



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 07:48 AM UTC

PDB ID : 8FWE / pdb_00008fwe
EMDB ID : EMD-29503
Title : Neck structure of Agrobacterium phage Milano, C3 symmetry
Authors : Sonani, R.R.; Wang, F.; Esteves, N.C.; Kelly, R.J.; Sebastian, A.;
Kreutzberger, M.A.B.; Leiman, P.G.; Scharf, B.E.; Egelman, E.H.
Deposited on : 2023-01-21
Resolution : 3.46 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

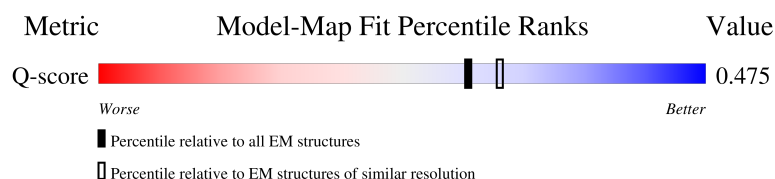
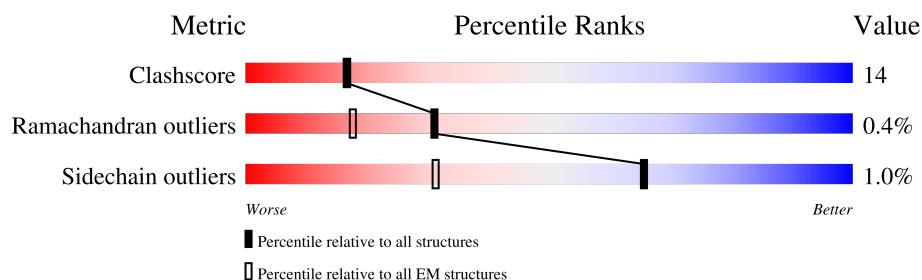
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.46 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13788 (2.96 - 3.96)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	230	5% 73% 23% .
1	1	230	. 72% 24% .
1	2	230	5% 71% 25% .
1	3	230	5% 72% 25% .

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Mol	Chain	Length	Quality of chain
1	4	230	
1	5	230	
1	6	230	
1	7	230	
1	8	230	
1	9	230	
1	A	230	
1	B	230	
1	C	230	
1	D	230	
1	E	230	
1	F	230	
1	G	230	
1	J	230	
1	K	230	
1	L	230	
1	M	230	
1	N	230	
1	O	230	
1	P	230	
1	Q	230	
1	R	230	
1	S	230	
1	T	230	
1	U	230	

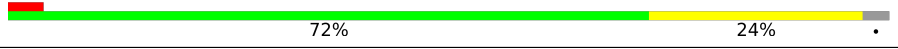
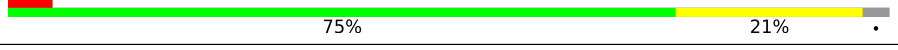
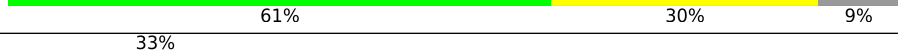
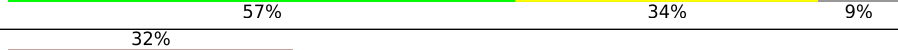
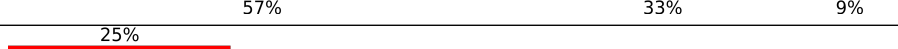
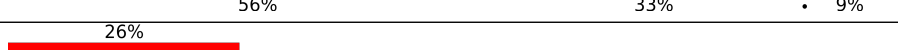
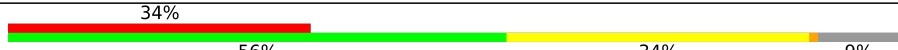
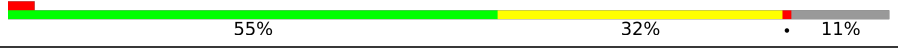
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Mol	Chain	Length	Quality of chain
1	V	230	
1	W	230	
1	X	230	
1	Y	230	
1	Z	230	
1	a	230	
1	b	230	
1	c	230	
1	d	230	
1	e	230	
1	f	230	
1	g	230	
1	h	230	
1	i	230	
1	j	230	
1	k	230	
1	l	230	
1	m	230	
1	n	230	
1	o	230	
1	p	230	
1	q	230	
1	r	230	
1	s	230	
1	t	230	

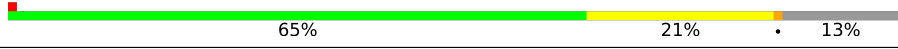
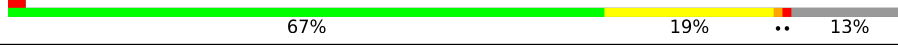
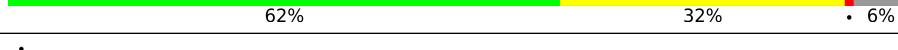
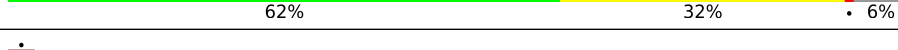
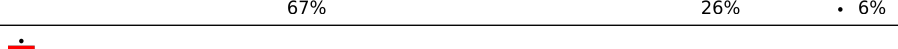
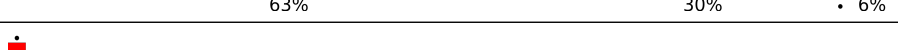
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Mol	Chain	Length	Quality of chain
1	u	230	
1	v	230	
1	w	230	
1	x	230	
1	y	230	
1	z	230	
2	AA	420	
2	AB	420	
2	AC	420	
2	AD	420	
2	AE	420	
2	AF	420	
2	AG	420	
2	AH	420	
2	AI	420	
2	AJ	420	
2	AK	420	
2	AL	420	
3	AM	141	
3	AN	141	
3	AO	141	
3	AP	141	
3	H	141	
3	I	141	
4	AQ	178	

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Mol	Chain	Length	Quality of chain
4	AR	178	
4	AS	178	
4	AT	178	
4	AW	178	
4	AX	178	
5	AU	136	
5	AV	136	
5	AY	136	
5	AZ	136	
5	Aa	136	
5	Ab	136	
6	R3	202	
6	R4	202	
6	R5	202	
6	S3	202	
6	S4	202	
6	S5	202	
6	T3	202	
6	T4	202	
6	T5	202	
6	U3	202	
6	U4	202	
6	U5	202	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 171990 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 Collar sheath protein, gp13.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	J	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	K	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	L	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	M	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	N	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	O	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	P	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	Q	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	R	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	S	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	T	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	U	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	V	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	W	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	X	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	Y	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	Z	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	b	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	c	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	d	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	e	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	f	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	g	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	h	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	i	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	j	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	k	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	l	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	m	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	n	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	o	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	p	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	q	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	r	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	s	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	t	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	u	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	v	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	w	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	x	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	y	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	z	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	1	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	2	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	4	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	5	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	6	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	7	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	8	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	9	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	0	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	A	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	B	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	C	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	D	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	E	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
1	F	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	G	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		

- Molecule 2 is a protein called Portal protein, gp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AA	381	Total	C	N	O	S	0	0
			2938	1860	504	560	14		
2	AB	381	Total	C	N	O	S	0	0
			2938	1860	504	560	14		
2	AC	381	Total	C	N	O	S	0	0
			2938	1860	504	560	14		
2	AD	381	Total	C	N	O	S	0	0
			2938	1860	504	560	14		
2	AE	381	Total	C	N	O	S	0	0
			2938	1860	504	560	14		
2	AF	381	Total	C	N	O	S	0	0
			2938	1860	504	560	14		
2	AG	381	Total	C	N	O	S	0	0
			2938	1860	504	560	14		
2	AH	381	Total	C	N	O	S	0	0
			2938	1860	504	560	14		
2	AI	381	Total	C	N	O	S	0	0
			2938	1860	504	560	14		
2	AJ	381	Total	C	N	O	S	0	0
			2938	1860	504	560	14		
2	AK	381	Total	C	N	O	S	0	0
			2938	1860	504	560	14		
2	AL	381	Total	C	N	O	S	0	0
			2938	1860	504	560	14		

- Molecule 3 is a protein called Neck 2 protein, gp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AM	125	Total	C	N	O	S	0	0
			997	621	183	185	8		
3	AP	125	Total	C	N	O	S	0	0
			997	621	183	185	8		
3	AN	125	Total	C	N	O	S	0	0
			997	621	183	185	8		
3	H	125	Total	C	N	O	S	0	0
			997	621	183	185	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	AO	125	Total	C	N	O	S	0	0
			997	621	183	185	8		
3	I	125	Total	C	N	O	S	0	0
			997	621	183	185	8		

- Molecule 4 is a protein called Tail-terminator protein, gp18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AQ	155	Total	C	N	O	S	0	0
			1251	798	207	243	3		
4	AR	155	Total	C	N	O	S	0	0
			1251	798	207	243	3		
4	AS	155	Total	C	N	O	S	0	0
			1251	798	207	243	3		
4	AT	155	Total	C	N	O	S	0	0
			1251	798	207	243	3		
4	AW	155	Total	C	N	O	S	0	0
			1251	798	207	243	3		
4	AX	155	Total	C	N	O	S	0	0
			1251	798	207	243	3		

- Molecule 5 is a protein called Tail-tube, gp21.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AU	128	Total	C	N	O	S	0	0
			977	606	162	202	7		
5	AZ	128	Total	C	N	O	S	0	0
			977	606	162	202	7		
5	AV	128	Total	C	N	O	S	0	0
			977	606	162	202	7		
5	Aa	128	Total	C	N	O	S	0	0
			977	606	162	202	7		
5	AY	128	Total	C	N	O	S	0	0
			977	606	162	202	7		
5	Ab	128	Total	C	N	O	S	0	0
			977	606	162	202	7		

- Molecule 6 is a protein called Neck 1 protein, gp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	R3	181	Total	C	N	O	S	0	0
			1395	887	249	255	4		

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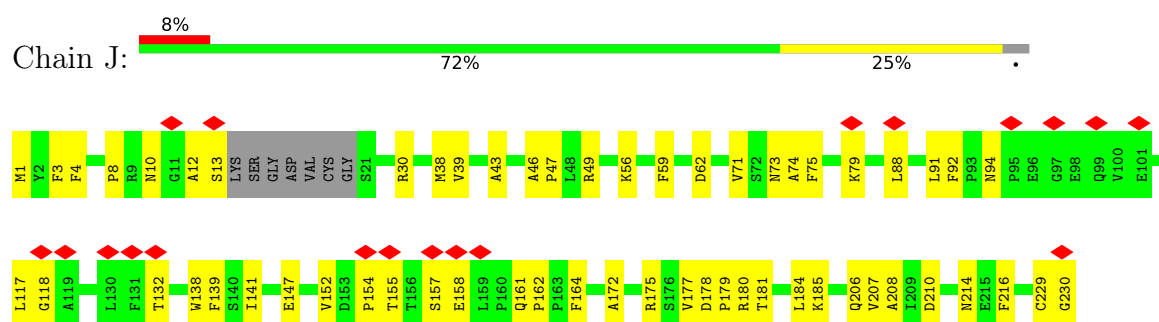
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Mol	Chain	Residues	Atoms					AltConf	Trace
6	S3	180	Total 1387	C 881	N 248	O 254	S 4	0	0
6	T3	179	Total 1379	C 875	N 247	O 253	S 4	0	0
6	U3	180	Total 1387	C 881	N 248	O 254	S 4	0	0
6	R4	181	Total 1395	C 887	N 249	O 255	S 4	0	0
6	S4	180	Total 1387	C 881	N 248	O 254	S 4	0	0
6	T4	179	Total 1379	C 875	N 247	O 253	S 4	0	0
6	U4	180	Total 1387	C 881	N 248	O 254	S 4	0	0
6	R5	181	Total 1395	C 887	N 249	O 255	S 4	0	0
6	S5	180	Total 1387	C 881	N 248	O 254	S 4	0	0
6	T5	179	Total 1379	C 875	N 247	O 253	S 4	0	0
6	U5	180	Total 1387	C 881	N 248	O 254	S 4	0	0

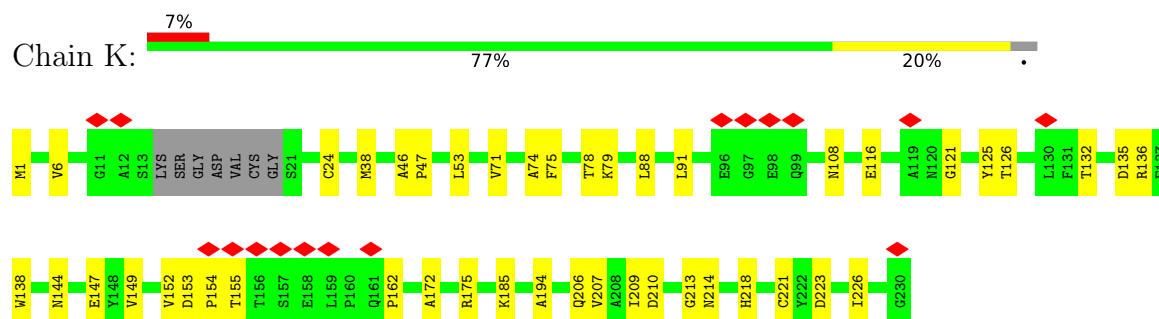
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

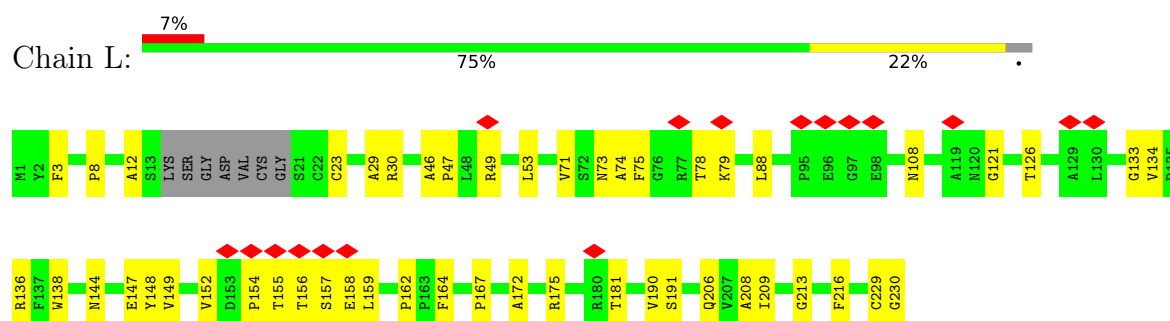
- Molecule 1: Collar sheath protein, gp13



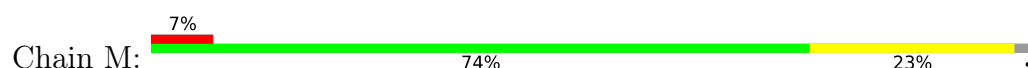
- Molecule 1: Collar sheath protein, gp13

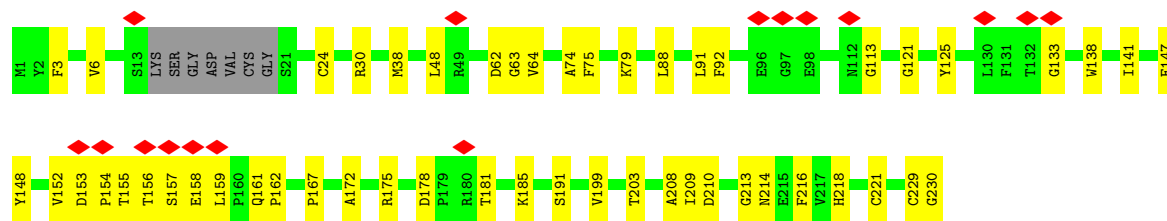


- Molecule 1: Collar sheath protein, gp13

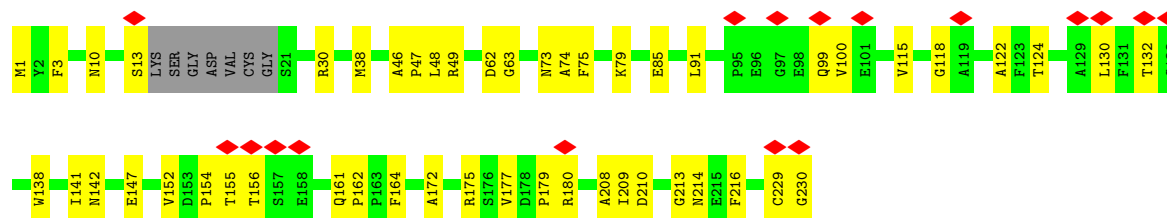
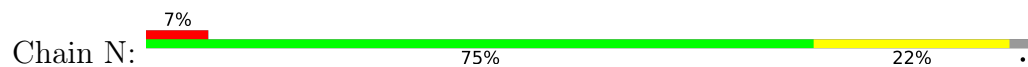


- Molecule 1: Collar sheath protein, gp13

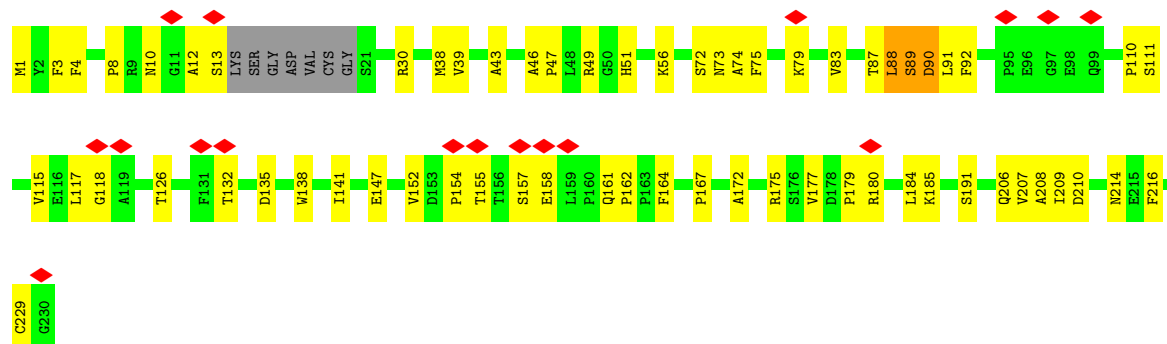




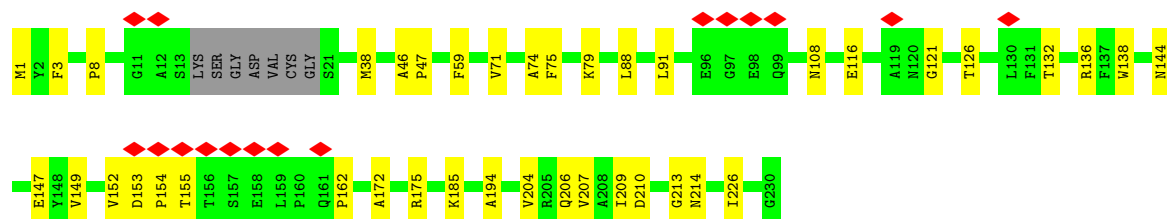
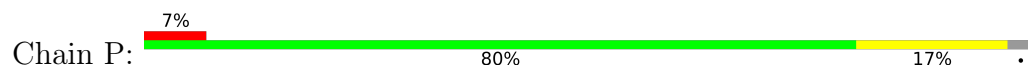
- Molecule 1: Collar sheath protein, gp13



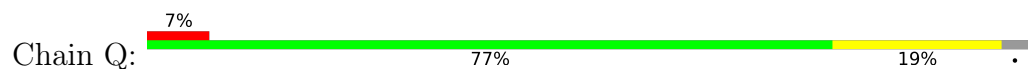
- Molecule 1: Collar sheath protein, gp13

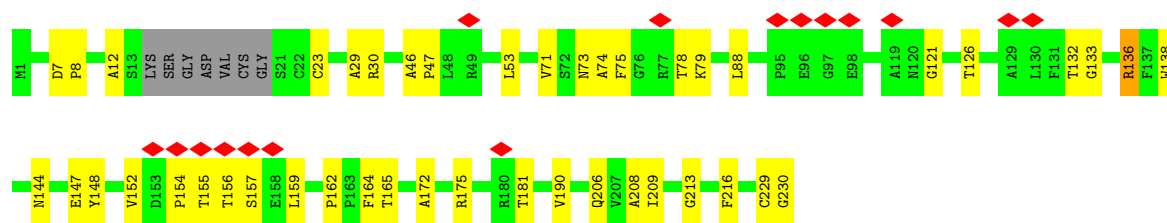


- Molecule 1: Collar sheath protein, gp13

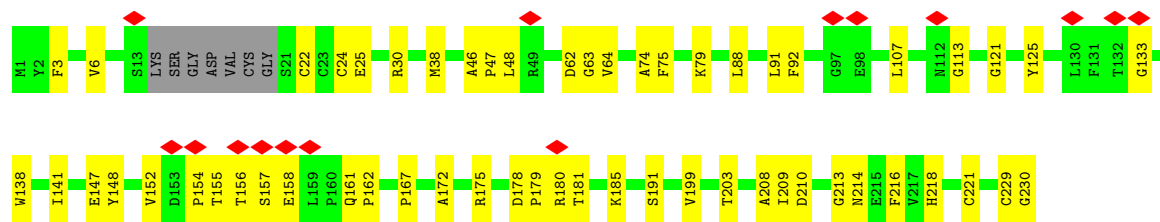


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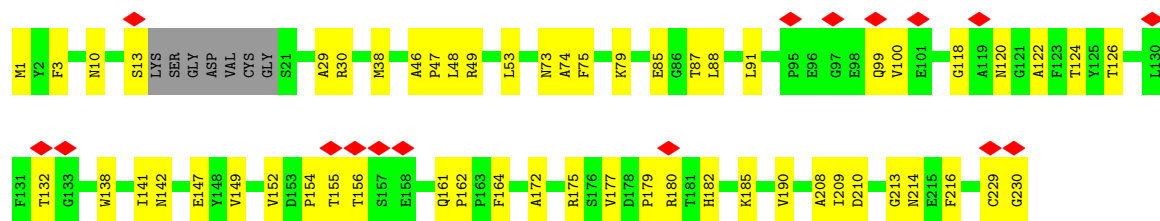
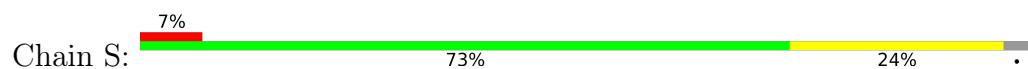




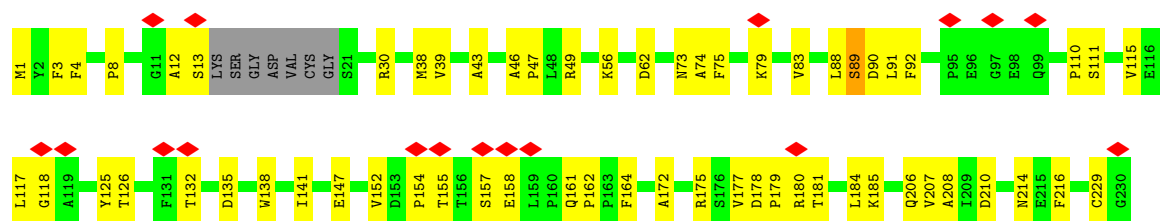
- Molecule 1: Collar sheath protein, gp13



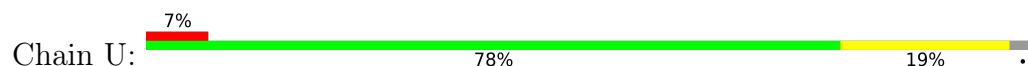
- Molecule 1: Collar sheath protein, gp13



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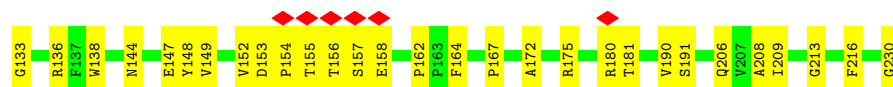
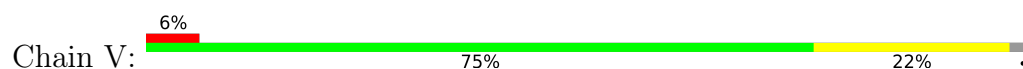


- Molecule 1: Collar sheath protein, gp13

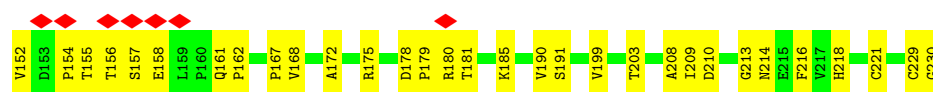
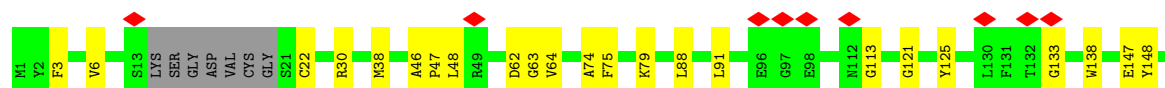
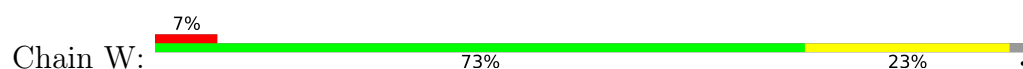




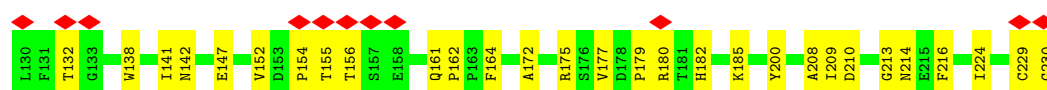
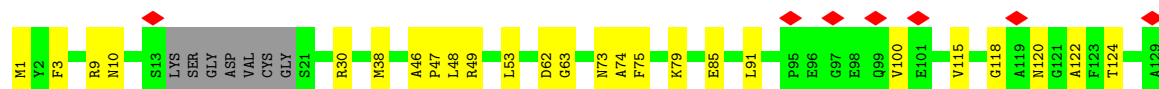
- Molecule 1: Collar sheath protein, gp13



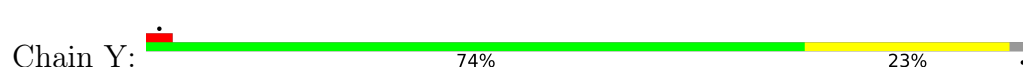
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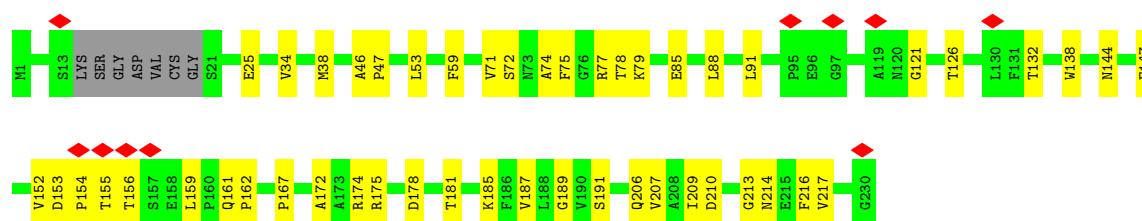


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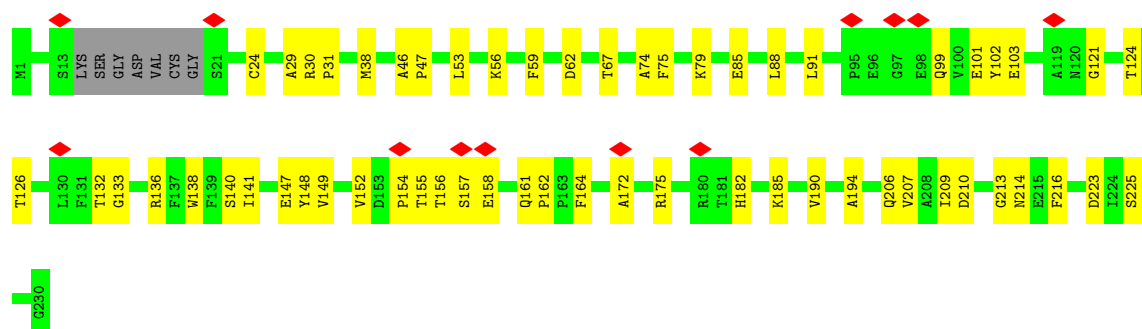
- Molecule 1: Collar sheath protein, gp13

Chain Z:  76% 21% .



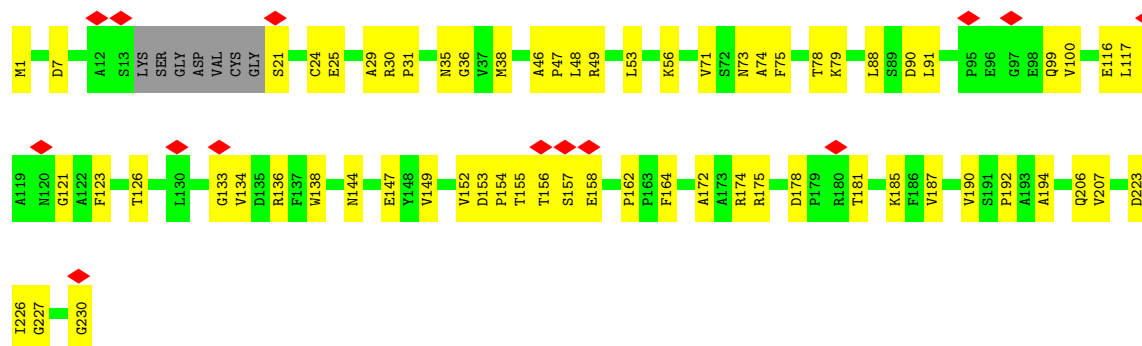
• Molecule 1: Collar sheath protein, gp13

Chain a:  71% 26% .



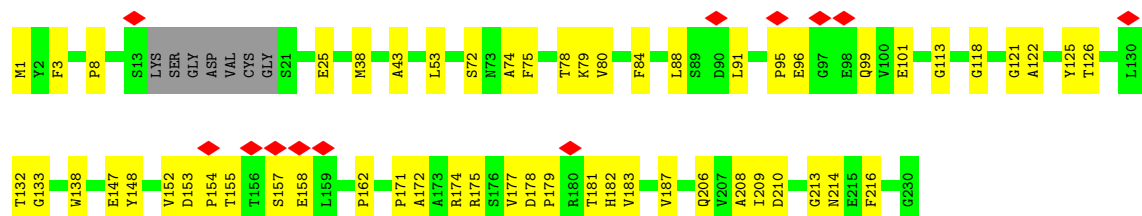
• Molecule 1: Collar sheath protein, gp13

Chain b:  68% 29% .

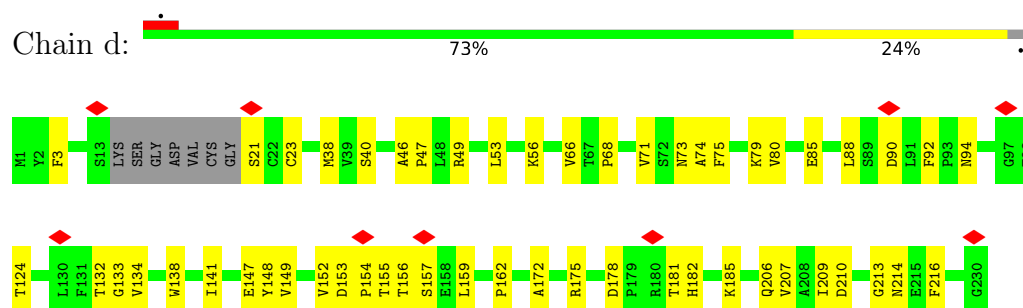


• Molecule 1: Collar sheath protein, gp13

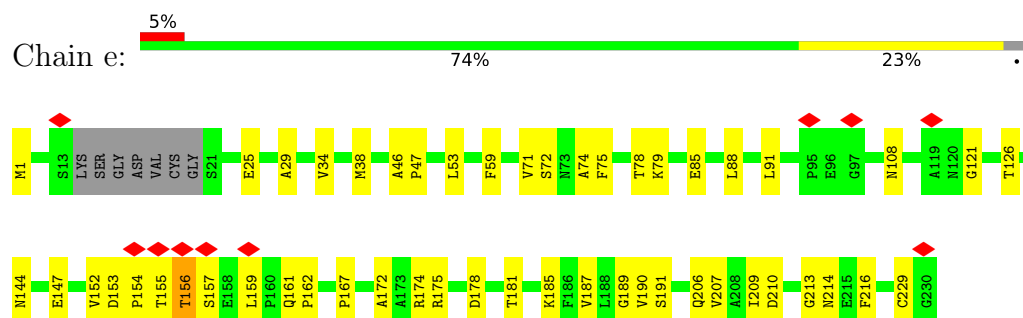
Chain c:  73% 24% .



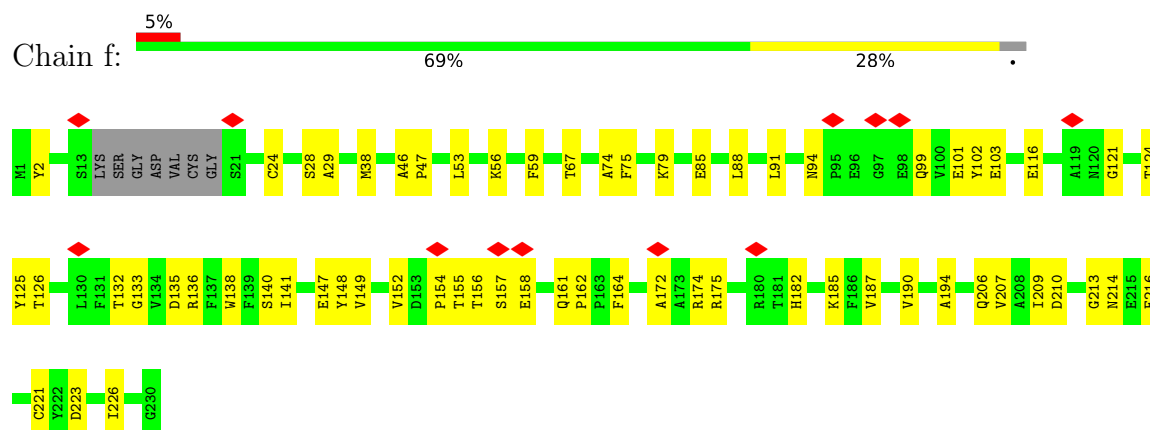
- Molecule 1: Collar sheath protein, gp13



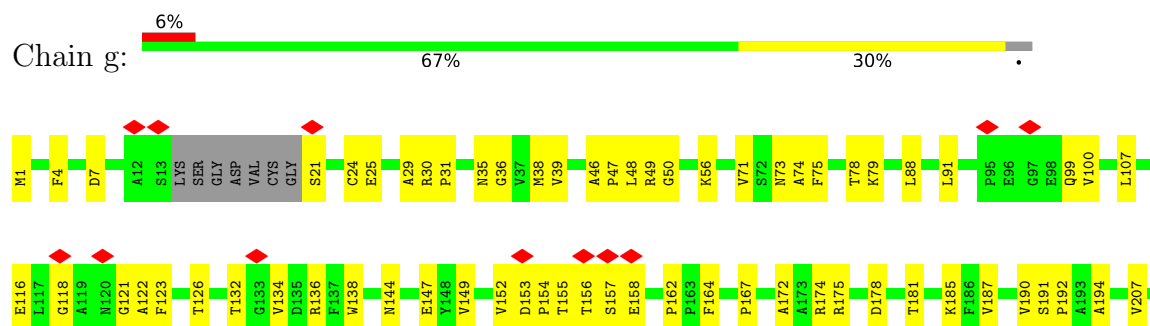
- Molecule 1: Collar sheath protein, gp13



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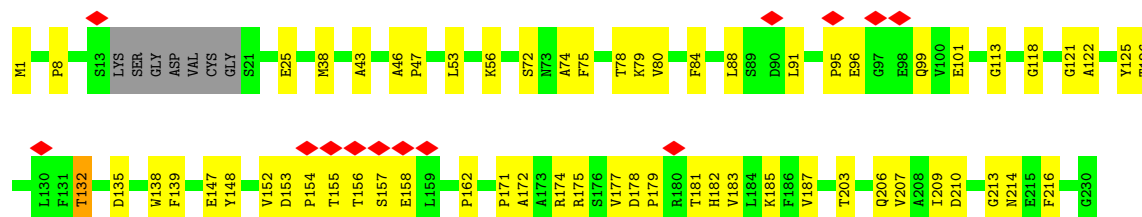


- Molecule 1: Collar sheath protein, gp13

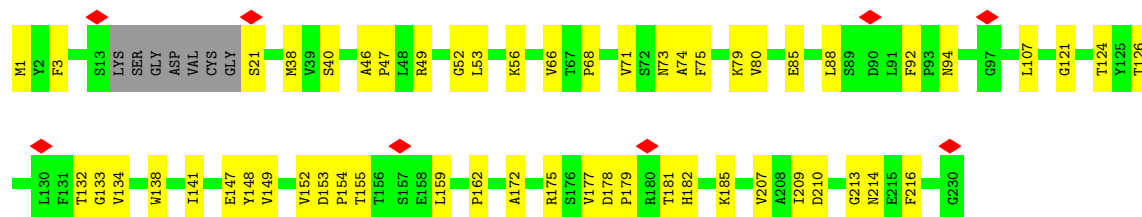




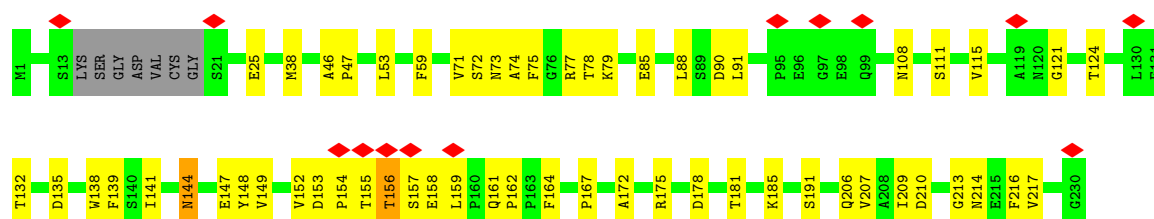
- Molecule 1: Collar sheath protein, gp13



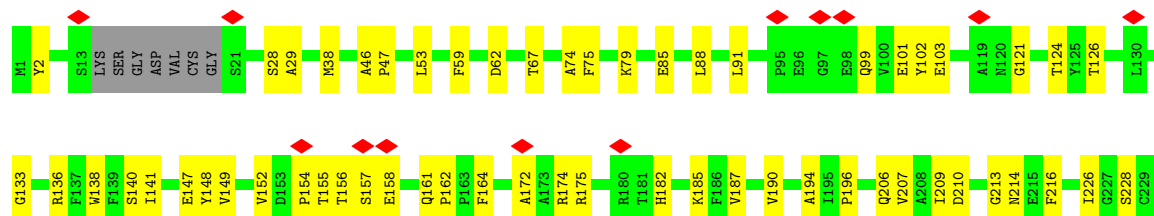
- Molecule 1: Collar sheath protein, gp13



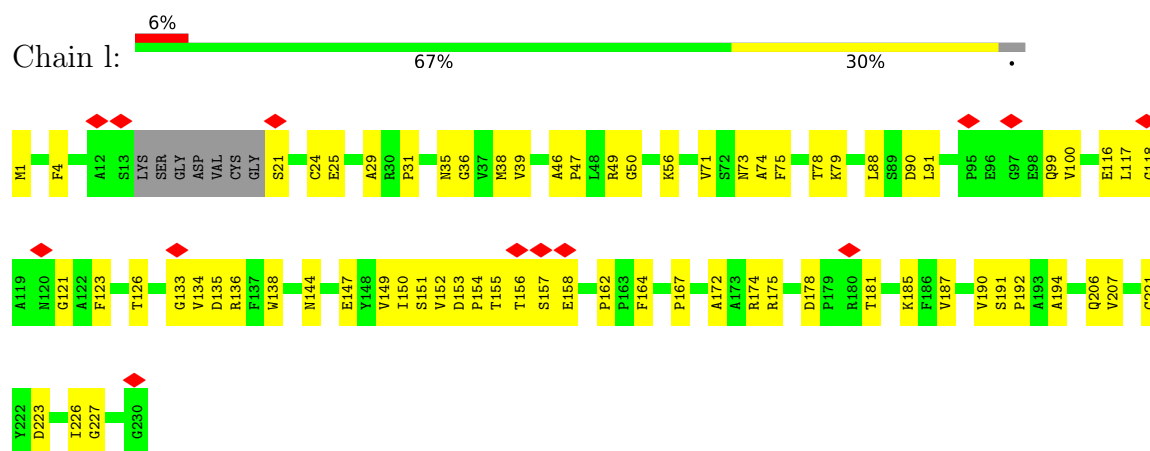
- Molecule 1: Collar sheath protein, gp13



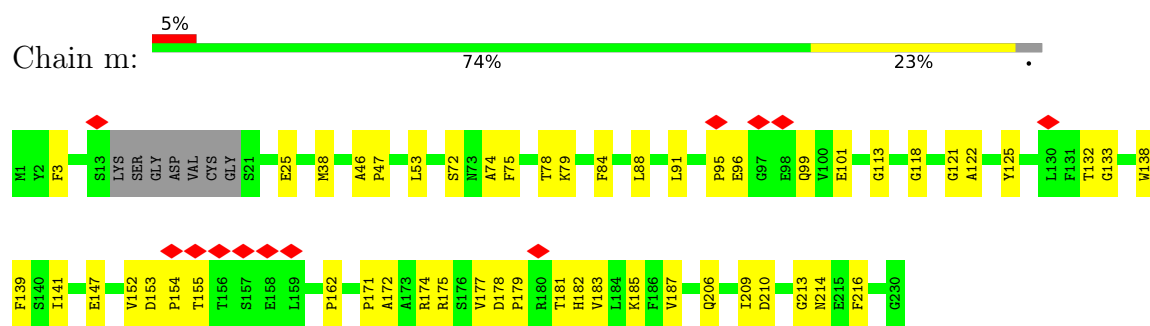
- Molecule 1: Collar sheath protein, gp13



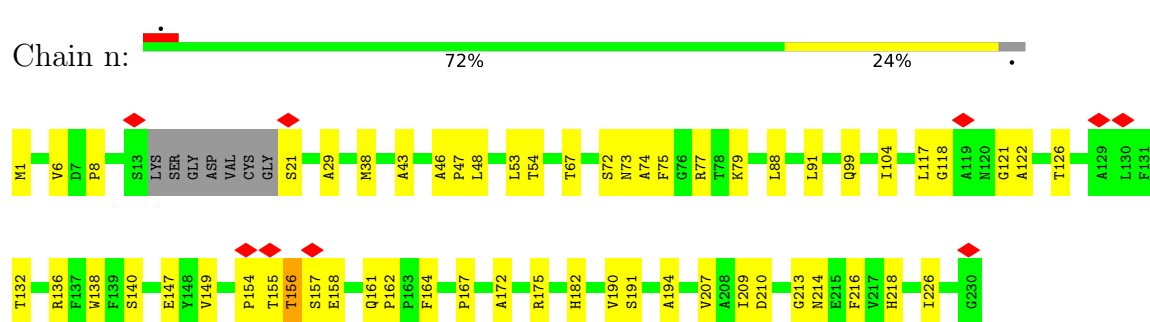
- Molecule 1: Collar sheath protein, gp13



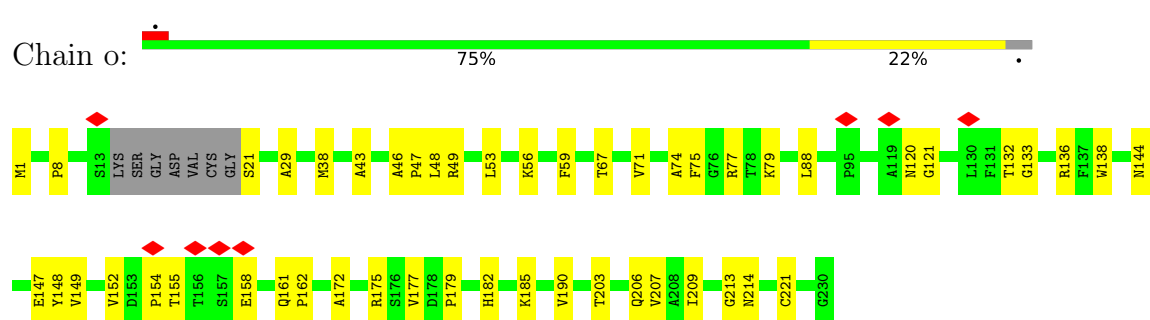
- Molecule 1: Collar sheath protein, gp13



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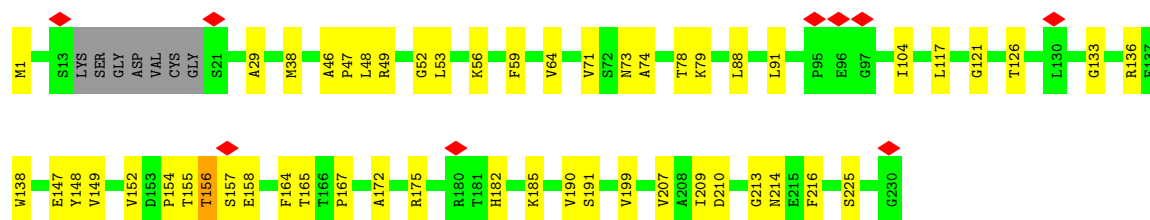


- Molecule 1: Collar sheath protein, gp13



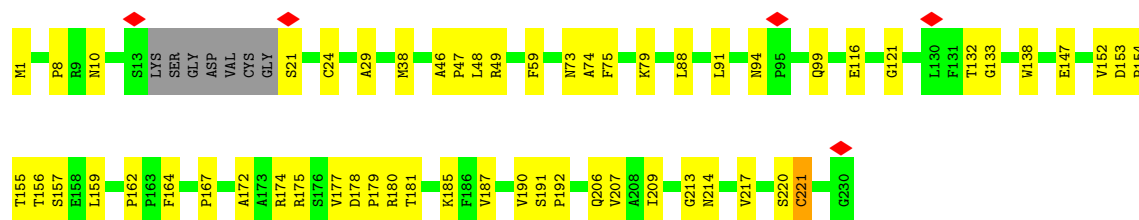
- Molecule 1: Collar sheath protein, gp13

Chain p:  74% 22%



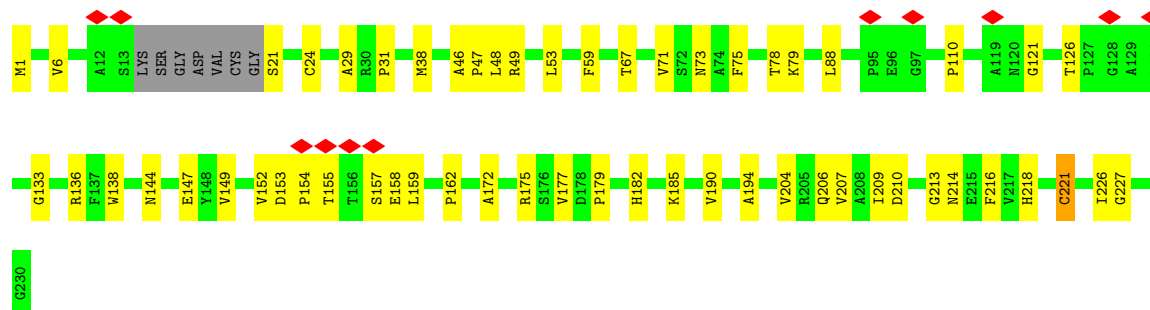
- Molecule 1: Collar sheath protein, gp13

Chain q:  72% 24%



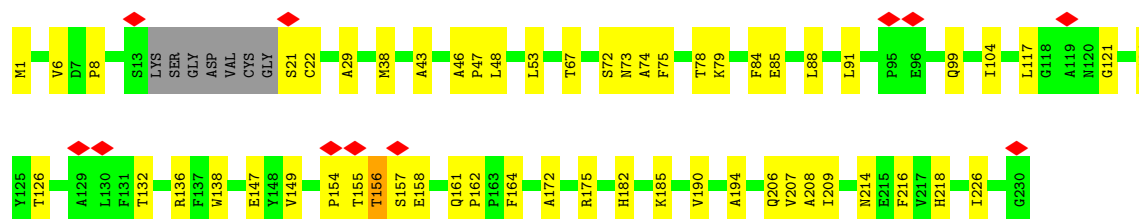
- Molecule 1: Collar sheath protein, gp13

Chain r:  5% 72% 24%



- Molecule 1: Collar sheath protein, gp13

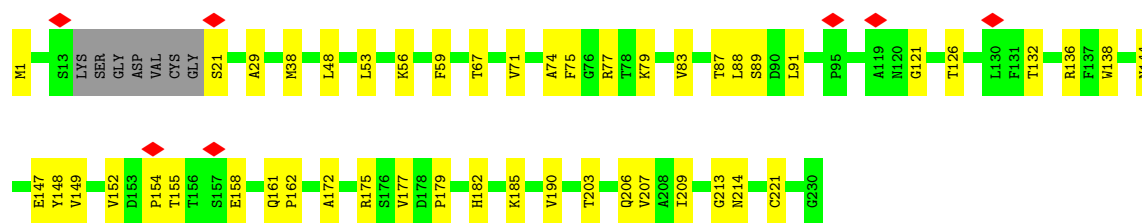
Chain s:  5% 73% 24%



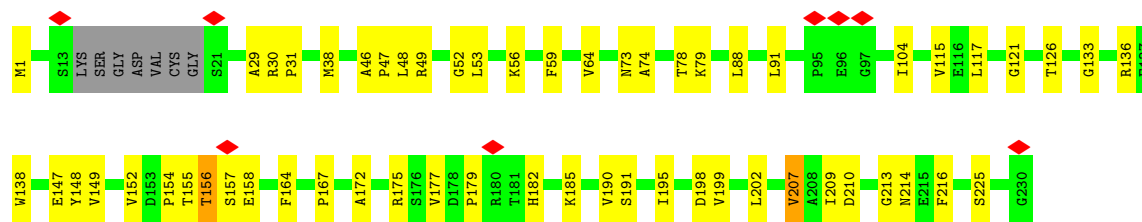
- Molecule 1: Collar sheath protein, gp13

Chain t:  76% 21%

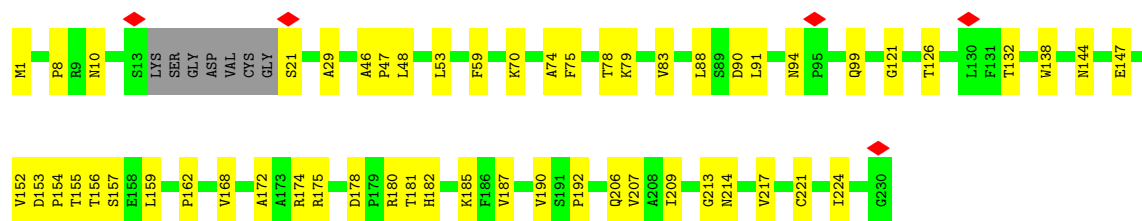




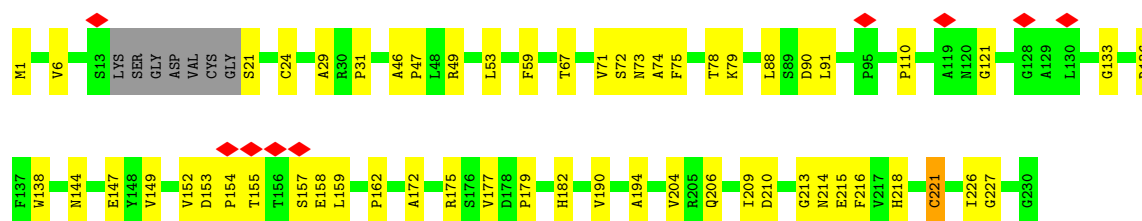
- Molecule 1: Collar sheath protein, gp13



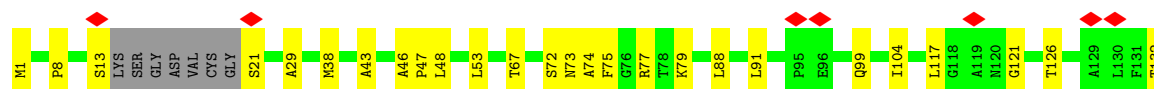
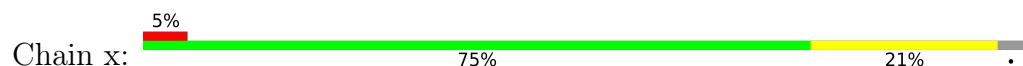
- Molecule 1: Collar sheath protein, gp13

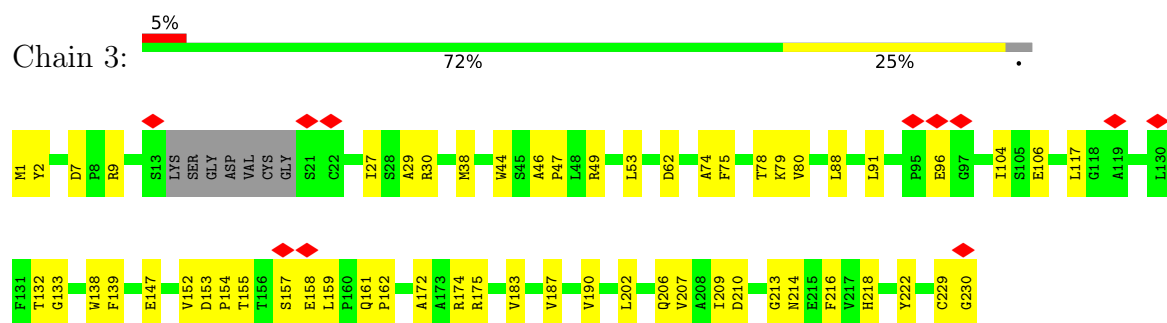


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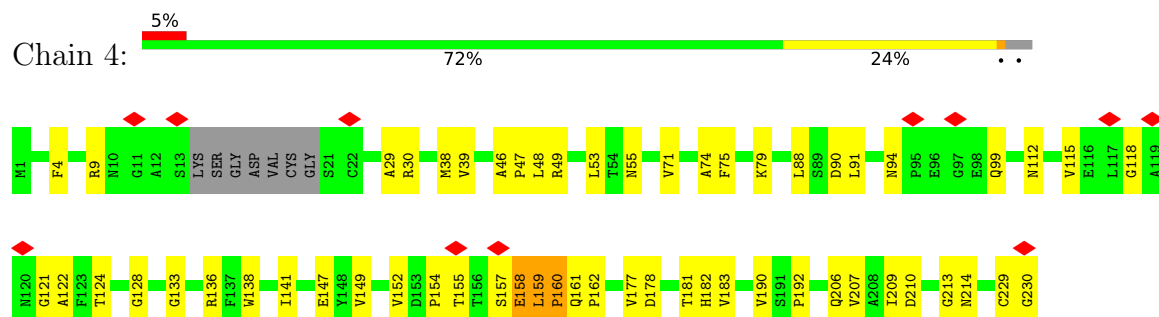


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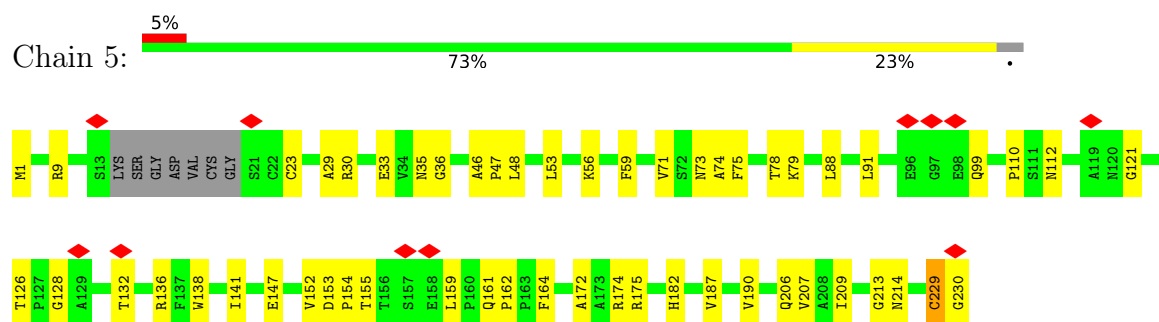




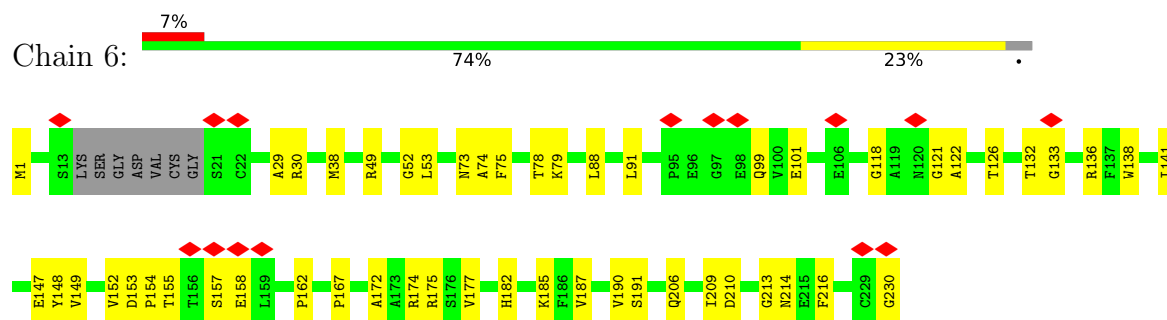
- Molecule 1: Collar sheath protein, gp13



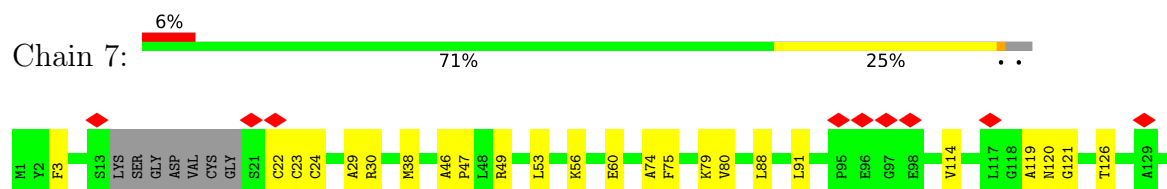
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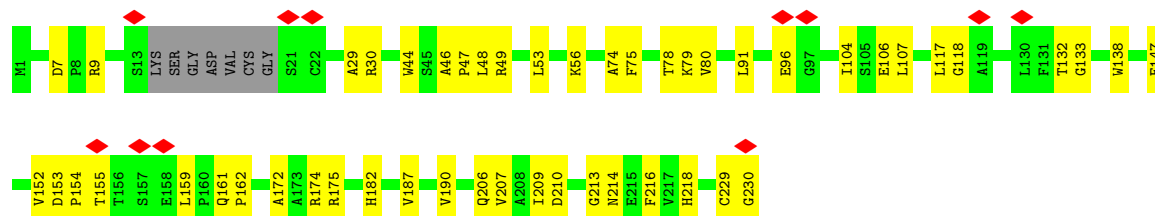
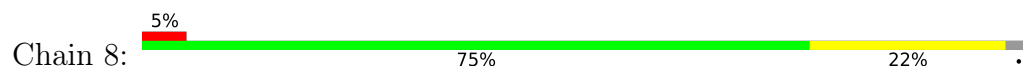


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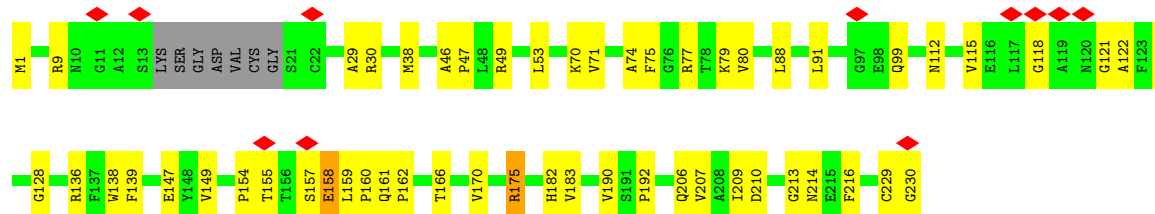
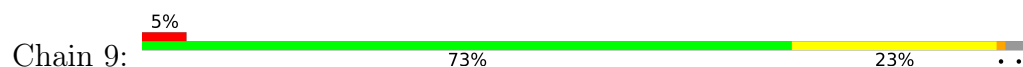




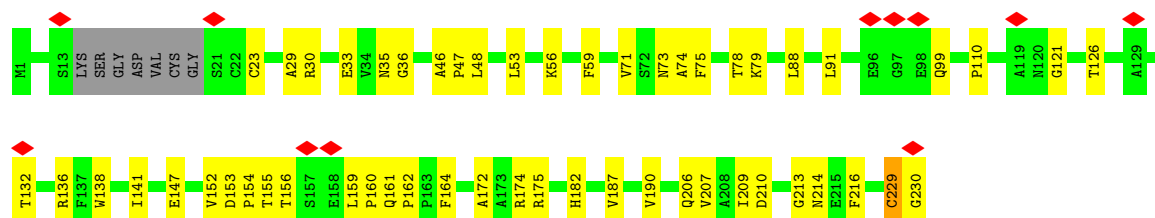
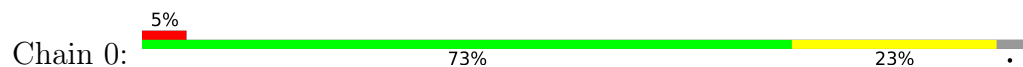
- Molecule 1: Collar sheath protein, gp13



