYS:SG	3.01	0.54
4:X:178:TYR:HD1	4:X:178:TYR:C	2.14	0.54
1:e:8:VAL:HG13	1:e:76:ARG:HG2	1.89	0.54
1:p:27:LEU:HD21	1:p:104:ILE:HG22	1.90	0.54
2:s:19:PRO:CG	2:t:711:GLU:OE2	2.56	0.54
2:w:341:PRO:HD3	2:w:378:TYR:CE2	2.42	0.54
2:x:184:GLN:HB2	2:x:187:HIS:CG	2.42	0.54
4:N:134:PHE:CD2	4:N:171:CYS:SG	3.01	0.54
4:T:168:ARG:HH11	4:T:172:MET:HE3	1.71	0.54
1:l:95:ARG:HB2	1:l:98:ASP:HB2	1.90	0.54
1:o:89:THR:HG21	2:s:641:THR:HA	1.90	0.54
2:t:727:TRP:CD2	4:T:38:ALA:HB2	2.43	0.54
2:u:602:ILE:HD12	2:u:662:LEU:O	2.08	0.54
2:v:190:ASN:HA	2:v:195:TRP:HZ3	1.73	0.54
2:w:370:ARG:HG2	2:w:390:PRO:HD3	1.89	0.54
2:x:204:MET:O	2:x:211:TRP:CH2	2.61	0.54
2:x:602:ILE:HD12	2:x:662:LEU:O	2.08	0.54
4:P:178:TYR:HD1	4:P:178:TYR:C	2.15	0.54
4:T:134:PHE:CD2	4:T:171:CYS:SG	3.01	0.54
4:X:168:ARG:HH11	4:X:172:MET:HE3	1.71	0.54
1:f:95:ARG:HB2	1:f:98:ASP:HB2	1.90	0.54
1:h:8:VAL:HG13	1:h:76:ARG:HG2	1.90	0.54
1:i:95:ARG:HB2	1:i:98:ASP:HB2	1.90	0.54
1:p:9:LEU:CG	4:O:72:ASP:OD2	2.55	0.54
1:r:13:LEU:HB2	1:r:71:THR:HA	1.90	0.54
2:s:369:SER:O	2:s:370:ARG:C	2.49	0.54
2:s:602:ILE:HD12	2:s:662:LEU:O	2.08	0.54
2:v:185:PRO:HD3	3:B:42:MET:HE2	1.89	0.54
2:w:602:ILE:HD12	2:w:662:LEU:O	2.08	0.54
2:x:727:TRP:CH2	4:Q:27:PRO:HB3	2.41	0.54
3:E:123:ALA:O	3:E:127:GLN:HB2	2.08	0.54
4:N:168:ARG:HH12	4:N:172:MET:HE1	1.68	0.54
4:U:50:ILE:HD12	4:U:142:ALA:HA	1.88	0.54
4:V:56:SER:O	4:V:57:ARG:C	2.51	0.54
1:a:9:LEU:HD21	4:M:72:ASP:CG	2.33	0.54
1:a:9:LEU:HD22	1:a:23:PRO:HG3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:c:13:LEU:HB2	1:c:71:THR:HA	1.90	0.54
1:k:36:LEU:H	1:k:42:LYS:H	1.53	0.54
1:o:51:ARG:C	1:o:53:ALA:N	2.65	0.54
2:t:437:LEU:HD12	2:t:437:LEU:H	1.72	0.54
2:u:204:MET:O	2:u:211:TRP:CH2	2.61	0.54
3:C:40:GLU:CB	3:C:43:ARG:HH21	2.20	0.54
4:O:148:ASN:HD21	4:P:159:VAL:HG11	1.73	0.54
1:c:93:ILE:HG12	2:w:638:GLY:CA	2.26	0.53
1:m:9:LEU:HD22	1:m:23:PRO:HG3	1.91	0.53
1:q:8:VAL:HG13	1:q:76:ARG:HG2	1.89	0.53
2:t:190:ASN:HA	2:t:195:TRP:HZ3	1.73	0.53
2:t:369:SER:O	2:t:370:ARG:C	2.49	0.53
2:v:727:TRP:HA	4:X:36:ALA:HB2	1.90	0.53
2:x:437:LEU:H	2:x:437:LEU:HD12	1.72	0.53
3:E:128:GLN:HG2	3:E:129:LEU:N	2.23	0.53
4:M:21:LEU:HB3	4:M:26:GLU:HB2	1.90	0.53
4:T:178:TYR:C	4:T:178:TYR:CD1	2.85	0.53
1:c:89:THR:HG21	2:w:641:THR:HA	1.89	0.53
1:j:27:LEU:HD21	1:j:104:ILE:HG22	1.90	0.53
1:o:95:ARG:HB2	1:o:98:ASP:HB2	1.90	0.53
2:s:562:TYR:HE1	2:s:575:ARG:HD3	1.74	0.53
2:w:564:ILE:HG12	2:w:573:LEU:HD13	1.91	0.53
2:x:184:GLN:HA	3:F:42:MET:CE	2.38	0.53
4:S:148:ASN:HD21	4:T:159:VAL:HG11	1.73	0.53
4:U:21:LEU:HB3	4:U:26:GLU:HB2	1.90	0.53
1:c:93:ILE:CD1	2:w:746:LEU:CA	2.67	0.53
1:n:8:VAL:HG13	1:n:76:ARG:HG2	1.89	0.53
2:s:460:PHE:CE1	2:s:471:HIS:HB2	2.44	0.53
2:s:727:TRP:CH2	4:S:27:PRO:HB3	2.41	0.53
2:v:341:PRO:HD3	2:v:378:TYR:CE2	2.42	0.53
2:v:727:TRP:CB	4:X:36:ALA:CB	2.83	0.53
4:O:21:LEU:HB3	4:O:26:GLU:HB2	1.91	0.53
4:P:178:TYR:C	4:P:178:TYR:CD1	2.85	0.53
4:Q:2:ARG:NH1	4:Q:124:LEU:HD21	2.13	0.53
4:Q:21:LEU:HB3	4:Q:26:GLU:HB2	1.91	0.53
1:j:9:LEU:HD22	1:j:23:PRO:HG3	1.90	0.53
1:p:9:LEU:HD21	4:O:72:ASP:CG	2.32	0.53
1:p:9:LEU:HD22	1:p:23:PRO:HG3	1.90	0.53
2:s:727:TRP:CD2	4:R:38:ALA:HB2	2.43	0.53
2:t:727:TRP:CH2	4:U:27:PRO:HB3	2.41	0.53
2:u:562:TYR:HE1	2:u:575:ARG:HD3	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:134:PHE:CD2	4:P:171:CYS:SG	3.01	0.53
4:S:21:LEU:HB3	4:S:26:GLU:HB2	1.90	0.53
1:c:95:ARG:HB2	1:c:98:ASP:HB2	1.90	0.53
1:d:50:TYR:HB2	1:d:58:ILE:HG13	1.90	0.53
1:f:13:LEU:HB2	1:f:71:THR:HA	1.91	0.53
2:s:161:TYR:CE1	3:E:46:ASN:HB3	2.44	0.53
2:s:590:TYR:O	2:s:591:ARG:C	2.52	0.53
2:t:357:ARG:HH11	2:t:368:LEU:HB3	1.73	0.53
2:t:602:ILE:HD12	2:t:662:LEU:O	2.08	0.53
2:u:727:TRP:CZ2	4:W:27:PRO:HB2	2.44	0.53
2:v:564:ILE:HG12	2:v:573:LEU:HD13	1.91	0.53
2:w:562:TYR:HE1	2:w:575:ARG:HD3	1.74	0.53
2:x:564:ILE:HG12	2:x:573:LEU:HD13	1.91	0.53
4:P:168:ARG:HH11	4:P:172:MET:HE3	1.71	0.53
4:U:148:ASN:HD21	4:V:159:VAL:HG11	1.72	0.53
1:d:9:LEU:HD22	1:d:23:PRO:HG3	1.91	0.53
1:m:27:LEU:HD21	1:m:104:ILE:HG22	1.90	0.53
2:s:357:ARG:HH11	2:s:368:LEU:HB3	1.74	0.53
2:t:460:PHE:CE1	2:t:471:HIS:HB2	2.44	0.53
2:v:602:ILE:HD12	2:v:662:LEU:O	2.08	0.53
2:w:460:PHE:CE1	2:w:471:HIS:HB2	2.44	0.53
2:x:357:ARG:HH11	2:x:368:LEU:HB3	1.74	0.53
2:x:460:PHE:CE1	2:x:471:HIS:HB2	2.44	0.53
4:W:148:ASN:HD21	4:X:159:VAL:HG11	1.72	0.53
1:m:50:TYR:HB2	1:m:58:ILE:HG13	1.90	0.53
2:t:590:TYR:O	2:t:591:ARG:C	2.52	0.53
2:u:55:GLY:H	2:u:571:THR:HG22	1.73	0.53
2:x:590:TYR:O	2:x:591:ARG:C	2.52	0.53
4:R:134:PHE:CD2	4:R:171:CYS:SG	3.01	0.53
4:W:21:LEU:HB3	4:W:26:GLU:HB2	1.91	0.53
1:i:51:ARG:C	1:i:53:ALA:N	2.65	0.53
1:k:13:LEU:HG	1:k:64:TRP:O	2.09	0.53
1:o:13:LEU:HB2	1:o:71:THR:HA	1.91	0.53
2:s:564:ILE:HG12	2:s:573:LEU:HD13	1.91	0.53
2:s:711:GLU:OE2	2:x:19:PRO:CG	2.55	0.53
2:t:562:TYR:HE1	2:t:575:ARG:HD3	1.74	0.53
2:u:357:ARG:HH11	2:u:368:LEU:HB3	1.74	0.53
2:u:564:ILE:HG12	2:u:573:LEU:HD13	1.91	0.53
2:w:204:MET:O	2:w:211:TRP:CH2	2.61	0.53
2:w:271:GLY:HA3	3:F:107:ILE:HG21	1.91	0.53
2:w:590:TYR:O	2:w:591:ARG:C	2.52	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:108:ARG:O	3:D:109:GLU:C	2.50	0.53
4:R:178:TYR:C	4:R:178:TYR:CD1	2.85	0.53
1:r:95:ARG:HB2	1:r:98:ASP:HB2	1.89	0.53
2:t:55:GLY:H	2:t:571:THR:HG22	1.74	0.53
2:u:590:TYR:O	2:u:591:ARG:C	2.52	0.53
2:v:55:GLY:H	2:v:571:THR:HG22	1.74	0.53
2:v:590:TYR:O	2:v:591:ARG:C	2.52	0.53
2:w:55:GLY:H	2:w:571:THR:HG22	1.74	0.53
2:w:357:ARG:HH11	2:w:368:LEU:HB3	1.74	0.53
2:x:55:GLY:H	2:x:571:THR:HG22	1.74	0.53
1:a:50:TYR:HB2	1:a:58:ILE:HG13	1.91	0.53
2:t:564:ILE:HG12	2:t:573:LEU:HD13	1.91	0.53
3:B:126:ALA:HA	3:B:129:LEU:HG	1.91	0.53
4:V:168:ARG:HH11	4:V:172:MET:HE3	1.71	0.53
4:V:174:TYR:C	4:V:174:TYR:CD1	2.87	0.53
1:f:51:ARG:C	1:f:53:ALA:N	2.65	0.52
2:x:328:SER:OG	2:x:376:ASN:HA	2.10	0.52
4:T:56:SER:O	4:T:57:ARG:C	2.51	0.52
1:b:8:VAL:HG13	1:b:76:ARG:HG2	1.89	0.52
1:g:9:LEU:HD22	1:g:23:PRO:HG3	1.91	0.52
1:j:50:TYR:HB2	1:j:58:ILE:HG13	1.91	0.52
1:k:8:VAL:HG13	1:k:76:ARG:HG2	1.90	0.52
2:v:357:ARG:HH11	2:v:368:LEU:HB3	1.74	0.52
2:v:460:PHE:CE1	2:v:471:HIS:HB2	2.44	0.52
2:v:562:TYR:HE1	2:v:575:ARG:HD3	1.74	0.52
2:w:328:SER:OG	2:w:376:ASN:HA	2.09	0.52
1:l:13:LEU:HB2	1:l:71:THR:HA	1.90	0.52
1:o:95:ARG:NH1	2:s:635:GLU:OE2	2.43	0.52
3:B:129:LEU:HD12	3:B:129:LEU:C	2.35	0.52
4:N:178:TYR:C	4:N:178:TYR:CD1	2.85	0.52
4:T:105:ASP:HB2	4:T:108:SER:HB3	1.91	0.52
1:b:13:LEU:HG	1:b:64:TRP:O	2.09	0.52
1:l:51:ARG:C	1:l:53:ALA:N	2.66	0.52
1:r:89:THR:HG21	2:x:641:THR:HA	1.91	0.52
2:v:727:TRP:CZ2	4:M:27:PRO:HB2	2.45	0.52
2:w:88:VAL:HG12	2:w:98:VAL:HG13	1.92	0.52
4:X:174:TYR:CD1	4:X:174:TYR:C	2.87	0.52
1:h:13:LEU:HG	1:h:64:TRP:O	2.09	0.52
1:j:9:LEU:HD21	4:S:72:ASP:CG	2.35	0.52
1:r:95:ARG:NH1	2:x:635:GLU:OE2	2.42	0.52
2:s:154:ILE:HG23	2:s:244:ILE:HG23	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:u:460:PHE:CE1	2:u:471:HIS:HB2	2.44	0.52
2:v:204:MET:O	2:v:211:TRP:CH2	2.61	0.52
2:w:190:ASN:HA	2:w:195:TRP:HZ3	1.73	0.52
2:x:727:TRP:HA	4:P:36:ALA:HB2	1.91	0.52
4:N:105:ASP:HB2	4:N:108:SER:HB3	1.91	0.52
4:P:56:SER:O	4:P:57:ARG:C	2.51	0.52
1:i:13:LEU:HB2	1:i:71:THR:HA	1.90	0.52
2:v:328:SER:OG	2:v:376:ASN:HA	2.10	0.52
2:w:727:TRP:HA	4:N:36:ALA:HB2	1.90	0.52
3:D:138:GLN:NE2	3:E:40:GLU:OE2	2.43	0.52
1:i:93:ILE:HB	2:u:638:GLY:C	2.27	0.52
1:m:9:LEU:HD21	4:Q:72:ASP:CG	2.34	0.52
1:n:13:LEU:HG	1:n:64:TRP:O	2.09	0.52
2:t:727:TRP:HA	4:T:36:ALA:HB2	1.90	0.52
2:u:727:TRP:CH2	4:W:27:PRO:CB	2.93	0.52
2:x:154:ILE:HG23	2:x:244:ILE:HG23	1.92	0.52
3:F:95:MET:O	3:F:98:ILE:HG22	2.10	0.52
4:P:105:ASP:HB2	4:P:108:SER:HB3	1.91	0.52
1:g:50:TYR:HB2	1:g:58:ILE:HG13	1.90	0.52
1:p:50:TYR:HB2	1:p:58:ILE:HG13	1.90	0.52
1:r:32:VAL:HG13	1:r:52:PHE:CZ	2.45	0.52
2:s:418:ASP:OD2	2:t:73:GLU:CG	2.36	0.52
2:u:727:TRP:HA	4:V:36:ALA:HB2	1.90	0.52
2:v:727:TRP:CH2	4:M:27:PRO:CB	2.93	0.52
2:x:88:VAL:HG12	2:x:98:VAL:HG13	1.92	0.52
2:x:562:TYR:HE1	2:x:575:ARG:HD3	1.74	0.52
4:P:174:TYR:CD1	4:P:174:TYR:C	2.87	0.52
4:V:98:ASN:ND2	4:W:129:GLU:HA	2.24	0.52
2:t:150:GLN:HB3	2:t:224:ALA:CA	2.40	0.52
2:w:154:ILE:HG23	2:w:244:ILE:HG23	1.92	0.52
2:w:727:TRP:CH2	4:O:27:PRO:CB	2.93	0.52
1:l:38:GLY:CA	1:l:70:TYR:HA	2.40	0.52
1:q:13:LEU:HG	1:q:64:TRP:O	2.09	0.52
2:s:443:PHE:CB	2:s:485:ALA:HB2	2.40	0.52
2:t:154:ILE:HG23	2:t:244:ILE:HG23	1.92	0.52
2:t:667:VAL:HG12	2:t:669:ILE:HG12	1.92	0.52
2:u:606:THR:O	2:u:607:TYR:HB3	2.10	0.52
2:v:254:PHE:HZ	3:A:112:MET:SD	2.32	0.52
3:D:105:GLN:HG2	3:D:108:ARG:HH22	1.75	0.52
4:P:126:ASP:OD1	4:P:127:TYR:N	2.43	0.52
4:V:105:ASP:HB2	4:V:108:SER:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:56:SER:O	4:X:57:ARG:C	2.51	0.52
1:c:51:ARG:C	1:c:53:ALA:N	2.67	0.51
1:o:38:GLY:CA	1:o:70:TYR:HA	2.41	0.51
2:s:55:GLY:H	2:s:571:THR:HG22	1.74	0.51
2:s:150:GLN:HB3	2:s:224:ALA:CA	2.39	0.51
2:s:667:VAL:HG12	2:s:669:ILE:HG12	1.92	0.51
2:t:328:SER:OG	2:t:376:ASN:HA	2.10	0.51
2:t:606:THR:O	2:t:607:TYR:HB3	2.10	0.51
2:u:183:SER:OG	3:C:42:MET:HE3	2.10	0.51
2:v:19:PRO:CG	2:w:711:GLU:OE2	2.55	0.51
2:x:150:GLN:HB3	2:x:224:ALA:CA	2.39	0.51
4:R:174:TYR:CD1	4:R:174:TYR:C	2.87	0.51
4:R:182:ASN:HB2	4:R:186:GLY:H	1.75	0.51
4:T:182:ASN:HB2	4:T:186:GLY:H	1.75	0.51
1:r:35:THR:HG22	1:r:37:ILE:HG12	1.93	0.51
2:t:48:LEU:HB2	2:t:595:ASP:O	2.11	0.51
2:t:254:PHE:CE2	3:D:65:ALA:HB1	2.45	0.51
2:u:667:VAL:HG12	2:u:669:ILE:HG12	1.92	0.51
2:v:443:PHE:CB	2:v:485:ALA:HB2	2.41	0.51
2:w:443:PHE:CB	2:w:485:ALA:HB2	2.41	0.51
4:N:56:SER:O	4:N:57:ARG:C	2.51	0.51
4:P:6:MET:HB3	4:P:8:VAL:HG12	1.92	0.51
1:r:38:GLY:CA	1:r:70:TYR:HA	2.41	0.51
2:u:161:TYR:CE1	3:C:46:ASN:HB3	2.45	0.51
2:u:200:LEU:HD23	2:u:200:LEU:H	1.75	0.51
2:v:88:VAL:HG12	2:v:98:VAL:HG13	1.92	0.51
2:w:69:ILE:HG12	2:w:77:TYR:O	2.11	0.51
2:w:150:GLN:HB3	2:w:224:ALA:CA	2.40	0.51
4:N:126:ASP:OD1	4:N:127:TYR:N	2.43	0.51
4:N:174:TYR:C	4:N:174:TYR:CD1	2.87	0.51
4:R:105:ASP:HB2	4:R:108:SER:HB3	1.91	0.51
1:l:35:THR:HG22	1:l:37:ILE:HG12	1.93	0.51
2:t:44:LYS:HD3	2:t:673:ILE:HD13	1.93	0.51
2:u:254:PHE:HZ	3:B:112:MET:SD	2.31	0.51
2:v:69:ILE:HG12	2:v:77:TYR:O	2.11	0.51
2:v:154:ILE:HG23	2:v:244:ILE:HG23	1.92	0.51
2:v:163:ARG:NH2	3:A:129:LEU:HD13	2.22	0.51
2:v:200:LEU:HD23	2:v:200:LEU:H	1.75	0.51
4:N:182:ASN:HB2	4:N:186:GLY:H	1.75	0.51
4:T:174:TYR:CD1	4:T:174:TYR:C	2.87	0.51
1:o:35:THR:HG22	1:o:37:ILE:HG12	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:r:32:VAL:O	1:r:32:VAL:HG22	2.11	0.51
2:s:328:SER:OG	2:s:376:ASN:HA	2.09	0.51
2:u:443:PHE:CB	2:u:485:ALA:HB2	2.41	0.51
2:w:727:TRP:CZ2	4:O:27:PRO:HB2	2.45	0.51
2:x:48:LEU:HB2	2:x:595:ASP:O	2.11	0.51
1:c:35:THR:HG22	1:c:37:ILE:HG12	1.93	0.51
1:e:13:LEU:HG	1:e:64:TRP:O	2.09	0.51
2:u:714:GLY:CA	2:u:774:THR:CG2	2.72	0.51
2:v:48:LEU:HB2	2:v:595:ASP:O	2.11	0.51
2:w:771:ASP:OD1	2:w:771:ASP:O	2.29	0.51
4:N:134:PHE:CA	4:N:171:CYS:SG	2.99	0.51
4:R:126:ASP:OD1	4:R:127:TYR:N	2.43	0.51
4:R:134:PHE:CA	4:R:171:CYS:SG	2.99	0.51
2:t:443:PHE:CB	2:t:485:ALA:HB2	2.40	0.51
2:u:44:LYS:HD3	2:u:673:ILE:HD13	1.93	0.51
2:u:69:ILE:HG12	2:u:77:TYR:O	2.11	0.51
2:u:281:TYR:CD1	2:u:333:GLY:HA3	2.44	0.51
2:x:771:ASP:O	2:x:771:ASP:OD1	2.29	0.51
4:R:56:SER:O	4:R:57:ARG:C	2.51	0.51
4:V:182:ASN:HB2	4:V:186:GLY:H	1.75	0.51
1:j:37:ILE:HG22	1:j:38:GLY:H	1.76	0.51
1:l:32:VAL:HG22	1:l:32:VAL:O	2.11	0.51
1:l:93:ILE:CD1	2:t:746:LEU:CA	2.68	0.51
1:q:50:TYR:HA	1:q:60:LEU:HA	1.93	0.51
2:t:281:TYR:CD1	2:t:333:GLY:HA3	2.44	0.51
2:v:667:VAL:HG12	2:v:669:ILE:HG12	1.92	0.51
2:v:771:ASP:OD1	2:v:771:ASP:O	2.29	0.51
4:M:6:MET:SD	4:N:6:MET:HB2	2.50	0.51
4:T:134:PHE:CA	4:T:171:CYS:SG	2.99	0.51
4:V:126:ASP:OD1	4:V:127:TYR:N	2.43	0.51
4:X:105:ASP:HB2	4:X:108:SER:HB3	1.91	0.51
4:X:126:ASP:OD1	4:X:127:TYR:N	2.43	0.51
4:X:134:PHE:CA	4:X:171:CYS:SG	2.99	0.51
1:i:38:GLY:CA	1:i:70:TYR:HA	2.41	0.51
2:t:88:VAL:HG12	2:t:98:VAL:HG13	1.92	0.51
2:v:606:THR:O	2:v:607:TYR:HB3	2.10	0.51
2:w:48:LEU:HB2	2:w:595:ASP:O	2.11	0.51
2:x:667:VAL:HG12	2:x:669:ILE:HG12	1.92	0.51
3:B:126:ALA:O	3:B:129:LEU:CG	2.52	0.51
4:N:82:ASP:OD1	4:N:82:ASP:N	2.44	0.51
4:T:126:ASP:OD1	4:T:127:TYR:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:32:VAL:O	1:f:32:VAL:HG22	2.11	0.51
1:f:93:ILE:CD1	2:v:746:LEU:CA	2.66	0.51
2:s:771:ASP:O	2:s:771:ASP:OD1	2.29	0.51
2:v:44:LYS:HD3	2:v:673:ILE:HD13	1.93	0.51
2:w:19:PRO:CG	2:x:711:GLU:OE2	2.57	0.51
2:x:190:ASN:HA	2:x:195:TRP:HZ3	1.73	0.51
4:M:148:ASN:HD21	4:N:159:VAL:HG11	1.72	0.51
4:P:134:PHE:CA	4:P:171:CYS:SG	2.99	0.51
1:i:35:THR:HG22	1:i:37:ILE:HG12	1.93	0.50
2:s:183:SER:O	3:E:42:MET:HE2	2.10	0.50
2:s:606:THR:O	2:s:607:TYR:HB3	2.10	0.50
2:u:114:ASN:HA	2:u:450:ARG:HH12	1.76	0.50
2:u:150:GLN:HB3	2:u:224:ALA:CA	2.40	0.50
2:u:562:TYR:CE1	2:u:575:ARG:HB2	2.47	0.50
2:v:60:LEU:HD11	2:v:80:VAL:HG11	1.93	0.50
2:w:60:LEU:HD11	2:w:80:VAL:HG11	1.93	0.50
2:x:69:ILE:HG12	2:x:77:TYR:O	2.11	0.50
2:x:727:TRP:CZ2	4:Q:27:PRO:HB2	2.47	0.50
4:W:182:ASN:OD1	4:W:185:ASP:N	2.45	0.50
1:c:38:GLY:CA	1:c:70:TYR:HA	2.40	0.50
1:f:35:THR:HG22	1:f:37:ILE:HG12	1.93	0.50
1:i:32:VAL:O	1:i:32:VAL:HG22	2.11	0.50
2:s:44:LYS:HD3	2:s:673:ILE:HD13	1.93	0.50
2:t:727:TRP:CZ2	4:U:27:PRO:HB2	2.46	0.50
2:u:48:LEU:HB2	2:u:595:ASP:O	2.11	0.50
2:u:86:ILE:O	2:u:98:VAL:HG21	2.12	0.50
2:u:167:VAL:HB	2:u:175:ALA:HB3	1.94	0.50
2:u:328:SER:OG	2:u:376:ASN:HA	2.10	0.50
2:v:562:TYR:CE1	2:v:575:ARG:HB2	2.46	0.50
3:E:83:ALA:O	3:E:87:GLU:HG2	2.12	0.50
4:P:4:TYR:O	4:P:6:MET:HG2	2.11	0.50
4:P:82:ASP:OD1	4:P:82:ASP:N	2.44	0.50
4:U:182:ASN:OD1	4:U:185:ASP:N	2.45	0.50
1:a:37:ILE:HG22	1:a:38:GLY:H	1.76	0.50
1:b:50:TYR:HA	1:b:60:LEU:HA	1.94	0.50
2:t:69:ILE:HG12	2:t:77:TYR:O	2.11	0.50
2:t:114:ASN:HA	2:t:450:ARG:HH12	1.77	0.50
2:t:562:TYR:CE1	2:t:575:ARG:HB2	2.47	0.50
2:u:154:ILE:HG23	2:u:244:ILE:HG23	1.92	0.50
2:u:771:ASP:OD1	2:u:771:ASP:O	2.29	0.50
2:v:114:ASN:HA	2:v:450:ARG:HH12	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:156:VAL:HG23	2:v:219:PHE:HA	1.93	0.50
2:w:257:LEU:HD12	2:w:258:PRO:HD2	1.94	0.50
4:O:80:TYR:HB2	4:O:103:VAL:HG12	1.93	0.50
4:X:182:ASN:HB2	4:X:186:GLY:H	1.75	0.50
1:g:37:ILE:HG22	1:g:38:GLY:H	1.76	0.50
2:s:69:ILE:HG12	2:s:77:TYR:O	2.11	0.50
2:s:562:TYR:CE1	2:s:575:ARG:HB2	2.47	0.50
2:s:727:TRP:HA	4:R:36:ALA:HB2	1.92	0.50
2:t:86:ILE:O	2:t:98:VAL:HG21	2.11	0.50
2:u:156:VAL:HG23	2:u:219:PHE:HA	1.93	0.50
2:w:562:TYR:CE1	2:w:575:ARG:HB2	2.47	0.50
2:x:86:ILE:O	2:x:98:VAL:HG21	2.12	0.50
2:x:257:LEU:HD12	2:x:258:PRO:HD2	1.94	0.50
2:x:370:ARG:HH12	3:F:82:ARG:HH12	1.59	0.50
4:N:153:ALA:HB3	4:N:156:VAL:HG12	1.93	0.50
1:h:24:PHE:CD1	1:h:77:ARG:HB2	2.47	0.50
1:o:46:ILE:HG22	1:o:52:PHE:CE2	2.46	0.50
1:p:37:ILE:HG22	1:p:38:GLY:H	1.76	0.50
2:t:200:LEU:HD23	2:t:200:LEU:H	1.75	0.50
2:w:128:VAL:HG21	2:w:351:VAL:CG2	2.34	0.50
2:w:277:ALA:CA	3:F:100:ARG:HG3	2.40	0.50
2:x:443:PHE:CB	2:x:485:ALA:HB2	2.41	0.50
2:x:562:TYR:CE1	2:x:575:ARG:HB2	2.47	0.50
4:Q:80:TYR:HB2	4:Q:103:VAL:HG12	1.93	0.50
4:S:89:SER:H	4:S:94:SER:HB2	1.77	0.50
2:s:128:VAL:HG21	2:s:351:VAL:CG2	2.34	0.50
2:s:190:ASN:HA	2:s:195:TRP:HZ3	1.73	0.50
2:u:88:VAL:HG12	2:u:98:VAL:HG13	1.92	0.50
2:v:86:ILE:O	2:v:98:VAL:HG21	2.12	0.50
2:w:200:LEU:HD23	2:w:200:LEU:H	1.75	0.50
3:A:40:GLU:CA	3:A:43:ARG:NH1	2.75	0.50
4:P:182:ASN:HB2	4:P:186:GLY:H	1.75	0.50
4:Q:89:SER:H	4:Q:94:SER:HB2	1.77	0.50
4:U:2:ARG:HH11	4:U:124:LEU:CD2	2.17	0.50
1:e:50:TYR:HA	1:e:60:LEU:HA	1.94	0.50
1:n:24:PHE:CD1	1:n:77:ARG:HB2	2.47	0.50
1:o:32:VAL:O	1:o:32:VAL:HG22	2.11	0.50
2:s:48:LEU:HB2	2:s:595:ASP:O	2.11	0.50
2:s:86:ILE:O	2:s:98:VAL:HG21	2.12	0.50
2:s:114:ASN:HA	2:s:450:ARG:HH12	1.76	0.50
2:s:727:TRP:CZ2	4:S:27:PRO:HB2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:771:ASP:OD1	2:t:771:ASP:O	2.29	0.50
2:w:44:LYS:HD3	2:w:673:ILE:HD13	1.93	0.50
2:w:373:LYS:HG3	3:A:82:ARG:NH2	2.27	0.50
2:w:715:THR:HG21	2:w:772:GLU:HB3	1.94	0.50
4:P:153:ALA:HB3	4:P:156:VAL:HG12	1.93	0.50
4:V:134:PHE:CA	4:V:171:CYS:SG	2.99	0.50
1:k:24:PHE:CD1	1:k:77:ARG:HB2	2.47	0.50
1:n:50:TYR:HA	1:n:60:LEU:HA	1.94	0.50
2:s:88:VAL:HG12	2:s:98:VAL:HG13	1.92	0.50
2:s:156:VAL:HG23	2:s:219:PHE:HA	1.93	0.50
2:s:257:LEU:HD12	2:s:258:PRO:HD2	1.94	0.50
2:t:300:GLU:HG2	2:t:340:TRP:CZ2	2.47	0.50
2:u:300:GLU:HG2	2:u:340:TRP:CZ2	2.47	0.50
2:v:150:GLN:HB3	2:v:224:ALA:CA	2.39	0.50
2:v:300:GLU:HG2	2:v:340:TRP:CZ2	2.47	0.50
2:w:86:ILE:O	2:w:98:VAL:HG21	2.11	0.50
2:w:606:THR:O	2:w:607:TYR:HB3	2.10	0.50
3:E:95:MET:O	3:E:98:ILE:HG22	2.12	0.50
4:P:94:SER:O	4:Q:178:TYR:CZ	2.65	0.50
4:R:158:GLY:O	4:R:161:GLN:HG3	2.12	0.50
4:S:182:ASN:OD1	4:S:185:ASP:N	2.45	0.50
4:V:158:GLY:O	4:V:161:GLN:HG3	2.12	0.50
1:q:94:LEU:HD11	2:x:741:LEU:HD21	1.94	0.50
1:r:13:LEU:HD21	1:r:64:TRP:HB3	1.94	0.50
2:s:60:LEU:HD11	2:s:80:VAL:HG11	1.93	0.50
2:t:183:SER:HB2	3:D:42:MET:CB	2.34	0.50
2:w:667:VAL:HG12	2:w:669:ILE:HG12	1.92	0.50
2:x:185:PRO:HD2	3:F:42:MET:HE1	1.82	0.50
2:x:606:THR:O	2:x:607:TYR:HB3	2.10	0.50
4:T:158:GLY:O	4:T:161:GLN:HG3	2.12	0.50
1:e:94:LEU:HD11	2:v:741:LEU:HD21	1.94	0.49
1:h:50:TYR:HA	1:h:60:LEU:HA	1.93	0.49
1:q:24:PHE:CD1	1:q:77:ARG:HB2	2.47	0.49
2:s:145:ASN:O	2:s:145:ASN:CG	2.54	0.49
2:t:715:THR:HG21	2:t:772:GLU:HB3	1.94	0.49
2:u:418:ASP:OD2	2:v:73:GLU:CG	2.35	0.49
2:v:257:LEU:HD12	2:v:258:PRO:HD2	1.94	0.49
3:C:137:SER:OG	3:D:43:ARG:CZ	2.61	0.49
4:P:158:GLY:O	4:P:161:GLN:HG3	2.12	0.49
4:V:153:ALA:HB3	4:V:156:VAL:HG12	1.93	0.49
1:j:88:PHE:CD1	1:l:99:LEU:HB3	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:715:THR:HG21	2:s:772:GLU:HB3	1.94	0.49
2:s:739:ASN:HD21	2:s:742:ARG:NH2	1.99	0.49
2:w:114:ASN:HA	2:w:450:ARG:HH12	1.77	0.49
2:w:165:LEU:HG	2:w:243:LEU:HD22	1.95	0.49
2:w:388:ASP:OD1	3:A:83:ALA:HB2	2.12	0.49
2:x:44:LYS:HD3	2:x:673:ILE:HD13	1.93	0.49
2:x:128:VAL:HG21	2:x:351:VAL:CG2	2.34	0.49
2:x:727:TRP:CH2	4:Q:27:PRO:CB	2.95	0.49
3:F:82:ARG:O	3:F:83:ALA:C	2.56	0.49
4:T:134:PHE:N	4:T:171:CYS:SG	2.86	0.49
4:U:80:TYR:HB2	4:U:103:VAL:HG12	1.93	0.49
1:d:37:ILE:HG22	1:d:38:GLY:H	1.76	0.49
1:n:94:LEU:HD11	2:s:741:LEU:HD21	1.94	0.49
2:s:300:GLU:HG2	2:s:340:TRP:CZ2	2.47	0.49
2:s:727:TRP:CB	4:R:36:ALA:CB	2.85	0.49
2:t:167:VAL:HB	2:t:175:ALA:HB3	1.94	0.49
2:t:257:LEU:HD12	2:t:258:PRO:HD2	1.94	0.49
2:t:437:LEU:CD1	3:C:90:LEU:CD1	2.85	0.49
2:v:146:TYR:HE1	2:v:148:PRO:HA	1.77	0.49
2:w:146:TYR:HE1	2:w:148:PRO:HA	1.78	0.49
2:w:167:VAL:HB	2:w:175:ALA:HB3	1.94	0.49
2:w:277:ALA:HB1	3:F:100:ARG:O	2.12	0.49
2:x:113:ARG:HD3	2:x:501:PHE:CD1	2.48	0.49
4:N:134:PHE:N	4:N:171:CYS:SG	2.86	0.49
4:V:134:PHE:N	4:V:171:CYS:SG	2.86	0.49
4:X:158:GLY:O	4:X:161:GLN:HG3	2.12	0.49
1:c:32:VAL:O	1:c:32:VAL:HG22	2.11	0.49
1:h:94:LEU:HD11	2:u:741:LEU:HD21	1.95	0.49
1:l:86:VAL:HG13	1:l:86:VAL:O	2.13	0.49
2:s:167:VAL:HB	2:s:175:ALA:HB3	1.94	0.49
2:t:60:LEU:HD11	2:t:80:VAL:HG11	1.93	0.49
2:t:727:TRP:CH2	4:U:27:PRO:CB	2.95	0.49
2:u:146:TYR:HE1	2:u:148:PRO:HA	1.77	0.49
2:w:113:ARG:HD3	2:w:501:PHE:CD1	2.48	0.49
2:w:156:VAL:HG23	2:w:219:PHE:HA	1.93	0.49
2:w:300:GLU:HG2	2:w:340:TRP:CZ2	2.47	0.49
2:x:156:VAL:HG23	2:x:219:PHE:HA	1.93	0.49
2:x:281:TYR:CD1	2:x:333:GLY:HA3	2.44	0.49
2:x:715:THR:HG21	2:x:772:GLU:HB3	1.93	0.49
3:C:108:ARG:O	3:C:111:ASN:N	2.45	0.49
4:M:80:TYR:HB2	4:M:103:VAL:HG12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U:89:SER:H	4:U:94:SER:HB2	1.77	0.49
1:b:24:PHE:CD1	1:b:77:ARG:HB2	2.47	0.49
1:e:24:PHE:CD1	1:e:77:ARG:HB2	2.47	0.49
1:k:50:TYR:HA	1:k:60:LEU:HA	1.94	0.49
1:o:86:VAL:HG13	1:o:86:VAL:O	2.12	0.49
2:s:113:ARG:HD3	2:s:501:PHE:CD1	2.48	0.49
2:t:357:ARG:NH2	2:t:371:THR:HB	2.28	0.49
2:t:600:TYR:CZ	2:t:602:ILE:HA	2.48	0.49
2:u:257:LEU:HD12	2:u:258:PRO:HD2	1.94	0.49
2:v:727:TRP:HH2	4:M:27:PRO:CB	2.25	0.49
2:w:727:TRP:HH2	4:O:27:PRO:CB	2.26	0.49
4:O:89:SER:H	4:O:94:SER:HB2	1.77	0.49
4:S:80:TYR:HB2	4:S:103:VAL:HG12	1.93	0.49
4:W:6:MET:SD	4:X:6:MET:HB2	2.51	0.49
4:W:80:TYR:HB2	4:W:103:VAL:HG12	1.94	0.49
4:X:153:ALA:HB3	4:X:156:VAL:HG12	1.93	0.49
1:i:13:LEU:HD21	1:i:64:TRP:HB3	1.94	0.49
1:o:13:LEU:HD21	1:o:64:TRP:HB3	1.94	0.49
2:s:357:ARG:NH2	2:s:371:THR:HB	2.28	0.49
2:u:60:LEU:HD11	2:u:80:VAL:HG11	1.93	0.49
2:u:357:ARG:NH2	2:u:371:THR:HB	2.28	0.49
2:x:146:TYR:HE1	2:x:148:PRO:HA	1.78	0.49
2:x:200:LEU:HD23	2:x:200:LEU:H	1.75	0.49
2:x:357:ARG:NH2	2:x:371:THR:HB	2.28	0.49
3:B:95:MET:O	3:B:98:ILE:HG22	2.12	0.49
3:C:74:LYS:HA	3:C:106:PHE:HE2	1.72	0.49
4:R:81:SER:OG	4:R:82:ASP:N	2.46	0.49
1:f:38:GLY:CA	1:f:70:TYR:HA	2.40	0.49
1:o:93:ILE:HG13	2:s:638:GLY:HA3	1.95	0.49
1:p:88:PHE:CD1	1:r:99:LEU:HB3	2.48	0.49
2:v:281:TYR:CD1	2:v:333:GLY:HA3	2.44	0.49
2:v:727:TRP:HZ2	4:M:27:PRO:HB2	1.78	0.49
2:x:165:LEU:HG	2:x:243:LEU:HD22	1.95	0.49
2:x:167:VAL:HB	2:x:175:ALA:HB3	1.94	0.49
2:x:727:TRP:CB	4:P:36:ALA:CB	2.82	0.49
3:C:95:MET:O	3:C:98:ILE:HG22	2.12	0.49
4:N:158:GLY:O	4:N:161:GLN:HG3	2.12	0.49
4:O:2:ARG:HH11	4:O:124:LEU:CD2	2.17	0.49
4:P:81:SER:OG	4:P:82:ASP:N	2.46	0.49
4:R:82:ASP:N	4:R:82:ASP:OD1	2.44	0.49
4:R:144:ARG:NH2	4:S:162:GLU:OE2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:94:LEU:HD11	2:w:741:LEU:HD21	1.95	0.49
1:d:88:PHE:CD1	1:f:99:LEU:HB3	2.48	0.49
1:f:13:LEU:HD21	1:f:64:TRP:HB3	1.94	0.49
1:f:86:VAL:O	1:f:86:VAL:HG13	2.12	0.49
1:m:37:ILE:HG22	1:m:38:GLY:H	1.76	0.49
2:s:163:ARG:NH2	3:D:129:LEU:HB3	2.27	0.49
2:s:176:LYS:HZ3	2:s:178:LYS:CE	2.16	0.49
2:s:600:TYR:CZ	2:s:602:ILE:HA	2.48	0.49
2:s:727:TRP:CH2	4:S:27:PRO:CB	2.95	0.49
2:t:156:VAL:HG23	2:t:219:PHE:HA	1.93	0.49
2:v:715:THR:HG21	2:v:772:GLU:HB3	1.94	0.49
2:x:708:VAL:HG13	2:x:778:ILE:HG23	1.94	0.49
4:P:134:PHE:N	4:P:171:CYS:SG	2.86	0.49
4:V:89:SER:OG	4:V:90:THR:N	2.46	0.49
1:c:13:LEU:HD21	1:c:64:TRP:HB3	1.94	0.49
1:i:84:ARG:C	1:i:86:VAL:N	2.68	0.49
2:t:450:ARG:HD2	2:t:501:PHE:O	2.12	0.49
2:v:167:VAL:HB	2:v:175:ALA:HB3	1.94	0.49
2:v:176:LYS:HZ3	2:v:178:LYS:CD	2.25	0.49
2:w:600:TYR:CZ	2:w:602:ILE:HA	2.48	0.49
2:x:60:LEU:HD11	2:x:80:VAL:HG11	1.93	0.49
3:D:95:MET:O	3:D:98:ILE:HG22	2.12	0.49
1:a:88:PHE:CD1	1:c:99:LEU:HB3	2.48	0.49
1:g:88:PHE:CD1	1:i:99:LEU:HB3	2.48	0.49
1:i:86:VAL:HG13	1:i:86:VAL:O	2.12	0.49
1:i:93:ILE:CG1	2:u:638:GLY:C	2.86	0.49
2:s:460:PHE:HE1	2:s:471:HIS:HB2	1.78	0.49
2:u:176:LYS:HZ3	2:u:178:LYS:CD	2.26	0.49
2:u:278:ASP:OD2	3:B:108:ARG:HG2	2.13	0.49
2:u:450:ARG:HD2	2:u:501:PHE:O	2.12	0.49
2:u:727:TRP:HZ2	4:W:27:PRO:HB2	1.77	0.49
2:x:86:ILE:C	2:x:98:VAL:HG11	2.30	0.49
2:x:450:ARG:HD2	2:x:501:PHE:O	2.12	0.49
4:O:65:GLU:O	4:O:66:GLY:C	2.56	0.49
4:Q:65:GLU:O	4:Q:66:GLY:C	2.55	0.49
4:R:89:SER:OG	4:R:90:THR:N	2.46	0.49
4:R:129:GLU:O	4:R:129:GLU:HG2	2.13	0.49
4:R:134:PHE:N	4:R:171:CYS:SG	2.86	0.49
4:X:89:SER:OG	4:X:90:THR:N	2.46	0.49
1:f:46:ILE:HG22	1:f:52:PHE:CE2	2.46	0.48
1:j:56:THR:HG23	4:T:7:ASN:OD1	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:277:ALA:HB1	3:C:100:ARG:O	2.13	0.48
2:v:113:ARG:HD3	2:v:501:PHE:CD1	2.48	0.48
2:v:278:ASP:OD2	3:A:108:ARG:HG2	2.12	0.48
2:x:600:TYR:CZ	2:x:602:ILE:HA	2.48	0.48
4:T:48:ASN:O	4:T:51:ASN:HB3	2.13	0.48
4:V:48:ASN:O	4:V:51:ASN:HB3	2.13	0.48
4:X:134:PHE:N	4:X:171:CYS:SG	2.86	0.48
1:g:56:THR:HG23	4:V:7:ASN:OD1	2.13	0.48
1:r:86:VAL:HG13	1:r:86:VAL:O	2.13	0.48
2:s:708:VAL:HG13	2:s:778:ILE:HG23	1.94	0.48
2:u:277:ALA:CA	3:B:100:ARG:HG3	2.39	0.48
2:w:450:ARG:HD2	2:w:501:PHE:O	2.12	0.48
2:w:708:VAL:HG13	2:w:778:ILE:HG23	1.94	0.48
2:x:114:ASN:HA	2:x:450:ARG:HH12	1.77	0.48
4:N:81:SER:OG	4:N:82:ASP:N	2.46	0.48
4:R:48:ASN:O	4:R:51:ASN:HB3	2.13	0.48
1:r:31:PHE:CD1	1:r:79:THR:HA	2.49	0.48
2:t:254:PHE:CE2	3:D:65:ALA:HB2	2.44	0.48
2:t:708:VAL:HG13	2:t:778:ILE:HG23	1.94	0.48
2:u:727:TRP:CB	4:V:36:ALA:CB	2.84	0.48
2:v:357:ARG:NH2	2:v:371:THR:HB	2.28	0.48
2:x:145:ASN:O	2:x:145:ASN:CG	2.54	0.48
3:C:40:GLU:HA	3:C:43:ARG:HH21	1.77	0.48
4:Q:182:ASN:OD1	4:Q:185:ASP:N	2.45	0.48
4:R:153:ALA:HB3	4:R:156:VAL:HG12	1.93	0.48
4:T:153:ALA:HB3	4:T:156:VAL:HG12	1.93	0.48
4:V:81:SER:OG	4:V:82:ASP:N	2.45	0.48
4:X:48:ASN:O	4:X:51:ASN:HB3	2.13	0.48
1:c:31:PHE:CD1	1:c:79:THR:HA	2.49	0.48
1:k:50:TYR:HB3	1:k:60:LEU:HG	1.96	0.48
1:m:88:PHE:CD1	1:o:99:LEU:HB3	2.48	0.48
1:r:46:ILE:HA	1:r:50:TYR:CE1	2.49	0.48
1:r:46:ILE:HG22	1:r:52:PHE:CE2	2.48	0.48
2:s:281:TYR:CD1	2:s:333:GLY:HA3	2.44	0.48
2:u:113:ARG:HD3	2:u:501:PHE:CD1	2.48	0.48
2:u:165:LEU:HG	2:u:243:LEU:HD22	1.95	0.48
2:v:450:ARG:HD2	2:v:501:PHE:O	2.12	0.48
4:X:81:SER:OG	4:X:82:ASP:N	2.46	0.48
1:o:31:PHE:CD1	1:o:79:THR:HA	2.49	0.48
2:s:19:PRO:HG3	2:t:711:GLU:HG3	1.96	0.48
2:s:146:TYR:HE1	2:s:148:PRO:HA	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:277:ALA:HB1	3:D:100:ARG:O	2.12	0.48
2:s:361:LEU:HA	2:s:361:LEU:HD12	1.67	0.48
2:t:146:TYR:HE1	2:t:148:PRO:HA	1.78	0.48
2:t:165:LEU:HG	2:t:243:LEU:HD22	1.95	0.48
2:x:300:GLU:HG2	2:x:340:TRP:CZ2	2.47	0.48
2:x:406:ALA:HB1	2:x:413:LEU:HD11	1.96	0.48
2:x:460:PHE:HE1	2:x:471:HIS:HB2	1.79	0.48
4:M:182:ASN:OD1	4:M:185:ASP:N	2.45	0.48
4:P:98:ASN:ND2	4:Q:129:GLU:HA	2.24	0.48
4:T:82:ASP:N	4:T:82:ASP:OD1	2.44	0.48
4:V:168:ARG:HH11	4:V:172:MET:CE	2.24	0.48
1:h:50:TYR:HB3	1:h:60:LEU:HG	1.96	0.48
1:k:94:LEU:HD11	2:t:741:LEU:HD21	1.96	0.48
1:m:27:LEU:HD13	1:m:27:LEU:HA	1.57	0.48
1:m:56:THR:HG23	4:R:7:ASN:OD1	2.13	0.48
2:u:715:THR:HG21	2:u:772:GLU:HB3	1.94	0.48
2:w:562:TYR:CE1	2:w:575:ARG:HD3	2.49	0.48
2:w:727:TRP:HZ2	4:O:27:PRO:HB2	1.78	0.48
4:M:178:TYR:CZ	4:X:94:SER:O	2.66	0.48
4:P:129:GLU:HG2	4:P:129:GLU:O	2.14	0.48
1:c:93:ILE:CG1	2:w:638:GLY:C	2.87	0.48
1:i:46:ILE:HG22	1:i:52:PHE:CE2	2.47	0.48
2:s:172:LYS:HB3	2:s:172:LYS:HE2	1.64	0.48
2:s:200:LEU:HD23	2:s:200:LEU:H	1.76	0.48
2:s:406:ALA:HB1	2:s:413:LEU:HD11	1.96	0.48
2:t:562:TYR:CE1	2:t:575:ARG:HD3	2.49	0.48
2:v:600:TYR:CZ	2:v:602:ILE:HA	2.48	0.48
2:w:406:ALA:HB1	2:w:413:LEU:HD11	1.96	0.48
2:w:460:PHE:HE1	2:w:471:HIS:HB2	1.79	0.48
4:N:94:SER:O	4:O:178:TYR:CZ	2.67	0.48
4:T:81:SER:OG	4:T:82:ASP:N	2.46	0.48
1:l:13:LEU:HD21	1:l:64:TRP:HB3	1.94	0.48
1:l:84:ARG:C	1:l:86:VAL:N	2.67	0.48
2:t:113:ARG:HD3	2:t:501:PHE:CD1	2.48	0.48
2:u:150:GLN:OE1	2:u:224:ALA:HB2	2.11	0.48
2:v:150:GLN:CB	2:v:224:ALA:HB1	2.27	0.48
2:v:165:LEU:HG	2:v:243:LEU:HD22	1.95	0.48
2:v:460:PHE:HE1	2:v:471:HIS:HB2	1.79	0.48
2:w:357:ARG:NH2	2:w:371:THR:HB	2.28	0.48
4:N:89:SER:OG	4:N:90:THR:N	2.46	0.48
4:W:2:ARG:HH11	4:W:124:LEU:CD2	2.17	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:129:GLU:HG2	4:X:129:GLU:O	2.13	0.48
1:c:86:VAL:O	1:c:86:VAL:HG13	2.13	0.48
1:f:31:PHE:CD1	1:f:79:THR:HA	2.49	0.48
1:h:44:LEU:H	1:h:44:LEU:HD22	1.79	0.48
1:j:62:LYS:HD2	1:j:62:LYS:HA	1.70	0.48
1:k:44:LEU:H	1:k:44:LEU:HD22	1.79	0.48
1:m:23:PRO:CB	4:Q:79:VAL:HG11	2.44	0.48
1:r:46:ILE:HG22	1:r:52:PHE:HE2	1.79	0.48
2:s:450:ARG:HD2	2:s:501:PHE:O	2.12	0.48
2:s:562:TYR:CE1	2:s:575:ARG:HD3	2.48	0.48
2:t:150:GLN:OE1	2:t:224:ALA:HB2	2.11	0.48
2:v:562:TYR:CE1	2:v:575:ARG:HD3	2.49	0.48
4:P:144:ARG:HA	4:P:160:LEU:HD23	1.96	0.48
2:s:165:LEU:HG	2:s:243:LEU:HD22	1.95	0.48
2:u:287:GLU:H	2:u:287:GLU:HG3	1.40	0.48
2:u:600:TYR:CZ	2:u:602:ILE:HA	2.48	0.48
2:v:277:ALA:HB1	3:A:100:ARG:O	2.14	0.48
2:w:281:TYR:CD1	2:w:333:GLY:HA3	2.44	0.48
2:w:356:ASN:ND2	3:A:86:GLY:O	2.47	0.48
4:M:65:GLU:O	4:M:66:GLY:C	2.56	0.48
4:P:48:ASN:O	4:P:51:ASN:HB3	2.13	0.48
4:Q:2:ARG:HH11	4:Q:124:LEU:CD2	2.17	0.48
4:W:89:SER:H	4:W:94:SER:HB2	1.77	0.48
1:c:46:ILE:HG22	1:c:52:PHE:CE2	2.49	0.47
1:e:44:LEU:H	1:e:44:LEU:HD22	1.79	0.47
1:i:31:PHE:CD1	1:i:79:THR:HA	2.49	0.47
1:l:31:PHE:CD1	1:l:79:THR:HA	2.49	0.47
2:u:708:VAL:HG13	2:u:778:ILE:HG23	1.94	0.47
2:v:19:PRO:HG3	2:w:711:GLU:HG3	1.96	0.47
2:v:277:ALA:CA	3:A:100:ARG:HG3	2.41	0.47
2:w:388:ASP:OD2	3:A:82:ARG:HB3	2.13	0.47
4:M:89:SER:H	4:M:94:SER:HB2	1.77	0.47
4:U:65:GLU:O	4:U:66:GLY:C	2.56	0.47
1:a:94:LEU:HG	2:w:741:LEU:HD23	1.96	0.47
1:c:106:THR:HA	1:c:109:VAL:HG12	1.96	0.47
1:i:51:ARG:C	1:i:53:ALA:H	2.23	0.47
2:s:175:ALA:HB2	2:s:204:MET:SD	2.54	0.47
2:s:463:PRO:HA	2:s:468:THR:HG22	1.96	0.47
2:t:175:ALA:HB2	2:t:204:MET:SD	2.55	0.47
2:u:175:ALA:HB2	2:u:204:MET:SD	2.55	0.47
4:M:10:THR:HB	4:M:13:GLU:CB	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:40:ALA:O	4:N:43:ALA:HB3	2.15	0.47
4:S:10:THR:HB	4:S:13:GLU:CB	2.44	0.47
4:S:65:GLU:O	4:S:66:GLY:C	2.56	0.47
4:T:89:SER:OG	4:T:90:THR:N	2.46	0.47
1:l:27:LEU:HD12	1:l:27:LEU:HA	1.74	0.47
2:t:19:PRO:HG3	2:u:711:GLU:HG3	1.96	0.47
2:t:460:PHE:HE1	2:t:471:HIS:HB2	1.79	0.47
2:u:562:TYR:CE1	2:u:575:ARG:HD3	2.49	0.47
2:v:708:VAL:HG13	2:v:778:ILE:HG23	1.94	0.47
2:w:714:GLY:CA	2:w:774:THR:CG2	2.72	0.47
2:x:175:ALA:HB2	2:x:204:MET:SD	2.55	0.47
4:N:48:ASN:O	4:N:51:ASN:HB3	2.13	0.47
4:O:182:ASN:OD1	4:O:185:ASP:N	2.45	0.47
4:P:89:SER:OG	4:P:90:THR:N	2.46	0.47
4:R:172:MET:O	4:R:176:MET:HG2	2.14	0.47
4:T:172:MET:O	4:T:176:MET:HG2	2.15	0.47
4:X:144:ARG:HA	4:X:160:LEU:HD23	1.96	0.47
1:f:106:THR:HA	1:f:109:VAL:HG12	1.96	0.47
1:n:44:LEU:H	1:n:44:LEU:HD22	1.79	0.47
2:s:254:PHE:HE1	3:D:112:MET:SD	2.37	0.47
2:t:463:PRO:HA	2:t:468:THR:HG22	1.96	0.47
2:u:176:LYS:HE2	2:u:178:LYS:HE3	1.96	0.47
2:v:176:LYS:HE2	2:v:178:LYS:HE3	1.96	0.47
4:M:2:ARG:HH11	4:M:124:LEU:CD2	2.17	0.47
4:O:1:MET:SD	4:P:15:SER:OG	2.66	0.47
4:P:40:ALA:O	4:P:43:ALA:HB3	2.15	0.47
1:g:94:LEU:HG	2:u:741:LEU:HD23	1.95	0.47
1:h:22:ILE:N	1:h:56:THR:O	2.47	0.47
1:o:9:LEU:HD21	1:o:23:PRO:CG	2.41	0.47
1:q:44:LEU:H	1:q:44:LEU:HD22	1.79	0.47
2:s:509:GLU:HB2	2:s:511:PHE:CE1	2.50	0.47
2:s:581:ASN:HD22	2:s:581:ASN:HA	1.56	0.47
2:u:277:ALA:HB1	3:B:100:ARG:O	2.13	0.47
2:v:86:ILE:C	2:v:98:VAL:HG11	2.30	0.47
2:v:146:TYR:CE1	2:v:148:PRO:HA	2.50	0.47
2:v:175:ALA:HB2	2:v:204:MET:SD	2.55	0.47
2:v:242:GLN:HE22	3:A:122:GLN:CD	2.23	0.47
2:v:714:GLY:CA	2:v:774:THR:CG2	2.72	0.47
1:r:106:THR:HA	1:r:109:VAL:HG12	1.96	0.47
2:t:727:TRP:HZ2	4:U:27:PRO:HB2	1.80	0.47
2:u:177:TYR:HB2	2:u:203:GLN:HE22	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:204:MET:HB3	2:v:211:TRP:CZ3	2.50	0.47
2:v:406:ALA:HB1	2:v:413:LEU:HD11	1.96	0.47
2:w:303:VAL:CG2	2:w:378:TYR:OH	2.63	0.47
2:x:183:SER:O	3:F:42:MET:HE2	2.14	0.47
2:x:562:TYR:CE1	2:x:575:ARG:HD3	2.48	0.47
4:N:129:GLU:HG2	4:N:129:GLU:O	2.13	0.47
4:X:40:ALA:O	4:X:43:ALA:HB3	2.15	0.47
1:b:44:LEU:HD22	1:b:44:LEU:H	1.79	0.47
1:f:93:ILE:HB	2:v:638:GLY:C	2.29	0.47
1:f:93:ILE:CG1	2:v:638:GLY:C	2.87	0.47
1:h:12:GLN:H	1:h:12:GLN:HG2	1.35	0.47
1:i:106:THR:HA	1:i:109:VAL:HG12	1.96	0.47
1:j:29:ARG:O	1:j:30:LYS:C	2.58	0.47
1:o:106:THR:HA	1:o:109:VAL:HG12	1.96	0.47
2:s:118:MET:HE3	2:s:118:MET:HB2	1.74	0.47
2:s:146:TYR:CE1	2:s:148:PRO:HA	2.50	0.47
2:s:188:VAL:HG21	3:E:46:ASN:OD1	2.12	0.47
2:s:204:MET:HB3	2:s:211:TRP:CZ3	2.50	0.47
2:s:700:ARG:HD3	2:s:760:ASN:OD1	2.15	0.47
2:t:128:VAL:HG21	2:t:351:VAL:CG2	2.34	0.47
2:t:163:ARG:HD3	2:t:163:ARG:HA	1.50	0.47
2:t:176:LYS:HZ3	2:t:178:LYS:HE3	1.68	0.47
2:t:254:PHE:HE1	3:C:112:MET:SD	2.37	0.47
2:t:357:ARG:HD2	2:t:368:LEU:HD13	1.97	0.47
2:t:396:SER:HB2	3:C:91:GLU:OE1	2.13	0.47
2:t:440:THR:HG23	2:t:441:THR:HG22	1.97	0.47
2:u:19:PRO:CG	2:v:711:GLU:CG	2.93	0.47
2:u:146:TYR:CE1	2:u:148:PRO:HA	2.50	0.47
2:w:19:PRO:HG3	2:x:711:GLU:HG3	1.96	0.47
2:w:175:ALA:HB2	2:w:204:MET:SD	2.55	0.47
2:x:52:ASN:HD22	2:x:52:ASN:HA	1.54	0.47
2:x:356:ASN:ND2	3:F:86:GLY:O	2.48	0.47
2:x:463:PRO:HA	2:x:468:THR:HG22	1.96	0.47
2:x:509:GLU:HB2	2:x:511:PHE:CE1	2.50	0.47
3:E:88:SER:HB2	3:E:90:LEU:HG	1.97	0.47
4:R:6:MET:HB3	4:R:6:MET:HE3	1.71	0.47
4:R:40:ALA:O	4:R:43:ALA:HB3	2.15	0.47
4:R:94:SER:O	4:S:178:TYR:CZ	2.68	0.47
4:S:182:ASN:OD1	4:S:185:ASP:CB	2.62	0.47
4:T:40:ALA:O	4:T:43:ALA:HB3	2.15	0.47
4:T:129:GLU:O	4:T:129:GLU:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:40:ALA:O	4:V:43:ALA:HB3	2.15	0.47
4:V:94:SER:O	4:W:178:TYR:CZ	2.68	0.47
4:X:172:MET:O	4:X:176:MET:HG2	2.15	0.47
1:b:50:TYR:HB3	1:b:60:LEU:HG	1.96	0.47
1:c:9:LEU:HD21	1:c:23:PRO:CG	2.41	0.47
1:f:51:ARG:C	1:f:53:ALA:H	2.22	0.47
1:m:104:ILE:O	1:m:105:GLN:C	2.56	0.47
2:s:711:GLU:CG	2:x:19:PRO:CG	2.93	0.47
2:t:509:GLU:HB2	2:t:511:PHE:CE1	2.50	0.47
2:u:211:TRP:HB2	2:u:222:VAL:HG13	1.97	0.47
2:u:700:ARG:HD3	2:u:760:ASN:OD1	2.15	0.47
2:v:177:TYR:HB2	2:v:203:GLN:HE22	1.80	0.47
2:v:284:TYR:HB2	2:v:291:TRP:CD2	2.50	0.47
2:x:700:ARG:HD3	2:x:760:ASN:OD1	2.15	0.47
3:A:119:ARG:HA	3:A:122:GLN:HG2	1.97	0.47
4:Q:10:THR:HB	4:Q:13:GLU:CB	2.45	0.47
1:b:22:ILE:N	1:b:56:THR:O	2.47	0.47
1:p:25:GLU:HB2	1:p:108:HIS:CE1	2.50	0.47
1:q:86:VAL:HG23	4:P:31:THR:HB	1.97	0.47
1:r:93:ILE:CD1	2:x:746:LEU:CA	2.66	0.47
2:t:177:TYR:HB2	2:t:203:GLN:HE22	1.80	0.47
2:u:460:PHE:HE1	2:u:471:HIS:HB2	1.79	0.47
2:u:463:PRO:HA	2:u:468:THR:HG22	1.96	0.47
2:u:509:GLU:HB2	2:u:511:PHE:CE1	2.50	0.47
2:v:727:TRP:CA	4:X:36:ALA:CB	2.92	0.47
2:w:727:TRP:CA	4:N:36:ALA:CB	2.92	0.47
2:x:746:LEU:H	2:x:746:LEU:HG	1.53	0.47
3:C:108:ARG:NH2	3:C:108:ARG:CB	2.77	0.47
4:N:125:ARG:HD3	4:N:129:GLU:OE2	2.15	0.47
4:N:172:MET:O	4:N:176:MET:HG2	2.15	0.47
4:O:182:ASN:OD1	4:O:185:ASP:CB	2.63	0.47
4:T:98:ASN:ND2	4:U:129:GLU:HA	2.28	0.47
4:U:10:THR:HB	4:U:13:GLU:CB	2.45	0.47
1:a:25:GLU:HB2	1:a:108:HIS:CE1	2.50	0.47
1:c:93:ILE:HB	2:w:638:GLY:C	2.29	0.47
1:g:55:ARG:HG2	4:V:5:ASP:OD1	2.15	0.47
1:l:93:ILE:CG1	2:t:638:GLY:C	2.87	0.47
2:s:239:TYR:CE2	3:D:129:LEU:HG	2.50	0.47
2:t:19:PRO:CG	2:u:711:GLU:CG	2.92	0.47
2:t:211:TRP:HB2	2:t:222:VAL:HG13	1.97	0.47
2:t:406:ALA:HB1	2:t:413:LEU:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:u:19:PRO:HG3	2:v:711:GLU:HG3	1.96	0.47
2:u:406:ALA:HB1	2:u:413:LEU:HD11	1.96	0.47
2:u:440:THR:HG23	2:u:441:THR:HG22	1.97	0.47
2:u:495:TYR:HD1	2:u:495:TYR:HA	1.65	0.47
2:v:147:ASN:HD22	2:v:150:GLN:CD	2.23	0.47
2:w:146:TYR:CE1	2:w:148:PRO:HA	2.50	0.47
2:w:591:ARG:HE	2:w:591:ARG:HB2	1.19	0.47
4:N:144:ARG:HA	4:N:160:LEU:HD23	1.97	0.47
4:O:53:GLN:HE21	4:O:53:GLN:HB3	1.49	0.47
1:a:104:ILE:O	1:a:105:GLN:C	2.56	0.46
1:g:25:GLU:HB2	1:g:108:HIS:CE1	2.50	0.46
2:s:711:GLU:HG3	2:x:19:PRO:HG3	1.96	0.46
2:t:204:MET:HB3	2:t:211:TRP:CZ3	2.50	0.46
2:u:204:MET:HB3	2:u:211:TRP:CZ3	2.50	0.46
2:v:440:THR:HG23	2:v:441:THR:HG22	1.97	0.46
2:w:145:ASN:O	2:w:145:ASN:CG	2.54	0.46
2:w:204:MET:HB3	2:w:211:TRP:CZ3	2.50	0.46
2:w:463:PRO:HA	2:w:468:THR:HG22	1.96	0.46
2:x:204:MET:HB3	2:x:211:TRP:CZ3	2.50	0.46
2:x:361:LEU:HD12	2:x:361:LEU:HA	1.67	0.46
3:B:126:ALA:CA	3:B:129:LEU:HG	2.44	0.46
4:V:172:MET:O	4:V:176:MET:HG2	2.15	0.46
1:j:55:ARG:HG2	4:T:5:ASP:OD1	2.15	0.46
1:n:50:TYR:HB3	1:n:60:LEU:HG	1.96	0.46
1:o:84:ARG:C	1:o:86:VAL:N	2.67	0.46
1:p:104:ILE:O	1:p:105:GLN:C	2.56	0.46
1:q:34:VAL:HA	1:q:74:GLU:O	2.15	0.46
1:q:50:TYR:HB3	1:q:60:LEU:HG	1.96	0.46
1:r:93:ILE:HB	2:x:638:GLY:C	2.32	0.46
2:s:303:VAL:CG2	2:s:378:TYR:OH	2.63	0.46
2:t:60:LEU:HD12	2:t:60:LEU:HA	1.62	0.46
2:t:242:GLN:HE22	3:C:122:GLN:CD	2.23	0.46
2:u:567:ASN:HD22	2:u:567:ASN:HA	1.53	0.46
2:v:19:PRO:CG	2:w:711:GLU:CG	2.93	0.46
2:v:150:GLN:OE1	2:v:224:ALA:HB2	2.11	0.46
2:v:211:TRP:HB2	2:v:222:VAL:HG13	1.97	0.46
2:x:146:TYR:CE1	2:x:148:PRO:HA	2.50	0.46
2:x:147:ASN:HD22	2:x:150:GLN:CD	2.24	0.46
2:x:303:VAL:CG2	2:x:378:TYR:OH	2.63	0.46
3:C:119:ARG:HA	3:C:122:GLN:HG2	1.97	0.46
4:N:136:TYR:OH	4:N:163:GLU:OE2	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:172:MET:O	4:P:176:MET:HG2	2.15	0.46
4:U:151:PHE:HD2	4:U:153:ALA:HB2	1.81	0.46
4:V:82:ASP:N	4:V:82:ASP:OD1	2.44	0.46
4:V:144:ARG:HA	4:V:160:LEU:HD23	1.96	0.46
1:b:27:LEU:HA	1:b:27:LEU:HD13	1.71	0.46
1:l:46:ILE:HG22	1:l:52:PHE:CE2	2.49	0.46
2:t:303:VAL:CG2	2:t:378:TYR:OH	2.63	0.46
2:u:284:TYR:HB2	2:u:291:TRP:CD2	2.50	0.46
2:u:357:ARG:HD2	2:u:368:LEU:HD13	1.97	0.46
2:w:509:GLU:HB2	2:w:511:PHE:CE1	2.50	0.46
2:x:300:GLU:HG2	2:x:340:TRP:HZ2	1.81	0.46
2:x:727:TRP:HZ2	4:Q:27:PRO:HB2	1.79	0.46
4:N:59:TRP:HB2	4:N:62:ASN:OD1	2.16	0.46
4:O:6:MET:CE	4:P:6:MET:HE2	2.44	0.46
4:P:136:TYR:OH	4:P:163:GLU:OE2	2.33	0.46
1:c:93:ILE:HG13	2:w:638:GLY:N	2.31	0.46
1:d:25:GLU:HB2	1:d:108:HIS:CE1	2.50	0.46
1:k:38:GLY:HA3	1:k:71:THR:H	1.80	0.46
1:l:6:LYS:H	1:l:6:LYS:HG2	1.52	0.46
1:n:34:VAL:HA	1:n:74:GLU:O	2.15	0.46
1:p:29:ARG:O	1:p:30:LYS:C	2.58	0.46
2:s:147:ASN:HD22	2:s:150:GLN:CD	2.24	0.46
2:t:185:PRO:HD2	3:D:42:MET:HE1	1.84	0.46
2:t:284:TYR:HB2	2:t:291:TRP:CD2	2.50	0.46
2:v:48:LEU:HD11	2:v:545:PHE:HE1	1.81	0.46
2:v:239:TYR:CD2	3:A:129:LEU:HD22	2.45	0.46
2:w:147:ASN:HD22	2:w:150:GLN:CD	2.24	0.46
4:M:20:ILE:HD11	4:M:47:LEU:HD13	1.98	0.46
4:U:182:ASN:OD1	4:U:185:ASP:CB	2.63	0.46
1:d:23:PRO:CB	4:W:79:VAL:HG11	2.45	0.46
1:e:50:TYR:HB3	1:e:60:LEU:HG	1.96	0.46
1:h:34:VAL:HA	1:h:74:GLU:O	2.15	0.46
1:l:106:THR:HA	1:l:109:VAL:HG12	1.96	0.46
2:s:177:TYR:HB2	2:s:203:GLN:HE22	1.80	0.46
2:t:176:LYS:HE2	2:t:178:LYS:HE3	1.96	0.46
2:t:700:ARG:HD3	2:t:760:ASN:OD1	2.15	0.46
2:u:147:ASN:HD22	2:u:150:GLN:CD	2.23	0.46
2:u:727:TRP:CA	4:V:36:ALA:CB	2.93	0.46
2:v:184:GLN:O	2:v:185:PRO:C	2.57	0.46
2:w:143:LEU:HD23	2:w:143:LEU:HA	1.70	0.46
2:w:581:ASN:HD22	2:w:581:ASN:HA	1.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:w:700:ARG:HD3	2:w:760:ASN:OD1	2.15	0.46
2:x:118:MET:HE3	2:x:118:MET:HB2	1.74	0.46
2:x:727:TRP:CA	4:P:36:ALA:CB	2.94	0.46
4:M:151:PHE:HD2	4:M:153:ALA:HB2	1.81	0.46
4:S:20:ILE:HD11	4:S:47:LEU:HD13	1.97	0.46
4:U:182:ASN:OD1	4:U:182:ASN:C	2.59	0.46
4:X:125:ARG:HD3	4:X:129:GLU:OE2	2.15	0.46
1:a:56:THR:HG23	4:N:7:ASN:OD1	2.15	0.46
1:b:34:VAL:HA	1:b:74:GLU:O	2.15	0.46
1:d:29:ARG:O	1:d:30:LYS:C	2.58	0.46
1:d:53:ALA:HB1	4:V:99:ARG:NH2	2.31	0.46
1:d:104:ILE:O	1:d:105:GLN:C	2.56	0.46
1:e:22:ILE:HG12	1:e:56:THR:HA	1.98	0.46
1:e:34:VAL:HA	1:e:74:GLU:O	2.15	0.46
1:e:90:ASP:HB2	4:W:4:TYR:HH	1.78	0.46
1:f:9:LEU:HD21	1:f:23:PRO:CG	2.41	0.46
1:j:18:ARG:NH2	1:j:63:ALA:HB2	2.31	0.46
1:q:22:ILE:HG12	1:q:56:THR:HA	1.98	0.46
2:s:284:TYR:HB2	2:s:291:TRP:CD2	2.50	0.46
2:s:300:GLU:HG2	2:s:340:TRP:HZ2	1.81	0.46
2:t:146:TYR:CE1	2:t:148:PRO:HA	2.50	0.46
2:t:296:GLY:H	2:t:333:GLY:HA2	1.81	0.46
2:u:161:TYR:HB3	2:u:162:GLY:H	1.61	0.46
2:v:428:GLY:O	2:v:429:THR:C	2.58	0.46
2:v:509:GLU:HB2	2:v:511:PHE:CE1	2.50	0.46
2:v:646:PRO:C	2:v:648:ALA:N	2.74	0.46
2:w:254:PHE:CE2	3:A:65:ALA:HB2	2.42	0.46
2:w:357:ARG:HD2	2:w:368:LEU:HD13	1.97	0.46
2:x:278:ASP:OD2	3:E:108:ARG:HG2	2.15	0.46
2:x:428:GLY:O	2:x:429:THR:C	2.58	0.46
3:B:119:ARG:NH1	3:C:61:GLU:OE1	2.49	0.46
4:N:98:ASN:ND2	4:O:129:GLU:HA	2.29	0.46
4:N:168:ARG:HH11	4:N:172:MET:CE	2.24	0.46
4:V:59:TRP:HB2	4:V:62:ASN:OD1	2.16	0.46
1:e:22:ILE:N	1:e:56:THR:O	2.47	0.46
1:f:6:LYS:H	1:f:6:LYS:HG2	1.51	0.46
2:s:177:TYR:HE2	2:s:196:LEU:CD2	2.29	0.46
2:s:202:LYS:HB3	2:s:202:LYS:HE2	1.64	0.46
2:t:428:GLY:O	2:t:429:THR:C	2.58	0.46
2:t:567:ASN:HD22	2:t:567:ASN:HA	1.53	0.46
2:u:150:GLN:OE1	2:u:224:ALA:HB3	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:u:296:GLY:H	2:u:333:GLY:HA2	1.81	0.46
2:v:150:GLN:OE1	2:v:224:ALA:HB3	2.13	0.46
2:v:463:PRO:HA	2:v:468:THR:HG22	1.96	0.46
2:v:700:ARG:HD3	2:v:760:ASN:OD1	2.15	0.46
2:w:176:LYS:HE2	2:w:178:LYS:HE3	1.96	0.46
4:M:182:ASN:OD1	4:M:182:ASN:C	2.59	0.46
4:P:59:TRP:HB2	4:P:62:ASN:OD1	2.16	0.46
4:R:14:LEU:HD11	4:R:30:SER:O	2.16	0.46
4:R:136:TYR:OH	4:R:163:GLU:OE2	2.33	0.46
4:T:96:TYR:HB3	4:T:103:VAL:HG13	1.98	0.46
1:b:22:ILE:HG12	1:b:56:THR:HA	1.98	0.46
1:d:56:THR:HG23	4:X:7:ASN:OD1	2.15	0.46
1:h:86:VAL:HG23	4:V:31:THR:HB	1.98	0.46
1:j:25:GLU:HB2	1:j:108:HIS:CE1	2.50	0.46
1:k:79:THR:HB	1:k:109:VAL:HG23	1.98	0.46
1:q:38:GLY:HA3	1:q:71:THR:H	1.80	0.46
1:r:46:ILE:HD11	2:x:610:ASP:HB3	1.95	0.46
2:s:277:ALA:CA	3:D:100:ARG:HG3	2.40	0.46
2:s:727:TRP:HZ2	4:S:27:PRO:HB2	1.80	0.46
2:v:145:ASN:O	2:v:145:ASN:CG	2.54	0.46
2:v:296:GLY:H	2:v:333:GLY:HA2	1.81	0.46
2:x:60:LEU:HA	2:x:60:LEU:HD12	1.62	0.46
3:A:126:ALA:HA	3:A:129:LEU:CG	2.45	0.46
4:X:14:LEU:HD11	4:X:30:SER:O	2.16	0.46
4:X:59:TRP:HB2	4:X:62:ASN:OD1	2.16	0.46
1:k:34:VAL:HA	1:k:74:GLU:O	2.15	0.46
1:m:25:GLU:HB2	1:m:108:HIS:CE1	2.50	0.46
2:s:150:GLN:OE1	2:s:224:ALA:HB2	2.11	0.46
2:s:161:TYR:CZ	3:E:46:ASN:HB3	2.51	0.46
2:s:388:ASP:OD1	3:E:83:ALA:HB2	2.16	0.46
2:t:184:GLN:CA	3:D:42:MET:HE1	2.35	0.46
2:u:48:LEU:HD11	2:u:545:PHE:HE1	1.81	0.46
2:u:60:LEU:HA	2:u:60:LEU:HD12	1.62	0.46
2:v:357:ARG:HD2	2:v:368:LEU:HD13	1.97	0.46
2:w:177:TYR:HB2	2:w:203:GLN:HE22	1.80	0.46
2:w:440:THR:HG23	2:w:441:THR:HG22	1.97	0.46
2:x:184:GLN:O	2:x:185:PRO:C	2.57	0.46
2:x:357:ARG:HD2	2:x:368:LEU:HD13	1.97	0.46
3:E:74:LYS:HA	3:E:106:PHE:CE2	2.51	0.46
4:O:151:PHE:HD2	4:O:153:ALA:HB2	1.81	0.46
4:R:96:TYR:HB3	4:R:103:VAL:HG13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:T:59:TRP:HB2	4:T:62:ASN:OD1	2.16	0.46
4:T:136:TYR:OH	4:T:163:GLU:OE2	2.33	0.46
4:T:170:LEU:HD12	4:T:170:LEU:HA	1.62	0.46
4:V:6:MET:HE3	4:V:6:MET:HB3	1.72	0.46
4:V:14:LEU:HD11	4:V:30:SER:O	2.16	0.46
4:V:96:TYR:HB3	4:V:103:VAL:HG13	1.98	0.46
4:W:20:ILE:HD11	4:W:47:LEU:HD13	1.98	0.46
4:X:96:TYR:HB3	4:X:103:VAL:HG13	1.98	0.46
1:a:18:ARG:NH2	1:a:63:ALA:HB2	2.31	0.46
1:h:22:ILE:HG12	1:h:56:THR:HA	1.98	0.46
1:h:38:GLY:HA3	1:h:71:THR:H	1.80	0.46
1:j:23:PRO:CB	4:S:79:VAL:HG11	2.45	0.46
1:p:94:LEU:HG	2:x:741:LEU:HD23	1.97	0.46
1:r:93:ILE:CG1	2:x:638:GLY:C	2.89	0.46
2:s:357:ARG:HD2	2:s:368:LEU:HD13	1.97	0.46
2:s:432:SER:CB	3:D:95:MET:HE1	2.44	0.46
2:t:147:ASN:HD22	2:t:150:GLN:CD	2.23	0.46
2:u:143:LEU:HD23	2:u:143:LEU:HA	1.70	0.46
2:w:48:LEU:HD11	2:w:545:PHE:HE1	1.81	0.46
2:x:177:TYR:HB2	2:x:203:GLN:HE22	1.80	0.46
2:x:211:TRP:HB2	2:x:222:VAL:HG13	1.97	0.46
3:D:74:LYS:HA	3:D:106:PHE:CE2	2.51	0.46
4:N:50:ILE:HG21	4:N:142:ALA:HB2	1.98	0.46
4:O:6:MET:HE3	4:P:8:VAL:HG11	1.98	0.46
4:O:182:ASN:OD1	4:O:182:ASN:C	2.59	0.46
4:V:136:TYR:OH	4:V:163:GLU:OE2	2.33	0.46
4:W:65:GLU:O	4:W:66:GLY:C	2.55	0.46
1:b:86:VAL:HG23	4:N:31:THR:HB	1.98	0.45
1:g:18:ARG:NH2	1:g:63:ALA:HB2	2.31	0.45
1:g:104:ILE:O	1:g:105:GLN:C	2.56	0.45
2:u:176:LYS:HZ1	2:u:178:LYS:CE	2.19	0.45
2:v:177:TYR:HE2	2:v:196:LEU:CD2	2.29	0.45
2:w:296:GLY:H	2:w:333:GLY:HA2	1.81	0.45
2:w:567:ASN:HD22	2:w:567:ASN:HA	1.53	0.45
2:x:284:TYR:HB2	2:x:291:TRP:CD2	2.50	0.45
3:B:74:LYS:HA	3:B:106:PHE:CE2	2.51	0.45
4:M:1:MET:SD	4:N:15:SER:OG	2.66	0.45
4:W:52:ARG:HD3	4:X:132:GLU:OE2	2.16	0.45
1:b:38:GLY:HA3	1:b:71:THR:H	1.80	0.45
1:f:93:ILE:HG13	2:v:638:GLY:N	2.30	0.45
1:o:51:ARG:C	1:o:53:ALA:H	2.22	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:296:GLY:H	2:s:333:GLY:HA2	1.81	0.45
2:s:440:THR:HG23	2:s:441:THR:HG22	1.97	0.45
2:s:646:PRO:C	2:s:648:ALA:N	2.74	0.45
2:t:99:ARG:HH12	2:t:319:ASN:HD22	1.65	0.45
2:v:153:LEU:HD12	2:v:153:LEU:HA	1.66	0.45
2:v:308:MET:SD	2:v:343:PHE:CZ	3.10	0.45
2:v:567:ASN:HD22	2:v:567:ASN:HA	1.53	0.45
2:w:177:TYR:HE2	2:w:196:LEU:CD2	2.29	0.45
2:w:284:TYR:HB2	2:w:291:TRP:CD2	2.50	0.45
2:w:308:MET:SD	2:w:343:PHE:CZ	3.09	0.45
2:x:145:ASN:OD1	2:x:145:ASN:C	2.59	0.45
2:x:153:LEU:HD12	2:x:153:LEU:HA	1.66	0.45
4:O:52:ARG:HD3	4:P:132:GLU:OE2	2.17	0.45
4:P:14:LEU:HD11	4:P:30:SER:O	2.16	0.45
4:P:61:PHE:HE1	4:P:134:PHE:CE2	2.34	0.45
4:Q:6:MET:HA	4:Q:6:MET:CE	2.45	0.45
4:Q:151:PHE:HD2	4:Q:153:ALA:HB2	1.81	0.45
4:R:125:ARG:HD3	4:R:129:GLU:OE2	2.16	0.45
1:d:18:ARG:NH2	1:d:63:ALA:HB2	2.31	0.45
1:e:27:LEU:HD13	1:e:27:LEU:HA	1.71	0.45
1:e:38:GLY:HA3	1:e:71:THR:H	1.80	0.45
1:j:104:ILE:O	1:j:105:GLN:C	2.56	0.45
1:k:22:ILE:HG12	1:k:56:THR:HA	1.98	0.45
2:s:41:GLY:O	2:s:42:LEU:C	2.59	0.45
2:s:145:ASN:OD1	2:s:145:ASN:C	2.59	0.45
2:t:308:MET:SD	2:t:343:PHE:CZ	3.10	0.45
2:u:99:ARG:HH12	2:u:319:ASN:HD22	1.64	0.45
2:x:258:PRO:HA	2:x:259:PRO:HD3	1.85	0.45
2:x:308:MET:SD	2:x:343:PHE:CZ	3.10	0.45
3:C:119:ARG:HA	3:C:119:ARG:HD3	1.76	0.45
4:M:52:ARG:HD3	4:N:132:GLU:OE2	2.17	0.45
4:R:61:PHE:HE1	4:R:134:PHE:CE2	2.34	0.45
4:R:98:ASN:ND2	4:S:129:GLU:HA	2.28	0.45
4:T:14:LEU:HD11	4:T:30:SER:O	2.16	0.45
4:T:94:SER:O	4:U:178:TYR:CZ	2.70	0.45
4:W:182:ASN:OD1	4:W:182:ASN:C	2.59	0.45
4:X:6:MET:HE3	4:X:6:MET:HB3	1.72	0.45
1:a:55:ARG:HG2	4:N:5:ASP:OD1	2.16	0.45
1:f:32:VAL:HG13	1:f:52:PHE:CE1	2.52	0.45
1:j:86:VAL:HG21	1:j:101:VAL:HB	1.99	0.45
1:l:93:ILE:HB	2:t:638:GLY:C	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:93:ILE:HG13	2:t:638:GLY:N	2.32	0.45
1:m:18:ARG:NH2	1:m:63:ALA:HB2	2.31	0.45
1:m:86:VAL:HG21	1:m:101:VAL:HB	1.99	0.45
1:n:22:ILE:HG12	1:n:56:THR:HA	1.98	0.45
1:n:38:GLY:HA3	1:n:71:THR:H	1.80	0.45
1:o:32:VAL:HG13	1:o:52:PHE:CE1	2.51	0.45
1:p:18:ARG:NH2	1:p:63:ALA:HB2	2.31	0.45
1:q:95:ARG:O	1:q:96:ALA:C	2.59	0.45
1:r:84:ARG:C	1:r:86:VAL:N	2.67	0.45
2:s:19:PRO:CG	2:t:711:GLU:CG	2.93	0.45
2:s:99:ARG:HH12	2:s:319:ASN:HD22	1.65	0.45
2:s:211:TRP:HB2	2:s:222:VAL:HG13	1.97	0.45
2:s:308:MET:SD	2:s:343:PHE:CZ	3.10	0.45
2:s:495:TYR:HD1	2:s:495:TYR:HA	1.65	0.45
2:s:779:ILE:HG12	2:x:22:LEU:HD23	1.91	0.45
2:u:177:TYR:HE2	2:u:196:LEU:CD2	2.29	0.45
2:u:204:MET:C	2:u:211:TRP:HZ3	2.25	0.45
2:w:9:LYS:HE2	2:w:9:LYS:HB3	1.78	0.45
2:w:19:PRO:CG	2:x:711:GLU:CG	2.94	0.45
2:x:296:GLY:H	2:x:333:GLY:HA2	1.81	0.45
4:N:61:PHE:HE1	4:N:134:PHE:CE2	2.34	0.45
4:P:125:ARG:HD3	4:P:129:GLU:OE2	2.15	0.45
4:Q:182:ASN:OD1	4:Q:185:ASP:CB	2.63	0.45
4:S:151:PHE:HD2	4:S:153:ALA:HB2	1.81	0.45
4:X:136:TYR:OH	4:X:163:GLU:OE2	2.33	0.45
1:g:86:VAL:HG21	1:g:101:VAL:HB	1.99	0.45
1:l:51:ARG:C	1:l:53:ALA:H	2.25	0.45
1:q:79:THR:HB	1:q:109:VAL:HG23	1.98	0.45
2:s:142:ASN:CB	2:s:295:LEU:HD11	2.44	0.45
2:s:557:ILE:HD13	2:s:557:ILE:HA	1.87	0.45
2:t:145:ASN:O	2:t:145:ASN:CG	2.54	0.45
2:t:161:TYR:CZ	3:D:46:ASN:HB3	2.51	0.45
2:t:727:TRP:CB	4:T:36:ALA:CB	2.84	0.45
2:u:35:TRP:CH2	2:u:527:LYS:HD3	2.52	0.45
2:v:47:PRO:HG3	2:v:593:PHE:HA	1.99	0.45
2:w:727:TRP:CB	4:N:36:ALA:CB	2.82	0.45
4:Q:182:ASN:OD1	4:Q:182:ASN:C	2.59	0.45
4:T:61:PHE:HE1	4:T:134:PHE:CE2	2.34	0.45
1:g:23:PRO:CB	4:U:79:VAL:HG11	2.46	0.45
1:r:93:ILE:HG23	2:x:745:ARG:O	2.16	0.45
2:s:143:LEU:O	2:s:298:ASN:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:177:TYR:HE2	2:t:196:LEU:CD2	2.29	0.45
2:t:184:GLN:O	2:t:185:PRO:C	2.57	0.45
2:t:204:MET:C	2:t:211:TRP:HZ3	2.25	0.45
2:t:591:ARG:HE	2:t:591:ARG:HB2	1.19	0.45
2:u:303:VAL:CG2	2:u:378:TYR:OH	2.63	0.45
2:u:308:MET:SD	2:u:343:PHE:CZ	3.09	0.45
2:u:428:GLY:O	2:u:429:THR:C	2.58	0.45
2:v:35:TRP:CH2	2:v:527:LYS:HD3	2.52	0.45
2:v:151:ASP:N	2:v:151:ASP:OD1	2.50	0.45
2:w:428:GLY:O	2:w:429:THR:C	2.58	0.45
2:x:48:LEU:HD11	2:x:545:PHE:HE1	1.81	0.45
4:N:14:LEU:HD11	4:N:30:SER:O	2.15	0.45
4:Q:20:ILE:HD11	4:Q:47:LEU:HD13	1.98	0.45
4:R:59:TRP:HB2	4:R:62:ASN:OD1	2.16	0.45
4:V:61:PHE:HE1	4:V:134:PHE:CE2	2.34	0.45
4:X:82:ASP:N	4:X:82:ASP:OD1	2.44	0.45
1:i:27:LEU:HD12	1:i:27:LEU:HA	1.74	0.45
1:i:32:VAL:HG13	1:i:52:PHE:CE1	2.52	0.45
1:r:17:ASN:HB3	1:r:20:PHE:CZ	2.52	0.45
1:r:63:ALA:O	1:r:64:TRP:C	2.60	0.45
2:s:134:ALA:HB3	2:s:344:VAL:HA	1.99	0.45
2:s:323:LYS:HE3	2:s:323:LYS:HB2	1.73	0.45
2:t:134:ALA:HB3	2:t:344:VAL:HA	1.99	0.45
2:t:727:TRP:CA	4:T:36:ALA:CB	2.94	0.45
2:u:66:ILE:HD12	2:u:80:VAL:HG22	1.99	0.45
2:u:143:LEU:O	2:u:298:ASN:HA	2.17	0.45
2:u:593:PHE:N	2:u:593:PHE:HD1	2.14	0.45
2:w:143:LEU:O	2:w:298:ASN:HA	2.17	0.45
2:w:300:GLU:HG2	2:w:340:TRP:HZ2	1.81	0.45
2:x:277:ALA:CA	3:E:100:ARG:HG3	2.41	0.45
2:x:581:ASN:HD22	2:x:581:ASN:HA	1.56	0.45
3:A:74:LYS:HA	3:A:106:PHE:CE2	2.51	0.45
4:N:96:TYR:HB3	4:N:103:VAL:HG13	1.98	0.45
4:Q:52:ARG:HD3	4:R:132:GLU:OE2	2.17	0.45
4:S:150:PHE:HE1	4:T:25:GLY:HA2	1.81	0.45
4:T:144:ARG:HA	4:T:160:LEU:HD23	1.98	0.45
4:U:20:ILE:HD11	4:U:47:LEU:HD13	1.98	0.45
1:c:63:ALA:O	1:c:64:TRP:C	2.60	0.45
1:h:79:THR:HB	1:h:109:VAL:HG23	1.98	0.45
1:n:95:ARG:O	1:n:96:ALA:C	2.59	0.45
2:s:47:PRO:HG3	2:s:593:PHE:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:48:LEU:HD11	2:s:545:PHE:HE1	1.81	0.45
2:s:176:LYS:HE2	2:s:178:LYS:HE3	1.96	0.45
2:s:204:MET:C	2:s:211:TRP:HZ3	2.25	0.45
2:s:428:GLY:O	2:s:429:THR:C	2.58	0.45
2:u:2:ALA:O	2:u:3:LEU:C	2.60	0.45
2:u:153:LEU:HD12	2:u:153:LEU:HA	1.66	0.45
2:u:300:GLU:HG2	2:u:340:TRP:HZ2	1.81	0.45
2:v:2:ALA:O	2:v:3:LEU:C	2.60	0.45
2:w:2:ALA:O	2:w:3:LEU:C	2.60	0.45
2:w:66:ILE:HD12	2:w:80:VAL:HG22	1.99	0.45
2:w:134:ALA:HB3	2:w:344:VAL:HA	1.99	0.45
2:w:211:TRP:HB2	2:w:222:VAL:HG13	1.97	0.45
2:x:177:TYR:HE2	2:x:196:LEU:CD2	2.29	0.45
2:x:287:GLU:H	2:x:287:GLU:HG3	1.40	0.45
2:x:440:THR:HG23	2:x:441:THR:HG22	1.97	0.45
2:x:525:MET:HE3	2:x:525:MET:HB3	1.67	0.45
4:T:125:ARG:HD3	4:T:129:GLU:OE2	2.15	0.45
4:W:151:PHE:HD2	4:W:153:ALA:HB2	1.80	0.45
1:i:9:LEU:HD21	1:i:23:PRO:CG	2.41	0.45
1:i:93:ILE:CD1	2:u:746:LEU:CA	2.68	0.45
1:k:36:LEU:HD22	1:k:73:ILE:HG12	1.99	0.45
1:m:94:LEU:HG	2:s:741:LEU:HD23	1.98	0.45
1:p:86:VAL:HG21	1:p:101:VAL:HB	1.99	0.45
2:s:86:ILE:C	2:s:98:VAL:HG11	2.30	0.45
2:t:48:LEU:HD11	2:t:545:PHE:HE1	1.81	0.45
2:t:127:ILE:HD12	2:t:322:PHE:HE1	1.82	0.45
2:u:271:GLY:HA3	3:B:107:ILE:HG21	1.99	0.45
2:w:47:PRO:HG3	2:w:593:PHE:HA	1.99	0.45
2:w:145:ASN:OD1	2:w:145:ASN:C	2.60	0.45
2:x:134:ALA:HB3	2:x:344:VAL:HA	1.99	0.45
3:A:90:LEU:HD13	3:A:95:MET:HG3	1.99	0.45
4:O:20:ILE:HD11	4:O:47:LEU:HD13	1.98	0.45
4:O:49:LYS:HE3	4:P:136:TYR:HE1	1.82	0.45
4:Q:1:MET:SD	4:R:15:SER:OG	2.65	0.45
4:V:166:GLU:O	4:V:169:ARG:HB3	2.17	0.45
1:f:84:ARG:O	1:f:85:LEU:C	2.59	0.45
1:g:29:ARG:O	1:g:30:LYS:C	2.58	0.45
1:h:36:LEU:HD22	1:h:73:ILE:HG12	1.99	0.45
1:o:9:LEU:HA	1:o:9:LEU:HD23	1.78	0.45
2:t:698:ILE:HG13	2:u:707:TRP:CH2	2.53	0.45
2:v:159:GLY:HA2	2:v:243:LEU:HD23	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:204:MET:C	2:v:211:TRP:HZ3	2.25	0.45
2:w:230:ILE:HG21	2:w:233:PHE:HB2	1.99	0.45
3:A:40:GLU:HA	3:A:43:ARG:NH1	2.31	0.45
3:B:82:ARG:O	3:B:83:ALA:C	2.59	0.45
4:P:96:TYR:HB3	4:P:103:VAL:HG13	1.98	0.45
4:R:144:ARG:HA	4:R:160:LEU:HD23	1.98	0.45
4:U:3:SER:OG	4:U:6:MET:SD	2.75	0.45
4:U:52:ARG:HD3	4:V:132:GLU:OE2	2.17	0.45
4:X:166:GLU:O	4:X:169:ARG:HB3	2.17	0.45
1:a:54:THR:O	1:a:55:ARG:C	2.60	0.44
1:d:62:LYS:HD2	1:d:62:LYS:HA	1.70	0.44
1:d:86:VAL:HG21	1:d:101:VAL:HB	1.99	0.44
1:i:93:ILE:HG13	2:u:638:GLY:N	2.29	0.44
1:l:3:ASN:HD22	1:l:3:ASN:HA	1.62	0.44
1:l:50:TYR:HB3	1:l:60:LEU:HB3	1.99	0.44
1:n:79:THR:HB	1:n:109:VAL:HG23	1.98	0.44
1:o:17:ASN:HB3	1:o:20:PHE:CZ	2.52	0.44
1:p:23:PRO:CB	4:O:79:VAL:HG11	2.48	0.44
2:s:127:ILE:HD12	2:s:322:PHE:HE1	1.82	0.44
2:t:118:MET:HE3	2:t:118:MET:HB2	1.74	0.44
2:t:230:ILE:HG21	2:t:233:PHE:HB2	1.99	0.44
2:u:127:ILE:HD12	2:u:322:PHE:HE1	1.82	0.44
2:v:99:ARG:HH12	2:v:319:ASN:HD22	1.64	0.44
2:w:151:ASP:N	2:w:151:ASP:OD1	2.50	0.44
2:x:99:ARG:HH12	2:x:319:ASN:HD22	1.65	0.44
2:x:150:GLN:OE1	2:x:224:ALA:HB3	2.13	0.44
2:x:230:ILE:HG21	2:x:233:PHE:HB2	1.99	0.44
2:x:254:PHE:CE2	3:F:65:ALA:HB2	2.43	0.44
2:x:340:TRP:O	2:x:341:PRO:C	2.60	0.44
3:C:40:GLU:HA	3:C:43:ARG:NE	2.30	0.44
3:E:119:ARG:HD3	3:E:119:ARG:HA	1.76	0.44
4:M:150:PHE:HE1	4:N:25:GLY:HA2	1.81	0.44
4:R:67:ILE:HG21	4:R:121:ILE:HG12	1.99	0.44
4:U:49:LYS:HE3	4:V:136:TYR:HE1	1.82	0.44
4:U:150:PHE:HE1	4:V:25:GLY:HA2	1.81	0.44
4:W:6:MET:HA	4:W:6:MET:HE3	2.00	0.44
1:a:9:LEU:CG	4:M:72:ASP:CG	2.90	0.44
1:e:36:LEU:HD22	1:e:73:ILE:HG12	1.99	0.44
1:e:79:THR:HB	1:e:109:VAL:HG23	1.98	0.44
2:s:230:ILE:HG21	2:s:233:PHE:HB2	1.99	0.44
2:s:686:GLN:HE21	2:s:694:SER:HB3	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:2:ALA:O	2:t:3:LEU:C	2.60	0.44
2:t:19:PRO:HG3	2:u:711:GLU:CG	2.48	0.44
2:t:557:ILE:HD13	2:t:557:ILE:HA	1.86	0.44
2:u:258:PRO:HA	2:u:259:PRO:HD3	1.85	0.44
2:v:150:GLN:HB3	2:v:224:ALA:HB1	1.84	0.44
2:w:470:ILE:O	2:w:488:ILE:HG12	2.17	0.44
2:x:143:LEU:O	2:x:298:ASN:HA	2.17	0.44
2:x:159:GLY:HA2	2:x:243:LEU:HD23	2.00	0.44
2:x:176:LYS:HE2	2:x:178:LYS:HE3	1.96	0.44
3:F:119:ARG:HD3	3:F:119:ARG:HA	1.76	0.44
4:M:28:PRO:HD3	4:X:42:ASN:OD1	2.18	0.44
4:P:50:ILE:HG21	4:P:142:ALA:HB2	1.98	0.44
4:T:166:GLU:O	4:T:169:ARG:HB3	2.17	0.44
4:W:150:PHE:HE1	4:X:25:GLY:HA2	1.81	0.44
1:c:50:TYR:HB3	1:c:60:LEU:HB3	1.99	0.44
1:d:55:ARG:HG2	4:X:5:ASP:OD1	2.17	0.44
1:e:86:VAL:HG23	4:X:31:THR:HB	2.00	0.44
1:f:13:LEU:HD12	1:f:73:ILE:HG12	2.00	0.44
1:f:84:ARG:C	1:f:86:VAL:N	2.67	0.44
1:i:17:ASN:HB3	1:i:20:PHE:CZ	2.52	0.44
1:m:29:ARG:O	1:m:30:LYS:C	2.58	0.44
1:m:55:ARG:HG2	4:R:5:ASP:OD1	2.17	0.44
1:n:36:LEU:HD22	1:n:73:ILE:HG12	1.99	0.44
2:s:159:GLY:HA2	2:s:243:LEU:HD23	2.00	0.44
2:u:746:LEU:H	2:u:746:LEU:HG	1.53	0.44
2:v:145:ASN:O	2:v:146:TYR:C	2.60	0.44
2:w:308:MET:SD	2:w:343:PHE:CE1	3.11	0.44
2:w:646:PRO:C	2:w:648:ALA:N	2.74	0.44
2:x:142:ASN:CB	2:x:295:LEU:HD11	2.44	0.44
2:x:557:ILE:HD13	2:x:557:ILE:HA	1.86	0.44
3:A:126:ALA:HA	3:A:129:LEU:CD2	2.48	0.44
4:R:166:GLU:O	4:R:169:ARG:HB3	2.17	0.44
4:S:10:THR:HB	4:S:13:GLU:HB3	2.00	0.44
4:S:182:ASN:OD1	4:S:182:ASN:C	2.59	0.44
4:T:50:ILE:HG21	4:T:142:ALA:HB2	1.98	0.44
4:T:172:MET:HE2	4:T:172:MET:HB2	1.87	0.44
4:U:10:THR:HB	4:U:13:GLU:HB3	2.00	0.44
1:a:86:VAL:HG21	1:a:101:VAL:HB	1.99	0.44
1:c:13:LEU:HD12	1:c:73:ILE:HG12	2.00	0.44
1:l:93:ILE:HG23	2:t:745:ARG:O	2.17	0.44
1:o:13:LEU:HD12	1:o:73:ILE:HG12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:r:46:ILE:H	1:r:46:ILE:HG12	1.59	0.44
2:t:143:LEU:O	2:t:298:ASN:HA	2.17	0.44
2:u:91:LEU:HD21	2:u:562:TYR:CD1	2.53	0.44
2:u:134:ALA:HB3	2:u:344:VAL:HA	1.99	0.44
2:v:491:HIS:HE1	2:v:540:TRP:HB2	1.83	0.44
2:w:159:GLY:HA2	2:w:243:LEU:HD23	2.00	0.44
2:w:491:HIS:HE1	2:w:540:TRP:HB2	1.83	0.44
2:x:161:TYR:CE1	3:F:46:ASN:HB3	2.52	0.44
2:x:204:MET:C	2:x:211:TRP:HZ3	2.25	0.44
2:x:470:ILE:O	2:x:488:ILE:HG12	2.17	0.44
3:C:88:SER:CB	3:C:90:LEU:HD13	2.34	0.44
4:N:166:GLU:O	4:N:169:ARG:HB3	2.17	0.44
4:P:166:GLU:O	4:P:169:ARG:HB3	2.17	0.44
4:S:52:ARG:HD3	4:T:132:GLU:OE2	2.17	0.44
4:X:144:ARG:NH1	4:X:164:GLU:OE1	2.50	0.44
1:b:79:THR:HB	1:b:109:VAL:HG23	1.98	0.44
1:c:17:ASN:HB3	1:c:20:PHE:CZ	2.52	0.44
1:d:99:LEU:HA	1:d:99:LEU:HD23	1.70	0.44
2:s:19:PRO:HG3	2:t:711:GLU:CG	2.48	0.44
2:s:470:ILE:O	2:s:488:ILE:HG12	2.17	0.44
2:s:727:TRP:CA	4:R:36:ALA:CB	2.95	0.44
2:t:41:GLY:O	2:t:42:LEU:C	2.59	0.44
2:t:300:GLU:HG2	2:t:340:TRP:HZ2	1.81	0.44
2:t:686:GLN:HE21	2:t:694:SER:HB3	1.83	0.44
2:u:22:LEU:HD23	2:v:779:ILE:HG12	1.90	0.44
2:u:47:PRO:HG3	2:u:593:PHE:HA	1.99	0.44
2:u:230:ILE:HG21	2:u:233:PHE:HB2	1.99	0.44
2:u:323:LYS:HE3	2:u:323:LYS:HB2	1.73	0.44
2:v:91:LEU:HD21	2:v:562:TYR:CD1	2.53	0.44
2:v:127:ILE:HD12	2:v:322:PHE:HE1	1.82	0.44
2:w:35:TRP:CH2	2:w:527:LYS:HD3	2.52	0.44
2:w:127:ILE:HD12	2:w:322:PHE:HE1	1.82	0.44
2:w:204:MET:C	2:w:211:TRP:HZ3	2.25	0.44
2:w:593:PHE:N	2:w:593:PHE:HD1	2.14	0.44
2:w:727:TRP:C	4:N:36:ALA:HB2	2.41	0.44
2:x:66:ILE:HD12	2:x:80:VAL:HG22	1.99	0.44
2:x:127:ILE:HD12	2:x:322:PHE:HE1	1.82	0.44
2:x:308:MET:SD	2:x:343:PHE:CE1	3.11	0.44
4:R:50:ILE:HG21	4:R:142:ALA:HB2	1.98	0.44
4:R:51:ASN:ND2	4:R:127:TYR:HA	2.33	0.44
1:c:93:ILE:HG23	2:w:745:ARG:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:d:94:LEU:HD22	2:v:741:LEU:HD22	1.98	0.44
1:f:17:ASN:HB3	1:f:20:PHE:CZ	2.52	0.44
1:f:63:ALA:O	1:f:64:TRP:C	2.60	0.44
1:i:30:LYS:HE3	1:i:31:PHE:CE1	2.53	0.44
1:l:13:LEU:HD12	1:l:73:ILE:HG12	2.00	0.44
1:l:30:LYS:HE3	1:l:31:PHE:CE1	2.53	0.44
2:s:35:TRP:CH2	2:s:527:LYS:HD3	2.52	0.44
2:t:35:TRP:CH2	2:t:527:LYS:HD3	2.52	0.44
2:t:47:PRO:HG3	2:t:593:PHE:HA	1.99	0.44
2:t:287:GLU:H	2:t:287:GLU:HG3	1.40	0.44
2:u:184:GLN:O	2:u:185:PRO:C	2.57	0.44
2:u:308:MET:SD	2:u:343:PHE:CE1	3.11	0.44
2:v:134:ALA:HB3	2:v:344:VAL:HA	1.99	0.44
2:v:143:LEU:O	2:v:298:ASN:HA	2.17	0.44
2:v:308:MET:SD	2:v:343:PHE:CE1	3.11	0.44
2:v:727:TRP:C	4:X:36:ALA:HB2	2.41	0.44
2:w:91:LEU:HD21	2:w:562:TYR:CD1	2.53	0.44
2:w:99:ARG:HH12	2:w:319:ASN:HD22	1.65	0.44
2:w:180:PRO:HD2	2:w:190:ASN:HB2	2.00	0.44
2:w:340:TRP:O	2:w:341:PRO:C	2.59	0.44
2:x:180:PRO:HD2	2:x:190:ASN:HB2	2.00	0.44
4:Q:49:LYS:HE3	4:R:136:TYR:HE1	1.82	0.44
4:X:61:PHE:HE1	4:X:134:PHE:CE2	2.34	0.44
1:i:15:GLY:HA2	1:i:66:PRO:HD2	2.00	0.44
1:o:84:ARG:O	1:o:85:LEU:C	2.59	0.44
1:r:93:ILE:HG13	2:x:638:GLY:N	2.33	0.44
2:s:180:PRO:HD2	2:s:190:ASN:HB2	2.00	0.44
2:s:183:SER:HB2	3:E:42:MET:CB	2.40	0.44
2:t:361:LEU:HD12	2:t:361:LEU:HA	1.67	0.44
2:t:593:PHE:N	2:t:593:PHE:HD1	2.14	0.44
2:v:9:LYS:HE2	2:v:9:LYS:HB3	1.78	0.44
2:v:66:ILE:HD12	2:v:80:VAL:HG22	1.99	0.44
2:v:230:ILE:HG21	2:v:233:PHE:HB2	1.99	0.44
2:v:271:GLY:HA3	3:A:107:ILE:HG21	2.00	0.44
2:v:361:LEU:HD12	2:v:361:LEU:HA	1.67	0.44
2:w:361:LEU:HD12	2:w:361:LEU:HA	1.67	0.44
2:x:2:ALA:O	2:x:3:LEU:C	2.60	0.44
2:x:145:ASN:O	2:x:146:TYR:C	2.59	0.44
2:x:277:ALA:HB1	3:E:100:ARG:O	2.17	0.44
2:x:686:GLN:HE21	2:x:694:SER:HB3	1.83	0.44
3:A:61:GLU:OE1	3:F:119:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:51:ASN:ND2	4:V:127:TYR:HA	2.33	0.44
4:W:49:LYS:HE3	4:X:136:TYR:HE1	1.82	0.44
1:c:32:VAL:HG13	1:c:52:PHE:CE1	2.53	0.44
1:i:13:LEU:HD12	1:i:73:ILE:HG12	2.00	0.44
1:l:32:VAL:HG13	1:l:52:PHE:CE1	2.53	0.44
1:l:63:ALA:O	1:l:64:TRP:C	2.60	0.44
1:r:13:LEU:HD12	1:r:73:ILE:HG12	2.00	0.44
2:s:308:MET:SD	2:s:343:PHE:CE1	3.11	0.44
2:s:360:PHE:N	2:s:360:PHE:CD1	2.84	0.44
2:s:602:ILE:HD11	2:s:606:THR:OG1	2.18	0.44
2:t:491:HIS:HE1	2:t:540:TRP:HB2	1.83	0.44
2:u:63:ALA:HB1	2:u:113:ARG:HE	1.83	0.44
2:u:491:HIS:HE1	2:u:540:TRP:HB2	1.83	0.44
2:w:142:ASN:CB	2:w:295:LEU:HD11	2.44	0.44
2:w:602:ILE:HD11	2:w:606:THR:OG1	2.18	0.44
2:w:698:ILE:HD13	2:w:699:GLY:N	2.33	0.44
2:x:373:LYS:HE3	3:F:82:ARG:NH2	2.33	0.44
3:B:126:ALA:CA	3:B:129:LEU:HD21	2.35	0.44
3:C:85:ILE:HG12	3:C:95:MET:HB3	1.99	0.44
3:C:90:LEU:HD23	3:C:95:MET:HG3	1.99	0.44
4:M:6:MET:HA	4:M:6:MET:HE3	2.00	0.44
4:S:49:LYS:HE3	4:T:136:TYR:HE1	1.83	0.44
4:V:50:ILE:HG21	4:V:142:ALA:HB2	1.98	0.44
4:X:50:ILE:HG21	4:X:142:ALA:HB2	1.98	0.44
4:X:51:ASN:ND2	4:X:127:TYR:HA	2.33	0.44
1:d:9:LEU:CG	4:W:72:ASP:CG	2.90	0.44
1:f:27:LEU:HA	1:f:27:LEU:HD12	1.74	0.44
1:l:15:GLY:HA2	1:l:66:PRO:HD2	2.00	0.44
1:o:3:ASN:HD22	1:o:3:ASN:HA	1.62	0.44
2:t:258:PRO:HA	2:t:259:PRO:HD3	1.84	0.44
2:t:470:ILE:O	2:t:488:ILE:HG12	2.17	0.44
2:u:118:MET:HE3	2:u:118:MET:HB2	1.74	0.44
2:u:151:ASP:OD1	2:u:151:ASP:N	2.50	0.44
2:u:340:TRP:O	2:u:341:PRO:C	2.60	0.44
2:u:698:ILE:HD13	2:u:699:GLY:N	2.33	0.44
2:v:470:ILE:O	2:v:488:ILE:HG12	2.17	0.44
2:v:602:ILE:HD11	2:v:606:THR:OG1	2.18	0.44
2:x:491:HIS:HE1	2:x:540:TRP:HB2	1.83	0.44
2:x:602:ILE:HD11	2:x:606:THR:OG1	2.18	0.44
4:M:49:LYS:HE3	4:N:136:TYR:HE1	1.82	0.44
4:N:42:ASN:OD1	4:O:28:PRO:HD3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:67:ILE:HG21	4:N:121:ILE:HG12	1.99	0.44
4:Q:150:PHE:HE1	4:R:25:GLY:HA2	1.81	0.44
1:b:36:LEU:HD22	1:b:73:ILE:HG12	1.99	0.43
1:b:95:ARG:O	1:b:96:ALA:C	2.59	0.43
1:c:84:ARG:C	1:c:86:VAL:N	2.67	0.43
1:i:63:ALA:O	1:i:64:TRP:C	2.60	0.43
1:p:97:TYR:CD1	4:O:6:MET:SD	3.11	0.43
1:q:36:LEU:HD22	1:q:73:ILE:HG12	1.99	0.43
2:s:185:PRO:CD	3:E:42:MET:HE3	2.16	0.43
2:t:91:LEU:HD21	2:t:562:TYR:CD1	2.53	0.43
2:t:143:LEU:HD23	2:t:143:LEU:HA	1.70	0.43
2:t:150:GLN:OE1	2:t:224:ALA:HB3	2.13	0.43
2:u:159:GLY:HA2	2:u:243:LEU:HD23	2.00	0.43
2:u:183:SER:HB2	3:C:42:MET:CB	2.40	0.43
2:u:388:ASP:OD1	3:C:83:ALA:HB2	2.17	0.43
2:u:535:LEU:HD12	2:u:535:LEU:HA	1.90	0.43
2:v:180:PRO:HD2	2:v:190:ASN:HB2	2.00	0.43
2:v:356:ASN:ND2	3:B:86:GLY:O	2.48	0.43
2:x:35:TRP:CH2	2:x:527:LYS:HD3	2.52	0.43
4:N:168:ARG:HH12	4:N:172:MET:HE3	1.63	0.43
4:P:51:ASN:ND2	4:P:127:TYR:HA	2.33	0.43
4:P:160:LEU:HA	4:P:160:LEU:HD12	1.73	0.43
4:T:67:ILE:HG21	4:T:121:ILE:HG12	1.99	0.43
1:l:17:ASN:HB3	1:l:20:PHE:CZ	2.52	0.43
1:o:106:THR:O	1:o:109:VAL:HG12	2.18	0.43
1:q:27:LEU:HA	1:q:27:LEU:HD13	1.71	0.43
1:q:92:SER:OG	4:P:30:SER:HB3	2.19	0.43
2:t:145:ASN:O	2:t:146:TYR:C	2.60	0.43
2:t:159:GLY:HA2	2:t:243:LEU:HD23	2.00	0.43
2:t:340:TRP:O	2:t:341:PRO:C	2.59	0.43
2:u:686:GLN:HE21	2:u:694:SER:HB3	1.83	0.43
2:v:525:MET:HE3	2:v:525:MET:HB3	1.67	0.43
2:w:360:PHE:N	2:w:360:PHE:CD1	2.85	0.43
2:w:618:ILE:H	2:w:618:ILE:HG13	1.58	0.43
2:x:47:PRO:HG3	2:x:593:PHE:HA	1.99	0.43
3:B:125:PHE:O	3:B:128:GLN:HG2	2.18	0.43
4:N:51:ASN:ND2	4:N:127:TYR:HA	2.33	0.43
4:T:51:ASN:ND2	4:T:127:TYR:HA	2.33	0.43
4:V:67:ILE:HG21	4:V:121:ILE:HG12	1.99	0.43
4:W:3:SER:OG	4:W:6:MET:SD	2.76	0.43
1:a:29:ARG:O	1:a:30:LYS:C	2.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i:3:ASN:HD22	1:i:3:ASN:HA	1.62	0.43
1:i:95:ARG:HD2	2:u:639:LYS:CD	2.48	0.43
1:k:86:VAL:HG23	4:T:31:THR:HB	2.00	0.43
1:r:84:ARG:O	1:r:85:LEU:C	2.59	0.43
2:s:48:LEU:HD21	2:s:545:PHE:CE1	2.54	0.43
2:s:151:ASP:OD1	2:s:151:ASP:N	2.50	0.43
2:s:340:TRP:O	2:s:341:PRO:C	2.60	0.43
2:s:491:HIS:HE1	2:s:540:TRP:HB2	1.83	0.43
2:s:580:LYS:H	2:s:580:LYS:HG2	1.46	0.43
2:t:308:MET:SD	2:t:343:PHE:CE1	3.11	0.43
2:t:314:ARG:O	2:t:314:ARG:CG	2.66	0.43
2:v:300:GLU:HG2	2:v:340:TRP:HZ2	1.81	0.43
2:v:360:PHE:N	2:v:360:PHE:CD1	2.84	0.43
2:w:503:ILE:HA	2:w:513:SER:O	2.19	0.43
2:w:686:GLN:HE21	2:w:694:SER:HB3	1.83	0.43
2:x:309:PRO:HB2	2:x:327:TRP:CZ2	2.53	0.43
2:x:698:ILE:HD13	2:x:699:GLY:N	2.33	0.43
3:E:127:GLN:C	3:E:127:GLN:CD	2.85	0.43
1:b:9:LEU:HD12	1:b:9:LEU:HA	1.82	0.43
1:c:84:ARG:O	1:c:85:LEU:C	2.59	0.43
1:f:93:ILE:HG23	2:v:745:ARG:O	2.17	0.43
1:g:29:ARG:C	1:g:31:PHE:N	2.75	0.43
1:n:12:GLN:H	1:n:12:GLN:HG2	1.35	0.43
1:q:46:ILE:HG13	1:q:47:ASN:H	1.84	0.43
1:r:60:LEU:HD12	1:r:64:TRP:CD1	2.54	0.43
2:t:66:ILE:HD12	2:t:80:VAL:HG22	1.99	0.43
2:t:72:ASP:O	2:t:73:GLU:C	2.62	0.43
2:t:646:PRO:C	2:t:648:ALA:N	2.74	0.43
2:u:19:PRO:HG3	2:v:711:GLU:CG	2.47	0.43
2:u:163:ARG:NH2	3:B:129:LEU:HB2	2.33	0.43
2:u:470:ILE:O	2:u:488:ILE:HG12	2.17	0.43
2:u:616:ILE:HG23	2:u:621:ILE:HG21	2.00	0.43
2:v:63:ALA:HB1	2:v:113:ARG:HE	1.83	0.43
2:v:148:PRO:O	2:v:249:HIS:HD2	2.02	0.43
2:v:202:LYS:HE2	2:v:202:LYS:HB3	1.64	0.43
2:v:686:GLN:HE21	2:v:694:SER:HB3	1.83	0.43
2:w:580:LYS:H	2:w:580:LYS:HG2	1.46	0.43
2:x:360:PHE:N	2:x:360:PHE:CD1	2.84	0.43
3:F:72:MET:HE3	3:F:72:MET:HB2	1.93	0.43
4:N:36:ALA:O	4:N:37:ASN:C	2.62	0.43
4:N:57:ARG:HE	4:N:57:ARG:HB2	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:150:PHE:HE1	4:P:25:GLY:HA2	1.82	0.43
4:R:160:LEU:HA	4:R:160:LEU:HD12	1.73	0.43
4:T:6:MET:HE3	4:T:6:MET:HB3	1.71	0.43
4:U:155:GLU:O	4:U:156:VAL:C	2.62	0.43
1:f:15:GLY:HA2	1:f:66:PRO:HD2	2.00	0.43
1:f:31:PHE:CG	1:f:79:THR:HA	2.53	0.43
1:j:93:ILE:HD12	2:t:739:ASN:HA	2.01	0.43
1:m:93:ILE:HD12	2:s:739:ASN:HA	2.01	0.43
1:q:55:ARG:HA	1:q:55:ARG:HD2	1.86	0.43
2:s:593:PHE:N	2:s:593:PHE:HD1	2.14	0.43
2:t:698:ILE:HD13	2:t:699:GLY:N	2.33	0.43
2:v:161:TYR:CE1	3:B:46:ASN:HB3	2.54	0.43
2:v:172:LYS:HB3	2:v:172:LYS:HE2	1.64	0.43
2:v:340:TRP:O	2:v:341:PRO:C	2.59	0.43
2:v:746:LEU:H	2:v:746:LEU:HG	1.53	0.43
2:x:151:ASP:OD1	2:x:151:ASP:N	2.50	0.43
3:A:40:GLU:CB	3:A:43:ARG:HH11	2.31	0.43
4:N:160:LEU:HD12	4:N:160:LEU:HA	1.73	0.43
4:P:67:ILE:HG21	4:P:121:ILE:HG12	1.99	0.43
4:X:67:ILE:HG21	4:X:121:ILE:HG12	1.99	0.43
1:b:46:ILE:HG13	1:b:47:ASN:H	1.84	0.43
1:c:60:LEU:HD12	1:c:64:TRP:CD1	2.54	0.43
1:e:46:ILE:HG13	1:e:47:ASN:H	1.84	0.43
1:m:9:LEU:CG	4:Q:72:ASP:CG	2.91	0.43
1:n:46:ILE:HG13	1:n:47:ASN:H	1.84	0.43
1:o:27:LEU:HA	1:o:27:LEU:HD12	1.74	0.43
2:s:711:GLU:CG	2:x:19:PRO:HG3	2.48	0.43
2:u:148:PRO:O	2:u:249:HIS:HD2	2.02	0.43
2:v:532:ASN:HB2	2:v:534:GLU:HG2	2.00	0.43
2:v:774:THR:HG22	2:v:775:PRO:O	2.19	0.43
2:x:593:PHE:N	2:x:593:PHE:HD1	2.14	0.43
3:B:129:LEU:CD1	3:B:130:GLY:N	2.71	0.43
4:M:3:SER:OG	4:M:6:MET:SD	2.76	0.43
4:M:155:GLU:O	4:M:156:VAL:C	2.62	0.43
4:R:32:LEU:HD23	4:R:32:LEU:HA	1.81	0.43
4:V:170:LEU:HD12	4:V:170:LEU:HA	1.62	0.43
4:W:182:ASN:OD1	4:W:185:ASP:CB	2.62	0.43
1:f:46:ILE:HD12	2:v:610:ASP:HB3	2.00	0.43
1:g:9:LEU:CG	4:U:72:ASP:CG	2.91	0.43
1:i:9:LEU:HA	1:i:9:LEU:HD23	1.78	0.43
1:i:31:PHE:CG	1:i:79:THR:HA	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:j:85:LEU:H	1:j:85:LEU:HG	1.65	0.43
1:l:84:ARG:O	1:l:85:LEU:C	2.59	0.43
1:n:55:ARG:HA	1:n:55:ARG:HD2	1.86	0.43
1:n:86:VAL:HG23	4:R:31:THR:HB	2.01	0.43
1:o:15:GLY:HA2	1:o:66:PRO:HD2	2.00	0.43
1:o:60:LEU:HD12	1:o:64:TRP:CD1	2.54	0.43
1:o:93:ILE:HD12	2:s:638:GLY:H	1.82	0.43
2:s:497:PRO:HG2	2:s:516:SER:HB3	2.00	0.43
2:s:567:ASN:HD22	2:s:567:ASN:HA	1.54	0.43
2:u:145:ASN:O	2:u:146:TYR:C	2.60	0.43
2:u:360:PHE:N	2:u:360:PHE:CD1	2.84	0.43
2:u:503:ILE:HA	2:u:513:SER:O	2.19	0.43
2:u:532:ASN:HB2	2:u:534:GLU:HG2	2.00	0.43
2:w:72:ASP:O	2:w:73:GLU:C	2.62	0.43
2:x:48:LEU:HD21	2:x:545:PHE:CE1	2.54	0.43
2:x:91:LEU:HD21	2:x:562:TYR:CD1	2.53	0.43
2:x:503:ILE:HA	2:x:513:SER:O	2.19	0.43
2:x:684:ILE:H	2:x:684:ILE:HG13	1.59	0.43
4:M:14:LEU:HD13	4:M:32:LEU:HB2	2.01	0.43
4:Q:14:LEU:HD13	4:Q:32:LEU:HB2	2.01	0.43
4:R:170:LEU:HD12	4:R:170:LEU:HA	1.62	0.43