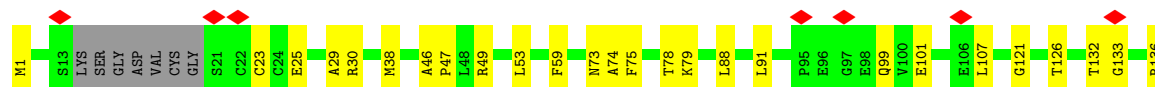
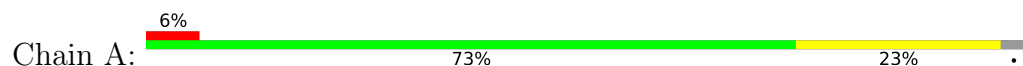
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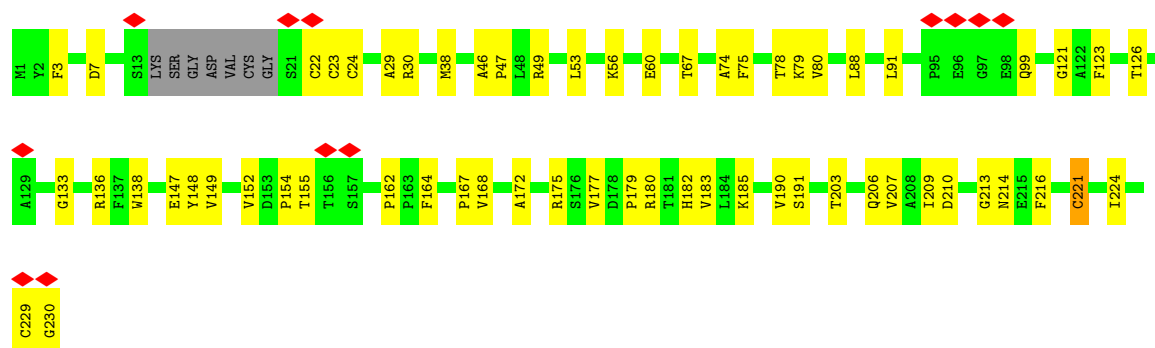


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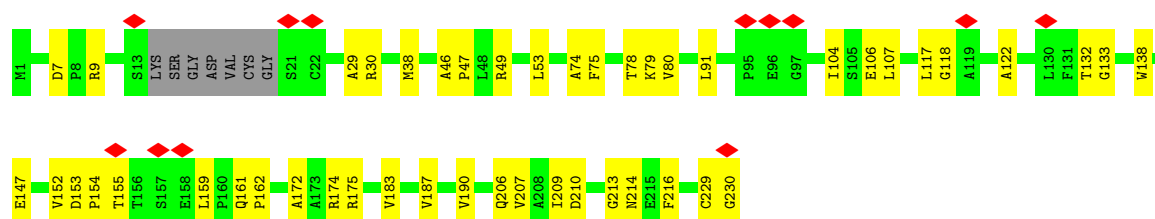
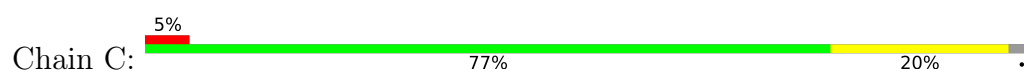




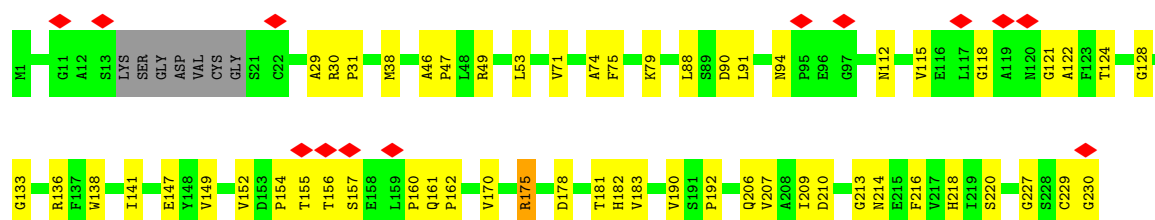
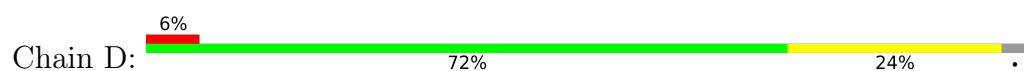
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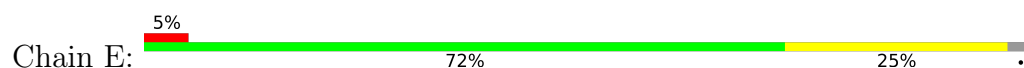
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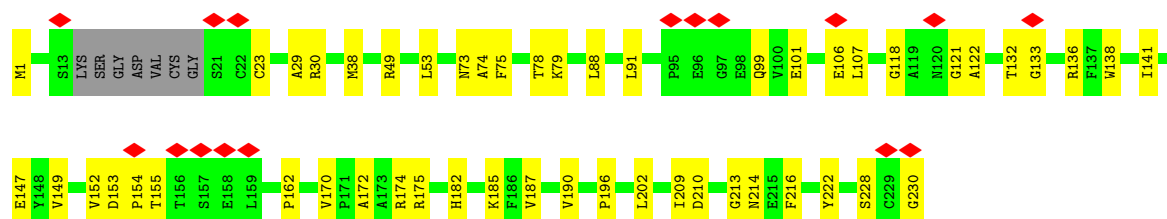
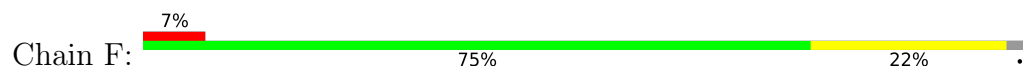


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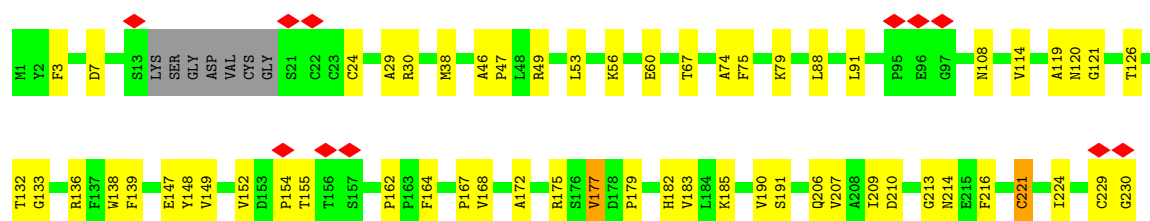




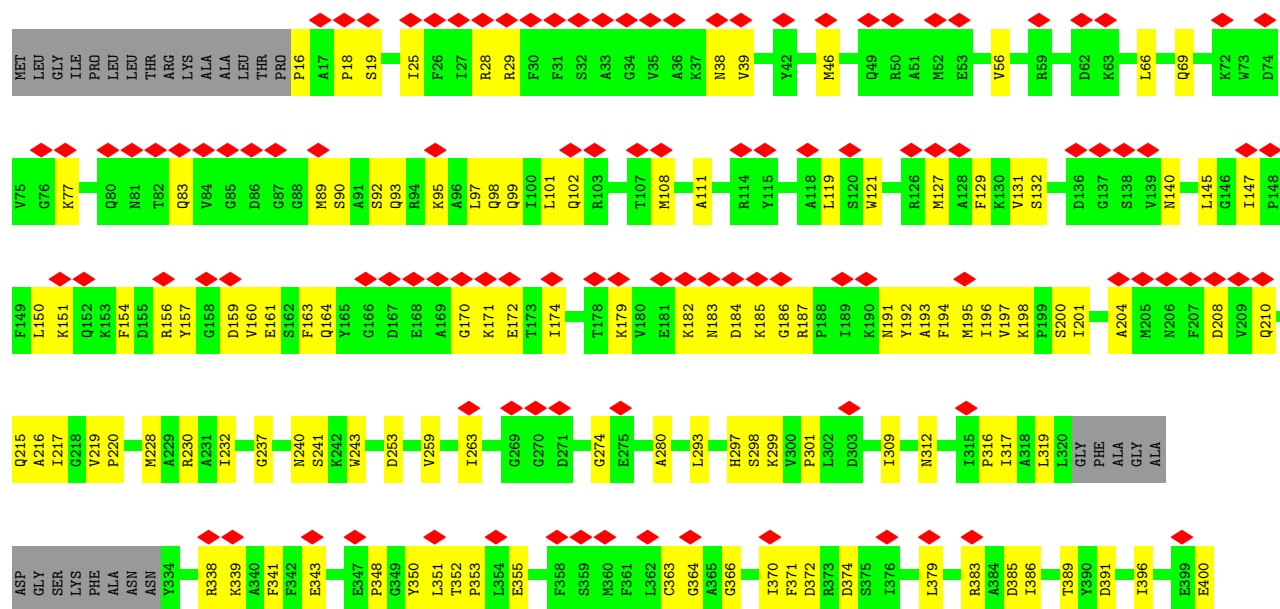
- Molecule 1: Collar sheath protein, gp13

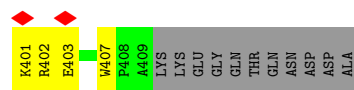


- Molecule 1: Collar sheath protein, gp13

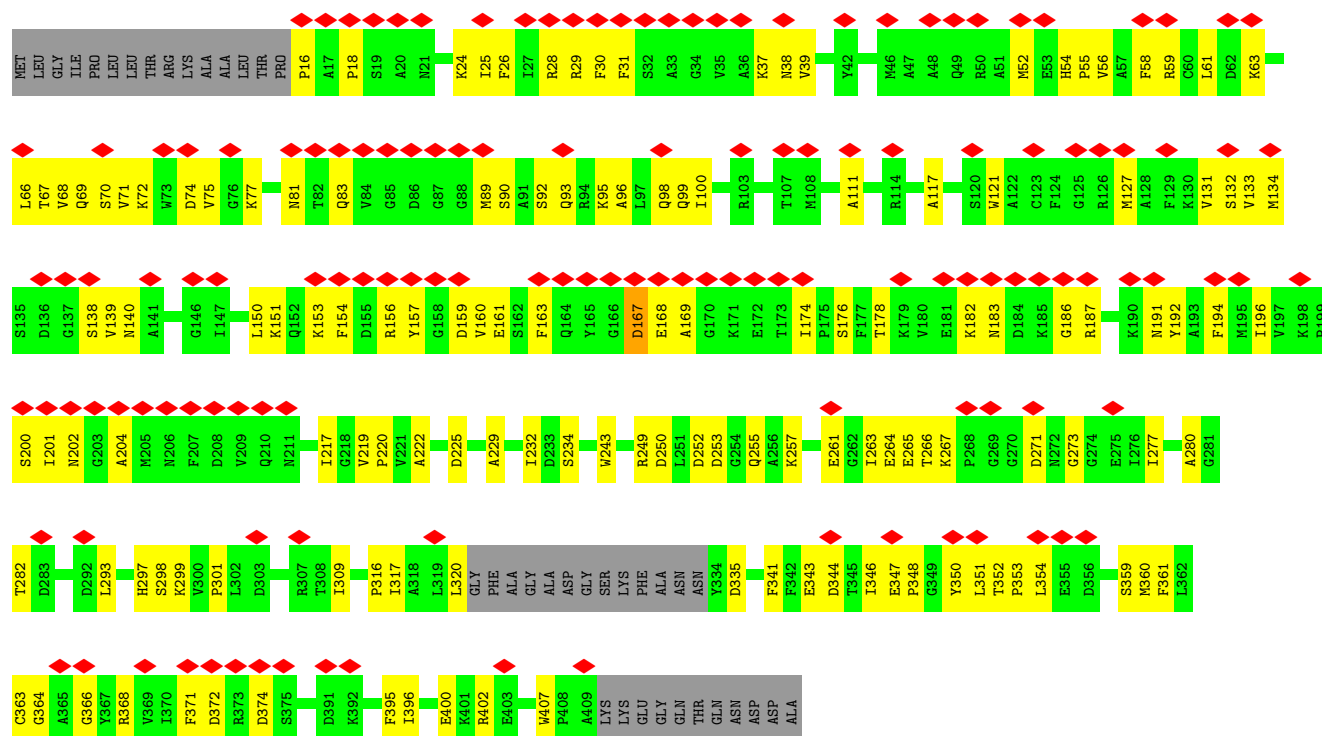


- Molecule 2: Portal protein, gp7

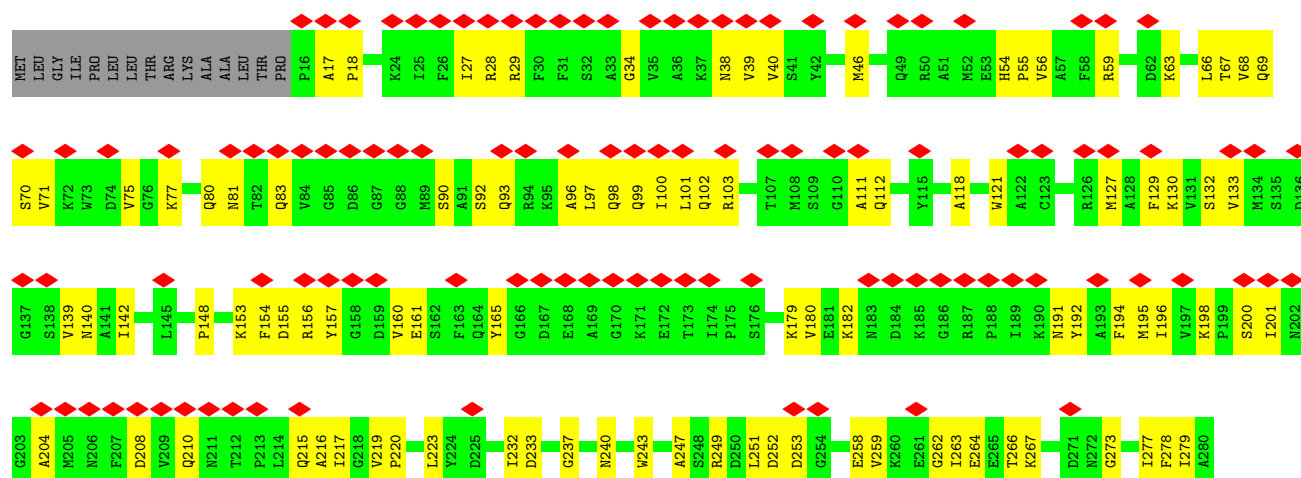


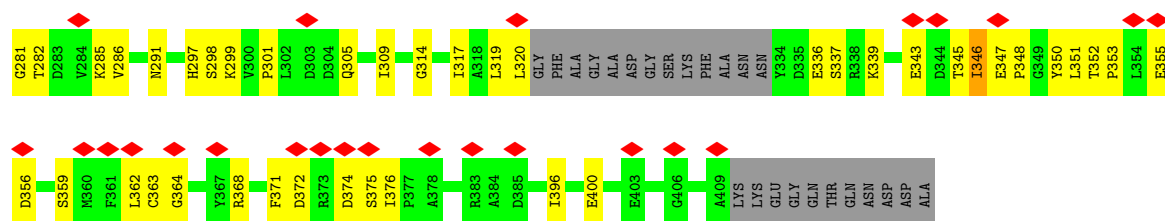


• Molecule 2: Portal protein, gp7

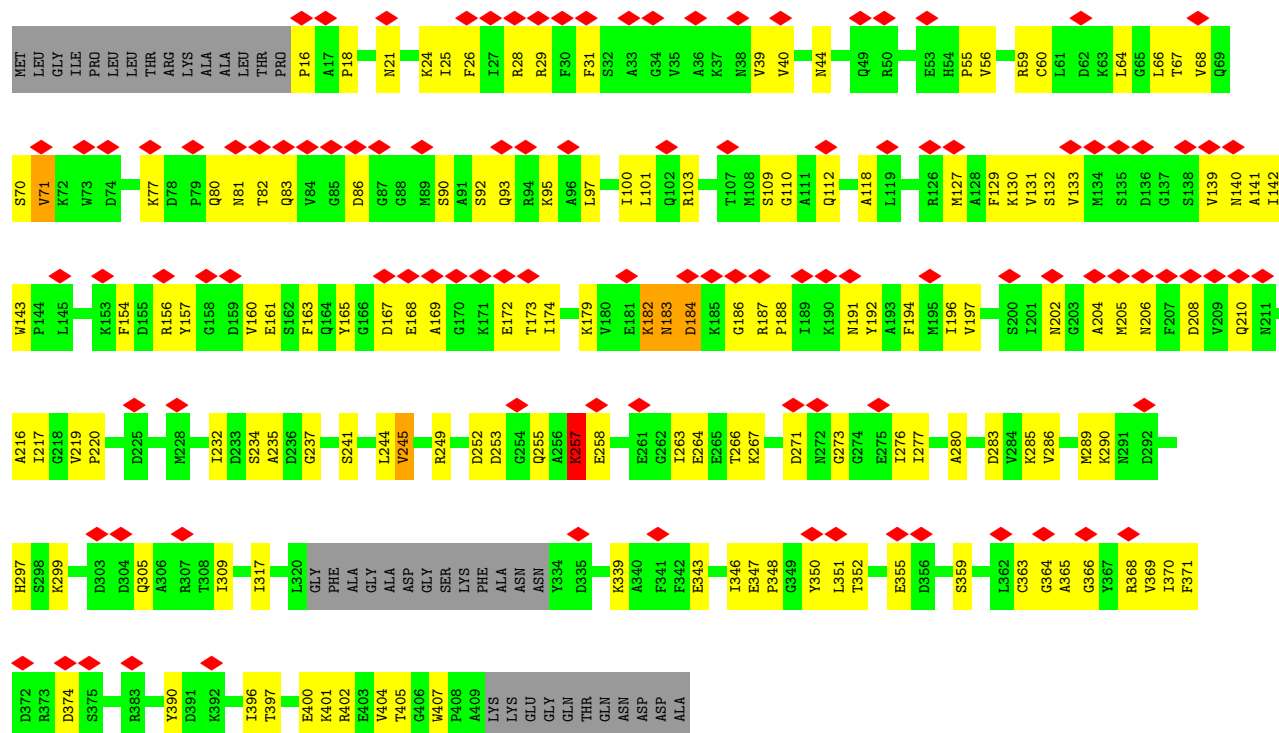


• Molecule 2: Portal protein, gp7

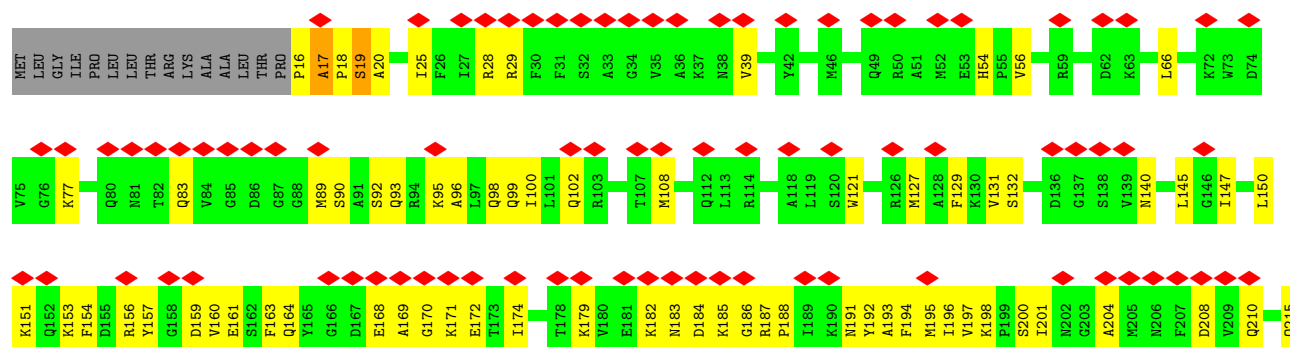


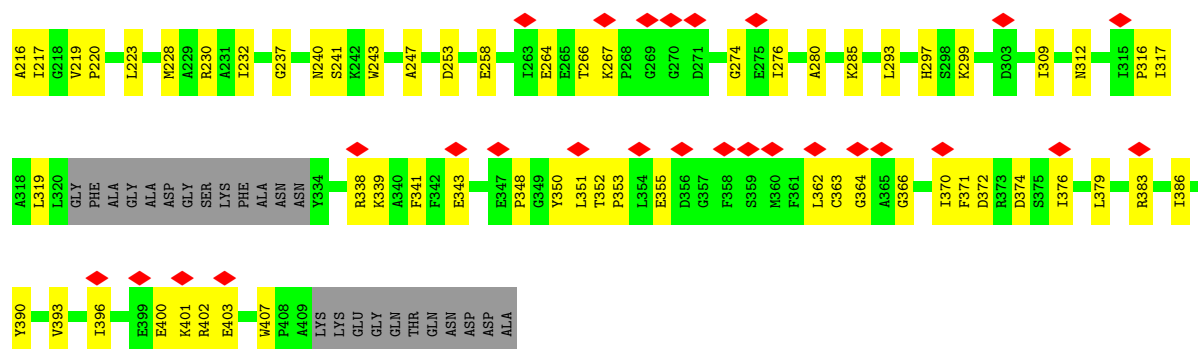


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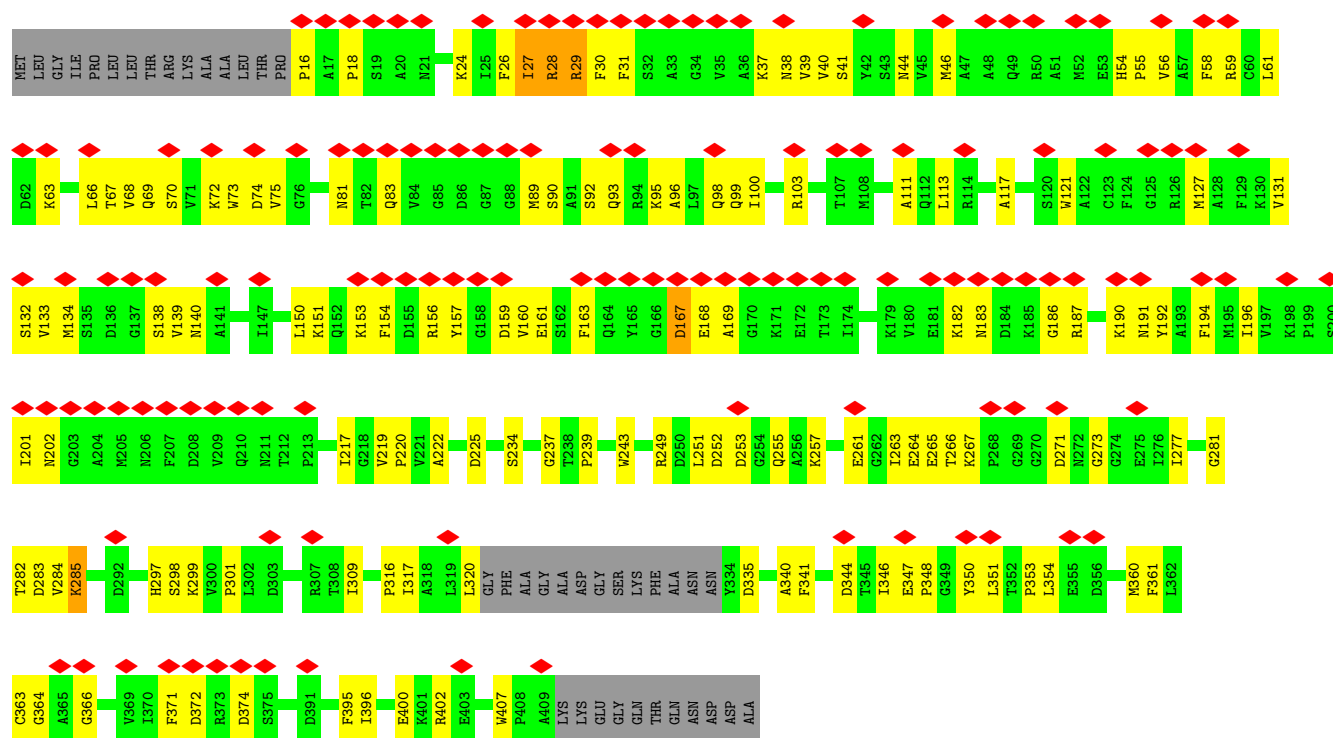


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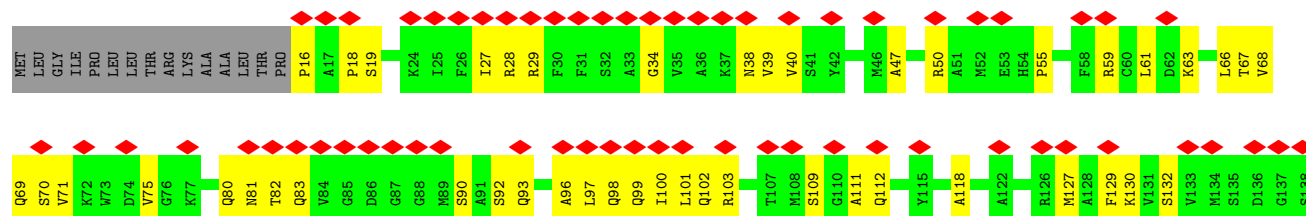


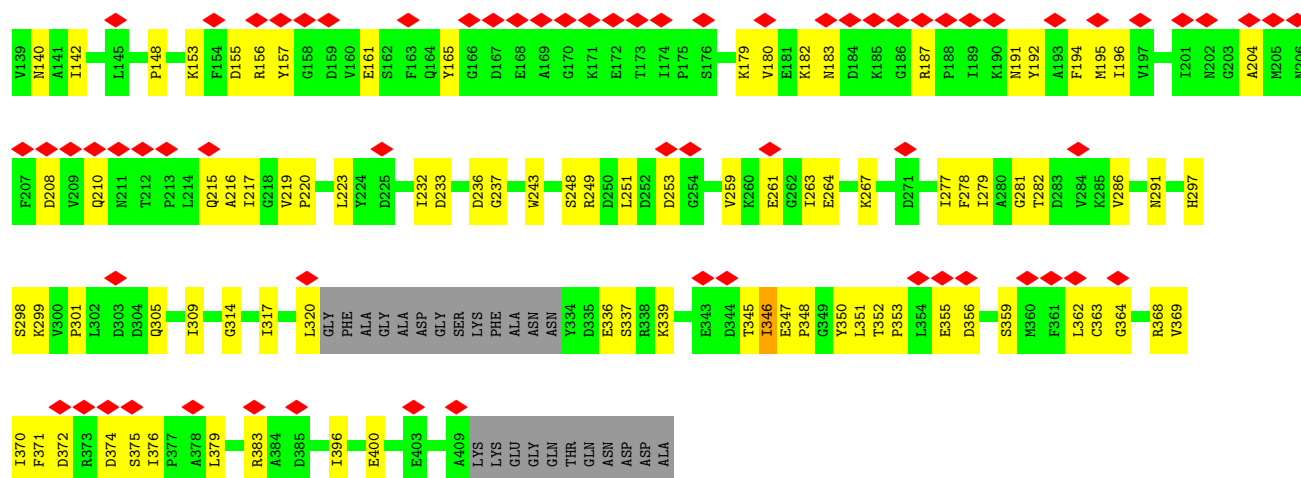


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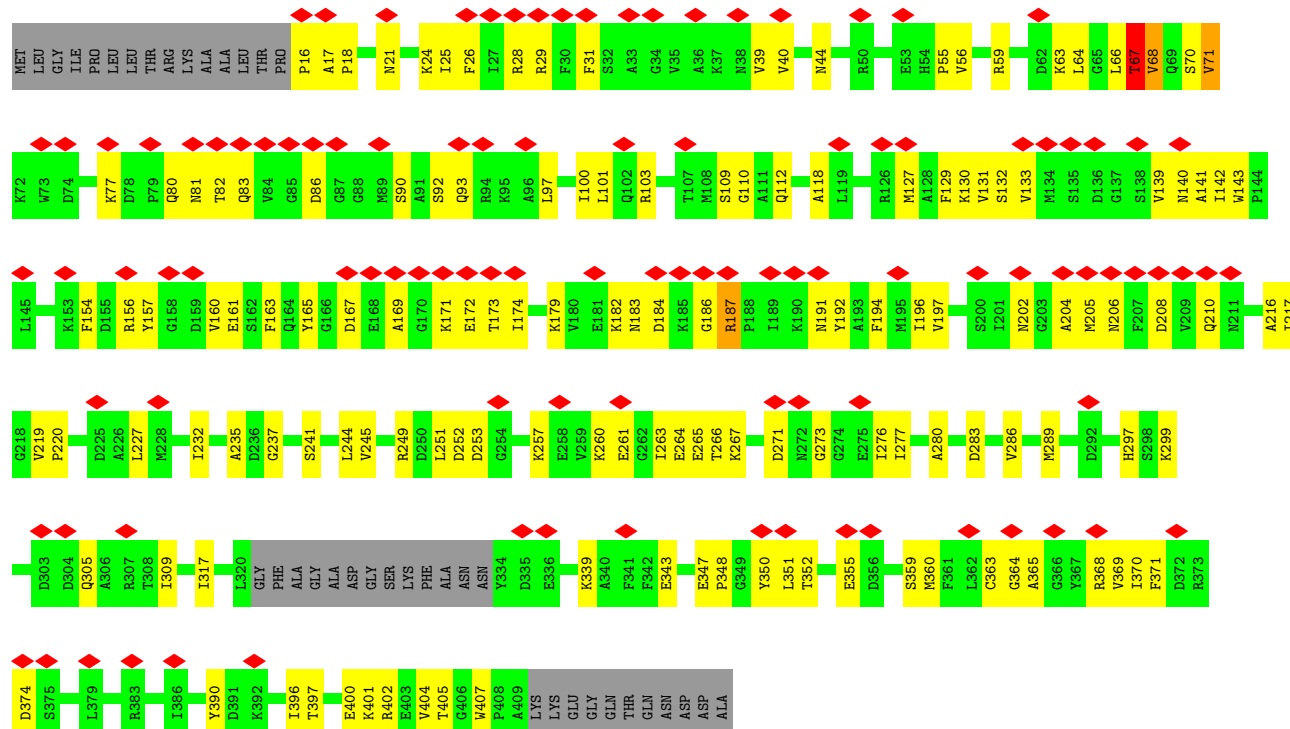


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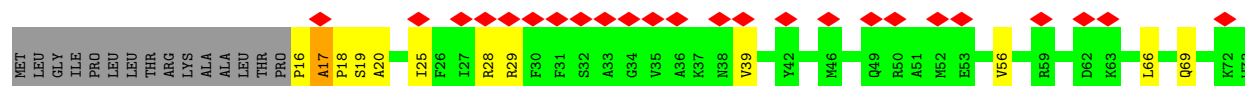


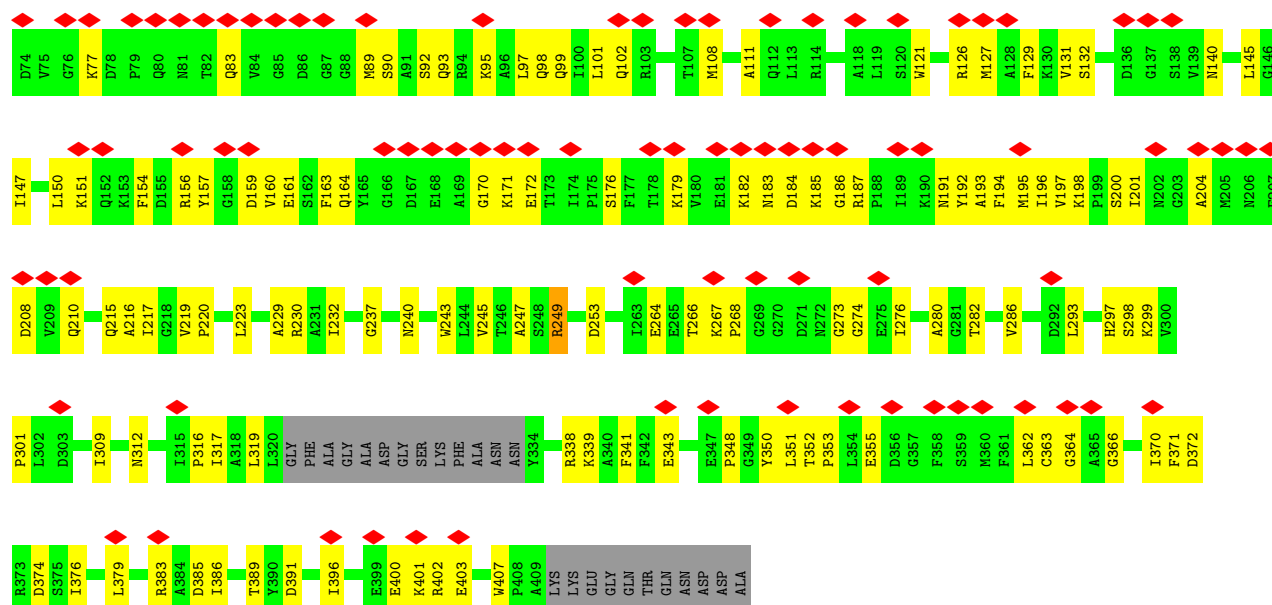


• Molecule 2: Portal protein, gp7

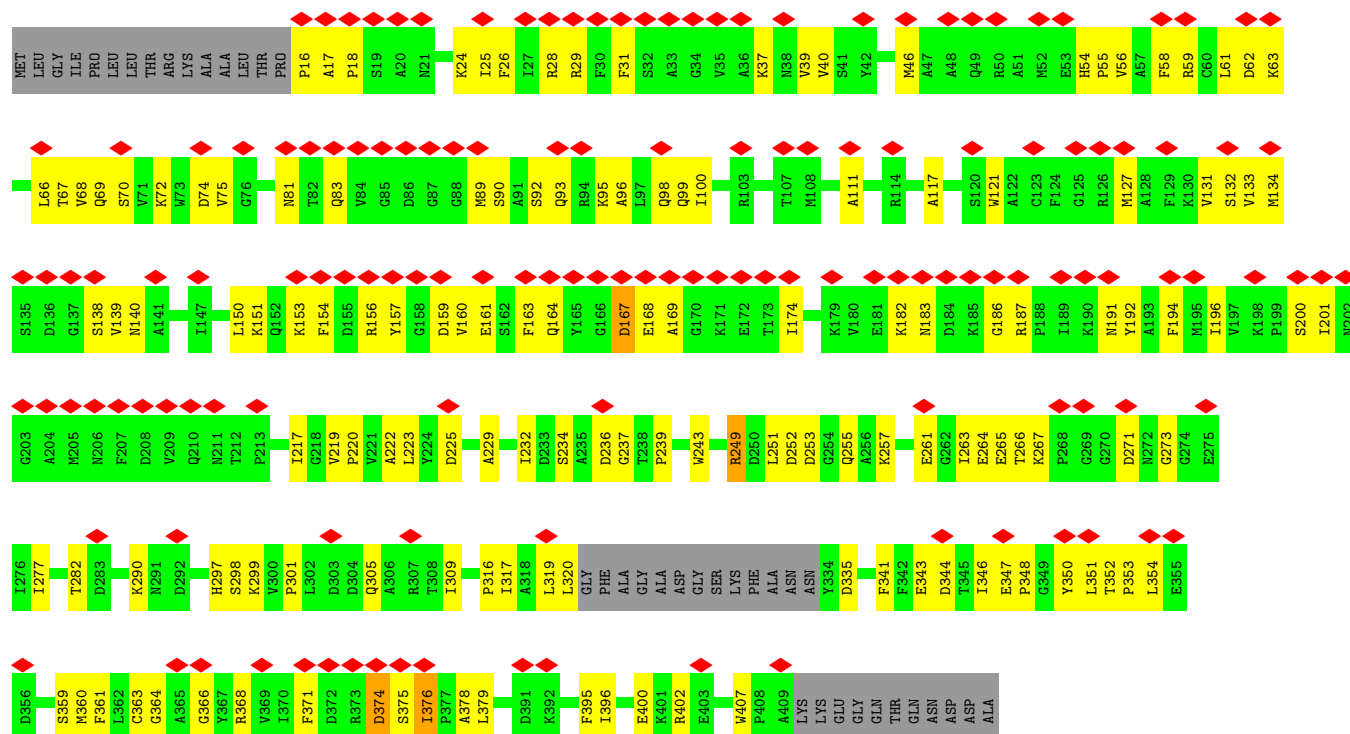


• Molecule 2: Portal protein, gp7



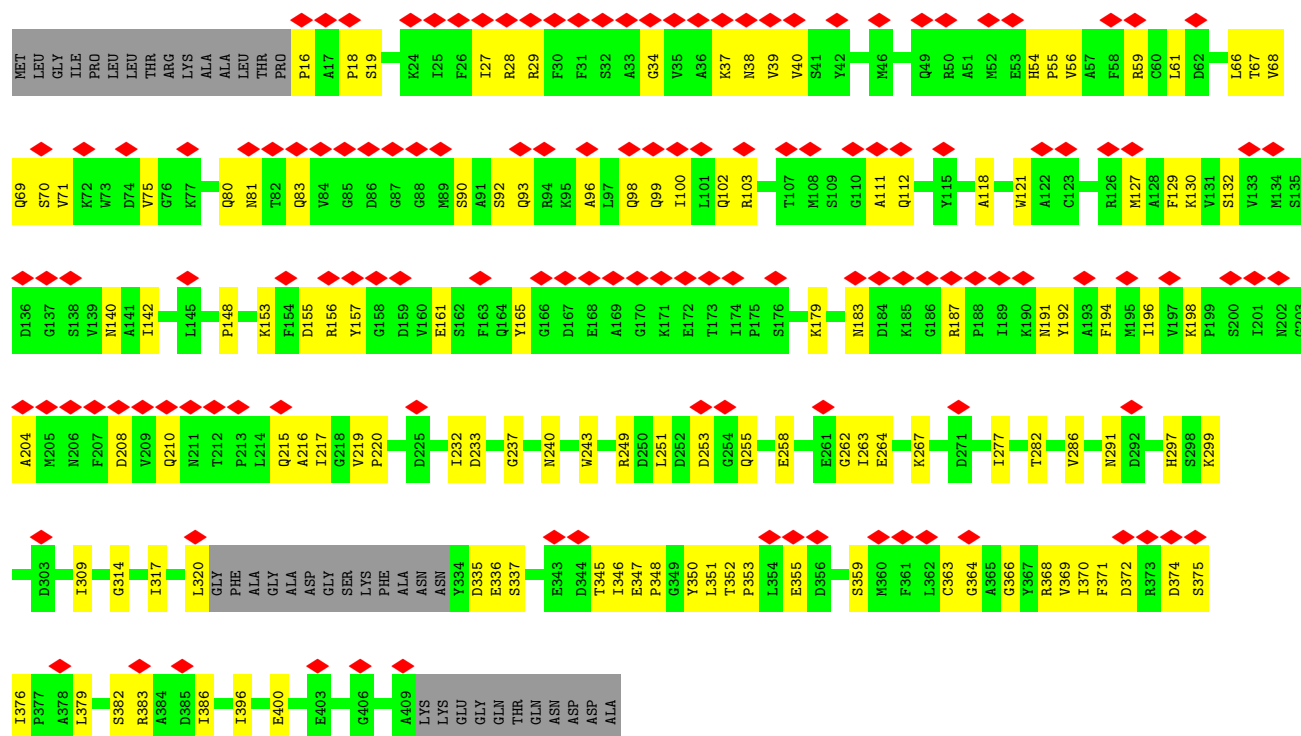


• Molecule 2: Portal protein, gp7

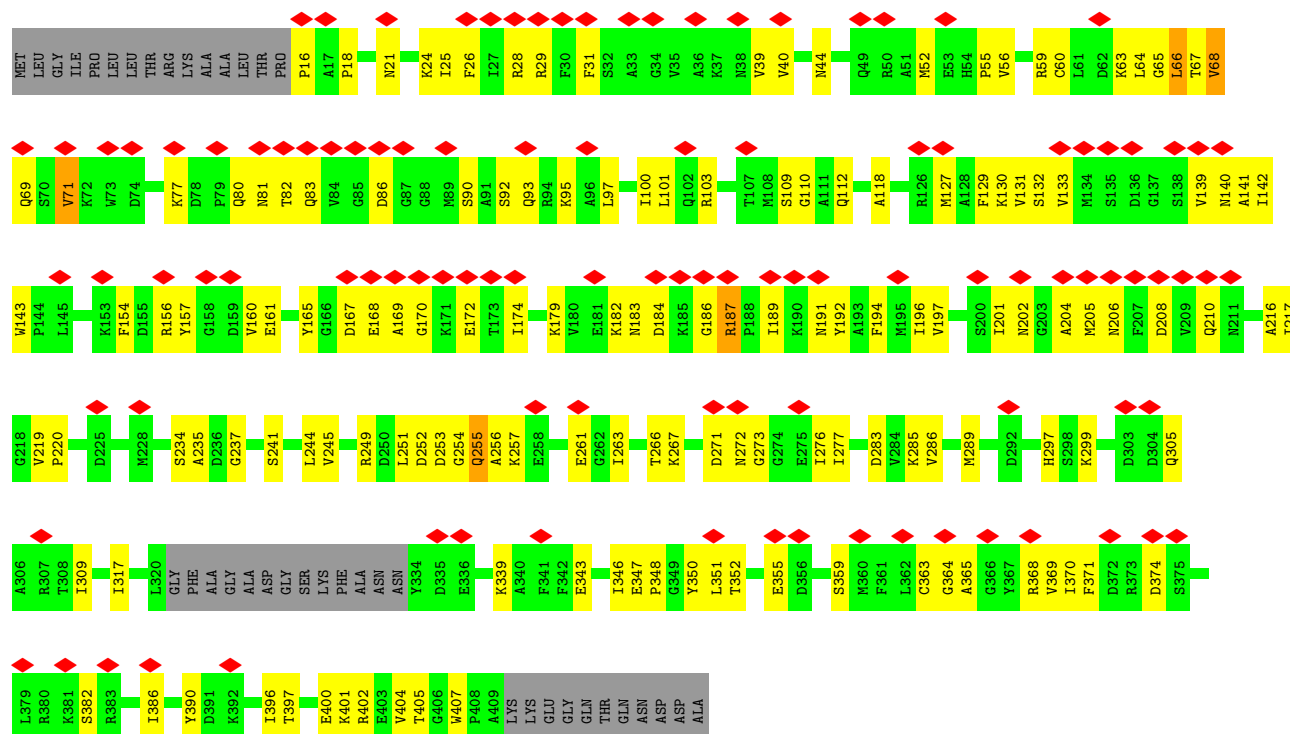


• Molecule 2: Portal protein, gp7



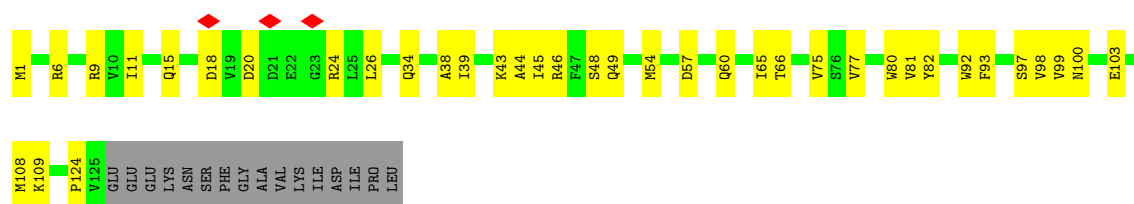


• Molecule 2: Portal protein, gp7



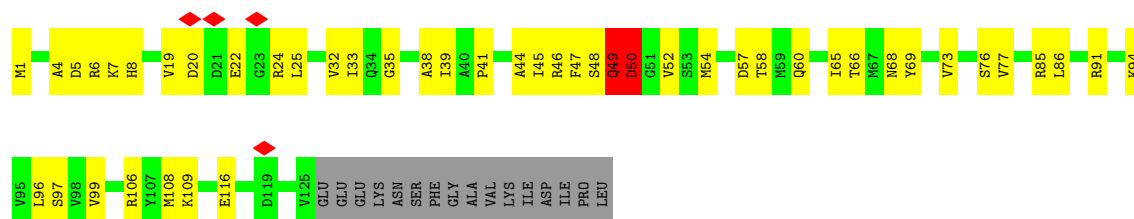
• Molecule 3: Neck 2 protein, gp15

Chain AM: 



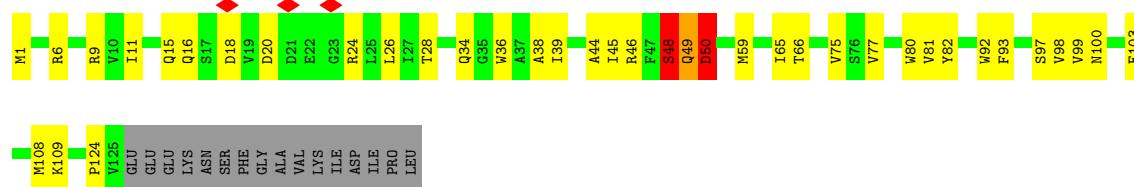
- Molecule 3: Neck 2 protein, gp15

Chain AP: 



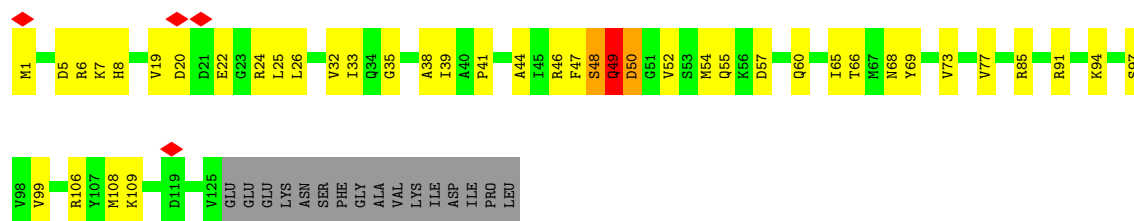
- Molecule 3: Neck 2 protein, gp15

Chain AN: 



- Molecule 3: Neck 2 protein, gp15

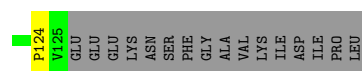
Chain H: 



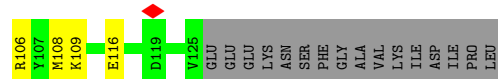
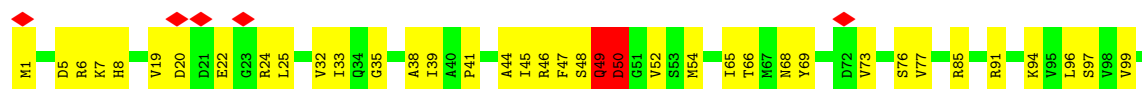
- Molecule 3: Neck 2 protein, gp15

Chain AO: 

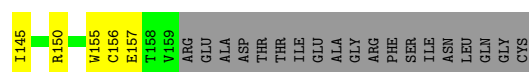
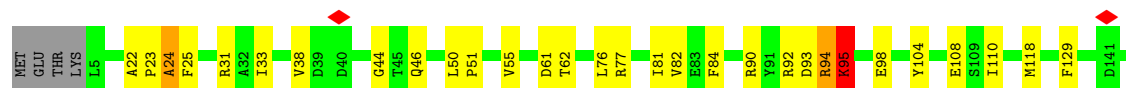




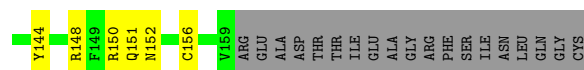
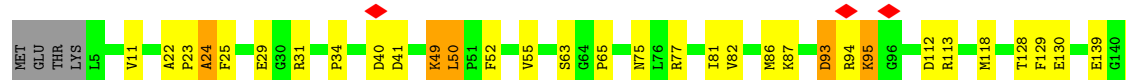
- Molecule 3: Neck 2 protein, gp15



- Molecule 4: Tail-terminator protein, gp18



- Molecule 4: Tail-terminator protein, gp18

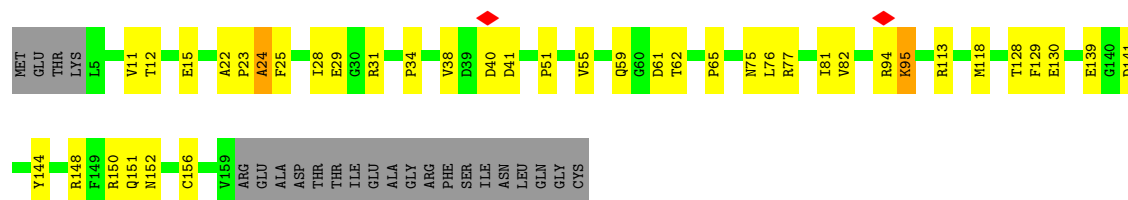


- Molecule 4: Tail-terminator protein, gp18

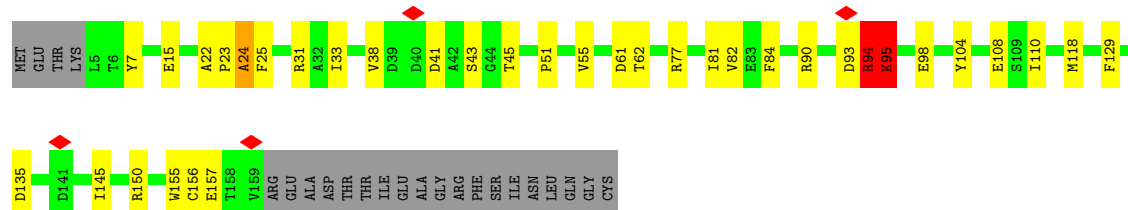


- Molecule 4: Tail-terminator protein, gp18

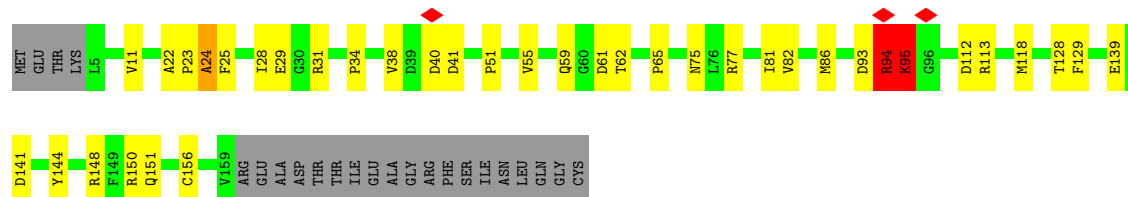




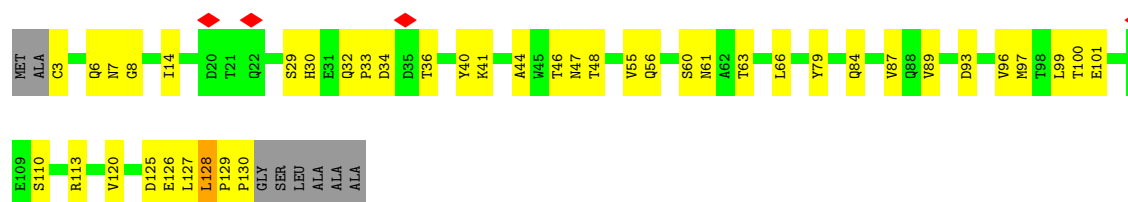
- Molecule 4: Tail-terminator protein, gp18



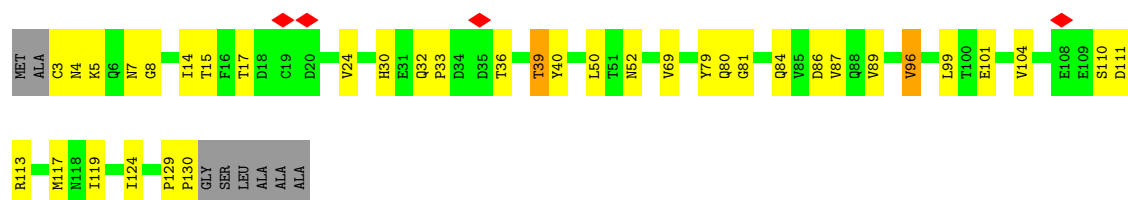
- Molecule 4: Tail-terminator protein, gp18



- Molecule 5: Tail-tube, gp21

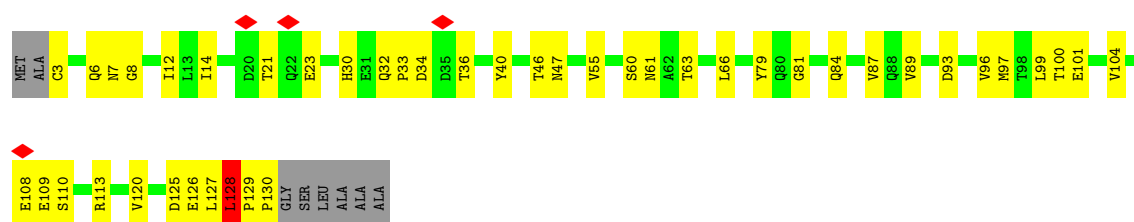


- Molecule 5: Tail-tube, gp21



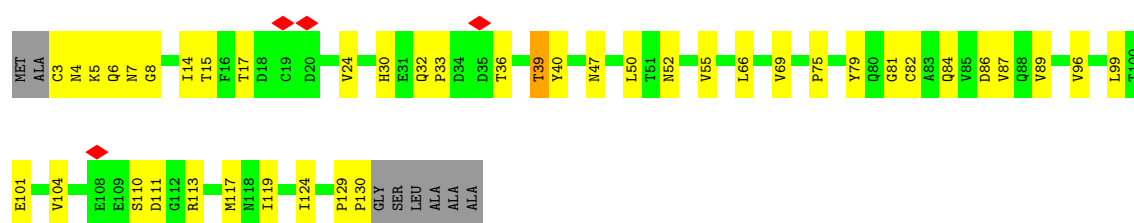
- Molecule 5: Tail-tube, gp21

Chain AV: 



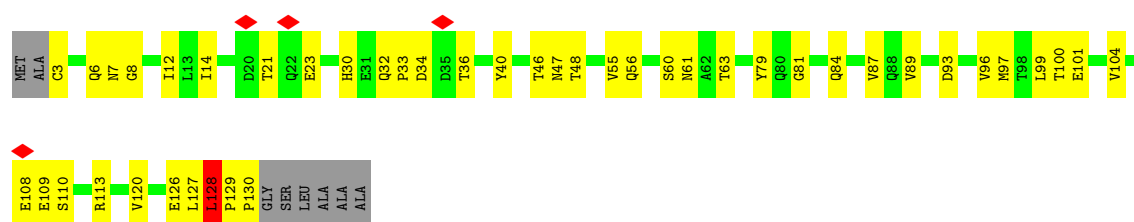
- Molecule 5: Tail-tube, gp21

Chain Aa: 



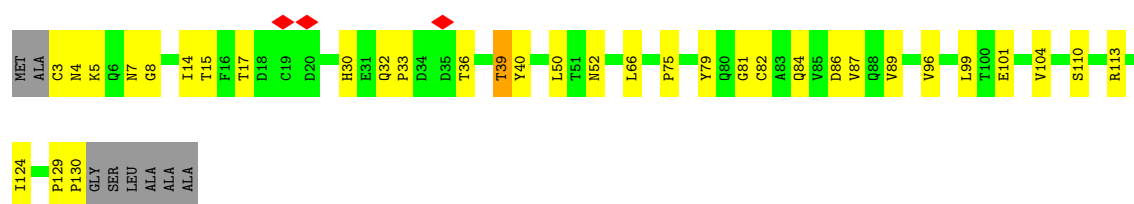
- Molecule 5: Tail-tube, gp21

Chain AY: 



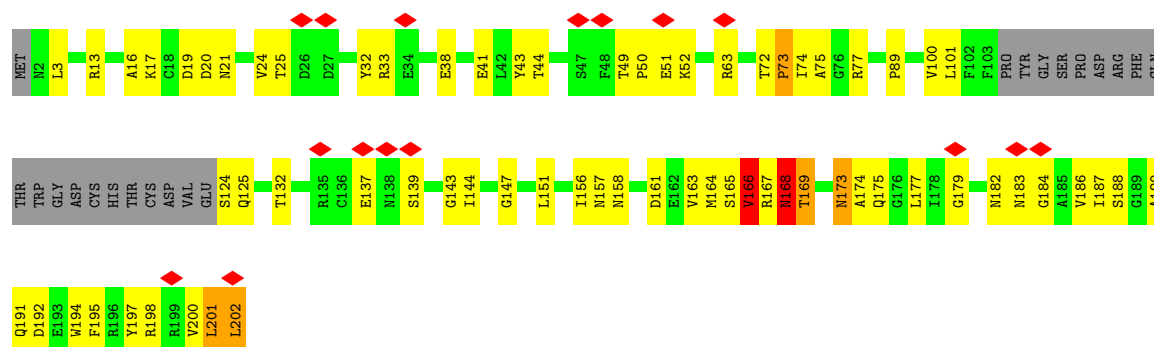
- Molecule 5: Tail-tube, gp21

Chain Ab: 

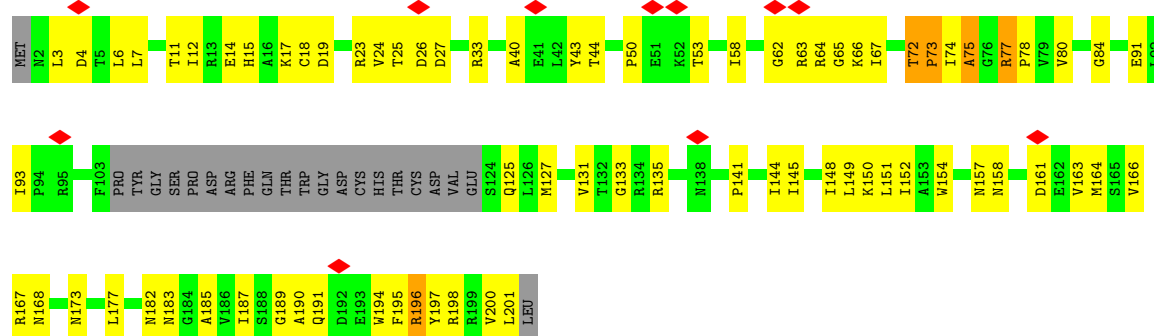


- Molecule 6: Neck 1 protein, gp14

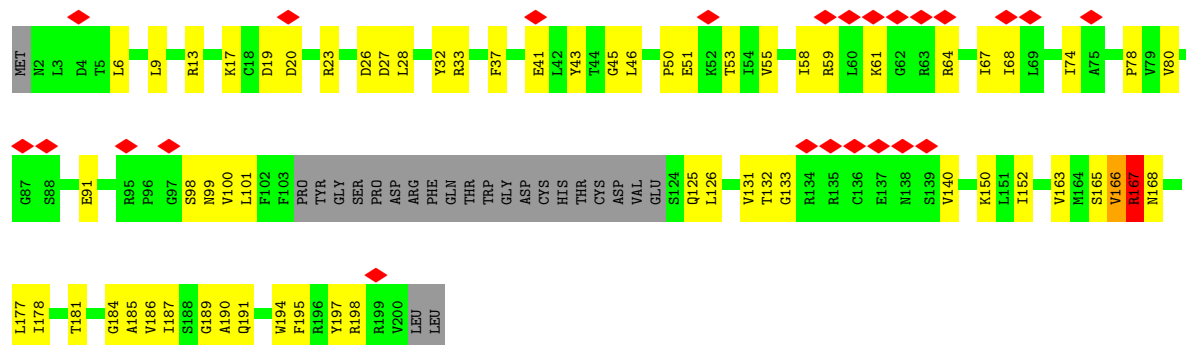
Chain R3: 