1:a:9:LEU:HD11	4:M:72:ASP:OD2	2.18	0.43
1:o:63:ALA:O	1:o:64:TRP:C	2.60	0.43
1:p:93:ILE:HD12	2:x:739:ASN:HA	2.01	0.43
1:r:30:LYS:HE3	1:r:31:PHE:CE1	2.53	0.43
2:s:66:ILE:HD12	2:s:80:VAL:HG22	1.99	0.43
2:s:407:VAL:HG23	2:s:414:LEU:HB2	2.01	0.43
2:s:616:ILE:HG23	2:s:621:ILE:HG21	2.00	0.43
2:s:698:ILE:HD13	2:s:699:GLY:N	2.33	0.43
2:t:148:PRO:O	2:t:249:HIS:HD2	2.02	0.43
2:t:407:VAL:HG23	2:t:414:LEU:HB2	2.01	0.43
2:u:618:ILE:H	2:u:618:ILE:HG13	1.58	0.43
2:v:303:VAL:CG2	2:v:378:TYR:OH	2.63	0.43
2:w:145:ASN:O	2:w:146:TYR:C	2.60	0.43
2:w:148:PRO:O	2:w:249:HIS:HD2	2.02	0.43
2:x:646:PRO:C	2:x:648:ALA:N	2.74	0.43
4:N:95:ILE:HG23	4:N:107:THR:HG23	2.01	0.43
4:P:114:ASP:OD1	4:P:115:SER:N	2.52	0.43
1:f:60:LEU:HD12	1:f:64:TRP:CD1	2.54	0.43
1:g:85:LEU:H	1:g:85:LEU:HG	1.65	0.43
1:h:46:ILE:HG13	1:h:47:ASN:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i:93:ILE:HG23	2:u:745:ARG:O	2.19	0.43
1:l:9:LEU:HA	1:l:9:LEU:HD23	1.78	0.43
1:o:30:LYS:HE3	1:o:31:PHE:CE1	2.53	0.43
1:q:94:LEU:HD23	2:x:736:LEU:HB2	2.01	0.43
2:s:91:LEU:HD21	2:s:562:TYR:CD1	2.53	0.43
2:s:611:THR:O	2:s:613:THR:N	2.48	0.43
2:t:48:LEU:HD21	2:t:545:PHE:CE1	2.54	0.43
2:t:377:PHE:O	2:t:390:PRO:HG3	2.19	0.43
2:u:634:LEU:HD13	2:u:640:ILE:HG12	2.01	0.43
2:u:698:ILE:HG13	2:v:707:TRP:CH2	2.54	0.43
2:v:143:LEU:HD23	2:v:143:LEU:HA	1.70	0.43
2:v:698:ILE:HD13	2:v:699:GLY:N	2.33	0.43
2:w:525:MET:HE3	2:w:525:MET:HB3	1.67	0.43
2:x:634:LEU:HD13	2:x:640:ILE:HG12	2.01	0.43
3:A:119:ARG:HA	3:A:119:ARG:HD3	1.76	0.43
3:C:125:PHE:O	3:C:128:GLN:HG2	2.18	0.43
4:M:21:LEU:HD23	4:M:21:LEU:HA	1.81	0.43
4:M:136:TYR:HE1	4:X:49:LYS:HZ1	1.67	0.43
4:N:63:ILE:HD11	4:N:120:ASN:HB3	2.01	0.43
4:N:178:TYR:O	4:N:178:TYR:CD1	2.69	0.43
4:Q:3:SER:OG	4:Q:6:MET:SD	2.76	0.43
4:R:36:ALA:O	4:R:37:ASN:C	2.62	0.43
4:S:1:MET:SD	4:T:15:SER:OG	2.65	0.43
4:S:155:GLU:O	4:S:156:VAL:C	2.62	0.43
4:W:14:LEU:HD13	4:W:32:LEU:HB2	2.01	0.43
4:X:95:ILE:HG23	4:X:107:THR:HG23	2.01	0.43
4:X:167:ALA:O	4:X:168:ARG:C	2.61	0.43
1:a:29:ARG:C	1:a:31:PHE:N	2.75	0.43
1:b:45:THR:O	1:b:46:ILE:C	2.62	0.43
1:c:31:PHE:CG	1:c:79:THR:HA	2.53	0.43
1:f:30:LYS:HE3	1:f:31:PHE:CE1	2.53	0.43
1:j:99:LEU:HD23	1:j:99:LEU:HA	1.70	0.43
1:p:9:LEU:CG	4:O:72:ASP:CG	2.91	0.43
1:r:6:LYS:H	1:r:6:LYS:HG2	1.52	0.43
1:r:9:LEU:HD21	1:r:23:PRO:CG	2.41	0.43
2:s:9:LYS:HE2	2:s:9:LYS:HB3	1.78	0.43
2:s:611:THR:C	2:s:613:THR:H	2.27	0.43
2:s:746:LEU:H	2:s:746:LEU:HG	1.53	0.43
2:t:180:PRO:HD2	2:t:190:ASN:HB2	2.00	0.43
2:t:634:LEU:HD13	2:t:640:ILE:HG12	2.01	0.43
2:u:145:ASN:O	2:u:145:ASN:CG	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:u:727:TRP:C	4:V:36:ALA:HB2	2.42	0.43
2:v:170:ASN:HD22	2:v:170:ASN:N	2.17	0.43
2:v:254:PHE:CE2	3:B:65:ALA:HB2	2.44	0.43
2:v:503:ILE:HA	2:v:513:SER:O	2.19	0.43
2:w:150:GLN:OE1	2:w:224:ALA:HB3	2.13	0.43
2:w:377:PHE:O	2:w:390:PRO:HG3	2.19	0.43
2:w:407:VAL:HG23	2:w:414:LEU:HB2	2.01	0.43
2:w:497:PRO:HG2	2:w:516:SER:HB3	2.00	0.43
2:w:611:THR:C	2:w:613:THR:H	2.27	0.43
2:x:377:PHE:O	2:x:390:PRO:HG3	2.19	0.43
2:x:662:LEU:HD23	2:x:662:LEU:HA	1.84	0.43
2:x:774:THR:HG22	2:x:775:PRO:O	2.19	0.43
3:E:126:ALA:O	3:E:129:LEU:N	2.52	0.43
3:F:111:ASN:HA	3:F:114:THR:HG22	2.01	0.43
4:M:75:SER:HB3	4:M:77:LEU:HG	2.01	0.43
4:M:129:GLU:HA	4:X:98:ASN:ND2	2.29	0.43
4:N:57:ARG:CG	4:O:170:LEU:HD11	2.26	0.43
4:Q:6:MET:SD	4:R:6:MET:HB2	2.59	0.43
4:R:63:ILE:HD11	4:R:120:ASN:HB3	2.01	0.43
4:T:144:ARG:HD2	4:T:161:GLN:HB3	2.01	0.43
1:i:46:ILE:HD12	2:u:610:ASP:HB3	2.00	0.42
1:k:46:ILE:HG13	1:k:47:ASN:H	1.84	0.42
1:l:60:LEU:HD12	1:l:64:TRP:CD1	2.54	0.42
1:o:50:TYR:HB3	1:o:60:LEU:HB3	2.01	0.42
1:r:31:PHE:CG	1:r:79:THR:HA	2.53	0.42
2:s:143:LEU:HA	2:s:143:LEU:HD23	1.70	0.42
2:s:145:ASN:O	2:s:146:TYR:C	2.60	0.42
2:s:150:GLN:OE1	2:s:224:ALA:HB3	2.13	0.42
2:s:525:MET:HE3	2:s:525:MET:HB3	1.67	0.42
2:t:309:PRO:HB2	2:t:327:TRP:CZ2	2.53	0.42
2:t:602:ILE:HD11	2:t:606:THR:OG1	2.18	0.42
2:t:616:ILE:HG23	2:t:621:ILE:HG21	2.00	0.42
2:u:161:TYR:CZ	3:C:46:ASN:HB3	2.53	0.42
2:u:170:ASN:HD22	2:u:170:ASN:N	2.17	0.42
2:u:172:LYS:HE2	2:u:172:LYS:HB3	1.64	0.42
2:u:180:PRO:HD2	2:u:190:ASN:HB2	2.00	0.42
2:u:521:SER:HA	2:u:549:VAL:O	2.19	0.42
2:v:314:ARG:O	2:v:314:ARG:CG	2.66	0.42
2:x:161:TYR:HB3	2:x:162:GLY:H	1.61	0.42
2:x:170:ASN:HD22	2:x:170:ASN:N	2.17	0.42
2:x:497:PRO:HG2	2:x:516:SER:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:129:LEU:HG	3:F:130:GLY:N	2.34	0.42
4:M:182:ASN:CG	4:M:185:ASP:HB3	2.43	0.42
4:O:14:LEU:HD13	4:O:32:LEU:HB2	2.01	0.42
4:P:63:ILE:HD11	4:P:120:ASN:HB3	2.01	0.42
4:S:75:SER:HB3	4:S:77:LEU:HG	2.01	0.42
4:T:36:ALA:O	4:T:37:ASN:C	2.62	0.42
4:V:95:ILE:HG23	4:V:107:THR:HG23	2.01	0.42
4:V:172:MET:HE2	4:V:172:MET:HB2	1.87	0.42
4:W:75:SER:HB3	4:W:77:LEU:HG	2.01	0.42
1:c:6:LYS:H	1:c:6:LYS:HG2	1.52	0.42
1:e:55:ARG:HA	1:e:55:ARG:HD2	1.86	0.42
1:j:54:THR:O	1:j:55:ARG:C	2.60	0.42
1:m:54:THR:O	1:m:55:ARG:C	2.60	0.42
1:o:31:PHE:CG	1:o:79:THR:HA	2.53	0.42
2:s:148:PRO:O	2:s:249:HIS:HD2	2.02	0.42
2:s:284:TYR:HB2	2:s:291:TRP:CE3	2.54	0.42
2:s:370:ARG:NH1	3:E:82:ARG:HH22	2.17	0.42
2:s:634:LEU:HD13	2:s:640:ILE:HG12	2.01	0.42
2:t:323:LYS:HB2	2:t:323:LYS:HE3	1.73	0.42
2:t:360:PHE:N	2:t:360:PHE:CD1	2.85	0.42
2:u:254:PHE:CE2	3:C:65:ALA:HB2	2.43	0.42
2:u:366:ILE:HB	2:u:393:VAL:HG23	2.01	0.42
2:u:497:PRO:HG2	2:u:516:SER:HB3	2.00	0.42
2:u:774:THR:HG22	2:u:775:PRO:O	2.19	0.42
2:w:172:LYS:HE2	2:w:172:LYS:HB3	1.64	0.42
2:w:323:LYS:HB2	2:w:323:LYS:HE3	1.73	0.42
2:w:521:SER:HA	2:w:549:VAL:O	2.19	0.42
2:w:634:LEU:HD13	2:w:640:ILE:HG12	2.01	0.42
2:w:774:THR:HG22	2:w:775:PRO:O	2.19	0.42
2:x:284:TYR:HB2	2:x:291:TRP:CE3	2.54	0.42
2:x:532:ASN:HB2	2:x:534:GLU:HG2	2.00	0.42
4:N:167:ALA:O	4:N:168:ARG:C	2.61	0.42
4:U:3:SER:OG	4:U:6:MET:HB2	2.19	0.42
4:W:21:LEU:HD23	4:W:21:LEU:HA	1.81	0.42
1:c:15:GLY:HA2	1:c:66:PRO:HD2	2.00	0.42
1:c:30:LYS:HE3	1:c:31:PHE:CE1	2.53	0.42
1:c:51:ARG:C	1:c:53:ALA:H	2.26	0.42
1:d:31:PHE:CG	1:d:79:THR:HA	2.54	0.42
1:d:85:LEU:H	1:d:85:LEU:HG	1.65	0.42
1:f:6:LYS:O	1:f:24:PHE:HB3	2.20	0.42
1:g:27:LEU:HD13	1:g:27:LEU:HA	1.57	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:36:LEU:N	1:h:42:LYS:H	2.17	0.42
1:j:31:PHE:CG	1:j:79:THR:HA	2.55	0.42
1:k:12:GLN:H	1:k:12:GLN:HG2	1.35	0.42
1:k:22:ILE:N	1:k:56:THR:O	2.47	0.42
1:l:95:ARG:HD2	2:t:639:LYS:CD	2.49	0.42
2:s:503:ILE:HA	2:s:513:SER:O	2.19	0.42
2:s:524:PHE:HD2	2:s:542:HIS:HB2	1.83	0.42
2:t:503:ILE:HA	2:t:513:SER:O	2.18	0.42
2:t:524:PHE:HD2	2:t:542:HIS:HB2	1.83	0.42
2:u:21:ILE:CG1	2:u:697:ASP:OD1	2.66	0.42
2:v:616:ILE:HG23	2:v:621:ILE:HG21	2.00	0.42
2:v:634:LEU:HD13	2:v:640:ILE:HG12	2.01	0.42
2:w:314:ARG:O	2:w:314:ARG:CG	2.66	0.42
4:M:31:THR:C	4:M:33:GLU:H	2.27	0.42
4:P:95:ILE:HG23	4:P:107:THR:HG23	2.01	0.42
4:Q:75:SER:HB3	4:Q:77:LEU:HG	2.01	0.42
4:S:14:LEU:HD13	4:S:32:LEU:HB2	2.01	0.42
4:T:57:ARG:HE	4:T:57:ARG:HB2	1.66	0.42
4:T:95:ILE:HG23	4:T:107:THR:HG23	2.01	0.42
4:T:168:ARG:HH11	4:T:172:MET:CE	2.25	0.42
4:W:155:GLU:O	4:W:156:VAL:C	2.62	0.42
4:X:63:ILE:HD11	4:X:120:ASN:HB3	2.01	0.42
1:a:31:PHE:CG	1:a:79:THR:HA	2.55	0.42
1:d:9:LEU:HD11	4:W:72:ASP:OD2	2.19	0.42
1:h:90:ASP:HB2	4:U:4:TYR:HH	1.83	0.42
2:t:151:ASP:N	2:t:151:ASP:OD1	2.50	0.42
2:t:366:ILE:HB	2:t:393:VAL:HG23	2.01	0.42
2:t:497:PRO:HG2	2:t:516:SER:HB3	2.00	0.42
2:u:356:ASN:ND2	3:C:86:GLY:O	2.50	0.42
2:u:602:ILE:HD11	2:u:606:THR:OG1	2.18	0.42
2:v:19:PRO:HG3	2:w:711:GLU:CG	2.48	0.42
2:v:142:ASN:CB	2:v:295:LEU:HD11	2.44	0.42
2:v:407:VAL:HG23	2:v:414:LEU:HB2	2.01	0.42
2:v:521:SER:HA	2:v:549:VAL:O	2.19	0.42
2:v:698:ILE:HG13	2:w:707:TRP:CH2	2.54	0.42
2:w:19:PRO:HG3	2:x:711:GLU:CG	2.49	0.42
4:N:114:ASP:OD1	4:N:115:SER:N	2.52	0.42
4:W:31:THR:C	4:W:33:GLU:H	2.27	0.42
4:X:36:ALA:O	4:X:37:ASN:C	2.62	0.42
1:a:93:ILE:HD12	2:w:739:ASN:HA	2.01	0.42
1:e:36:LEU:N	1:e:42:LYS:H	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:r:9:LEU:HD23	1:r:9:LEU:HA	1.78	0.42
2:s:377:PHE:O	2:s:390:PRO:HG3	2.19	0.42
2:s:707:TRP:CH2	2:x:698:ILE:HG13	2.55	0.42
2:t:145:ASN:OD1	2:t:145:ASN:C	2.59	0.42
2:t:633:VAL:HG22	2:t:669:ILE:HD13	2.01	0.42
2:u:407:VAL:HG23	2:u:414:LEU:HB2	2.01	0.42
2:u:646:PRO:C	2:u:648:ALA:N	2.74	0.42
2:v:48:LEU:HD21	2:v:545:PHE:CE1	2.54	0.42
2:v:377:PHE:O	2:v:390:PRO:HG3	2.19	0.42
2:w:170:ASN:HD22	2:w:170:ASN:N	2.17	0.42
2:w:746:LEU:H	2:w:746:LEU:HG	1.53	0.42
2:x:256:LYS:HB2	2:x:256:LYS:HE3	1.84	0.42
2:x:407:VAL:HG23	2:x:414:LEU:HB2	2.01	0.42
2:x:464:ARG:HE	2:x:464:ARG:HB2	1.62	0.42
4:O:62:ASN:O	4:O:63:ILE:C	2.62	0.42
4:P:167:ALA:O	4:P:168:ARG:C	2.61	0.42
4:T:167:ALA:O	4:T:168:ARG:C	2.61	0.42
4:V:42:ASN:OD1	4:W:28:PRO:HD3	2.20	0.42
4:X:168:ARG:HH11	4:X:172:MET:CE	2.24	0.42
1:i:60:LEU:HD12	1:i:64:TRP:CD1	2.54	0.42
1:j:29:ARG:C	1:j:31:PHE:N	2.75	0.42
1:r:15:GLY:HA2	1:r:66:PRO:HD2	2.00	0.42
2:s:170:ASN:HD22	2:s:170:ASN:N	2.17	0.42
2:t:170:ASN:HD22	2:t:170:ASN:N	2.17	0.42
2:t:433:LYS:H	2:t:433:LYS:HG3	1.71	0.42
2:t:521:SER:HA	2:t:549:VAL:O	2.19	0.42
2:v:41:GLY:O	2:v:42:LEU:C	2.59	0.42
2:v:109:THR:CG2	2:v:112:PRO:HA	2.50	0.42
2:v:258:PRO:HA	2:v:259:PRO:HD3	1.84	0.42
2:x:29:SER:O	2:x:678:GLU:HB2	2.20	0.42
2:x:72:ASP:O	2:x:73:GLU:C	2.62	0.42
4:M:3:SER:OG	4:M:6:MET:HB2	2.20	0.42
4:P:178:TYR:O	4:P:178:TYR:CD1	2.69	0.42
4:W:3:SER:OG	4:W:6:MET:HB2	2.19	0.42
1:c:6:LYS:O	1:c:24:PHE:HB3	2.20	0.42
1:i:95:ARG:CD	2:u:639:LYS:CG	2.97	0.42
1:j:62:LYS:O	1:j:63:ALA:C	2.63	0.42
1:k:95:ARG:O	1:k:96:ALA:C	2.59	0.42
1:l:9:LEU:HD21	1:l:23:PRO:CG	2.41	0.42
1:l:31:PHE:CG	1:l:79:THR:HA	2.53	0.42
1:m:31:PHE:CG	1:m:79:THR:HA	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:287:GLU:H	2:s:287:GLU:HG3	1.40	0.42
2:t:449:ALA:HB2	2:t:461:ALA:O	2.20	0.42
2:t:774:THR:HG22	2:t:775:PRO:O	2.19	0.42
2:u:109:THR:CG2	2:u:112:PRO:HA	2.50	0.42
2:u:309:PRO:HB2	2:u:327:TRP:CZ2	2.53	0.42
2:v:143:LEU:HB3	2:v:298:ASN:H	1.85	0.42
2:v:161:TYR:HB3	2:v:162:GLY:H	1.61	0.42
2:x:143:LEU:HB3	2:x:298:ASN:H	1.85	0.42
2:x:202:LYS:HA	2:x:205:ARG:HH11	1.85	0.42
2:x:323:LYS:HE3	2:x:323:LYS:HB2	1.73	0.42
2:x:366:ILE:HB	2:x:393:VAL:HG23	2.01	0.42
2:x:616:ILE:HG23	2:x:621:ILE:HG21	2.00	0.42
3:F:125:PHE:O	3:F:128:GLN:HG2	2.19	0.42
4:O:155:GLU:O	4:O:156:VAL:C	2.62	0.42
4:P:54:ILE:HD13	4:P:54:ILE:HA	1.84	0.42
4:Q:62:ASN:O	4:Q:63:ILE:C	2.62	0.42
4:R:172:MET:HE2	4:R:172:MET:HB2	1.87	0.42
1:k:45:THR:O	1:k:46:ILE:C	2.62	0.42
1:l:6:LYS:O	1:l:24:PHE:HB3	2.20	0.42
1:n:22:ILE:N	1:n:56:THR:O	2.48	0.42
1:q:22:ILE:N	1:q:56:THR:O	2.47	0.42
1:r:106:THR:O	1:r:109:VAL:HG12	2.20	0.42
2:s:176:LYS:HZ3	2:s:178:LYS:CD	2.31	0.42
2:s:532:ASN:HB2	2:s:534:GLU:HG2	2.00	0.42
2:s:591:ARG:HE	2:s:591:ARG:HB2	1.19	0.42
2:t:640:ILE:H	2:t:640:ILE:HG13	1.63	0.42
2:u:35:TRP:CH2	2:u:511:PHE:HB3	2.55	0.42
2:v:72:ASP:O	2:v:73:GLU:C	2.62	0.42
2:w:21:ILE:CG1	2:w:697:ASP:OD1	2.66	0.42
2:w:48:LEU:HD21	2:w:545:PHE:CE1	2.54	0.42
2:w:137:ASN:HD22	2:w:137:ASN:HA	1.73	0.42
2:w:532:ASN:HB2	2:w:534:GLU:HG2	2.00	0.42
2:x:148:PRO:O	2:x:249:HIS:HD2	2.02	0.42
2:x:521:SER:HA	2:x:549:VAL:O	2.19	0.42
2:x:567:ASN:HD22	2:x:567:ASN:HA	1.54	0.42
2:x:664:GLY:O	2:x:665:ARG:HG2	2.20	0.42
3:B:104:GLY:O	3:B:108:ARG:HG3	2.20	0.42
3:E:104:GLY:O	3:E:108:ARG:HG3	2.20	0.42
4:N:170:LEU:HA	4:N:170:LEU:HD12	1.62	0.42
4:X:7:ASN:HD22	4:X:7:ASN:HA	1.67	0.42
1:d:55:ARG:HH21	4:W:6:MET:HG2	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:e:45:THR:O	1:e:46:ILE:C	2.62	0.42
1:e:92:SER:OG	4:X:30:SER:HB3	2.20	0.42
1:g:9:LEU:HD11	4:U:72:ASP:OD2	2.20	0.42
1:g:62:LYS:HD2	1:g:62:LYS:HA	1.70	0.42
1:i:6:LYS:O	1:i:24:PHE:HB3	2.20	0.42
1:j:9:LEU:CG	4:S:72:ASP:CG	2.92	0.42
1:j:27:LEU:HD13	1:j:27:LEU:HA	1.57	0.42
1:m:62:LYS:HD2	1:m:62:LYS:HA	1.70	0.42
1:n:94:LEU:HD23	2:s:736:LEU:HB2	2.02	0.42
1:p:54:THR:O	1:p:55:ARG:C	2.60	0.42
2:s:2:ALA:O	2:s:3:LEU:C	2.60	0.42
2:s:70:ASN:ND2	2:x:419:GLU:OE1	2.53	0.42
2:s:109:THR:CG2	2:s:112:PRO:HA	2.50	0.42
2:s:202:LYS:HA	2:s:205:ARG:HH11	1.85	0.42
2:s:309:PRO:HB2	2:s:327:TRP:CZ2	2.53	0.42
2:s:521:SER:HA	2:s:549:VAL:O	2.19	0.42
2:t:109:THR:CG2	2:t:112:PRO:HA	2.50	0.42
2:t:202:LYS:HA	2:t:205:ARG:HH11	1.85	0.42
2:t:256:LYS:HE3	2:t:256:LYS:HB2	1.84	0.42
2:t:532:ASN:HB2	2:t:534:GLU:HG2	2.00	0.42
2:t:611:THR:C	2:t:613:THR:H	2.27	0.42
2:u:41:GLY:O	2:u:42:LEU:C	2.59	0.42
2:v:497:PRO:HG2	2:v:516:SER:HB3	2.00	0.42
2:v:611:THR:C	2:v:613:THR:H	2.27	0.42
2:v:633:VAL:HG22	2:v:669:ILE:HD13	2.01	0.42
2:w:366:ILE:HB	2:w:393:VAL:HG23	2.01	0.42
2:w:616:ILE:HG23	2:w:621:ILE:HG21	2.00	0.42
2:x:109:THR:CG2	2:x:112:PRO:HA	2.50	0.42
2:x:185:PRO:CD	3:F:42:MET:HE3	2.24	0.42
3:A:125:PHE:O	3:A:128:GLN:HG2	2.19	0.42
4:Q:31:THR:C	4:Q:33:GLU:H	2.27	0.42
4:R:114:ASP:OD1	4:R:115:SER:N	2.52	0.42
4:U:14:LEU:HD13	4:U:32:LEU:HB2	2.01	0.42
4:V:160:LEU:HD12	4:V:160:LEU:HA	1.73	0.42
4:X:114:ASP:OD1	4:X:115:SER:N	2.52	0.42
1:b:92:SER:OG	4:N:30:SER:HB3	2.19	0.42
1:f:106:THR:O	1:f:109:VAL:HG12	2.20	0.42
1:h:92:SER:OG	4:V:30:SER:HB3	2.20	0.42
1:p:31:PHE:CG	1:p:79:THR:HA	2.55	0.42
2:s:29:SER:O	2:s:678:GLU:HB2	2.20	0.42
2:s:72:ASP:O	2:s:73:GLU:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:356:ASN:ND2	3:E:86:GLY:O	2.52	0.42
2:s:664:GLY:O	2:s:665:ARG:HG2	2.20	0.42
2:t:11:LEU:HD23	2:t:11:LEU:HA	1.50	0.42
2:t:177:TYR:HE2	2:t:196:LEU:HD21	1.85	0.42
2:t:277:ALA:CA	3:C:100:ARG:HG3	2.43	0.42
2:t:359:GLY:C	2:t:360:PHE:CD1	2.95	0.42
2:u:143:LEU:HB3	2:u:298:ASN:H	1.85	0.42
2:u:202:LYS:HA	2:u:205:ARG:HH11	1.85	0.42
2:u:633:VAL:HG22	2:u:669:ILE:HD13	2.01	0.42
2:v:202:LYS:HA	2:v:205:ARG:HH11	1.85	0.42
2:v:328:SER:CB	2:v:376:ASN:HA	2.50	0.42
2:v:366:ILE:HB	2:v:393:VAL:HG23	2.01	0.42
2:v:695:THR:H	2:v:695:THR:HG23	1.62	0.42
2:w:29:SER:O	2:w:678:GLU:HB2	2.20	0.42
2:w:63:ALA:HB1	2:w:113:ARG:HE	1.83	0.42
2:w:109:THR:CG2	2:w:112:PRO:HA	2.50	0.42
2:w:161:TYR:CE1	3:A:46:ASN:HB3	2.55	0.42
2:w:359:GLY:C	2:w:360:PHE:CD1	2.95	0.42
2:w:370:ARG:NH1	3:A:82:ARG:HH22	2.18	0.42
2:w:535:LEU:HD12	2:w:535:LEU:HA	1.90	0.42
2:w:591:ARG:O	2:w:593:PHE:CD1	2.73	0.42
2:w:713:SER:OG	2:w:714:GLY:N	2.53	0.42
2:x:9:LYS:HE2	2:x:9:LYS:HB3	1.78	0.42
4:O:20:ILE:HG23	4:O:143:SER:HA	2.02	0.42
4:O:75:SER:HB3	4:O:77:LEU:HG	2.01	0.42
4:R:95:ILE:HG23	4:R:107:THR:HG23	2.01	0.42
1:a:62:LYS:O	1:a:63:ALA:C	2.63	0.41
1:e:9:LEU:HD12	1:e:9:LEU:HA	1.82	0.41
1:f:50:TYR:HB3	1:f:60:LEU:HB3	2.01	0.41
1:i:13:LEU:HB2	1:i:71:THR:CA	2.50	0.41
1:o:93:ILE:HD13	1:o:93:ILE:HG21	1.73	0.41
1:p:9:LEU:HD11	4:O:72:ASP:OD2	2.19	0.41
2:s:161:TYR:HB2	3:E:47:ILE:HD13	2.01	0.41
2:s:715:THR:HG23	2:s:715:THR:O	2.20	0.41
2:t:184:GLN:C	3:D:42:MET:CE	2.93	0.41
2:t:664:GLY:O	2:t:665:ARG:HG2	2.20	0.41
2:u:48:LEU:HD21	2:u:545:PHE:CE1	2.54	0.41
2:u:314:ARG:O	2:u:314:ARG:CG	2.66	0.41
2:u:377:PHE:O	2:u:390:PRO:HG3	2.19	0.41
2:u:449:ALA:HB2	2:u:461:ALA:O	2.20	0.41
2:u:472:ARG:HG2	2:u:473:TYR:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:u:591:ARG:O	2:u:593:PHE:CD1	2.73	0.41
2:u:640:ILE:H	2:u:640:ILE:HG13	1.63	0.41
2:v:60:LEU:HD12	2:v:60:LEU:HA	1.63	0.41
2:v:591:ARG:O	2:v:593:PHE:CD1	2.73	0.41
2:v:713:SER:OG	2:v:714:GLY:N	2.53	0.41
2:v:735:ARG:HH11	4:W:38:ALA:CB	2.33	0.41
2:w:184:GLN:O	2:w:185:PRO:C	2.57	0.41
2:w:633:VAL:HG22	2:w:669:ILE:HD13	2.01	0.41
2:x:524:PHE:HD2	2:x:542:HIS:HB2	1.83	0.41
3:A:43:ARG:HG3	3:A:43:ARG:H	1.55	0.41
3:D:49:ASN:OD1	3:D:128:GLN:NE2	2.52	0.41
4:N:54:ILE:HD13	4:N:54:ILE:HA	1.85	0.41
4:S:20:ILE:HG23	4:S:143:SER:HA	2.02	0.41
4:T:63:ILE:HD11	4:T:120:ASN:HB3	2.01	0.41
1:b:36:LEU:N	1:b:42:LYS:H	2.18	0.41
1:d:54:THR:O	1:d:55:ARG:C	2.60	0.41
1:k:36:LEU:N	1:k:42:LYS:H	2.18	0.41
1:m:97:TYR:HE1	4:R:6:MET:SD	2.43	0.41
1:n:45:THR:O	1:n:46:ILE:C	2.62	0.41
1:q:12:GLN:H	1:q:12:GLN:HG2	1.35	0.41
2:s:449:ALA:HB2	2:s:461:ALA:O	2.20	0.41
2:s:640:ILE:H	2:s:640:ILE:HG13	1.63	0.41
2:s:774:THR:HG22	2:s:775:PRO:O	2.19	0.41
2:t:35:TRP:CH2	2:t:511:PHE:HB3	2.55	0.41
2:t:143:LEU:HB3	2:t:298:ASN:H	1.85	0.41
2:t:284:TYR:HB2	2:t:291:TRP:CE3	2.54	0.41
2:t:328:SER:CB	2:t:376:ASN:HA	2.50	0.41
2:t:472:ARG:HG2	2:t:473:TYR:N	2.35	0.41
2:t:645:GLN:HA	2:t:650:TRP:CZ2	2.56	0.41
2:t:746:LEU:H	2:t:746:LEU:HG	1.53	0.41
2:u:524:PHE:HD2	2:u:542:HIS:HB2	1.82	0.41
2:u:645:GLN:HA	2:u:650:TRP:CZ2	2.55	0.41
2:u:664:GLY:O	2:u:665:ARG:HG2	2.20	0.41
2:v:524:PHE:HD2	2:v:542:HIS:HB2	1.83	0.41
2:x:580:LYS:H	2:x:580:LYS:HG2	1.46	0.41
2:x:611:THR:C	2:x:613:THR:H	2.27	0.41
3:D:119:ARG:HA	3:D:119:ARG:HD3	1.76	0.41
4:O:31:THR:C	4:O:33:GLU:H	2.28	0.41
4:O:80:TYR:HD2	4:O:103:VAL:HG12	1.85	0.41
4:S:31:THR:C	4:S:33:GLU:H	2.27	0.41
4:T:42:ASN:OD1	4:U:28:PRO:HD3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U:6:MET:HA	4:U:6:MET:HE3	2.03	0.41
4:V:36:ALA:O	4:V:37:ASN:C	2.62	0.41
4:X:178:TYR:O	4:X:178:TYR:CD1	2.69	0.41
1:a:23:PRO:CB	4:M:79:VAL:HG11	2.47	0.41
1:a:55:ARG:HH21	4:M:6:MET:HG2	1.85	0.41
1:g:31:PHE:CG	1:g:79:THR:HA	2.55	0.41
1:o:6:LYS:O	1:o:24:PHE:HB3	2.20	0.41
1:p:25:GLU:HB2	1:p:108:HIS:HE1	1.86	0.41
2:s:35:TRP:CH2	2:s:511:PHE:HB3	2.55	0.41
2:t:86:ILE:C	2:t:98:VAL:HG11	2.30	0.41
2:t:277:ALA:CB	3:C:103:GLU:HB3	2.50	0.41
2:t:591:ARG:O	2:t:593:PHE:CD1	2.73	0.41
2:u:713:SER:OG	2:u:714:GLY:N	2.53	0.41
2:v:21:ILE:CG1	2:v:697:ASP:OD1	2.66	0.41
2:v:284:TYR:HB2	2:v:291:TRP:CE3	2.54	0.41
2:w:495:TYR:HD1	2:w:495:TYR:HA	1.65	0.41
2:x:35:TRP:CH2	2:x:511:PHE:HB3	2.55	0.41
2:x:715:THR:O	2:x:715:THR:HG23	2.20	0.41
3:A:126:ALA:O	3:A:129:LEU:HG	2.20	0.41
3:E:72:MET:HE3	3:E:72:MET:HB2	1.93	0.41
3:F:49:ASN:OD1	3:F:128:GLN:NE2	2.52	0.41
4:P:36:ALA:O	4:P:37:ASN:C	2.62	0.41
4:Q:21:LEU:HD23	4:Q:21:LEU:HA	1.81	0.41
4:U:31:THR:C	4:U:33:GLU:H	2.27	0.41
4:U:75:SER:HB3	4:U:77:LEU:HG	2.01	0.41
1:d:93:ILE:HD12	2:v:739:ASN:HA	2.01	0.41
1:h:45:THR:O	1:h:46:ILE:C	2.62	0.41
1:i:106:THR:O	1:i:109:VAL:HG12	2.20	0.41
1:p:29:ARG:C	1:p:31:PHE:N	2.75	0.41
1:p:62:LYS:O	1:p:63:ALA:C	2.63	0.41
1:r:13:LEU:HB2	1:r:71:THR:CA	2.50	0.41
2:s:143:LEU:HB3	2:s:298:ASN:H	1.85	0.41
2:s:633:VAL:HG22	2:s:669:ILE:HD13	2.01	0.41
2:s:739:ASN:O	2:s:742:ARG:HG3	2.21	0.41
2:s:779:ILE:HD12	2:s:779:ILE:HA	1.87	0.41
2:t:116:LEU:HD12	2:t:127:ILE:HG22	2.03	0.41
2:u:735:ARG:HH11	4:U:38:ALA:CB	2.34	0.41
2:v:664:GLY:O	2:v:665:ARG:HG2	2.20	0.41
2:w:35:TRP:CH2	2:w:511:PHE:HB3	2.55	0.41
2:w:202:LYS:HE2	2:w:202:LYS:HB3	1.64	0.41
2:w:309:PRO:HB2	2:w:327:TRP:CZ2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:111:ASN:HA	3:B:114:THR:HG22	2.02	0.41
3:E:125:PHE:O	3:E:126:ALA:C	2.64	0.41
4:M:62:ASN:O	4:M:63:ILE:C	2.62	0.41
4:O:21:LEU:HA	4:O:21:LEU:HD23	1.81	0.41
4:P:42:ASN:OD1	4:Q:28:PRO:HD3	2.20	0.41
4:P:168:ARG:HH12	4:P:172:MET:HE3	1.63	0.41
4:U:80:TYR:HD2	4:U:103:VAL:HG12	1.85	0.41
4:V:51:ASN:HD21	4:V:127:TYR:HA	1.86	0.41
1:c:95:ARG:HD2	2:w:639:LYS:CD	2.50	0.41
1:g:54:THR:O	1:g:55:ARG:C	2.60	0.41
1:r:6:LYS:O	1:r:24:PHE:HB3	2.20	0.41
2:s:254:PHE:CE2	3:E:65:ALA:HB2	2.42	0.41
2:t:21:ILE:CG1	2:t:697:ASP:OD1	2.66	0.41
2:t:525:MET:HB3	2:t:525:MET:HE3	1.67	0.41
2:u:328:SER:CB	2:u:376:ASN:HA	2.50	0.41
2:v:154:ILE:HG23	2:v:244:ILE:CG2	2.51	0.41
2:v:176:LYS:HZ1	2:v:178:LYS:CE	2.21	0.41
2:v:177:TYR:HE2	2:v:196:LEU:HD21	1.86	0.41
2:v:591:ARG:HE	2:v:591:ARG:HB2	1.19	0.41
2:v:593:PHE:N	2:v:593:PHE:HD1	2.14	0.41
2:w:11:LEU:HA	2:w:11:LEU:HD23	1.50	0.41
2:w:256:LYS:HE3	2:w:256:LYS:HB2	1.84	0.41
2:w:715:THR:O	2:w:715:THR:HG23	2.20	0.41
2:x:591:ARG:O	2:x:593:PHE:CD1	2.73	0.41
2:x:713:SER:OG	2:x:714:GLY:N	2.53	0.41
3:A:111:ASN:HA	3:A:114:THR:HG22	2.03	0.41
4:R:76:ASN:HD22	4:R:76:ASN:HA	1.66	0.41
4:S:62:ASN:O	4:S:63:ILE:C	2.62	0.41
4:T:114:ASP:OD1	4:T:115:SER:N	2.52	0.41
4:W:1:MET:SD	4:X:15:SER:OG	2.66	0.41
4:X:51:ASN:HD21	4:X:127:TYR:HA	1.86	0.41
1:d:62:LYS:O	1:d:63:ALA:C	2.63	0.41
1:h:27:LEU:HD13	1:h:27:LEU:HA	1.71	0.41
1:h:95:ARG:O	1:h:96:ALA:C	2.59	0.41
1:m:25:GLU:HB2	1:m:108:HIS:HE1	1.86	0.41
1:m:62:LYS:O	1:m:63:ALA:C	2.63	0.41
1:n:36:LEU:N	1:n:42:LYS:H	2.17	0.41
1:q:36:LEU:N	1:q:42:LYS:H	2.17	0.41
2:s:116:LEU:HD12	2:s:127:ILE:HG22	2.03	0.41
2:s:472:ARG:HG2	2:s:473:TYR:N	2.35	0.41
2:s:645:GLN:HA	2:s:650:TRP:CZ2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:739:ASN:O	2:t:742:ARG:HG3	2.21	0.41
2:u:116:LEU:HD12	2:u:127:ILE:HG22	2.03	0.41
2:u:142:ASN:CB	2:u:295:LEU:HD11	2.43	0.41
2:v:35:TRP:CH2	2:v:511:PHE:HB3	2.55	0.41
2:v:145:ASN:OD1	2:v:145:ASN:C	2.59	0.41
2:v:163:ARG:NH2	3:A:129:LEU:HB2	2.35	0.41
2:v:449:ALA:HB2	2:v:461:ALA:O	2.20	0.41
2:v:472:ARG:HG2	2:v:473:TYR:N	2.35	0.41
2:w:150:GLN:OE1	2:w:224:ALA:HB2	2.11	0.41
2:w:202:LYS:HA	2:w:205:ARG:HH11	1.85	0.41
2:w:284:TYR:HB2	2:w:291:TRP:CE3	2.54	0.41
2:w:524:PHE:HD2	2:w:542:HIS:HB2	1.83	0.41
2:x:314:ARG:O	2:x:314:ARG:CG	2.66	0.41
3:A:104:GLY:O	3:A:108:ARG:HG3	2.20	0.41
3:B:85:ILE:HG12	3:B:95:MET:HB3	2.03	0.41
4:M:78:ILE:HB	4:M:103:VAL:HG22	2.03	0.41
4:M:182:ASN:OD1	4:M:185:ASP:CB	2.62	0.41
4:Q:80:TYR:HD2	4:Q:103:VAL:HG12	1.85	0.41
4:T:51:ASN:HD21	4:T:127:TYR:HA	1.86	0.41
4:U:20:ILE:HG23	4:U:143:SER:HA	2.02	0.41
4:V:7:ASN:HD22	4:V:7:ASN:HA	1.67	0.41
1:a:25:GLU:HB2	1:a:108:HIS:HE1	1.86	0.41
1:d:97:TYR:HE1	4:X:6:MET:SD	2.42	0.41
1:f:13:LEU:HB2	1:f:71:THR:CA	2.50	0.41
1:i:84:ARG:O	1:i:85:LEU:C	2.59	0.41
1:j:25:GLU:HB2	1:j:108:HIS:HE1	1.86	0.41
2:s:60:LEU:HD12	2:s:60:LEU:HA	1.62	0.41
2:s:535:LEU:O	2:s:536:ARG:C	2.64	0.41
2:s:617:HIS:CE1	2:s:654:PRO:HB2	2.56	0.41
2:s:788:LEU:HD13	2:s:788:LEU:HA	1.93	0.41
2:v:323:LYS:HB2	2:v:323:LYS:HE3	1.73	0.41
2:v:617:HIS:CE1	2:v:654:PRO:HB2	2.56	0.41
2:w:328:SER:CB	2:w:376:ASN:HA	2.50	0.41
2:w:664:GLY:O	2:w:665:ARG:HG2	2.20	0.41
2:w:684:ILE:H	2:w:684:ILE:HG13	1.60	0.41
3:A:119:ARG:NH1	3:B:61:GLU:OE1	2.53	0.41
3:B:102:THR:O	3:B:105:GLN:HB2	2.21	0.41
4:Q:20:ILE:HG23	4:Q:143:SER:HA	2.03	0.41
4:V:63:ILE:HD11	4:V:120:ASN:HB3	2.01	0.41
4:W:78:ILE:HB	4:W:103:VAL:HG22	2.03	0.41
4:X:54:ILE:HD13	4:X:54:ILE:HA	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:c:27:LEU:HD12	1:c:27:LEU:HA	1.74	0.41
1:e:95:ARG:O	1:e:96:ALA:C	2.59	0.41
1:g:25:GLU:HB2	1:g:108:HIS:HE1	1.86	0.41
1:g:62:LYS:O	1:g:63:ALA:C	2.63	0.41
1:i:50:TYR:HB3	1:i:60:LEU:HB3	2.02	0.41
2:t:29:SER:O	2:t:678:GLU:HB2	2.20	0.41
2:t:788:LEU:HD13	2:t:788:LEU:HA	1.93	0.41
2:u:154:ILE:HG23	2:u:244:ILE:CG2	2.51	0.41
2:u:284:TYR:HB2	2:u:291:TRP:CE3	2.54	0.41
2:v:419:GLU:OE1	2:w:70:ASN:ND2	2.54	0.41
2:v:715:THR:H	2:v:715:THR:HG22	1.57	0.41
2:w:735:ARG:HH11	4:M:38:ALA:CB	2.34	0.41
2:x:449:ALA:HB2	2:x:461:ALA:O	2.20	0.41
2:x:645:GLN:HA	2:x:650:TRP:CZ2	2.56	0.41
4:N:51:ASN:HD21	4:N:127:TYR:HA	1.86	0.41
4:P:24:ILE:H	4:P:24:ILE:HG12	1.79	0.41
4:Q:53:GLN:HE21	4:Q:53:GLN:HB3	1.48	0.41
4:Q:155:GLU:O	4:Q:156:VAL:C	2.62	0.41
4:R:42:ASN:OD1	4:S:28:PRO:HD3	2.21	0.41
4:X:160:LEU:HA	4:X:160:LEU:HD12	1.73	0.41
1:d:25:GLU:HB2	1:d:108:HIS:HE1	1.86	0.41
1:d:94:LEU:HD21	1:d:99:LEU:CD1	2.49	0.41
1:g:97:TYR:HE1	4:V:6:MET:SD	2.43	0.41
1:h:55:ARG:HD2	1:h:55:ARG:HA	1.86	0.41
1:h:94:LEU:O	1:h:95:ARG:C	2.64	0.41
1:r:95:ARG:HD2	2:x:639:LYS:CD	2.51	0.41
2:s:184:GLN:O	2:s:185:PRO:C	2.57	0.41
2:s:277:ALA:CB	3:D:103:GLU:HB3	2.50	0.41
2:s:288:ARG:O	2:s:290:VAL:HG22	2.21	0.41
2:s:328:SER:CB	2:s:376:ASN:HA	2.50	0.41
2:s:684:ILE:H	2:s:684:ILE:HG13	1.60	0.41
2:t:153:LEU:HA	2:t:153:LEU:HD12	1.66	0.41
2:t:617:HIS:CE1	2:t:654:PRO:HB2	2.56	0.41
2:u:72:ASP:O	2:u:73:GLU:C	2.62	0.41
2:u:254:PHE:HE1	3:B:112:MET:SD	2.44	0.41
2:u:256:LYS:HB2	2:u:256:LYS:HE3	1.84	0.41
2:u:277:ALA:CB	3:B:103:GLU:HB3	2.51	0.41
2:u:715:THR:O	2:u:715:THR:HG23	2.21	0.41
2:v:29:SER:O	2:v:678:GLU:HB2	2.20	0.41
2:v:46:PRO:HA	2:v:47:PRO:HD3	1.90	0.41
2:v:116:LEU:HD12	2:v:127:ILE:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:118:MET:HE3	2:v:118:MET:HB2	1.74	0.41
2:w:60:LEU:HA	2:w:60:LEU:HD12	1.62	0.41
2:w:154:ILE:HG23	2:w:244:ILE:CG2	2.51	0.41
2:w:288:ARG:O	2:w:290:VAL:HG22	2.21	0.41
2:w:449:ALA:HB2	2:w:461:ALA:O	2.20	0.41
2:w:645:GLN:HA	2:w:650:TRP:CZ2	2.56	0.41
2:w:739:ASN:O	2:w:742:ARG:HG3	2.21	0.41
2:x:61:GLY:HA2	2:x:566:ARG:NH1	2.36	0.41
2:x:328:SER:CB	2:x:376:ASN:HA	2.50	0.41
2:x:739:ASN:O	2:x:742:ARG:HG3	2.21	0.41
3:A:102:THR:O	3:A:105:GLN:HB2	2.21	0.41
4:M:20:ILE:HG23	4:M:143:SER:HA	2.02	0.41
4:P:51:ASN:HD21	4:P:127:TYR:HA	1.86	0.41
4:Q:6:MET:CE	4:R:6:MET:HB2	2.51	0.41
4:R:51:ASN:HD21	4:R:127:TYR:HA	1.85	0.41
4:S:78:ILE:HB	4:S:103:VAL:HG22	2.03	0.41
4:U:78:ILE:HB	4:U:103:VAL:HG22	2.03	0.41
4:V:76:ASN:HD22	4:V:76:ASN:HA	1.66	0.41
4:V:114:ASP:OD1	4:V:115:SER:N	2.52	0.41
4:W:80:TYR:HD2	4:W:103:VAL:HG12	1.86	0.41
1:a:9:LEU:HD23	1:a:11:TYR:CE1	2.56	0.41
1:c:106:THR:O	1:c:109:VAL:HG12	2.21	0.41
1:d:9:LEU:HD23	1:d:11:TYR:CE1	2.56	0.41
1:k:65:GLY:C	1:k:67:ALA:N	2.79	0.41
1:k:94:LEU:HD11	2:t:741:LEU:CD1	2.51	0.41
1:m:11:TYR:CD2	4:Q:70:LEU:O	2.73	0.41
1:o:13:LEU:HB2	1:o:71:THR:CA	2.50	0.41
2:s:591:ARG:O	2:s:593:PHE:CD1	2.73	0.41
2:t:202:LYS:HE2	2:t:202:LYS:HB3	1.64	0.41
2:t:633:VAL:HG11	2:t:658:LEU:HD21	2.04	0.41
2:t:715:THR:HG23	2:t:715:THR:O	2.20	0.41
2:v:256:LYS:HE3	2:v:256:LYS:HB2	1.84	0.41
2:v:715:THR:HG23	2:v:715:THR:O	2.20	0.41
2:w:52:ASN:HD22	2:w:52:ASN:HA	1.53	0.41
2:w:143:LEU:HB3	2:w:298:ASN:H	1.85	0.41
2:w:419:GLU:OE1	2:x:70:ASN:ND2	2.54	0.41
2:w:698:ILE:HG13	2:x:707:TRP:CH2	2.56	0.41
2:x:21:ILE:CG1	2:x:697:ASP:OD1	2.66	0.41
2:x:172:LYS:HB3	2:x:172:LYS:HE2	1.64	0.41
2:x:617:HIS:CE1	2:x:654:PRO:HB2	2.56	0.41
3:E:84:ALA:O	3:E:87:GLU:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:102:THR:O	3:E:105:GLN:HB2	2.21	0.41
4:S:80:TYR:HD2	4:S:103:VAL:HG12	1.85	0.41
4:U:46:ILE:HD13	4:U:46:ILE:HA	1.94	0.41
4:X:16:ALA:HB2	4:X:127:TYR:CZ	2.56	0.41
1:k:110:ALA:O	1:k:111:GLU:C	2.63	0.40
1:m:9:LEU:HD11	4:Q:72:ASP:OD2	2.21	0.40
1:p:9:LEU:HD23	1:p:11:TYR:CE1	2.56	0.40
2:t:184:GLN:CA	3:D:42:MET:CE	2.94	0.40
2:u:355:ARG:HD3	2:u:355:ARG:HA	1.95	0.40
2:u:361:LEU:HA	2:u:361:LEU:HD12	1.67	0.40
2:w:611:THR:O	2:w:613:THR:N	2.48	0.40
2:x:271:GLY:HA3	3:E:107:ILE:HG21	2.02	0.40
2:x:288:ARG:O	2:x:290:VAL:HG22	2.21	0.40
3:C:111:ASN:HA	3:C:114:THR:HG22	2.03	0.40
4:O:78:ILE:HB	4:O:103:VAL:HG22	2.03	0.40
4:P:170:LEU:HD12	4:P:170:LEU:HA	1.63	0.40
4:Q:78:ILE:HB	4:Q:103:VAL:HG22	2.03	0.40
1:g:9:LEU:HD23	1:g:11:TYR:CE1	2.56	0.40
1:j:30:LYS:HE2	1:j:30:LYS:HB3	1.93	0.40
1:l:13:LEU:HB2	1:l:71:THR:C	2.46	0.40
1:o:13:LEU:HB2	1:o:71:THR:C	2.46	0.40
1:p:30:LYS:HE2	1:p:30:LYS:HB3	1.93	0.40
2:s:366:ILE:HB	2:s:393:VAL:HG23	2.01	0.40
2:t:288:ARG:O	2:t:290:VAL:HG22	2.21	0.40
2:u:29:SER:O	2:u:678:GLU:HB2	2.20	0.40
2:v:249:HIS:HE1	2:v:265:TYR:CE2	2.40	0.40
2:v:309:PRO:HB2	2:v:327:TRP:CZ2	2.53	0.40
2:v:359:GLY:C	2:v:360:PHE:CD1	2.95	0.40
2:v:373:LYS:HE3	3:B:82:ARG:CZ	2.51	0.40
2:w:61:GLY:HA2	2:w:566:ARG:NH1	2.36	0.40
2:w:177:TYR:HE2	2:w:196:LEU:HD21	1.85	0.40
2:w:249:HIS:HE1	2:w:265:TYR:CE2	2.39	0.40
2:x:150:GLN:OE1	2:x:224:ALA:HB2	2.11	0.40
2:x:593:PHE:HD1	2:x:593:PHE:H	1.70	0.40
3:A:67:LEU:HD23	3:A:67:LEU:HA	1.95	0.40
3:B:119:ARG:HH12	3:C:61:GLU:CD	2.28	0.40
4:N:7:ASN:HD22	4:N:7:ASN:HA	1.67	0.40
4:V:167:ALA:O	4:V:168:ARG:C	2.61	0.40
1:c:35:THR:HG21	1:c:41:ARG:HD2	2.04	0.40
1:f:13:LEU:HB2	1:f:71:THR:C	2.47	0.40
1:j:9:LEU:HD11	4:S:72:ASP:OD2	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:q:9:LEU:HD12	1:q:9:LEU:HA	1.82	0.40
2:s:61:GLY:HA2	2:s:566:ARG:NH1	2.36	0.40
2:s:593:PHE:HD1	2:s:593:PHE:H	1.69	0.40
2:s:698:ILE:HG13	2:t:707:TRP:CH2	2.56	0.40
2:s:713:SER:OG	2:s:714:GLY:N	2.53	0.40
2:u:163:ARG:HH21	3:B:129:LEU:CD1	2.28	0.40
2:u:617:HIS:CE1	2:u:654:PRO:HB2	2.56	0.40
2:u:739:ASN:O	2:u:742:ARG:HG3	2.21	0.40
2:v:761:ALA:O	2:v:762:LYS:C	2.65	0.40
2:w:161:TYR:HB3	2:w:162:GLY:H	1.61	0.40
2:w:472:ARG:HG2	2:w:473:TYR:N	2.35	0.40
2:w:617:HIS:CE1	2:w:654:PRO:HB2	2.56	0.40
2:x:116:LEU:HD12	2:x:127:ILE:HG22	2.03	0.40
2:x:633:VAL:HG22	2:x:669:ILE:HD13	2.01	0.40
3:C:102:THR:O	3:C:105:GLN:HB2	2.21	0.40
3:C:110:ALA:O	3:C:113:VAL:HG12	2.22	0.40
4:N:16:ALA:HB2	4:N:127:TYR:CZ	2.57	0.40
4:V:16:ALA:HB2	4:V:127:TYR:CZ	2.57	0.40
4:W:20:ILE:HG23	4:W:143:SER:HA	2.02	0.40
4:W:182:ASN:CG	4:W:185:ASP:HB3	2.46	0.40
4:X:20:ILE:O	4:X:23:SER:HB3	2.22	0.40
1:b:11:TYR:HD1	1:b:11:TYR:HA	1.75	0.40
1:c:13:LEU:HB2	1:c:71:THR:CA	2.50	0.40
1:k:39:VAL:HG13	1:k:40:ASP:H	1.86	0.40
1:m:29:ARG:C	1:m:31:PHE:N	2.75	0.40
2:t:150:GLN:CG	2:t:224:ALA:CB	2.75	0.40
2:u:359:GLY:C	2:u:360:PHE:CD1	2.95	0.40
2:u:633:VAL:HG11	2:u:658:LEU:HD21	2.04	0.40
2:v:254:PHE:HE1	3:A:112:MET:SD	2.44	0.40
2:v:645:GLN:HA	2:v:650:TRP:CZ2	2.56	0.40
2:v:739:ASN:O	2:v:742:ARG:HG3	2.21	0.40
2:w:116:LEU:HD12	2:w:127:ILE:HG22	2.03	0.40
2:w:535:LEU:O	2:w:536:ARG:C	2.63	0.40
2:w:593:PHE:HD1	2:w:593:PHE:H	1.70	0.40
2:x:788:LEU:HD13	2:x:788:LEU:HA	1.93	0.40
3:E:85:ILE:HG12	3:E:95:MET:HB3	2.03	0.40
4:S:21:LEU:HD23	4:S:21:LEU:HA	1.81	0.40
4:S:53:GLN:HE21	4:S:53:GLN:HB3	1.49	0.40
4:U:1:MET:SD	4:V:15:SER:OG	2.66	0.40
1:a:35:THR:HB	1:a:74:GLU:HB3	2.04	0.40
1:c:95:ARG:HD2	2:w:639:LYS:HD3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:j:9:LEU:HD23	1:j:11:TYR:CE1	2.56	0.40
1:l:106:THR:O	1:l:109:VAL:HG12	2.21	0.40
1:m:9:LEU:HD23	1:m:11:TYR:CE1	2.56	0.40
1:n:110:ALA:O	1:n:111:GLU:C	2.63	0.40
2:s:153:LEU:HD12	2:s:153:LEU:HA	1.66	0.40
2:s:314:ARG:O	2:s:314:ARG:CG	2.66	0.40
2:t:154:ILE:HG23	2:t:244:ILE:CG2	2.51	0.40
2:t:172:LYS:HE2	2:t:172:LYS:HB3	1.64	0.40
2:u:249:HIS:HE1	2:u:265:TYR:CE2	2.40	0.40
2:v:288:ARG:O	2:v:290:VAL:HG22	2.21	0.40
2:v:535:LEU:O	2:v:536:ARG:C	2.64	0.40
2:v:633:VAL:HG11	2:v:658:LEU:HD21	2.04	0.40
2:w:86:ILE:C	2:w:98:VAL:HG11	2.30	0.40
2:x:202:LYS:HB3	2:x:202:LYS:HE2	1.64	0.40
2:x:249:HIS:HE1	2:x:265:TYR:CE2	2.40	0.40
2:x:384:ASN:HD22	3:F:75:VAL:HG23	1.87	0.40
3:A:88:SER:HB3	3:A:90:LEU:HG	2.03	0.40
3:A:110:ALA:O	3:A:113:VAL:HG12	2.22	0.40
4:Q:183:MET:H	4:Q:183:MET:HG2	1.74	0.40
4:S:6:MET:SD	4:T:6:MET:HB2	2.61	0.40
4:U:182:ASN:CG	4:U:185:ASP:HB3	2.47	0.40
4:W:31:THR:C	4:W:33:GLU:N	2.80	0.40
4:X:32:LEU:HA	4:X:32:LEU:HD23	1.81	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	113/553 (20%)	102 (90%)	10 (9%)	1 (1%)	14 50
1	b	113/553 (20%)	107 (95%)	4 (4%)	2 (2%)	7 34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	c	113/553 (20%)	107 (95%)	5 (4%)	1 (1%)	14	50
1	d	113/553 (20%)	102 (90%)	10 (9%)	1 (1%)	14	50
1	e	113/553 (20%)	107 (95%)	4 (4%)	2 (2%)	7	34
1	f	113/553 (20%)	107 (95%)	5 (4%)	1 (1%)	14	50
1	g	113/553 (20%)	102 (90%)	10 (9%)	1 (1%)	14	50
1	h	113/553 (20%)	107 (95%)	4 (4%)	2 (2%)	7	34
1	i	113/553 (20%)	107 (95%)	5 (4%)	1 (1%)	14	50
1	j	113/553 (20%)	102 (90%)	10 (9%)	1 (1%)	14	50
1	k	113/553 (20%)	107 (95%)	4 (4%)	2 (2%)	7	34
1	l	113/553 (20%)	107 (95%)	5 (4%)	1 (1%)	14	50
1	m	113/553 (20%)	102 (90%)	10 (9%)	1 (1%)	14	50
1	n	113/553 (20%)	107 (95%)	4 (4%)	2 (2%)	7	34
1	o	113/553 (20%)	108 (96%)	4 (4%)	1 (1%)	14	50
1	p	113/553 (20%)	102 (90%)	10 (9%)	1 (1%)	14	50
1	q	113/553 (20%)	107 (95%)	4 (4%)	2 (2%)	7	34
1	r	113/553 (20%)	107 (95%)	6 (5%)	0	100	100
2	s	787/794 (99%)	735 (93%)	46 (6%)	6 (1%)	16	53
2	t	787/794 (99%)	735 (93%)	46 (6%)	6 (1%)	16	53
2	u	787/794 (99%)	735 (93%)	46 (6%)	6 (1%)	16	53
2	v	787/794 (99%)	735 (93%)	46 (6%)	6 (1%)	16	53
2	w	787/794 (99%)	734 (93%)	47 (6%)	6 (1%)	16	53
2	x	787/794 (99%)	734 (93%)	47 (6%)	6 (1%)	16	53
3	A	100/196 (51%)	100 (100%)	0	0	100	100
3	B	100/196 (51%)	99 (99%)	1 (1%)	0	100	100
3	C	100/196 (51%)	100 (100%)	0	0	100	100
3	D	100/196 (51%)	99 (99%)	1 (1%)	0	100	100
3	E	100/196 (51%)	100 (100%)	0	0	100	100
3	F	100/196 (51%)	100 (100%)	0	0	100	100
4	M	193/196 (98%)	183 (95%)	10 (5%)	0	100	100
4	N	191/196 (97%)	180 (94%)	11 (6%)	0	100	100
4	O	193/196 (98%)	184 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	P	191/196 (97%)	179 (94%)	11 (6%)	1 (0%)	25	63
4	Q	193/196 (98%)	184 (95%)	9 (5%)	0	100	100
4	R	191/196 (97%)	180 (94%)	11 (6%)	0	100	100
4	S	193/196 (98%)	183 (95%)	10 (5%)	0	100	100
4	T	191/196 (97%)	180 (94%)	11 (6%)	0	100	100
4	U	193/196 (98%)	182 (94%)	11 (6%)	0	100	100
4	V	191/196 (97%)	179 (94%)	12 (6%)	0	100	100
4	W	193/196 (98%)	183 (95%)	10 (5%)	0	100	100
4	X	191/196 (97%)	180 (94%)	11 (6%)	0	100	100
All	All	9660/18246 (53%)	9080 (94%)	520 (5%)	60 (1%)	24	59

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	c	46	ILE
1	f	46	ILE
1	i	46	ILE
1	l	46	ILE
1	o	46	ILE
2	s	62	GLN
2	t	62	GLN
2	u	62	GLN
2	v	62	GLN
2	w	62	GLN
2	x	62	GLN
4	P	8	VAL
1	a	63	ALA
1	d	63	ALA
1	g	63	ALA
1	j	63	ALA
1	m	63	ALA
1	p	63	ALA
2	s	190	ASN
2	s	607	TYR
2	t	190	ASN
2	t	607	TYR
2	u	190	ASN
2	u	607	TYR
2	v	190	ASN

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Mol	Chain	Res	Type
2	v	607	TYR
2	w	190	ASN
2	w	607	TYR
2	x	190	ASN
2	x	607	TYR
2	s	334	ASP
2	s	639	LYS
2	t	334	ASP
2	t	639	LYS
2	u	334	ASP
2	u	639	LYS
2	v	334	ASP
2	v	639	LYS
2	w	334	ASP
2	w	639	LYS
2	x	334	ASP
2	x	639	LYS
1	b	90	ASP
1	e	90	ASP
1	h	90	ASP
1	k	90	ASP
1	n	90	ASP
1	q	90	ASP
1	b	23	PRO
1	e	23	PRO
1	h	23	PRO
1	k	23	PRO
1	n	23	PRO
1	q	23	PRO
2	s	484	ASN
2	t	484	ASN
2	u	484	ASN
2	v	484	ASN
2	w	484	ASN
2	x	484	ASN