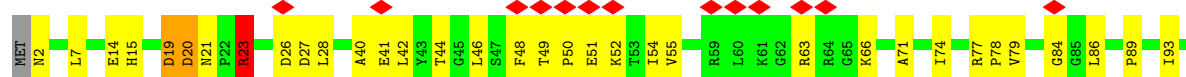
• Molecule 6: Neck 1 protein, gp14

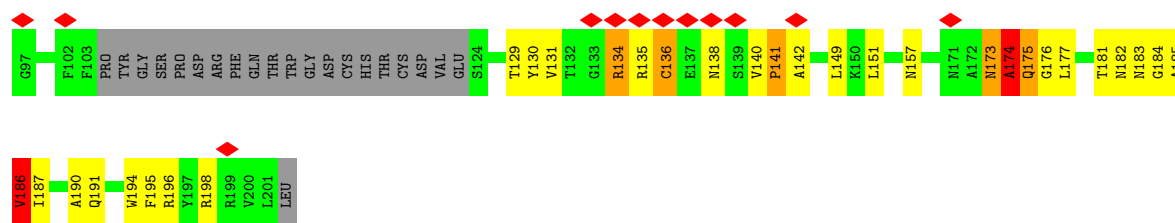


• Molecule 6: Neck 1 protein, gp14

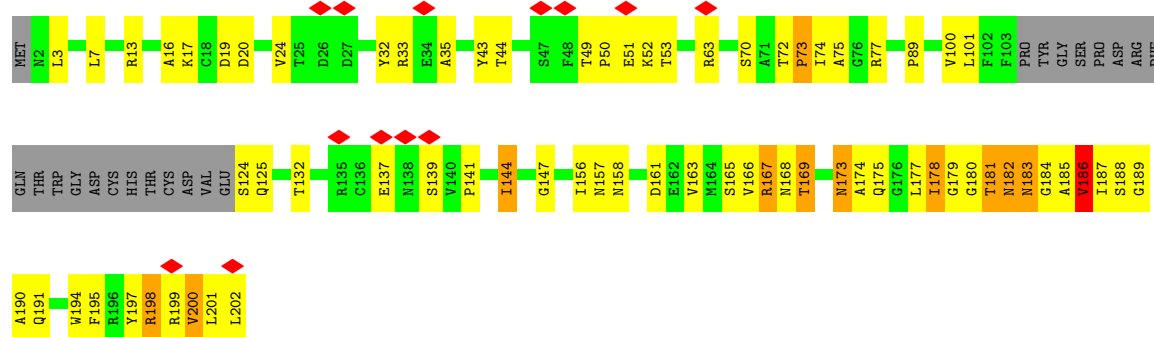


• Molecule 6: Neck 1 protein, gp14

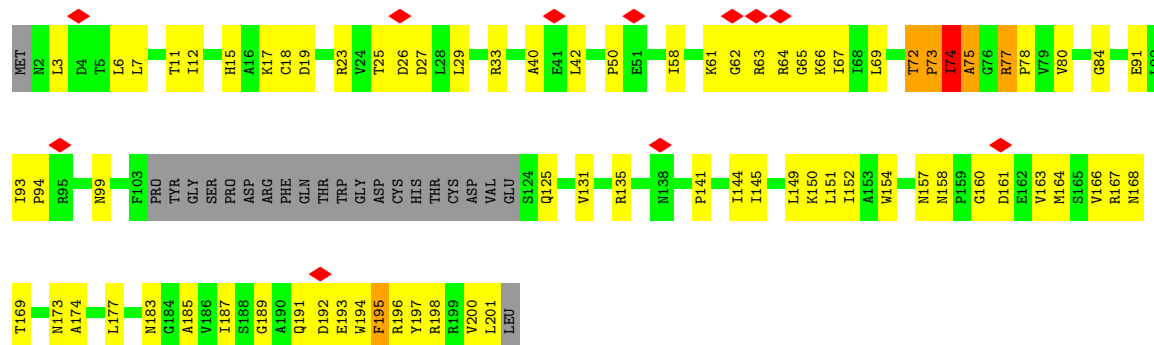




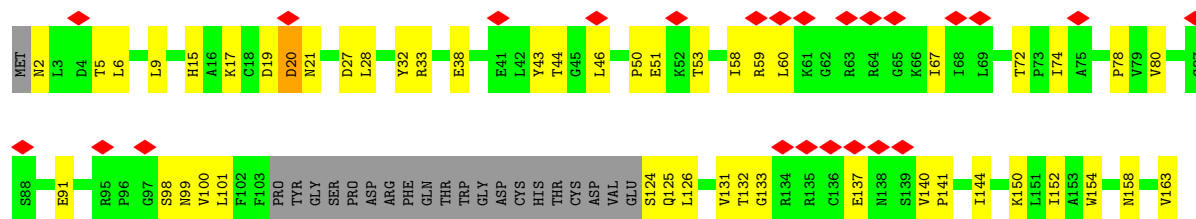
• Molecule 6: Neck 1 protein, gp14

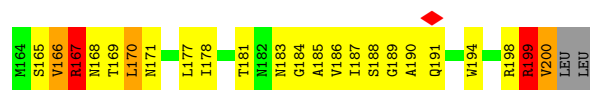


• Molecule 6: Neck 1 protein, gp14

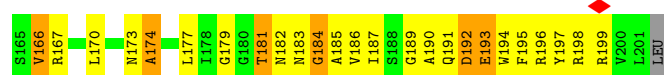
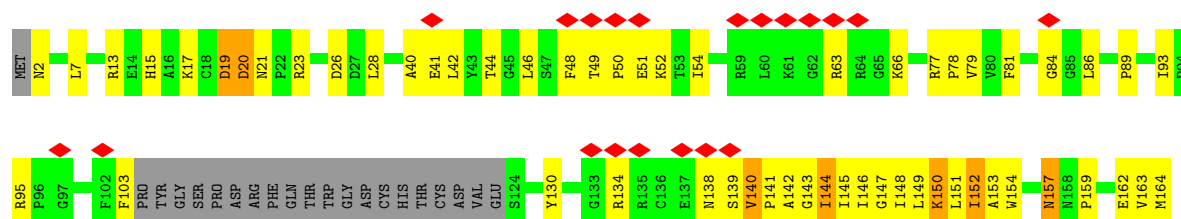


• Molecule 6: Neck 1 protein, gp14

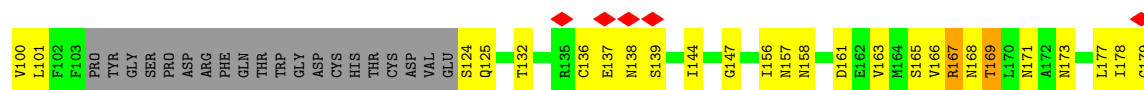
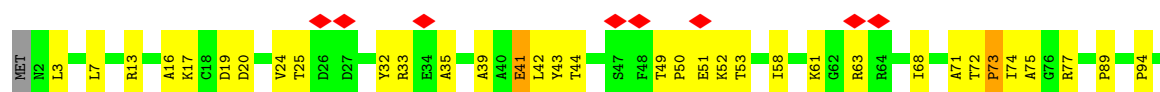




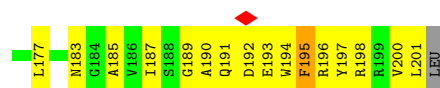
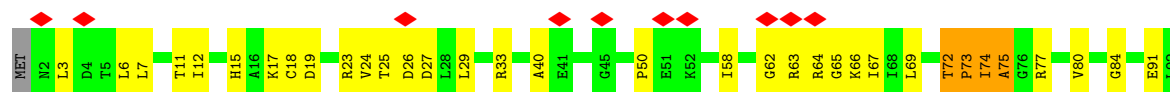
- Molecule 6: Neck 1 protein, gp14



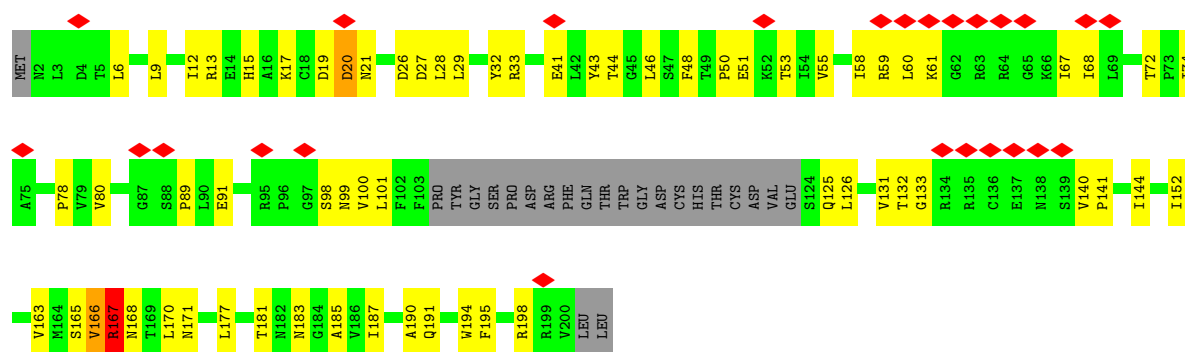
- Molecule 6: Neck 1 protein, gp14



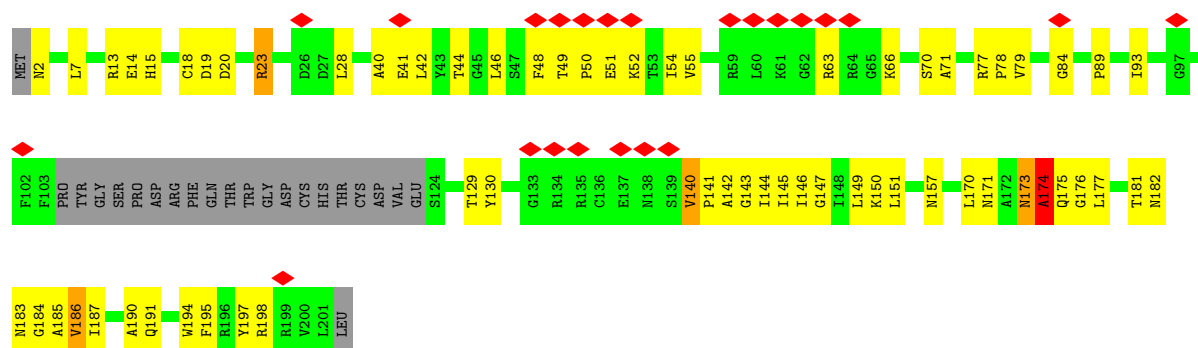
- Molecule 6: Neck 1 protein, gp14



- Molecule 6: Neck 1 protein, gp14



- Molecule 6: Neck 1 protein, gp14



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10216	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.780	Depositor
Minimum map value	-0.421	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	483.84003, 483.84003, 483.84003	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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	0	0.35	0/1723	0.49	0/2353
1	1	0.39	0/1723	0.52	0/2353
1	2	0.40	0/1723	0.51	0/2353
1	3	0.33	0/1723	0.48	0/2353
1	4	0.34	0/1723	0.47	0/2353
1	5	0.35	0/1723	0.49	0/2353
1	6	0.33	0/1723	0.48	0/2353
1	7	0.34	0/1723	0.51	0/2353
1	8	0.33	0/1723	0.48	0/2353
1	9	0.35	0/1723	0.48	0/2353
1	A	0.33	0/1723	0.50	0/2353
1	B	0.34	0/1723	0.51	0/2353
1	C	0.33	0/1723	0.49	0/2353
1	D	0.34	0/1723	0.47	0/2353
1	E	0.35	0/1723	0.48	0/2353
1	F	0.33	0/1723	0.47	0/2353
1	G	0.34	0/1723	0.50	0/2353
1	J	0.38	0/1723	0.51	0/2353
1	K	0.38	0/1723	0.51	0/2353
1	L	0.37	0/1723	0.48	0/2353
1	M	0.36	0/1723	0.49	0/2353
1	N	0.36	0/1723	0.50	0/2353
1	O	0.38	0/1723	0.50	0/2353
1	P	0.38	0/1723	0.52	0/2353
1	Q	0.38	0/1723	0.49	0/2353
1	R	0.35	0/1723	0.50	0/2353
1	S	0.36	0/1723	0.50	0/2353
1	T	0.38	0/1723	0.53	1/2353 (0.0%)
1	U	0.38	0/1723	0.52	0/2353
1	V	0.37	0/1723	0.51	0/2353
1	W	0.35	0/1723	0.50	0/2353
1	X	0.36	0/1723	0.51	0/2353
1	Y	0.39	0/1723	0.50	0/2353
1	Z	0.38	0/1723	0.50	0/2353

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.39	0/1723	0.50	0/2353
1	b	0.38	0/1723	0.48	0/2353
1	c	0.39	0/1723	0.51	0/2353
1	d	0.39	0/1723	0.50	0/2353
1	e	0.39	0/1723	0.51	0/2353
1	f	0.39	0/1723	0.50	0/2353
1	g	0.38	0/1723	0.48	0/2353
1	h	0.39	0/1723	0.50	0/2353
1	i	0.39	0/1723	0.50	0/2353
1	j	0.39	0/1723	0.50	0/2353
1	k	0.39	0/1723	0.50	0/2353
1	l	0.38	0/1723	0.47	0/2353
1	m	0.39	0/1723	0.51	0/2353
1	n	0.38	0/1723	0.49	0/2353
1	o	0.39	0/1723	0.49	0/2353
1	p	0.38	0/1723	0.50	0/2353
1	q	0.39	0/1723	0.52	0/2353
1	r	0.40	0/1723	0.51	0/2353
1	s	0.39	0/1723	0.50	0/2353
1	t	0.39	0/1723	0.49	0/2353
1	u	0.38	0/1723	0.50	0/2353
1	v	0.39	0/1723	0.53	0/2353
1	w	0.39	0/1723	0.51	0/2353
1	x	0.39	0/1723	0.50	0/2353
1	y	0.39	0/1723	0.49	0/2353
1	z	0.38	0/1723	0.49	0/2353
2	AA	0.31	0/3000	0.49	0/4056
2	AB	0.30	0/3000	0.54	2/4056 (0.0%)
2	AC	0.29	0/3000	0.50	0/4056
2	AD	0.31	0/3000	0.53	1/4056 (0.0%)
2	AE	0.30	0/3000	0.51	0/4056
2	AF	0.30	0/3000	0.54	4/4056 (0.1%)
2	AG	0.29	0/3000	0.50	0/4056
2	AH	0.30	0/3000	0.52	0/4056
2	AI	0.31	0/3000	0.48	0/4056
2	AJ	0.29	0/3000	0.55	4/4056 (0.1%)
2	AK	0.29	0/3000	0.51	0/4056
2	AL	0.31	0/3000	0.53	1/4056 (0.0%)
3	AM	0.36	0/1017	0.46	0/1381
3	AN	0.38	0/1017	0.46	0/1381
3	AO	0.36	0/1017	0.46	0/1381
3	AP	0.39	0/1017	0.51	1/1381 (0.1%)
3	H	0.39	0/1017	0.48	0/1381

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	I	0.38	0/1017	0.51	1/1381 (0.1%)
4	AQ	0.39	0/1281	0.46	0/1734
4	AR	0.41	0/1281	0.48	0/1734
4	AS	0.39	0/1281	0.50	1/1734 (0.1%)
4	AT	0.38	0/1281	0.46	0/1734
4	AW	0.39	0/1281	0.48	1/1734 (0.1%)
4	AX	0.41	0/1281	0.47	1/1734 (0.1%)
5	AU	0.41	0/993	0.48	0/1358
5	AV	0.40	0/993	0.47	0/1358
5	AY	0.40	0/993	0.46	0/1358
5	AZ	0.37	0/993	0.44	0/1358
5	Aa	0.36	0/993	0.44	0/1358
5	Ab	0.37	0/993	0.44	0/1358
6	R3	0.45	0/1420	0.57	0/1927
6	R4	0.49	1/1420 (0.1%)	0.59	0/1927
6	R5	0.46	0/1420	0.60	2/1927 (0.1%)
6	S3	0.43	0/1412	0.61	0/1916
6	S4	0.44	0/1412	0.60	1/1916 (0.1%)
6	S5	0.44	0/1412	0.61	1/1916 (0.1%)
6	T3	0.37	0/1404	0.55	0/1905
6	T4	0.38	0/1404	0.57	1/1905 (0.1%)
6	T5	0.37	0/1404	0.55	0/1905
6	U3	0.48	0/1412	0.71	5/1916 (0.3%)
6	U4	0.62	0/1412	0.80	4/1916 (0.2%)
6	U5	0.50	0/1412	0.68	4/1916 (0.2%)
All	All	0.37	1/176070 (0.0%)	0.51	36/239682 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	R4	181	THR	CA-C	-6.41	1.49	1.52

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	U4	42	LEU	N-CA-C	-7.76	104.70	114.56
6	U3	42	LEU	N-CA-C	-7.66	104.84	114.56
6	U5	42	LEU	N-CA-C	-7.56	104.96	114.56
2	AJ	167	ASP	CA-C-N	-7.27	110.43	122.79
2	AJ	167	ASP	C-N-CA	-7.27	110.43	122.79
2	AF	167	ASP	CA-C-N	-7.23	110.50	122.79
2	AF	167	ASP	C-N-CA	-7.23	110.50	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	U4	184	GLY	N-CA-C	-7.17	102.20	112.81
2	AB	167	ASP	CA-C-N	-7.00	110.90	122.79
2	AB	167	ASP	C-N-CA	-7.00	110.90	122.79
4	AX	95	LYS	N-CA-C	-6.70	96.52	110.80
6	U4	189	GLY	N-CA-C	-6.46	105.97	115.72
6	R5	41	GLU	N-CA-C	-6.32	97.34	110.80
6	U3	174	ALA	N-CA-C	-6.27	97.44	110.80
6	R5	39	ALA	N-CA-C	-6.27	105.59	113.18
6	U5	174	ALA	N-CA-C	-6.25	97.50	110.80
6	T4	199	ARG	N-CA-C	6.21	115.63	108.49
4	AS	95	LYS	N-CA-C	-5.93	98.17	110.80
6	U3	19	ASP	N-CA-C	-5.92	99.70	108.99
4	AW	95	LYS	N-CA-C	-5.88	98.28	110.80
6	U4	193	GLU	N-CA-C	-5.77	106.16	113.43
3	AP	50	ASP	N-CA-C	-5.75	98.56	110.80
6	S4	195	PHE	N-CA-C	-5.66	106.92	113.88
2	AD	257	LYS	N-CA-C	-5.55	105.31	111.36
6	U3	173	ASN	N-CA-C	-5.53	102.47	111.04
1	T	89	SER	N-CA-C	-5.50	107.22	114.04
6	U5	186	VAL	N-CA-C	-5.46	107.53	112.12
2	AJ	249	ARG	CA-C-N	-5.33	114.59	123.33
2	AJ	249	ARG	C-N-CA	-5.33	114.59	123.33
6	U3	186	VAL	N-CA-C	-5.29	107.67	112.12
2	AL	255	GLN	N-CA-C	-5.28	104.99	111.75
2	AF	249	ARG	CA-C-N	-5.27	114.69	123.33
2	AF	249	ARG	C-N-CA	-5.27	114.69	123.33
6	U5	173	ASN	N-CA-C	-5.24	102.92	111.04
6	S5	195	PHE	N-CA-C	-5.21	107.31	113.97
3	I	50	ASP	N-CA-C	-5.08	99.98	110.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	1679	0	1610	42	0
1	1	1679	0	1609	41	0
1	2	1679	0	1609	41	0
1	3	1679	0	1610	40	0
1	4	1679	0	1610	42	0
1	5	1679	0	1610	41	0
1	6	1679	0	1610	39	0
1	7	1679	0	1610	41	0
1	8	1679	0	1610	40	0
1	9	1679	0	1610	41	0
1	A	1679	0	1610	39	0
1	B	1679	0	1610	46	0
1	C	1679	0	1610	36	0
1	D	1679	0	1610	42	0
1	E	1679	0	1610	47	0
1	F	1679	0	1610	38	0
1	G	1679	0	1610	45	0
1	J	1679	0	1610	45	0
1	K	1679	0	1610	29	0
1	L	1679	0	1610	35	0
1	M	1679	0	1610	35	0
1	N	1679	0	1610	39	0
1	O	1679	0	1610	47	0
1	P	1679	0	1610	26	0
1	Q	1679	0	1610	31	0
1	R	1679	0	1610	39	0
1	S	1679	0	1610	40	0
1	T	1679	0	1610	47	0
1	U	1679	0	1610	28	0
1	V	1679	0	1610	34	0
1	W	1679	0	1610	36	0
1	X	1679	0	1610	39	0
1	Y	1679	0	1609	36	0
1	Z	1679	0	1609	33	0
1	a	1679	0	1609	45	0
1	b	1679	0	1609	45	0
1	c	1679	0	1609	42	0
1	d	1679	0	1609	41	0
1	e	1679	0	1609	38	0
1	f	1679	0	1609	47	0
1	g	1679	0	1609	45	0
1	h	1679	0	1609	47	0
1	i	1679	0	1609	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	j	1679	0	1609	41	0
1	k	1679	0	1609	42	0
1	l	1679	0	1609	48	0
1	m	1679	0	1609	39	0
1	n	1679	0	1609	41	0
1	o	1679	0	1609	35	0
1	p	1679	0	1609	38	0
1	q	1679	0	1609	40	0
1	r	1679	0	1609	41	0
1	s	1679	0	1609	40	0
1	t	1679	0	1609	33	0
1	u	1679	0	1609	42	0
1	v	1679	0	1609	36	0
1	w	1679	0	1609	40	0
1	x	1679	0	1609	37	0
1	y	1679	0	1609	36	0
1	z	1679	0	1609	41	0
2	AA	2938	0	2906	115	0
2	AB	2938	0	2906	130	0
2	AC	2938	0	2906	156	0
2	AD	2938	0	2906	149	0
2	AE	2938	0	2906	122	0
2	AF	2938	0	2906	136	0
2	AG	2938	0	2906	131	0
2	AH	2938	0	2906	148	0
2	AI	2938	0	2906	121	0
2	AJ	2938	0	2906	130	0
2	AK	2938	0	2906	113	0
2	AL	2938	0	2906	143	0
3	AM	997	0	999	33	0
3	AN	997	0	999	33	0
3	AO	997	0	999	31	0
3	AP	997	0	999	51	0
3	H	997	0	999	41	0
3	I	997	0	999	43	0
4	AQ	1251	0	1189	24	0
4	AR	1251	0	1189	27	0
4	AS	1251	0	1189	31	0
4	AT	1251	0	1189	25	0
4	AW	1251	0	1189	25	0
4	AX	1251	0	1189	27	0
5	AU	977	0	949	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	AV	977	0	949	39	0
5	AY	977	0	949	41	0
5	AZ	977	0	949	30	0
5	Aa	977	0	949	33	0
5	Ab	977	0	949	28	0
6	R3	1395	0	1428	77	0
6	R4	1395	0	1428	89	0
6	R5	1395	0	1428	89	0
6	S3	1387	0	1417	64	0
6	S4	1387	0	1417	71	0
6	S5	1387	0	1417	68	0
6	T3	1379	0	1406	54	0
6	T4	1379	0	1406	60	0
6	T5	1379	0	1406	60	0
6	U3	1387	0	1417	53	0
6	U4	1387	0	1417	78	0
6	U5	1387	0	1417	53	0
All	All	171990	0	167268	4761	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 14.