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain 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 sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	102/451 (23%)	77 (76%)	25 (24%)	0	3
1	b	102/451 (23%)	78 (76%)	24 (24%)	0	4
1	c	102/451 (23%)	82 (80%)	20 (20%)	1	7
1	d	102/451 (23%)	78 (76%)	24 (24%)	0	4
1	e	102/451 (23%)	78 (76%)	24 (24%)	0	4
1	f	102/451 (23%)	82 (80%)	20 (20%)	1	7
1	g	102/451 (23%)	77 (76%)	25 (24%)	0	3
1	h	102/451 (23%)	78 (76%)	24 (24%)	0	4
1	i	102/451 (23%)	82 (80%)	20 (20%)	1	7
1	j	102/451 (23%)	78 (76%)	24 (24%)	0	4
1	k	102/451 (23%)	78 (76%)	24 (24%)	0	4
1	l	102/451 (23%)	82 (80%)	20 (20%)	1	7
1	m	102/451 (23%)	77 (76%)	25 (24%)	0	3
1	n	102/451 (23%)	78 (76%)	24 (24%)	0	4
1	o	102/451 (23%)	82 (80%)	20 (20%)	1	7
1	p	102/451 (23%)	77 (76%)	25 (24%)	0	3
1	q	102/451 (23%)	78 (76%)	24 (24%)	0	4
1	r	102/451 (23%)	82 (80%)	20 (20%)	1	7
2	s	684/688 (99%)	562 (82%)	122 (18%)	1	9
2	t	684/688 (99%)	562 (82%)	122 (18%)	1	9
2	u	684/688 (99%)	562 (82%)	122 (18%)	1	9
2	v	684/688 (99%)	562 (82%)	122 (18%)	1	9
2	w	684/688 (99%)	562 (82%)	122 (18%)	1	9
2	x	684/688 (99%)	562 (82%)	122 (18%)	1	9
3	A	83/149 (56%)	79 (95%)	4 (5%)	21	44
3	B	83/149 (56%)	81 (98%)	2 (2%)	44	64
3	C	83/149 (56%)	78 (94%)	5 (6%)	16	38
3	D	83/149 (56%)	80 (96%)	3 (4%)	30	52
3	E	83/149 (56%)	79 (95%)	4 (5%)	21	44
3	F	83/149 (56%)	81 (98%)	2 (2%)	44	64
4	M	168/169 (99%)	158 (94%)	10 (6%)	16	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	N	166/169 (98%)	151 (91%)	15 (9%)	8 25
4	O	168/169 (99%)	158 (94%)	10 (6%)	16 38
4	P	166/169 (98%)	154 (93%)	12 (7%)	12 32
4	Q	168/169 (99%)	158 (94%)	10 (6%)	16 38
4	R	166/169 (98%)	152 (92%)	14 (8%)	9 28
4	S	168/169 (99%)	158 (94%)	10 (6%)	16 38
4	T	166/169 (98%)	153 (92%)	13 (8%)	10 30
4	U	168/169 (99%)	158 (94%)	10 (6%)	16 38
4	V	166/169 (98%)	153 (92%)	13 (8%)	10 30
4	W	168/169 (99%)	157 (94%)	11 (6%)	14 36
4	X	166/169 (98%)	152 (92%)	14 (8%)	9 28
All	All	8442/15168 (56%)	7136 (84%)	1306 (16%)	4 12