All (4761) 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:AC:282:THR:H	2:AD:249:ARG:CG	1.60	1.15
2:AB:282:THR:HG23	2:AC:249:ARG:HH21	1.09	1.12
2:AC:281:GLY:CA	2:AD:249:ARG:HG2	1.91	1.00
6:R3:164:MET:HE3	6:R3:168:ASN:HD22	1.27	0.99
2:AG:282:THR:H	2:AH:249:ARG:CG	1.77	0.96
2:AB:282:THR:CG2	2:AC:249:ARG:HH21	1.79	0.95
2:AD:28:ARG:HG3	2:AD:29:ARG:H	1.32	0.94
6:S3:74:ILE:HD11	6:S3:77:ARG:HB2	1.48	0.94
2:AH:260:LYS:CD	6:R4:201:LEU:HD21	1.96	0.94
2:AL:28:ARG:HG3	2:AL:29:ARG:H	1.31	0.93
2:AK:262:GLY:HA3	6:R3:202:LEU:HB2	1.49	0.93
2:AB:282:THR:CG2	2:AC:249:ARG:NH2	2.32	0.92
6:R4:32:TYR:HH	6:U4:15:HIS:HD1	1.18	0.92
2:AH:28:ARG:HG3	2:AH:29:ARG:H	1.32	0.91
2:AB:282:THR:HG23	2:AC:249:ARG:NH2	1.86	0.90
2:AC:282:THR:N	2:AD:249:ARG:CG	2.33	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:R5:32:TYR:HH	6:U5:15:HIS:HD1	1.20	0.89
6:R3:164:MET:CE	6:R3:168:ASN:HD22	1.85	0.89
1:P:8:PRO:HG3	6:S3:53:THR:HG21	1.56	0.88
6:R3:164:MET:CE	6:R3:168:ASN:ND2	2.36	0.87
4:AS:94:ARG:H	4:AS:94:ARG:HH21	1.22	0.86
6:R3:32:TYR:HH	6:U3:15:HIS:HD1	1.23	0.85
5:AZ:15:THR:HB	5:AZ:86:ASP:HB2	1.59	0.85
6:S3:74:ILE:HG22	6:S3:133:GLY:CA	2.06	0.85
2:AC:282:THR:H	2:AD:249:ARG:HG3	1.41	0.85
2:AC:277:ILE:HG23	6:R5:202:LEU:HD21	1.58	0.85
6:R3:164:MET:HE2	6:R3:168:ASN:ND2	1.93	0.84
1:3:210:ASP:HB3	1:3:216:PHE:HE2	1.43	0.84
2:AC:281:GLY:HA3	2:AD:249:ARG:HG2	1.60	0.84
2:AF:127:MET:HB2	2:AF:196:ILE:HB	1.60	0.83
2:AG:251:LEU:HD13	2:AG:282:THR:HG21	1.61	0.83
1:8:210:ASP:HB3	1:8:216:PHE:HE2	1.44	0.82
2:AB:127:MET:HB2	2:AB:196:ILE:HB	1.61	0.82
2:AJ:127:MET:HB2	2:AJ:196:ILE:HB	1.61	0.82
6:S5:74:ILE:HG21	6:S5:77:ARG:HB2	1.62	0.81
2:AH:71:VAL:HG21	2:AH:351:LEU:HD21	1.63	0.81
1:u:133:GLY:H	1:u:152:VAL:HG23	1.43	0.81
2:AC:282:THR:H	2:AD:249:ARG:CD	1.93	0.81
5:AV:30:HIS:HE2	5:AV:79:TYR:HH	1.29	0.81
1:p:133:GLY:H	1:p:152:VAL:HG23	1.45	0.80
2:AK:396:ILE:HG23	2:AK:400:GLU:HG3	1.63	0.80
2:AC:396:ILE:HG23	2:AC:400:GLU:HG3	1.62	0.80
5:Ab:15:THR:HB	5:Ab:86:ASP:HB2	1.63	0.80
1:C:210:ASP:HB3	1:C:216:PHE:HE2	1.46	0.80
2:AC:251:LEU:HD13	2:AC:282:THR:HG21	1.62	0.80
6:S3:74:ILE:HG22	6:S3:133:GLY:HA2	1.61	0.80
2:AG:396:ILE:HG23	2:AG:400:GLU:HG3	1.64	0.80
2:AF:69:GLN:HE21	2:AF:111:ALA:HB1	1.47	0.79
6:R5:186:VAL:HG21	6:R5:191:GLN:HE21	1.46	0.79
2:AK:251:LEU:HD13	2:AK:282:THR:HG21	1.64	0.79
6:S4:173:ASN:HD21	6:S4:177:LEU:HB2	1.48	0.79
2:AE:161:GLU:HB3	2:AE:179:LYS:HE2	1.65	0.79
2:AJ:69:GLN:HE21	2:AJ:111:ALA:HB1	1.46	0.79
3:H:33:ILE:HD11	3:H:73:VAL:HG21	1.66	0.78
3:I:33:ILE:HD11	3:I:73:VAL:HG21	1.66	0.78
2:AB:69:GLN:HE21	2:AB:111:ALA:HB1	1.48	0.78
6:S3:173:ASN:HD21	6:S3:177:LEU:HB2	1.49	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:74:ALA:HB2	1:5:91:LEU:HD11	1.65	0.77
6:S5:173:ASN:HD21	6:S5:177:LEU:HB2	1.49	0.77
2:AJ:167:ASP:H	2:AK:28:ARG:HH12	1.31	0.77
2:AB:167:ASP:H	2:AC:28:ARG:HH12	1.32	0.77
3:AP:33:ILE:HD11	3:AP:73:VAL:HG21	1.67	0.77
5:Aa:15:THR:HB	5:Aa:86:ASP:HB2	1.66	0.77
2:AF:167:ASP:H	2:AG:28:ARG:HH12	1.32	0.77
2:AD:71:VAL:HG21	2:AD:351:LEU:HD21	1.67	0.77
1:R:179:PRO:HD2	1:R:180:ARG:HH21	1.51	0.76
2:AI:28:ARG:HG3	2:AI:29:ARG:H	1.50	0.76
1:b:133:GLY:H	1:b:152:VAL:HG23	1.49	0.76
1:g:136:ARG:HG2	1:g:149:VAL:HG22	1.67	0.76
1:l:74:ALA:HB2	1:l:91:LEU:HD11	1.68	0.76
2:AB:282:THR:HG22	2:AC:249:ARG:NH2	2.00	0.76
1:0:74:ALA:HB2	1:0:91:LEU:HD11	1.66	0.76
1:E:74:ALA:HB2	1:E:91:LEU:HD11	1.66	0.76
4:AS:25:PHE:HZ	4:AS:110:ILE:HA	1.50	0.76
4:AQ:25:PHE:HZ	4:AQ:110:ILE:HA	1.51	0.76
1:2:133:GLY:H	1:2:152:VAL:HG23	1.51	0.75
2:AJ:28:ARG:HG3	2:AJ:29:ARG:H	1.51	0.75
2:AC:282:THR:HA	2:AD:249:ARG:HH11	1.50	0.75
1:b:74:ALA:HB2	1:b:91:LEU:HD11	1.69	0.75
3:AP:39:ILE:HG22	3:AP:65:ILE:HG12	1.69	0.75
6:R3:186:VAL:HG21	6:R3:191:GLN:HE21	1.50	0.75
1:6:88:LEU:N	1:6:121:GLY:O	2.20	0.75
1:0:48:LEU:HD23	1:A:1:MET:HE3	1.68	0.75
6:S3:151:LEU:HD13	6:S3:185:ALA:HB2	1.68	0.75
2:AH:260:LYS:HD2	6:R4:201:LEU:CD2	2.17	0.75
1:l:133:GLY:H	1:l:152:VAL:HG23	1.52	0.74
6:S5:80:VAL:HG12	6:S5:91:GLU:HG2	1.69	0.74
1:F:88:LEU:N	1:F:121:GLY:O	2.20	0.74
1:z:74:ALA:HB2	1:z:91:LEU:HD11	1.70	0.74
3:H:39:ILE:HG22	3:H:65:ILE:HG12	1.67	0.74
1:g:74:ALA:HB2	1:g:91:LEU:HD11	1.68	0.74
2:AB:28:ARG:HG3	2:AB:29:ARG:H	1.52	0.74
1:b:136:ARG:HG2	1:b:149:VAL:HG22	1.69	0.74
1:3:172:ALA:O	1:3:175:ARG:NH1	2.21	0.74
1:e:74:ALA:HB2	1:e:91:LEU:HD11	1.69	0.74
2:AA:339:LYS:HE3	2:AA:379:LEU:HD22	1.70	0.74
1:n:74:ALA:HB2	1:n:91:LEU:HD11	1.70	0.74
1:w:133:GLY:H	1:w:152:VAL:HG23	1.51	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:n:21:SER:HB2	1:3:49:ARG:HB3	1.68	0.74
1:9:74:ALA:HB2	1:9:91:LEU:HD11	1.70	0.74
6:R3:74:ILE:HG21	6:R3:77:ARG:HB3	1.70	0.74
3:I:39:ILE:HG22	3:I:65:ILE:HG12	1.68	0.74
1:x:21:SER:HB2	1:C:49:ARG:HB3	1.69	0.73
1:z:133:GLY:H	1:z:152:VAL:HG23	1.53	0.73
2:AE:402:ARG:HH21	2:AE:407:TRP:HB3	1.53	0.73
1:R:133:GLY:H	1:R:152:VAL:HG13	1.53	0.73
4:AW:25:PHE:HZ	4:AW:110:ILE:HA	1.51	0.73
6:S4:80:VAL:HG12	6:S4:91:GLU:HG2	1.69	0.73
3:I:19:VAL:HA	3:I:25:LEU:HA	1.69	0.73
1:W:133:GLY:H	1:W:152:VAL:HG13	1.54	0.73
2:AC:282:THR:N	2:AD:249:ARG:HG2	2.02	0.73
5:AZ:81:GLY:HA2	5:AZ:104:VAL:HB	1.70	0.73
6:R3:143:GLY:HA3	6:R3:197:TYR:HE1	1.53	0.73
6:S3:80:VAL:HG12	6:S3:91:GLU:HG2	1.70	0.73
1:p:79:LYS:HE3	1:p:155:THR:HA	1.71	0.73
2:AG:232:ILE:HD11	2:AH:219:VAL:HG13	1.68	0.73
1:l:136:ARG:HG2	1:l:149:VAL:HG22	1.68	0.73
1:o:77:ARG:NH2	1:o:158:GLU:OE1	2.22	0.73
1:s:21:SER:HB2	1:8:49:ARG:HB3	1.69	0.73
2:AH:260:LYS:HD2	6:R4:201:LEU:HD21	1.70	0.73
6:S4:151:LEU:HD13	6:S4:185:ALA:HB2	1.68	0.73
2:AI:402:ARG:HH21	2:AI:407:TRP:HB3	1.54	0.73
1:V:136:ARG:HG2	1:V:149:VAL:HG22	1.71	0.73
1:8:172:ALA:O	1:8:175:ARG:NH1	2.21	0.73
2:AA:16:PRO:O	2:AL:140:ASN:ND2	2.20	0.73
6:R3:173:ASN:C	6:R3:175:GLN:H	1.97	0.73
6:R3:183:ASN:OD1	6:R3:184:GLY:N	2.21	0.73
4:AS:31:ARG:NH1	4:AS:51:PRO:O	2.22	0.73
2:AK:258:GLU:OE1	6:R3:202:LEU:HB3	1.88	0.72
1:W:179:PRO:HD2	1:W:180:ARG:HH21	1.54	0.72
1:p:74:ALA:HB2	1:p:91:LEU:HD11	1.72	0.72
1:5:48:LEU:HD23	1:6:1:MET:HE3	1.71	0.72
2:AE:28:ARG:HG3	2:AE:29:ARG:H	1.52	0.72
1:M:88:LEU:N	1:M:121:GLY:O	2.22	0.72
1:W:88:LEU:N	1:W:121:GLY:O	2.22	0.72
1:k:99:GLN:OE1	1:k:99:GLN:N	2.21	0.72
1:u:74:ALA:HB2	1:u:91:LEU:HD11	1.71	0.72
1:x:74:ALA:HB2	1:x:91:LEU:HD11	1.71	0.72
2:AL:71:VAL:HG21	2:AL:351:LEU:HD21	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AI:140:ASN:ND2	2:AJ:16:PRO:O	2.23	0.72
1:k:74:ALA:HB2	1:k:91:LEU:HD11	1.71	0.72
1:s:74:ALA:HB2	1:s:91:LEU:HD11	1.71	0.72
1:4:74:ALA:HB2	1:4:91:LEU:HD11	1.71	0.72
2:AL:28:ARG:HG3	2:AL:29:ARG:N	2.04	0.72
1:j:77:ARG:NH2	1:j:158:GLU:OE1	2.23	0.72
1:u:79:LYS:HE3	1:u:155:THR:HA	1.71	0.72
1:6:74:ALA:HB2	1:6:91:LEU:HD11	1.71	0.72
2:AC:263:ILE:HD13	2:AC:277:ILE:HG12	1.72	0.72
1:t:77:ARG:NH2	1:t:158:GLU:OE2	2.23	0.72
1:z:79:LYS:HE3	1:z:155:THR:HA	1.71	0.72
2:AC:282:THR:N	2:AD:249:ARG:HD3	2.05	0.72
2:AD:235:ALA:O	2:AE:230:ARG:NH1	2.23	0.72
1:j:74:ALA:HB2	1:j:91:LEU:HD11	1.71	0.71
1:L:136:ARG:HG2	1:L:149:VAL:HG22	1.72	0.71
1:W:79:LYS:HE3	1:W:155:THR:HA	1.72	0.71
2:AE:140:ASN:ND2	2:AF:16:PRO:O	2.22	0.71
1:a:74:ALA:HB2	1:a:91:LEU:HD11	1.71	0.71
1:a:99:GLN:N	1:a:99:GLN:OE1	2.21	0.71
2:AB:249:ARG:NH2	6:T5:43:TYR:OH	2.24	0.71
2:AH:235:ALA:O	2:AI:230:ARG:NH1	2.23	0.71
1:R:88:LEU:N	1:R:121:GLY:O	2.22	0.71
1:c:79:LYS:HE3	1:c:155:THR:HA	1.71	0.71
2:AK:263:ILE:HD13	2:AK:277:ILE:HG12	1.71	0.71
1:O:210:ASP:OD1	1:O:214:ASN:N	2.23	0.71
1:M:75:PHE:HE1	1:M:162:PRO:HD2	1.55	0.71
1:r:133:GLY:H	1:r:152:VAL:HG23	1.55	0.71
2:AA:402:ARG:HH21	2:AA:407:TRP:HB3	1.55	0.71
5:AU:30:HIS:HE2	5:AU:79:TYR:HH	1.39	0.71
4:AW:31:ARG:NH1	4:AW:51:PRO:O	2.24	0.71
1:s:88:LEU:N	1:s:121:GLY:O	2.24	0.71
1:A:30:ARG:HD2	1:A:230:GLY:H	1.56	0.71
2:AA:201:ILE:HD11	2:AL:52:MET:HE3	1.73	0.71
2:AK:69:GLN:HE21	2:AK:111:ALA:HB1	1.56	0.71
6:S5:151:LEU:HD13	6:S5:185:ALA:HB2	1.72	0.71
2:AB:182:LYS:HE3	2:AB:186:GLY:HA2	1.72	0.70
6:R3:166:VAL:O	6:R3:169:THR:HG22	1.91	0.70
1:f:136:ARG:HG2	1:f:149:VAL:HG22	1.73	0.70
1:C:79:LYS:HE3	1:C:155:THR:HA	1.73	0.70
2:AH:260:LYS:NZ	6:R4:201:LEU:HD21	2.06	0.70
1:3:79:LYS:HE3	1:3:155:THR:HA	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:30:ARG:HD2	1:6:230:GLY:H	1.56	0.70
1:k:136:ARG:HG2	1:k:149:VAL:HG22	1.72	0.70
1:Z:74:ALA:HB2	1:Z:91:LEU:HD11	1.71	0.70
1:g:79:LYS:HE3	1:g:155:THR:HA	1.71	0.70
1:D:74:ALA:HB2	1:D:91:LEU:HD11	1.72	0.70
1:M:210:ASP:OD1	1:M:214:ASN:N	2.24	0.70
1:p:209:ILE:HD11	1:p:213:GLY:HA2	1.73	0.70
1:C:172:ALA:O	1:C:175:ARG:NH1	2.24	0.70
1:d:133:GLY:H	1:d:152:VAL:HG23	1.57	0.70
2:AC:281:GLY:CA	2:AD:249:ARG:CG	2.68	0.70
2:AL:297:HIS:HE1	2:AL:299:LYS:HB2	1.57	0.70
1:0:75:PHE:HE1	1:0:162:PRO:HD2	1.56	0.70
1:k:172:ALA:O	1:k:175:ARG:NH1	2.24	0.70
2:AF:127:MET:HE1	2:AF:354:LEU:HD12	1.74	0.70
2:AH:260:LYS:CD	6:R4:201:LEU:CD2	2.70	0.70
2:AJ:25:ILE:O	2:AJ:28:ARG:NE	2.25	0.70
2:AL:77:LYS:HD2	2:AL:81:ASN:HD22	1.57	0.70
6:R4:188:SER:C	6:R4:190:ALA:H	2.00	0.70
1:7:136:ARG:HG2	1:7:149:VAL:HG22	1.74	0.70
2:AA:237:GLY:HA2	2:AL:267:LYS:HD3	1.74	0.70
1:r:209:ILE:HD11	1:r:213:GLY:HA2	1.74	0.69
1:2:209:ILE:HD11	1:2:213:GLY:HA2	1.74	0.69
2:AG:281:GLY:CA	2:AH:249:ARG:HG2	2.22	0.69
6:U4:7:LEU:HD11	6:U4:149:LEU:HD21	1.73	0.69
6:R5:74:ILE:HG21	6:R5:77:ARG:HB3	1.74	0.69
1:W:75:PHE:HE1	1:W:162:PRO:HD2	1.55	0.69
1:8:75:PHE:HE1	1:8:162:PRO:HD2	1.57	0.69
1:E:75:PHE:HE1	1:E:162:PRO:HD2	1.57	0.69
6:R4:158:ASN:ND2	6:S4:161:ASP:OD1	2.24	0.69
1:a:172:ALA:O	1:a:175:ARG:NH1	2.25	0.69
1:9:38:MET:HE3	1:9:183:VAL:HG21	1.74	0.69
2:AA:140:ASN:ND2	2:AB:16:PRO:O	2.24	0.69
2:AH:260:LYS:HD3	6:R4:201:LEU:HD21	1.73	0.69
1:l:79:LYS:HE3	1:l:155:THR:HA	1.73	0.69
3:AP:19:VAL:HA	3:AP:25:LEU:HA	1.73	0.69
6:T3:186:VAL:HG22	6:T3:191:GLN:HG3	1.73	0.69
1:T:210:ASP:OD1	1:T:214:ASN:N	2.25	0.69
1:e:132:THR:HA	1:e:152:VAL:HG23	1.74	0.69
1:A:74:ALA:HB2	1:A:91:LEU:HD11	1.73	0.69
2:AE:240:ASN:ND2	2:AF:234:SER:OG	2.25	0.69
1:c:172:ALA:O	1:c:175:ARG:NH1	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:R5:167:ARG:HH21	6:T5:171:ASN:H	1.39	0.69
1:M:133:GLY:H	1:M:152:VAL:HG13	1.57	0.69
1:N:79:LYS:HE3	1:N:155:THR:HA	1.74	0.69
1:f:102:TYR:HD1	1:f:141:ILE:HD12	1.58	0.69
1:F:74:ALA:HB2	1:F:91:LEU:HD11	1.73	0.69
2:AH:297:HIS:HE1	2:AH:299:LYS:HB2	1.57	0.69
1:L:133:GLY:H	1:L:152:VAL:HG23	1.58	0.69
1:M:79:LYS:HE3	1:M:155:THR:HA	1.73	0.69
1:R:79:LYS:HE3	1:R:155:THR:HA	1.73	0.69
1:b:79:LYS:HE3	1:b:155:THR:HA	1.73	0.69
1:f:74:ALA:HB2	1:f:91:LEU:HD11	1.73	0.69
1:h:79:LYS:HE3	1:h:155:THR:HA	1.73	0.69
1:o:133:GLY:H	1:o:152:VAL:HG23	1.56	0.69
1:x:88:LEU:N	1:x:121:GLY:O	2.26	0.69
1:z:209:ILE:HD11	1:z:213:GLY:HA2	1.75	0.69
1:8:79:LYS:HE3	1:8:155:THR:HA	1.72	0.69
1:9:75:PHE:CE1	1:9:161:GLN:HG2	2.27	0.69
2:AD:28:ARG:HG3	2:AD:29:ARG:N	2.04	0.69
6:T4:186:VAL:HG22	6:T4:191:GLN:HG3	1.73	0.69
5:AY:93:ASP:OD2	5:Ab:113:ARG:NH1	2.26	0.69
1:K:74:ALA:HB2	1:K:91:LEU:HD11	1.75	0.69
1:5:75:PHE:HE1	1:5:162:PRO:HD2	1.56	0.69
2:AC:69:GLN:HE21	2:AC:111:ALA:HB1	1.57	0.69
1:V:133:GLY:H	1:V:152:VAL:HG23	1.58	0.69
1:f:99:GLN:N	1:f:99:GLN:OE1	2.22	0.69
2:AC:232:ILE:HD11	2:AD:219:VAL:HG13	1.75	0.69
2:AG:249:ARG:HG3	2:AG:249:ARG:O	1.91	0.69
1:W:210:ASP:OD1	1:W:214:ASN:N	2.24	0.68
1:Y:133:GLY:H	1:Y:152:VAL:HG23	1.58	0.68
1:a:136:ARG:HG2	1:a:149:VAL:HG22	1.74	0.68
1:m:79:LYS:HE3	1:m:155:THR:HA	1.74	0.68
1:q:74:ALA:HB2	1:q:91:LEU:HD11	1.75	0.68
1:y:77:ARG:NH2	1:y:158:GLU:OE1	2.26	0.68
2:AH:77:LYS:HD2	2:AH:81:ASN:HD22	1.57	0.68
6:R5:158:ASN:ND2	6:S5:161:ASP:OD1	2.26	0.68
1:J:210:ASP:OD1	1:J:214:ASN:N	2.25	0.68
1:h:172:ALA:O	1:h:175:ARG:NH1	2.26	0.68
2:AL:263:ILE:HD13	2:AL:277:ILE:HG12	1.75	0.68
6:R5:183:ASN:OD1	6:R5:184:GLY:N	2.22	0.68
1:R:210:ASP:OD1	1:R:214:ASN:N	2.24	0.68
2:AD:297:HIS:HE1	2:AD:299:LYS:HB2	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:R4:74:ILE:HG21	6:R4:77:ARG:HB3	1.76	0.68
1:X:208:ALA:HB3	1:X:216:PHE:HB2	1.73	0.68
1:F:30:ARG:HD2	1:F:230:GLY:H	1.58	0.68
5:AY:30:HIS:HE2	5:AY:79:TYR:HH	1.42	0.68
2:AA:161:GLU:HB3	2:AA:179:LYS:HE2	1.76	0.68
2:AB:25:ILE:O	2:AB:28:ARG:NE	2.26	0.68
2:AD:77:LYS:HD2	2:AD:81:ASN:HD22	1.58	0.68
2:AI:161:GLU:HB3	2:AI:179:LYS:HE2	1.75	0.68
2:AK:28:ARG:HG3	2:AK:29:ARG:H	1.58	0.68
5:AV:93:ASP:OD2	5:Aa:113:ARG:NH1	2.27	0.68
1:U:79:LYS:HE3	1:U:155:THR:HA	1.76	0.68
2:AA:230:ARG:NH1	2:AL:235:ALA:O	2.26	0.68
2:AG:263:ILE:HD13	2:AG:277:ILE:HG12	1.73	0.68
3:AM:9:ARG:HH21	3:AM:34:GLN:HG2	1.59	0.68
1:2:38:MET:HG2	1:2:185:LYS:HG2	1.76	0.68
1:C:75:PHE:HE1	1:C:162:PRO:HD2	1.58	0.68
1:E:29:ALA:HB1	1:E:190:VAL:HG21	1.75	0.68
1:E:30:ARG:HD2	1:E:230:GLY:H	1.58	0.68
2:AH:263:ILE:HD13	2:AH:277:ILE:HG12	1.75	0.68
4:AQ:31:ARG:NH1	4:AQ:51:PRO:O	2.26	0.68
1:R:75:PHE:HE1	1:R:162:PRO:HD2	1.57	0.68
1:E:48:LEU:HD23	1:F:1:MET:HE3	1.76	0.68
6:U3:185:ALA:O	6:U3:191:GLN:HG2	1.93	0.68
1:P:74:ALA:HB2	1:P:91:LEU:HD11	1.75	0.67
1:X:79:LYS:HE3	1:X:155:THR:HA	1.75	0.67
1:c:74:ALA:HB2	1:c:91:LEU:HD11	1.75	0.67
1:F:136:ARG:HG2	1:F:149:VAL:HG22	1.76	0.67
2:AG:140:ASN:ND2	2:AH:16:PRO:O	2.25	0.67
3:AO:20:ASP:OD2	3:AO:24:ARG:NH1	2.27	0.67
1:S:79:LYS:HE3	1:S:155:THR:HA	1.74	0.67
1:Z:132:THR:HA	1:Z:152:VAL:HG23	1.74	0.67
3:AN:20:ASP:OD2	3:AN:24:ARG:NH1	2.26	0.67
1:K:79:LYS:HE3	1:K:155:THR:HA	1.76	0.67
1:v:132:THR:HA	1:v:152:VAL:HG23	1.77	0.67
1:B:136:ARG:HG2	1:B:149:VAL:HG22	1.75	0.67
2:AL:249:ARG:O	2:AL:249:ARG:HG2	1.93	0.67
6:U5:7:LEU:HD11	6:U5:149:LEU:HD21	1.76	0.67
2:AC:28:ARG:HG3	2:AC:29:ARG:H	1.59	0.67
3:H:19:VAL:HA	3:H:25:LEU:HA	1.75	0.67
1:Y:79:LYS:HE3	1:Y:155:THR:HA	1.75	0.67
1:i:133:GLY:H	1:i:152:VAL:HG23	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:79:LYS:HE3	1:P:155:THR:HA	1.76	0.67
1:i:79:LYS:HE3	1:i:155:THR:HA	1.77	0.67
1:i:172:ALA:O	1:i:175:ARG:NH1	2.27	0.67
1:l:209:ILE:HD11	1:l:213:GLY:HA2	1.77	0.67
1:t:132:THR:HA	1:t:152:VAL:HG23	1.76	0.67
1:l:74:ALA:HB2	1:l:91:LEU:HD11	1.76	0.67
3:AM:20:ASP:OD2	3:AM:24:ARG:NH1	2.28	0.67
6:R3:158:ASN:ND2	6:S3:161:ASP:OD1	2.28	0.67
6:R3:191:GLN:HA	6:R3:194:TRP:CE3	2.29	0.67
6:S3:166:VAL:HG23	6:T3:177:LEU:HB3	1.77	0.67
1:j:132:THR:HA	1:j:152:VAL:HG23	1.76	0.67
1:n:88:LEU:N	1:n:121:GLY:O	2.25	0.67
1:u:209:ILE:HD11	1:u:213:GLY:HA2	1.77	0.67
6:S4:166:VAL:HG23	6:T4:177:LEU:HB3	1.76	0.67
3:AO:6:ARG:NH2	6:R5:17:LYS:O	2.27	0.67
1:h:74:ALA:HB2	1:h:91:LEU:HD11	1.76	0.67
1:3:75:PHE:HE1	1:3:162:PRO:HD2	1.59	0.67
6:S3:74:ILE:CD1	6:S3:77:ARG:HB2	2.24	0.67
1:d:172:ALA:O	1:d:175:ARG:NH1	2.28	0.66
6:R3:143:GLY:HA3	6:R3:197:TYR:CE1	2.29	0.66
1:w:209:ILE:HD11	1:w:213:GLY:HA2	1.78	0.66
2:AC:282:THR:CA	2:AD:249:ARG:HD3	2.25	0.66
2:AK:232:ILE:HD11	2:AL:219:VAL:HG13	1.75	0.66
1:L:209:ILE:HD11	1:L:213:GLY:HA2	1.77	0.66
1:X:172:ALA:O	1:X:175:ARG:NH1	2.28	0.66
2:AD:217:ILE:HB	2:AD:309:ILE:HG22	1.77	0.66
3:AM:39:ILE:HG22	3:AM:65:ILE:HG12	1.78	0.66
3:AM:46:ARG:HE	3:AP:77:VAL:HG23	1.60	0.66
1:T:132:THR:HA	1:T:152:VAL:HG23	1.78	0.66
1:f:172:ALA:O	1:f:175:ARG:NH1	2.29	0.66
2:AG:28:ARG:HG3	2:AG:29:ARG:H	1.59	0.66
1:J:132:THR:HA	1:J:152:VAL:HG23	1.77	0.66
1:6:136:ARG:HG2	1:6:149:VAL:HG22	1.76	0.66
1:G:136:ARG:HG2	1:G:149:VAL:HG22	1.77	0.66
2:AA:83:GLN:HE21	2:AA:366:GLY:H	1.43	0.66
1:m:172:ALA:O	1:m:175:ARG:NH1	2.29	0.66
1:0:30:ARG:HD2	1:0:230:GLY:H	1.61	0.66
4:AW:55:VAL:HG22	4:AW:82:VAL:HG22	1.78	0.66
3:I:32:VAL:HG12	3:I:33:ILE:HG13	1.77	0.66
1:K:210:ASP:OD1	1:K:214:ASN:N	2.26	0.66
1:v:74:ALA:HB2	1:v:91:LEU:HD11	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:132:SER:HA	2:AB:191:ASN:HD22	1.60	0.66
5:AU:93:ASP:OD2	5:AZ:113:ARG:NH1	2.27	0.66
6:R4:167:ARG:HH21	6:T4:171:ASN:H	1.43	0.66
3:AO:46:ARG:HE	3:I:77:VAL:HG23	1.60	0.66
2:AA:28:ARG:HG3	2:AA:29:ARG:H	1.61	0.66
2:AJ:132:SER:HA	2:AJ:191:ASN:HD22	1.59	0.66
1:V:209:ILE:HD11	1:V:213:GLY:HA2	1.78	0.66
2:AE:83:GLN:HE21	2:AE:366:GLY:H	1.44	0.66
6:U5:185:ALA:O	6:U5:191:GLN:HG2	1.95	0.66
4:AQ:55:VAL:HG22	4:AQ:82:VAL:HG22	1.78	0.66
1:K:206:GLN:OE1	1:K:207:VAL:N	2.29	0.65
2:AG:69:GLN:HE21	2:AG:111:ALA:HB1	1.60	0.65
2:AH:140:ASN:HD21	2:AI:16:PRO:C	2.03	0.65
1:U:132:THR:HA	1:U:152:VAL:HG23	1.78	0.65
1:p:210:ASP:HB3	1:p:216:PHE:HE2	1.60	0.65
2:AG:282:THR:H	2:AH:249:ARG:CD	2.09	0.65
3:AN:9:ARG:HH21	3:AN:34:GLN:HG2	1.61	0.65
6:U5:182:ASN:HA	6:U5:187:ILE:HD11	1.79	0.65
1:Z:172:ALA:O	1:Z:175:ARG:NH1	2.30	0.65
1:m:133:GLY:H	1:m:152:VAL:HG23	1.60	0.65
2:AC:90:SER:HG	2:AC:93:GLN:H	1.44	0.65
1:M:208:ALA:HB3	1:M:216:PHE:HB2	1.78	0.65
1:U:136:ARG:HG2	1:U:149:VAL:HG22	1.78	0.65
1:4:38:MET:HE3	1:4:183:VAL:HG21	1.78	0.65
2:AC:140:ASN:ND2	2:AD:16:PRO:O	2.25	0.65
3:AO:9:ARG:HH21	3:AO:34:GLN:HG2	1.60	0.65
1:J:75:PHE:HE1	1:J:162:PRO:HD2	1.62	0.65
1:Q:209:ILE:HD11	1:Q:213:GLY:HA2	1.79	0.65
1:6:209:ILE:HD11	1:6:213:GLY:HA2	1.78	0.65
2:AB:249:ARG:O	2:AB:249:ARG:HG3	1.93	0.65
1:U:74:ALA:HB2	1:U:91:LEU:HD11	1.77	0.65
1:d:79:LYS:HE3	1:d:155:THR:HA	1.79	0.65
2:AF:27:ILE:HA	2:AF:31:PHE:HB3	1.79	0.65
2:AJ:396:ILE:HG23	2:AJ:400:GLU:HG3	1.78	0.65
1:K:132:THR:HA	1:K:152:VAL:HG23	1.79	0.65
1:R:167:PRO:HA	1:R:191:SER:HB3	1.78	0.65
1:t:136:ARG:HG2	1:t:149:VAL:HG22	1.79	0.65
2:AF:132:SER:HA	2:AF:191:ASN:HD22	1.61	0.65
6:S5:163:VAL:HG23	6:S5:164:MET:H	1.62	0.65
1:l:4:PHE:HB2	1:l:39:VAL:HG12	1.78	0.65
1:7:74:ALA:HB2	1:7:91:LEU:HD11	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AE:280:ALA:HB1	6:T4:198:ARG:HH11	1.62	0.65
2:AF:168:GLU:HG2	2:AF:169:ALA:N	2.12	0.65
2:AI:240:ASN:ND2	2:AJ:234:SER:OG	2.30	0.65
2:AL:404:VAL:HG13	2:AL:405:THR:HG23	1.79	0.65
1:P:210:ASP:OD1	1:P:214:ASN:N	2.25	0.65
1:U:206:GLN:OE1	1:U:207:VAL:N	2.30	0.65
1:k:210:ASP:HB3	1:k:216:PHE:HE2	1.62	0.65
1:r:172:ALA:O	1:r:175:ARG:NH1	2.30	0.65
1:5:29:ALA:HB1	1:5:190:VAL:HG21	1.79	0.65
6:S3:195:PHE:C	6:S3:197:TYR:H	2.04	0.65
1:K:209:ILE:HD11	1:K:213:GLY:HA2	1.79	0.65
2:AA:312:ASN:ND2	2:AL:59:ARG:HB2	2.11	0.65
2:AD:140:ASN:HD21	2:AE:16:PRO:C	2.04	0.65
1:q:207:VAL:HG12	1:q:217:VAL:HG22	1.79	0.64
1:w:172:ALA:O	1:w:175:ARG:NH1	2.30	0.64
2:AG:282:THR:H	2:AH:249:ARG:HG2	1.61	0.64
2:AH:217:ILE:HB	2:AH:309:ILE:HG22	1.79	0.64
1:r:88:LEU:N	1:r:121:GLY:O	2.30	0.64
1:A:79:LYS:HE3	1:A:155:THR:HA	1.79	0.64
2:AC:277:ILE:HG23	6:R5:202:LEU:CD2	2.25	0.64
2:AG:297:HIS:HE1	2:AG:299:LYS:HB2	1.62	0.64
2:AJ:168:GLU:HG2	2:AJ:169:ALA:N	2.12	0.64
6:U4:184:GLY:C	6:U4:186:VAL:H	2.05	0.64
1:X:141:ILE:HG22	1:X:142:ASN:HD22	1.62	0.64
1:u:210:ASP:HB3	1:u:216:PHE:HE2	1.62	0.64
1:2:172:ALA:O	1:2:175:ARG:NH1	2.30	0.64
2:AD:263:ILE:HD13	2:AD:277:ILE:HG12	1.78	0.64
3:AN:6:ARG:NH2	6:R4:17:LYS:O	2.29	0.64
1:O:132:THR:HA	1:O:152:VAL:HG23	1.79	0.64
1:q:48:LEU:HD23	1:r:1:MET:HE3	1.80	0.64
2:AC:281:GLY:C	2:AD:249:ARG:HG2	2.22	0.64
2:AK:183:ASN:HD22	2:AK:187:ARG:HB2	1.63	0.64
1:h:132:THR:HA	1:h:152:VAL:HG23	1.79	0.64
1:m:74:ALA:HB2	1:m:91:LEU:HD11	1.78	0.64
1:e:172:ALA:O	1:e:175:ARG:NH1	2.30	0.64
1:E:210:ASP:OD1	1:E:214:ASN:N	2.31	0.64
2:AH:28:ARG:HG3	2:AH:29:ARG:N	2.04	0.64
2:AH:404:VAL:HG13	2:AH:405:THR:HG23	1.79	0.64
2:AL:132:SER:HA	2:AL:191:ASN:HD22	1.62	0.64
2:AL:217:ILE:HB	2:AL:309:ILE:HG22	1.80	0.64
5:AV:32:GLN:NE2	5:AV:36:THR:O	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:208:ALA:HB3	1:N:216:PHE:HB2	1.79	0.64
1:U:210:ASP:OD1	1:U:214:ASN:N	2.24	0.64
1:a:59:PHE:HE2	1:a:175:ARG:HE	1.46	0.64
2:AK:140:ASN:ND2	2:AL:16:PRO:O	2.24	0.64
1:k:59:PHE:HE2	1:k:175:ARG:HE	1.45	0.64
1:m:99:GLN:OE1	1:m:99:GLN:N	2.31	0.64
1:7:133:GLY:H	1:7:152:VAL:HG13	1.63	0.64
1:B:133:GLY:H	1:B:152:VAL:HG13	1.63	0.64
2:AK:66:LEU:HD21	2:AL:348:PRO:HG2	1.79	0.64
4:AQ:92:ARG:HB3	4:AQ:94:ARG:HH22	1.60	0.64
6:U4:140:VAL:O	6:U4:141:PRO:C	2.39	0.64
1:J:172:ALA:O	1:J:175:ARG:NH1	2.30	0.64
1:P:132:THR:HA	1:P:152:VAL:HG23	1.79	0.64
1:V:30:ARG:HD2	1:V:230:GLY:H	1.63	0.64
1:g:4:PHE:HB2	1:g:39:VAL:HG12	1.80	0.64
2:AG:98:GLN:HG2	2:AH:82:THR:HG21	1.80	0.64
3:AN:46:ARG:HE	3:H:77:VAL:HG23	1.62	0.64
6:S4:84:GLY:N	6:S4:125:GLN:O	2.31	0.64
1:P:206:GLN:OE1	1:P:207:VAL:N	2.31	0.64
1:2:88:LEU:N	1:2:121:GLY:O	2.30	0.64
1:F:79:LYS:HE3	1:F:155:THR:HA	1.80	0.64
2:AB:168:GLU:HG2	2:AB:169:ALA:N	2.12	0.64
2:AB:183:ASN:N	2:AB:187:ARG:O	2.29	0.64
2:AL:25:ILE:O	2:AL:28:ARG:HG2	1.98	0.64
6:U3:7:LEU:HD11	6:U3:149:LEU:HD21	1.80	0.64
1:W:208:ALA:HB3	1:W:216:PHE:HB2	1.80	0.63
1:c:99:GLN:OE1	1:c:99:GLN:N	2.31	0.63
2:AF:140:ASN:HD22	2:AG:18:PRO:HG3	1.63	0.63
2:AF:190:LYS:HG2	2:AF:191:ASN:H	1.62	0.63
1:O:75:PHE:HE1	1:O:162:PRO:HD2	1.63	0.63
1:9:159:LEU:HG	1:9:160:PRO:HD2	1.80	0.63
1:G:38:MET:HG2	1:G:185:LYS:HG2	1.79	0.63
2:AC:66:LEU:HD21	2:AD:348:PRO:HG2	1.81	0.63
2:AD:404:VAL:HG13	2:AD:405:THR:HG23	1.79	0.63
2:AJ:39:VAL:HG23	2:AJ:40:VAL:HG13	1.80	0.63
2:AK:102:GLN:HE21	2:AL:80:GLN:HG3	1.62	0.63
6:S3:84:GLY:N	6:S3:125:GLN:O	2.31	0.63
6:S5:69:LEU:HD12	6:S5:73:PRO:HD3	1.80	0.63
1:A:136:ARG:HG2	1:A:149:VAL:HG22	1.79	0.63
2:AJ:140:ASN:HD22	2:AK:18:PRO:HG3	1.63	0.63
6:S4:163:VAL:HG23	6:S4:164:MET:H	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:R5:191:GLN:HA	6:R5:194:TRP:CE3	2.33	0.63
1:a:206:GLN:OE1	1:a:207:VAL:N	2.31	0.63
1:h:99:GLN:OE1	1:h:99:GLN:N	2.30	0.63
1:j:172:ALA:O	1:j:175:ARG:NH1	2.31	0.63
2:AC:98:GLN:HG2	2:AD:82:THR:HG21	1.80	0.63
6:R4:191:GLN:HA	6:R4:194:TRP:CE3	2.34	0.63
1:q:209:ILE:HD11	1:q:213:GLY:HA2	1.81	0.63
2:AF:183:ASN:N	2:AF:187:ARG:O	2.29	0.63
6:S3:163:VAL:HG23	6:S3:164:MET:H	1.62	0.63
4:AS:55:VAL:HG22	4:AS:82:VAL:HG22	1.81	0.63
6:R5:182:ASN:HA	6:R5:187:ILE:HG13	1.80	0.63
6:T5:132:THR:HG22	6:T5:133:GLY:H	1.62	0.63
1:U:209:ILE:HD11	1:U:213:GLY:HA2	1.80	0.63
1:g:156:THR:HG23	1:g:157:SER:H	1.64	0.63
1:k:79:LYS:HE3	1:k:155:THR:HA	1.80	0.63
2:AG:66:LEU:HD21	2:AH:348:PRO:HG2	1.80	0.63
3:AM:6:ARG:NH2	6:R3:17:LYS:O	2.32	0.63
6:S5:84:GLY:N	6:S5:125:GLN:O	2.32	0.63
1:f:206:GLN:OE1	1:f:207:VAL:N	2.31	0.63
1:f:210:ASP:HB3	1:f:216:PHE:HE2	1.63	0.63
1:x:136:ARG:HG2	1:x:149:VAL:HG22	1.81	0.63
1:G:74:ALA:HB2	1:G:91:LEU:HD11	1.80	0.63
6:S3:50:PRO:HA	6:S3:135:ARG:HA	1.79	0.63
6:T3:132:THR:HG22	6:T3:133:GLY:H	1.64	0.63
4:AX:11:VAL:HG22	4:AX:151:GLN:HE22	1.63	0.63
1:g:172:ALA:O	1:g:175:ARG:NH1	2.32	0.63
1:w:74:ALA:HB2	1:w:91:LEU:HD11	1.80	0.63
1:G:210:ASP:HB3	1:G:216:PHE:HE2	1.64	0.63
2:AA:200:SER:OG	2:AA:201:ILE:N	2.32	0.63
2:AD:183:ASN:N	2:AD:187:ARG:O	2.32	0.63
2:AI:351:LEU:HB3	2:AI:371:PHE:CZ	2.34	0.63
4:AR:81:ILE:HG22	4:AR:148:ARG:HG3	1.81	0.63
6:U5:44:THR:HG22	6:U5:46:LEU:HD13	1.81	0.63
1:K:24:CYS:HB2	1:K:223:ASP:OD2	1.99	0.62
1:a:79:LYS:HE3	1:a:155:THR:HA	1.81	0.62
1:b:156:THR:HG23	1:b:157:SER:H	1.64	0.62
1:f:59:PHE:HE2	1:f:175:ARG:HE	1.47	0.62
1:n:75:PHE:HE1	1:n:162:PRO:HD2	1.64	0.62
2:AA:351:LEU:HB3	2:AA:371:PHE:CZ	2.34	0.62
2:AH:25:ILE:O	2:AH:28:ARG:HG2	1.99	0.62
5:AU:32:GLN:NE2	5:AU:36:THR:O	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AU:40:TYR:N	5:AZ:110:SER:O	2.30	0.62
1:x:104:ILE:HG12	1:x:117:LEU:HD13	1.82	0.62
1:B:168:VAL:HG11	1:B:224:ILE:HD13	1.82	0.62
1:E:99:GLN:OE1	1:E:99:GLN:N	2.32	0.62
2:AJ:182:LYS:HE3	2:AJ:186:GLY:HA2	1.80	0.62
1:u:172:ALA:O	1:u:175:ARG:NH1	2.31	0.62
1:v:79:LYS:HE3	1:v:155:THR:HA	1.80	0.62
1:7:38:MET:HG2	1:7:185:LYS:HG2	1.80	0.62
1:7:79:LYS:HE3	1:7:155:THR:HA	1.81	0.62
1:0:209:ILE:HD11	1:0:213:GLY:HA2	1.82	0.62
2:AC:278:PHE:HD2	6:R5:201:LEU:HD21	1.64	0.62
2:AL:156:ARG:HG3	2:AL:157:TYR:HD1	1.64	0.62
3:AP:6:ARG:NH2	6:T3:17:LYS:O	2.32	0.62
6:R4:147:GLY:HA3	6:R4:194:TRP:NE1	2.14	0.62
6:S5:157:ASN:O	6:S5:158:ASN:ND2	2.32	0.62
1:Q:156:THR:HG23	1:Q:157:SER:H	1.64	0.62
1:b:172:ALA:O	1:b:175:ARG:NH1	2.32	0.62
1:l:156:THR:HG23	1:l:157:SER:H	1.64	0.62
1:l:172:ALA:O	1:l:175:ARG:NH1	2.32	0.62
1:0:99:GLN:N	1:0:99:GLN:OE1	2.31	0.62
1:B:210:ASP:HB3	1:B:216:PHE:HE2	1.62	0.62
2:AC:297:HIS:HE1	2:AC:299:LYS:HB2	1.64	0.62
2:AH:156:ARG:HG3	2:AH:157:TYR:HD1	1.64	0.62
2:AK:98:GLN:HG2	2:AL:82:THR:HG21	1.81	0.62
6:R5:199:ARG:O	6:R5:200:VAL:C	2.41	0.62
1:S:172:ALA:O	1:S:175:ARG:NH1	2.32	0.62
1:d:21:SER:O	1:r:49:ARG:NH2	2.33	0.62
1:j:209:ILE:HD11	1:j:213:GLY:HA2	1.81	0.62
1:o:38:MET:SD	1:o:185:LYS:NZ	2.71	0.62
1:z:172:ALA:O	1:z:175:ARG:NH1	2.33	0.62
1:1:79:LYS:HE3	1:1:155:THR:HA	1.80	0.62
1:B:38:MET:HG2	1:B:185:LYS:HG2	1.82	0.62
2:AE:351:LEU:HB3	2:AE:371:PHE:CZ	2.33	0.62
2:AJ:266:THR:HA	2:AJ:273:GLY:HA2	1.82	0.62
1:9:210:ASP:OD1	1:9:214:ASN:N	2.31	0.62
2:AC:39:VAL:HG23	2:AC:40:VAL:HG13	1.80	0.62
2:AH:132:SER:HA	2:AH:191:ASN:HD22	1.64	0.62
4:AS:33:ILE:HG12	3:H:25:LEU:HD13	1.81	0.62
6:R4:173:ASN:C	6:R4:175:GLN:H	2.07	0.62
1:N:172:ALA:O	1:N:175:ARG:NH1	2.33	0.62
1:Q:30:ARG:HD2	1:Q:230:GLY:H	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:79:LYS:HE3	1:f:155:THR:HA	1.81	0.62
1:4:88:LEU:N	1:4:121:GLY:O	2.32	0.62
1:5:99:GLN:OE1	1:5:99:GLN:N	2.31	0.62
1:D:210:ASP:OD1	1:D:214:ASN:N	2.33	0.62
2:AI:69:GLN:HE21	2:AI:111:ALA:HB1	1.64	0.62
4:AQ:33:ILE:HG12	3:AP:25:LEU:HD13	1.81	0.62
6:S5:50:PRO:HA	6:S5:135:ARG:HA	1.82	0.62
1:Y:172:ALA:O	1:Y:175:ARG:NH1	2.32	0.62
1:a:210:ASP:HB3	1:a:216:PHE:HE2	1.65	0.62
1:u:156:THR:HG23	1:u:157:SER:H	1.65	0.62
1:9:88:LEU:N	1:9:121:GLY:O	2.32	0.62
2:AF:243:TRP:HE1	2:AG:291:ASN:HD21	1.46	0.62
1:O:172:ALA:O	1:O:175:ARG:NH1	2.32	0.62
1:T:75:PHE:HE1	1:T:162:PRO:HD2	1.65	0.62
1:k:206:GLN:OE1	1:k:207:VAL:N	2.33	0.62
1:5:30:ARG:HD2	1:5:230:GLY:H	1.64	0.62
2:AD:156:ARG:HG3	2:AD:157:TYR:HD1	1.64	0.62
2:AG:34:GLY:HA2	2:AG:153:LYS:HE3	1.80	0.62
2:AG:282:THR:N	2:AH:249:ARG:CG	2.57	0.62
4:AR:55:VAL:HG22	4:AR:82:VAL:HG22	1.82	0.62
6:S4:15:HIS:ND1	6:T4:32:TYR:OH	2.32	0.62
1:r:210:ASP:HB3	1:r:216:PHE:HE2	1.65	0.62
2:AD:132:SER:HA	2:AD:191:ASN:HD22	1.63	0.62
6:S3:157:ASN:O	6:S3:158:ASN:ND2	2.33	0.62
6:U3:44:THR:HG22	6:U3:46:LEU:HD13	1.82	0.62
1:z:210:ASP:HB3	1:z:216:PHE:HE2	1.64	0.61
1:D:88:LEU:N	1:D:121:GLY:O	2.31	0.61
2:AA:316:PRO:HB2	2:AA:319:LEU:HD23	1.82	0.61
6:S4:50:PRO:HA	6:S4:135:ARG:HA	1.82	0.61
6:U4:44:THR:HG22	6:U4:46:LEU:HD13	1.82	0.61
1:L:156:THR:HG23	1:L:157:SER:H	1.65	0.61
1:T:172:ALA:O	1:T:175:ARG:NH1	2.32	0.61
1:6:79:LYS:HE3	1:6:155:THR:HA	1.81	0.61
2:AB:140:ASN:HD22	2:AC:18:PRO:HG3	1.64	0.61
2:AB:266:THR:HA	2:AB:273:GLY:HA2	1.81	0.61
2:AE:200:SER:OG	2:AE:201:ILE:N	2.32	0.61
5:AU:61:ASN:ND2	5:Ab:50:LEU:O	2.27	0.61
6:T4:132:THR:HG22	6:T4:133:GLY:H	1.64	0.61
6:S5:7:LEU:HD12	6:S5:145:ILE:HG23	1.81	0.61
1:f:24:CYS:HB2	1:f:223:ASP:OD2	2.00	0.61
1:y:209:ILE:HD11	1:y:213:GLY:HA2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:29:ALA:HB1	1:O:190:VAL:HG21	1.82	0.61
2:AA:240:ASN:ND2	2:AB:234:SER:OG	2.32	0.61
1:T:74:ALA:HB2	1:T:91:LEU:HD11	1.82	0.61
1:b:24:CYS:HB2	1:b:223:ASP:OD2	2.00	0.61
2:AA:297:HIS:HE1	2:AA:299:LYS:HB2	1.66	0.61
2:AG:259:VAL:HA	6:R4:202:LEU:O	2.01	0.61
2:AI:280:ALA:HB1	6:T3:198:ARG:HH11	1.65	0.61
2:AK:297:HIS:HE1	2:AK:299:LYS:HB2	1.65	0.61
1:O:74:ALA:HB2	1:O:91:LEU:HD11	1.83	0.61
2:AD:25:ILE:O	2:AD:28:ARG:HG2	2.00	0.61
5:AV:40:TYR:N	5:Aa:110:SER:O	2.32	0.61
1:W:168:VAL:HG12	1:W:190:VAL:HG22	1.83	0.61
1:i:21:SER:O	1:w:49:ARG:NH2	2.33	0.61
2:AI:108:MET:H	2:AJ:360:MET:HE1	1.64	0.61
2:AK:90:SER:HG	2:AK:93:GLN:H	1.45	0.61
1:W:203:THR:HG22	1:W:221:CYS:HB3	1.82	0.61
1:h:209:ILE:HD11	1:h:213:GLY:HA2	1.81	0.61
1:p:156:THR:HG23	1:p:157:SER:H	1.65	0.61
1:q:79:LYS:HE3	1:q:155:THR:HA	1.80	0.61
1:t:59:PHE:HE2	1:t:175:ARG:HE	1.49	0.61
2:AJ:347:GLU:HA	2:AJ:351:LEU:HB2	1.83	0.61
6:S5:62:GLY:O	6:S5:65:GLY:N	2.25	0.61
1:N:48:LEU:HD23	1:O:1:MET:HE3	1.81	0.61
1:W:64:VAL:HB	1:W:199:VAL:HG23	1.82	0.61
1:Z:209:ILE:HD11	1:Z:213:GLY:HA2	1.81	0.61
1:p:172:ALA:O	1:p:175:ARG:NH1	2.34	0.61
1:v:209:ILE:HD11	1:v:213:GLY:HA2	1.83	0.61
2:AK:39:VAL:HG23	2:AK:40:VAL:HG13	1.82	0.61
6:S4:157:ASN:O	6:S4:158:ASN:ND2	2.33	0.61
1:S:48:LEU:HD23	1:T:1:MET:HE3	1.83	0.61
1:1:110:PRO:HG3	1:1:115:VAL:HG13	1.83	0.61
1:G:133:GLY:H	1:G:152:VAL:HG13	1.65	0.61
2:AC:262:GLY:C	6:R5:202:LEU:HD22	2.26	0.61
2:AI:140:ASN:HD21	2:AJ:16:PRO:C	2.08	0.61
3:AM:100:ASN:ND2	3:AM:103:GLU:OE1	2.33	0.61
4:AS:90:ARG:NH1	4:AS:98:GLU:OE2	2.34	0.61
4:AX:81:ILE:HG22	4:AX:148:ARG:HG3	1.82	0.61
1:L:30:ARG:HD2	1:L:230:GLY:H	1.65	0.61
1:a:88:LEU:N	1:a:121:GLY:O	2.32	0.61
1:f:88:LEU:N	1:f:121:GLY:O	2.30	0.61
1:g:24:CYS:HB2	1:g:223:ASP:OD2	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:s:136:ARG:HG2	1:s:149:VAL:HG22	1.82	0.61
1:z:156:THR:HG23	1:z:157:SER:H	1.65	0.61
2:AL:249:ARG:NH1	6:R3:192:ASP:OD1	2.34	0.61
6:R4:163:VAL:HG21	6:R4:177:LEU:HG	1.83	0.61
1:J:1:MET:HE3	1:X:48:LEU:HD23	1.83	0.60
1:A:73:ASN:OD1	1:A:147:GLU:N	2.26	0.60
2:AA:69:GLN:HE21	2:AA:111:ALA:HB1	1.65	0.60
2:AF:127:MET:O	2:AF:196:ILE:N	2.34	0.60
6:S5:192:ASP:OD2	6:T5:183:ASN:ND2	2.34	0.60
1:l:24:CYS:HB2	1:l:223:ASP:OD2	2.01	0.60
6:S4:74:ILE:HG13	6:S4:131:VAL:HG23	1.82	0.60
1:s:104:ILE:HG12	1:s:117:LEU:HD13	1.82	0.60
1:A:138:TRP:CZ3	1:A:147:GLU:HB3	2.36	0.60
2:AB:372:ASP:HB3	2:AB:374:ASP:OD1	2.02	0.60
2:AE:316:PRO:HB2	2:AE:319:LEU:HD23	1.82	0.60
2:AI:83:GLN:HE21	2:AI:366:GLY:H	1.49	0.60
4:AR:11:VAL:HG22	4:AR:151:GLN:HE22	1.64	0.60
1:S:208:ALA:HB3	1:S:216:PHE:HB2	1.84	0.60
1:y:59:PHE:HE2	1:y:175:ARG:HE	1.47	0.60
1:3:74:ALA:HB2	1:3:91:LEU:HD11	1.83	0.60
2:AJ:167:ASP:N	2:AK:28:ARG:HH12	1.99	0.60
5:AU:93:ASP:N	5:AU:93:ASP:OD1	2.33	0.60
4:AW:90:ARG:NH1	4:AW:98:GLU:OE2	2.34	0.60
5:AY:32:GLN:NE2	5:AY:36:THR:O	2.30	0.60
1:J:74:ALA:HB2	1:J:91:LEU:HD11	1.83	0.60
1:P:136:ARG:HG2	1:P:149:VAL:HG22	1.81	0.60
1:B:79:LYS:HE3	1:B:155:THR:HA	1.82	0.60
2:AC:259:VAL:O	6:R5:202:LEU:HD13	2.01	0.60
2:AG:90:SER:HG	2:AG:93:GLN:H	1.46	0.60
5:AV:93:ASP:N	5:AV:93:ASP:OD1	2.35	0.60
4:AT:11:VAL:HG22	4:AT:151:GLN:HE22	1.65	0.60
6:S5:166:VAL:HG23	6:T5:177:LEU:HB3	1.83	0.60
1:M:64:VAL:HB	1:M:199:VAL:HG23	1.83	0.60
1:V:208:ALA:HB3	1:V:216:PHE:HB2	1.82	0.60
1:k:88:LEU:N	1:k:121:GLY:O	2.31	0.60
1:n:104:ILE:HG12	1:n:117:LEU:HD13	1.83	0.60
1:F:138:TRP:CZ3	1:F:147:GLU:HB3	2.36	0.60
2:AI:90:SER:HG	2:AI:93:GLN:H	1.50	0.60
2:AK:103:ARG:HH22	2:AL:365:ALA:HA	1.66	0.60
6:R3:165:SER:HB2	6:R3:169:THR:HG23	1.84	0.60
6:R3:182:ASN:HA	6:R3:187:ILE:HG13	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S3:7:LEU:HD12	6:S3:145:ILE:HG23	1.84	0.60
6:U4:139:SER:O	6:U4:140:VAL:C	2.44	0.60
4:AW:38:VAL:HG11	4:AW:81:ILE:HD11	1.83	0.60
1:Z:75:PHE:HE1	1:Z:162:PRO:HD2	1.67	0.60
1:t:203:THR:HG22	1:t:221:CYS:HB3	1.84	0.60
1:E:79:LYS:HE3	1:E:155:THR:HA	1.83	0.60
2:AE:108:MET:H	2:AF:360:MET:HE1	1.65	0.60
5:AY:93:ASP:N	5:AY:93:ASP:OD1	2.33	0.60
1:T:180:ARG:HH22	6:R4:124:SER:HA	1.65	0.60
1:V:79:LYS:HE3	1:V:155:THR:HA	1.84	0.60
2:AA:140:ASN:HD21	2:AB:16:PRO:C	2.09	0.60
2:AH:260:LYS:HZ3	6:R4:201:LEU:HD21	1.66	0.60
1:K:136:ARG:HG2	1:K:149:VAL:HG22	1.82	0.60
1:c:132:THR:HA	1:c:152:VAL:HG23	1.83	0.60
1:s:75:PHE:HE1	1:s:162:PRO:HD2	1.67	0.60
2:AD:266:THR:HA	2:AD:273:GLY:HA2	1.84	0.60
2:AF:251:LEU:HD11	2:AF:282:THR:HG23	1.84	0.60
4:AQ:90:ARG:NH1	4:AQ:98:GLU:OE2	2.35	0.60
6:R4:125:GLN:HE22	6:U4:93:ILE:H	1.49	0.60
4:AW:33:ILE:HG12	3:I:25:LEU:HD13	1.82	0.60
1:R:64:VAL:HB	1:R:199:VAL:HG23	1.83	0.60
1:Y:21:SER:O	1:2:49:ARG:NH2	2.35	0.60
1:e:209:ILE:HD11	1:e:213:GLY:HA2	1.84	0.60
1:0:88:LEU:N	1:0:121:GLY:O	2.35	0.60
1:D:136:ARG:HG2	1:D:149:VAL:HG22	1.83	0.60
1:G:168:VAL:HG11	1:G:224:ILE:HD13	1.84	0.60
2:AA:280:ALA:HB1	6:T5:198:ARG:HH11	1.66	0.60
2:AB:267:LYS:HD2	2:AC:237:GLY:HA2	1.84	0.60
2:AB:347:GLU:HA	2:AB:351:LEU:HB2	1.84	0.60
2:AC:102:GLN:HE21	2:AD:80:GLN:HG3	1.67	0.60
4:AQ:38:VAL:HG11	4:AQ:81:ILE:HD11	1.82	0.60
1:7:177:VAL:O	1:7:179:PRO:HD3	2.02	0.59
2:AB:127:MET:O	2:AB:196:ILE:N	2.34	0.59
2:AC:127:MET:HB2	2:AC:196:ILE:HB	1.84	0.59
2:AF:26:PHE:O	2:AF:31:PHE:N	2.35	0.59
2:AH:396:ILE:HG23	2:AH:400:GLU:HG3	1.84	0.59
6:U3:140:VAL:O	6:U3:141:PRO:C	2.45	0.59
3:AO:39:ILE:HG22	3:AO:65:ILE:HG12	1.83	0.59
1:S:30:ARG:HD2	1:S:230:GLY:H	1.67	0.59
1:o:88:LEU:N	1:o:121:GLY:O	2.34	0.59
1:w:210:ASP:HB3	1:w:216:PHE:HE2	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4:136:ARG:HG2	1:4:149:VAL:HG22	1.83	0.59
1:8:74:ALA:HB2	1:8:91:LEU:HD11	1.83	0.59
2:AE:140:ASN:HD21	2:AF:16:PRO:C	2.10	0.59
2:AF:263:ILE:HD13	2:AF:277:ILE:HG12	1.84	0.59
2:AH:127:MET:HB2	2:AH:196:ILE:HB	1.82	0.59
2:AK:127:MET:HB2	2:AK:196:ILE:HB	1.84	0.59
2:AG:261:GLU:OE2	6:S4:61:LYS:NZ	2.27	0.59
6:R4:179:GLY:O	6:R4:180:GLY:C	2.46	0.59
6:S4:69:LEU:HD12	6:S4:73:PRO:HD3	1.84	0.59
6:S4:193:GLU:O	6:S4:196:ARG:NH1	2.35	0.59
5:AY:40:TYR:N	5:Ab:110:SER:O	2.35	0.59
1:k:133:GLY:H	1:k:152:VAL:HG23	1.68	0.59
1:n:136:ARG:HG2	1:n:149:VAL:HG22	1.83	0.59
1:s:99:GLN:OE1	1:s:99:GLN:N	2.33	0.59
1:7:210:ASP:HB3	1:7:216:PHE:HE2	1.67	0.59
1:B:29:ALA:HB1	1:B:190:VAL:HG21	1.84	0.59
2:AA:108:MET:H	2:AB:360:MET:HE1	1.66	0.59
2:AH:253:ASP:HB2	6:R4:198:ARG:HD2	1.84	0.59
2:AK:156:ARG:HG3	2:AK:157:TYR:HD1	1.68	0.59
2:AL:396:ILE:HG23	2:AL:400:GLU:HG3	1.84	0.59
3:AN:39:ILE:HG22	3:AN:65:ILE:HG12	1.84	0.59
4:AX:93:ASP:O	4:AX:94:ARG:C	2.46	0.59
6:R5:163:VAL:HG21	6:R5:177:LEU:HG	1.84	0.59
6:U5:77:ARG:HD2	6:U5:78:PRO:HD2	1.85	0.59
1:P:209:ILE:HD11	1:P:213:GLY:HA2	1.83	0.59
1:R:208:ALA:HB3	1:R:216:PHE:HB2	1.84	0.59
1:k:156:THR:HG23	1:k:157:SER:H	1.68	0.59
2:AG:297:HIS:CE1	2:AG:299:LYS:HB2	2.38	0.59
4:AR:93:ASP:HB2	4:AR:95:LYS:HE2	1.84	0.59
2:AC:282:THR:H	2:AD:249:ARG:HD3	1.62	0.59
2:AD:112:GLN:NE2	2:AE:197:VAL:O	2.36	0.59
2:AG:156:ARG:HG3	2:AG:157:TYR:HD1	1.68	0.59
2:AK:132:SER:HA	2:AK:191:ASN:HD22	1.68	0.59
2:AK:267:LYS:HD2	2:AL:237:GLY:HA2	1.85	0.59
6:U3:182:ASN:HA	6:U3:187:ILE:HD11	1.85	0.59
1:1:156:THR:HG23	1:1:157:SER:H	1.68	0.59
1:0:75:PHE:CE1	1:0:162:PRO:HD2	2.38	0.59
2:AB:243:TRP:HE1	2:AC:291:ASN:HD21	1.49	0.59
2:AD:219:VAL:HB	2:AD:220:PRO:HD3	1.85	0.59
5:AU:113:ARG:HD2	5:Ab:7:ASN:HB2	1.83	0.59
4:AS:61:ASP:OD1	4:AS:62:THR:N	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S4:7:LEU:HD12	6:S4:145:ILE:HG23	1.82	0.59
6:U4:77:ARG:HD2	6:U4:78:PRO:HD2	1.85	0.59
4:AX:55:VAL:HG22	4:AX:82:VAL:HG22	1.84	0.59
1:K:78:THR:HG23	1:K:152:VAL:HG12	1.85	0.59
1:n:99:GLN:N	1:n:99:GLN:OE1	2.34	0.59
1:p:48:LEU:HD23	1:q:1:MET:HE3	1.85	0.59
1:s:132:THR:HG21	1:s:154:PRO:HB3	1.85	0.59
1:y:88:LEU:HD12	1:y:91:LEU:HD12	1.85	0.59
1:6:138:TRP:CZ3	1:6:147:GLU:HB3	2.37	0.59
2:AC:103:ARG:HH22	2:AD:365:ALA:HA	1.67	0.59
2:AC:156:ARG:HG3	2:AC:157:TYR:HD1	1.68	0.59
2:AD:127:MET:HB2	2:AD:196:ILE:HB	1.84	0.59
2:AD:161:GLU:HB2	2:AD:179:LYS:HE2	1.84	0.59
2:AH:339:LYS:O	2:AH:343:GLU:HG2	2.03	0.59
6:T4:44:THR:HG22	6:T4:46:LEU:HD23	1.83	0.59
6:S5:72:THR:O	6:S5:73:PRO:C	2.45	0.59
1:M:167:PRO:HA	1:M:191:SER:HB3	1.85	0.59
1:a:156:THR:HG23	1:a:157:SER:H	1.68	0.59
1:v:156:THR:HG23	1:v:157:SER:H	1.68	0.59
1:y:203:THR:HG22	1:y:221:CYS:HB3	1.85	0.59
1:5:79:LYS:HE3	1:5:155:THR:HA	1.85	0.59
1:9:136:ARG:HG2	1:9:149:VAL:HG22	1.83	0.59
2:AJ:243:TRP:HE1	2:AK:291:ASN:HD21	1.50	0.59
3:AP:32:VAL:HG12	3:AP:33:ILE:HG13	1.84	0.59
1:V:156:THR:HG23	1:V:157:SER:H	1.67	0.59
1:2:79:LYS:HE3	1:2:155:THR:HA	1.85	0.59
2:AA:25:ILE:O	2:AA:28:ARG:HG2	2.03	0.59
2:AI:151:LYS:O	2:AI:164:GLN:N	2.32	0.59
2:AJ:263:ILE:HD13	2:AJ:277:ILE:HG12	1.85	0.59
2:AL:219:VAL:HB	2:AL:220:PRO:HD3	1.84	0.59
6:U3:77:ARG:HD2	6:U3:78:PRO:HD2	1.85	0.59
6:T5:58:ILE:HB	6:T5:126:LEU:HD22	1.85	0.59
1:R:38:MET:HG2	1:R:185:LYS:HG2	1.84	0.58
1:W:75:PHE:CE1	1:W:162:PRO:HD2	2.37	0.58
1:a:209:ILE:HD11	1:a:213:GLY:HA2	1.85	0.58
1:w:88:LEU:N	1:w:121:GLY:O	2.36	0.58
1:x:29:ALA:HB1	1:x:190:VAL:HG21	1.84	0.58
1:4:210:ASP:OD1	1:4:214:ASN:N	2.35	0.58
2:AC:281:GLY:HA2	2:AD:249:ARG:CG	2.32	0.58
2:AG:282:THR:H	2:AH:249:ARG:HG3	1.63	0.58
2:AH:205:MET:N	2:AH:205:MET:SD	2.76	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AJ:127:MET:O	2:AJ:196:ILE:N	2.35	0.58
2:AJ:183:ASN:N	2:AJ:187:ARG:O	2.30	0.58
5:AU:96:VAL:HG12	5:AU:127:LEU:HB2	1.84	0.58
6:T4:166:VAL:O	6:T4:167:ARG:C	2.47	0.58
1:j:71:VAL:HG13	1:j:144:ASN:HB2	1.84	0.58
1:G:79:LYS:HE3	1:G:155:THR:HA	1.85	0.58
2:AB:396:ILE:HG23	2:AB:400:GLU:HG3	1.86	0.58