All (1306) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	a	4	VAL
1	a	8	VAL
1	a	9	LEU
1	a	10	THR
1	a	21	ASN
1	a	22	ILE
1	a	25	GLU
1	a	27	LEU
1	a	32	VAL
1	a	33	VAL
1	a	37	ILE
1	a	39	VAL
1	a	43	VAL
1	a	46	ILE
1	a	52	PHE
1	a	56	THR
1	a	58	ILE
1	a	72	THR
1	a	73	ILE
1	a	81	THR
1	a	83	ASP
1	a	86	VAL

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Mol	Chain	Res	Type
1	a	94	LEU
1	a	98	ASP
1	a	112	GLU
1	b	4	VAL
1	b	8	VAL
1	b	10	THR
1	b	12	GLN
1	b	27	LEU
1	b	32	VAL
1	b	33	VAL
1	b	39	VAL
1	b	43	VAL
1	b	44	LEU
1	b	54	THR
1	b	57	THR
1	b	58	ILE
1	b	72	THR
1	b	73	ILE
1	b	74	GLU
1	b	81	THR
1	b	84	ARG
1	b	86	VAL
1	b	89	THR
1	b	94	LEU
1	b	100	ASN
1	b	106	THR
1	b	109	VAL
1	c	5	ILE
1	c	6	LYS
1	c	7	THR
1	c	13	LEU
1	c	16	SER
1	c	29	ARG
1	c	32	VAL
1	c	36	LEU
1	c	37	ILE
1	c	39	VAL
1	c	43	VAL
1	c	46	ILE
1	c	57	THR
1	c	58	ILE
1	c	60	LEU

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Mol	Chain	Res	Type
1	c	62	LYS
1	c	89	THR
1	c	111	GLU
1	c	116	LEU
1	c	117	THR
1	d	4	VAL
1	d	8	VAL
1	d	9	LEU
1	d	10	THR
1	d	21	ASN
1	d	22	ILE
1	d	25	GLU
1	d	27	LEU
1	d	32	VAL
1	d	33	VAL
1	d	37	ILE
1	d	39	VAL
1	d	43	VAL
1	d	46	ILE
1	d	52	PHE
1	d	56	THR
1	d	58	ILE
1	d	72	THR
1	d	73	ILE
1	d	81	THR
1	d	83	ASP
1	d	86	VAL
1	d	98	ASP
1	d	112	GLU
1	e	4	VAL
1	e	8	VAL
1	e	10	THR
1	e	12	GLN
1	e	27	LEU
1	e	32	VAL
1	e	33	VAL
1	e	39	VAL
1	e	43	VAL
1	e	44	LEU
1	e	54	THR
1	e	57	THR
1	e	58	ILE