2:AE:338:ARG:NE	2:AF:344:ASP:OD1	2.36	0.58
2:AG:132:SER:HA	2:AG:191:ASN:HD22	1.68	0.58
6:S4:62:GLY:O	6:S4:65:GLY:N	2.26	0.58
6:U4:166:VAL:HG12	6:U4:167:ARG:H	1.67	0.58
1:J:79:LYS:HE3	1:J:155:THR:HA	1.84	0.58
1:J:180:ARG:HH22	6:R5:124:SER:HA	1.68	0.58
1:q:156:THR:HG23	1:q:157:SER:H	1.68	0.58
1:5:88:LEU:N	1:5:121:GLY:O	2.36	0.58
1:0:79:LYS:HE3	1:0:155:THR:HA	1.84	0.58
1:C:74:ALA:HB2	1:C:91:LEU:HD11	1.85	0.58
2:AH:55:PRO:HA	2:AI:216:ALA:HB1	1.85	0.58
2:AJ:28:ARG:HG3	2:AJ:29:ARG:N	2.18	0.58
6:R3:20:ASP:OD1	6:R3:20:ASP:N	2.36	0.58
1:f:156:THR:HG23	1:f:157:SER:H	1.69	0.58
1:k:209:ILE:HD11	1:k:213:GLY:HA2	1.84	0.58
2:AB:351:LEU:HB3	2:AB:371:PHE:CZ	2.39	0.58
2:AE:132:SER:HA	2:AE:191:ASN:HD22	1.67	0.58
2:AG:39:VAL:HG23	2:AG:40:VAL:HG13	1.85	0.58
1:P:71:VAL:HG13	1:P:144:ASN:HB2	1.85	0.58
1:X:75:PHE:HE1	1:X:162:PRO:HD2	1.69	0.58
1:x:99:GLN:OE1	1:x:99:GLN:N	2.33	0.58
2:AA:151:LYS:O	2:AA:164:GLN:N	2.31	0.58
2:AF:266:THR:HA	2:AF:273:GLY:HA2	1.84	0.58
2:AG:352:THR:HA	2:AG:355:GLU:HG2	1.84	0.58
2:AH:267:LYS:HD3	2:AI:237:GLY:HA2	1.85	0.58
2:AJ:26:PHE:O	2:AJ:31:PHE:N	2.35	0.58
1:T:79:LYS:HE3	1:T:155:THR:HA	1.85	0.58
1:s:79:LYS:HE3	1:s:155:THR:HA	1.86	0.58
1:5:75:PHE:CE1	1:5:162:PRO:HD2	2.37	0.58
1:A:154:PRO:O	1:A:155:THR:HG22	2.04	0.58
2:AE:90:SER:HG	2:AE:93:GLN:H	1.51	0.58
4:AQ:61:ASP:OD1	4:AQ:62:THR:N	2.29	0.58
5:AZ:17:THR:HG22	5:AZ:24:VAL:HG13	1.85	0.58
6:R3:195:PHE:C	6:R3:197:TYR:N	2.59	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:167:PRO:HA	1:W:191:SER:HB3	1.86	0.58
1:Z:71:VAL:HG13	1:Z:144:ASN:HB2	1.86	0.58
1:d:156:THR:HG23	1:d:157:SER:H	1.69	0.58
1:m:210:ASP:OD1	1:m:214:ASN:N	2.33	0.58
1:y:172:ALA:O	1:y:175:ARG:NH1	2.37	0.58
1:B:74:ALA:HB2	1:B:91:LEU:HD11	1.84	0.58
1:F:154:PRO:O	1:F:155:THR:HG22	2.04	0.58
2:AC:210:GLN:O	2:AC:215:GLN:NE2	2.36	0.58
2:AD:77:LYS:NZ	2:AD:86:ASP:OD2	2.36	0.58
3:H:6:ARG:NH2	6:T4:17:LYS:O	2.37	0.58
6:R4:161:ASP:HB2	6:U4:157:ASN:CG	2.29	0.58
6:T5:44:THR:HG22	6:T5:46:LEU:HD23	1.86	0.58
1:U:71:VAL:HG13	1:U:144:ASN:HB2	1.85	0.58
1:k:75:PHE:CE1	1:k:162:PRO:HD2	2.39	0.58
1:7:168:VAL:HG11	1:7:224:ILE:HD13	1.85	0.58
1:B:209:ILE:HD11	1:B:213:GLY:HA2	1.85	0.58
2:AD:339:LYS:O	2:AD:343:GLU:HG2	2.03	0.58
2:AG:103:ARG:HH22	2:AH:365:ALA:HA	1.68	0.58
6:S4:192:ASP:OD2	6:T4:183:ASN:ND2	2.37	0.58
6:S5:15:HIS:CD2	6:S5:149:LEU:HB3	2.39	0.58
1:5:209:ILE:HD11	1:5:213:GLY:HA2	1.85	0.58
1:6:154:PRO:O	1:6:155:THR:HG22	2.04	0.58
2:AD:44:ASN:HD22	2:AD:210:GLN:HG2	1.69	0.58
2:AE:258:GLU:OE2	6:T4:200:VAL:HG13	2.04	0.58
2:AF:167:ASP:N	2:AG:28:ARG:HH12	1.99	0.58
2:AL:252:ASP:O	2:AL:253:ASP:C	2.47	0.58
5:AZ:7:ASN:HB2	5:AV:113:ARG:HD2	1.84	0.58
5:Aa:50:LEU:O	5:AY:61:ASN:ND2	2.27	0.58
6:U4:134:ARG:NH1	6:U4:138:ASN:HA	2.19	0.58
1:o:203:THR:HG22	1:o:221:CYS:HB3	1.86	0.58
2:AF:243:TRP:HE1	2:AG:291:ASN:ND2	2.01	0.58
2:AH:112:GLN:NE2	2:AI:197:VAL:O	2.37	0.58
2:AH:352:THR:HA	2:AH:355:GLU:HG2	1.86	0.58
6:S3:15:HIS:CD2	6:S3:149:LEU:HB3	2.39	0.58
5:Aa:30:HIS:HE2	5:Aa:79:TYR:HH	1.52	0.58
6:S5:144:ILE:H	6:S5:144:ILE:HD12	1.67	0.58
1:o:172:ALA:O	1:o:175:ARG:NH1	2.37	0.57
1:p:88:LEU:N	1:p:121:GLY:O	2.36	0.57
1:w:79:LYS:HE3	1:w:155:THR:HA	1.85	0.57
1:y:132:THR:HA	1:y:152:VAL:HG23	1.86	0.57
1:2:210:ASP:HB3	1:2:216:PHE:HE2	1.67	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AC:298:SER:HB3	2:AC:301:PRO:HG2	1.86	0.57
2:AF:347:GLU:HA	2:AF:351:LEU:HB2	1.86	0.57
2:AH:161:GLU:HB2	2:AH:179:LYS:HE2	1.84	0.57
2:AL:77:LYS:NZ	2:AL:86:ASP:OD2	2.37	0.57
5:AU:7:ASN:OD1	5:AU:8:GLY:N	2.37	0.57
4:AR:77:ARG:HD2	4:AR:150:ARG:HD3	1.86	0.57
6:T3:166:VAL:O	6:T3:167:ARG:C	2.47	0.57
5:Aa:7:ASN:HB2	5:AY:113:ARG:HD2	1.86	0.57
6:U4:141:PRO:HG2	6:U4:144:ILE:HG13	1.85	0.57
6:S5:18:CYS:SG	6:S5:23:ARG:NH2	2.70	0.57
6:U5:40:ALA:HB2	6:U5:194:TRP:CZ2	2.39	0.57
1:W:38:MET:HG2	1:W:185:LYS:HG2	1.85	0.57
1:f:75:PHE:CE1	1:f:162:PRO:HD2	2.39	0.57
1:x:75:PHE:HE1	1:x:162:PRO:HD2	1.69	0.57
1:y:88:LEU:N	1:y:121:GLY:O	2.37	0.57
1:y:133:GLY:H	1:y:152:VAL:HG23	1.68	0.57
1:6:73:ASN:OD1	1:6:147:GLU:N	2.28	0.57
1:G:177:VAL:O	1:G:179:PRO:HD3	2.03	0.57
2:AD:271:ASP:HB3	6:U5:66:LYS:HD2	1.85	0.57
2:AE:151:LYS:O	2:AE:164:GLN:N	2.31	0.57
2:AG:282:THR:N	2:AH:249:ARG:HG2	2.18	0.57
2:AI:132:SER:HA	2:AI:191:ASN:HD22	1.69	0.57
2:AL:352:THR:HA	2:AL:355:GLU:HG2	1.86	0.57
3:AP:4:ALA:HB2	6:U4:159:PRO:HD3	1.85	0.57
6:R3:179:GLY:HA2	6:R3:182:ASN:HD21	1.69	0.57
6:R4:19:ASP:N	6:R4:19:ASP:OD1	2.37	0.57
1:M:75:PHE:CE1	1:M:162:PRO:HD2	2.38	0.57
1:X:154:PRO:O	1:X:155:THR:HG22	2.04	0.57
1:e:71:VAL:HG13	1:e:144:ASN:HB2	1.86	0.57
1:z:59:PHE:HE2	1:z:175:ARG:HE	1.50	0.57
1:4:209:ILE:HD11	1:4:213:GLY:HA2	1.86	0.57
2:AA:90:SER:HG	2:AA:93:GLN:H	1.52	0.57
2:AA:197:VAL:O	2:AL:112:GLN:NE2	2.37	0.57
2:AB:90:SER:HG	2:AB:93:GLN:H	1.50	0.57
2:AC:132:SER:HA	2:AC:191:ASN:HD22	1.69	0.57
2:AK:210:GLN:O	2:AK:215:GLN:NE2	2.37	0.57
6:R3:173:ASN:O	6:R3:175:GLN:N	2.38	0.57
5:Aa:17:THR:HG22	5:Aa:24:VAL:HG13	1.86	0.57
1:R:62:ASP:OD2	1:R:63:GLY:N	2.37	0.57
1:j:156:THR:HG23	1:j:157:SER:H	1.69	0.57
2:AD:204:ALA:HB3	2:AD:208:ASP:HB2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AD:253:ASP:H	6:R5:198:ARG:NH1	2.02	0.57
1:K:71:VAL:HG13	1:K:144:ASN:HB2	1.86	0.57
1:R:203:THR:HG22	1:R:221:CYS:HB3	1.86	0.57
1:h:210:ASP:HB3	1:h:216:PHE:HE2	1.69	0.57
1:y:136:ARG:HG2	1:y:149:VAL:HG22	1.86	0.57
2:AC:336:GLU:HG2	2:AC:337:SER:N	2.19	0.57
3:AP:85:ARG:HH22	3:AP:91:ARG:CZ	2.18	0.57
6:S3:18:CYS:SG	6:S3:23:ARG:NH2	2.72	0.57
6:R5:147:GLY:HA3	6:R5:194:TRP:NE1	2.18	0.57
1:L:79:LYS:HE3	1:L:155:THR:HA	1.85	0.57
1:Q:154:PRO:O	1:Q:155:THR:HG22	2.05	0.57
1:T:110:PRO:HG3	1:T:115:VAL:HG23	1.87	0.57
1:n:79:LYS:HE3	1:n:155:THR:HA	1.85	0.57
1:o:59:PHE:HE2	1:o:175:ARG:HE	1.53	0.57
1:8:206:GLN:OE1	1:8:207:VAL:N	2.38	0.57
1:E:75:PHE:CE1	1:E:162:PRO:HD2	2.38	0.57
2:AC:267:LYS:HD2	2:AD:237:GLY:HA2	1.86	0.57
2:AD:100:ILE:HD11	2:AD:141:ALA:HA	1.87	0.57
2:AD:205:MET:SD	2:AD:205:MET:N	2.77	0.57
2:AF:28:ARG:HD3	2:AF:29:ARG:CG	2.35	0.57
2:AF:396:ILE:HG23	2:AF:400:GLU:HG3	1.86	0.57
2:AI:121:TRP:CZ2	2:AI:198:LYS:HD3	2.39	0.57
5:AZ:30:HIS:HE2	5:AZ:79:TYR:HH	1.51	0.57
6:R3:163:VAL:HG21	6:R3:177:LEU:HG	1.85	0.57
6:S4:18:CYS:SG	6:S4:23:ARG:NH2	2.71	0.57
1:L:154:PRO:O	1:L:155:THR:HG22	2.05	0.57
1:W:30:ARG:HD2	1:W:230:GLY:H	1.70	0.57
1:4:75:PHE:CZ	1:4:161:GLN:HG2	2.39	0.57
1:A:75:PHE:CE1	1:A:162:PRO:HD2	2.40	0.57
3:AM:48:SER:O	3:AM:48:SER:OG	2.18	0.57
6:S4:33:ARG:HA	6:S4:152:ILE:HD11	1.87	0.57
6:U4:170:LEU:H	6:U4:170:LEU:HD23	1.70	0.57
1:N:154:PRO:O	1:N:155:THR:HG22	2.04	0.57
1:n:156:THR:HG23	1:n:157:SER:H	1.70	0.57
1:F:75:PHE:CE1	1:F:162:PRO:HD2	2.40	0.57
2:AA:132:SER:HA	2:AA:191:ASN:HD22	1.69	0.57
5:AU:96:VAL:HG12	5:AU:127:LEU:CB	2.34	0.57
5:AV:7:ASN:OD1	5:AV:8:GLY:N	2.38	0.57
6:U5:195:PHE:HD1	6:U5:198:ARG:HE	1.53	0.57
1:i:210:ASP:HB3	1:i:216:PHE:HE2	1.69	0.57
1:q:116:GLU:N	1:q:116:GLU:OE2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:r:136:ARG:HG2	1:r:149:VAL:HG22	1.86	0.57
2:AD:396:ILE:HG23	2:AD:400:GLU:HG3	1.85	0.57
2:AH:77:LYS:NZ	2:AH:86:ASP:OD2	2.38	0.57
6:U3:40:ALA:HB2	6:U3:194:TRP:CZ2	2.39	0.57
1:M:62:ASP:OD2	1:M:63:GLY:N	2.38	0.57
1:S:154:PRO:O	1:S:155:THR:HG22	2.04	0.57
1:U:116:GLU:N	1:U:116:GLU:OE2	2.38	0.57
1:s:156:THR:HG23	1:s:157:SER:H	1.70	0.57
1:x:132:THR:HG21	1:x:154:PRO:HB3	1.87	0.57
1:D:38:MET:HE3	1:D:183:VAL:HG21	1.85	0.57
2:AK:217:ILE:HB	2:AK:309:ILE:HG22	1.87	0.57
2:AL:127:MET:HB2	2:AL:196:ILE:HB	1.87	0.57
6:R5:20:ASP:OD1	6:R5:20:ASP:N	2.33	0.57
6:T5:13:ARG:NH2	6:T5:26:ASP:OD1	2.30	0.57
1:P:116:GLU:N	1:P:116:GLU:OE2	2.38	0.56
1:R:75:PHE:CE1	1:R:162:PRO:HD2	2.39	0.56
1:X:100:VAL:HA	1:X:142:ASN:HD21	1.69	0.56
1:Z:154:PRO:O	1:Z:155:THR:HG22	2.05	0.56
1:e:25:GLU:OE1	1:e:25:GLU:N	2.36	0.56
1:e:75:PHE:HE1	1:e:162:PRO:HD2	1.69	0.56
1:t:209:ILE:HD11	1:t:213:GLY:HA2	1.87	0.56
1:E:88:LEU:N	1:E:121:GLY:O	2.37	0.56
2:AD:169:ALA:HB3	2:AE:28:ARG:HD3	1.87	0.56
4:AX:77:ARG:HD2	4:AX:150:ARG:HD3	1.86	0.56
3:I:77:VAL:O	3:I:94:LYS:NZ	2.36	0.56
3:I:85:ARG:HH22	3:I:91:ARG:CZ	2.18	0.56
6:U5:175:GLN:O	6:U5:177:LEU:N	2.36	0.56
1:U:153:ASP:OD1	1:U:155:THR:N	2.38	0.56
1:Y:153:ASP:HA	1:Y:159:LEU:HD23	1.87	0.56
1:o:136:ARG:HG2	1:o:149:VAL:HG22	1.87	0.56
1:t:138:TRP:CZ3	1:t:147:GLU:HB3	2.40	0.56
1:t:172:ALA:O	1:t:175:ARG:NH1	2.38	0.56
1:z:48:LEU:HD23	1:1:1:MET:HE3	1.87	0.56
1:6:210:ASP:OD1	1:6:214:ASN:N	2.37	0.56
1:G:30:ARG:HD2	1:G:230:GLY:H	1.70	0.56
2:AB:176:SER:OG	2:AB:178:THR:OG1	2.22	0.56
2:AC:351:LEU:HD23	2:AC:371:PHE:CE2	2.40	0.56
2:AC:352:THR:HA	2:AC:355:GLU:HG2	1.86	0.56
5:Aa:40:TYR:OH	5:Aa:89:VAL:HG11	2.05	0.56
6:S4:58:ILE:HD12	6:S4:67:ILE:HD12	1.87	0.56
3:AO:48:SER:OG	3:AO:48:SER:O	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:172:ALA:O	1:P:175:ARG:NH1	2.38	0.56
1:Y:134:VAL:HG11	1:Y:162:PRO:HG3	1.87	0.56
1:Z:79:LYS:HE3	1:Z:155:THR:HA	1.87	0.56
1:w:31:PRO:HD3	1:w:227:GLY:O	2.06	0.56
1:x:79:LYS:HE3	1:x:155:THR:HA	1.87	0.56
1:z:88:LEU:N	1:z:121:GLY:O	2.38	0.56
1:2:31:PRO:HD3	1:2:227:GLY:O	2.05	0.56
1:4:75:PHE:CE1	1:4:161:GLN:HG2	2.40	0.56
2:AC:282:THR:N	2:AD:249:ARG:CD	2.59	0.56
2:AK:28:ARG:HG3	2:AK:29:ARG:N	2.20	0.56
6:R3:43:TYR:CZ	6:R3:198:ARG:HD3	2.39	0.56
6:T3:80:VAL:HG12	6:T3:91:GLU:HG2	1.87	0.56
3:H:85:ARG:HH22	3:H:91:ARG:CZ	2.18	0.56
4:AW:61:ASP:OD1	4:AW:62:THR:N	2.29	0.56
5:AY:7:ASN:OD1	5:AY:8:GLY:N	2.38	0.56
1:e:209:ILE:HG13	1:e:214:ASN:O	2.06	0.56
1:n:29:ALA:HB1	1:n:190:VAL:HG21	1.88	0.56
2:AB:263:ILE:HD13	2:AB:277:ILE:HG12	1.86	0.56
2:AD:245:VAL:HB	2:AD:286:VAL:HG12	1.87	0.56
2:AG:102:GLN:HE21	2:AH:80:GLN:HG3	1.70	0.56
2:AL:205:MET:N	2:AL:205:MET:SD	2.77	0.56
2:AL:257:LYS:O	2:AL:261:GLU:HG2	2.05	0.56
5:AV:63:THR:HG22	5:AV:120:VAL:HG22	1.87	0.56
5:Aa:4:ASN:HD21	5:AY:113:ARG:HE	1.53	0.56
6:R4:173:ASN:O	6:R4:175:GLN:N	2.38	0.56
6:S4:15:HIS:CD2	6:S4:149:LEU:HB3	2.41	0.56
6:S4:74:ILE:HG22	6:S4:75:ALA:N	2.20	0.56
1:N:75:PHE:HE1	1:N:162:PRO:HD2	1.71	0.56
1:m:38:MET:HE3	1:m:183:VAL:HG21	1.88	0.56
1:p:104:ILE:HG12	1:p:117:LEU:HD13	1.88	0.56
1:5:53:LEU:HD23	1:5:182:HIS:HA	1.87	0.56
1:F:73:ASN:OD1	1:F:147:GLU:N	2.26	0.56
1:F:75:PHE:HE1	1:F:162:PRO:HD2	1.71	0.56
2:AB:243:TRP:HE1	2:AC:291:ASN:ND2	2.03	0.56
2:AC:372:ASP:O	2:AC:375:SER:OG	2.22	0.56
2:AG:28:ARG:HG3	2:AG:29:ARG:N	2.21	0.56
2:AI:229:ALA:HA	2:AI:232:ILE:HD12	1.87	0.56
2:AL:252:ASP:HB2	2:AL:255:GLN:HG3	1.88	0.56
3:AO:100:ASN:ND2	3:AO:103:GLU:OE1	2.37	0.56
1:R:30:ARG:HD2	1:R:230:GLY:H	1.70	0.56
1:R:156:THR:HG23	1:R:157:SER:H	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:r:79:LYS:HE3	1:r:155:THR:HA	1.85	0.56
2:AI:204:ALA:HB3	2:AI:208:ASP:HB2	1.88	0.56
2:AI:282:THR:HG23	2:AJ:249:ARG:HD3	1.88	0.56
2:AK:336:GLU:HG2	2:AK:337:SER:N	2.21	0.56
6:S5:33:ARG:HA	6:S5:152:ILE:HD11	1.88	0.56
1:X:3:PHE:HD1	1:X:38:MET:HE2	1.71	0.56
1:g:118:GLY:N	1:g:122:ALA:O	2.24	0.56
1:D:118:GLY:N	1:D:122:ALA:O	2.31	0.56
2:AB:28:ARG:HG3	2:AB:29:ARG:N	2.18	0.56
2:AC:217:ILE:HB	2:AC:309:ILE:HG22	1.88	0.56
2:AE:297:HIS:HE1	2:AE:299:LYS:HB2	1.71	0.56
3:AP:49:GLN:O	3:AP:50:ASP:HB2	2.05	0.56
5:AY:128:LEU:HD21	5:Ab:75:PRO:HA	1.87	0.56
1:V:154:PRO:O	1:V:155:THR:HG22	2.06	0.56
1:d:73:ASN:OD1	1:d:147:GLU:N	2.28	0.56
1:u:88:LEU:N	1:u:121:GLY:O	2.38	0.56
1:5:132:THR:HA	1:5:152:VAL:HG23	1.88	0.56
1:7:209:ILE:HD11	1:7:213:GLY:HA2	1.87	0.56
2:AA:156:ARG:HG3	2:AA:157:TYR:HD1	1.71	0.56
2:AC:262:GLY:HA3	6:R5:202:LEU:HB3	1.86	0.56
2:AF:90:SER:HG	2:AF:93:GLN:H	1.53	0.56
5:AZ:50:LEU:O	5:AV:61:ASN:ND2	2.27	0.56
6:R5:19:ASP:OD1	6:R5:19:ASP:N	2.38	0.56
1:g:21:SER:HB2	1:u:49:ARG:HB3	1.87	0.56
1:g:29:ALA:HB1	1:g:190:VAL:HG21	1.87	0.56
1:k:62:ASP:N	1:k:62:ASP:OD2	2.38	0.56
1:1:88:LEU:N	1:1:121:GLY:O	2.39	0.56
1:1:133:GLY:H	1:1:152:VAL:HG23	1.70	0.56
2:AD:140:ASN:HD22	2:AE:18:PRO:HG3	1.71	0.56
2:AG:351:LEU:HD23	2:AG:371:PHE:CE2	2.41	0.56
2:AK:297:HIS:CE1	2:AK:299:LYS:HB2	2.41	0.56
6:R3:19:ASP:OD1	6:R3:19:ASP:N	2.38	0.56
6:U3:173:ASN:CG	6:U3:177:LEU:HB2	2.30	0.56
1:M:156:THR:HG23	1:M:157:SER:H	1.71	0.56
1:X:132:THR:HA	1:X:152:VAL:HG13	1.88	0.56
1:a:75:PHE:CE1	1:a:162:PRO:HD2	2.41	0.56
1:b:21:SER:HB2	1:p:49:ARG:HB3	1.87	0.56
1:p:59:PHE:HE2	1:p:175:ARG:HE	1.53	0.56
1:q:132:THR:HA	1:q:152:VAL:HG23	1.87	0.56
1:u:48:LEU:HD23	1:v:1:MET:HE3	1.87	0.56
1:5:154:PRO:O	1:5:155:THR:HG22	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:PHE:HE1	1:A:162:PRO:HD2	1.71	0.56
1:B:30:ARG:HD2	1:B:230:GLY:H	1.70	0.56
1:F:132:THR:HA	1:F:152:VAL:HG23	1.88	0.56
2:AA:338:ARG:NH2	2:AB:344:ASP:OD2	2.39	0.56
2:AE:396:ILE:HG23	2:AE:400:GLU:HG3	1.88	0.56
2:AG:127:MET:HB2	2:AG:196:ILE:HB	1.88	0.56
2:AJ:297:HIS:HE1	2:AJ:299:LYS:HB2	1.70	0.56
3:AN:49:GLN:CD	3:AN:49:GLN:H	2.13	0.56
1:N:3:PHE:HD1	1:N:38:MET:HE2	1.72	0.55
1:W:74:ALA:HB2	1:W:91:LEU:HD11	1.88	0.55
1:t:88:LEU:N	1:t:121:GLY:O	2.38	0.55
2:AB:167:ASP:N	2:AC:28:ARG:HH12	2.00	0.55
2:AC:28:ARG:HG3	2:AC:29:ARG:N	2.21	0.55
2:AE:169:ALA:HB2	2:AF:28:ARG:HG3	1.87	0.55
2:AH:100:ILE:HD11	2:AH:141:ALA:HA	1.86	0.55
2:AH:154:PHE:HA	2:AH:160:VAL:HA	1.88	0.55
2:AI:195:MET:HA	2:AI:195:MET:HE3	1.87	0.55
2:AI:396:ILE:HG23	2:AI:400:GLU:HG3	1.88	0.55
5:AZ:40:TYR:OH	5:AZ:89:VAL:HG11	2.06	0.55
6:S4:174:ALA:HA	6:U4:170:LEU:HD22	1.88	0.55
6:T5:32:TYR:HB3	6:T5:152:ILE:HG23	1.87	0.55
1:W:156:THR:HG23	1:W:157:SER:H	1.71	0.55
1:X:38:MET:HG2	1:X:185:LYS:HG2	1.88	0.55
1:c:75:PHE:CE1	1:c:162:PRO:HD2	2.41	0.55
1:j:75:PHE:HE1	1:j:162:PRO:HD2	1.70	0.55
1:l:21:SER:HB2	1:z:49:ARG:HB3	1.89	0.55
1:v:172:ALA:O	1:v:175:ARG:NH1	2.39	0.55
1:2:73:ASN:OD1	1:2:147:GLU:N	2.30	0.55
1:6:75:PHE:CE1	1:6:162:PRO:HD2	2.41	0.55
2:AA:204:ALA:HB3	2:AA:208:ASP:HB2	1.88	0.55
2:AI:363:CYS:SG	2:AI:364:GLY:N	2.79	0.55
2:AJ:243:TRP:HE1	2:AK:291:ASN:ND2	2.03	0.55
2:AJ:267:LYS:HD2	2:AK:237:GLY:HA2	1.88	0.55
2:AL:252:ASP:HA	6:R3:43:TYR:CD1	2.40	0.55
4:AS:38:VAL:HG11	4:AS:81:ILE:HD11	1.87	0.55
6:U4:145:ILE:O	6:U4:146:ILE:C	2.49	0.55
6:T5:166:VAL:O	6:T5:167:ARG:C	2.48	0.55
1:O:79:LYS:HE3	1:O:155:THR:HA	1.86	0.55
1:Q:79:LYS:HE3	1:Q:155:THR:HA	1.87	0.55
1:e:156:THR:HG23	1:e:157:SER:H	1.70	0.55
1:j:25:GLU:OE1	1:j:25:GLU:N	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:26:PHE:O	2:AB:31:PHE:N	2.38	0.55
2:AE:228:MET:O	2:AE:232:ILE:HG13	2.06	0.55
2:AF:55:PRO:HA	2:AG:216:ALA:HB1	1.88	0.55
2:AG:217:ILE:HB	2:AG:309:ILE:HG22	1.89	0.55
2:AG:298:SER:HB3	2:AG:301:PRO:HG2	1.88	0.55
2:AL:161:GLU:HB2	2:AL:179:LYS:HE2	1.88	0.55
4:AQ:84:PHE:HB2	4:AQ:145:ILE:HB	1.89	0.55
4:AR:139:GLU:HB3	4:AR:144:TYR:HE2	1.70	0.55
4:AT:81:ILE:HG22	4:AT:148:ARG:HG3	1.87	0.55
1:Y:71:VAL:HG11	1:Y:141:ILE:HB	1.86	0.55
1:q:154:PRO:O	1:q:155:THR:HG22	2.07	0.55
1:x:206:GLN:OE1	1:x:207:VAL:N	2.40	0.55
1:y:154:PRO:O	1:y:155:THR:HG22	2.07	0.55
1:C:154:PRO:O	1:C:155:THR:HG22	2.07	0.55
2:AG:336:GLU:HG2	2:AG:337:SER:N	2.20	0.55
2:AI:316:PRO:HB2	2:AI:319:LEU:HD23	1.86	0.55
6:S3:33:ARG:HA	6:S3:152:ILE:HD11	1.88	0.55
6:S3:164:MET:HE1	6:T3:163:VAL:HG12	1.88	0.55
5:AY:96:VAL:HG12	5:AY:127:LEU:HB2	1.87	0.55
1:M:203:THR:HG22	1:M:221:CYS:HB3	1.87	0.55
1:P:153:ASP:OD1	1:P:155:THR:N	2.40	0.55
1:W:62:ASP:OD2	1:W:63:GLY:N	2.40	0.55
1:u:59:PHE:HE2	1:u:175:ARG:HE	1.55	0.55
1:v:154:PRO:O	1:v:155:THR:HG22	2.06	0.55
1:3:154:PRO:O	1:3:155:THR:HG22	2.07	0.55
1:0:154:PRO:O	1:0:155:THR:HG22	2.07	0.55
2:AD:90:SER:HG	2:AD:93:GLN:H	1.52	0.55
2:AE:339:LYS:HE3	2:AE:379:LEU:HD22	1.89	0.55
2:AG:282:THR:H	2:AH:249:ARG:HD3	1.70	0.55
2:AI:121:TRP:HB2	2:AI:127:MET:HE3	1.89	0.55
5:AZ:84:GLN:NE2	5:AZ:101:GLU:HB2	2.22	0.55
6:S3:15:HIS:ND1	6:T3:32:TYR:OH	2.39	0.55
6:R5:125:GLN:HE22	6:U5:93:ILE:H	1.54	0.55
1:M:48:LEU:HD23	1:N:1:MET:HE3	1.88	0.55
1:Z:206:GLN:OE1	1:Z:207:VAL:N	2.39	0.55
1:c:38:MET:HE3	1:c:183:VAL:HG21	1.88	0.55
1:i:71:VAL:HG11	1:i:141:ILE:HB	1.88	0.55
1:u:167:PRO:HA	1:u:191:SER:HB3	1.89	0.55
1:C:210:ASP:OD1	1:C:214:ASN:N	2.40	0.55
1:D:154:PRO:O	1:D:155:THR:HG22	2.07	0.55
2:AF:281:GLY:HA2	2:AG:248:SER:HA	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AH:167:ASP:OD1	2:AI:28:ARG:NH1	2.40	0.55
2:AL:347:GLU:HA	2:AL:351:LEU:HD12	1.89	0.55
3:AN:1:MET:HE2	3:AN:66:THR:HG21	1.88	0.55
1:W:154:PRO:O	1:W:155:THR:HG22	2.07	0.55
1:Y:73:ASN:OD1	1:Y:147:GLU:N	2.27	0.55
1:n:132:THR:HG21	1:n:154:PRO:HB3	1.89	0.55
1:r:154:PRO:O	1:r:155:THR:HG22	2.07	0.55
1:E:154:PRO:O	1:E:155:THR:HG22	2.07	0.55
2:AA:145:LEU:HD23	2:AA:150:LEU:HD13	1.88	0.55
2:AA:396:ILE:HG23	2:AA:400:GLU:HG3	1.88	0.55
2:AE:121:TRP:CZ2	2:AE:198:LYS:HD3	2.41	0.55
2:AG:210:GLN:O	2:AG:215:GLN:NE2	2.39	0.55
2:AI:339:LYS:O	2:AI:343:GLU:HG2	2.07	0.55
3:AP:77:VAL:O	3:AP:94:LYS:NZ	2.40	0.55
6:S4:195:PHE:C	6:S4:197:TYR:H	2.15	0.55
6:S5:58:ILE:HD12	6:S5:67:ILE:HD12	1.88	0.55
1:d:209:ILE:HG13	1:d:214:ASN:O	2.07	0.55
1:i:154:PRO:O	1:i:155:THR:HG22	2.07	0.55
1:v:88:LEU:N	1:v:121:GLY:O	2.39	0.55
1:x:46:ALA:HB3	1:x:47:PRO:HD3	1.89	0.55
2:AD:352:THR:HA	2:AD:355:GLU:HG2	1.87	0.55
2:AI:200:SER:OG	2:AI:201:ILE:N	2.40	0.55
2:AL:67:THR:HG21	2:AL:346:ILE:HG13	1.89	0.55
6:S3:58:ILE:HD12	6:S3:67:ILE:HD12	1.88	0.55
6:S3:74:ILE:HG13	6:S3:75:ALA:H	1.72	0.55
4:AT:77:ARG:HD2	4:AT:150:ARG:HD3	1.89	0.55
6:R5:188:SER:C	6:R5:190:ALA:H	2.15	0.55
1:N:30:ARG:HD2	1:N:230:GLY:H	1.72	0.55
1:o:154:PRO:O	1:o:155:THR:HG22	2.07	0.55
1:x:48:LEU:HD23	1:y:1:MET:HE3	1.89	0.55
1:x:156:THR:HG23	1:x:157:SER:H	1.71	0.55
1:4:79:LYS:HE3	1:4:155:THR:HA	1.88	0.55
1:8:75:PHE:CE1	1:8:162:PRO:HD2	2.41	0.55
1:G:154:PRO:O	1:G:155:THR:HG22	2.07	0.55
2:AA:28:ARG:HH11	2:AL:170:GLY:H	1.55	0.55
2:AA:228:MET:O	2:AA:232:ILE:HG13	2.07	0.55
2:AD:182:LYS:HD2	2:AD:186:GLY:O	2.07	0.55
2:AE:363:CYS:SG	2:AE:364:GLY:N	2.79	0.55
2:AK:34:GLY:HA2	2:AK:153:LYS:HE3	1.88	0.55
6:U3:134:ARG:HG2	6:U3:136:CYS:H	1.72	0.55
3:AN:100:ASN:ND2	3:AN:103:GLU:OE1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:154:PRO:O	1:M:155:THR:HG22	2.06	0.55
1:R:154:PRO:O	1:R:155:THR:HG22	2.07	0.55
1:h:75:PHE:CE1	1:h:162:PRO:HD2	2.41	0.55
1:r:210:ASP:OD1	1:r:214:ASN:N	2.37	0.55
1:w:154:PRO:O	1:w:155:THR:HG22	2.07	0.55
1:9:79:LYS:HE3	1:9:155:THR:HA	1.88	0.55
1:C:133:GLY:H	1:C:152:VAL:HG13	1.72	0.55
1:E:209:ILE:HG13	1:E:214:ASN:O	2.08	0.55
2:AE:195:MET:HA	2:AE:195:MET:HE3	1.88	0.55
2:AI:156:ARG:HG3	2:AI:157:TYR:HD1	1.72	0.55
6:R3:157:ASN:ND2	6:S3:161:ASP:OD2	2.40	0.55
5:AY:12:ILE:HG12	5:AY:89:VAL:HG23	1.89	0.55
5:AY:34:ASP:OD1	5:AY:36:THR:HG22	2.07	0.55
1:M:30:ARG:HD2	1:M:230:GLY:H	1.72	0.54
1:j:209:ILE:HG13	1:j:214:ASN:O	2.07	0.54
1:q:21:SER:HB3	1:6:49:ARG:HB3	1.88	0.54
2:AE:204:ALA:HB3	2:AE:208:ASP:HB2	1.88	0.54
2:AI:339:LYS:HE3	2:AI:379:LEU:HD22	1.88	0.54
3:H:85:ARG:HH22	3:H:91:ARG:NH1	2.06	0.54
5:Ab:81:GLY:HA2	5:Ab:104:VAL:HB	1.89	0.54
1:K:153:ASP:OD1	1:K:155:THR:N	2.40	0.54
1:Y:154:PRO:O	1:Y:155:THR:HG22	2.07	0.54
1:e:167:PRO:HA	1:e:191:SER:HB3	1.89	0.54
1:m:75:PHE:CE1	1:m:162:PRO:HD2	2.42	0.54
1:t:154:PRO:O	1:t:155:THR:HG22	2.07	0.54
1:6:210:ASP:HB3	1:6:216:PHE:HE2	1.72	0.54
2:AD:182:LYS:HA	2:AD:188:PRO:HA	1.89	0.54
2:AH:44:ASN:HD22	2:AH:210:GLN:HG2	1.72	0.54
3:AP:44:ALA:HB1	3:AN:97:SER:OG	2.07	0.54
4:AS:13:LEU:O	4:AS:14:PRO:C	2.49	0.54
1:d:88:LEU:N	1:d:121:GLY:O	2.40	0.54
1:d:210:ASP:HB3	1:d:216:PHE:HE2	1.70	0.54
1:m:209:ILE:HG13	1:m:214:ASN:O	2.08	0.54
1:2:136:ARG:HG2	1:2:149:VAL:HG22	1.88	0.54
1:3:75:PHE:CE1	1:3:162:PRO:HD2	2.42	0.54
1:8:154:PRO:O	1:8:155:THR:HG22	2.07	0.54
2:AA:195:MET:HA	2:AA:195:MET:HE3	1.88	0.54
2:AA:210:GLN:O	2:AA:215:GLN:NE2	2.40	0.54
2:AD:252:ASP:HA	6:R5:43:TYR:CD1	2.43	0.54
2:AI:145:LEU:HD23	2:AI:150:LEU:HD13	1.88	0.54
3:AM:97:SER:OG	3:I:44:ALA:HB1	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AX:65:PRO:HD2	4:AX:75:ASN:HD22	1.72	0.54
6:R5:157:ASN:ND2	6:S5:161:ASP:OD2	2.39	0.54
1:S:132:THR:HA	1:S:152:VAL:HG13	1.89	0.54
1:Y:88:LEU:N	1:Y:121:GLY:O	2.41	0.54
1:Z:75:PHE:CE1	1:Z:162:PRO:HD2	2.42	0.54
1:e:154:PRO:O	1:e:155:THR:HG22	2.08	0.54
1:m:38:MET:SD	1:m:185:LYS:NZ	2.80	0.54
1:p:136:ARG:HG2	1:p:149:VAL:HG22	1.90	0.54
1:D:79:LYS:HE3	1:D:155:THR:HA	1.88	0.54
1:F:29:ALA:HB1	1:F:190:VAL:HG21	1.89	0.54
2:AL:100:ILE:HD11	2:AL:141:ALA:HA	1.88	0.54
6:S3:25:THR:OG1	6:S3:26:ASP:N	2.39	0.54
6:S3:62:GLY:O	6:S3:65:GLY:N	2.26	0.54
6:T3:58:ILE:HB	6:T3:126:LEU:HD22	1.89	0.54
6:U4:195:PHE:HD1	6:U4:198:ARG:HE	1.56	0.54
3:I:6:ARG:NH2	6:T5:17:LYS:O	2.40	0.54
1:O:138:TRP:CZ3	1:O:147:GLU:HB3	2.42	0.54
1:a:62:ASP:OD2	1:a:62:ASP:N	2.39	0.54
1:o:138:TRP:CZ3	1:o:147:GLU:HB3	2.43	0.54
1:q:138:TRP:CZ3	1:q:147:GLU:HB3	2.43	0.54
1:t:79:LYS:HE3	1:t:155:THR:HA	1.88	0.54
1:C:75:PHE:CE1	1:C:162:PRO:HD2	2.41	0.54
1:E:132:THR:HA	1:E:152:VAL:HG23	1.90	0.54
2:AF:182:LYS:HE3	2:AF:186:GLY:HA2	1.87	0.54
2:AL:44:ASN:HD22	2:AL:210:GLN:HG2	1.72	0.54
2:AL:182:LYS:HD2	2:AL:186:GLY:O	2.08	0.54
6:T3:67:ILE:HB	6:T3:101:LEU:HB2	1.90	0.54
6:U4:153:ALA:O	6:U4:154:TRP:C	2.51	0.54
6:U4:181:THR:O	6:U4:183:ASN:N	2.41	0.54
6:S5:183:ASN:O	6:S5:187:ILE:HG23	2.07	0.54
1:T:89:SER:C	1:T:91:LEU:H	2.14	0.54
1:o:209:ILE:HD11	1:o:213:GLY:HA2	1.90	0.54
1:1:116:GLU:N	1:1:116:GLU:OE2	2.41	0.54
1:9:118:GLY:N	1:9:122:ALA:O	2.31	0.54
1:0:132:THR:HA	1:0:152:VAL:HG23	1.88	0.54
1:A:209:ILE:HD11	1:A:213:GLY:HA2	1.89	0.54
2:AA:339:LYS:O	2:AA:343:GLU:HG2	2.07	0.54
2:AC:34:GLY:HA2	2:AC:153:LYS:HE3	1.89	0.54
2:AE:89:MET:HE3	2:AE:185:LYS:HB3	1.90	0.54
2:AE:348:PRO:HA	2:AE:352:THR:HG22	1.90	0.54
2:AH:266:THR:HA	2:AH:273:GLY:HA2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:R3:164:MET:HE3	6:R3:168:ASN:ND2	2.02	0.54
5:AV:129:PRO:O	5:AV:130:PRO:C	2.51	0.54
6:R4:157:ASN:ND2	6:S4:161:ASP:OD2	2.40	0.54
6:R4:185:ALA:O	6:R4:186:VAL:C	2.50	0.54
1:K:172:ALA:O	1:K:175:ARG:NH1	2.40	0.54
1:i:153:ASP:HA	1:i:159:LEU:HD23	1.89	0.54
1:q:24:CYS:HB3	1:q:221:CYS:O	2.08	0.54
1:s:161:GLN:HE22	1:s:164:PHE:HE2	1.56	0.54
1:v:59:PHE:HE2	1:v:175:ARG:HE	1.56	0.54
1:A:29:ALA:HB1	1:A:190:VAL:HG21	1.89	0.54
1:D:209:ILE:HD11	1:D:213:GLY:HA2	1.88	0.54
2:AB:297:HIS:HE1	2:AB:299:LYS:HB2	1.71	0.54
2:AC:347:GLU:HA	2:AC:351:LEU:HB2	1.90	0.54
2:AI:297:HIS:HE1	2:AI:299:LYS:HB2	1.71	0.54
6:R3:195:PHE:C	6:R3:197:TYR:H	2.15	0.54
3:AN:20:ASP:N	3:AN:24:ARG:O	2.40	0.54
1:J:206:GLN:OE1	1:J:207:VAL:N	2.41	0.54
1:c:209:ILE:HD11	1:c:213:GLY:HA2	1.89	0.54
1:1:24:CYS:HB3	1:1:221:CYS:O	2.07	0.54
1:2:154:PRO:O	1:2:155:THR:HG22	2.07	0.54
1:4:154:PRO:O	1:4:155:THR:HG22	2.08	0.54
1:6:29:ALA:HB1	1:6:190:VAL:HG21	1.89	0.54
1:7:30:ARG:HD2	1:7:230:GLY:H	1.73	0.54
1:9:154:PRO:O	1:9:155:THR:HG22	2.08	0.54
1:9:206:GLN:OE1	1:9:207:VAL:N	2.41	0.54
1:A:132:THR:HA	1:A:152:VAL:HG23	1.89	0.54
2:AJ:90:SER:HG	2:AJ:93:GLN:H	1.54	0.54
2:AK:96:ALA:O	2:AK:100:ILE:HG12	2.07	0.54
4:AS:7:TYR:OH	4:AX:112:ASP:OD2	2.20	0.54
3:H:44:ALA:HB1	3:AO:97:SER:OG	2.08	0.54
5:Aa:81:GLY:HA2	5:Aa:104:VAL:HB	1.89	0.54
6:T5:67:ILE:HB	6:T5:101:LEU:HB2	1.89	0.54
1:Z:209:ILE:HG13	1:Z:214:ASN:O	2.07	0.54
1:c:210:ASP:OD1	1:c:214:ASN:N	2.36	0.54
1:f:209:ILE:HD11	1:f:213:GLY:HA2	1.88	0.54
1:h:156:THR:HG23	1:h:157:SER:H	1.72	0.54
1:j:154:PRO:O	1:j:155:THR:HG22	2.08	0.54
1:q:24:CYS:HB3	1:q:221:CYS:C	2.33	0.54
1:7:29:ALA:HB1	1:7:190:VAL:HG21	1.89	0.54
1:0:53:LEU:HD23	1:0:182:HIS:HA	1.89	0.54
1:G:138:TRP:CZ3	1:G:147:GLU:HB3	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AD:374:ASP:N	2:AD:374:ASP:OD1	2.39	0.54
2:AH:253:ASP:H	6:R4:198:ARG:HH11	1.55	0.54
2:AI:338:ARG:NH2	2:AJ:344:ASP:OD2	2.40	0.54
2:AK:140:ASN:HD22	2:AL:18:PRO:HG3	1.73	0.54
5:AU:113:ARG:HE	5:Ab:4:ASN:HD21	1.54	0.54
6:U5:147:GLY:O	6:U5:150:LYS:N	2.41	0.54
1:e:79:LYS:HE3	1:e:155:THR:HA	1.89	0.54
1:o:21:SER:HB2	1:4:49:ARG:HB3	1.90	0.54
1:1:154:PRO:O	1:1:155:THR:HG22	2.07	0.54
1:0:209:ILE:HG13	1:0:214:ASN:O	2.08	0.54
2:AA:348:PRO:HA	2:AA:352:THR:HG22	1.90	0.54
2:AC:140:ASN:HD22	2:AD:18:PRO:HG3	1.73	0.54
2:AF:351:LEU:HB3	2:AF:371:PHE:CZ	2.43	0.54
2:AL:266:THR:HA	2:AL:273:GLY:HA2	1.90	0.54
3:AM:18:ASP:OD2	3:AM:18:ASP:N	2.40	0.54
6:S3:144:ILE:HD12	6:S3:144:ILE:H	1.73	0.54
1:M:38:MET:HG2	1:M:185:LYS:HG2	1.90	0.53
1:M:138:TRP:CZ3	1:M:147:GLU:HB3	2.43	0.53
1:N:132:THR:HA	1:N:152:VAL:HG13	1.89	0.53
1:d:154:PRO:O	1:d:155:THR:HG22	2.08	0.53
1:h:210:ASP:OD1	1:h:214:ASN:N	2.39	0.53
1:o:79:LYS:HE3	1:o:155:THR:HA	1.89	0.53
1:r:31:PRO:HD3	1:r:227:GLY:O	2.07	0.53
1:z:167:PRO:HA	1:z:191:SER:HB3	1.90	0.53
1:1:138:TRP:CZ3	1:1:147:GLU:HB3	2.42	0.53
1:7:154:PRO:O	1:7:155:THR:HG22	2.08	0.53
1:B:46:ALA:HB3	1:B:47:PRO:HD3	1.90	0.53
1:B:154:PRO:O	1:B:155:THR:HG22	2.09	0.53
2:AA:121:TRP:HB2	2:AA:127:MET:HE3	1.90	0.53
2:AB:38:ASN:HB2	2:AB:151:LYS:NZ	2.23	0.53
2:AE:156:ARG:HG3	2:AE:157:TYR:HD1	1.73	0.53
2:AH:90:SER:HG	2:AH:93:GLN:H	1.54	0.53
2:AL:154:PHE:HA	2:AL:160:VAL:HA	1.91	0.53
6:S3:74:ILE:HG23	6:S3:131:VAL:HG23	1.90	0.53
4:AS:84:PHE:HB2	4:AS:145:ILE:HB	1.89	0.53
6:T4:80:VAL:HG12	6:T4:91:GLU:HG2	1.89	0.53
3:AO:81:VAL:HB	3:AO:93:PHE:HB2	1.90	0.53
1:L:8:PRO:HG3	6:T5:53:THR:HG21	1.90	0.53
1:R:74:ALA:HB2	1:R:91:LEU:HD11	1.90	0.53
1:n:75:PHE:CE1	1:n:162:PRO:HD2	2.42	0.53
1:3:210:ASP:OD1	1:3:214:ASN:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:8:132:THR:HA	1:8:152:VAL:HG13	1.91	0.53
1:E:138:TRP:CE3	1:E:147:GLU:HB3	2.42	0.53
1:L:154:PRO:HG2	1:L:156:THR:HG22	1.90	0.53
1:d:153:ASP:HA	1:d:159:LEU:HD23	1.90	0.53
1:g:73:ASN:HB3	1:g:164:PHE:HE1	1.74	0.53
1:1:172:ALA:O	1:1:175:ARG:NH1	2.42	0.53
1:E:56:LYS:HB3	1:E:207:VAL:HG11	1.90	0.53
2:AE:182:LYS:HD2	2:AE:186:GLY:O	2.09	0.53
2:AJ:351:LEU:HB3	2:AJ:371:PHE:CZ	2.43	0.53
5:AV:87:VAL:HG12	5:AV:99:LEU:HB3	1.89	0.53
6:R4:188:SER:O	6:R4:190:ALA:N	2.41	0.53
5:AY:6:GLN:NE2	4:AX:128:THR:OG1	2.41	0.53
6:S5:195:PHE:C	6:S5:197:TYR:H	2.16	0.53
1:T:206:GLN:OE1	1:T:207:VAL:N	2.41	0.53
1:m:138:TRP:CZ3	1:m:147:GLU:HB3	2.43	0.53
1:s:75:PHE:CE1	1:s:162:PRO:HD2	2.43	0.53
2:AB:95:LYS:O	2:AB:99:GLN:HG2	2.08	0.53
2:AC:282:THR:HA	2:AD:249:ARG:NH1	2.23	0.53
2:AD:100:ILE:HD12	2:AD:103:ARG:O	2.08	0.53
2:AG:372:ASP:O	2:AG:375:SER:OG	2.22	0.53
2:AH:271:ASP:HB3	6:U4:66:LYS:HD2	1.90	0.53
3:AM:1:MET:HE2	3:AM:66:THR:HG21	1.89	0.53
4:AR:50:LEU:HD23	4:AR:52:PHE:HE1	1.73	0.53
6:R3:188:SER:C	6:R3:190:ALA:H	2.14	0.53
5:AV:34:ASP:OD1	5:AV:36:THR:HG22	2.09	0.53
5:AV:96:VAL:HG12	5:AV:127:LEU:HB2	1.90	0.53
1:M:74:ALA:HB2	1:M:91:LEU:HD11	1.90	0.53
1:Q:8:PRO:HG3	6:T3:53:THR:HG21	1.91	0.53
1:a:38:MET:HG2	1:a:185:LYS:HG2	1.89	0.53
1:k:138:TRP:CZ3	1:k:147:GLU:HB3	2.43	0.53
1:p:210:ASP:OD1	1:p:214:ASN:N	2.40	0.53
1:s:161:GLN:NE2	1:s:164:PHE:HE2	2.06	0.53
1:t:21:SER:HB2	1:9:49:ARG:HB3	1.89	0.53
1:1:48:LEU:HD23	1:2:1:MET:HE3	1.90	0.53
1:7:138:TRP:CZ3	1:7:147:GLU:HB3	2.43	0.53
1:0:59:PHE:HE2	1:0:175:ARG:HE	1.56	0.53
2:AJ:55:PRO:HA	2:AK:216:ALA:HB1	1.90	0.53
6:S3:7:LEU:HD21	6:S3:12:ILE:HG13	1.91	0.53
6:U3:19:ASP:O	6:U3:20:ASP:C	2.48	0.53
6:R4:191:GLN:HA	6:R4:194:TRP:CZ3	2.44	0.53
6:S4:72:THR:O	6:S4:73:PRO:C	2.52	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S4:183:ASN:O	6:S4:187:ILE:HG23	2.08	0.53
1:T:111:SER:OG	1:T:135:ASP:OD1	2.21	0.53
1:V:172:ALA:O	1:V:175:ARG:NH1	2.42	0.53
1:h:125:TYR:OH	1:h:135:ASP:OD2	2.21	0.53
1:s:46:ALA:HB3	1:s:47:PRO:HD3	1.91	0.53
1:u:210:ASP:OD1	1:u:214:ASN:N	2.39	0.53
1:w:29:ALA:HB1	1:w:190:VAL:HG21	1.90	0.53
1:y:53:LEU:HD23	1:y:182:HIS:HA	1.90	0.53
1:4:133:GLY:H	1:4:152:VAL:HG13	1.73	0.53
2:AG:282:THR:N	2:AH:249:ARG:HD3	2.23	0.53
2:AH:68:VAL:HG11	2:AH:118:ALA:CB	2.38	0.53
2:AL:100:ILE:HD12	2:AL:103:ARG:O	2.08	0.53
1:o:53:LEU:HD23	1:o:182:HIS:HA	1.90	0.53
1:1:207:VAL:HG12	1:1:217:VAL:HG22	1.91	0.53
1:3:210:ASP:HB3	1:3:216:PHE:CE2	2.34	0.53
1:E:209:ILE:HD11	1:E:213:GLY:HA2	1.90	0.53
1:G:46:ALA:HB3	1:G:47:PRO:HD3	1.89	0.53
2:AD:351:LEU:HB3	2:AD:371:PHE:CZ	2.44	0.53
2:AE:145:LEU:HD23	2:AE:150:LEU:HD13	1.91	0.53
2:AH:347:GLU:HA	2:AH:351:LEU:HD12	1.90	0.53
6:S3:154:TRP:CH2	6:S3:187:ILE:HD11	2.44	0.53
6:R4:73:PRO:O	6:R4:132:THR:HA	2.09	0.53
6:R5:13:ARG:NH2	6:R5:24:VAL:O	2.36	0.53
1:Y:209:ILE:HG13	1:Y:214:ASN:O	2.08	0.53
1:b:126:THR:O	1:b:126:THR:OG1	2.27	0.53
1:i:134:VAL:HG11	1:i:162:PRO:HG3	1.91	0.53
1:v:138:TRP:CZ3	1:v:147:GLU:HB3	2.44	0.53
1:7:46:ALA:HB3	1:7:47:PRO:HD3	1.90	0.53
1:D:210:ASP:HB3	1:D:216:PHE:HE2	1.73	0.53
2:AE:339:LYS:O	2:AE:343:GLU:HG2	2.09	0.53
6:T3:132:THR:HG22	6:T3:133:GLY:N	2.24	0.53
3:AN:18:ASP:OD2	3:AN:18:ASP:N	2.40	0.53
6:S5:164:MET:HE1	6:T5:163:VAL:HG12	1.91	0.53
1:J:138:TRP:CZ3	1:J:147:GLU:HB3	2.43	0.53
1:O:180:ARG:HH22	6:R3:124:SER:N	2.07	0.53
1:h:38:MET:SD	1:h:185:LYS:NZ	2.82	0.53
1:3:132:THR:HA	1:3:152:VAL:HG13	1.91	0.53
1:8:133:GLY:H	1:8:152:VAL:HG13	1.73	0.53
1:E:53:LEU:HD23	1:E:182:HIS:HA	1.91	0.53
2:AA:216:ALA:HB1	2:AL:55:PRO:HA	1.90	0.53
2:AC:243:TRP:CZ2	2:AD:289:MET:HG3	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AF:28:ARG:HD3	2:AF:29:ARG:HG2	1.90	0.53
2:AF:95:LYS:O	2:AF:99:GLN:HG2	2.08	0.53
2:AH:363:CYS:SG	2:AH:364:GLY:N	2.81	0.53
2:AH:374:ASP:OD1	2:AH:374:ASP:N	2.40	0.53
2:AJ:95:LYS:O	2:AJ:99:GLN:HG2	2.09	0.53
3:AP:85:ARG:HH22	3:AP:91:ARG:NH1	2.07	0.53
6:S4:25:THR:OG1	6:S4:26:ASP:N	2.40	0.53
6:U4:143:GLY:HA3	6:U4:197:TYR:OH	2.09	0.53
4:AX:40:ASP:OD2	4:AX:41:ASP:N	2.42	0.53
1:N:73:ASN:HB2	1:N:164:PHE:HE1	1.74	0.53
1:h:138:TRP:CZ3	1:h:147:GLU:HB3	2.44	0.53
1:j:206:GLN:OE1	1:j:207:VAL:N	2.41	0.53
1:k:38:MET:HG2	1:k:185:LYS:HG2	1.91	0.53
1:t:29:ALA:HB1	1:t:190:VAL:HG21	1.90	0.53
2:AB:55:PRO:HA	2:AC:216:ALA:HB1	1.90	0.53
2:AD:347:GLU:HA	2:AD:351:LEU:HD12	1.90	0.53
2:AF:38:ASN:HB2	2:AF:151:LYS:HZ3	1.74	0.53
2:AH:260:LYS:HD2	6:R4:201:LEU:HD23	1.89	0.53
2:AL:374:ASP:N	2:AL:374:ASP:OD1	2.40	0.53
5:AU:34:ASP:OD1	5:AU:36:THR:HG22	2.09	0.53
4:AT:40:ASP:OD2	4:AT:41:ASP:N	2.42	0.53
6:U4:54:ILE:HD11	6:U4:130:TYR:CZ	2.44	0.53
6:T5:141:PRO:HD2	6:T5:144:ILE:HD12	1.91	0.53
1:a:154:PRO:O	1:a:155:THR:HG22	2.09	0.52
1:g:75:PHE:HE1	1:g:162:PRO:HD2	1.73	0.52
1:r:73:ASN:OD1	1:r:147:GLU:N	2.31	0.52
1:t:75:PHE:HE1	1:t:162:PRO:HD2	1.73	0.52
1:v:207:VAL:HG12	1:v:217:VAL:HG22	1.90	0.52
1:0:138:TRP:CE3	1:0:147:GLU:HB3	2.44	0.52
2:AA:140:ASN:HD22	2:AB:18:PRO:HG3	1.73	0.52
2:AE:154:PHE:HA	2:AE:160:VAL:HA	1.91	0.52
2:AF:297:HIS:HE1	2:AF:299:LYS:HB2	1.73	0.52
2:AI:348:PRO:HA	2:AI:352:THR:HG22	1.89	0.52
6:U3:175:GLN:O	6:U3:177:LEU:N	2.40	0.52
1:J:62:ASP:OD2	1:J:62:ASP:N	2.42	0.52
1:U:209:ILE:HG13	1:U:214:ASN:O	2.10	0.52
1:X:73:ASN:HB2	1:X:164:PHE:HE1	1.73	0.52
1:Z:167:PRO:HA	1:Z:191:SER:HB3	1.91	0.52
1:c:210:ASP:HB3	1:c:216:PHE:HE2	1.74	0.52
1:f:29:ALA:HB1	1:f:190:VAL:HG21	1.91	0.52
1:f:154:PRO:O	1:f:155:THR:HG22	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:o:75:PHE:HE1	1:o:162:PRO:HD2	1.74	0.52
2:AB:219:VAL:HB	2:AB:220:PRO:HD3	1.91	0.52
2:AI:140:ASN:HD22	2:AJ:18:PRO:HG3	1.75	0.52
2:AL:363:CYS:SG	2:AL:364:GLY:N	2.82	0.52
6:T3:13:ARG:NH2	6:T3:26:ASP:OD1	2.32	0.52
5:AY:129:PRO:O	5:AY:130:PRO:C	2.52	0.52
4:AX:139:GLU:HB3	4:AX:144:TYR:HE2	1.74	0.52
3:I:85:ARG:HH22	3:I:91:ARG:NH1	2.06	0.52
6:U5:151:LEU:HD13	6:U5:185:ALA:HB2	1.90	0.52
1:Q:154:PRO:HG2	1:Q:156:THR:HG22	1.91	0.52
1:g:75:PHE:CE1	1:g:162:PRO:HD2	2.45	0.52
1:r:194:ALA:HB1	1:r:226:ILE:HG21	1.91	0.52
1:s:48:LEU:HD23	1:t:1:MET:HE3	1.92	0.52
1:v:168:VAL:HG11	1:v:224:ILE:HD13	1.91	0.52
1:3:133:GLY:H	1:3:152:VAL:HG13	1.73	0.52
1:6:133:GLY:H	1:6:152:VAL:HG23	1.74	0.52
2:AB:253:ASP:OD2	6:T5:198:ARG:NE	2.42	0.52
2:AD:154:PHE:HA	2:AD:160:VAL:HA	1.90	0.52
2:AD:402:ARG:HH21	2:AD:407:TRP:HB3	1.74	0.52
2:AF:168:GLU:HG2	2:AF:169:ALA:H	1.74	0.52
2:AF:267:LYS:HD2	2:AG:237:GLY:HA2	1.91	0.52
2:AI:89:MET:HE3	2:AI:185:LYS:HB3	1.91	0.52
2:AK:37:LYS:NZ	2:AK:38:ASN:O	2.41	0.52
2:AL:204:ALA:HB3	2:AL:208:ASP:HB2	1.91	0.52
3:AP:4:ALA:HB2	6:U4:159:PRO:CD	2.39	0.52
3:H:77:VAL:O	3:H:94:LYS:NZ	2.42	0.52
6:T4:6:LEU:HD22	6:T4:140:VAL:HG11	1.91	0.52
6:U4:173:ASN:O	6:U4:174:ALA:HB2	2.08	0.52
1:L:208:ALA:HB3	1:L:216:PHE:HB2	1.92	0.52
1:O:154:PRO:O	1:O:155:THR:HG22	2.10	0.52
1:T:56:LYS:HB3	1:T:207:VAL:HG11	1.92	0.52
1:T:154:PRO:O	1:T:155:THR:HG22	2.10	0.52
1:U:172:ALA:O	1:U:175:ARG:NH1	2.41	0.52
1:d:154:PRO:HG2	1:d:156:THR:HG22	1.91	0.52
1:e:75:PHE:CE1	1:e:162:PRO:HD2	2.44	0.52
1:n:46:ALA:HB3	1:n:47:PRO:HD3	1.90	0.52
1:p:167:PRO:HA	1:p:191:SER:HB3	1.92	0.52
1:u:104:ILE:HG12	1:u:117:LEU:HD13	1.91	0.52
1:w:136:ARG:HG2	1:w:149:VAL:HG22	1.91	0.52
1:y:138:TRP:CZ3	1:y:147:GLU:HB3	2.44	0.52
2:AA:89:MET:HE3	2:AA:185:LYS:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AA:363:CYS:SG	2:AA:364:GLY:N	2.82	0.52
2:AB:156:ARG:HG3	2:AB:157:TYR:HD1	1.75	0.52
2:AG:267:LYS:HD2	2:AH:237:GLY:HA2	1.91	0.52
2:AH:100:ILE:HD12	2:AH:103:ARG:O	2.09	0.52
2:AH:351:LEU:HB3	2:AH:371:PHE:CZ	2.45	0.52
2:AJ:156:ARG:HG3	2:AJ:157:TYR:HD1	1.74	0.52
3:AM:6:ARG:HA	3:AM:38:ALA:HB2	1.92	0.52
1:T:138:TRP:CZ3	1:T:147:GLU:HB3	2.44	0.52
1:l:126:THR:O	1:l:126:THR:OG1	2.27	0.52
1:q:99:GLN:N	1:q:99:GLN:OE1	2.42	0.52
1:x:161:GLN:NE2	1:x:164:PHE:HE2	2.07	0.52
1:y:79:LYS:HE3	1:y:155:THR:HA	1.92	0.52
1:5:138:TRP:CE3	1:5:147:GLU:HB3	2.45	0.52
2:AE:121:TRP:HB2	2:AE:127:MET:HE3	1.91	0.52
2:AG:140:ASN:HD22	2:AH:18:PRO:HG3	1.74	0.52
2:AI:210:GLN:O	2:AI:215:GLN:NE2	2.43	0.52
2:AJ:219:VAL:HB	2:AJ:220:PRO:HD3	1.91	0.52
6:T4:43:TYR:HE2	6:T4:194:TRP:HB2	1.75	0.52
6:T4:78:PRO:HB3	6:T4:91:GLU:HB3	1.91	0.52
1:K:38:MET:HG2	1:K:185:LYS:HG2	1.91	0.52
1:O:89:SER:C	1:O:91:LEU:H	2.17	0.52
1:S:75:PHE:HE1	1:S:162:PRO:HD2	1.74	0.52
1:e:138:TRP:CZ3	1:e:147:GLU:HB3	2.45	0.52
1:g:88:LEU:N	1:g:121:GLY:O	2.42	0.52
1:j:167:PRO:HA	1:j:191:SER:HB3	1.92	0.52
1:y:21:SER:HB2	1:D:49:ARG:HB3	1.90	0.52
6:T3:168:ASN:OD1	6:U4:162:GLU:HA	2.10	0.52
6:S4:3:LEU:O	6:S4:6:LEU:N	2.43	0.52
6:T4:67:ILE:HB	6:T4:101:LEU:HB2	1.91	0.52
1:c:209:ILE:HG13	1:c:214:ASN:O	2.10	0.52
1:q:29:ALA:HB1	1:q:190:VAL:HG21	1.92	0.52
1:v:180:ARG:HG2	1:v:180:ARG:HH11	1.75	0.52
1:w:210:ASP:OD1	1:w:214:ASN:N	2.37	0.52
2:AA:121:TRP:CZ2	2:AA:198:LYS:HD3	2.45	0.52
2:AA:182:LYS:HD2	2:AA:186:GLY:O	2.10	0.52
2:AC:121:TRP:CZ2	2:AC:198:LYS:HD3	2.45	0.52
2:AF:243:TRP:NE1	2:AG:291:ASN:HD21	2.07	0.52
2:AG:192:TYR:HE2	2:AG:194:PHE:HE1	1.57	0.52
2:AI:339:LYS:HZ1	2:AI:379:LEU:HD13	1.75	0.52
3:AM:103:GLU:HG2	3:I:41:PRO:HD3	1.92	0.52
6:S3:183:ASN:O	6:S3:187:ILE:HG23	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S5:154:TRP:CH2	6:S5:187:ILE:HD11	2.44	0.52
1:a:210:ASP:OD1	1:a:214:ASN:N	2.42	0.52
1:j:138:TRP:CZ3	1:j:147:GLU:HB3	2.45	0.52
1:n:210:ASP:OD1	1:n:214:ASN:N	2.40	0.52
1:r:59:PHE:CD1	1:r:204:VAL:HG12	2.45	0.52
1:t:53:LEU:HD23	1:t:182:HIS:HA	1.91	0.52
1:6:132:THR:HA	1:6:152:VAL:HG23	1.91	0.52
1:B:88:LEU:N	1:B:121:GLY:O	2.43	0.52
1:B:126:THR:O	1:B:126:THR:OG1	2.26	0.52
2:AA:92:SER:HA	2:AA:95:LYS:HE2	1.90	0.52
2:AE:25:ILE:O	2:AE:28:ARG:HG2	2.09	0.52
2:AG:264:GLU:O	2:AG:267:LYS:HG3	2.09	0.52
2:AI:317:ILE:H	2:AI:317:ILE:HD12	1.75	0.52
4:AT:65:PRO:HD2	4:AT:75:ASN:HD22	1.75	0.52
6:S4:154:TRP:CH2	6:S4:187:ILE:HD11	2.44	0.52
5:Ab:40:TYR:OH	5:Ab:89:VAL:HG11	2.09	0.52
6:U5:41:GLU:HG2	6:U5:48:PHE:CE1	2.45	0.52
1:T:115:VAL:HG22	1:T:125:TYR:HD2	1.75	0.52
1:j:79:LYS:HE3	1:j:155:THR:HA	1.91	0.52
1:r:153:ASP:HA	1:r:159:LEU:HD23	1.92	0.52
1:x:154:PRO:O	1:x:155:THR:HG22	2.10	0.52
1:z:104:ILE:HG12	1:z:117:LEU:HD13	1.92	0.52
1:9:210:ASP:HB3	1:9:216:PHE:HE2	1.75	0.52
1:G:29:ALA:HB1	1:G:190:VAL:HG21	1.90	0.52
1:G:172:ALA:O	1:G:175:ARG:NH1	2.43	0.52
2:AL:39:VAL:HG23	2:AL:40:VAL:HG13	1.92	0.52
2:AL:402:ARG:HH21	2:AL:407:TRP:HB3	1.75	0.52
3:AN:6:ARG:HA	3:AN:38:ALA:HB2	1.91	0.52
6:S5:19:ASP:OD1	6:S5:19:ASP:N	2.43	0.52
6:T5:72:THR:O	6:T5:132:THR:HG23	2.09	0.52
1:f:210:ASP:OD1	1:f:214:ASN:N	2.43	0.52
1:r:53:LEU:HD23	1:r:182:HIS:HA	1.92	0.52
1:s:154:PRO:O	1:s:155:THR:HG22	2.10	0.52
1:2:153:ASP:HA	1:2:159:LEU:HD23	1.91	0.52
1:3:209:ILE:HG13	1:3:214:ASN:O	2.10	0.52
1:5:209:ILE:HG13	1:5:214:ASN:O	2.10	0.52
2:AA:317:ILE:H	2:AA:317:ILE:HD12	1.75	0.52