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Mol	Chain	Res	Type
1	e	72	THR
1	e	73	ILE
1	e	74	GLU
1	e	81	THR
1	e	84	ARG
1	e	86	VAL
1	e	89	THR
1	e	94	LEU
1	e	100	ASN
1	e	106	THR
1	e	109	VAL
1	f	5	ILE
1	f	6	LYS
1	f	7	THR
1	f	13	LEU
1	f	16	SER
1	f	29	ARG
1	f	32	VAL
1	f	36	LEU
1	f	37	ILE
1	f	39	VAL
1	f	43	VAL
1	f	46	ILE
1	f	57	THR
1	f	58	ILE
1	f	60	LEU
1	f	62	LYS
1	f	89	THR
1	f	111	GLU
1	f	116	LEU
1	f	117	THR
1	g	4	VAL
1	g	8	VAL
1	g	9	LEU
1	g	10	THR
1	g	21	ASN
1	g	22	ILE
1	g	25	GLU
1	g	27	LEU
1	g	32	VAL
1	g	33	VAL
1	g	37	ILE

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Mol	Chain	Res	Type
1	g	39	VAL
1	g	43	VAL
1	g	46	ILE
1	g	52	PHE
1	g	56	THR
1	g	58	ILE
1	g	72	THR
1	g	73	ILE
1	g	81	THR
1	g	83	ASP
1	g	86	VAL
1	g	94	LEU
1	g	98	ASP
1	g	112	GLU
1	h	4	VAL
1	h	8	VAL
1	h	10	THR
1	h	12	GLN
1	h	27	LEU
1	h	32	VAL
1	h	33	VAL
1	h	39	VAL
1	h	43	VAL
1	h	44	LEU
1	h	54	THR
1	h	57	THR
1	h	58	ILE
1	h	72	THR
1	h	73	ILE
1	h	74	GLU
1	h	81	THR
1	h	84	ARG
1	h	86	VAL
1	h	89	THR
1	h	94	LEU
1	h	100	ASN
1	h	106	THR
1	h	109	VAL
1	i	5	ILE
1	i	6	LYS
1	i	7	THR
1	i	13	LEU

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Mol	Chain	Res	Type
1	i	16	SER
1	i	29	ARG
1	i	32	VAL
1	i	36	LEU
1	i	37	ILE
1	i	39	VAL
1	i	43	VAL
1	i	46	ILE
1	i	57	THR
1	i	58	ILE
1	i	60	LEU
1	i	62	LYS
1	i	89	THR
1	i	111	GLU
1	i	116	LEU
1	i	117	THR
1	j	4	VAL
1	j	8	VAL
1	j	9	LEU
1	j	10	THR
1	j	21	ASN
1	j	22	ILE
1	j	25	GLU
1	j	27	LEU
1	j	32	VAL
1	j	33	VAL
1	j	37	ILE
1	j	39	VAL
1	j	43	VAL
1	j	46	ILE
1	j	52	PHE
1	j	56	THR
1	j	58	ILE
1	j	72	THR
1	j	73	ILE
1	j	81	THR
1	j	83	ASP
1	j	86	VAL
1	j	98	ASP
1	j	112	GLU
1	k	4	VAL
1	k	8	VAL

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Mol	Chain	Res	Type
1	k	10	THR
1	k	12	GLN
1	k	27	LEU
1	k	32	VAL
1	k	33	VAL
1	k	39	VAL
1	k	43	VAL
1	k	44	LEU
1	k	54	THR
1	k	57	THR
1	k	58	ILE
1	k	72	THR
1	k	73	ILE
1	k	74	GLU
1	k	81	THR
1	k	84	ARG
1	k	86	VAL
1	k	89	THR
1	k	94	LEU
1	k	100	ASN
1	k	106	THR
1	k	109	VAL
1	l	5	ILE
1	l	6	LYS
1	l	7	THR
1	l	13	LEU
1	l	16	SER
1	l	29	ARG
1	l	32	VAL
1	l	36	LEU
1	l	37	ILE
1	l	39	VAL
1	l	43	VAL
1	l	46	ILE
1	l	57	THR
1	l	58	ILE
1	l	60	LEU
1	l	62	LYS
1	l	89	THR
1	l	111	GLU
1	l	116	LEU
1	l	117	THR

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Mol	Chain	Res	Type
1	m	4	VAL
1	m	8	VAL
1	m	9	LEU
1	m	10	THR
1	m	21	ASN
1	m	22	ILE
1	m	25	GLU
1	m	27	LEU
1	m	32	VAL
1	m	33	VAL
1	m	37	ILE
1	m	39	VAL
1	m	43	VAL
1	m	46	ILE
1	m	52	PHE
1	m	56	THR
1	m	58	ILE
1	m	72	THR
1	m	73	ILE
1	m	81	THR
1	m	83	ASP
1	m	86	VAL
1	m	94	LEU
1	m	98	ASP
1	m	112	GLU
1	n	4	VAL
1	n	8	VAL
1	n	10	THR
1	n	12	GLN
1	n	27	LEU
1	n	32	VAL
1	n	33	VAL
1	n	39	VAL
1	n	43	VAL
1	n	44	LEU
1	n	54	THR
1	n	57	THR
1	n	58	ILE
1	n	72	THR
1	n	73	ILE
1	n	74	GLU
1	n	81	THR

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Mol	Chain	Res	Type
1	n	84	ARG
1	n	86	VAL
1	n	89	THR
1	n	94	LEU
1	n	100	ASN
1	n	106	THR
1	n	109	VAL
1	o	5	ILE
1	o	6	LYS
1	o	7	THR
1	o	13	LEU
1	o	16	SER
1	o	29	ARG
1	o	32	VAL
1	o	36	LEU
1	o	37	ILE
1	o	39	VAL
1	o	43	VAL
1	o	46	ILE
1	o	57	THR
1	o	58	ILE
1	o	60	LEU
1	o	62	LYS
1	o	89	THR
1	o	111	GLU
1	o	116	LEU
1	o	117	THR
1	p	4	VAL
1	p	8	VAL
1	p	9	LEU
1	p	10	THR
1	p	21	ASN
1	p	22	ILE
1	p	25	GLU
1	p	27	LEU
1	p	32	VAL
1	p	33	VAL
1	p	37	ILE
1	p	39	VAL
1	p	43	VAL
1	p	46	ILE
1	p	52	PHE

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Mol	Chain	Res	Type
1	p	56	THR
1	p	58	ILE
1	p	72	THR
1	p	73	ILE
1	p	81	THR
1	p	83	ASP
1	p	86	VAL
1	p	94	LEU
1	p	98	ASP
1	p	112	GLU
1	q	4	VAL
1	q	8	VAL
1	q	10	THR
1	q	12	GLN
1	q	27	LEU
1	q	32	VAL
1	q	33	VAL
1	q	39	VAL
1	q	43	VAL
1	q	44	LEU
1	q	54	THR
1	q	57	THR
1	q	58	ILE
1	q	72	THR
1	q	73	ILE
1	q	74	GLU
1	q	81	THR
1	q	84	ARG
1	q	86	VAL
1	q	89	THR
1	q	94	LEU
1	q	100	ASN
1	q	106	THR
1	q	109	VAL
1	r	5	ILE
1	r	6	LYS
1	r	7	THR
1	r	13	LEU
1	r	16	SER
1	r	29	ARG
1	r	32	VAL
1	r	36	LEU

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Mol	Chain	Res	Type
1	r	37	ILE
1	r	39	VAL
1	r	43	VAL
1	r	46	ILE
1	r	57	THR
1	r	58	ILE
1	r	60	LEU
1	r	62	LYS
1	r	89	THR
1	r	111	GLU
1	r	116	LEU
1	r	117	THR
2	s	15	ILE
2	s	50	PHE
2	s	52	ASN
2	s	66	ILE
2	s	78	TYR
2	s	82	THR
2	s	86	ILE
2	s	88	VAL
2	s	98	VAL
2	s	109	THR
2	s	119	VAL
2	s	121	VAL
2	s	141	VAL
2	s	143	LEU
2	s	151	ASP
2	s	154	ILE
2	s	161	TYR
2	s	166	ILE
2	s	170	ASN
2	s	174	VAL
2	s	186	GLU
2	s	188	VAL
2	s	200	LEU
2	s	213	VAL
2	s	214	ASN
2	s	215	VAL
2	s	220	ILE
2	s	234	THR
2	s	235	THR
2	s	237	ASP

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Mol	Chain	Res	Type
2	s	250	TYR
2	s	256	LYS
2	s	272	ASP
2	s	287	GLU
2	s	288	ARG
2	s	292	THR
2	s	295	LEU
2	s	298	ASN
2	s	300	GLU
2	s	303	VAL
2	s	304	LEU
2	s	312	LEU
2	s	313	VAL
2	s	325	LEU
2	s	326	GLU
2	s	330	LYS
2	s	335	VAL
2	s	337	THR
2	s	348	ILE
2	s	353	PHE
2	s	367	ILE
2	s	371	THR
2	s	378	TYR
2	s	385	LEU
2	s	387	ASP
2	s	393	VAL
2	s	395	VAL
2	s	397	THR
2	s	399	ARG
2	s	407	VAL
2	s	413	LEU
2	s	430	LEU
2	s	436	GLU
2	s	441	THR
2	s	442	GLN
2	s	454	ILE
2	s	457	ASN
2	s	458	VAL
2	s	460	PHE
2	s	476	VAL
2	s	479	VAL
2	s	482	VAL

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Mol	Chain	Res	Type
2	s	486	GLU
2	s	490	SER
2	s	492	VAL
2	s	495	TYR
2	s	496	ILE
2	s	504	CYS
2	s	514	VAL
2	s	515	LEU
2	s	525	MET
2	s	542	HIS
2	s	552	LEU
2	s	563	VAL
2	s	567	ASN
2	s	581	ASN
2	s	583	ILE
2	s	591	ARG
2	s	593	PHE
2	s	595	ASP
2	s	600	TYR
2	s	602	ILE
2	s	606	THR
2	s	611	THR
2	s	618	ILE
2	s	621	ILE
2	s	632	THR
2	s	633	VAL
2	s	641	THR
2	s	642	VAL
2	s	657	ARG
2	s	658	LEU
2	s	669	ILE
2	s	673	ILE
2	s	683	LEU
2	s	684	ILE
2	s	698	ILE
2	s	703	LEU
2	s	715	THR
2	s	730	THR
2	s	740	THR
2	s	741	LEU
2	s	746	LEU
2	s	748	LEU

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Mol	Chain	Res	Type
2	s	757	VAL
2	s	765	THR
2	s	766	VAL
2	s	768	ILE
2	s	772	GLU
2	s	774	THR
2	s	779	ILE
2	s	790	ARG
2	t	15	ILE
2	t	50	PHE
2	t	52	ASN
2	t	66	ILE
2	t	78	TYR
2	t	82	THR
2	t	86	ILE
2	t	88	VAL
2	t	98	VAL
2	t	109	THR
2	t	119	VAL
2	t	121	VAL
2	t	141	VAL
2	t	143	LEU
2	t	151	ASP
2	t	154	ILE
2	t	161	TYR
2	t	166	ILE
2	t	170	ASN
2	t	174	VAL
2	t	186	GLU
2	t	188	VAL
2	t	200	LEU
2	t	213	VAL
2	t	214	ASN
2	t	215	VAL
2	t	220	ILE
2	t	234	THR
2	t	235	THR
2	t	237	ASP
2	t	250	TYR
2	t	256	LYS
2	t	272	ASP
2	t	287	GLU

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Mol	Chain	Res	Type
2	t	288	ARG
2	t	292	THR
2	t	295	LEU
2	t	298	ASN
2	t	300	GLU
2	t	303	VAL
2	t	304	LEU
2	t	312	LEU
2	t	313	VAL
2	t	325	LEU
2	t	326	GLU
2	t	330	LYS
2	t	335	VAL
2	t	337	THR
2	t	348	ILE
2	t	353	PHE
2	t	367	ILE
2	t	371	THR
2	t	378	TYR
2	t	385	LEU
2	t	387	ASP
2	t	393	VAL
2	t	395	VAL
2	t	397	THR
2	t	399	ARG
2	t	407	VAL
2	t	413	LEU
2	t	430	LEU
2	t	436	GLU
2	t	441	THR
2	t	442	GLN
2	t	454	ILE
2	t	457	ASN
2	t	458	VAL
2	t	460	PHE
2	t	476	VAL
2	t	479	VAL
2	t	482	VAL
2	t	486	GLU
2	t	490	SER
2	t	492	VAL
2	t	495	TYR

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Mol	Chain	Res	Type
2	t	496	ILE
2	t	504	CYS
2	t	514	VAL
2	t	515	LEU
2	t	525	MET
2	t	542	HIS
2	t	552	LEU
2	t	563	VAL
2	t	567	ASN
2	t	581	ASN
2	t	583	ILE
2	t	591	ARG
2	t	593	PHE
2	t	595	ASP
2	t	600	TYR
2	t	602	ILE
2	t	606	THR
2	t	611	THR
2	t	618	ILE
2	t	621	ILE
2	t	632	THR
2	t	633	VAL
2	t	641	THR
2	t	642	VAL
2	t	657	ARG
2	t	658	LEU
2	t	669	ILE
2	t	673	ILE
2	t	683	LEU
2	t	684	ILE
2	t	698	ILE
2	t	703	LEU
2	t	715	THR
2	t	730	THR
2	t	740	THR
2	t	741	LEU
2	t	746	LEU
2	t	748	LEU
2	t	757	VAL
2	t	765	THR
2	t	766	VAL
2	t	768	ILE

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Mol	Chain	Res	Type
2	t	772	GLU
2	t	774	THR
2	t	779	ILE
2	t	790	ARG
2	u	15	ILE
2	u	50	PHE
2	u	52	ASN
2	u	66	ILE
2	u	78	TYR
2	u	82	THR
2	u	86	ILE
2	u	88	VAL
2	u	98	VAL
2	u	109	THR
2	u	119	VAL
2	u	121	VAL
2	u	141	VAL
2	u	143	LEU
2	u	151	ASP
2	u	154	ILE
2	u	161	TYR
2	u	166	ILE
2	u	170	ASN
2	u	174	VAL
2	u	186	GLU
2	u	188	VAL
2	u	200	LEU
2	u	213	VAL
2	u	214	ASN
2	u	215	VAL
2	u	220	ILE
2	u	234	THR
2	u	235	THR
2	u	237	ASP
2	u	250	TYR
2	u	256	LYS
2	u	272	ASP
2	u	287	GLU
2	u	288	ARG
2	u	292	THR
2	u	295	LEU
2	u	298	ASN

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Mol	Chain	Res	Type
2	u	300	GLU
2	u	303	VAL
2	u	304	LEU
2	u	312	LEU
2	u	313	VAL
2	u	325	LEU
2	u	326	GLU
2	u	330	LYS
2	u	335	VAL
2	u	337	THR
2	u	348	ILE
2	u	353	PHE
2	u	367	ILE
2	u	371	THR
2	u	378	TYR
2	u	385	LEU
2	u	387	ASP
2	u	393	VAL
2	u	395	VAL
2	u	397	THR
2	u	399	ARG
2	u	407	VAL
2	u	413	LEU
2	u	430	LEU
2	u	436	GLU
2	u	441	THR
2	u	442	GLN
2	u	454	ILE
2	u	457	ASN
2	u	458	VAL
2	u	460	PHE
2	u	476	VAL
2	u	479	VAL
2	u	482	VAL
2	u	486	GLU
2	u	490	SER
2	u	492	VAL
2	u	495	TYR
2	u	496	ILE
2	u	504	CYS
2	u	514	VAL
2	u	515	LEU

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Mol	Chain	Res	Type
2	u	525	MET
2	u	542	HIS
2	u	552	LEU
2	u	563	VAL
2	u	567	ASN
2	u	581	ASN
2	u	583	ILE
2	u	591	ARG
2	u	593	PHE
2	u	595	ASP
2	u	600	TYR
2	u	602	ILE
2	u	606	THR
2	u	611	THR
2	u	618	ILE
2	u	621	ILE
2	u	632	THR
2	u	633	VAL
2	u	641	THR
2	u	642	VAL
2	u	657	ARG
2	u	658	LEU
2	u	669	ILE
2	u	673	ILE
2	u	683	LEU
2	u	684	ILE
2	u	698	ILE
2	u	703	LEU
2	u	715	THR
2	u	730	THR
2	u	740	THR
2	u	741	LEU
2	u	746	LEU
2	u	748	LEU
2	u	757	VAL
2	u	765	THR
2	u	766	VAL
2	u	768	ILE
2	u	772	GLU
2	u	774	THR
2	u	779	ILE
2	u	790	ARG

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Mol	Chain	Res	Type
2	v	15	ILE
2	v	50	PHE
2	v	52	ASN
2	v	66	ILE
2	v	78	TYR
2	v	82	THR
2	v	86	ILE
2	v	88	VAL
2	v	98	VAL
2	v	109	THR
2	v	119	VAL
2	v	121	VAL
2	v	141	VAL
2	v	143	LEU
2	v	151	ASP
2	v	154	ILE
2	v	161	TYR
2	v	166	ILE
2	v	170	ASN
2	v	174	VAL
2	v	186	GLU
2	v	188	VAL
2	v	200	LEU
2	v	213	VAL
2	v	214	ASN
2	v	215	VAL
2	v	220	ILE
2	v	234	THR
2	v	235	THR
2	v	237	ASP
2	v	250	TYR
2	v	256	LYS
2	v	272	ASP
2	v	287	GLU
2	v	288	ARG
2	v	292	THR
2	v	295	LEU
2	v	298	ASN
2	v	300	GLU
2	v	303	VAL
2	v	304	LEU
2	v	312	LEU

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Mol	Chain	Res	Type
2	v	313	VAL
2	v	325	LEU
2	v	326	GLU
2	v	330	LYS
2	v	335	VAL
2	v	337	THR
2	v	348	ILE
2	v	353	PHE
2	v	367	ILE
2	v	371	THR
2	v	378	TYR
2	v	385	LEU
2	v	387	ASP
2	v	393	VAL
2	v	395	VAL
2	v	397	THR
2	v	399	ARG
2	v	407	VAL
2	v	413	LEU
2	v	430	LEU
2	v	436	GLU
2	v	441	THR
2	v	442	GLN
2	v	454	ILE
2	v	457	ASN
2	v	458	VAL
2	v	460	PHE
2	v	476	VAL
2	v	479	VAL
2	v	482	VAL
2	v	486	GLU
2	v	490	SER
2	v	492	VAL
2	v	495	TYR
2	v	496	ILE
2	v	504	CYS
2	v	514	VAL
2	v	515	LEU
2	v	525	MET
2	v	542	HIS
2	v	552	LEU
2	v	563	VAL

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Mol	Chain	Res	Type
2	v	567	ASN
2	v	581	ASN
2	v	583	ILE
2	v	591	ARG
2	v	593	PHE
2	v	595	ASP
2	v	600	TYR
2	v	602	ILE
2	v	606	THR
2	v	611	THR
2	v	618	ILE
2	v	621	ILE
2	v	632	THR
2	v	633	VAL
2	v	641	THR
2	v	642	VAL
2	v	657	ARG
2	v	658	LEU
2	v	669	ILE
2	v	673	ILE
2	v	683	LEU
2	v	684	ILE
2	v	698	ILE
2	v	703	LEU
2	v	715	THR
2	v	730	THR
2	v	740	THR
2	v	741	LEU
2	v	746	LEU
2	v	748	LEU
2	v	757	VAL
2	v	765	THR
2	v	766	VAL
2	v	768	ILE
2	v	772	GLU
2	v	774	THR
2	v	779	ILE
2	v	790	ARG
2	w	15	ILE
2	w	50	PHE
2	w	52	ASN
2	w	66	ILE

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Mol	Chain	Res	Type
2	w	78	TYR
2	w	82	THR
2	w	86	ILE
2	w	88	VAL
2	w	98	VAL
2	w	109	THR
2	w	119	VAL
2	w	121	VAL
2	w	141	VAL
2	w	143	LEU
2	w	151	ASP
2	w	154	ILE
2	w	161	TYR
2	w	166	ILE
2	w	170	ASN
2	w	174	VAL
2	w	186	GLU
2	w	188	VAL
2	w	200	LEU
2	w	213	VAL
2	w	214	ASN
2	w	215	VAL
2	w	220	ILE
2	w	234	THR
2	w	235	THR
2	w	237	ASP
2	w	250	TYR
2	w	256	LYS
2	w	272	ASP
2	w	287	GLU
2	w	288	ARG
2	w	292	THR
2	w	295	LEU
2	w	298	ASN
2	w	300	GLU
2	w	303	VAL
2	w	304	LEU
2	w	312	LEU
2	w	313	VAL
2	w	325	LEU
2	w	326	GLU
2	w	330	LYS

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Mol	Chain	Res	Type
2	w	335	VAL
2	w	337	THR
2	w	348	ILE
2	w	353	PHE
2	w	367	ILE
2	w	371	THR
2	w	378	TYR
2	w	385	LEU
2	w	387	ASP
2	w	393	VAL
2	w	395	VAL
2	w	397	THR
2	w	399	ARG
2	w	407	VAL
2	w	413	LEU
2	w	430	LEU
2	w	436	GLU
2	w	441	THR
2	w	442	GLN
2	w	454	ILE
2	w	457	ASN
2	w	458	VAL
2	w	460	PHE
2	w	476	VAL
2	w	479	VAL
2	w	482	VAL
2	w	486	GLU
2	w	490	SER
2	w	492	VAL
2	w	495	TYR
2	w	496	ILE
2	w	504	CYS
2	w	514	VAL
2	w	515	LEU
2	w	525	MET
2	w	542	HIS
2	w	552	LEU
2	w	563	VAL
2	w	567	ASN
2	w	581	ASN
2	w	583	ILE
2	w	591	ARG

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Mol	Chain	Res	Type
2	w	593	PHE
2	w	595	ASP
2	w	600	TYR
2	w	602	ILE
2	w	606	THR
2	w	611	THR
2	w	618	ILE
2	w	621	ILE
2	w	632	THR
2	w	633	VAL
2	w	641	THR
2	w	642	VAL
2	w	657	ARG
2	w	658	LEU
2	w	669	ILE
2	w	673	ILE
2	w	683	LEU
2	w	684	ILE
2	w	698	ILE
2	w	703	LEU
2	w	715	THR
2	w	730	THR
2	w	740	THR
2	w	741	LEU
2	w	746	LEU
2	w	748	LEU
2	w	757	VAL
2	w	765	THR
2	w	766	VAL
2	w	768	ILE
2	w	772	GLU
2	w	774	THR
2	w	779	ILE
2	w	790	ARG
2	x	15	ILE
2	x	50	PHE
2	x	52	ASN
2	x	66	ILE
2	x	78	TYR
2	x	82	THR
2	x	86	ILE
2	x	88	VAL

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Mol	Chain	Res	Type
2	x	98	VAL
2	x	109	THR
2	x	119	VAL
2	x	121	VAL
2	x	141	VAL
2	x	143	LEU
2	x	151	ASP
2	x	154	ILE
2	x	161	TYR
2	x	166	ILE
2	x	170	ASN
2	x	174	VAL
2	x	186	GLU
2	x	188	VAL
2	x	200	LEU
2	x	213	VAL
2	x	214	ASN
2	x	215	VAL
2	x	220	ILE
2	x	234	THR
2	x	235	THR
2	x	237	ASP
2	x	250	TYR
2	x	256	LYS
2	x	272	ASP
2	x	287	GLU
2	x	288	ARG
2	x	292	THR
2	x	295	LEU
2	x	298	ASN
2	x	300	GLU
2	x	303	VAL
2	x	304	LEU
2	x	312	LEU
2	x	313	VAL
2	x	325	LEU
2	x	326	GLU
2	x	330	LYS
2	x	335	VAL
2	x	337	THR
2	x	348	ILE
2	x	353	PHE

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Mol	Chain	Res	Type
2	x	367	ILE
2	x	371	THR
2	x	378	TYR
2	x	385	LEU
2	x	387	ASP
2	x	393	VAL
2	x	395	VAL
2	x	397	THR
2	x	399	ARG
2	x	407	VAL
2	x	413	LEU
2	x	430	LEU
2	x	436	GLU
2	x	441	THR
2	x	442	GLN
2	x	454	ILE
2	x	457	ASN
2	x	458	VAL
2	x	460	PHE
2	x	476	VAL
2	x	479	VAL
2	x	482	VAL
2	x	486	GLU
2	x	490	SER
2	x	492	VAL
2	x	495	TYR
2	x	496	ILE
2	x	504	CYS
2	x	514	VAL
2	x	515	LEU
2	x	525	MET
2	x	542	HIS
2	x	552	LEU
2	x	563	VAL
2	x	567	ASN
2	x	581	ASN
2	x	583	ILE
2	x	591	ARG
2	x	593	PHE
2	x	595	ASP
2	x	600	TYR
2	x	602	ILE

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Mol	Chain	Res	Type
2	x	606	THR
2	x	611	THR
2	x	618	ILE
2	x	621	ILE
2	x	632	THR
2	x	633	VAL
2	x	641	THR
2	x	642	VAL
2	x	657	ARG
2	x	658	LEU
2	x	669	ILE
2	x	673	ILE
2	x	683	LEU
2	x	684	ILE
2	x	698	ILE
2	x	703	LEU
2	x	715	THR
2	x	730	THR
2	x	740	THR
2	x	741	LEU
2	x	746	LEU
2	x	748	LEU
2	x	757	VAL
2	x	765	THR
2	x	766	VAL
2	x	768	ILE
2	x	772	GLU
2	x	774	THR
2	x	779	ILE
2	x	790	ARG
3	A	41	ILE
3	A	43	ARG
3	A	90	LEU
3	A	129	LEU
3	B	90	LEU
3	B	91	GLU
3	C	90	LEU
3	C	91	GLU
3	C	107	ILE
3	C	108	ARG
3	C	129	LEU
3	D	82	ARG

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Mol	Chain	Res	Type
3	D	90	LEU
3	D	129	LEU
3	E	90	LEU
3	E	91	GLU
3	E	128	GLN
3	E	129	LEU
3	F	90	LEU
3	F	129	LEU
4	M	6	MET
4	M	24	ILE
4	M	53	GLN
4	M	57	ARG
4	M	73	VAL
4	M	77	LEU
4	M	160	LEU
4	M	163	GLU
4	M	181	TYR
4	M	190	THR
4	N	6	MET
4	N	7	ASN
4	N	8	VAL
4	N	24	ILE
4	N	26	GLU
4	N	39	ASP
4	N	68	THR
4	N	73	VAL
4	N	77	LEU
4	N	103	VAL
4	N	144	ARG
4	N	170	LEU
4	N	171	CYS
4	N	184	LEU
4	N	190	THR
4	O	10	THR
4	O	24	ILE
4	O	53	GLN
4	O	57	ARG
4	O	73	VAL
4	O	77	LEU
4	O	160	LEU
4	O	163	GLU
4	O	181	TYR

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Mol	Chain	Res	Type
4	O	190	THR
4	P	8	VAL
4	P	24	ILE
4	P	26	GLU
4	P	39	ASP
4	P	68	THR
4	P	73	VAL
4	P	77	LEU
4	P	103	VAL
4	P	170	LEU
4	P	171	CYS
4	P	184	LEU
4	P	190	THR
4	Q	6	MET
4	Q	24	ILE
4	Q	53	GLN
4	Q	57	ARG
4	Q	73	VAL
4	Q	77	LEU
4	Q	160	LEU
4	Q	163	GLU
4	Q	181	TYR
4	Q	190	THR
4	R	6	MET
4	R	7	ASN
4	R	8	VAL
4	R	24	ILE
4	R	26	GLU
4	R	39	ASP
4	R	68	THR
4	R	73	VAL
4	R	77	LEU
4	R	103	VAL
4	R	170	LEU
4	R	171	CYS
4	R	184	LEU
4	R	190	THR
4	S	6	MET
4	S	24	ILE
4	S	53	GLN
4	S	57	ARG
4	S	73	VAL

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Mol	Chain	Res	Type
4	S	77	LEU
4	S	160	LEU
4	S	163	GLU
4	S	181	TYR
4	S	190	THR
4	T	6	MET
4	T	8	VAL
4	T	24	ILE
4	T	26	GLU
4	T	39	ASP
4	T	68	THR
4	T	73	VAL
4	T	77	LEU
4	T	103	VAL
4	T	170	LEU
4	T	171	CYS
4	T	184	LEU
4	T	190	THR
4	U	6	MET
4	U	24	ILE
4	U	53	GLN
4	U	57	ARG
4	U	73	VAL
4	U	77	LEU
4	U	160	LEU
4	U	163	GLU
4	U	181	TYR
4	U	190	THR
4	V	6	MET
4	V	8	VAL
4	V	24	ILE
4	V	26	GLU
4	V	39	ASP
4	V	68	THR
4	V	73	VAL
4	V	77	LEU
4	V	103	VAL
4	V	170	LEU
4	V	171	CYS
4	V	184	LEU
4	V	190	THR
4	W	6	MET

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Mol	Chain	Res	Type
4	W	10	THR
4	W	24	ILE
4	W	53	GLN
4	W	57	ARG
4	W	73	VAL
4	W	77	LEU
4	W	160	LEU
4	W	163	GLU
4	W	181	TYR
4	W	190	THR
4	X	6	MET
4	X	8	VAL
4	X	24	ILE
4	X	26	GLU
4	X	39	ASP
4	X	52	ARG
4	X	68	THR
4	X	73	VAL
4	X	77	LEU
4	X	103	VAL
4	X	170	LEU
4	X	171	CYS
4	X	184	LEU
4	X	190	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (244) such sidechains are listed below:

Mol	Chain	Res	Type
1	a	3	ASN
1	a	108	HIS
1	b	12	GLN
1	b	47	ASN
1	c	3	ASN
1	c	100	ASN
1	d	3	ASN
1	d	108	HIS
1	e	12	GLN
1	e	47	ASN
1	f	3	ASN
1	f	100	ASN
1	g	3	ASN
1	g	108	HIS

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Mol	Chain	Res	Type
1	h	12	GLN
1	h	47	ASN
1	i	3	ASN
1	i	100	ASN
1	j	3	ASN
1	j	108	HIS
1	k	12	GLN
1	k	47	ASN
1	l	3	ASN
1	l	100	ASN
1	m	3	ASN
1	n	12	GLN
1	n	47	ASN
1	o	3	ASN
1	o	100	ASN
1	p	3	ASN
1	p	108	HIS
1	q	12	GLN
1	q	47	ASN
1	r	3	ASN
1	r	100	ASN
2	s	18	GLN
2	s	52	ASN
2	s	97	GLN
2	s	137	ASN
2	s	147	ASN
2	s	170	ASN
2	s	189	ASN
2	s	229	GLN
2	s	310	HIS
2	s	319	ASN
2	s	356	ASN
2	s	384	ASN
2	s	457	ASN
2	s	498	ASN
2	s	538	GLN
2	s	567	ASN
2	s	581	ASN
2	s	608	ASN
2	s	651	ASN
2	s	661	ASN
2	s	709	ASN

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Mol	Chain	Res	Type
2	s	723	GLN
2	s	726	ASN
2	t	18	GLN
2	t	52	ASN
2	t	97	GLN
2	t	137	ASN
2	t	147	ASN
2	t	170	ASN
2	t	189	ASN
2	t	229	GLN
2	t	242	GLN
2	t	310	HIS
2	t	319	ASN
2	t	356	ASN
2	t	421	GLN
2	t	457	ASN
2	t	491	HIS
2	t	498	ASN
2	t	538	GLN
2	t	567	ASN
2	t	581	ASN
2	t	608	ASN
2	t	651	ASN
2	t	661	ASN
2	t	709	ASN
2	t	723	GLN
2	t	726	ASN
2	u	18	GLN
2	u	52	ASN
2	u	97	GLN
2	u	137	ASN
2	u	147	ASN
2	u	170	ASN
2	u	189	ASN
2	u	229	GLN
2	u	310	HIS
2	u	319	ASN
2	u	356	ASN
2	u	384	ASN
2	u	421	GLN
2	u	491	HIS
2	u	498	ASN

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Mol	Chain	Res	Type
2	u	538	GLN
2	u	567	ASN
2	u	581	ASN
2	u	608	ASN
2	u	651	ASN
2	u	661	ASN
2	u	709	ASN
2	u	723	GLN
2	u	726	ASN
2	v	18	GLN
2	v	52	ASN
2	v	97	GLN
2	v	137	ASN
2	v	147	ASN
2	v	170	ASN
2	v	189	ASN
2	v	229	GLN
2	v	242	GLN
2	v	310	HIS
2	v	319	ASN
2	v	384	ASN
2	v	421	GLN
2	v	457	ASN
2	v	491	HIS
2	v	498	ASN
2	v	538	GLN
2	v	567	ASN
2	v	581	ASN
2	v	608	ASN
2	v	651	ASN
2	v	661	ASN
2	v	709	ASN
2	v	723	GLN
2	v	726	ASN
2	w	18	GLN
2	w	52	ASN
2	w	97	GLN
2	w	137	ASN
2	w	147	ASN
2	w	170	ASN
2	w	189	ASN
2	w	229	GLN

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Mol	Chain	Res	Type
2	w	310	HIS
2	w	319	ASN
2	w	356	ASN
2	w	384	ASN
2	w	457	ASN
2	w	491	HIS
2	w	498	ASN
2	w	538	GLN
2	w	567	ASN
2	w	581	ASN
2	w	608	ASN
2	w	651	ASN
2	w	661	ASN
2	w	709	ASN
2	w	723	GLN
2	w	726	ASN
2	x	18	GLN
2	x	52	ASN
2	x	97	GLN
2	x	137	ASN
2	x	147	ASN
2	x	170	ASN
2	x	189	ASN
2	x	229	GLN
2	x	310	HIS
2	x	319	ASN
2	x	356	ASN
2	x	384	ASN
2	x	421	GLN
2	x	457	ASN
2	x	491	HIS
2	x	498	ASN
2	x	538	GLN
2	x	567	ASN
2	x	581	ASN
2	x	608	ASN
2	x	651	ASN
2	x	661	ASN
2	x	709	ASN
2	x	723	GLN
2	x	726	ASN
3	A	44	GLN

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Mol	Chain	Res	Type
3	A	48	GLN
3	B	44	GLN
3	B	46	ASN
3	B	48	GLN
3	C	44	GLN
3	C	48	GLN
3	C	133	GLN
3	D	44	GLN
3	D	48	GLN
3	D	138	GLN
3	E	44	GLN
3	E	48	GLN
3	F	44	GLN
3	F	48	GLN
4	M	48	ASN
4	M	53	GLN
4	M	76	ASN
4	M	120	ASN
4	N	51	ASN
4	N	55	GLN
4	N	76	ASN
4	N	109	GLN
4	N	147	ASN
4	O	53	GLN
4	O	76	ASN
4	P	7	ASN
4	P	51	ASN
4	P	55	GLN
4	P	76	ASN
4	P	109	GLN
4	P	147	ASN
4	Q	48	ASN
4	Q	53	GLN
4	Q	76	ASN
4	R	51	ASN
4	R	55	GLN
4	R	76	ASN
4	R	109	GLN
4	R	147	ASN
4	S	53	GLN
4	S	76	ASN
4	T	51	ASN

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Mol	Chain	Res	Type
4	T	55	GLN
4	T	76	ASN
4	T	109	GLN
4	T	147	ASN
4	U	53	GLN
4	U	76	ASN
4	V	51	ASN
4	V	55	GLN
4	V	76	ASN
4	V	109	GLN
4	V	147	ASN
4	W	48	ASN
4	W	53	GLN
4	W	76	ASN
4	W	120	ASN
4	X	51	ASN
4	X	55	GLN
4	X	76	ASN
4	X	109	GLN
4	X	147	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

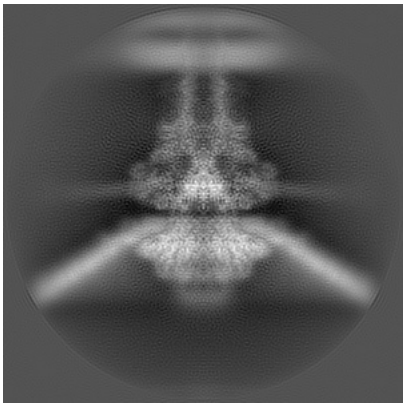
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-31321. These allow visual inspection of the internal detail of the map and identification of artifacts.