2:AC:148:PRO:HG2	2:AD:202:ASN:HB3	1.92	0.52
2:AJ:350:TYR:C	2:AJ:353:PRO:HD2	2.35	0.52
2:AK:347:GLU:HG2	2:AK:351:LEU:HD22	1.91	0.52
6:U3:181:THR:O	6:U3:183:ASN:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AN:15:GLN:OE1	3:AN:80:TRP:NE1	2.39	0.52
5:AV:128:LEU:O	5:AV:129:PRO:C	2.52	0.52
5:Ab:84:GLN:NE2	5:Ab:101:GLU:HB2	2.24	0.52
1:L:3:PHE:CD2	6:S5:77:ARG:HG2	2.44	0.51
1:d:71:VAL:HG11	1:d:141:ILE:HB	1.91	0.51
1:d:134:VAL:HG11	1:d:162:PRO:HG3	1.92	0.51
1:g:132:THR:HA	1:g:152:VAL:HG23	1.92	0.51
1:m:101:GLU:OE1	1:m:101:GLU:N	2.44	0.51
1:r:138:TRP:CZ3	1:r:147:GLU:HB3	2.45	0.51
1:y:75:PHE:HE1	1:y:162:PRO:HD2	1.75	0.51
1:7:75:PHE:CE1	1:7:162:PRO:HD2	2.45	0.51
1:G:88:LEU:N	1:G:121:GLY:O	2.43	0.51
2:AH:257:LYS:O	2:AH:261:GLU:HG2	2.10	0.51
2:AL:252:ASP:HA	6:R3:43:TYR:HD1	1.74	0.51
3:AP:86:LEU:HD12	6:U4:19:ASP:HA	1.91	0.51
5:AZ:4:ASN:HD21	5:AV:113:ARG:HE	1.56	0.51
3:AN:45:ILE:N	3:H:97:SER:OG	2.42	0.51
3:H:26:LEU:HD13	4:AX:93:ASP:OD2	2.10	0.51
6:S4:7:LEU:HD21	6:S4:12:ILE:HG13	1.92	0.51
1:Y:210:ASP:HB3	1:Y:216:PHE:HE2	1.74	0.51
1:c:101:GLU:OE1	1:c:101:GLU:N	2.43	0.51
1:k:154:PRO:O	1:k:155:THR:HG22	2.10	0.51
1:m:210:ASP:HB3	1:m:216:PHE:HE2	1.76	0.51
1:q:59:PHE:HE2	1:q:175:ARG:HE	1.58	0.51
1:u:73:ASN:HB3	1:u:164:PHE:HE1	1.75	0.51
1:2:29:ALA:HB1	1:2:190:VAL:HG21	1.92	0.51
1:3:174:ARG:CZ	1:3:187:VAL:HG21	2.40	0.51
2:AA:56:VAL:HB	2:AA:309:ILE:HD11	1.91	0.51
2:AF:156:ARG:HG3	2:AF:157:TYR:HD1	1.75	0.51
2:AG:148:PRO:HG2	2:AH:202:ASN:HB3	1.92	0.51
2:AG:347:GLU:HA	2:AG:351:LEU:HB2	1.91	0.51
2:AK:264:GLU:O	2:AK:267:LYS:HG3	2.10	0.51
2:AL:297:HIS:CE1	2:AL:299:LYS:HB2	2.43	0.51
4:AS:13:LEU:HB2	4:AS:14:PRO:HD3	1.92	0.51
6:R4:43:TYR:CD2	6:R4:44:THR:HG23	2.45	0.51
3:AO:49:GLN:HB3	3:I:76:SER:HB2	1.91	0.51
6:S5:15:HIS:ND1	6:T5:32:TYR:OH	2.40	0.51
1:K:209:ILE:HG13	1:K:214:ASN:O	2.10	0.51
1:z:136:ARG:HG2	1:z:149:VAL:HG22	1.92	0.51
1:C:132:THR:HA	1:C:152:VAL:HG13	1.92	0.51
2:AD:348:PRO:HA	2:AD:352:THR:HG22	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AE:217:ILE:HB	2:AE:309:ILE:HG22	1.92	0.51
2:AH:317:ILE:H	2:AH:317:ILE:HD12	1.75	0.51
5:AZ:117:MET:HE2	5:AZ:119:ILE:HD11	1.92	0.51
6:U3:54:ILE:HD11	6:U3:130:TYR:CZ	2.46	0.51
6:R4:20:ASP:OD1	6:R4:20:ASP:N	2.35	0.51
6:T4:72:THR:O	6:T4:132:THR:HG23	2.10	0.51
3:AO:20:ASP:N	3:AO:24:ARG:O	2.41	0.51
1:h:138:TRP:CE3	1:h:147:GLU:HB3	2.45	0.51
1:1:59:PHE:HE2	1:1:175:ARG:HE	1.57	0.51
1:6:209:ILE:HG13	1:6:214:ASN:O	2.11	0.51
1:7:75:PHE:HE1	1:7:162:PRO:HD2	1.75	0.51
1:F:99:GLN:CD	1:F:99:GLN:H	2.19	0.51
1:G:209:ILE:HD11	1:G:213:GLY:HA2	1.92	0.51
2:AA:372:ASP:HB2	2:AA:374:ASP:OD1	2.10	0.51
2:AB:163:PHE:HB2	2:AB:174:ILE:HG13	1.93	0.51
2:AB:347:GLU:HB3	2:AB:348:PRO:HD3	1.92	0.51
5:Aa:84:GLN:NE2	5:Aa:101:GLU:HB2	2.24	0.51
6:R4:173:ASN:C	6:R4:175:GLN:N	2.67	0.51
6:S4:164:MET:HE1	6:T4:163:VAL:HG12	1.91	0.51
3:I:48:SER:O	3:I:49:GLN:C	2.53	0.51
6:U5:181:THR:O	6:U5:183:ASN:N	2.43	0.51
1:J:154:PRO:O	1:J:155:THR:HG22	2.11	0.51
1:V:8:PRO:HG3	6:T4:53:THR:HG21	1.91	0.51
1:n:154:PRO:O	1:n:155:THR:HG22	2.10	0.51
1:4:138:TRP:CH2	1:4:192:PRO:HD2	2.45	0.51
1:D:178:ASP:OD2	1:D:181:THR:OG1	2.21	0.51
2:AA:18:PRO:HG3	2:AL:140:ASN:HD22	1.76	0.51
2:AB:127:MET:HE1	2:AB:354:LEU:HD12	1.92	0.51
2:AB:134:MET:SD	2:AB:138:SER:OG	2.69	0.51
2:AC:348:PRO:HA	2:AC:352:THR:HG22	1.93	0.51
2:AF:347:GLU:HB3	2:AF:348:PRO:HD3	1.92	0.51
3:AM:49:GLN:HB3	3:AP:76:SER:HB2	1.92	0.51
3:AP:48:SER:O	3:AP:49:GLN:C	2.54	0.51
6:T3:78:PRO:HB3	6:T3:91:GLU:HB3	1.91	0.51
3:AN:16:GLN:OE1	3:AN:28:THR:OG1	2.24	0.51
4:AT:55:VAL:HG22	4:AT:82:VAL:HG22	1.91	0.51
6:U4:184:GLY:C	6:U4:186:VAL:N	2.69	0.51
5:AY:63:THR:HG22	5:AY:120:VAL:HG22	1.92	0.51
1:n:161:GLN:HE22	1:n:164:PHE:HE2	1.59	0.51
1:u:154:PRO:O	1:u:155:THR:HG22	2.11	0.51
1:y:138:TRP:CE3	1:y:147:GLU:HB3	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:75:PHE:HE1	1:6:162:PRO:HD2	1.74	0.51
2:AB:168:GLU:HG2	2:AB:169:ALA:H	1.74	0.51
2:AC:264:GLU:O	2:AC:267:LYS:HG3	2.11	0.51
2:AD:317:ILE:H	2:AD:317:ILE:HD12	1.75	0.51
2:AE:280:ALA:HB1	6:T4:198:ARG:NH1	2.26	0.51
2:AG:317:ILE:HD12	2:AG:317:ILE:H	1.76	0.51
2:AI:372:ASP:HB2	2:AI:374:ASP:OD1	2.11	0.51
2:AJ:168:GLU:HG2	2:AJ:169:ALA:H	1.74	0.51
2:AJ:253:ASP:OD2	6:T3:198:ARG:NE	2.43	0.51
2:AJ:376:ILE:HG21	2:AJ:379:LEU:HD23	1.93	0.51
2:AL:351:LEU:HB3	2:AL:371:PHE:CZ	2.45	0.51
5:AU:30:HIS:NE2	5:AU:79:TYR:OH	2.34	0.51
6:R3:166:VAL:HG11	6:T3:177:LEU:HD13	1.91	0.51
1:n:73:ASN:HB3	1:n:164:PHE:HE1	1.76	0.51
1:z:154:PRO:O	1:z:155:THR:HG22	2.11	0.51
1:B:75:PHE:CE1	1:B:162:PRO:HD2	2.45	0.51
1:B:138:TRP:CZ3	1:B:147:GLU:HB3	2.46	0.51
1:G:75:PHE:CE1	1:G:162:PRO:HD2	2.46	0.51
2:AE:210:GLN:O	2:AE:215:GLN:NE2	2.43	0.51
2:AE:317:ILE:H	2:AE:317:ILE:HD12	1.74	0.51
2:AF:29:ARG:C	2:AF:31:PHE:N	2.68	0.51
2:AH:44:ASN:ND2	2:AH:210:GLN:HG2	2.26	0.51
3:AM:20:ASP:N	3:AM:24:ARG:O	2.42	0.51
3:AN:46:ARG:NE	3:H:77:VAL:HG23	2.25	0.51
3:H:106:ARG:HH21	6:S4:17:LYS:HZ1	1.58	0.51
6:U4:190:ALA:C	6:U4:192:ASP:H	2.19	0.51
1:S:13:SER:O	1:S:13:SER:OG	2.29	0.51
1:S:100:VAL:HA	1:S:142:ASN:HD21	1.75	0.51
1:V:153:ASP:OD1	1:V:155:THR:N	2.44	0.51
1:a:75:PHE:HB2	1:a:164:PHE:CZ	2.46	0.51
1:f:138:TRP:CZ3	1:f:147:GLU:HB3	2.46	0.51
1:p:154:PRO:O	1:p:155:THR:HG22	2.11	0.51
1:x:75:PHE:CE1	1:x:162:PRO:HD2	2.46	0.51
1:x:161:GLN:HE22	1:x:164:PHE:HE2	1.59	0.51
1:D:138:TRP:CH2	1:D:192:PRO:HD2	2.46	0.51
2:AA:183:ASN:N	2:AA:187:ARG:O	2.37	0.51
2:AB:153:LYS:HZ1	2:AB:161:GLU:HB2	1.76	0.51
2:AE:183:ASN:N	2:AE:187:ARG:O	2.36	0.51
2:AF:350:TYR:C	2:AF:353:PRO:HD2	2.35	0.51
2:AI:183:ASN:OD1	2:AI:184:ASP:N	2.43	0.51
2:AK:55:PRO:HA	2:AL:216:ALA:HB1	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:R4:188:SER:C	6:R4:190:ALA:N	2.62	0.51
6:S4:144:ILE:H	6:S4:144:ILE:HD12	1.76	0.51
1:1:24:CYS:HB3	1:1:221:CYS:C	2.35	0.51
1:8:210:ASP:OD1	1:8:214:ASN:N	2.42	0.51
2:AE:92:SER:HA	2:AE:95:LYS:HE2	1.92	0.51
2:AK:352:THR:HA	2:AK:355:GLU:HG2	1.92	0.51
6:R3:125:GLN:HE22	6:U3:93:ILE:H	1.58	0.51
3:I:99:VAL:HG13	3:I:109:LYS:HB3	1.93	0.51
6:U5:170:LEU:HD23	6:U5:170:LEU:H	1.76	0.51
1:b:194:ALA:HB1	1:b:226:ILE:HG21	1.93	0.51
1:k:75:PHE:HB2	1:k:164:PHE:CZ	2.46	0.51
1:m:78:THR:HB	1:m:84:PHE:HD2	1.75	0.51
1:n:161:GLN:NE2	1:n:164:PHE:HE2	2.07	0.51
1:s:206:GLN:OE1	1:s:207:VAL:N	2.44	0.51
1:v:29:ALA:HB1	1:v:190:VAL:HG21	1.93	0.51
1:2:138:TRP:CZ3	1:2:147:GLU:HB3	2.45	0.51
1:B:177:VAL:O	1:B:179:PRO:HD3	2.10	0.51
1:G:38:MET:SD	1:G:185:LYS:HE2	2.51	0.51
1:G:75:PHE:HE1	1:G:162:PRO:HD2	1.76	0.51
2:AA:312:ASN:HD22	2:AL:59:ARG:HB2	1.76	0.51
2:AD:182:LYS:HD3	2:AD:188:PRO:HG3	1.93	0.51
2:AF:217:ILE:HB	2:AF:309:ILE:HG22	1.93	0.51
2:AH:297:HIS:CE1	2:AH:299:LYS:HB2	2.43	0.51
2:AI:25:ILE:O	2:AI:28:ARG:NE	2.44	0.51
2:AJ:347:GLU:HB3	2:AJ:348:PRO:HD3	1.92	0.51
2:AL:183:ASN:OD1	2:AL:184:ASP:N	2.42	0.51
5:Ab:30:HIS:HE2	5:Ab:79:TYR:HH	1.57	0.51
6:S5:25:THR:OG1	6:S5:26:ASP:N	2.41	0.51
6:U5:54:ILE:HD11	6:U5:130:TYR:CZ	2.46	0.51
1:K:116:GLU:N	1:K:116:GLU:OE2	2.44	0.50
1:Q:133:GLY:H	1:Q:152:VAL:HG23	1.76	0.50
1:T:62:ASP:OD2	1:T:62:ASP:N	2.42	0.50
1:X:75:PHE:CE1	1:X:162:PRO:HD2	2.46	0.50
1:c:138:TRP:CZ3	1:c:147:GLU:HB3	2.47	0.50
1:c:154:PRO:O	1:c:155:THR:HG22	2.12	0.50
1:e:25:GLU:H	1:e:25:GLU:CD	2.19	0.50
1:h:101:GLU:OE1	1:h:101:GLU:N	2.43	0.50
1:s:73:ASN:HB3	1:s:164:PHE:HE1	1.76	0.50
1:w:75:PHE:CE1	1:w:162:PRO:HD2	2.45	0.50
1:w:153:ASP:HA	1:w:159:LEU:HD23	1.92	0.50
1:1:180:ARG:HH11	1:1:180:ARG:HG2	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:8:174:ARG:CZ	1:8:187:VAL:HG21	2.41	0.50
1:9:75:PHE:HE1	1:9:162:PRO:HD2	1.76	0.50
1:9:209:ILE:HD11	1:9:213:GLY:HA2	1.91	0.50
1:B:38:MET:SD	1:B:185:LYS:HE2	2.52	0.50
1:F:209:ILE:HD11	1:F:213:GLY:HA2	1.93	0.50
2:AG:348:PRO:HA	2:AG:352:THR:HG22	1.92	0.50
2:AI:182:LYS:HD2	2:AI:186:GLY:O	2.10	0.50
2:AK:165:TYR:CG	2:AL:25:ILE:HD11	2.46	0.50
2:AL:68:VAL:HG21	2:AL:118:ALA:HB2	1.93	0.50
5:Aa:99:LEU:HD12	5:Aa:124:ILE:HD11	1.92	0.50
6:S5:15:HIS:HD1	6:T5:32:TYR:HH	1.58	0.50
6:T5:185:ALA:O	6:T5:191:GLN:HG2	2.11	0.50
1:Q:172:ALA:O	1:Q:175:ARG:NH1	2.44	0.50
1:a:138:TRP:CZ3	1:a:147:GLU:HB3	2.47	0.50
1:c:138:TRP:CE3	1:c:147:GLU:HB3	2.46	0.50
1:o:29:ALA:HB1	1:o:190:VAL:HG21	1.93	0.50
1:2:210:ASP:OD1	1:2:214:ASN:N	2.37	0.50
1:3:29:ALA:HB1	1:3:190:VAL:HG21	1.93	0.50
1:7:138:TRP:CE3	1:7:147:GLU:HB3	2.46	0.50
1:7:210:ASP:OD1	1:7:214:ASN:N	2.41	0.50
1:9:138:TRP:CH2	1:9:192:PRO:HD2	2.47	0.50
1:A:99:GLN:CD	1:A:99:GLN:H	2.20	0.50
2:AK:81:ASN:OD1	2:AK:83:GLN:HG2	2.12	0.50
2:AL:65:GLY:O	2:AL:66:LEU:C	2.54	0.50
4:AR:40:ASP:OD2	4:AR:41:ASP:N	2.44	0.50
6:R3:73:PRO:O	6:R3:132:THR:HA	2.11	0.50
6:U3:41:GLU:HG2	6:U3:48:PHE:CE1	2.45	0.50
1:P:209:ILE:HG13	1:P:214:ASN:O	2.11	0.50
1:g:126:THR:O	1:g:126:THR:OG1	2.27	0.50
1:1:132:THR:HA	1:1:152:VAL:HG23	1.93	0.50
1:4:99:GLN:OE1	1:4:99:GLN:N	2.45	0.50
1:8:29:ALA:HB1	1:8:190:VAL:HG21	1.93	0.50
1:8:209:ILE:HG13	1:8:214:ASN:O	2.11	0.50
1:8:209:ILE:HD11	1:8:213:GLY:HA2	1.93	0.50
1:9:99:GLN:OE1	1:9:99:GLN:N	2.44	0.50
2:AB:282:THR:HG22	2:AC:249:ARG:HH22	1.74	0.50
2:AG:278:PHE:O	6:R4:201:LEU:O	2.29	0.50
2:AG:347:GLU:HG2	2:AG:351:LEU:HD22	1.93	0.50
2:AL:339:LYS:O	2:AL:343:GLU:HG2	2.11	0.50
6:S4:27:ASP:OD2	6:S4:27:ASP:N	2.45	0.50
6:T4:58:ILE:HB	6:T4:126:LEU:HD22	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:U4:41:GLU:HG2	6:U4:48:PHE:CE1	2.46	0.50
6:R5:73:PRO:O	6:R5:132:THR:HA	2.12	0.50
6:R5:165:SER:HB2	6:R5:169:THR:HG23	1.93	0.50
6:S5:74:ILE:CG2	6:S5:77:ARG:HB2	2.39	0.50
1:d:209:ILE:HD11	1:d:213:GLY:HA2	1.92	0.50
1:g:138:TRP:CZ3	1:g:147:GLU:HB3	2.47	0.50
1:h:154:PRO:O	1:h:155:THR:HG22	2.12	0.50
1:s:29:ALA:HB1	1:s:190:VAL:HG21	1.92	0.50
1:s:172:ALA:O	1:s:175:ARG:NH1	2.45	0.50
1:w:138:TRP:CZ3	1:w:147:GLU:HB3	2.46	0.50
1:z:210:ASP:OD1	1:z:214:ASN:N	2.40	0.50
1:1:140:SER:O	1:1:140:SER:OG	2.26	0.50
2:AB:350:TYR:C	2:AB:353:PRO:HD2	2.37	0.50
2:AC:67:THR:O	2:AC:70:SER:OG	2.24	0.50
2:AE:372:ASP:HB2	2:AE:374:ASP:OD1	2.11	0.50
2:AG:282:THR:HA	2:AH:249:ARG:HH11	1.76	0.50
2:AH:402:ARG:HE	2:AH:407:TRP:HB3	1.76	0.50
2:AJ:282:THR:CG2	2:AK:249:ARG:HD2	2.42	0.50
4:AR:112:ASP:OD2	4:AW:7:TYR:OH	2.20	0.50
6:S3:74:ILE:CG2	6:S3:131:VAL:HG23	2.41	0.50
6:T3:165:SER:OG	6:T3:166:VAL:N	2.45	0.50
3:AO:15:GLN:OE1	3:AO:80:TRP:NE1	2.42	0.50
1:R:3:PHE:HD1	1:R:38:MET:HE2	1.76	0.50
1:m:154:PRO:O	1:m:155:THR:HG22	2.11	0.50
1:q:172:ALA:O	1:q:175:ARG:NH1	2.45	0.50
1:B:99:GLN:OE1	1:B:99:GLN:N	2.44	0.50
2:AA:183:ASN:OD1	2:AA:184:ASP:N	2.42	0.50
2:AB:271:ASP:OD2	6:T5:59:ARG:NH1	2.44	0.50
2:AF:121:TRP:HE3	2:AF:127:MET:HG3	1.77	0.50
2:AH:64:LEU:O	2:AH:68:VAL:HG12	2.12	0.50
2:AJ:131:VAL:HG21	2:AJ:192:TYR:CZ	2.46	0.50
2:AJ:153:LYS:HZ1	2:AJ:161:GLU:HB2	1.76	0.50
2:AK:67:THR:O	2:AK:70:SER:OG	2.26	0.50
6:U4:13:ARG:HH12	6:U4:26:ASP:CG	2.19	0.50
1:J:13:SER:O	1:J:13:SER:OG	2.30	0.50
1:b:154:PRO:O	1:b:155:THR:HG22	2.12	0.50
1:k:99:GLN:HG2	1:k:101:GLU:OE1	2.12	0.50
1:4:206:GLN:OE1	1:4:207:VAL:N	2.45	0.50
1:5:59:PHE:HE2	1:5:175:ARG:HE	1.59	0.50
1:6:99:GLN:CD	1:6:99:GLN:H	2.20	0.50
1:7:88:LEU:N	1:7:121:GLY:O	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:243:TRP:NE1	2:AC:291:ASN:HD21	2.09	0.50
2:AC:165:TYR:CG	2:AD:25:ILE:HD11	2.47	0.50
2:AD:165:TYR:CG	2:AE:25:ILE:HD11	2.47	0.50
2:AF:219:VAL:HB	2:AF:220:PRO:HD3	1.92	0.50
2:AG:165:TYR:CG	2:AH:25:ILE:HD11	2.46	0.50
2:AI:92:SER:HA	2:AI:95:LYS:HE2	1.94	0.50
2:AJ:217:ILE:HB	2:AJ:309:ILE:HG22	1.92	0.50
2:AJ:265:GLU:OE2	2:AJ:271:ASP:HB3	2.12	0.50
2:AJ:374:ASP:O	2:AJ:375:SER:C	2.53	0.50
6:U3:185:ALA:O	6:U3:190:ALA:HB3	2.12	0.50
6:U3:195:PHE:HD2	6:U3:196:ARG:HH11	1.60	0.50
5:Aa:7:ASN:OD1	5:Aa:8:GLY:N	2.45	0.50
6:R4:184:GLY:O	6:R4:185:ALA:C	2.54	0.50
1:W:3:PHE:HD1	1:W:38:MET:HE2	1.76	0.50
1:X:10:ASN:ND2	6:U5:77:ARG:HH22	2.10	0.50
1:i:40:SER:O	1:i:40:SER:OG	2.29	0.50
1:q:88:LEU:N	1:q:121:GLY:O	2.42	0.50
1:r:29:ALA:HB1	1:r:190:VAL:HG21	1.93	0.50
1:w:73:ASN:OD1	1:w:147:GLU:N	2.29	0.50
1:y:38:MET:HG2	1:y:185:LYS:HG2	1.93	0.50
2:AA:131:VAL:HG21	2:AA:192:TYR:CZ	2.47	0.50
2:AC:317:ILE:H	2:AC:317:ILE:HD12	1.76	0.50
2:AE:16:PRO:O	2:AE:17:ALA:C	2.53	0.50
2:AH:67:THR:O	2:AH:68:VAL:C	2.53	0.50
2:AH:219:VAL:HB	2:AH:220:PRO:HD3	1.93	0.50
2:AK:192:TYR:HE2	2:AK:194:PHE:HE1	1.60	0.50
6:R3:13:ARG:NH2	6:R3:24:VAL:O	2.36	0.50
5:Aa:14:ILE:HG12	5:Aa:87:VAL:HG23	1.94	0.50
6:U4:183:ASN:HB3	6:U4:186:VAL:HG12	1.94	0.50
5:AY:3:CYS:HA	4:AX:156:CYS:SG	2.52	0.50
6:S5:62:GLY:O	6:S5:64:ARG:N	2.45	0.50
1:N:13:SER:O	1:N:13:SER:OG	2.28	0.50
1:g:154:PRO:O	1:g:155:THR:HG22	2.12	0.50
1:p:73:ASN:HB3	1:p:164:PHE:HE1	1.77	0.50
2:AA:28:ARG:CD	2:AL:169:ALA:HB3	2.42	0.50
2:AA:119:LEU:HD22	2:AB:201:ILE:HG12	1.92	0.50
2:AE:131:VAL:HG21	2:AE:192:TYR:CZ	2.47	0.50
2:AF:67:THR:O	2:AF:70:SER:OG	2.23	0.50
2:AH:402:ARG:HH21	2:AH:407:TRP:HB3	1.75	0.50
2:AJ:89:MET:HB2	2:AJ:93:GLN:OE1	2.12	0.50
2:AJ:121:TRP:HE3	2:AJ:127:MET:HG3	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AU:129:PRO:O	5:AU:130:PRO:C	2.54	0.50
5:AZ:4:ASN:OD1	5:AV:113:ARG:NH2	2.44	0.50
3:H:7:LYS:HB2	6:U5:23:ARG:HG3	1.92	0.50
6:R4:182:ASN:N	6:R4:182:ASN:OD1	2.45	0.50
5:Ab:32:GLN:NE2	5:Ab:36:THR:O	2.45	0.50
6:R5:195:PHE:C	6:R5:197:TYR:N	2.69	0.50
6:T5:43:TYR:HE2	6:T5:194:TRP:HB2	1.77	0.50
6:U5:55:VAL:HG13	6:U5:129:THR:HG22	1.93	0.50
1:L:29:ALA:HB1	1:L:190:VAL:HG21	1.94	0.50
1:M:3:PHE:HD1	1:M:38:MET:HE2	1.77	0.50
1:M:172:ALA:O	1:M:175:ARG:NH1	2.45	0.50
1:Y:209:ILE:HD11	1:Y:213:GLY:HA2	1.93	0.50
1:a:46:ALA:HB3	1:a:47:PRO:HD3	1.93	0.50
1:b:88:LEU:N	1:b:121:GLY:O	2.45	0.50
1:m:138:TRP:CE3	1:m:147:GLU:HB3	2.47	0.50
1:r:126:THR:O	1:r:126:THR:OG1	2.27	0.50
1:4:75:PHE:HE1	1:4:162:PRO:HD2	1.75	0.50
1:7:167:PRO:HA	1:7:191:SER:HB3	1.93	0.50
2:AD:67:THR:HG21	2:AD:346:ILE:HG13	1.94	0.50
2:AE:339:LYS:HZ1	2:AE:379:LEU:HD13	1.77	0.50
2:AG:47:ALA:HA	2:AG:50:ARG:NH1	2.27	0.50
2:AG:281:GLY:HA3	2:AH:249:ARG:HG2	1.94	0.50
2:AH:359:SER:OG	2:AH:368:ARG:HB2	2.11	0.50
2:AI:249:ARG:HD3	6:U4:195:PHE:CD1	2.46	0.50
2:AK:121:TRP:CZ2	2:AK:198:LYS:HD3	2.47	0.50
2:AK:127:MET:O	2:AK:196:ILE:N	2.45	0.50
2:AL:26:PHE:O	2:AL:31:PHE:N	2.45	0.50
3:AM:44:ALA:HB1	3:AP:97:SER:OG	2.12	0.50
6:S3:40:ALA:HB2	6:S3:194:TRP:CZ3	2.46	0.50
6:S5:7:LEU:HD21	6:S5:12:ILE:HG13	1.94	0.50
1:N:10:ASN:ND2	6:U3:77:ARG:HH22	2.09	0.49
1:X:138:TRP:CZ3	1:X:147:GLU:HB3	2.47	0.49
1:b:75:PHE:HE1	1:b:162:PRO:HD2	1.77	0.49
1:e:154:PRO:HG2	1:e:156:THR:HG22	1.94	0.49
1:k:102:TYR:HD1	1:k:141:ILE:HD12	1.77	0.49
1:C:53:LEU:HD12	1:C:206:GLN:NE2	2.27	0.49
2:AD:402:ARG:HE	2:AD:407:TRP:HB3	1.77	0.49
2:AF:89:MET:HB2	2:AF:93:GLN:OE1	2.12	0.49
2:AF:264:GLU:O	2:AF:267:LYS:HG3	2.12	0.49
2:AI:16:PRO:O	2:AI:17:ALA:C	2.55	0.49
2:AL:317:ILE:H	2:AL:317:ILE:HD12	1.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AU:14:ILE:HG12	5:AU:87:VAL:HG23	1.94	0.49
5:AU:84:GLN:HE21	5:AU:101:GLU:HA	1.77	0.49
4:AT:139:GLU:HB3	4:AT:144:TYR:HE2	1.77	0.49
5:Aa:4:ASN:OD1	5:AY:113:ARG:NH2	2.45	0.49
6:R5:167:ARG:O	6:R5:168:ASN:C	2.54	0.49
1:Y:3:PHE:HD1	1:Y:38:MET:HE2	1.77	0.49
1:a:29:ALA:HB1	1:a:190:VAL:HG21	1.93	0.49
1:a:99:GLN:HG2	1:a:101:GLU:OE1	2.12	0.49
1:i:209:ILE:HG13	1:i:214:ASN:O	2.12	0.49
1:l:154:PRO:O	1:l:155:THR:HG22	2.12	0.49
1:q:180:ARG:HG2	1:q:180:ARG:HH11	1.76	0.49
1:u:56:LYS:HB3	1:u:207:VAL:HG11	1.94	0.49
1:4:118:GLY:N	1:4:122:ALA:O	2.32	0.49
1:C:7:ASP:OD1	1:C:7:ASP:N	2.43	0.49
2:AA:28:ARG:HG3	2:AA:29:ARG:N	2.28	0.49
2:AB:131:VAL:HG21	2:AB:192:TYR:CZ	2.47	0.49
2:AB:217:ILE:HB	2:AB:309:ILE:HG22	1.94	0.49
2:AC:262:GLY:CA	6:R5:202:LEU:HD22	2.42	0.49
2:AE:267:LYS:HD2	2:AF:237:GLY:HA2	1.93	0.49
2:AJ:127:MET:HE1	2:AJ:354:LEU:HD12	1.92	0.49
2:AJ:271:ASP:OD2	6:T3:59:ARG:NH1	2.45	0.49
5:AU:113:ARG:NH2	5:Ab:4:ASN:OD1	2.44	0.49
5:AZ:52:ASN:N	5:AV:61:ASN:OD1	2.45	0.49
6:S3:19:ASP:N	6:S3:19:ASP:OD1	2.43	0.49
6:S4:62:GLY:O	6:S4:64:ARG:N	2.45	0.49
6:R5:195:PHE:O	6:R5:197:TYR:N	2.45	0.49
1:L:71:VAL:HG13	1:L:144:ASN:HB2	1.94	0.49
1:O:117:LEU:HG	1:O:118:GLY:O	2.13	0.49
1:T:117:LEU:HG	1:T:118:GLY:O	2.12	0.49
1:Y:75:PHE:HD1	1:Y:149:VAL:HG13	1.77	0.49
1:b:134:VAL:HG21	1:b:162:PRO:HG3	1.94	0.49
1:d:3:PHE:HD1	1:d:38:MET:HE2	1.77	0.49
1:h:95:PRO:HG2	1:h:96:GLU:OE2	2.12	0.49
1:h:209:ILE:HG13	1:h:214:ASN:O	2.12	0.49
1:j:154:PRO:HG2	1:j:156:THR:HG22	1.95	0.49
1:z:133:GLY:H	1:z:152:VAL:CG2	2.25	0.49
1:3:80:VAL:HG12	1:3:155:THR:HB	1.93	0.49
2:AD:252:ASP:HA	6:R5:43:TYR:HD1	1.78	0.49
2:AD:363:CYS:SG	2:AD:364:GLY:N	2.85	0.49
2:AG:282:THR:CA	2:AH:249:ARG:HD3	2.41	0.49
2:AH:26:PHE:O	2:AH:31:PHE:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AI:131:VAL:HG21	2:AI:192:TYR:CZ	2.47	0.49
2:AK:161:GLU:HB3	2:AK:179:LYS:HE2	1.94	0.49
6:U3:23:ARG:HG3	3:I:7:LYS:HB2	1.93	0.49
6:U3:184:GLY:C	6:U3:186:VAL:H	2.20	0.49
3:AN:99:VAL:HB	3:AN:109:LYS:HB3	1.94	0.49
6:R4:13:ARG:NH2	6:R4:24:VAL:O	2.33	0.49
6:R4:181:THR:O	6:R4:182:ASN:C	2.55	0.49
3:AO:1:MET:HE2	3:AO:66:THR:HG21	1.93	0.49
6:R5:43:TYR:CD2	6:R5:44:THR:HG23	2.47	0.49
6:U5:185:ALA:O	6:U5:190:ALA:HB3	2.13	0.49
1:K:125:TYR:OH	1:K:135:ASP:OD2	2.26	0.49
1:R:138:TRP:CZ3	1:R:147:GLU:HB3	2.47	0.49
1:Z:46:ALA:HB3	1:Z:47:PRO:HD3	1.94	0.49
1:f:75:PHE:HB2	1:f:164:PHE:CZ	2.47	0.49
1:i:88:LEU:N	1:i:121:GLY:O	2.44	0.49
1:l:138:TRP:CH2	1:l:192:PRO:HD2	2.48	0.49
1:q:133:GLY:H	1:q:152:VAL:HG23	1.76	0.49
1:r:75:PHE:CE1	1:r:162:PRO:HD2	2.48	0.49
1:7:38:MET:SD	1:7:185:LYS:HE2	2.51	0.49
1:G:209:ILE:HG13	1:G:214:ASN:O	2.12	0.49
2:AB:348:PRO:HA	2:AB:352:THR:HG22	1.94	0.49
2:AH:348:PRO:HA	2:AH:352:THR:HG22	1.94	0.49
3:AP:106:ARG:HH21	6:S3:17:LYS:HZ1	1.59	0.49
6:R3:183:ASN:HD22	6:U3:187:ILE:C	2.21	0.49
6:S3:62:GLY:O	6:S3:64:ARG:N	2.45	0.49
6:T5:6:LEU:HD22	6:T5:140:VAL:HG11	1.94	0.49
1:S:138:TRP:CZ3	1:S:147:GLU:HB3	2.47	0.49
1:V:126:THR:O	1:V:126:THR:OG1	2.30	0.49
1:i:138:TRP:CZ3	1:i:147:GLU:HB3	2.48	0.49
1:j:75:PHE:CE1	1:j:162:PRO:HD2	2.46	0.49
1:l:29:ALA:HB1	1:l:190:VAL:HG21	1.94	0.49
1:o:74:ALA:HB3	1:o:148:TYR:CD1	2.47	0.49
1:t:38:MET:HG2	1:t:185:LYS:HG2	1.94	0.49
1:u:73:ASN:HB3	1:u:164:PHE:CE1	2.47	0.49
1:x:53:LEU:HD23	1:x:182:HIS:HA	1.95	0.49
1:x:72:SER:O	1:x:91:LEU:HD12	2.13	0.49
1:z:126:THR:O	1:z:126:THR:OG1	2.31	0.49
1:B:210:ASP:OD1	1:B:214:ASN:N	2.41	0.49
1:C:29:ALA:HB1	1:C:190:VAL:HG21	1.95	0.49
2:AF:253:ASP:OD2	6:T4:198:ARG:NE	2.45	0.49
2:AI:232:ILE:HG22	6:R4:63:ARG:HH22	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AK:317:ILE:H	2:AK:317:ILE:HD12	1.77	0.49
2:AK:348:PRO:HA	2:AK:352:THR:HG22	1.94	0.49
3:AN:44:ALA:HB1	3:H:97:SER:OG	2.11	0.49
5:Aa:52:ASN:N	5:AY:61:ASN:OD1	2.45	0.49
6:S4:19:ASP:OD1	6:S4:19:ASP:N	2.43	0.49
1:f:46:ALA:HB3	1:f:47:PRO:HD3	1.95	0.49
1:f:85:GLU:OE1	1:f:124:THR:HG22	2.13	0.49
1:n:75:PHE:CE1	1:n:161:GLN:HG2	2.47	0.49
1:3:138:TRP:CE3	1:3:147:GLU:HB3	2.48	0.49
1:6:79:LYS:HD2	1:6:153:ASP:HB2	1.95	0.49
1:G:210:ASP:OD1	1:G:214:ASN:N	2.40	0.49
2:AE:121:TRP:HZ2	2:AE:198:LYS:HD3	1.77	0.49
2:AH:169:ALA:HB3	2:AI:28:ARG:HD3	1.94	0.49
2:AL:402:ARG:HE	2:AL:407:TRP:HB3	1.76	0.49
3:AP:46:ARG:NE	3:AN:77:VAL:HG23	2.28	0.49
6:R3:32:TYR:CD2	6:R3:156:ILE:HG22	2.47	0.49
5:AV:84:GLN:HE21	5:AV:101:GLU:HA	1.78	0.49
5:AY:87:VAL:HG12	5:AY:99:LEU:HB3	1.93	0.49
1:N:62:ASP:OD1	1:N:63:GLY:N	2.46	0.49
1:T:13:SER:HB3	6:R4:52:LYS:HA	1.94	0.49
1:g:48:LEU:HD23	1:h:1:MET:HE3	1.95	0.49
1:j:78:THR:O	1:j:152:VAL:HA	2.12	0.49
1:r:48:LEU:HD23	1:s:1:MET:HE3	1.95	0.49
1:w:72:SER:O	1:w:91:LEU:HD12	2.13	0.49
1:2:157:SER:OG	1:2:158:GLU:N	2.45	0.49
1:E:210:ASP:HB3	1:E:216:PHE:HE2	1.76	0.49
2:AB:374:ASP:OD1	2:AB:374:ASP:N	2.45	0.49
2:AC:55:PRO:HA	2:AD:216:ALA:HB1	1.95	0.49
2:AC:374:ASP:OD1	2:AC:374:ASP:N	2.44	0.49
2:AI:274:GLY:HA3	2:AK:233:ASP:OD2	2.12	0.49
3:AM:46:ARG:NE	3:AP:77:VAL:HG23	2.26	0.49
5:AU:3:CYS:HA	4:AR:156:CYS:SG	2.52	0.49
6:U3:186:VAL:HB	6:U3:191:GLN:HG3	1.95	0.49
4:AS:156:CYS:HB3	5:Aa:3:CYS:HA	1.95	0.49
5:AV:89:VAL:HG12	5:AV:97:MET:HB2	1.94	0.49
6:S4:154:TRP:CZ2	6:S4:187:ILE:HD11	2.48	0.49
3:AO:44:ALA:HB1	3:I:97:SER:OG	2.13	0.49
6:S5:3:LEU:O	6:S5:6:LEU:N	2.46	0.49
1:V:78:THR:HG23	1:V:152:VAL:HG12	1.93	0.49
1:V:167:PRO:HA	1:V:191:SER:HB3	1.95	0.49
1:Y:99:GLN:H	1:Y:99:GLN:CD	2.21	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:138:TRP:CZ3	1:Z:147:GLU:HB3	2.48	0.49
1:b:75:PHE:CE1	1:b:162:PRO:HD2	2.48	0.49
1:k:138:TRP:CE3	1:k:147:GLU:HB3	2.48	0.49
1:m:95:PRO:HG2	1:m:96:GLU:OE2	2.13	0.49
1:l:29:ALA:HB1	1:l:190:VAL:HG21	1.94	0.49
1:D:156:THR:OG1	1:D:157:SER:N	2.46	0.49
2:AC:112:GLN:NE2	2:AD:197:VAL:O	2.46	0.49
2:AD:26:PHE:O	2:AD:31:PHE:N	2.45	0.49
2:AD:97:LEU:O	2:AD:101:LEU:HB2	2.13	0.49
2:AF:220:PRO:HB2	2:AF:309:ILE:HG23	1.94	0.49
2:AG:71:VAL:HG22	2:AG:376:ILE:HD11	1.95	0.49
2:AG:81:ASN:OD1	2:AG:83:GLN:HG2	2.13	0.49
2:AG:127:MET:O	2:AG:196:ILE:N	2.46	0.49
2:AH:165:TYR:CG	2:AI:25:ILE:HD11	2.47	0.49
2:AI:267:LYS:HD2	2:AJ:237:GLY:HA2	1.94	0.49
2:AL:348:PRO:HA	2:AL:352:THR:HG22	1.95	0.49
6:R3:179:GLY:HA2	6:R3:182:ASN:ND2	2.28	0.49
6:S3:11:THR:HG23	6:T3:28:LEU:HD12	1.95	0.49
6:T3:181:THR:O	6:T3:187:ILE:HG13	2.13	0.49
5:Aa:17:THR:OG1	5:Aa:84:GLN:HB3	2.12	0.49
3:AO:6:ARG:HA	3:AO:38:ALA:HB2	1.94	0.49
1:W:138:TRP:CZ3	1:W:147:GLU:HB3	2.48	0.49
1:l:75:PHE:CE1	1:l:162:PRO:HD2	2.47	0.49
1:o:48:LEU:HD23	1:p:1:MET:HE3	1.95	0.49
1:v:48:LEU:HD23	1:w:1:MET:HE3	1.95	0.49
1:x:73:ASN:HB3	1:x:164:PHE:HE1	1.78	0.49
1:C:80:VAL:HG12	1:C:155:THR:HB	1.95	0.49
1:C:210:ASP:HB3	1:C:216:PHE:CE2	2.36	0.49
2:AB:89:MET:HB2	2:AB:93:GLN:OE1	2.12	0.49
2:AC:81:ASN:OD1	2:AC:83:GLN:HG2	2.13	0.49
2:AD:44:ASN:ND2	2:AD:210:GLN:HG2	2.28	0.49
2:AD:132:SER:HA	2:AD:191:ASN:ND2	2.27	0.49
2:AG:374:ASP:N	2:AG:374:ASP:OD1	2.45	0.49
2:AI:183:ASN:N	2:AI:187:ARG:O	2.37	0.49
2:AL:97:LEU:O	2:AL:101:LEU:HB2	2.13	0.49
5:AU:110:SER:O	5:Ab:39:THR:HG22	2.13	0.49
5:AZ:99:LEU:HD12	5:AZ:124:ILE:HD11	1.95	0.49
6:U3:26:ASP:OD1	6:U3:27:ASP:N	2.46	0.49
3:H:46:ARG:NE	3:AO:77:VAL:HG23	2.28	0.49
6:S4:167:ARG:HG2	6:S4:168:ASN:O	2.13	0.49
5:Ab:7:ASN:OD1	5:Ab:8:GLY:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:108:ASN:HB3	1:K:138:TRP:CD1	2.48	0.49
1:L:172:ALA:O	1:L:175:ARG:NH1	2.46	0.49
1:O:56:LYS:HB3	1:O:207:VAL:HG11	1.95	0.49
1:X:30:ARG:HD2	1:X:230:GLY:H	1.77	0.49
1:b:25:GLU:OE1	1:b:25:GLU:N	2.45	0.49
1:b:46:ALA:HB3	1:b:47:PRO:HD3	1.94	0.49
1:d:40:SER:O	1:d:40:SER:OG	2.28	0.49
1:e:46:ALA:HB3	1:e:47:PRO:HD3	1.95	0.49
1:m:132:THR:HA	1:m:152:VAL:HG23	1.94	0.49
1:m:209:ILE:HD11	1:m:213:GLY:HA2	1.95	0.49
1:v:99:GLN:N	1:v:99:GLN:OE1	2.46	0.49
1:x:67:THR:O	1:x:67:THR:OG1	2.31	0.49
1:3:206:GLN:OE1	1:3:207:VAL:N	2.45	0.49
1:A:209:ILE:HG13	1:A:214:ASN:O	2.13	0.49
1:C:30:ARG:HD2	1:C:230:GLY:H	1.78	0.49
1:E:9:ARG:NH2	1:F:230:GLY:OXT	2.40	0.49
2:AB:67:THR:O	2:AB:70:SER:OG	2.24	0.49
2:AD:39:VAL:HG23	2:AD:40:VAL:HG13	1.95	0.49
2:AK:258:GLU:HG2	6:R3:202:LEU:HD13	1.95	0.49
3:AP:86:LEU:HD12	6:U4:20:ASP:H	1.78	0.49
5:AZ:32:GLN:NE2	5:AZ:36:THR:O	2.46	0.49
5:AV:3:CYS:HA	4:AT:156:CYS:SG	2.53	0.49
6:R4:32:TYR:CD2	6:R4:156:ILE:HG22	2.48	0.49
6:T4:181:THR:O	6:T4:187:ILE:HG13	2.12	0.49
6:U5:145:ILE:O	6:U5:146:ILE:C	2.54	0.49
1:S:73:ASN:HB2	1:S:164:PHE:HE1	1.77	0.48
1:T:39:VAL:HG23	1:T:184:LEU:HB3	1.95	0.48
1:b:38:MET:HG2	1:b:185:LYS:HG2	1.95	0.48
1:f:38:MET:HG2	1:f:185:LYS:HG2	1.94	0.48
1:k:46:ALA:HB3	1:k:47:PRO:HD3	1.95	0.48
1:o:138:TRP:CE3	1:o:147:GLU:HB3	2.48	0.48
1:s:75:PHE:CE1	1:s:161:GLN:HG2	2.48	0.48
1:u:136:ARG:HG2	1:u:149:VAL:HG22	1.95	0.48
1:7:209:ILE:HG13	1:7:214:ASN:O	2.12	0.48
1:8:56:LYS:HB3	1:8:207:VAL:CG1	2.42	0.48
1:B:138:TRP:CE3	1:B:147:GLU:HB3	2.48	0.48
2:AA:25:ILE:HD11	2:AL:165:TYR:CG	2.48	0.48
2:AB:316:PRO:HD2	2:AB:341:PHE:HB2	1.95	0.48
2:AD:305:GLN:O	2:AD:309:ILE:HG12	2.11	0.48
2:AE:338:ARG:NH2	2:AF:344:ASP:OD2	2.46	0.48
2:AF:153:LYS:HZ1	2:AF:161:GLU:HB2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AM:49:GLN:OE1	3:AM:49:GLN:N	2.46	0.48
5:AU:63:THR:HG22	5:AU:120:VAL:HG22	1.95	0.48
3:I:69:TYR:HD2	3:I:108:MET:HG3	1.77	0.48
1:R:172:ALA:O	1:R:175:ARG:NH1	2.45	0.48
1:U:38:MET:HG2	1:U:185:LYS:HG2	1.93	0.48
1:U:126:THR:O	1:U:126:THR:OG1	2.30	0.48
1:X:30:ARG:NH1	1:X:229:CYS:HA	2.28	0.48
1:j:46:ALA:HB3	1:j:47:PRO:HD3	1.95	0.48
1:p:73:ASN:HB3	1:p:164:PHE:CE1	2.48	0.48
1:r:210:ASP:CG	1:r:214:ASN:HD22	2.21	0.48
1:y:74:ALA:HB3	1:y:148:TYR:CD1	2.48	0.48
1:0:174:ARG:NE	1:0:187:VAL:HG21	2.28	0.48
1:B:53:LEU:HD23	1:B:182:HIS:HA	1.94	0.48
1:G:3:PHE:HD1	1:G:38:MET:HE2	1.79	0.48
2:AF:251:LEU:CD1	2:AF:282:THR:HG23	2.42	0.48
2:AJ:317:ILE:HD12	2:AJ:317:ILE:H	1.78	0.48
2:AK:262:GLY:CA	6:R3:202:LEU:HD12	2.42	0.48
2:AK:347:GLU:HA	2:AK:351:LEU:HB2	1.95	0.48
6:S3:195:PHE:C	6:S3:197:TYR:N	2.61	0.48
6:T3:43:TYR:HE2	6:T3:194:TRP:HB2	1.78	0.48
6:U4:142:ALA:O	6:U4:143:GLY:C	2.53	0.48
6:R5:183:ASN:HD22	6:U5:187:ILE:C	2.21	0.48
6:U5:186:VAL:HB	6:U5:191:GLN:HG3	1.95	0.48
1:S:30:ARG:NH1	1:S:229:CYS:HA	2.28	0.48
1:h:177:VAL:O	1:h:179:PRO:HD3	2.13	0.48
1:k:29:ALA:HB1	1:k:190:VAL:HG21	1.95	0.48
1:l:134:VAL:HG21	1:l:162:PRO:HG3	1.96	0.48
1:n:77:ARG:NH2	1:n:158:GLU:OE2	2.47	0.48
1:3:53:LEU:HD12	1:3:206:GLN:NE2	2.28	0.48
1:B:209:ILE:HG13	1:B:214:ASN:O	2.13	0.48
1:C:174:ARG:CZ	1:C:187:VAL:HG21	2.43	0.48
2:AB:200:SER:OG	2:AB:201:ILE:N	2.46	0.48
2:AF:374:ASP:N	2:AF:374:ASP:OD1	2.45	0.48
2:AG:66:LEU:HG	2:AH:348:PRO:O	2.14	0.48
2:AG:277:ILE:HD11	2:AH:241:SER:OG	2.13	0.48
2:AI:121:TRP:HE3	2:AI:127:MET:HG3	1.78	0.48
2:AI:350:TYR:C	2:AI:353:PRO:HD2	2.39	0.48
2:AJ:134:MET:SD	2:AJ:138:SER:OG	2.68	0.48
2:AK:148:PRO:HG2	2:AL:202:ASN:HB3	1.95	0.48
6:S4:11:THR:HG23	6:T4:28:LEU:HD12	1.94	0.48
5:Ab:87:VAL:HG12	5:Ab:99:LEU:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:38:MET:HG2	1:P:185:LYS:HG2	1.95	0.48
1:U:108:ASN:HB3	1:U:138:TRP:CD1	2.47	0.48
1:Z:78:THR:O	1:Z:152:VAL:HA	2.13	0.48
1:h:72:SER:O	1:h:91:LEU:HD12	2.13	0.48
1:l:46:ALA:HB3	1:l:47:PRO:HD3	1.95	0.48
1:w:59:PHE:CD1	1:w:204:VAL:HG12	2.48	0.48
1:w:157:SER:OG	1:w:158:GLU:N	2.45	0.48
1:z:209:ILE:HG13	1:z:214:ASN:O	2.13	0.48
1:2:53:LEU:HD23	1:2:182:HIS:HA	1.95	0.48
1:2:194:ALA:HB1	1:2:226:ILE:HG21	1.94	0.48
1:B:75:PHE:HE1	1:B:162:PRO:HD2	1.77	0.48
1:B:167:PRO:HA	1:B:191:SER:HB3	1.95	0.48
1:G:138:TRP:CE3	1:G:147:GLU:HB3	2.48	0.48
2:AA:154:PHE:HA	2:AA:160:VAL:HA	1.95	0.48
2:AA:400:GLU:HA	2:AA:403:GLU:HG3	1.96	0.48
2:AB:154:PHE:HA	2:AB:160:VAL:HA	1.95	0.48
2:AE:140:ASN:HD22	2:AF:18:PRO:HG3	1.77	0.48
2:AG:363:CYS:SG	2:AG:364:GLY:N	2.87	0.48
2:AH:204:ALA:HB3	2:AH:208:ASP:HB2	1.96	0.48
2:AJ:74:ASP:OD1	2:AJ:74:ASP:N	2.45	0.48
2:AJ:140:ASN:ND2	2:AK:16:PRO:O	2.23	0.48
2:AJ:264:GLU:O	2:AJ:267:LYS:HG3	2.13	0.48
2:AL:44:ASN:ND2	2:AL:210:GLN:HG2	2.27	0.48
2:AL:220:PRO:HB2	2:AL:309:ILE:HG23	1.94	0.48
5:AU:61:ASN:OD1	5:Ab:52:ASN:N	2.46	0.48
3:I:49:GLN:O	3:I:50:ASP:HB2	2.13	0.48
6:S5:27:ASP:OD2	6:S5:27:ASP:N	2.46	0.48
1:J:49:ARG:HD2	6:R5:89:PRO:O	2.14	0.48
1:K:75:PHE:HE1	1:K:162:PRO:HD2	1.79	0.48
1:V:29:ALA:HB1	1:V:190:VAL:HG21	1.95	0.48
1:V:88:LEU:N	1:V:121:GLY:O	2.46	0.48
1:n:209:ILE:HD11	1:n:213:GLY:HA2	1.95	0.48
1:y:67:THR:O	1:y:67:THR:OG1	2.32	0.48
1:z:21:SER:HB3	1:E:49:ARG:HB3	1.95	0.48
2:AB:317:ILE:H	2:AB:317:ILE:HD12	1.78	0.48
2:AF:282:THR:HG22	2:AF:283:ASP:H	1.78	0.48
2:AI:266:THR:HA	2:AI:273:GLY:HA2	1.96	0.48
2:AJ:243:TRP:NE1	2:AK:291:ASN:HD21	2.09	0.48
2:AL:90:SER:HG	2:AL:93:GLN:H	1.60	0.48
2:AL:131:VAL:HG21	2:AL:192:TYR:CZ	2.48	0.48
2:AL:132:SER:HA	2:AL:191:ASN:ND2	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AR:31:ARG:NH2	4:AR:49:LYS:HD3	2.29	0.48
4:AW:22:ALA:HB3	4:AW:23:PRO:HD3	1.95	0.48
1:L:78:THR:HG23	1:L:152:VAL:HG12	1.96	0.48
1:L:88:LEU:N	1:L:121:GLY:O	2.46	0.48
1:N:30:ARG:NH1	1:N:229:CYS:HA	2.28	0.48
1:O:8:PRO:HB3	1:O:43:ALA:HB1	1.96	0.48
1:P:75:PHE:HE1	1:P:162:PRO:HD2	1.77	0.48
1:X:75:PHE:CE1	1:X:161:GLN:HG2	2.49	0.48
1:c:95:PRO:HG2	1:c:96:GLU:OE2	2.13	0.48
1:e:78:THR:O	1:e:152:VAL:HA	2.14	0.48
1:g:73:ASN:HB3	1:g:164:PHE:CE1	2.48	0.48
1:4:30:ARG:HD2	1:4:230:GLY:H	1.78	0.48
1:4:178:ASP:OD2	1:4:181:THR:OG1	2.25	0.48
1:8:210:ASP:HB3	1:8:216:PHE:CE2	2.34	0.48
1:B:206:GLN:OE1	1:B:207:VAL:N	2.46	0.48
2:AA:121:TRP:HE3	2:AA:127:MET:HG3	1.78	0.48
2:AA:132:SER:HA	2:AA:191:ASN:ND2	2.28	0.48
2:AA:350:TYR:C	2:AA:353:PRO:HD2	2.38	0.48
2:AB:264:GLU:O	2:AB:267:LYS:HG3	2.13	0.48
2:AC:66:LEU:HG	2:AD:348:PRO:O	2.13	0.48
2:AC:192:TYR:HE2	2:AC:194:PHE:HE1	1.61	0.48
2:AD:167:ASP:OD2	2:AD:168:GLU:N	2.47	0.48
2:AE:172:GLU:OE2	2:AF:24:LYS:HE3	2.14	0.48
2:AG:161:GLU:HB3	2:AG:179:LYS:HE2	1.95	0.48
2:AG:243:TRP:CZ2	2:AH:289:MET:HG3	2.48	0.48
2:AH:305:GLN:O	2:AH:309:ILE:HG12	2.14	0.48
2:AI:28:ARG:HG3	2:AI:29:ARG:N	2.22	0.48
2:AI:56:VAL:HB	2:AI:309:ILE:HD11	1.95	0.48
2:AJ:316:PRO:HD2	2:AJ:341:PHE:HB2	1.95	0.48
5:AZ:7:ASN:OD1	5:AZ:8:GLY:N	2.46	0.48
3:H:99:VAL:HG13	3:H:109:LYS:HB3	1.95	0.48
5:Ab:99:LEU:HD12	5:Ab:124:ILE:HD11	1.94	0.48
1:J:117:LEU:HG	1:J:118:GLY:O	2.14	0.48
1:M:75:PHE:CE1	1:M:161:GLN:HG2	2.49	0.48
1:O:206:GLN:OE1	1:O:207:VAL:N	2.47	0.48
1:Q:208:ALA:HB3	1:Q:216:PHE:HB2	1.95	0.48
1:T:8:PRO:HB3	1:T:43:ALA:HB1	1.96	0.48
1:V:53:LEU:HD12	1:V:206:GLN:CD	2.39	0.48
1:V:71:VAL:HG13	1:V:144:ASN:HB2	1.96	0.48
1:a:85:GLU:OE1	1:a:124:THR:HG22	2.14	0.48
1:e:126:THR:O	1:e:126:THR:OG1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:x:75:PHE:CE1	1:x:161:GLN:HG2	2.48	0.48
1:x:208:ALA:HB3	1:x:216:PHE:HB2	1.95	0.48
1:z:73:ASN:HB3	1:z:164:PHE:CE1	2.49	0.48
1:1:168:VAL:HG11	1:1:224:ILE:HD13	1.95	0.48
1:5:153:ASP:OD1	1:5:159:LEU:HB2	2.13	0.48
1:A:79:LYS:HD2	1:A:153:ASP:HB2	1.95	0.48
2:AF:131:VAL:HG21	2:AF:192:TYR:CZ	2.49	0.48
2:AF:340:ALA:O	2:AF:344:ASP:HB2	2.13	0.48
3:AP:8:HIS:CD2	3:AP:39:ILE:HG12	2.48	0.48
4:AS:22:ALA:HB3	4:AS:23:PRO:HD3	1.95	0.48
4:AW:84:PHE:HB2	4:AW:145:ILE:HB	1.94	0.48
1:J:8:PRO:HB3	1:J:43:ALA:HB1	1.95	0.48
1:K:154:PRO:O	1:K:155:THR:HG22	2.14	0.48
1:N:75:PHE:CE1	1:N:162:PRO:HD2	2.47	0.48
1:N:138:TRP:CZ3	1:N:147:GLU:HB3	2.47	0.48
1:U:154:PRO:O	1:U:155:THR:HG22	2.14	0.48
1:d:38:MET:HG2	1:d:185:LYS:HG2	1.96	0.48
1:n:1:MET:HE2	1:n:38:MET:HG3	1.96	0.48
1:n:210:ASP:HB3	1:n:216:PHE:HE2	1.78	0.48
1:p:209:ILE:HG13	1:p:214:ASN:O	2.14	0.48
1:x:1:MET:HE2	1:x:38:MET:HG3	1.95	0.48
1:8:7:ASP:OD2	1:8:7:ASP:N	2.44	0.48
1:9:75:PHE:CZ	1:9:161:GLN:HG2	2.48	0.48
2:AB:121:TRP:HE3	2:AB:127:MET:HG3	1.78	0.48
2:AE:383:ARG:O	2:AE:386:ILE:HG22	2.14	0.48
2:AF:154:PHE:HA	2:AF:160:VAL:HA	1.95	0.48
2:AG:196:ILE:H	2:AG:196:ILE:HD12	1.79	0.48
3:AP:99:VAL:HG13	3:AP:109:LYS:HB3	1.94	0.48
6:R4:201:LEU:O	6:R4:202:LEU:C	2.55	0.48
1:X:118:GLY:N	1:X:122:ALA:O	2.30	0.48
1:Z:38:MET:HG2	1:Z:185:LYS:HG2	1.96	0.48
1:l:35:ASN:OD1	1:l:36:GLY:N	2.43	0.48
1:l:194:ALA:HB1	1:l:226:ILE:HG21	1.96	0.48
1:w:53:LEU:HD23	1:w:182:HIS:HA	1.95	0.48
1:4:209:ILE:HG13	1:4:214:ASN:O	2.14	0.48
1:B:56:LYS:HB3	1:B:207:VAL:CG1	2.43	0.48
2:AC:96:ALA:O	2:AC:100:ILE:HG12	2.14	0.48
2:AD:131:VAL:HG21	2:AD:192:TYR:CZ	2.48	0.48
2:AG:183:ASN:N	2:AG:187:ARG:O	2.41	0.48
2:AH:97:LEU:O	2:AH:101:LEU:HB2	2.14	0.48
2:AJ:75:VAL:H	2:AJ:98:GLN:HE22	1.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AJ:200:SER:OG	2:AJ:201:ILE:N	2.46	0.48
2:AK:372:ASP:O	2:AK:375:SER:OG	2.24	0.48
4:AR:65:PRO:HD2	4:AR:75:ASN:HD22	1.78	0.48
6:R3:32:TYR:OH	6:U3:15:HIS:ND1	2.29	0.48
3:H:46:ARG:HB3	3:H:54:MET:HB2	1.96	0.48
3:AO:99:VAL:HB	3:AO:109:LYS:HB3	1.96	0.48
5:AY:14:ILE:HG12	5:AY:87:VAL:HG23	1.95	0.48
6:S5:74:ILE:HG23	6:S5:75:ALA:H	1.78	0.48
6:S5:167:ARG:HG2	6:S5:168:ASN:O	2.13	0.48
6:T5:80:VAL:HG12	6:T5:91:GLU:HG2	1.94	0.48
1:X:62:ASP:OD2	1:X:63:GLY:N	2.47	0.48
1:b:48:LEU:HD23	1:c:1:MET:HE3	1.96	0.48
1:s:53:LEU:HD23	1:s:182:HIS:HA	1.96	0.48
1:v:21:SER:HB3	1:A:49:ARG:HB3	1.96	0.48
1:7:3:PHE:HD1	1:7:38:MET:HE2	1.79	0.48
1:D:206:GLN:OE1	1:D:207:VAL:N	2.46	0.48
1:E:30:ARG:HD2	1:E:230:GLY:N	2.27	0.48
2:AA:172:GLU:OE2	2:AB:24:LYS:HE3	2.13	0.48
2:AF:317:ILE:H	2:AF:317:ILE:HD12	1.78	0.48
2:AH:141:ALA:HB3	2:AH:143:TRP:CH2	2.49	0.48
2:AK:102:GLN:OE1	2:AK:102:GLN:HA	2.14	0.48
5:AU:6:GLN:NE2	4:AR:128:THR:OG1	2.46	0.48
6:R3:43:TYR:CD2	6:R3:44:THR:HG23	2.48	0.48
6:R3:72:THR:O	6:R3:72:THR:OG1	2.30	0.48
6:S3:167:ARG:HG2	6:S3:168:ASN:O	2.13	0.48
6:T3:19:ASP:OD1	6:T3:19:ASP:N	2.46	0.48
3:H:20:ASP:N	3:H:24:ARG:O	2.47	0.48
5:Ab:17:THR:OG1	5:Ab:84:GLN:HB3	2.14	0.48
6:R5:41:GLU:O	6:R5:42:LEU:C	2.56	0.48
1:J:75:PHE:CE1	1:J:162:PRO:HD2	2.46	0.47
1:R:75:PHE:CE1	1:R:161:GLN:HG2	2.48	0.47
1:T:83:VAL:HG23	1:T:126:THR:HA	1.96	0.47
1:a:74:ALA:HB3	1:a:148:TYR:CD1	2.49	0.47
1:d:23:CYS:HB2	1:e:229:CYS:HB3	1.66	0.47
1:e:206:GLN:OE1	1:e:207:VAL:N	2.46	0.47
1:f:2:TYR:OH	1:f:28:SER:OG	2.31	0.47
1:h:53:LEU:HD12	1:h:206:GLN:CD	2.39	0.47
1:k:75:PHE:HE1	1:k:162:PRO:HD2	1.78	0.47
1:l:138:TRP:CZ3	1:l:147:GLU:HB3	2.49	0.47
1:r:157:SER:OG	1:r:158:GLU:N	2.46	0.47
1:v:206:GLN:OE1	1:v:207:VAL:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:y:29:ALA:HB1	1:y:190:VAL:HG21	1.96	0.47
1:z:104:ILE:HG21	1:z:115:VAL:HG21	1.95	0.47
1:1:21:SER:HB3	1:F:49:ARG:HB3	1.96	0.47
1:7:53:LEU:HD23	1:7:182:HIS:HA	1.96	0.47
1:0:153:ASP:OD1	1:0:159:LEU:HB2	2.14	0.47
1:0:210:ASP:HB3	1:0:216:PHE:HE2	1.79	0.47
1:B:3:PHE:HD1	1:B:38:MET:HE2	1.79	0.47
1:G:56:LYS:HB3	1:G:207:VAL:CG1	2.44	0.47
2:AA:99:GLN:HE22	2:AB:83:GLN:HB3	1.78	0.47
2:AA:217:ILE:HB	2:AA:309:ILE:HG22	1.95	0.47
2:AA:339:LYS:NZ	2:AA:379:LEU:HA	2.29	0.47
3:AM:81:VAL:HB	3:AM:93:PHE:HB2	1.94	0.47
5:AU:97:MET:SD	5:AU:126:GLU:HG2	2.53	0.47
1:J:157:SER:OG	1:J:158:GLU:N	2.47	0.47
1:L:53:LEU:HD12	1:L:206:GLN:CD	2.39	0.47
1:N:100:VAL:HA	1:N:142:ASN:HD21	1.78	0.47
1:N:141:ILE:HG22	1:N:142:ASN:HD22	1.79	0.47
1:R:209:ILE:HD11	1:R:213:GLY:HA2	1.95	0.47
1:Y:47:PRO:O	1:Y:49:ARG:HG2	2.14	0.47
1:a:194:ALA:HB1	1:a:226:ILE:HG21	1.95	0.47
1:i:3:PHE:HD1	1:i:38:MET:HE2	1.78	0.47
1:j:207:VAL:HG12	1:j:217:VAL:HG22	1.96	0.47
1:l:75:PHE:HE1	1:l:162:PRO:HD2	1.79	0.47
1:s:72:SER:O	1:s:91:LEU:HD12	2.14	0.47
1:u:209:ILE:HG13	1:u:214:ASN:O	2.15	0.47
1:w:210:ASP:CG	1:w:214:ASN:HD22	2.21	0.47
1:x:209:ILE:HD11	1:x:213:GLY:HA2	1.95	0.47
1:5:71:VAL:HG11	1:5:141:ILE:HB	1.96	0.47
1:C:206:GLN:OE1	1:C:207:VAL:N	2.47	0.47
2:AA:280:ALA:HB1	6:T5:198:ARG:NH1	2.28	0.47
2:AD:130:LYS:O	2:AD:142:ILE:HA	2.14	0.47
2:AH:131:VAL:HG21	2:AH:192:TYR:CZ	2.49	0.47
2:AJ:96:ALA:O	2:AJ:100:ILE:HG12	2.14	0.47
2:AK:363:CYS:SG	2:AK:364:GLY:N	2.87	0.47
3:AP:41:PRO:HD3	3:AN:103:GLU:HG2	1.96	0.47
5:AZ:87:VAL:HG12	5:AZ:99:LEU:HB3	1.97	0.47
3:H:5:ASP:O	3:H:7:LYS:N	2.48	0.47
5:AY:97:MET:SD	5:AY:126:GLU:HG2	2.54	0.47
3:I:8:HIS:CD2	3:I:39:ILE:HG12	2.49	0.47
1:K:88:LEU:N	1:K:121:GLY:O	2.47	0.47
1:P:108:ASN:HB3	1:P:138:TRP:CD1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:g:46:ALA:HB3	1:g:47:PRO:HD3	1.96	0.47
1:j:38:MET:HG2	1:j:185:LYS:HG2	1.96	0.47
1:k:85:GLU:OE1	1:k:124:THR:HG22	2.14	0.47
1:l:88:LEU:N	1:l:121:GLY:O	2.46	0.47
1:s:67:THR:O	1:s:67:THR:OG1	2.30	0.47
1:4:112:ASN:O	1:4:128:GLY:N	2.46	0.47
1:D:46:ALA:HB3	1:D:47:PRO:HD3	1.96	0.47
2:AB:132:SER:HA	2:AB:191:ASN:ND2	2.28	0.47
2:AB:168:GLU:OE2	2:AB:168:GLU:N	2.47	0.47
2:AE:132:SER:HA	2:AE:191:ASN:ND2	2.29	0.47
2:AF:28:ARG:HH11	2:AF:29:ARG:HB3	1.79	0.47
2:AF:316:PRO:HD2	2:AF:341:PHE:HB2	1.96	0.47
2:AI:129:PHE:HB2	2:AI:194:PHE:CD2	2.49	0.47
2:AK:66:LEU:HG	2:AL:348:PRO:O	2.14	0.47
2:AL:130:LYS:O	2:AL:142:ILE:HA	2.13	0.47
5:AU:87:VAL:HG12	5:AU:99:LEU:HB3	1.95	0.47
5:AU:89:VAL:HG12	5:AU:97:MET:HB2	1.96	0.47
6:R3:147:GLY:HA3	6:R3:194:TRP:NE1	2.29	0.47
6:R4:166:VAL:O	6:R4:167:ARG:HB2	2.13	0.47
6:U4:78:PRO:HB3	6:U4:93:ILE:HG12	1.96	0.47
6:U4:150:LYS:O	6:U4:151:LEU:C	2.56	0.47
3:AO:45:ILE:N	3:I:97:SER:OG	2.47	0.47
5:AY:100:THR:HB	5:AY:101:GLU:OE1	2.13	0.47
5:AY:128:LEU:O	5:AY:129:PRO:C	2.55	0.47
1:M:209:ILE:HD11	1:M:213:GLY:HA2	1.96	0.47
1:O:38:MET:HG2	1:O:185:LYS:HG2	1.95	0.47
1:P:88:LEU:N	1:P:121:GLY:O	2.47	0.47
1:U:75:PHE:HE1	1:U:162:PRO:HD2	1.80	0.47