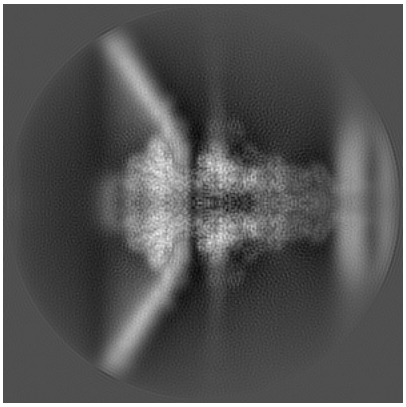
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

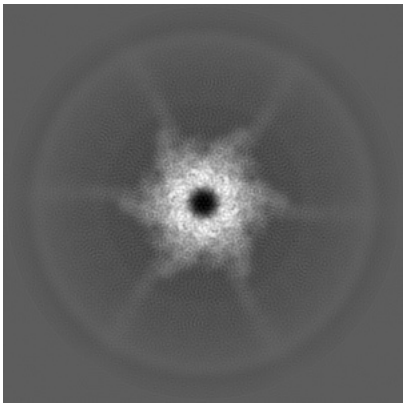
6.1.1 Primary map



X



Y

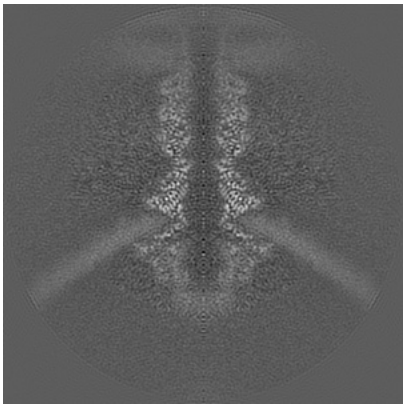


Z

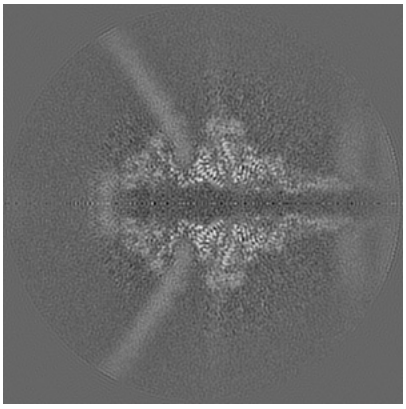
The images above show the map projected in three orthogonal directions.

6.2 Central slices

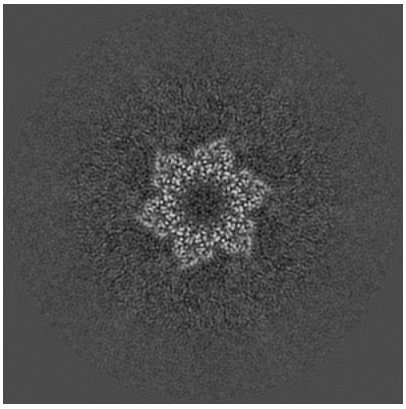
6.2.1 Primary map



X Index: 200



Y Index: 200

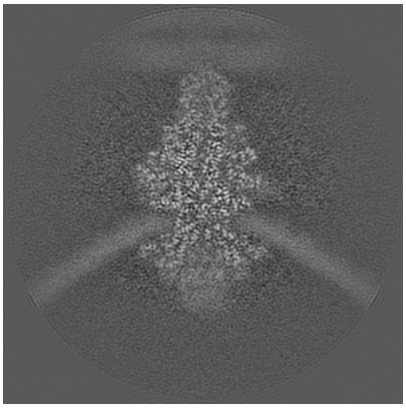


Z Index: 200

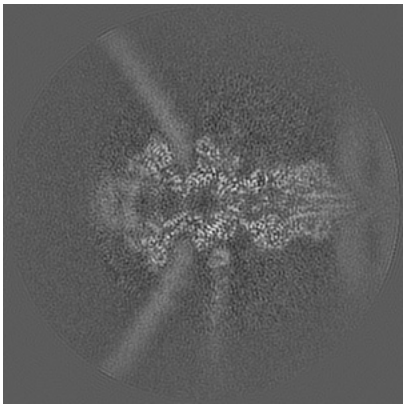
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

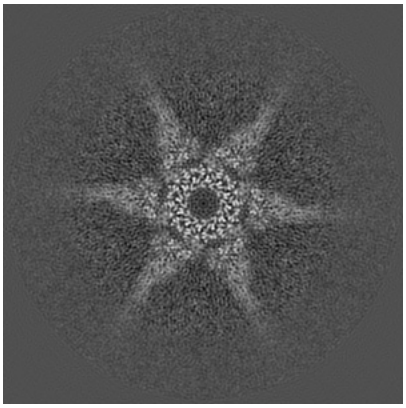
6.3.1 Primary map



X Index: 177



Y Index: 216

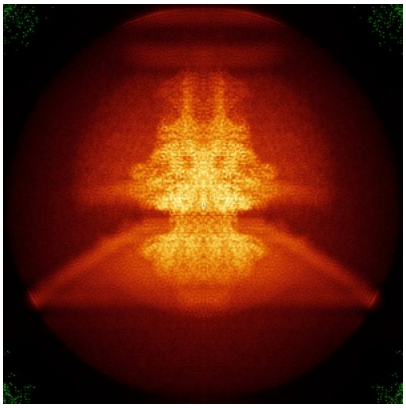


Z Index: 217

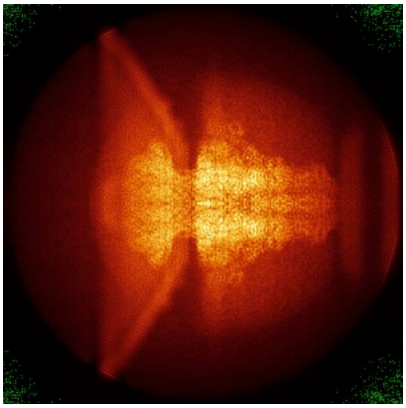
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

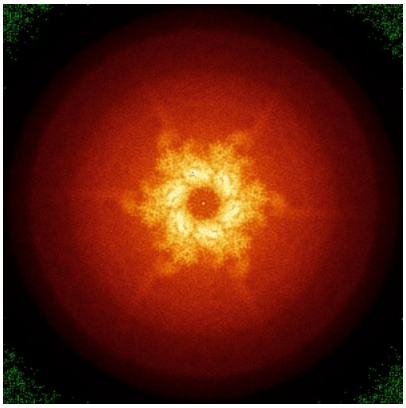
6.4.1 Primary map



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

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 8.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

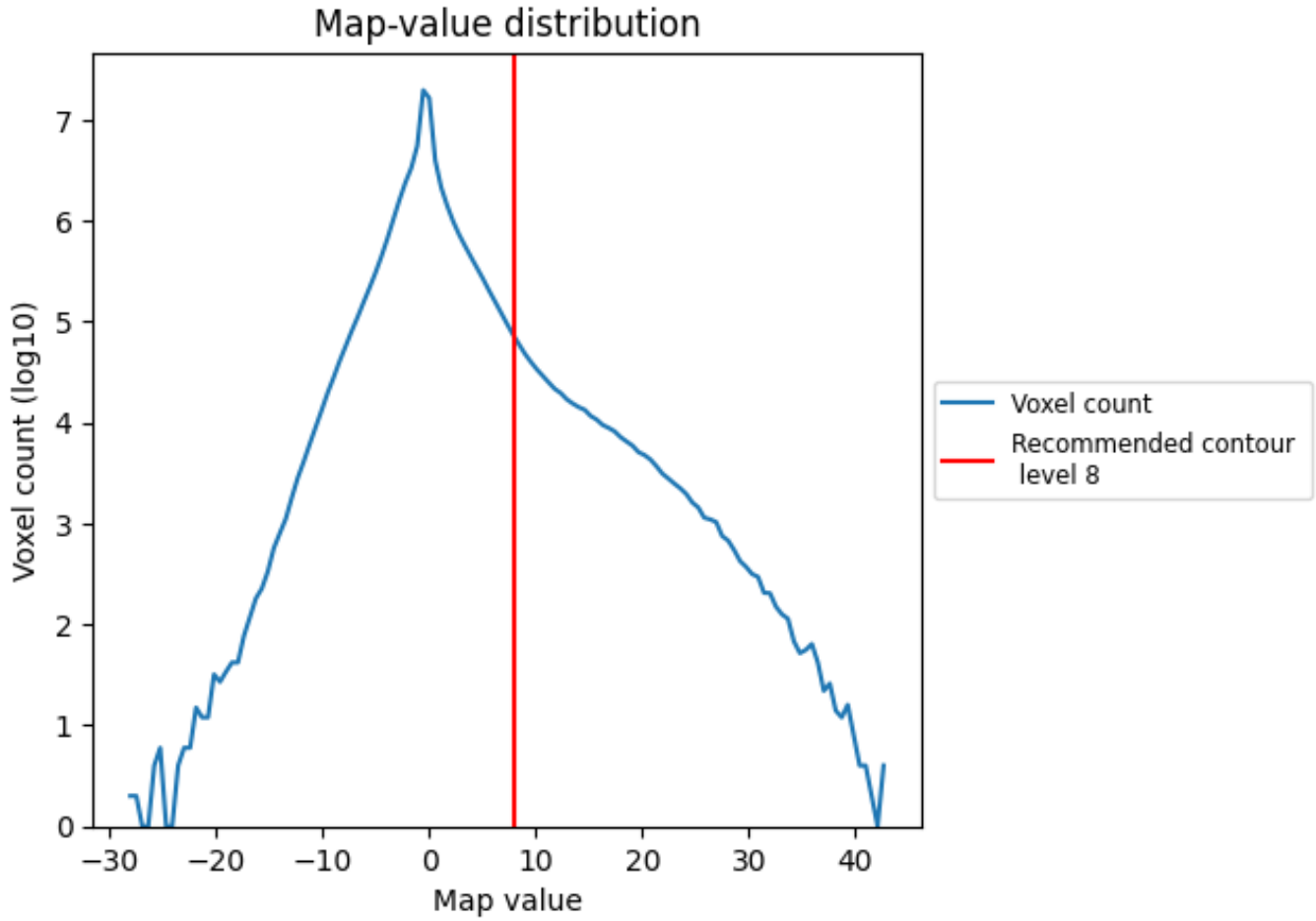
6.6 Mask visualisation (i)

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

7 Map analysis

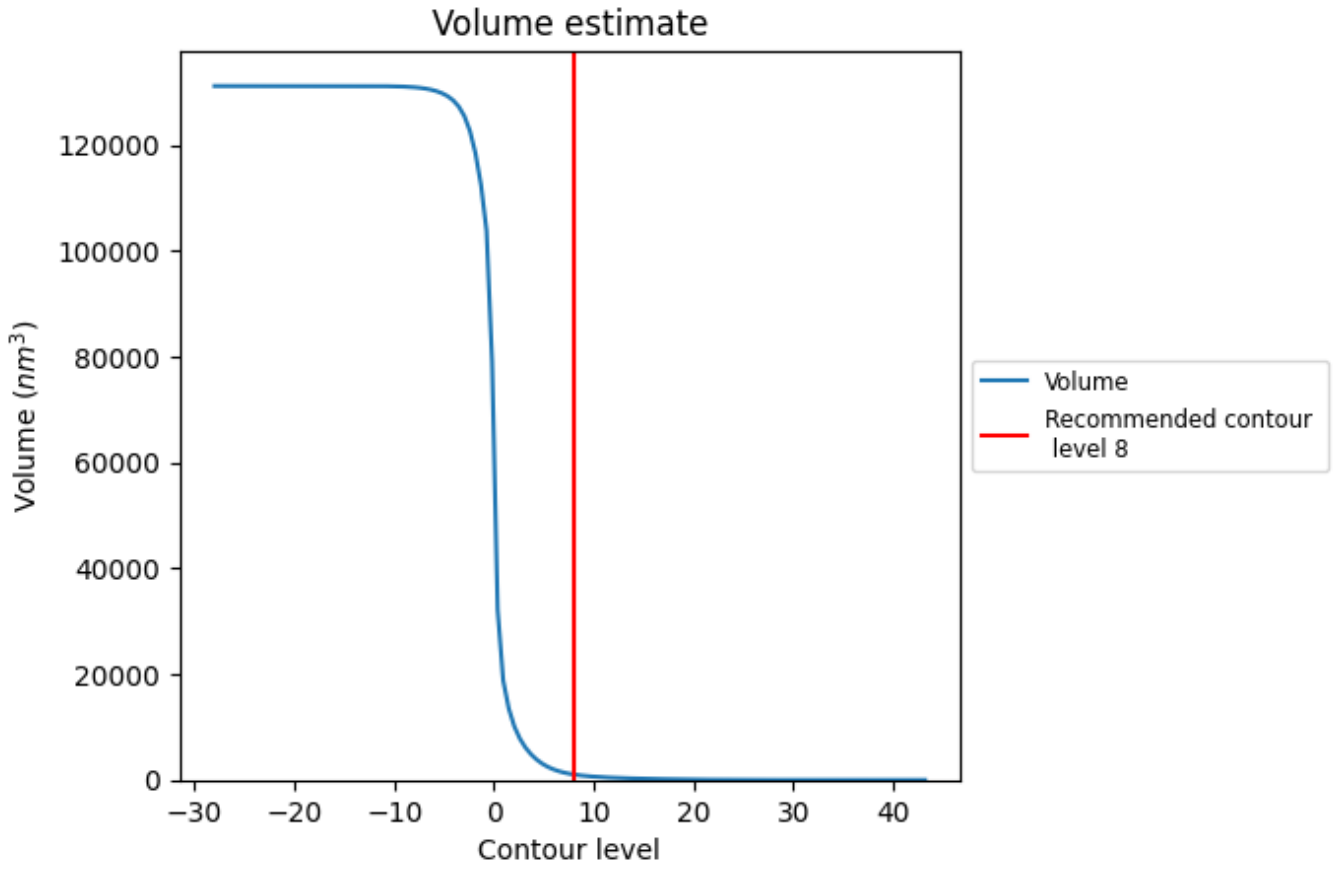
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

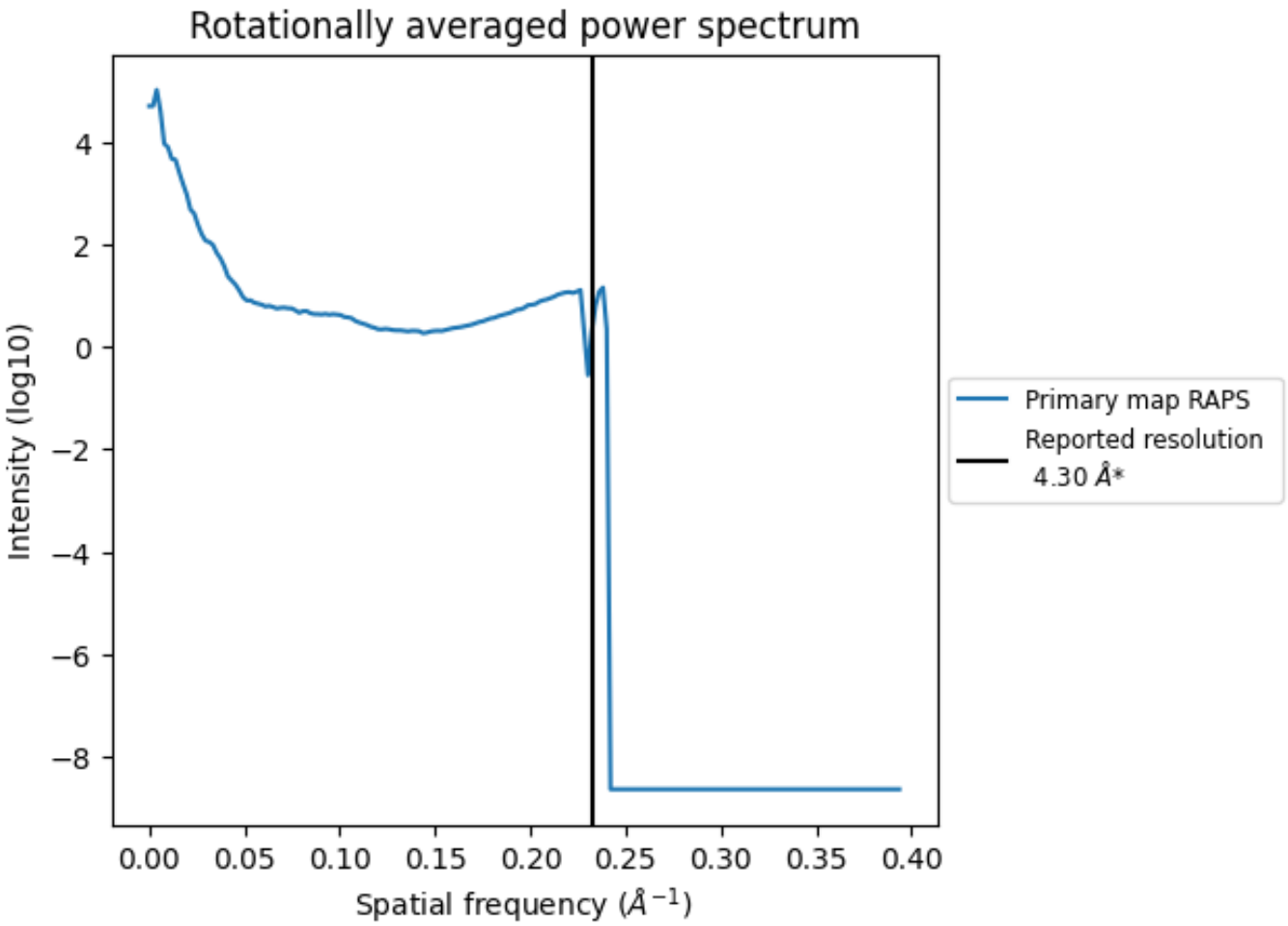
7.2 Volume estimate



The volume at the recommended contour level is 1038 nm^3; this corresponds to an approximate mass of 938 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 (i)



*Reported resolution corresponds to spatial frequency of 0.233 Å^{-1}

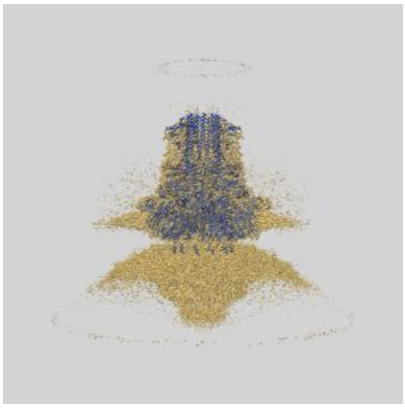
8 Fourier-Shell correlation

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

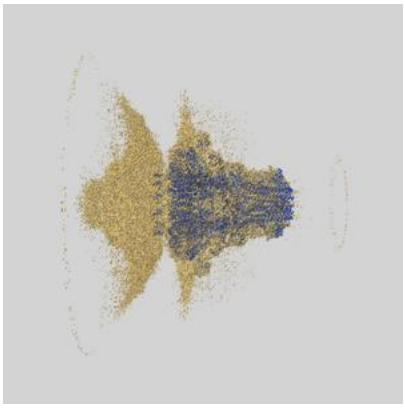
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-31321 and PDB model 7EY7. Per-residue inclusion information can be found in section 3 on page 8.

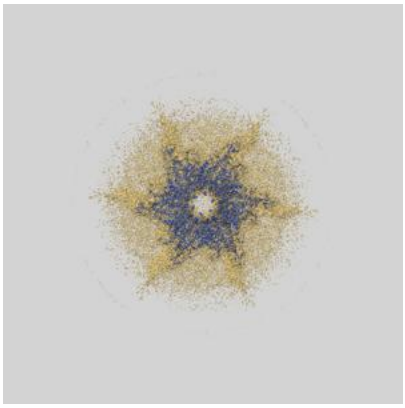
9.1 Map-model overlay



X



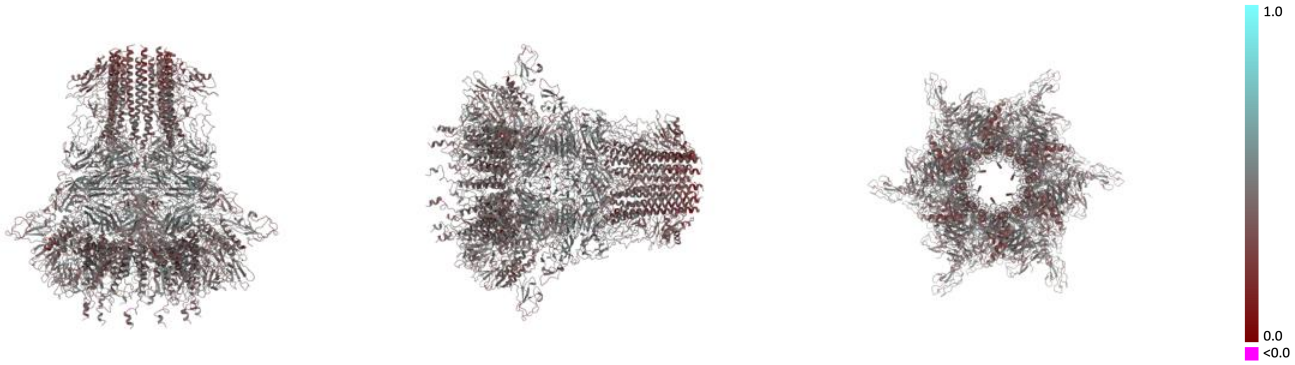
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 8.0 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.

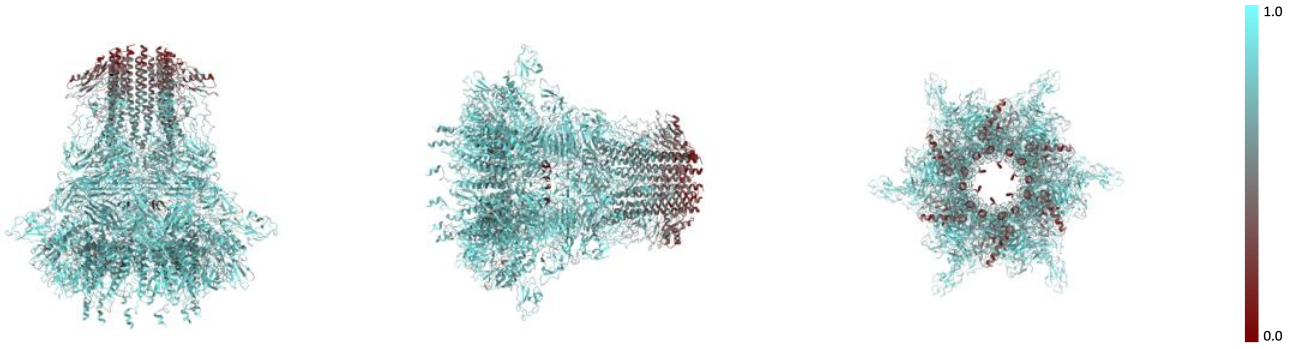
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

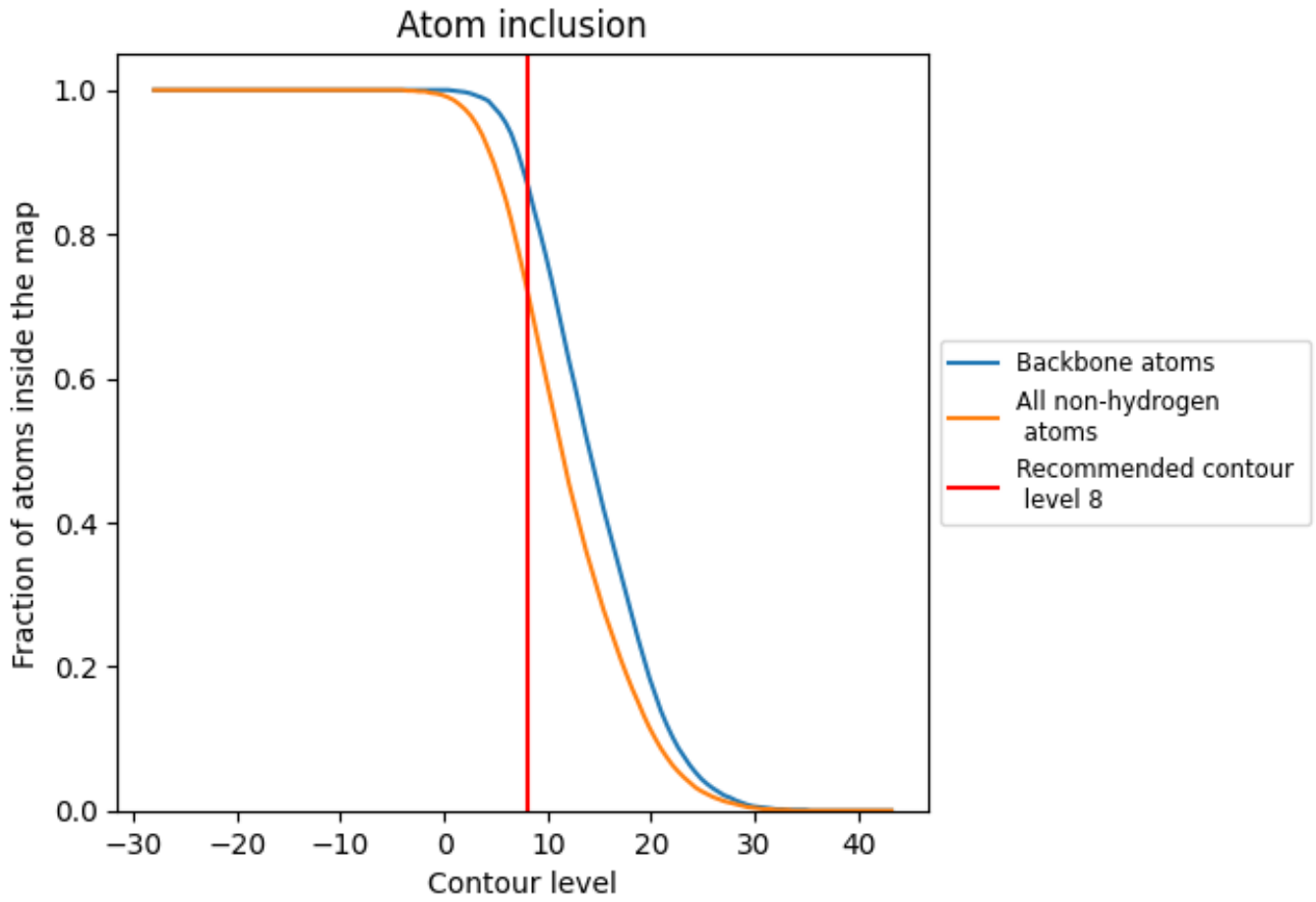
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (8).

9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 72% 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 (8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7250	0.4200
A	0.5180	0.3430
B	0.5150	0.3450
C	0.5190	0.3450
D	0.5400	0.3540
E	0.5160	0.3450
F	0.5200	0.3530
M	0.7660	0.4190
N	0.7750	0.4130
O	0.7650	0.4190
P	0.7740	0.4120
Q	0.7640	0.4180
R	0.7800	0.4130
S	0.7670	0.4180
T	0.7770	0.4150
U	0.7650	0.4190
V	0.7720	0.4150
W	0.7640	0.4190
X	0.7840	0.4130
a	0.7990	0.4370
b	0.6940	0.4050
c	0.7590	0.4100
d	0.7920	0.4330
e	0.6890	0.4000
f	0.7530	0.4060
g	0.7930	0.4360
h	0.6930	0.4020
i	0.7510	0.4080
j	0.7970	0.4400
k	0.6890	0.4040
l	0.7570	0.4110
m	0.7950	0.4370
n	0.6850	0.4000
o	0.7510	0.4050
p	0.7920	0.4370

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Chain	Atom inclusion	Q-score
q	0.6940	0.4040
r	0.7520	0.4050
s	0.7190	0.4340
t	0.7170	0.4310
u	0.7170	0.4320
v	0.7190	0.4340
w	0.7190	0.4320
x	0.7170	0.4320