1:c:118:GLY:N	1:c:122:ALA:O	2.28	0.47
1:f:99:GLN:HG2	1:f:101:GLU:OE1	2.14	0.47
1:i:38:MET:HG2	1:i:185:LYS:HG2	1.97	0.47
1:j:59:PHE:HE2	1:j:175:ARG:NE	2.11	0.47
1:n:48:LEU:HD23	1:o:1:MET:HE3	1.97	0.47
1:n:53:LEU:HD23	1:n:182:HIS:HA	1.96	0.47
1:z:29:ALA:HB1	1:z:190:VAL:HG21	1.97	0.47
1:1:46:ALA:HB3	1:1:47:PRO:HD3	1.95	0.47
1:4:75:PHE:CE1	1:4:162:PRO:HD2	2.50	0.47
1:9:46:ALA:HB3	1:9:47:PRO:HD3	1.96	0.47
2:AB:29:ARG:HD2	2:AB:30:PHE:N	2.28	0.47
2:AC:277:ILE:HD11	2:AD:241:SER:OG	2.14	0.47
2:AG:112:GLN:NE2	2:AH:197:VAL:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AH:140:ASN:HD22	2:AI:18:PRO:HG3	1.78	0.47
2:AK:19:SER:O	2:AK:19:SER:OG	2.33	0.47
3:AM:15:GLN:OE1	3:AM:80:TRP:NE1	2.45	0.47
4:AR:141:ASP:HB3	3:I:52:VAL:HG21	1.96	0.47
6:R3:186:VAL:HB	6:R3:191:GLN:HB2	1.96	0.47
6:R5:166:VAL:O	6:R5:167:ARG:HB2	2.14	0.47
1:Q:126:THR:O	1:Q:126:THR:OG1	2.30	0.47
1:T:8:PRO:HG3	6:R4:53:THR:HG21	1.96	0.47
1:a:209:ILE:HG13	1:a:214:ASN:O	2.14	0.47
1:b:31:PRO:HD3	1:b:227:GLY:O	2.14	0.47
1:g:194:ALA:HB1	1:g:226:ILE:HG21	1.95	0.47
1:i:80:VAL:HG12	1:i:155:THR:HB	1.97	0.47
1:m:25:GLU:OE1	1:m:25:GLU:N	2.48	0.47
1:y:38:MET:SD	1:y:185:LYS:HE2	2.54	0.47
1:z:73:ASN:HB3	1:z:164:PHE:HE1	1.80	0.47
1:2:209:ILE:HG13	1:2:214:ASN:O	2.15	0.47
1:D:75:PHE:HE1	1:D:162:PRO:HD2	1.78	0.47
2:AD:55:PRO:HA	2:AE:216:ALA:HB1	1.95	0.47
2:AH:183:ASN:OD1	2:AH:184:ASP:N	2.40	0.47
2:AJ:348:PRO:HA	2:AJ:352:THR:HG22	1.96	0.47
4:AT:22:ALA:HB3	4:AT:23:PRO:HD3	1.96	0.47
6:R4:166:VAL:HA	6:S4:163:VAL:CG2	2.45	0.47
6:U4:143:GLY:O	6:U4:144:ILE:C	2.56	0.47
5:AY:32:GLN:HG3	5:AY:33:PRO:HD2	1.97	0.47
1:b:29:ALA:HB1	1:b:190:VAL:HG21	1.97	0.47
1:b:138:TRP:CZ3	1:b:147:GLU:HB3	2.49	0.47
1:m:72:SER:O	1:m:91:LEU:HD12	2.14	0.47
1:n:126:THR:O	1:n:126:THR:OG1	2.32	0.47
1:u:52:GLY:O	1:u:209:ILE:HG22	2.14	0.47
1:u:138:TRP:CZ3	1:u:147:GLU:HB3	2.49	0.47
1:3:153:ASP:HA	1:3:159:LEU:HD23	1.97	0.47
1:4:48:LEU:HD23	1:5:1:MET:HE3	1.96	0.47
1:4:159:LEU:HD12	1:4:160:PRO:HD3	1.96	0.47
1:G:126:THR:O	1:G:126:THR:OG1	2.26	0.47
2:AC:363:CYS:SG	2:AC:364:GLY:N	2.88	0.47
2:AD:183:ASN:O	2:AD:184:ASP:C	2.57	0.47
2:AE:56:VAL:HB	2:AE:309:ILE:HD11	1.96	0.47
2:AE:376:ILE:HG21	2:AE:379:LEU:HD23	1.95	0.47
2:AF:261:GLU:O	2:AF:265:GLU:HG2	2.14	0.47
2:AI:90:SER:C	2:AI:92:SER:H	2.23	0.47
2:AI:172:GLU:OE2	2:AJ:24:LYS:HE3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AJ:154:PHE:HA	2:AJ:160:VAL:HA	1.96	0.47
2:AK:243:TRP:CZ2	2:AL:289:MET:HG3	2.50	0.47
4:AQ:22:ALA:HB3	4:AQ:23:PRO:HD3	1.95	0.47
3:AN:92:TRP:CH2	3:AN:124:PRO:HG3	2.50	0.47
3:H:8:HIS:CD2	3:H:39:ILE:HG12	2.49	0.47
3:H:69:TYR:HD2	3:H:108:MET:HG3	1.80	0.47
5:AY:84:GLN:HE21	5:AY:101:GLU:HA	1.78	0.47
1:J:13:SER:HB3	6:R5:52:LYS:HA	1.96	0.47
1:N:75:PHE:CE1	1:N:161:GLN:HG2	2.50	0.47
1:O:39:VAL:HG23	1:O:184:LEU:HB3	1.96	0.47
1:P:154:PRO:O	1:P:155:THR:HG22	2.14	0.47
1:Q:23:CYS:HB3	1:R:229:CYS:HB3	1.76	0.47
1:R:113:GLY:HA3	1:R:125:TYR:CE2	2.50	0.47
1:S:141:ILE:HG22	1:S:142:ASN:HD22	1.80	0.47
1:X:10:ASN:HD21	6:U5:77:ARG:HH22	1.62	0.47
1:Z:25:GLU:OE1	1:Z:25:GLU:N	2.27	0.47
1:b:79:LYS:HD2	1:b:153:ASP:HB2	1.97	0.47
1:b:90:ASP:OD1	1:b:90:ASP:N	2.42	0.47
1:b:116:GLU:O	1:b:123:PHE:HA	2.14	0.47
1:c:78:THR:HB	1:c:84:PHE:HD2	1.79	0.47
1:c:177:VAL:O	1:c:179:PRO:HD3	2.15	0.47
1:d:75:PHE:HD1	1:d:149:VAL:HG13	1.80	0.47
1:g:116:GLU:O	1:g:123:PHE:HA	2.15	0.47
1:j:90:ASP:OD1	1:j:90:ASP:N	2.46	0.47
1:k:67:THR:O	1:k:67:THR:OG1	2.31	0.47
1:k:75:PHE:CZ	1:k:161:GLN:HG2	2.49	0.47
1:q:46:ALA:HB3	1:q:47:PRO:HD3	1.96	0.47
1:r:78:THR:O	1:r:152:VAL:HA	2.14	0.47
1:s:73:ASN:HB3	1:s:164:PHE:CE1	2.50	0.47
1:t:74:ALA:HB3	1:t:148:TYR:CD1	2.49	0.47
1:t:138:TRP:CE3	1:t:147:GLU:HB3	2.50	0.47
1:v:174:ARG:CZ	1:v:187:VAL:HG21	2.44	0.47
1:w:78:THR:O	1:w:152:VAL:HA	2.15	0.47
1:2:59:PHE:CD1	1:2:204:VAL:HG12	2.50	0.47
1:7:172:ALA:O	1:7:175:ARG:NH1	2.48	0.47
1:8:30:ARG:HD2	1:8:230:GLY:H	1.80	0.47
1:9:53:LEU:HD12	1:9:206:GLN:NE2	2.29	0.47
1:9:112:ASN:O	1:9:128:GLY:N	2.47	0.47
1:9:209:ILE:HG13	1:9:214:ASN:O	2.15	0.47
1:0:30:ARG:NH1	1:0:229:CYS:HA	2.30	0.47
1:E:174:ARG:NE	1:E:187:VAL:HG21	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AA:69:GLN:HE22	2:AB:352:THR:HG23	1.78	0.47
2:AA:99:GLN:NE2	2:AB:83:GLN:HB3	2.29	0.47
2:AA:129:PHE:HB2	2:AA:194:PHE:CD2	2.50	0.47
2:AA:219:VAL:HB	2:AA:220:PRO:HD3	1.97	0.47
2:AB:74:ASP:OD2	2:AB:74:ASP:N	2.47	0.47
2:AC:282:THR:OG1	2:AD:249:ARG:HD3	2.15	0.47
2:AD:133:VAL:HA	2:AD:139:VAL:HA	1.96	0.47
2:AD:297:HIS:CE1	2:AD:299:LYS:HB2	2.45	0.47
2:AE:121:TRP:HE3	2:AE:127:MET:HG3	1.80	0.47
2:AE:350:TYR:C	2:AE:353:PRO:HD2	2.40	0.47
2:AH:130:LYS:O	2:AH:142:ILE:HA	2.15	0.47
2:AI:150:LEU:HD11	2:AI:163:PHE:HB3	1.96	0.47
2:AI:219:VAL:HB	2:AI:220:PRO:HD3	1.96	0.47
2:AK:351:LEU:HB3	2:AK:371:PHE:CZ	2.50	0.47
3:AM:99:VAL:HB	3:AM:109:LYS:HB3	1.97	0.47
6:T3:6:LEU:HD22	6:T3:140:VAL:HG11	1.96	0.47
6:T3:32:TYR:HB3	6:T3:152:ILE:HG23	1.97	0.47
4:AS:155:TRP:CZ3	4:AS:157:GLU:HB3	2.50	0.47
5:AV:97:MET:SD	5:AV:126:GLU:HG2	2.55	0.47
6:R4:7:LEU:HD12	6:R4:7:LEU:HA	1.75	0.47
6:R4:200:VAL:O	6:R4:201:LEU:C	2.54	0.47
6:S4:74:ILE:HG13	6:S4:131:VAL:O	2.15	0.47
6:S4:164:MET:HE3	6:S4:164:MET:HB3	1.74	0.47
6:T4:32:TYR:HB3	6:T4:152:ILE:HG23	1.96	0.47
6:U4:50:PRO:HB3	6:U4:138:ASN:HB3	1.96	0.47
6:R5:32:TYR:CD2	6:R5:156:ILE:HG22	2.50	0.47
6:S5:11:THR:HG23	6:T5:28:LEU:HD12	1.96	0.47
6:S5:74:ILE:O	6:S5:75:ALA:HB2	2.13	0.47
1:J:75:PHE:CE1	1:J:161:GLN:HG2	2.50	0.47
1:O:4:PHE:HB2	1:O:39:VAL:HG12	1.97	0.47
1:O:13:SER:HB3	6:R3:52:LYS:HA	1.97	0.47
1:O:75:PHE:CE1	1:O:161:GLN:HG2	2.50	0.47
1:T:92:PHE:HB2	1:T:141:ILE:HG21	1.96	0.47
1:f:75:PHE:HE1	1:f:162:PRO:HD2	1.80	0.47
1:i:75:PHE:HD1	1:i:149:VAL:HG13	1.78	0.47
1:v:46:ALA:HB3	1:v:47:PRO:HD3	1.97	0.47
1:3:30:ARG:HD2	1:3:230:GLY:H	1.79	0.47
1:5:30:ARG:NH1	1:5:229:CYS:HA	2.30	0.47
1:C:138:TRP:CE3	1:C:147:GLU:HB3	2.49	0.47
1:G:167:PRO:HA	1:G:191:SER:HB3	1.97	0.47
2:AB:54:HIS:HE1	2:AB:56:VAL:HB	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AC:278:PHE:CD2	6:R5:201:LEU:HD21	2.47	0.47
2:AJ:194:PHE:CD1	2:AJ:361:PHE:HE2	2.33	0.47
2:AK:90:SER:C	2:AK:92:SER:H	2.22	0.47
2:AL:141:ALA:HB3	2:AL:143:TRP:CH2	2.50	0.47
4:AR:22:ALA:HB3	4:AR:23:PRO:HD3	1.97	0.47
6:R3:202:LEU:N	6:R3:202:LEU:HD23	2.29	0.47
5:AV:14:ILE:HG12	5:AV:87:VAL:HG23	1.97	0.47
6:U4:40:ALA:HB1	6:U4:41:GLU:OE1	2.15	0.47
6:U4:148:ILE:HA	6:U4:194:TRP:HZ2	1.80	0.47
4:AW:104:TYR:OH	4:AW:108:GLU:OE1	2.33	0.47
1:P:126:THR:O	1:P:126:THR:OG1	2.30	0.47
1:P:194:ALA:HB1	1:P:226:ILE:HG21	1.95	0.47
1:S:3:PHE:HD1	1:S:38:MET:HE2	1.80	0.47
1:S:75:PHE:CE1	1:S:162:PRO:HD2	2.49	0.47
1:S:209:ILE:HG13	1:S:214:ASN:O	2.15	0.47
1:Y:107:LEU:HD23	1:Y:107:LEU:HA	1.70	0.47
1:c:178:ASP:OD2	1:c:181:THR:HG22	2.15	0.47
1:i:73:ASN:OD1	1:i:147:GLU:N	2.28	0.47
1:k:74:ALA:HB3	1:k:148:TYR:CD1	2.49	0.47
1:v:75:PHE:CE1	1:v:162:PRO:HD2	2.50	0.47
1:2:78:THR:O	1:2:152:VAL:HA	2.14	0.47
1:B:38:MET:HE3	1:B:183:VAL:HG21	1.97	0.47
1:C:104:ILE:HG12	1:C:117:LEU:HD12	1.96	0.47
1:D:112:ASN:O	1:D:128:GLY:N	2.47	0.47
1:G:53:LEU:HD23	1:G:182:HIS:HA	1.95	0.47
2:AB:194:PHE:CD1	2:AB:361:PHE:HE2	2.33	0.47
2:AE:129:PHE:HB2	2:AE:194:PHE:CD2	2.50	0.47
2:AH:283:ASP:OD2	2:AH:283:ASP:N	2.48	0.47
2:AJ:68:VAL:HG23	2:AJ:346:ILE:HD12	1.97	0.47
2:AL:305:GLN:O	2:AL:309:ILE:HG12	2.15	0.47
3:AP:20:ASP:N	3:AP:24:ARG:O	2.47	0.47
6:U3:40:ALA:HB1	6:U3:41:GLU:OE1	2.15	0.47
5:Ab:129:PRO:HA	5:Ab:130:PRO:HD3	1.83	0.47
6:R5:200:VAL:HG23	6:R5:200:VAL:O	2.15	0.47
6:U5:13:ARG:HD3	6:U5:18:CYS:HB3	1.96	0.47
1:Q:78:THR:HG23	1:Q:152:VAL:HG12	1.98	0.47
1:W:209:ILE:HD11	1:W:213:GLY:HA2	1.97	0.47
1:X:85:GLU:OE1	1:X:124:THR:HG22	2.14	0.47
1:k:210:ASP:OD1	1:k:214:ASN:N	2.47	0.47
1:m:118:GLY:N	1:m:122:ALA:O	2.28	0.47
1:s:208:ALA:HB3	1:s:216:PHE:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:56:LYS:HB3	1:u:207:VAL:CG1	2.45	0.47
1:y:75:PHE:CZ	1:y:161:GLN:HG2	2.50	0.47
1:7:177:VAL:HG11	1:7:206:GLN:HE22	1.80	0.47
1:E:71:VAL:HG11	1:E:141:ILE:HB	1.98	0.47
1:E:153:ASP:OD1	1:E:159:LEU:HB2	2.15	0.47
2:AB:335:ASP:N	2:AB:335:ASP:OD1	2.48	0.47
2:AC:68:VAL:HG11	2:AC:118:ALA:CB	2.45	0.47
2:AC:262:GLY:HA3	6:R5:202:LEU:HD22	1.97	0.47
2:AE:98:GLN:O	2:AE:102:GLN:HG2	2.15	0.47
2:AE:258:GLU:OE2	6:T4:199:ARG:HB2	2.15	0.47
2:AH:56:VAL:HB	2:AH:309:ILE:HD11	1.97	0.47
2:AI:338:ARG:NH2	2:AJ:343:GLU:OE1	2.38	0.47
2:AI:400:GLU:HA	2:AI:403:GLU:HG3	1.96	0.47
2:AJ:261:GLU:O	2:AJ:265:GLU:HG2	2.15	0.47
2:AK:374:ASP:OD1	2:AK:374:ASP:N	2.43	0.47
6:R5:194:TRP:O	6:R5:195:PHE:C	2.58	0.47
6:T5:19:ASP:N	6:T5:19:ASP:OD1	2.46	0.47
6:U5:184:GLY:C	6:U5:186:VAL:H	2.22	0.47
1:L:167:PRO:HA	1:L:191:SER:HB3	1.97	0.46
1:O:49:ARG:HD2	6:R3:89:PRO:O	2.14	0.46
1:Q:71:VAL:HG13	1:Q:144:ASN:HB2	1.97	0.46
1:U:75:PHE:CE1	1:U:162:PRO:HD2	2.51	0.46
1:Y:80:VAL:HG12	1:Y:155:THR:HB	1.97	0.46
1:e:210:ASP:HB3	1:e:216:PHE:HE2	1.80	0.46
1:g:35:ASN:OD1	1:g:36:GLY:N	2.42	0.46
1:h:206:GLN:OE1	1:h:207:VAL:N	2.47	0.46
1:j:25:GLU:CD	1:j:25:GLU:H	2.18	0.46
1:p:52:GLY:O	1:p:209:ILE:HG22	2.15	0.46
1:6:126:THR:O	1:6:126:THR:OG1	2.32	0.46
1:8:138:TRP:CE3	1:8:147:GLU:HB3	2.50	0.46
1:9:75:PHE:CE1	1:9:162:PRO:HD2	2.50	0.46
1:E:73:ASN:HB3	1:E:164:PHE:HE1	1.79	0.46
2:AB:265:GLU:OE1	2:AB:271:ASP:HB3	2.14	0.46
2:AG:55:PRO:HA	2:AH:216:ALA:HB1	1.96	0.46
2:AG:279:ILE:HG23	6:R4:200:VAL:HG21	1.96	0.46
2:AH:167:ASP:O	2:AH:171:LYS:NZ	2.48	0.46
2:AI:18:PRO:C	2:AI:20:ALA:H	2.23	0.46
2:AI:25:ILE:O	2:AI:28:ARG:HG2	2.15	0.46
2:AI:280:ALA:HB1	6:T3:198:ARG:NH1	2.29	0.46
2:AJ:133:VAL:HA	2:AJ:139:VAL:HA	1.97	0.46
2:AJ:252:ASP:HA	6:T3:43:TYR:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AK:71:VAL:HG22	2:AK:376:ILE:HD11	1.97	0.46
2:AK:155:ASP:HB3	2:AK:161:GLU:OE2	2.16	0.46
3:AM:66:THR:HA	3:AM:108:MET:O	2.15	0.46
6:S3:154:TRP:CZ2	6:S3:187:ILE:HD11	2.49	0.46
6:R4:165:SER:HB2	6:R4:169:THR:HG23	1.97	0.46
6:U4:41:GLU:OE1	6:U4:41:GLU:N	2.48	0.46
6:U4:134:ARG:HH11	6:U4:138:ASN:HA	1.80	0.46
1:J:56:LYS:HB3	1:J:207:VAL:HG11	1.96	0.46
1:Q:53:LEU:HD12	1:Q:206:GLN:CD	2.40	0.46
1:T:49:ARG:HD2	6:R4:89:PRO:O	2.15	0.46
1:T:208:ALA:HB3	1:T:216:PHE:HB2	1.95	0.46
1:Y:138:TRP:CZ3	1:Y:147:GLU:HB3	2.49	0.46
1:g:79:LYS:HD2	1:g:153:ASP:HB2	1.97	0.46
1:w:194:ALA:HB1	1:w:226:ILE:HG21	1.96	0.46
1:D:75:PHE:CZ	1:D:161:GLN:HG2	2.50	0.46
1:D:209:ILE:HG13	1:D:214:ASN:O	2.16	0.46
2:AD:141:ALA:HB3	2:AD:143:TRP:CH2	2.49	0.46
2:AD:280:ALA:HA	2:AE:247:ALA:HB3	1.96	0.46
2:AG:67:THR:O	2:AG:70:SER:OG	2.27	0.46
2:AG:90:SER:C	2:AG:92:SER:H	2.23	0.46
2:AI:132:SER:HA	2:AI:191:ASN:ND2	2.30	0.46
2:AL:133:VAL:HA	2:AL:139:VAL:HA	1.96	0.46
6:R3:32:TYR:HH	6:U3:15:HIS:CE1	2.32	0.46
5:AV:100:THR:HB	5:AV:101:GLU:OE2	2.15	0.46
6:R4:74:ILE:HG13	6:R4:75:ALA:H	1.79	0.46
3:I:5:ASP:O	3:I:7:LYS:N	2.48	0.46
3:I:48:SER:O	3:I:48:SER:OG	2.31	0.46
1:K:75:PHE:CE1	1:K:162:PRO:HD2	2.50	0.46
1:U:138:TRP:CZ3	1:U:147:GLU:HB3	2.50	0.46
1:Y:38:MET:HG2	1:Y:185:LYS:HG2	1.97	0.46
1:f:126:THR:O	1:f:126:THR:OG1	2.33	0.46
1:o:132:THR:HA	1:o:152:VAL:HG23	1.96	0.46
1:p:78:THR:O	1:p:152:VAL:HA	2.15	0.46
1:s:21:SER:OG	1:s:22:CYS:N	2.47	0.46
1:s:85:GLU:OE1	1:s:124:THR:OG1	2.26	0.46
1:x:73:ASN:HB3	1:x:164:PHE:CE1	2.51	0.46
1:C:209:ILE:HG13	1:C:214:ASN:O	2.14	0.46
1:E:138:TRP:CZ3	1:E:147:GLU:HB3	2.51	0.46
1:F:38:MET:HG2	1:F:185:LYS:HG2	1.97	0.46
1:F:79:LYS:HD2	1:F:153:ASP:HB2	1.98	0.46
1:F:172:ALA:O	1:F:175:ARG:NH1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:66:LEU:HD22	2:AC:348:PRO:O	2.15	0.46
2:AB:257:LYS:O	2:AB:261:GLU:HG2	2.15	0.46
2:AB:261:GLU:O	2:AB:265:GLU:HG2	2.15	0.46
2:AF:257:LYS:O	2:AF:261:GLU:HG2	2.15	0.46
2:AG:19:SER:O	2:AG:19:SER:OG	2.34	0.46
2:AG:96:ALA:O	2:AG:100:ILE:HG12	2.16	0.46
2:AG:155:ASP:HB3	2:AG:161:GLU:OE2	2.15	0.46
2:AG:286:VAL:HG11	2:AH:244:LEU:HD13	1.97	0.46
2:AI:98:GLN:O	2:AI:102:GLN:HG2	2.15	0.46
2:AJ:375:SER:O	2:AJ:376:ILE:C	2.59	0.46
2:AK:277:ILE:HD11	2:AL:241:SER:OG	2.16	0.46
3:AM:48:SER:HB3	3:AM:54:MET:CG	2.46	0.46
5:AU:32:GLN:HG3	5:AU:33:PRO:HD2	1.97	0.46
6:T3:98:SER:OG	6:T3:99:ASN:N	2.49	0.46
6:R4:181:THR:C	6:R4:183:ASN:N	2.70	0.46
3:AO:49:GLN:OE1	3:AO:49:GLN:N	2.48	0.46
5:AY:46:THR:HG23	5:AY:60:SER:OG	2.15	0.46
3:I:20:ASP:N	3:I:24:ARG:O	2.48	0.46
1:S:210:ASP:OD1	1:S:213:GLY:N	2.48	0.46
1:W:3:PHE:CD1	1:W:38:MET:HE2	2.51	0.46
1:X:210:ASP:OD1	1:X:213:GLY:N	2.48	0.46
1:Z:59:PHE:HE2	1:Z:175:ARG:NE	2.13	0.46
1:Z:75:PHE:CE1	1:Z:161:GLN:HG2	2.50	0.46
1:h:53:LEU:HD23	1:h:182:HIS:HA	1.97	0.46
1:k:194:ALA:HB1	1:k:226:ILE:HG21	1.97	0.46
2:AB:38:ASN:OD1	2:AB:39:VAL:N	2.49	0.46
2:AE:232:ILE:HG22	6:R5:63:ARG:HH22	1.81	0.46
3:AP:48:SER:O	3:AP:48:SER:OG	2.32	0.46
4:AS:77:ARG:HD2	4:AS:150:ARG:HD3	1.96	0.46
5:Aa:87:VAL:HG12	5:Aa:99:LEU:HB3	1.97	0.46
6:T4:5:THR:OG1	6:T4:137:GLU:OE1	2.25	0.46
6:T4:19:ASP:OD1	6:T4:19:ASP:N	2.45	0.46
6:U4:166:VAL:HG21	6:U4:187:ILE:HG23	1.97	0.46
3:AO:11:ILE:HD13	3:AO:82:TYR:HD2	1.80	0.46
6:S5:154:TRP:CZ2	6:S5:187:ILE:HD11	2.50	0.46
6:U5:41:GLU:N	6:U5:41:GLU:OE1	2.48	0.46
6:U5:66:LYS:HB2	6:U5:66:LYS:HE3	1.57	0.46
1:N:74:ALA:HB2	1:N:91:LEU:HD11	1.97	0.46
1:T:56:LYS:HB3	1:T:207:VAL:CG1	2.46	0.46
1:U:225:SER:O	1:U:225:SER:OG	2.31	0.46
1:W:172:ALA:O	1:W:175:ARG:NH1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:180:ARG:NH2	6:U5:84:GLY:O	2.49	0.46
1:u:78:THR:O	1:u:152:VAL:HA	2.16	0.46
1:z:46:ALA:HB3	1:z:47:PRO:HD3	1.97	0.46
1:1:75:PHE:CE1	1:1:162:PRO:HD2	2.51	0.46
1:2:46:ALA:HB3	1:2:47:PRO:HD3	1.97	0.46
1:E:73:ASN:HB3	1:E:164:PHE:CE1	2.50	0.46
2:AC:90:SER:C	2:AC:92:SER:H	2.24	0.46
2:AH:187:ARG:HA	2:AH:187:ARG:HD2	1.56	0.46
2:AI:69:GLN:HE22	2:AJ:352:THR:HG23	1.79	0.46
2:AI:245:VAL:HB	2:AI:286:VAL:HG22	1.98	0.46
2:AJ:132:SER:HA	2:AJ:191:ASN:ND2	2.28	0.46
4:AQ:155:TRP:CZ3	4:AQ:157:GLU:HB3	2.51	0.46
6:R3:74:ILE:HG13	6:R3:75:ALA:H	1.79	0.46
6:U3:28:LEU:HD23	6:U3:28:LEU:HA	1.77	0.46
4:AT:130:GLU:OE2	4:AT:152:ASN:ND2	2.48	0.46
6:S4:195:PHE:C	6:S4:197:TYR:N	2.73	0.46
1:V:138:TRP:CZ3	1:V:147:GLU:HB3	2.51	0.46
1:e:75:PHE:CE1	1:e:161:GLN:HG2	2.50	0.46
1:e:108:ASN:HB3	1:e:138:TRP:CD1	2.51	0.46
1:r:6:VAL:HG21	1:r:218:HIS:CE1	2.50	0.46
1:z:52:GLY:O	1:z:209:ILE:HG22	2.16	0.46
1:z:78:THR:O	1:z:152:VAL:HA	2.15	0.46
1:4:157:SER:OG	1:4:158:GLU:N	2.49	0.46
1:0:30:ARG:HD2	1:0:230:GLY:N	2.28	0.46
1:A:88:LEU:HG	1:A:141:ILE:HD11	1.98	0.46
1:D:30:ARG:HD2	1:D:230:GLY:H	1.80	0.46
2:AA:338:ARG:NH2	2:AB:343:GLU:OE1	2.35	0.46
2:AB:117:ALA:HB1	2:AB:127:MET:HE2	1.98	0.46
2:AD:359:SER:OG	2:AD:368:ARG:HB2	2.16	0.46
2:AE:90:SER:C	2:AE:92:SER:H	2.24	0.46
3:AM:77:VAL:HG23	3:I:46:ARG:NE	2.30	0.46
3:H:6:ARG:NH2	3:H:68:ASN:HD21	2.13	0.46
6:T4:98:SER:OG	6:T4:100:VAL:HG22	2.16	0.46
1:W:75:PHE:CE1	1:W:161:GLN:HG2	2.50	0.46
1:j:72:SER:O	1:j:91:LEU:HD12	2.16	0.46
1:k:209:ILE:HG13	1:k:214:ASN:O	2.15	0.46
1:m:178:ASP:OD2	1:m:181:THR:HG22	2.16	0.46
1:1:174:ARG:CZ	1:1:187:VAL:HG21	2.45	0.46
1:2:75:PHE:CE1	1:2:162:PRO:HD2	2.50	0.46
1:2:210:ASP:CG	1:2:214:ASN:HD22	2.20	0.46
1:8:153:ASP:HA	1:8:159:LEU:HD23	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:88:LEU:HG	1:O:141:ILE:HD11	1.96	0.46
1:B:56:LYS:HB3	1:B:207:VAL:HG11	1.96	0.46
1:D:175:ARG:HE	1:D:175:ARG:HB3	1.30	0.46
2:AG:68:VAL:HG11	2:AG:118:ALA:CB	2.46	0.46
2:AH:133:VAL:HA	2:AH:139:VAL:HA	1.97	0.46
2:AH:289:MET:HE2	2:AH:289:MET:HA	1.98	0.46
2:AI:127:MET:O	2:AI:196:ILE:N	2.47	0.46
3:AM:45:ILE:N	3:AP:97:SER:OG	2.46	0.46
5:AU:100:THR:HB	5:AU:101:GLU:OE1	2.15	0.46
4:AR:49:LYS:HB2	4:AR:49:LYS:HE2	1.44	0.46
6:T4:167:ARG:O	6:T4:168:ASN:C	2.59	0.46
4:AX:22:ALA:HB3	4:AX:23:PRO:HD3	1.97	0.46
6:S5:195:PHE:C	6:S5:197:TYR:N	2.72	0.46
1:M:113:GLY:HA3	1:M:125:TYR:CE2	2.50	0.46
1:R:3:PHE:CD1	1:R:38:MET:HE2	2.51	0.46
1:V:3:PHE:CD2	6:S4:77:ARG:HG2	2.51	0.46
1:V:78:THR:O	1:V:152:VAL:HA	2.15	0.46
1:V:108:ASN:HB3	1:V:138:TRP:CD1	2.51	0.46
1:X:120:ASN:N	1:X:120:ASN:OD1	2.49	0.46
1:Z:72:SER:O	1:Z:91:LEU:HD12	2.16	0.46
1:Z:88:LEU:N	1:Z:121:GLY:O	2.49	0.46
1:z:154:PRO:HG2	1:z:156:THR:HG22	1.98	0.46
1:4:138:TRP:CZ3	1:4:147:GLU:HB3	2.51	0.46
1:8:80:VAL:HG12	1:8:155:THR:HB	1.97	0.46
1:E:30:ARG:NH1	1:E:229:CYS:HA	2.31	0.46
1:F:99:GLN:HG2	1:F:101:GLU:OE2	2.15	0.46
2:AC:127:MET:O	2:AC:196:ILE:N	2.44	0.46
2:AD:220:PRO:HB2	2:AD:309:ILE:HG23	1.97	0.46
2:AF:68:VAL:HG23	2:AF:346:ILE:HD12	1.97	0.46
2:AF:285:LYS:HB2	2:AF:285:LYS:NZ	2.31	0.46
2:AG:279:ILE:HG23	6:R4:200:VAL:CG2	2.45	0.46
2:AH:260:LYS:NZ	6:R4:201:LEU:HD11	2.31	0.46
2:AI:99:GLN:NE2	2:AJ:83:GLN:HB3	2.30	0.46
2:AJ:153:LYS:NZ	2:AJ:161:GLU:HB2	2.31	0.46
2:AL:289:MET:HE2	2:AL:289:MET:HA	1.98	0.46
4:AR:95:LYS:HB2	4:AR:95:LYS:HE3	1.36	0.46
3:AP:86:LEU:HB2	6:U4:20:ASP:H	1.81	0.46
6:R3:25:THR:HG23	6:U3:14:GLU:OE2	2.15	0.46
4:AS:128:THR:OG1	5:Aa:6:GLN:NE2	2.49	0.46
5:Aa:39:THR:HG22	5:AY:110:SER:O	2.15	0.46
6:R4:35:ALA:HB2	6:U4:142:ALA:CB	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S4:69:LEU:CD1	6:S4:73:PRO:HD3	2.46	0.46
3:AO:46:ARG:NE	3:I:77:VAL:HG23	2.29	0.46
6:R5:195:PHE:O	6:R5:196:ARG:C	2.59	0.46
6:T5:78:PRO:HB3	6:T5:91:GLU:HB3	1.98	0.46
6:T5:98:SER:OG	6:T5:99:ASN:N	2.49	0.46
1:O:157:SER:OG	1:O:158:GLU:N	2.48	0.46
1:O:208:ALA:HB3	1:O:216:PHE:HB2	1.98	0.46
1:c:75:PHE:HE1	1:c:162:PRO:HD2	1.79	0.46
1:e:88:LEU:N	1:e:121:GLY:O	2.48	0.46
1:f:209:ILE:HG13	1:f:214:ASN:O	2.15	0.46
1:g:31:PRO:HD3	1:g:227:GLY:O	2.16	0.46
1:j:75:PHE:CE1	1:j:161:GLN:HG2	2.51	0.46
1:n:73:ASN:HB3	1:n:164:PHE:CE1	2.50	0.46
1:v:138:TRP:CH2	1:v:192:PRO:HD2	2.51	0.46
1:2:6:VAL:HG21	1:2:218:HIS:CE1	2.51	0.46
1:6:172:ALA:O	1:6:175:ARG:NH1	2.49	0.46
2:AA:90:SER:C	2:AA:92:SER:H	2.24	0.46
2:AB:71:VAL:HG22	2:AB:371:PHE:HB2	1.97	0.46
2:AC:258:GLU:OE2	6:R5:200:VAL:HG23	2.15	0.46
2:AD:68:VAL:C	2:AD:70:SER:N	2.74	0.46
2:AE:169:ALA:CB	2:AF:28:ARG:HG3	2.46	0.46
2:AE:274:GLY:HA3	2:AG:233:ASP:OD2	2.16	0.46
2:AE:401:LYS:HD2	2:AF:395:PHE:CE1	2.51	0.46
2:AF:54:HIS:HE1	2:AF:56:VAL:HB	1.81	0.46
2:AH:132:SER:HA	2:AH:191:ASN:ND2	2.28	0.46
2:AL:254:GLY:O	2:AL:255:GLN:C	2.58	0.46
3:AP:5:ASP:O	3:AP:7:LYS:N	2.49	0.46
6:R4:32:TYR:OH	6:U4:15:HIS:ND1	2.28	0.46
6:T4:2:ASN:OD1	6:T4:137:GLU:HG2	2.15	0.46
4:AX:38:VAL:HG21	4:AX:81:ILE:HG13	1.98	0.46
1:N:85:GLU:OE1	1:N:124:THR:HG22	2.16	0.46
1:a:126:THR:O	1:a:126:THR:OG1	2.33	0.46
1:c:126:THR:O	1:c:126:THR:OG1	2.33	0.46
1:d:80:VAL:HG12	1:d:155:THR:HB	1.98	0.46
1:e:210:ASP:OD1	1:e:214:ASN:N	2.47	0.46
1:i:66:VAL:HG23	1:i:68:PRO:HD3	1.98	0.46
1:i:132:THR:HG21	1:i:154:PRO:HB3	1.97	0.46
1:i:209:ILE:HD11	1:i:213:GLY:HA2	1.96	0.46
1:i:210:ASP:HB3	1:i:216:PHE:CE2	2.50	0.46
1:l:47:PRO:O	1:l:49:ARG:N	2.49	0.46
1:o:120:ASN:OD1	1:o:120:ASN:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:7:ASP:OD1	1:3:7:ASP:N	2.49	0.46
1:5:56:LYS:HB3	1:5:207:VAL:HG11	1.97	0.46
1:5:126:THR:O	1:5:126:THR:OG1	2.33	0.46
1:7:22:CYS:SG	1:7:23:CYS:N	2.89	0.46
1:8:53:LEU:HD12	1:8:206:GLN:NE2	2.30	0.46
1:D:138:TRP:CZ3	1:D:147:GLU:HB3	2.51	0.46
2:AB:68:VAL:HG23	2:AB:346:ILE:HD12	1.98	0.46
2:AB:220:PRO:HB2	2:AB:309:ILE:HG23	1.97	0.46
2:AC:204:ALA:O	2:AC:208:ASP:HB2	2.16	0.46
2:AC:346:ILE:HD13	2:AC:346:ILE:HA	1.83	0.46
2:AE:99:GLN:HE22	2:AF:83:GLN:HB3	1.80	0.46
2:AE:183:ASN:OD1	2:AE:184:ASP:N	2.42	0.46
2:AE:400:GLU:HA	2:AE:403:GLU:HG3	1.97	0.46
2:AF:74:ASP:N	2:AF:74:ASP:OD1	2.47	0.46
2:AG:282:THR:HA	2:AH:249:ARG:HD3	1.98	0.46
2:AJ:159:ASP:OD1	2:AJ:159:ASP:N	2.49	0.46
2:AJ:252:ASP:HB2	2:AJ:255:GLN:HE21	1.80	0.46
2:AJ:298:SER:HB3	2:AJ:301:PRO:HG2	1.98	0.46
2:AL:359:SER:OG	2:AL:368:ARG:HB2	2.15	0.46
5:AU:44:ALA:HB1	5:AU:60:SER:O	2.15	0.46
3:AP:46:ARG:HB3	3:AP:54:MET:HB2	1.98	0.46
6:R3:177:LEU:CD2	6:T5:166:VAL:HG11	2.46	0.46
3:H:52:VAL:HG21	4:AX:141:ASP:HB3	1.98	0.46
6:R5:171:ASN:ND2	6:R5:173:ASN:HB2	2.31	0.46
1:J:208:ALA:HB3	1:J:216:PHE:HB2	1.98	0.45
1:L:78:THR:O	1:L:152:VAL:HA	2.16	0.45
1:L:138:TRP:CZ3	1:L:147:GLU:HB3	2.51	0.45
1:R:92:PHE:HB2	1:R:141:ILE:HG21	1.98	0.45
1:d:206:GLN:OE1	1:d:207:VAL:N	2.49	0.45
1:e:72:SER:O	1:e:91:LEU:HD12	2.16	0.45
1:i:126:THR:O	1:i:126:THR:OG1	2.32	0.45
1:j:210:ASP:HB3	1:j:216:PHE:HE2	1.80	0.45
1:z:56:LYS:HB3	1:z:207:VAL:CG1	2.46	0.45
1:1:99:GLN:OE1	1:1:99:GLN:N	2.50	0.45
1:4:46:ALA:HB3	1:4:47:PRO:HD3	1.97	0.45
1:7:126:THR:O	1:7:126:THR:OG1	2.26	0.45
1:C:46:ALA:HB3	1:C:47:PRO:HD3	1.98	0.45
2:AC:297:HIS:CE1	2:AC:299:LYS:HB2	2.47	0.45
2:AF:252:ASP:HA	6:T4:43:TYR:HA	1.97	0.45
2:AF:402:ARG:HH21	2:AF:407:TRP:HB3	1.81	0.45
2:AI:154:PHE:HA	2:AI:160:VAL:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AM:92:TRP:CH2	3:AM:124:PRO:HG3	2.51	0.45
6:R3:151:LEU:HD22	6:R3:194:TRP:HH2	1.81	0.45
6:U3:86:LEU:HD12	6:U3:86:LEU:HA	1.78	0.45
4:AT:95:LYS:HZ3	4:AT:95:LYS:N	2.15	0.45
6:U4:40:ALA:HB2	6:U4:194:TRP:CZ2	2.52	0.45
6:R5:74:ILE:HG13	6:R5:75:ALA:H	1.81	0.45
1:M:3:PHE:CD1	1:M:38:MET:HE2	2.51	0.45
1:Q:46:ALA:HB3	1:Q:47:PRO:HD3	1.98	0.45
1:S:38:MET:SD	1:S:185:LYS:HE2	2.56	0.45
1:Y:85:GLU:OE1	1:Y:124:THR:OG1	2.29	0.45
1:g:38:MET:HG2	1:g:185:LYS:HG2	1.99	0.45
1:i:53:LEU:HD23	1:i:182:HIS:HA	1.99	0.45
1:p:138:TRP:CZ3	1:p:147:GLU:HB3	2.51	0.45
1:q:174:ARG:CZ	1:q:187:VAL:HG21	2.46	0.45
1:s:75:PHE:CZ	1:s:161:GLN:HG2	2.51	0.45
1:D:75:PHE:CE1	1:D:162:PRO:HD2	2.51	0.45
1:F:209:ILE:HG13	1:F:214:ASN:O	2.16	0.45
2:AC:286:VAL:HG11	2:AD:244:LEU:HD13	1.98	0.45
2:AF:372:ASP:HB3	2:AF:374:ASP:OD1	2.16	0.45
2:AH:260:LYS:CE	6:R4:201:LEU:HD21	2.44	0.45
2:AI:99:GLN:HE22	2:AJ:83:GLN:HB3	1.80	0.45
4:AR:118:MET:HE3	4:AR:129:PHE:HD2	1.81	0.45
3:AP:6:ARG:NH2	3:AP:68:ASN:HD21	2.14	0.45
3:AP:52:VAL:HG21	4:AT:141:ASP:HB3	1.97	0.45
6:T3:195:PHE:C	6:T3:197:TYR:H	2.25	0.45
3:H:32:VAL:HG12	3:H:33:ILE:HG13	1.98	0.45
4:AX:61:ASP:OD2	4:AX:62:THR:N	2.46	0.45
3:I:6:ARG:NH2	3:I:68:ASN:HD21	2.14	0.45
1:J:38:MET:HG2	1:J:185:LYS:HG2	1.98	0.45
1:Q:88:LEU:N	1:Q:121:GLY:O	2.48	0.45
1:S:85:GLU:OE1	1:S:124:THR:HG22	2.16	0.45
1:T:157:SER:OG	1:T:158:GLU:N	2.48	0.45
1:X:74:ALA:HB2	1:X:91:LEU:HD11	1.99	0.45
1:c:53:LEU:HD12	1:c:206:GLN:CD	2.42	0.45
1:f:75:PHE:CZ	1:f:161:GLN:HG2	2.51	0.45
1:h:78:THR:HB	1:h:84:PHE:HD2	1.79	0.45
1:t:53:LEU:HD12	1:t:206:GLN:CD	2.42	0.45
1:w:215:GLU:N	1:w:215:GLU:OE2	2.48	0.45
1:z:71:VAL:HG23	1:z:91:LEU:O	2.17	0.45
1:4:53:LEU:HD12	1:4:206:GLN:CD	2.42	0.45
1:6:88:LEU:HG	1:6:141:ILE:HD11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:7:60:GLU:HG3	1:8:106:GLU:OE1	2.16	0.45
1:A:30:ARG:HD2	1:A:230:GLY:N	2.29	0.45
1:A:59:PHE:HE2	1:A:175:ARG:HE	1.64	0.45
2:AA:232:ILE:HG22	6:R3:63:ARG:HH22	1.81	0.45
2:AB:96:ALA:O	2:AB:100:ILE:HG12	2.16	0.45
2:AC:38:ASN:OD1	2:AC:39:VAL:N	2.50	0.45
2:AD:169:ALA:HB3	2:AE:28:ARG:CD	2.46	0.45
2:AE:28:ARG:HG3	2:AE:29:ARG:N	2.25	0.45
2:AE:127:MET:O	2:AE:196:ILE:N	2.49	0.45
2:AE:219:VAL:HB	2:AE:220:PRO:HD3	1.96	0.45
2:AF:28:ARG:HH11	2:AF:28:ARG:HG2	1.81	0.45
2:AF:168:GLU:OE2	2:AF:168:GLU:N	2.44	0.45
2:AJ:83:GLN:HE21	2:AJ:366:GLY:H	1.65	0.45
2:AJ:168:GLU:OE2	2:AJ:168:GLU:N	2.46	0.45
2:AJ:220:PRO:HB2	2:AJ:309:ILE:HG23	1.97	0.45
5:AV:128:LEU:HD21	5:Aa:75:PRO:HA	1.98	0.45
6:T5:9:LEU:HD21	6:T5:33:ARG:NH2	2.31	0.45
6:U5:40:ALA:HB1	6:U5:41:GLU:OE1	2.16	0.45
1:L:133:GLY:H	1:L:152:VAL:CG2	2.28	0.45
1:P:75:PHE:CE1	1:P:162:PRO:HD2	2.51	0.45
1:T:138:TRP:CE3	1:T:147:GLU:HB3	2.52	0.45
1:W:113:GLY:HA3	1:W:125:TYR:CE2	2.51	0.45
1:Z:207:VAL:HG12	1:Z:217:VAL:HG22	1.99	0.45
1:b:47:PRO:O	1:b:49:ARG:N	2.49	0.45
1:d:47:PRO:O	1:d:49:ARG:N	2.50	0.45
1:d:53:LEU:HD23	1:d:182:HIS:HA	1.98	0.45
1:m:78:THR:HB	1:m:84:PHE:CD2	2.51	0.45
1:t:48:LEU:HD23	1:u:1:MET:HE3	1.97	0.45
1:y:75:PHE:CE1	1:y:162:PRO:HD2	2.52	0.45
1:6:30:ARG:HD2	1:6:230:GLY:N	2.30	0.45
1:9:9:ARG:NE	1:0:33:GLU:OE2	2.50	0.45
1:C:9:ARG:NH2	1:D:230:GLY:OXT	2.41	0.45
1:G:132:THR:HA	1:G:152:VAL:HG13	1.99	0.45
2:AA:383:ARG:O	2:AA:386:ILE:HG22	2.16	0.45
2:AC:90:SER:OG	2:AC:93:GLN:N	2.29	0.45
2:AC:282:THR:HA	2:AD:249:ARG:HD3	1.97	0.45
2:AD:232:ILE:HD13	2:AE:223:LEU:HD13	1.98	0.45
2:AF:96:ALA:O	2:AF:100:ILE:HG12	2.16	0.45
2:AF:132:SER:O	2:AF:140:ASN:HB2	2.16	0.45
2:AF:265:GLU:OE2	2:AF:271:ASP:HB3	2.16	0.45
4:AS:11:VAL:HG21	4:AS:129:PHE:HZ	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AV:32:GLN:HG3	5:AV:33:PRO:HD2	1.98	0.45
6:S4:169:THR:HA	6:U5:174:ALA:O	2.16	0.45
3:I:52:VAL:HG12	3:I:116:GLU:HB3	1.98	0.45
1:N:180:ARG:NH2	6:U3:84:GLY:O	2.49	0.45
1:O:13:SER:O	1:O:13:SER:OG	2.30	0.45
1:O:75:PHE:CE1	1:O:162:PRO:HD2	2.47	0.45
1:Q:78:THR:O	1:Q:152:VAL:HA	2.16	0.45
1:R:178:ASP:CG	1:R:181:THR:HG22	2.42	0.45
1:S:120:ASN:OD1	1:S:120:ASN:N	2.50	0.45
1:U:194:ALA:HB1	1:U:226:ILE:HG21	1.98	0.45
1:a:67:THR:O	1:a:67:THR:OG1	2.32	0.45
1:c:80:VAL:HG12	1:c:155:THR:HB	1.99	0.45
1:h:171:PRO:HD2	1:h:187:VAL:HG23	1.98	0.45
1:n:172:ALA:O	1:n:175:ARG:NH1	2.49	0.45
1:u:126:THR:O	1:u:126:THR:OG1	2.32	0.45
1:v:90:ASP:OD1	1:v:90:ASP:N	2.49	0.45
1:z:64:VAL:HG12	1:z:199:VAL:O	2.16	0.45
1:4:115:VAL:HA	1:4:124:THR:O	2.17	0.45
1:9:157:SER:OG	1:9:158:GLU:N	2.47	0.45
2:AA:127:MET:O	2:AA:196:ILE:N	2.50	0.45
2:AB:363:CYS:SG	2:AB:364:GLY:N	2.90	0.45
2:AC:240:ASN:ND2	2:AD:234:SER:OG	2.49	0.45
2:AF:83:GLN:HE21	2:AF:366:GLY:H	1.65	0.45
2:AG:103:ARG:NH2	2:AH:365:ALA:HA	2.31	0.45
2:AL:60:CYS:O	2:AL:64:LEU:HG	2.16	0.45
6:T3:37:PHE:O	6:T3:41:GLU:HG3	2.17	0.45
6:U3:175:GLN:HG2	6:U3:177:LEU:HD13	1.98	0.45
6:R5:61:LYS:HE2	6:R5:68:ILE:HD12	1.99	0.45
6:T5:165:SER:OG	6:T5:166:VAL:N	2.44	0.45
1:N:10:ASN:HD21	6:U3:77:ARG:HH22	1.63	0.45
1:S:180:ARG:NH2	6:U4:84:GLY:O	2.49	0.45
1:T:30:ARG:NH1	1:T:229:CYS:HA	2.32	0.45
1:T:177:VAL:O	1:T:179:PRO:HD3	2.17	0.45
1:Z:210:ASP:OD1	1:Z:214:ASN:N	2.47	0.45
1:e:1:MET:HE2	1:e:38:MET:HG3	1.98	0.45
1:e:29:ALA:HB1	1:e:190:VAL:HG21	1.99	0.45
1:f:74:ALA:HB3	1:f:148:TYR:CD1	2.51	0.45
1:l:73:ASN:HB3	1:l:164:PHE:CE1	2.52	0.45
1:l:116:GLU:O	1:l:123:PHE:HA	2.16	0.45
1:m:88:LEU:N	1:m:121:GLY:O	2.50	0.45
1:n:54:THR:HG23	1:n:207:VAL:HG23	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:s:126:THR:O	1:s:126:THR:OG1	2.32	0.45
1:2:47:PRO:O	1:2:49:ARG:N	2.49	0.45
1:7:206:GLN:OE1	1:7:207:VAL:N	2.50	0.45
2:AB:132:SER:O	2:AB:140:ASN:HB2	2.16	0.45
2:AC:282:THR:CA	2:AD:249:ARG:HH11	2.24	0.45
2:AF:41:SER:HB2	2:AF:44:ASN:ND2	2.31	0.45
2:AG:350:TYR:C	2:AG:353:PRO:HD2	2.42	0.45
2:AI:161:GLU:O	2:AI:176:SER:N	2.34	0.45
2:AI:217:ILE:HB	2:AI:309:ILE:HG22	1.97	0.45
2:AJ:63:LYS:O	2:AJ:67:THR:HG23	2.17	0.45
2:AK:240:ASN:ND2	2:AL:234:SER:OG	2.50	0.45
6:S3:190:ALA:HB1	6:S3:194:TRP:CZ2	2.51	0.45
6:T3:177:LEU:HD12	6:T3:177:LEU:HA	1.83	0.45
4:AT:29:GLU:N	4:AT:29:GLU:OE2	2.50	0.45
3:H:48:SER:O	3:H:50:ASP:N	2.50	0.45
6:U5:50:PRO:C	6:U5:51:GLU:HG3	2.41	0.45
1:M:138:TRP:CE3	1:M:147:GLU:HB3	2.52	0.45
1:a:75:PHE:CZ	1:a:161:GLN:HG2	2.51	0.45
1:h:56:LYS:HB3	1:h:207:VAL:HG11	1.98	0.45
1:q:178:ASP:OD2	1:q:181:THR:HG22	2.17	0.45
1:r:46:ALA:HB3	1:r:47:PRO:HD3	1.98	0.45
1:u:154:PRO:HG2	1:u:156:THR:HG22	1.97	0.45
1:2:110:PRO:HA	1:2:136:ARG:O	2.17	0.45
1:5:174:ARG:NE	1:5:187:VAL:HG21	2.32	0.45
1:7:38:MET:HE3	1:7:183:VAL:HG21	1.99	0.45
1:0:46:ALA:HB3	1:0:47:PRO:HD3	1.99	0.45
1:F:106:GLU:OE1	1:F:106:GLU:N	2.43	0.45
1:G:38:MET:HE3	1:G:183:VAL:HG21	1.97	0.45
2:AB:59:ARG:NH1	2:AB:320:LEU:HB3	2.31	0.45
2:AC:59:ARG:NH1	2:AC:320:LEU:HD13	2.32	0.45
2:AD:21:ASN:O	2:AD:24:LYS:HE2	2.17	0.45
2:AD:369:VAL:O	2:AD:370:ILE:HD13	2.17	0.45
2:AF:335:ASP:N	2:AF:335:ASP:OD1	2.49	0.45
2:AH:252:ASP:HA	6:R4:43:TYR:HD1	1.81	0.45
2:AI:121:TRP:HZ2	2:AI:198:LYS:HD3	1.79	0.45
2:AI:355:GLU:OE2	2:AI:370:ILE:HA	2.17	0.45
2:AI:401:LYS:HD2	2:AJ:395:PHE:CE1	2.52	0.45
4:AQ:77:ARG:HD2	4:AQ:150:ARG:HD3	1.99	0.45
5:AZ:39:THR:HG22	5:AV:110:SER:O	2.15	0.45
6:R4:141:PRO:HD2	6:R4:144:ILE:HD13	1.99	0.45
6:U4:148:ILE:O	6:U4:149:LEU:C	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AW:155:TRP:CZ3	4:AW:157:GLU:HB3	2.52	0.45
6:R5:49:THR:OG1	6:R5:50:PRO:HD2	2.17	0.45
6:T5:181:THR:O	6:T5:187:ILE:HG13	2.16	0.45
1:O:30:ARG:NH1	1:O:229:CYS:HA	2.32	0.45
1:S:74:ALA:HB2	1:S:91:LEU:HD11	1.98	0.45
1:S:177:VAL:O	1:S:179:PRO:HD3	2.17	0.45
1:a:24:CYS:HB2	1:a:223:ASP:OD1	2.17	0.45
1:c:25:GLU:OE1	1:c:25:GLU:N	2.48	0.45
1:e:38:MET:HG2	1:e:185:LYS:HG2	1.98	0.45
1:g:167:PRO:HA	1:g:191:SER:HB3	1.99	0.45
1:h:126:THR:O	1:h:126:THR:OG1	2.33	0.45
1:i:47:PRO:O	1:i:49:ARG:N	2.50	0.45
1:l:38:MET:HG2	1:l:185:LYS:HG2	1.98	0.45
1:m:177:VAL:O	1:m:179:PRO:HD3	2.16	0.45
1:p:157:SER:OG	1:p:158:GLU:N	2.50	0.45
1:s:1:MET:HE2	1:s:38:MET:HG3	1.98	0.45
1:t:38:MET:SD	1:t:185:LYS:HE2	2.56	0.45
1:v:178:ASP:OD2	1:v:181:THR:HG22	2.17	0.45
1:x:157:SER:OG	1:x:158:GLU:N	2.49	0.45
1:3:78:THR:O	1:3:152:VAL:HA	2.16	0.45
1:5:73:ASN:HB3	1:5:164:PHE:HE1	1.82	0.45
1:A:133:GLY:H	1:A:152:VAL:HG23	1.80	0.45
1:B:22:CYS:SG	1:B:23:CYS:N	2.89	0.45
1:B:75:PHE:HB2	1:B:164:PHE:CZ	2.52	0.45
1:B:172:ALA:O	1:B:175:ARG:NH1	2.50	0.45
1:E:59:PHE:HE2	1:E:175:ARG:HE	1.63	0.45
2:AB:402:ARG:HH21	2:AB:407:TRP:HB3	1.82	0.45
2:AE:99:GLN:NE2	2:AF:83:GLN:HB3	2.32	0.45
2:AF:153:LYS:NZ	2:AF:161:GLU:HB2	2.32	0.45
2:AF:271:ASP:OD2	6:T4:59:ARG:NH1	2.49	0.45
2:AG:75:VAL:H	2:AG:98:GLN:NE2	2.15	0.45
3:AP:49:GLN:O	3:AP:50:ASP:CB	2.64	0.45
6:R3:49:THR:OG1	6:R3:50:PRO:HD2	2.17	0.45
5:AV:46:THR:HG23	5:AV:60:SER:OG	2.16	0.45
3:H:6:ARG:HA	3:H:38:ALA:HB2	1.99	0.45
5:Aa:32:GLN:HG3	5:Aa:33:PRO:HD2	1.98	0.45
6:R5:35:ALA:HB2	6:U5:142:ALA:HB1	1.99	0.45
6:R5:179:GLY:HA2	6:R5:182:ASN:OD1	2.17	0.45
1:Q:132:THR:HA	1:Q:152:VAL:HG23	1.98	0.45
1:T:46:ALA:HB3	1:T:47:PRO:HD3	1.99	0.45
1:T:75:PHE:CE1	1:T:161:GLN:HG2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:75:PHE:CE1	1:T:162:PRO:HD2	2.48	0.45
1:T:89:SER:C	1:T:91:LEU:N	2.75	0.45
1:m:171:PRO:HD2	1:m:187:VAL:HG23	1.98	0.45
1:s:157:SER:OG	1:s:158:GLU:N	2.49	0.45
1:t:88:LEU:HD12	1:t:91:LEU:HD22	1.99	0.45
1:7:56:LYS:HB3	1:7:207:VAL:CG1	2.46	0.45
1:0:53:LEU:HD12	1:0:206:GLN:CD	2.42	0.45
2:AC:161:GLU:HB3	2:AC:179:LYS:HE2	1.98	0.45
2:AC:263:ILE:HG12	6:R5:202:LEU:HD11	1.99	0.45
2:AF:363:CYS:SG	2:AF:364:GLY:N	2.90	0.45
6:T3:98:SER:OG	6:T3:100:VAL:HG22	2.16	0.45
6:U3:41:GLU:OE1	6:U3:41:GLU:N	2.50	0.45
5:Aa:32:GLN:NE2	5:Aa:36:THR:O	2.50	0.45
6:T4:9:LEU:HD21	6:T4:33:ARG:NH2	2.32	0.45
6:T4:98:SER:OG	6:T4:99:ASN:N	2.49	0.45
6:R5:186:VAL:HB	6:R5:191:GLN:HB2	1.98	0.45
1:W:138:TRP:CE3	1:W:147:GLU:HB3	2.52	0.45
1:W:209:ILE:HG13	1:W:214:ASN:O	2.17	0.45
1:p:29:ALA:HB1	1:p:190:VAL:HG21	1.99	0.45
1:p:46:ALA:HB3	1:p:47:PRO:HD3	1.99	0.45
1:1:178:ASP:OD2	1:1:181:THR:HG22	2.17	0.45
1:5:73:ASN:HB3	1:5:164:PHE:CE1	2.52	0.45
1:5:110:PRO:HA	1:5:136:ARG:O	2.16	0.45
1:0:73:ASN:HB3	1:0:164:PHE:CE1	2.52	0.45
1:A:23:CYS:HB3	1:B:229:CYS:HB3	1.85	0.45
1:C:153:ASP:HA	1:C:159:LEU:HD23	1.98	0.45
2:AB:153:LYS:NZ	2:AB:161:GLU:HB2	2.31	0.45
2:AB:249:ARG:NH2	6:T5:195:PHE:HD2	2.15	0.45
2:AE:19:SER:O	2:AE:19:SER:OG	2.35	0.45
2:AE:168:GLU:HB3	2:AF:28:ARG:HE	1.82	0.45
2:AF:61:LEU:HA	2:AF:61:LEU:HD23	1.77	0.45
2:AH:369:VAL:O	2:AH:370:ILE:HD13	2.17	0.45
2:AJ:117:ALA:HB1	2:AJ:127:MET:HE2	1.98	0.45
2:AJ:257:LYS:O	2:AJ:261:GLU:HG2	2.16	0.45
2:AJ:363:CYS:SG	2:AJ:364:GLY:N	2.90	0.45
4:AR:29:GLU:N	4:AR:29:GLU:OE2	2.50	0.45
3:AP:57:ASP:OD2	3:AP:60:GLN:NE2	2.37	0.45
3:AN:66:THR:HA	3:AN:108:MET:O	2.17	0.45
3:H:35:GLY:HA3	6:T4:20:ASP:OD2	2.17	0.45
6:R4:179:GLY:HA2	6:R4:182:ASN:ND2	2.32	0.45
6:T4:124:SER:O	6:T4:124:SER:OG	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:U4:181:THR:O	6:U4:187:ILE:HD11	2.16	0.45
5:AY:89:VAL:HG12	5:AY:97:MET:HB2	1.99	0.45
3:I:1:MET:SD	3:I:1:MET:N	2.77	0.45
6:T5:166:VAL:HG12	6:T5:167:ARG:H	1.81	0.45
1:J:230:GLY:OXT	1:X:9:ARG:NH2	2.33	0.44
1:L:108:ASN:HB3	1:L:138:TRP:CD1	2.52	0.44
1:O:138:TRP:CE3	1:O:147:GLU:HB3	2.51	0.44
1:R:25:GLU:H	1:R:25:GLU:HG2	1.65	0.44
1:X:209:ILE:HG13	1:X:214:ASN:O	2.17	0.44
1:b:78:THR:O	1:b:152:VAL:HA	2.17	0.44
1:j:111:SER:OG	1:j:135:ASP:OD1	2.32	0.44
1:j:210:ASP:OD1	1:j:214:ASN:N	2.48	0.44
1:l:73:ASN:HB3	1:l:164:PHE:HE1	1.81	0.44
1:m:53:LEU:HD12	1:m:206:GLN:CD	2.41	0.44
1:t:75:PHE:CZ	1:t:161:GLN:HG2	2.52	0.44
1:v:153:ASP:HA	1:v:159:LEU:HD23	1.99	0.44
1:x:77:ARG:NH2	1:x:158:GLU:OE2	2.50	0.44
1:9:71:VAL:HG11	1:9:139:PHE:HE2	1.81	0.44
1:0:78:THR:HG23	1:0:152:VAL:HG12	1.99	0.44
1:E:126:THR:O	1:E:126:THR:OG1	2.33	0.44
2:AA:192:TYR:CE2	2:AA:194:PHE:HE1	2.35	0.44
2:AD:277:ILE:HD11	2:AE:241:SER:OG	2.17	0.44
2:AI:97:LEU:O	2:AI:101:LEU:HD23	2.17	0.44
5:AU:46:THR:HG23	5:AU:60:SER:OG	2.17	0.44
3:AP:57:ASP:O	3:AP:58:THR:OG1	2.30	0.44
5:Aa:5:LYS:O	5:AY:113:ARG:NH2	2.51	0.44
5:Aa:117:MET:HE2	5:Aa:119:ILE:HD11	1.99	0.44
6:R4:72:THR:O	6:R4:72:THR:OG1	2.31	0.44
6:S4:69:LEU:HD12	6:S4:73:PRO:CD	2.48	0.44
6:T4:60:LEU:HD12	6:T4:67:ILE:HD11	1.99	0.44
3:I:106:ARG:HH21	6:S5:17:LYS:HZ1	1.63	0.44
3:I:106:ARG:HE	6:S5:17:LYS:NZ	2.15	0.44
6:T5:21:ASN:OD1	6:T5:21:ASN:N	2.48	0.44
1:J:46:ALA:HB3	1:J:47:PRO:HD3	1.99	0.44
1:S:10:ASN:ND2	6:U4:77:ARG:HH22	2.14	0.44
1:T:38:MET:HG2	1:T:185:LYS:HG2	1.98	0.44
1:a:102:TYR:HD1	1:a:141:ILE:HD12	1.80	0.44
1:a:149:VAL:HG11	1:a:162:PRO:HG2	1.99	0.44
1:b:73:ASN:HB3	1:b:164:PHE:HE1	1.82	0.44
1:g:47:PRO:O	1:g:49:ARG:N	2.49	0.44
1:g:71:VAL:HG13	1:g:144:ASN:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i:154:PRO:HD3	1:i:159:LEU:HD21	1.99	0.44
1:r:67:THR:O	1:r:67:THR:OG1	2.32	0.44
1:t:67:THR:O	1:t:67:THR:OG1	2.32	0.44
1:y:48:LEU:HD23	1:z:1:MET:HE3	1.98	0.44
1:4:53:LEU:HD12	1:4:206:GLN:NE2	2.32	0.44
1:8:133:GLY:H	1:8:152:VAL:CG1	2.30	0.44
1:0:73:ASN:HB3	1:0:164:PHE:HE1	1.81	0.44
1:A:38:MET:HG2	1:A:185:LYS:HG2	1.98	0.44
1:D:71:VAL:HG23	1:D:91:LEU:O	2.17	0.44
2:AA:150:LEU:HD11	2:AA:163:PHE:HB3	1.98	0.44
2:AC:39:VAL:HG11	2:AC:195:MET:HE3	2.00	0.44
2:AD:59:ARG:HD3	2:AE:312:ASN:HA	1.99	0.44
2:AD:60:CYS:O	2:AD:64:LEU:HG	2.17	0.44
2:AG:347:GLU:HB2	2:AG:348:PRO:HD3	2.00	0.44
2:AH:163:PHE:O	2:AH:173:THR:HA	2.17	0.44
2:AH:252:ASP:HA	6:R4:43:TYR:CD1	2.52	0.44
2:AI:383:ARG:HA	2:AI:386:ILE:HG22	1.99	0.44
2:AK:59:ARG:NH1	2:AK:320:LEU:HD13	2.32	0.44
3:AP:69:TYR:HD2	3:AP:108:MET:HG3	1.82	0.44
5:AZ:32:GLN:HG3	5:AZ:33:PRO:HD2	1.98	0.44
3:AN:81:VAL:HB	3:AN:93:PHE:HB2	2.00	0.44
4:AS:118:MET:HE3	4:AS:129:PHE:CD2	2.52	0.44
4:AT:38:VAL:HG21	4:AT:81:ILE:HG13	1.99	0.44
6:S4:72:THR:HA	6:S4:73:PRO:HD2	1.77	0.44
3:AO:92:TRP:CH2	3:AO:124:PRO:HG3	2.52	0.44
4:AX:29:GLU:OE2	4:AX:29:GLU:N	2.50	0.44
3:I:6:ARG:HA	3:I:38:ALA:HB2	1.99	0.44
3:I:46:ARG:HB3	3:I:54:MET:HB2	1.98	0.44
5:Ab:32:GLN:HG3	5:Ab:33:PRO:HD2	1.99	0.44
6:T5:61:LYS:HB2	6:T5:61:LYS:HE3	1.69	0.44
1:O:87:THR:OG1	1:O:88:LEU:N	2.51	0.44
1:S:118:GLY:N	1:S:122:ALA:O	2.30	0.44
1:U:88:LEU:N	1:U:121:GLY:O	2.49	0.44
1:W:178:ASP:CG	1:W:181:THR:HG22	2.42	0.44
1:Y:132:THR:HG21	1:Y:154:PRO:HB3	1.98	0.44
1:b:99:GLN:HG3	1:b:100:VAL:H	1.82	0.44
1:f:138:TRP:CE3	1:f:147:GLU:HB3	2.52	0.44
1:r:209:ILE:HG13	1:r:214:ASN:O	2.16	0.44
1:t:75:PHE:CE1	1:t:162:PRO:HD2	2.51	0.44
1:y:120:ASN:N	1:y:120:ASN:OD1	2.50	0.44
1:0:78:THR:O	1:0:152:VAL:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:GLN:HG2	1:A:101:GLU:OE2	2.17	0.44
1:E:46:ALA:HB3	1:E:47:PRO:HD3	1.99	0.44
1:E:136:ARG:HG2	1:E:149:VAL:HG22	1.99	0.44
2:AA:98:GLN:O	2:AA:102:GLN:HG2	2.16	0.44
2:AA:312:ASN:HA	2:AL:59:ARG:HD3	1.99	0.44
2:AB:252:ASP:HA	6:T5:43:TYR:HA	1.98	0.44
2:AF:194:PHE:CD1	2:AF:361:PHE:HE2	2.34	0.44
2:AG:204:ALA:O	2:AG:208:ASP:HB2	2.17	0.44
2:AJ:72:LYS:NZ	2:AK:80:GLN:HB3	2.33	0.44
2:AK:192:TYR:CE2	2:AK:194:PHE:HE1	2.36	0.44
2:AL:21:ASN:O	2:AL:24:LYS:HE2	2.18	0.44
2:AL:272:ASN:OD1	2:AL:272:ASN:N	2.51	0.44
3:AP:52:VAL:HG12	3:AP:116:GLU:HB3	2.00	0.44
6:R3:161:ASP:HB2	6:U3:157:ASN:HD21	1.82	0.44
6:S3:77:ARG:HA	6:S3:78:PRO:HD3	1.85	0.44
5:AV:6:GLN:NE2	4:AT:128:THR:OG1	2.50	0.44
6:U4:147:GLY:O	6:U4:148:ILE:C	2.58	0.44
1:J:177:VAL:O	1:J:179:PRO:HD3	2.18	0.44
1:L:46:ALA:HB3	1:L:47:PRO:HD3	1.98	0.44
1:S:29:ALA:HB1	1:S:190:VAL:HG21	1.99	0.44
1:V:73:ASN:HB3	1:V:164:PHE:CE1	2.53	0.44
1:Y:28:SER:OG	1:Y:230:GLY:OXT	2.34	0.44
1:a:133:GLY:H	1:a:152:VAL:HG23	1.82	0.44
1:c:72:SER:O	1:c:91:LEU:HD12	2.16	0.44
1:p:71:VAL:HG23	1:p:91:LEU:O	2.17	0.44
1:5:53:LEU:HD12	1:5:206:GLN:CD	2.43	0.44
1:6:177:VAL:HG11	1:6:206:GLN:HE22	1.82	0.44
1:7:75:PHE:HB2	1:7:164:PHE:CZ	2.53	0.44
1:A:126:THR:O	1:A:126:THR:OG1	2.32	0.44
1:D:53:LEU:HD12	1:D:206:GLN:CD	2.42	0.44
1:E:56:LYS:HB3	1:E:207:VAL:CG1	2.47	0.44
2:AA:159:ASP:OD1	2:AA:159:ASP:N	2.50	0.44
2:AB:52:MET:HE2	2:AC:201:ILE:HG13	1.98	0.44
2:AB:69:GLN:HE22	2:AC:352:THR:HG23	1.82	0.44
2:AB:159:ASP:OD1	2:AB:159:ASP:N	2.50	0.44
2:AC:196:ILE:H	2:AC:196:ILE:HD12	1.82	0.44
2:AC:339:LYS:HB3	2:AC:339:LYS:HE2	1.74	0.44
2:AI:95:LYS:HE3	2:AI:95:LYS:HB2	1.75	0.44
2:AJ:54:HIS:HE1	2:AJ:56:VAL:HB	1.81	0.44
2:AL:90:SER:C	2:AL:92:SER:H	2.26	0.44
2:AL:369:VAL:O	2:AL:370:ILE:HD13	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AQ:118:MET:HE3	4:AQ:129:PHE:HD2	1.82	0.44
6:U4:152:ILE:O	6:U4:153:ALA:C	2.60	0.44
5:AY:96:VAL:HG12	5:AY:127:LEU:CB	2.47	0.44
3:I:66:THR:HA	3:I:108:MET:O	2.18	0.44
6:R5:167:ARG:HH21	6:T5:171:ASN:N	2.11	0.44
1:J:30:ARG:NH1	1:J:229:CYS:HA	2.33	0.44
1:M:209:ILE:HG13	1:M:214:ASN:O	2.18	0.44
1:N:209:ILE:HG13	1:N:214:ASN:O	2.17	0.44
1:Q:133:GLY:H	1:Q:152:VAL:CG2	2.30	0.44
1:R:157:SER:OG	1:R:158:GLU:N	2.50	0.44
1:a:225:SER:O	1:a:225:SER:OG	2.36	0.44
1:d:66:VAL:HG23	1:d:68:PRO:HD3	2.00	0.44
1:e:59:PHE:HE2	1:e:175:ARG:NE	2.16	0.44
1:f:125:TYR:OH	1:f:135:ASP:OD2	2.21	0.44
1:h:113:GLY:HA3	1:h:125:TYR:CE2	2.53	0.44
1:l:135:ASP:N	1:l:150:ILE:O	2.37	0.44
1:m:174:ARG:NH2	1:m:187:VAL:HG11	2.33	0.44
1:o:75:PHE:CZ	1:o:161:GLN:HG2	2.53	0.44
1:t:83:VAL:HG23	1:t:126:THR:HG22	2.00	0.44
1:u:157:SER:OG	1:u:158:GLU:N	2.50	0.44
1:5:46:ALA:HB3	1:5:47:PRO:HD3	1.99	0.44
1:5:78:THR:O	1:5:152:VAL:HA	2.18	0.44
1:7:80:VAL:HG12	1:7:155:THR:HB	1.99	0.44
1:8:30:ARG:NH1	1:8:229:CYS:HA	2.33	0.44
2:AC:71:VAL:HG22	2:AC:376:ILE:HD11	2.00	0.44
2:AD:68:VAL:HG11	2:AD:118:ALA:CB	2.47	0.44
2:AD:90:SER:C	2:AD:92:SER:H	2.26	0.44
2:AE:18:PRO:C	2:AE:20:ALA:H	2.24	0.44
2:AE:192:TYR:CE2	2:AE:194:PHE:HE1	2.35	0.44
2:AH:264:GLU:O	2:AH:267:LYS:HG3	2.17	0.44
6:S3:74:ILE:HD11	6:S3:77:ARG:CB	2.32	0.44
6:T3:166:VAL:C	6:T3:168:ASN:N	2.76	0.44
3:H:66:THR:HA	3:H:108:MET:O	2.17	0.44
6:R4:35:ALA:HB2	6:U4:142:ALA:HB1	1.99	0.44
3:I:35:GLY:HA3	6:T5:20:ASP:OD2	2.18	0.44
3:I:49:GLN:O	3:I:50:ASP:CB	2.64	0.44
6:R5:35:ALA:HB2	6:U5:142:ALA:CB	2.47	0.44
6:R5:100:VAL:C	6:R5:101:LEU:HD22	2.43	0.44
1:O:110:PRO:HG3	1:O:115:VAL:HG23	2.00	0.44
1:P:46:ALA:HB3	1:P:47:PRO:HD3	1.99	0.44
1:S:126:THR:O	1:S:126:THR:OG1	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:49:ARG:HD2	6:U5:89:PRO:O	2.18	0.44
1:Y:46:ALA:HB3	1:Y:47:PRO:HD3	1.99	0.44
1:Y:66:VAL:HG23	1:Y:68:PRO:HD3	1.98	0.44
1:c:53:LEU:HD23	1:c:182:HIS:HA	2.00	0.44
1:d:92:PHE:CZ	1:d:94:ASN:HB3	2.52	0.44
1:C:133:GLY:H	1:C:152:VAL:CG1	2.30	0.44
1:C:209:ILE:HD11	1:C:213:GLY:HA2	1.99	0.44
1:G:75:PHE:HB2	1:G:164:PHE:CZ	2.51	0.44
2:AB:90:SER:C	2:AB:92:SER:H	2.25	0.44
2:AB:252:ASP:HB2	2:AB:255:GLN:HE21	1.83	0.44
2:AF:90:SER:C	2:AF:92:SER:H	2.26	0.44
2:AG:90:SER:OG	2:AG:93:GLN:N	2.31	0.44
2:AH:39:VAL:HG23	2:AH:40:VAL:HG13	1.98	0.44
2:AI:253:ASP:OD2	6:U4:198:ARG:HG2	2.18	0.44
2:AL:109:SER:OG	2:AL:110:GLY:N	2.51	0.44
6:R3:165:SER:O	6:R3:166:VAL:C	2.61	0.44
6:R4:178:ILE:C	6:R4:180:GLY:H	2.24	0.44
6:S4:77:ARG:HA	6:S4:78:PRO:HD3	1.88	0.44
6:U4:2:ASN:N	6:U4:2:ASN:OD1	2.50	0.44
6:U4:166:VAL:HB	6:U4:181:THR:HG21	2.00	0.44
6:U4:193:GLU:HG2	6:U4:196:ARG:HH22	1.82	0.44
4:AX:118:MET:HE3	4:AX:129:PHE:HD2	1.82	0.44
6:R5:25:THR:HG23	6:U5:14:GLU:OE2	2.17	0.44
1:N:130:LEU:HD23	1:N:130:LEU:HA	1.86	0.44
1:d:154:PRO:HD3	1:d:159:LEU:HD21	2.00	0.44
1:h:118:GLY:N	1:h:122:ALA:O	2.27	0.44
1:m:53:LEU:HD23	1:m:182:HIS:HA	2.00	0.44
1:w:71:VAL:HG13	1:w:144:ASN:HB2	1.99	0.44
1:4:90:ASP:N	1:4:90:ASP:OD1	2.48	0.44
1:6:52:GLY:O	1:6:209:ILE:HG22	2.18	0.44
1:8:48:LEU:HD23	1:9:1:MET:HE3	2.00	0.44
1:A:133:GLY:H	1:A:152:VAL:CG2	2.31	0.44
1:C:78:THR:O	1:C:152:VAL:HA	2.18	0.44
1:G:67:THR:O	1:G:67:THR:OG1	2.36	0.44
2:AA:253:ASP:OD2	6:U3:198:ARG:HG2	2.18	0.44
2:AC:130:LYS:O	2:AC:142:ILE:HA	2.17	0.44
2:AD:217:ILE:C	2:AD:220:PRO:HD2	2.43	0.44
2:AF:39:VAL:HG23	2:AF:40:VAL:HG13	1.99	0.44
2:AG:59:ARG:NH1	2:AG:320:LEU:HD13	2.32	0.44
2:AG:130:LYS:O	2:AG:142:ILE:HA	2.18	0.44
2:AI:39:VAL:HG21	2:AI:147:ILE:HD11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AJ:46:MET:HA	2:AJ:46:MET:HE2	2.00	0.44
2:AJ:376:ILE:HG22	2:AJ:378:ALA:H	1.82	0.44
2:AK:204:ALA:O	2:AK:208:ASP:HB2	2.17	0.44
2:AK:372:ASP:HB3	2:AK:374:ASP:OD1	2.18	0.44
6:R3:100:VAL:C	6:R3:101:LEU:HD22	2.43	0.44
5:AV:96:VAL:HG12	5:AV:127:LEU:CB	2.48	0.44
5:Aa:47:ASN:HB3	5:Aa:55:VAL:HG21	1.99	0.44
5:Aa:89:VAL:O	5:Aa:96:VAL:HG23	2.17	0.44
6:T4:165:SER:OG	6:T4:166:VAL:N	2.44	0.44
4:AW:156:CYS:HB3	5:Ab:3:CYS:HA	1.99	0.44
6:R5:136:CYS:SG	6:R5:138:ASN:HB2	2.58	0.44
6:S5:29:LEU:HD12	6:S5:29:LEU:HA	1.89	0.44
6:S5:77:ARG:HE	6:S5:77:ARG:HB3	1.68	0.44
6:T5:166:VAL:C	6:T5:168:ASN:N	2.75	0.44
1:K:1:MET:HE2	1:K:38:MET:HG3	2.00	0.44
1:L:154:PRO:HD3	1:L:159:LEU:HD21	2.00	0.44
1:T:90:ASP:OD1	1:T:90:ASP:N	2.50	0.44
1:V:154:PRO:HG2	1:V:156:THR:HG22	1.99	0.44
1:j:75:PHE:HD1	1:j:149:VAL:HG13	1.83	0.44
1:n:118:GLY:N	1:n:122:ALA:O	2.38	0.44
1:q:167:PRO:HA	1:q:191:SER:HB3	2.00	0.44
1:q:206:GLN:OE1	1:q:207:VAL:N	2.50	0.44
1:u:53:LEU:HD23	1:u:182:HIS:HA	2.00	0.44
1:y:53:LEU:HD12	1:y:206:GLN:CD	2.43	0.44
1:1:209:ILE:HG13	1:1:214:ASN:O	2.18	0.44
1:3:106:GLU:OE1	1:G:60:GLU:HG3	2.17	0.44
1:9:53:LEU:HD23	1:9:182:HIS:HA	1.99	0.44
1:0:126:THR:O	1:0:126:THR:OG1	2.33	0.44
1:B:210:ASP:HB3	1:B:216:PHE:CE2	2.48	0.44
2:AA:274:GLY:HA3	2:AC:233:ASP:OD2	2.18	0.44
2:AA:401:LYS:HD2	2:AB:395:PHE:CE1	2.52	0.44
2:AB:83:GLN:HE21	2:AB:366:GLY:H	1.66	0.44
2:AC:102:GLN:OE1	2:AC:102:GLN:HA	2.18	0.44
2:AF:27:ILE:HG23	2:AF:31:PHE:HD2	1.82	0.44
2:AF:72:LYS:NZ	2:AG:80:GLN:HB3	2.33	0.44
2:AG:109:SER:HA	2:AH:360:MET:HE3	1.98	0.44
2:AH:220:PRO:HB2	2:AH:309:ILE:HG23	1.99	0.44
5:AU:113:ARG:NH2	5:Ab:5:LYS:O	2.51	0.44
3:AP:46:ARG:HE	3:AN:77:VAL:HG23	1.82	0.44
6:R3:3:LEU:O	6:R3:33:ARG:NH1	2.51	0.44
6:R4:16:ALA:HB1	6:R4:156:ILE:HD11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S4:40:ALA:HB2	6:S4:194:TRP:CH2	2.53	0.44
6:R5:3:LEU:O	6:R5:33:ARG:NH1	2.51	0.44
6:R5:32:TYR:HH	6:U5:15:HIS:CE1	2.36	0.44
6:T5:60:LEU:HD12	6:T5:67:ILE:HD11	2.00	0.44
1:J:10:ASN:HD22	6:R5:77:ARG:NH1	2.16	0.44
1:J:56:LYS:HB3	1:J:207:VAL:CG1	2.48	0.44
1:J:138:TRP:CE3	1:J:147:GLU:HB3	2.53	0.44
1:L:149:VAL:HG11	1:L:162:PRO:HG2	2.00	0.44
1:O:46:ALA:HB3	1:O:47:PRO:HD3	1.99	0.44
1:R:209:ILE:HG13	1:R:214:ASN:O	2.17	0.44
1:X:38:MET:SD	1:X:185:LYS:HE2	2.57	0.44
1:X:177:VAL:O	1:X:179:PRO:HD3	2.18	0.44
1:f:194:ALA:HB1	1:f:226:ILE:HG21	1.99	0.44
1:h:25:GLU:OE1	1:h:25:GLU:N	2.47	0.44
1:h:75:PHE:HE1	1:h:162:PRO:HD2	1.82	0.44
1:h:88:LEU:N	1:h:121:GLY:O	2.51	0.44
1:l:31:PRO:HD3	1:l:227:GLY:O	2.17	0.44
1:n:67:THR:O	1:n:67:THR:OG1	2.31	0.44
1:q:75:PHE:CE1	1:q:162:PRO:HD2	2.53	0.44
1:u:46:ALA:HB3	1:u:47:PRO:HD3	1.99	0.44
1:w:21:SER:HB3	1:B:49:ARG:HB3	2.00	0.44
1:z:138:TRP:CZ3	1:z:147:GLU:HB3	2.52	0.44
1:5:78:THR:HG23	1:5:152:VAL:HG12	1.99	0.44
1:7:24:CYS:HB3	1:7:221:CYS:HB2	1.63	0.44
1:8:46:ALA:HB3	1:8:47:PRO:HD3	2.00	0.44
1:9:30:ARG:HD2	1:9:230:GLY:H	1.83	0.44
1:O:210:ASP:OD1	1:O:214:ASN:N	2.49	0.44
1:D:88:LEU:HG	1:D:141:ILE:HD11	2.00	0.44
2:AB:280:ALA:HA	2:AC:247:ALA:HB3	2.00	0.44
2:AC:350:TYR:C	2:AC:353:PRO:HD2	2.43	0.44
2:AF:69:GLN:HE22	2:AG:352:THR:HG23	1.82	0.44
2:AF:159:ASP:N	2:AF:159:ASP:OD1	2.50	0.44
2:AJ:67:THR:O	2:AJ:70:SER:OG	2.24	0.44
2:AJ:163:PHE:HB2	2:AJ:174:ILE:HG13	1.99	0.44
2:AK:165:TYR:CD1	2:AL:25:ILE:HD11	2.53	0.44
2:AK:196:ILE:H	2:AK:196:ILE:HD12	1.82	0.44
3:AM:11:ILE:HD13	3:AM:82:TYR:HD2	1.83	0.44
4:AR:130:GLU:OE2	4:AR:152:ASN:ND2	2.51	0.44
3:AP:25:LEU:HD23	3:AP:25:LEU:H	1.83	0.44
6:T3:178:ILE:HD12	6:T3:178:ILE:HA	1.87	0.44
6:S4:93:ILE:H	6:T4:125:GLN:HE22	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AW:41:ASP:O	4:AW:45:THR:OG1	2.22	0.44
4:AW:77:ARG:HD2	4:AW:150:ARG:HD3	1.99	0.44
6:R5:195:PHE:HA	6:R5:198:ARG:HG3	1.99	0.44
6:T5:27:ASP:OD1	6:T5:27:ASP:N	2.50	0.44
6:T5:167:ARG:O	6:T5:168:ASN:C	2.61	0.44
1:M:157:SER:OG	1:M:158:GLU:N	2.51	0.43
1:Z:210:ASP:HB3	1:Z:216:PHE:HE2	1.81	0.43
1:b:25:GLU:H	1:b:25:GLU:CD	2.26	0.43
1:c:78:THR:HB	1:c:84:PHE:CD2	2.53	0.43
1:c:133:GLY:H	1:c:152:VAL:HG23	1.83	0.43
1:f:53:LEU:HD23	1:f:182:HIS:HA	2.00	0.43
1:j:53:LEU:HD12	1:j:206:GLN:CD	2.43	0.43
1:j:88:LEU:N	1:j:121:GLY:O	2.50	0.43
1:x:126:THR:O	1:x:126:THR:OG1	2.31	0.43
1:1:1:MET:HE2	1:1:38:MET:HG3	2.00	0.43
1:2:24:CYS:HB3	1:2:221:CYS:HB2	1.53	0.43
1:4:29:ALA:HB1	1:4:190:VAL:HG21	2.00	0.43
1:0:172:ALA:O	1:0:175:ARG:NH1	2.51	0.43
1:A:177:VAL:HG11	1:A:206:GLN:HE22	1.83	0.43
2:AA:46:MET:HE2	2:AA:46:MET:HA	1.99	0.43
2:AA:170:GLY:O	2:AA:171:LYS:HD2	2.18	0.43
2:AB:54:HIS:CE1	2:AB:56:VAL:H	2.36	0.43
2:AF:63:LYS:O	2:AF:67:THR:HG23	2.17	0.43
2:AH:21:ASN:O	2:AH:24:LYS:HE2	2.18	0.43
2:AI:163:PHE:CD2	2:AI:193:ALA:HB3	2.53	0.43
2:AI:170:GLY:O	2:AI:171:LYS:HD2	2.18	0.43
2:AI:362:LEU:HD23	2:AI:362:LEU:HA	1.76	0.43
2:AI:372:ASP:N	2:AI:372:ASP:OD1	2.51	0.43
4:AQ:118:MET:HE3	4:AQ:129:PHE:CD2	2.53	0.43
6:S3:3:LEU:O	6:S3:6:LEU:N	2.51	0.43
6:S3:74:ILE:CG1	6:S3:77:ARG:HB2	2.48	0.43
6:R4:180:GLY:HA3	6:S4:177:LEU:HA	1.99	0.43
6:T4:27:ASP:N	6:T4:27:ASP:OD1	2.51	0.43
1:b:71:VAL:HG13	1:b:144:ASN:HB2	2.00	0.43
1:d:132:THR:HG21	1:d:154:PRO:HB3	1.99	0.43
1:d:210:ASP:HB3	1:d:216:PHE:CE2	2.49	0.43
1:p:225:SER:O	1:p:225:SER:OG	2.36	0.43
1:r:71:VAL:HG13	1:r:144:ASN:HB2	1.99	0.43
1:w:177:VAL:O	1:w:179:PRO:HD3	2.18	0.43
1:y:47:PRO:O	1:y:49:ARG:N	2.52	0.43
1:z:157:SER:OG	1:z:158:GLU:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:7:75:PHE:HB2	1:7:164:PHE:HZ	1.82	0.43
1:9:30:ARG:NH1	1:9:229:CYS:HA	2.33	0.43
1:E:78:THR:O	1:E:152:VAL:HA	2.17	0.43
1:F:23:CYS:HB3	1:G:229:CYS:HB3	1.85	0.43
1:F:133:GLY:H	1:F:152:VAL:HG23	1.84	0.43
1:G:206:GLN:OE1	1:G:207:VAL:N	2.50	0.43
2:AA:97:LEU:O	2:AA:101:LEU:HD23	2.18	0.43
2:AB:61:LEU:HD23	2:AB:61:LEU:HA	1.77	0.43
2:AB:298:SER:HB3	2:AB:301:PRO:HG2	2.00	0.43
2:AC:314:GLY:O	2:AC:345:THR:HG21	2.17	0.43
2:AD:66:LEU:HG	2:AE:348:PRO:O	2.17	0.43
2:AD:289:MET:HE2	2:AD:289:MET:HA	1.99	0.43
2:AE:293:LEU:HD12	2:AE:293:LEU:HA	1.82	0.43
2:AF:252:ASP:OD1	2:AF:255:GLN:NE2	2.52	0.43
2:AF:283:ASP:O	2:AF:284:VAL:C	2.61	0.43
2:AG:400:GLU:H	2:AG:400:GLU:HG2	1.64	0.43
2:AI:282:THR:HG22	2:AJ:249:ARG:NH2	2.33	0.43
2:AI:385:ASP:O	2:AI:389:THR:HG22	2.18	0.43
2:AJ:54:HIS:CE1	2:AJ:56:VAL:H	2.36	0.43
2:AK:69:GLN:HE22	2:AL:352:THR:HG23	1.83	0.43
2:AL:382:SER:O	2:AL:386:ILE:HG12	2.19	0.43
4:AQ:95:LYS:HB2	4:AQ:95:LYS:HE3	1.42	0.43
3:AP:106:ARG:HE	6:S3:17:LYS:NZ	2.16	0.43
3:AN:75:VAL:HB	3:AN:98:VAL:HG11	2.00	0.43
4:AS:118:MET:HE3	4:AS:129:PHE:HD2	1.83	0.43
5:AV:47:ASN:HB3	5:AV:55:VAL:CG2	2.48	0.43
5:Aa:33:PRO:HB3	5:Aa:69:VAL:HG23	2.00	0.43
3:AO:48:SER:HB3	3:AO:54:MET:CG	2.47	0.43
1:N:177:VAL:O	1:N:179:PRO:HD3	2.18	0.43
1:N:210:ASP:OD1	1:N:213:GLY:N	2.51	0.43
1:U:53:LEU:HD12	1:U:206:GLN:CD	2.43	0.43
1:l:167:PRO:HA	1:l:191:SER:HB3	1.99	0.43
1:r:53:LEU:HD12	1:r:206:GLN:CD	2.43	0.43
1:D:115:VAL:HA	1:D:124:THR:O	2.18	0.43
2:AA:19:SER:O	2:AA:19:SER:OG	2.36	0.43
2:AA:83:GLN:HE21	2:AA:366:GLY:N	2.15	0.43
2:AB:63:LYS:O	2:AB:67:THR:HG23	2.18	0.43
2:AF:252:ASP:HB2	2:AF:255:GLN:HG2	1.99	0.43
2:AG:165:TYR:CD1	2:AH:25:ILE:HD11	2.53	0.43
2:AH:90:SER:C	2:AH:92:SER:H	2.26	0.43
2:AH:182:LYS:HD2	2:AH:186:GLY:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AH:217:ILE:C	2:AH:220:PRO:HD2	2.43	0.43
2:AH:245:VAL:HB	2:AH:286:VAL:HG12	1.99	0.43
6:R3:52:LYS:HE2	6:R3:52:LYS:HB3	1.75	0.43
6:U3:182:ASN:ND2	6:T5:187:ILE:HA	2.33	0.43
3:AN:59:MET:HE3	3:AN:59:MET:HB3	1.88	0.43
3:AN:82:TYR:HB2	3:AN:92:TRP:CZ3	2.53	0.43
4:AT:28:ILE:HG22	4:AT:51:PRO:HG2	2.00	0.43
6:T4:184:GLY:C	6:T4:186:VAL:H	2.26	0.43
6:U4:49:THR:HB	6:U4:52:LYS:NZ	2.34	0.43
6:R5:71:ALA:O	6:R5:72:THR:OG1	2.36	0.43
1:J:92:PHE:HB2	1:J:141:ILE:HG21	2.00	0.43
1:Q:75:PHE:CE1	1:Q:162:PRO:HD2	2.54	0.43
1:W:157:SER:OG	1:W:158:GLU:N	2.51	0.43
1:a:59:PHE:HE2	1:a:175:ARG:NE	2.14	0.43
1:a:157:SER:O	1:a:158:GLU:HG2	2.19	0.43
1:f:132:THR:HA	1:f:152:VAL:HG23	2.00	0.43
1:j:115:VAL:HA	1:j:124:THR:O	2.18	0.43
1:l:78:THR:O	1:l:152:VAL:HA	2.18	0.43
1:q:59:PHE:HE2	1:q:175:ARG:NE	2.16	0.43
1:w:47:PRO:O	1:w:49:ARG:N	2.52	0.43
1:1:206:GLN:OE1	1:1:207:VAL:N	2.49	0.43
1:0:71:VAL:HG11	1:0:141:ILE:HB	2.01	0.43
2:AE:25:ILE:O	2:AE:28:ARG:NE	2.51	0.43
2:AH:167:ASP:OD1	2:AH:167:ASP:N	2.46	0.43
2:AH:280:ALA:HA	2:AI:247:ALA:HB3	2.01	0.43
2:AI:192:TYR:CE2	2:AI:194:PHE:HE1	2.36	0.43
2:AJ:150:LEU:HD11	2:AJ:163:PHE:HB3	1.99	0.43
2:AJ:402:ARG:HH21	2:AJ:407:TRP:HB3	1.83	0.43
2:AK:103:ARG:NH2	2:AL:365:ALA:HA	2.32	0.43
2:AL:172:GLU:O	2:AL:174:ILE:HD12	2.19	0.43
3:AP:8:HIS:CE1	6:U4:21:ASN:HD21	2.37	0.43
6:S3:27:ASP:N	6:S3:27:ASP:OD2	2.50	0.43
6:T3:195:PHE:C	6:T3:197:TYR:N	2.77	0.43
6:R4:3:LEU:O	6:R4:33:ARG:NH1	2.51	0.43
6:R5:161:ASP:HB2	6:U5:157:ASN:HD21	1.83	0.43
6:S5:72:THR:HA	6:S5:73:PRO:HD2	1.83	0.43
6:S5:127:MET:HE3	6:S5:127:MET:HB3	1.77	0.43
6:S5:194:TRP:O	6:S5:194:TRP:CD1	2.72	0.43
6:U5:2:ASN:OD1	6:U5:2:ASN:N	2.51	0.43
1:J:10:ASN:HD22	6:R5:77:ARG:HH12	1.67	0.43
1:Q:154:PRO:HD3	1:Q:159:LEU:HD21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:75:PHE:CE1	1:S:161:GLN:HG2	2.53	0.43
1:W:48:LEU:HD21	1:X:1:MET:HB2	2.00	0.43
1:a:53:LEU:HD12	1:a:206:GLN:CD	2.44	0.43
1:f:24:CYS:HB3	1:f:221:CYS:C	2.43	0.43
1:i:85:GLU:OE1	1:i:124:THR:OG1	2.28	0.43
1:j:85:GLU:OE1	1:j:85:GLU:N	2.52	0.43
1:u:78:THR:HG23	1:u:152:VAL:HG12	2.01	0.43
1:w:46:ALA:HB3	1:w:47:PRO:HD3	1.99	0.43
1:4:30:ARG:NH1	1:4:229:CYS:HA	2.33	0.43
1:9:53:LEU:HD12	1:9:206:GLN:CD	2.43	0.43
1:0:56:LYS:HB3	1:0:207:VAL:HG11	2.00	0.43
1:A:172:ALA:O	1:A:175:ARG:NH1	2.52	0.43
1:F:78:THR:O	1:F:152:VAL:HA	2.18	0.43
2:AB:77:LYS:HE2	2:AB:77:LYS:HB2	1.85	0.43
2:AB:83:GLN:OE1	2:AB:83:GLN:N	2.50	0.43
2:AD:167:ASP:OD2	2:AE:28:ARG:NH1	2.51	0.43
2:AD:285:LYS:HE3	2:AD:285:LYS:HB3	1.67	0.43
2:AE:159:ASP:N	2:AE:159:ASP:OD1	2.51	0.43
2:AF:66:LEU:HD22	2:AG:348:PRO:O	2.18	0.43
2:AF:201:ILE:O	2:AF:202:ASN:ND2	2.52	0.43
2:AG:27:ILE:HD13	2:AG:155:ASP:O	2.18	0.43
2:AJ:132:SER:O	2:AJ:140:ASN:HB2	2.17	0.43
2:AK:75:VAL:H	2:AK:98:GLN:NE2	2.16	0.43
2:AK:112:GLN:NE2	2:AL:197:VAL:O	2.51	0.43
2:AL:56:VAL:HB	2:AL:309:ILE:HD11	2.00	0.43
2:AL:285:LYS:HB3	2:AL:285:LYS:HE3	1.68	0.43
3:AP:7:LYS:HB2	6:U4:23:ARG:HG3	1.99	0.43
5:AZ:14:ILE:HG12	5:AZ:87:VAL:HG23	2.00	0.43
6:S3:195:PHE:O	6:S3:197:TYR:N	2.51	0.43
6:T3:27:ASP:OD1	6:T3:27:ASP:N	2.50	0.43
5:AV:46:THR:HG23	5:AV:60:SER:CB	2.48	0.43
3:AO:66:THR:HA	3:AO:108:MET:O	2.18	0.43
1:M:178:ASP:CG	1:M:181:THR:HG22	2.43	0.43
1:R:6:VAL:HG21	1:R:218:HIS:CE1	2.53	0.43
1:R:24:CYS:HB3	1:R:221:CYS:C	2.43	0.43
1:R:48:LEU:HD23	1:S:1:MET:HE3	1.99	0.43
1:S:141:ILE:HG22	1:S:142:ASN:ND2	2.33	0.43
1:S:154:PRO:O	1:S:156:THR:HG23	2.18	0.43
1:Z:53:LEU:HD12	1:Z:206:GLN:CD	2.44	0.43
1:Z:154:PRO:O	1:Z:156:THR:HG23	2.17	0.43
1:c:88:LEU:N	1:c:121:GLY:O	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:w:209:ILE:HG13	1:w:214:ASN:O	2.18	0.43
1:2:177:VAL:O	1:2:179:PRO:HD3	2.18	0.43
1:0:110:PRO:HA	1:0:136:ARG:O	2.19	0.43
1:E:110:PRO:HA	1:E:136:ARG:O	2.19	0.43
1:G:210:ASP:HB3	1:G:216:PHE:CE2	2.50	0.43
2:AA:77:LYS:HB2	2:AA:77:LYS:HE2	1.82	0.43
2:AA:163:PHE:CD2	2:AA:193:ALA:HB3	2.53	0.43
2:AB:201:ILE:HG22	2:AB:202:ASN:H	1.84	0.43
2:AC:362:LEU:HD23	2:AC:362:LEU:HA	1.89	0.43
2:AF:37:LYS:HE3	2:AF:37:LYS:HB2	1.93	0.43
2:AH:251:LEU:HD12	2:AH:251:LEU:HA	1.87	0.43
2:AI:293:LEU:HA	2:AI:293:LEU:HD12	1.80	0.43
2:AJ:54:HIS:O	2:AJ:58:PHE:HB3	2.19	0.43
2:AK:68:VAL:HG11	2:AK:118:ALA:CB	2.47	0.43
2:AK:220:PRO:HB2	2:AK:309:ILE:HG23	1.99	0.43
2:AK:347:GLU:HB2	2:AK:348:PRO:HD3	1.99	0.43
2:AL:64:LEU:HD13	2:AL:350:TYR:OH	2.18	0.43
2:AL:133:VAL:HG13	2:AL:189:ILE:O	2.17	0.43
2:AL:283:ASP:OD2	2:AL:283:ASP:N	2.49	0.43
4:AR:50:LEU:HD23	4:AR:52:PHE:CE1	2.53	0.43
6:U3:50:PRO:C	6:U3:51:GLU:HG3	2.42	0.43
6:U3:141:PRO:O	6:U3:142:ALA:C	2.59	0.43
3:H:25:LEU:HD23	3:H:25:LEU:H	1.84	0.43
5:Ab:14:ILE:HG12	5:Ab:87:VAL:HG23	2.01	0.43
6:R5:52:LYS:HE2	6:R5:52:LYS:HB3	1.73	0.43
6:S5:23:ARG:O	6:S5:24:VAL:HG13	2.18	0.43
6:S5:194:TRP:O	6:S5:194:TRP:HD1	2.01	0.43
1:L:23:CYS:HB3	1:M:229:CYS:HB3	1.90	0.43
1:O:56:LYS:HB3	1:O:207:VAL:CG1	2.49	0.43
1:T:3:PHE:HD1	1:T:38:MET:HE2	1.83	0.43
1:f:133:GLY:H	1:f:152:VAL:HG23	1.83	0.43
1:h:78:THR:HB	1:h:84:PHE:CD2	2.54	0.43
1:o:8:PRO:HB3	1:o:43:ALA:HB1	2.00	0.43
1:u:29:ALA:HB1	1:u:190:VAL:HG21	2.00	0.43
1:3:104:ILE:HG12	1:3:117:LEU:HD12	2.00	0.43
1:5:35:ASN:OD1	1:5:36:GLY:N	2.46	0.43
1:8:56:LYS:HB3	1:8:207:VAL:HG11	1.99	0.43
1:9:170:VAL:HG12	1:9:175:ARG:NH2	2.34	0.43
1:B:123:PHE:HZ	1:B:148:TYR:CE2	2.37	0.43
1:F:210:ASP:HB3	1:F:216:PHE:HE2	1.84	0.43
2:AA:25:ILE:HG23	2:AA:28:ARG:NH2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:81:ASN:ND2	2:AB:366:GLY:O	2.52	0.43
2:AG:38:ASN:OD1	2:AG:39:VAL:N	2.52	0.43
2:AG:102:GLN:OE1	2:AG:102:GLN:HA	2.18	0.43
2:AG:243:TRP:CH2	2:AH:289:MET:HG3	2.54	0.43
2:AI:266:THR:OG1	2:AJ:239:PRO:HB3	2.17	0.43
2:AK:28:ARG:CG	2:AK:29:ARG:H	2.30	0.43
2:AK:251:LEU:HD12	2:AK:251:LEU:HA	1.81	0.43
3:AP:66:THR:HA	3:AP:108:MET:O	2.19	0.43
6:T3:9:LEU:HD21	6:T3:33:ARG:NH2	2.33	0.43
6:T3:45:GLY:O	6:T3:46:LEU:HD23	2.18	0.43
6:T3:74:ILE:HG23	6:T3:131:VAL:O	2.18	0.43
6:U3:66:LYS:HE3	6:U3:66:LYS:HB2	1.80	0.43
4:AS:94:ARG:H	4:AS:94:ARG:NH2	2.02	0.43
3:H:106:ARG:HE	6:S4:17:LYS:NZ	2.17	0.43
6:R4:49:THR:OG1	6:R4:50:PRO:HD2	2.18	0.43
6:R4:167:ARG:HH21	6:T4:171:ASN:N	2.14	0.43
6:S4:150:LYS:HD3	6:S4:189:GLY:HA3	2.00	0.43
6:R5:166:VAL:HA	6:S5:163:VAL:CG2	2.48	0.43
6:S5:164:MET:HE3	6:S5:164:MET:HB3	1.73	0.43
6:S5:185:ALA:O	6:S5:191:GLN:HG2	2.19	0.43
6:T5:98:SER:OG	6:T5:100:VAL:HG22	2.19	0.43
1:K:46:ALA:HB3	1:K:47:PRO:HD3	2.00	0.43
1:Q:29:ALA:HB1	1:Q:190:VAL:HG21	1.99	0.43
1:X:132:THR:HG21	1:X:154:PRO:HB3	2.00	0.43
1:b:56:LYS:HB3	1:b:207:VAL:CG1	2.49	0.43
1:b:174:ARG:NE	1:b:187:VAL:HG21	2.33	0.43
1:d:46:ALA:HB3	1:d:47:PRO:HD3	2.01	0.43
1:h:38:MET:HE3	1:h:183:VAL:HG11	2.01	0.43
1:i:92:PHE:HB2	1:i:141:ILE:HG21	2.01	0.43
1:l:71:VAL:HG13	1:l:144:ASN:HB2	2.00	0.43
1:m:46:ALA:HB3	1:m:47:PRO:HD3	2.00	0.43
1:s:8:PRO:HB3	1:s:43:ALA:HB1	2.01	0.43
1:3:30:ARG:NH1	1:3:229:CYS:HA	2.33	0.43
1:B:75:PHE:HB2	1:B:164:PHE:HZ	1.84	0.43
1:G:75:PHE:HB2	1:G:164:PHE:HZ	1.83	0.43
2:AC:103:ARG:NH2	2:AD:365:ALA:HA	2.33	0.43
2:AC:133:VAL:HA	2:AC:139:VAL:HA	2.00	0.43
2:AD:56:VAL:HB	2:AD:309:ILE:HD11	2.01	0.43
2:AF:140:ASN:ND2	2:AG:16:PRO:O	2.24	0.43
2:AG:251:LEU:HD12	2:AG:251:LEU:HA	1.80	0.43
2:AJ:66:LEU:HD22	2:AK:348:PRO:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AJ:69:GLN:HE22	2:AK:352:THR:HG23	1.83	0.43
2:AJ:90:SER:C	2:AJ:92:SER:H	2.26	0.43
2:AJ:151:LYS:O	2:AJ:164:GLN:N	2.47	0.43
2:AK:27:ILE:HD13	2:AK:155:ASP:O	2.19	0.43
2:AK:61:LEU:HD23	2:AK:61:LEU:HA	1.86	0.43
2:AL:217:ILE:C	2:AL:220:PRO:HD2	2.44	0.43
2:AL:256:ALA:O	2:AL:257:LYS:C	2.59	0.43
6:S3:185:ALA:O	6:S3:191:GLN:HG2	2.19	0.43
6:U3:49:THR:HB	6:U3:52:LYS:NZ	2.34	0.43
3:AN:45:ILE:C	3:H:97:SER:HG	2.25	0.43
6:T4:188:SER:O	6:T4:188:SER:OG	2.31	0.43
4:AW:95:LYS:HB2	4:AW:95:LYS:HE2	1.53	0.43
5:AY:47:ASN:HD22	5:AY:55:VAL:HG21	1.84	0.43
1:Z:178:ASP:OD2	1:Z:181:THR:HG22	2.19	0.43
1:b:7:ASP:OD1	1:b:7:ASP:N	2.51	0.43
1:d:74:ALA:HB3	1:d:148:TYR:CD1	2.54	0.43
1:e:174:ARG:CZ	1:e:187:VAL:HG21	2.48	0.43
1:f:103:GLU:HB3	1:f:140:SER:OG	2.19	0.43
1:g:99:GLN:HG3	1:g:100:VAL:H	1.84	0.43
1:h:203:THR:OG1	1:i:107:LEU:HD11	2.19	0.43
1:k:59:PHE:HE2	1:k:175:ARG:NE	2.15	0.43
1:k:126:THR:O	1:k:126:THR:OG1	2.34	0.43
1:l:79:LYS:HD2	1:l:153:ASP:HB2	2.01	0.43
1:o:53:LEU:HD12	1:o:206:GLN:CD	2.43	0.43
1:r:47:PRO:O	1:r:49:ARG:N	2.52	0.43
1:v:53:LEU:HD23	1:v:182:HIS:HA	2.01	0.43
1:w:67:THR:O	1:w:67:THR:OG1	2.36	0.43
1:x:172:ALA:O	1:x:175:ARG:NH1	2.52	0.43
1:3:133:GLY:H	1:3:152:VAL:CG1	2.30	0.43
1:3:202:LEU:O	1:3:222:TYR:N	2.49	0.43
1:9:115:VAL:HA	1:9:124:THR:O	2.18	0.43
1:0:35:ASN:OD1	1:0:36:GLY:N	2.44	0.43
1:A:174:ARG:CZ	1:A:187:VAL:HG21	2.49	0.43
1:D:30:ARG:NH1	1:D:229:CYS:HA	2.33	0.43
1:D:90:ASP:OD1	1:D:90:ASP:N	2.51	0.43
1:E:35:ASN:OD1	1:E:36:GLY:N	2.46	0.43
2:AA:38:ASN:ND2	2:AA:39:VAL:H	2.17	0.43
2:AA:338:ARG:NE	2:AB:344:ASP:OD1	2.52	0.43
2:AB:72:LYS:NZ	2:AC:80:GLN:HB3	2.34	0.43
2:AD:109:SER:OG	2:AD:110:GLY:N	2.51	0.43
2:AL:167:ASP:OD2	2:AL:168:GLU:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AL:347:GLU:HB3	2:AL:348:PRO:HD3	2.01	0.43
2:AL:368:ARG:HG3	2:AL:370:ILE:HD11	2.01	0.43
6:R3:38:GLU:HA	6:R3:41:GLU:HB3	1.99	0.43
6:T3:184:GLY:C	6:T3:186:VAL:H	2.26	0.43
4:AT:118:MET:HE3	4:AT:129:PHE:HD2	1.84	0.43
6:U4:50:PRO:C	6:U4:51:GLU:HG3	2.44	0.43
3:I:25:LEU:H	3:I:25:LEU:HD23	1.84	0.43
6:R5:193:GLU:CD	6:R5:196:ARG:HH21	2.26	0.43
6:U5:70:SER:O	6:U5:70:SER:OG	2.29	0.43
1:Q:138:TRP:CZ3	1:Q:147:GLU:HB3	2.54	0.43
1:U:46:ALA:HB3	1:U:47:PRO:HD3	2.00	0.43
1:V:23:CYS:HB3	1:W:229:CYS:HB3	1.80	0.43
1:Y:210:ASP:HB3	1:Y:216:PHE:CE2	2.52	0.43
1:Z:85:GLU:OE1	1:Z:85:GLU:N	2.52	0.43
1:c:3:PHE:CD1	1:c:38:MET:HE2	2.54	0.43
1:c:171:PRO:HD2	1:c:187:VAL:HG23	2.00	0.43
1:e:53:LEU:HD12	1:e:206:GLN:CD	2.44	0.43
1:f:94:ASN:OD1	1:f:94:ASN:N	2.51	0.43
1:h:78:THR:O	1:h:152:VAL:HA	2.19	0.43
1:l:25:GLU:H	1:l:25:GLU:CD	2.27	0.43
1:p:38:MET:HG2	1:p:185:LYS:HG2	2.00	0.43
1:p:56:LYS:HB3	1:p:207:VAL:CG1	2.49	0.43
1:q:1:MET:HE1	1:q:185:LYS:NZ	2.34	0.43
1:u:104:ILE:HG21	1:u:115:VAL:HG21	2.01	0.43
1:1:9:ARG:HH12	1:2:230:GLY:HA2	1.83	0.43
1:2:53:LEU:HD12	1:2:206:GLN:CD	2.44	0.43
1:3:46:ALA:HB3	1:3:47:PRO:HD3	1.99	0.43
1:6:78:THR:O	1:6:152:VAL:HA	2.19	0.43
1:8:53:LEU:HD23	1:8:182:HIS:HA	2.01	0.43
1:9:138:TRP:CZ3	1:9:147:GLU:HB3	2.54	0.43
1:D:138:TRP:CE3	1:D:147:GLU:HB3	2.54	0.43
1:E:153:ASP:HA	1:E:159:LEU:HD23	2.00	0.43
1:F:202:LEU:O	1:F:222:TYR:N	2.47	0.43
1:G:133:GLY:H	1:G:152:VAL:CG1	2.32	0.43
2:AF:54:HIS:O	2:AF:58:PHE:HB3	2.19	0.43
2:AG:61:LEU:HD23	2:AG:61:LEU:HA	1.89	0.43
2:AH:154:PHE:HE1	2:AH:206:ASN:HD22	1.66	0.43
3:AP:1:MET:SD	3:AP:1:MET:N	2.75	0.43
6:R3:188:SER:C	6:R3:190:ALA:N	2.76	0.43
3:H:46:ARG:HE	3:AO:77:VAL:HG23	1.83	0.43
6:T4:21:ASN:OD1	6:T4:21:ASN:N	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T4:199:ARG:HH12	6:T4:200:VAL:HG22	1.83	0.43
6:U4:184:GLY:O	6:U4:185:ALA:HB3	2.18	0.43
1:Y:210:ASP:OD1	1:Y:214:ASN:N	2.52	0.42
1:Z:153:ASP:HA	1:Z:159:LEU:HD23	2.01	0.42
1:b:56:LYS:HB3	1:b:207:VAL:HG11	2.01	0.42
1:b:73:ASN:HB3	1:b:164:PHE:CE1	2.53	0.42
1:k:2:TYR:OH	1:k:28:SER:OG	2.31	0.42
1:l:56:LYS:HB3	1:l:207:VAL:CG1	2.50	0.42
1:l:78:THR:HG23	1:l:152:VAL:HG12	2.01	0.42
1:p:74:ALA:HB3	1:p:148:TYR:CD1	2.54	0.42
1:p:154:PRO:HG2	1:p:156:THR:HG22	2.00	0.42
1:u:74:ALA:HB3	1:u:148:TYR:CD1	2.54	0.42
1:4:53:LEU:HD23	1:4:182:HIS:HA	2.01	0.42
1:5:9:ARG:NH2	1:6:230:GLY:OXT	2.46	0.42
1:6:38:MET:HG2	1:6:185:LYS:HG2	2.00	0.42
1:9:29:ALA:HB1	1:9:190:VAL:HG21	2.00	0.42
1:E:53:LEU:HD12	1:E:206:GLN:CD	2.44	0.42
1:E:112:ASN:O	1:E:128:GLY:N	2.50	0.42
1:G:177:VAL:HG11	1:G:206:GLN:HE22	1.84	0.42
2:AB:75:VAL:H	2:AB:98:GLN:HE22	1.67	0.42
2:AB:252:ASP:OD1	6:T5:43:TYR:HB2	2.19	0.42
2:AC:219:VAL:HB	2:AC:220:PRO:HD3	2.01	0.42
2:AJ:17:ALA:HA	2:AJ:18:PRO:HD3	1.92	0.42
2:AK:314:GLY:O	2:AK:345:THR:HG21	2.18	0.42
6:T3:68:ILE:HD12	6:T3:68:ILE:HA	1.86	0.42
6:T3:167:ARG:O	6:T3:168:ASN:C	2.60	0.42
6:R4:100:VAL:C	6:R4:101:LEU:HD22	2.44	0.42
6:U4:193:GLU:C	6:U4:195:PHE:H	2.25	0.42
5:AY:40:TYR:OH	5:AY:89:VAL:HG11	2.19	0.42
6:U5:49:THR:HB	6:U5:52:LYS:NZ	2.34	0.42
1:N:118:GLY:N	1:N:122:ALA:O	2.30	0.42
1:V:73:ASN:HB3	1:V:164:PHE:HE1	1.84	0.42
1:W:6:VAL:HG21	1:W:218:HIS:CE1	2.54	0.42
1:Z:79:LYS:HD2	1:Z:153:ASP:HB2	2.01	0.42
1:b:157:SER:O	1:b:158:GLU:HG2	2.19	0.42
1:f:102:TYR:CD1	1:f:141:ILE:HD12	2.47	0.42
1:j:108:ASN:HB3	1:j:138:TRP:CD1	2.53	0.42
1:k:157:SER:O	1:k:158:GLU:HG2	2.19	0.42
1:k:196:PRO:HB3	1:k:228:SER:HB3	2.01	0.42
1:s:78:THR:HB	1:s:84:PHE:HD2	1.84	0.42
1:v:59:PHE:HE2	1:v:175:ARG:NE	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:w:53:LEU:HD12	1:w:206:GLN:CD	2.44	0.42
1:4:71:VAL:HG23	1:4:91:LEU:O	2.18	0.42
1:7:119:ALA:O	1:7:120:ASN:ND2	2.49	0.42
1:8:104:ILE:HG12	1:8:117:LEU:HD12	2.01	0.42
1:C:30:ARG:NH1	1:C:229:CYS:HA	2.33	0.42
2:AC:97:LEU:O	2:AC:101:LEU:HB2	2.19	0.42
2:AD:276:ILE:HG22	2:AE:243:TRP:HB2	2.02	0.42
2:AG:369:VAL:O	2:AG:370:ILE:HD13	2.18	0.42
2:AH:68:VAL:C	2:AH:70:SER:N	2.74	0.42
2:AK:130:LYS:O	2:AK:142:ILE:HA	2.19	0.42
2:AL:80:GLN:H	2:AL:80:GLN:CD	2.28	0.42
3:AM:26:LEU:HA	4:AQ:98:GLU:O	2.19	0.42
6:S3:66:LYS:O	6:S3:67:ILE:HD13	2.19	0.42
6:S3:93:ILE:H	6:T3:125:GLN:HE22	1.66	0.42
5:AV:81:GLY:HA2	5:AV:104:VAL:HB	1.99	0.42
3:H:41:PRO:HD3	3:AO:103:GLU:HG2	2.01	0.42
6:R4:195:PHE:C	6:R4:197:TYR:N	2.75	0.42
6:S4:194:TRP:CD1	6:S4:194:TRP:O	2.72	0.42
3:AO:12:VAL:HB	3:AO:33:ILE:HB	2.01	0.42
3:AO:26:LEU:HA	4:AW:98:GLU:O	2.19	0.42
4:AW:93:ASP:O	4:AW:94:ARG:C	2.62	0.42
1:J:8:PRO:HG3	6:R5:53:THR:HG21	2.01	0.42
1:M:6:VAL:HG21	1:M:218:HIS:CE1	2.54	0.42
1:R:138:TRP:CE3	1:R:147:GLU:HB3	2.54	0.42
1:V:46:ALA:HB3	1:V:47:PRO:HD3	2.00	0.42
1:Y:88:LEU:HA	1:Y:91:LEU:HD13	2.00	0.42
1:a:30:ARG:HG3	1:a:31:PRO:HD2	2.01	0.42
1:f:174:ARG:NE	1:f:187:VAL:HG21	2.34	0.42
1:g:78:THR:O	1:g:152:VAL:HA	2.19	0.42
1:n:8:PRO:HB3	1:n:43:ALA:HB1	2.01	0.42
1:p:53:LEU:HD23	1:p:182:HIS:HA	2.01	0.42
1:p:136:ARG:HH21	1:p:165:THR:HG22	1.84	0.42
1:q:94:ASN:OD1	1:q:94:ASN:N	2.52	0.42
1:r:177:VAL:O	1:r:179:PRO:HD3	2.19	0.42
1:w:6:VAL:HG21	1:w:218:HIS:CE1	2.54	0.42
1:x:75:PHE:CZ	1:x:161:GLN:HG2	2.54	0.42
1:1:180:ARG:HG2	1:1:180:ARG:NH1	2.34	0.42
1:5:138:TRP:CZ3	1:5:147:GLU:HB3	2.54	0.42
1:8:53:LEU:HD12	1:8:206:GLN:CD	2.44	0.42
1:8:78:THR:O	1:8:152:VAL:HA	2.18	0.42
1:0:138:TRP:CZ3	1:0:147:GLU:HB3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:133:GLY:H	1:F:152:VAL:CG2	2.32	0.42
2:AC:279:ILE:HD11	6:R5:202:LEU:HG	2.01	0.42
2:AD:172:GLU:O	2:AD:174:ILE:HD12	2.19	0.42
2:AE:66:LEU:HD22	2:AF:348:PRO:O	2.20	0.42
2:AF:28:ARG:HD3	2:AF:29:ARG:HG3	2.02	0.42
2:AF:222:ALA:HA	2:AF:225:ASP:OD2	2.20	0.42
2:AG:219:VAL:HB	2:AG:220:PRO:HD3	2.01	0.42
2:AI:159:ASP:N	2:AI:159:ASP:OD1	2.51	0.42
2:AJ:335:ASP:OD1	2:AJ:335:ASP:N	2.49	0.42
6:U3:2:ASN:N	6:U3:2:ASN:OD1	2.53	0.42
3:H:1:MET:SD	3:H:1:MET:N	2.77	0.42
6:S4:194:TRP:O	6:S4:194:TRP:HD1	2.02	0.42
6:U4:190:ALA:C	6:U4:192:ASP:N	2.78	0.42
3:AO:43:LYS:HE2	3:AO:43:LYS:HB2	1.84	0.42
5:AY:128:LEU:HA	5:AY:128:LEU:HD13	1.73	0.42
1:J:3:PHE:HD1	1:J:38:MET:HE2	1.85	0.42
1:J:4:PHE:HB2	1:J:39:VAL:HG12	2.02	0.42
1:J:12:ALA:HB1	6:R5:51:GLU:O	2.18	0.42
1:K:53:LEU:HD12	1:K:206:GLN:CD	2.44	0.42
1:M:74:ALA:HB3	1:M:148:TYR:CD1	2.54	0.42
1:S:180:ARG:HD2	1:S:180:ARG:HA	1.90	0.42
1:a:38:MET:SD	1:a:185:LYS:HE2	2.60	0.42
1:g:1:MET:HE2	1:g:38:MET:HG3	2.01	0.42
1:g:138:TRP:CH2	1:g:192:PRO:HD2	2.54	0.42
1:h:74:ALA:HB3	1:h:148:TYR:CD1	2.54	0.42
1:h:174:ARG:NH2	1:h:187:VAL:HG11	2.33	0.42
1:i:46:ALA:HB3	1:i:47:PRO:HD3	2.01	0.42
1:n:75:PHE:CZ	1:n:161:GLN:HG2	2.54	0.42
1:o:47:PRO:O	1:o:49:ARG:N	2.52	0.42
1:z:157:SER:O	1:z:158:GLU:HG2	2.20	0.42
1:4:88:LEU:HG	1:4:141:ILE:HD11	2.01	0.42
1:G:119:ALA:O	1:G:120:ASN:ND2	2.51	0.42
2:AB:229:ALA:HA	2:AB:232:ILE:HG22	2.01	0.42
2:AC:192:TYR:CE2	2:AC:194:PHE:HE1	2.37	0.42
2:AC:220:PRO:HB2	2:AC:309:ILE:HG23	2.00	0.42
2:AD:368:ARG:HG3	2:AD:370:ILE:HD11	2.02	0.42
2:AE:25:ILE:HG23	2:AE:28:ARG:NH2	2.35	0.42
2:AF:59:ARG:NH1	2:AF:320:LEU:HB3	2.35	0.42
2:AI:264:GLU:O	2:AI:267:LYS:HG3	2.18	0.42
2:AI:297:HIS:CE1	2:AI:299:LYS:HB2	2.54	0.42
2:AJ:249:ARG:HD2	2:AJ:249:ARG:HA	1.79	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AM:75:VAL:HB	3:AM:98:VAL:HG11	2.01	0.42
6:S3:164:MET:HE3	6:S3:164:MET:HB3	1.75	0.42
4:AS:104:TYR:OH	4:AS:108:GLU:OE1	2.37	0.42
6:S4:191:GLN:C	6:S4:193:GLU:N	2.77	0.42
6:T4:185:ALA:O	6:T4:191:GLN:HG2	2.20	0.42
6:U4:147:GLY:HA3	6:U4:194:TRP:NE1	2.34	0.42
4:AX:28:ILE:HG22	4:AX:51:PRO:HG2	2.01	0.42
1:K:24:CYS:HB3	1:K:221:CYS:C	2.44	0.42
1:b:78:THR:HG23	1:b:152:VAL:HG12	2.00	0.42
1:r:24:CYS:HB3	1:r:221:CYS:HB2	1.54	0.42
1:v:180:ARG:HG2	1:v:180:ARG:NH1	2.34	0.42
1:w:110:PRO:HA	1:w:136:ARG:O	2.19	0.42
1:6:133:GLY:H	1:6:152:VAL:CG2	2.31	0.42
1:0:56:LYS:HB3	1:0:207:VAL:CG1	2.49	0.42
1:A:78:THR:O	1:A:152:VAL:HA	2.19	0.42
1:F:88:LEU:HG	1:F:141:ILE:HD11	2.01	0.42
1:F:118:GLY:N	1:F:122:ALA:O	2.31	0.42
2:AA:297:HIS:CE1	2:AA:299:LYS:HB2	2.48	0.42
2:AB:400:GLU:H	2:AB:400:GLU:HG2	1.69	0.42
2:AC:46:MET:HE2	2:AC:46:MET:HB2	1.89	0.42
2:AD:163:PHE:O	2:AD:173:THR:HA	2.19	0.42
2:AE:39:VAL:HG21	2:AE:147:ILE:HD11	2.01	0.42
2:AE:253:ASP:OD2	6:U5:198:ARG:HG2	2.19	0.42
2:AF:117:ALA:HB1	2:AF:127:MET:HE2	2.01	0.42
2:AF:150:LEU:HD11	2:AF:163:PHE:HB3	2.02	0.42
2:AF:201:ILE:HG22	2:AF:202:ASN:N	2.34	0.42
2:AJ:359:SER:CB	2:AJ:368:ARG:HB2	2.50	0.42
3:AP:35:GLY:HA3	6:T3:20:ASP:OD2	2.18	0.42
6:S3:127:MET:HE3	6:S3:127:MET:HB3	1.78	0.42
6:U3:173:ASN:OD1	6:U3:175:GLN:HG2	2.19	0.42
3:AN:26:LEU:HA	4:AS:98:GLU:O	2.19	0.42
6:U4:28:LEU:HD23	6:U4:28:LEU:HA	1.77	0.42
4:AW:118:MET:HE3	4:AW:129:PHE:CD2	2.54	0.42
1:J:39:VAL:HG23	1:J:184:LEU:HB3	2.00	0.42
1:K:126:THR:O	1:K:126:THR:OG1	2.30	0.42
1:N:154:PRO:O	1:N:156:THR:HG23	2.19	0.42
1:O:90:ASP:OD1	1:O:90:ASP:N	2.53	0.42
1:P:138:TRP:CZ3	1:P:147:GLU:HB3	2.55	0.42
1:R:74:ALA:HB3	1:R:148:TYR:CD1	2.55	0.42
1:T:73:ASN:HB3	1:T:164:PHE:HE1	1.84	0.42
1:W:22:CYS:SG	1:l:50:GLY:HA2	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:53:LEU:HD23	1:Y:182:HIS:HA	2.01	0.42
1:Y:154:PRO:HD3	1:Y:159:LEU:HD21	2.02	0.42
1:Z:34:VAL:HA	1:Z:189:GLY:HA2	2.02	0.42
1:c:78:THR:O	1:c:152:VAL:HA	2.19	0.42
1:i:107:LEU:HD23	1:i:107:LEU:HA	1.84	0.42
1:l:206:GLN:OE1	1:l:207:VAL:N	2.51	0.42
1:m:88:LEU:HD11	1:m:139:PHE:CG	2.55	0.42
1:p:64:VAL:HG12	1:p:199:VAL:O	2.20	0.42
1:s:194:ALA:HB1	1:s:226:ILE:HG21	2.01	0.42
1:v:209:ILE:HG13	1:v:214:ASN:O	2.19	0.42
1:1:153:ASP:HA	1:1:159:LEU:HD23	2.01	0.42
1:0:75:PHE:CZ	1:0:161:GLN:HG2	2.55	0.42
1:B:60:GLU:HG3	1:C:106:GLU:OE2	2.20	0.42
1:D:29:ALA:HB1	1:D:190:VAL:HG21	2.02	0.42
1:D:53:LEU:HD23	1:D:182:HIS:HA	2.02	0.42
2:AC:28:ARG:CG	2:AC:29:ARG:H	2.30	0.42
2:AD:83:GLN:HE21	2:AD:366:GLY:H	1.67	0.42
2:AE:96:ALA:O	2:AE:100:ILE:HG12	2.19	0.42
2:AE:182:LYS:HA	2:AE:188:PRO:HA	2.02	0.42
2:AF:54:HIS:CE1	2:AF:56:VAL:H	2.37	0.42
2:AF:98:GLN:HG2	2:AG:82:THR:HG21	2.01	0.42
2:AH:63:LYS:HE3	2:AH:63:LYS:HB2	1.94	0.42
2:AH:172:GLU:O	2:AH:174:ILE:HD12	2.20	0.42
2:AL:210:GLN:H	2:AL:210:GLN:HG3	1.60	0.42
2:AL:245:VAL:HB	2:AL:286:VAL:HG12	2.02	0.42
3:AM:97:SER:OG	3:I:45:ILE:N	2.52	0.42
4:AQ:76:LEU:HD12	4:AQ:155:TRP:HB2	2.02	0.42
4:AQ:104:TYR:OH	4:AQ:108:GLU:OE1	2.37	0.42
5:AU:47:ASN:HB3	5:AU:55:VAL:CG2	2.50	0.42
4:AR:86:MET:HE3	4:AR:86:MET:HB3	1.91	0.42
5:AV:47:ASN:HB3	5:AV:55:VAL:HG21	2.01	0.42
6:S4:73:PRO:HB3	6:S4:94:PRO:HG3	2.00	0.42
6:T4:187:ILE:HA	6:U5:182:ASN:ND2	2.34	0.42
6:U4:145:ILE:HD13	6:U4:145:ILE:HA	1.87	0.42
6:U4:184:GLY:O	6:U4:186:VAL:N	2.52	0.42
5:AY:47:ASN:HB3	5:AY:55:VAL:CG2	2.50	0.42
4:AX:34:PRO:HA	4:AX:55:VAL:O	2.20	0.42
6:T5:74:ILE:HG23	6:T5:131:VAL:O	2.19	0.42
1:J:59:PHE:HE2	1:J:175:ARG:NE	2.18	0.42
1:N:132:THR:HG21	1:N:154:PRO:HB3	2.01	0.42
1:P:3:PHE:CD1	1:P:38:MET:HE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:132:THR:HG21	1:S:154:PRO:HB3	2.00	0.42
1:Z:126:THR:O	1:Z:126:THR:OG1	2.32	0.42
1:d:138:TRP:CZ3	1:d:147:GLU:HB3	2.55	0.42
1:f:157:SER:O	1:f:158:GLU:HG2	2.19	0.42
1:h:46:ALA:HB3	1:h:47:PRO:HD3	2.02	0.42
1:i:92:PHE:CZ	1:i:94:ASN:HB3	2.54	0.42
1:j:79:LYS:HD2	1:j:153:ASP:HB2	2.01	0.42
1:k:53:LEU:HD12	1:k:206:GLN:CD	2.44	0.42
1:r:206:GLN:OE1	1:r:207:VAL:N	2.52	0.42
1:s:6:VAL:HG21	1:s:218:HIS:CE1	2.55	0.42
1:t:59:PHE:HE2	1:t:175:ARG:NE	2.17	0.42
1:3:209:ILE:HD11	1:3:213:GLY:HA2	2.01	0.42
1:5:153:ASP:HA	1:5:159:LEU:HD23	2.02	0.42
1:D:75:PHE:CE1	1:D:161:GLN:HG2	2.54	0.42
1:D:170:VAL:HG12	1:D:175:ARG:NH2	2.35	0.42
2:AC:80:GLN:H	2:AC:80:GLN:CD	2.28	0.42
2:AC:347:GLU:HB2	2:AC:348:PRO:HD3	2.00	0.42
2:AF:182:LYS:HE3	2:AF:182:LYS:HB2	1.86	0.42
2:AJ:81:ASN:ND2	2:AJ:366:GLY:O	2.53	0.42
2:AK:359:SER:HB3	2:AK:368:ARG:HB2	2.01	0.42
2:AL:95:LYS:HE3	2:AL:95:LYS:HB3	1.80	0.42
2:AL:154:PHE:HE1	2:AL:206:ASN:HD22	1.66	0.42
6:S3:148:ILE:HG13	6:S3:194:TRP:HZ3	1.85	0.42
6:S3:150:LYS:HD3	6:S3:189:GLY:HA3	2.02	0.42
6:T3:190:ALA:HB1	6:T3:194:TRP:CH2	2.55	0.42
6:R4:147:GLY:HA3	6:R4:194:TRP:CE2	2.55	0.42
6:T4:74:ILE:HG23	6:T4:131:VAL:O	2.20	0.42
6:T4:178:ILE:HD12	6:T4:178:ILE:HA	1.86	0.42
4:AW:24:ALA:O	4:AW:25:PHE:C	2.63	0.42
6:S5:66:LYS:O	6:S5:67:ILE:HD13	2.19	0.42
1:N:115:VAL:HA	1:N:124:THR:O	2.20	0.42
1:N:180:ARG:HD2	1:N:180:ARG:HA	1.91	0.42
1:O:157:SER:O	1:O:158:GLU:HG2	2.20	0.42
1:O:177:VAL:O	1:O:179:PRO:HD3	2.19	0.42
1:S:46:ALA:HB3	1:S:47:PRO:HD3	2.01	0.42
1:S:53:LEU:HD23	1:S:182:HIS:HA	2.02	0.42
1:S:75:PHE:HD1	1:S:149:VAL:HG13	1.84	0.42
1:W:74:ALA:HB3	1:W:148:TYR:CD1	2.55	0.42
1:b:138:TRP:CH2	1:b:192:PRO:HD2	2.54	0.42
1:e:153:ASP:HA	1:e:159:LEU:HD23	2.01	0.42
1:h:153:ASP:C	1:h:155:THR:H	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:k:103:GLU:HB3	1:k:140:SER:OG	2.18	0.42
1:k:174:ARG:NE	1:k:187:VAL:HG21	2.34	0.42
1:l:99:GLN:HG3	1:l:100:VAL:H	1.83	0.42
1:l:178:ASP:OD2	1:l:181:THR:HG22	2.20	0.42
1:q:180:ARG:HG2	1:q:180:ARG:NH1	2.35	0.42
1:5:75:PHE:CZ	1:5:161:GLN:HG2	2.53	0.42
1:5:172:ALA:O	1:5:175:ARG:NH1	2.52	0.42
1:D:218:HIS:HE1	1:D:220:SER:HB3	1.84	0.42
1:F:174:ARG:CZ	1:F:187:VAL:HG21	2.50	0.42
2:AA:293:LEU:HA	2:AA:293:LEU:HD12	1.80	0.42
2:AE:132:SER:OG	2:AE:140:ASN:HB3	2.19	0.42
2:AE:316:PRO:CD	2:AE:341:PHE:HB2	2.50	0.42
2:AF:131:VAL:HG21	2:AF:192:TYR:CE1	2.55	0.42
2:AF:132:SER:HA	2:AF:191:ASN:ND2	2.29	0.42
2:AG:161:GLU:OE1	2:AG:179:LYS:HG2	2.19	0.42
2:AH:109:SER:OG	2:AH:110:GLY:N	2.52	0.42
2:AH:232:ILE:HD13	2:AI:223:LEU:HD13	2.02	0.42
2:AJ:83:GLN:OE1	2:AJ:83:GLN:N	2.50	0.42
2:AJ:319:LEU:O	2:AJ:320:LEU:HD23	2.20	0.42
2:AK:219:VAL:HB	2:AK:220:PRO:HD3	2.00	0.42
6:R3:21:ASN:HB3	6:R3:24:VAL:HG22	2.01	0.42
6:U3:151:LEU:HD13	6:U3:185:ALA:HB2	2.01	0.42
3:AN:11:ILE:HD13	3:AN:82:TYR:HD2	1.85	0.42
4:AT:34:PRO:HA	4:AT:55:VAL:O	2.19	0.42
6:U4:190:ALA:O	6:U4:192:ASP:N	2.53	0.42
3:AO:75:VAL:HB	3:AO:98:VAL:HG11	2.01	0.42
1:J:73:ASN:HB3	1:J:164:PHE:HE1	1.84	0.42
1:L:73:ASN:HB3	1:L:164:PHE:CE1	2.54	0.42
1:L:126:THR:O	1:L:126:THR:OG1	2.30	0.42
1:Q:74:ALA:HB3	1:Q:148:TYR:CD1	2.55	0.42
1:a:75:PHE:HE1	1:a:162:PRO:HD2	1.81	0.42
1:g:56:LYS:HB3	1:g:207:VAL:HG11	2.02	0.42
1:i:56:LYS:HB3	1:i:207:VAL:CG1	2.50	0.42
1:l:90:ASP:N	1:l:90:ASP:OD1	2.46	0.42
1:m:25:GLU:CD	1:m:25:GLU:H	2.26	0.42
1:m:75:PHE:HE1	1:m:162:PRO:HD2	1.83	0.42
1:n:140:SER:O	1:n:140:SER:OG	2.30	0.42
1:o:75:PHE:CE1	1:o:162:PRO:HD2	2.53	0.42
1:r:110:PRO:HA	1:r:136:ARG:O	2.19	0.42
1:y:209:ILE:HG13	1:y:214:ASN:O	2.20	0.42
1:z:56:LYS:HB3	1:z:207:VAL:HG11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:59:PHE:HE2	1:1:175:ARG:NE	2.18	0.42
1:1:138:TRP:CH2	1:1:192:PRO:HD2	2.55	0.42
1:8:75:PHE:CE1	1:8:161:GLN:HG2	2.55	0.42
1:A:88:LEU:HB3	1:A:121:GLY:CA	2.50	0.42
1:A:138:TRP:CE3	1:A:147:GLU:HB3	2.54	0.42
1:A:167:PRO:HA	1:A:191:SER:HB3	2.01	0.42
1:F:138:TRP:CE3	1:F:147:GLU:HB3	2.55	0.42
2:AA:241:SER:OG	2:AL:277:ILE:HD11	2.20	0.42
2:AE:400:GLU:H	2:AE:400:GLU:HG2	1.62	0.42
2:AF:264:GLU:OE1	2:AF:267:LYS:HD3	2.20	0.42
2:AG:39:VAL:HG11	2:AG:195:MET:HE2	2.01	0.42
2:AG:346:ILE:HD13	2:AG:346:ILE:HA	1.84	0.42
2:AG:362:LEU:HD23	2:AG:362:LEU:HA	1.91	0.42
2:AH:64:LEU:HD13	2:AH:350:TYR:OH	2.20	0.42
6:T3:185:ALA:O	6:T3:191:GLN:HG2	2.20	0.42
6:T3:194:TRP:O	6:T3:195:PHE:C	2.62	0.42
4:AW:118:MET:HE3	4:AW:129:PHE:HD2	1.84	0.42
6:S5:190:ALA:O	6:S5:191:GLN:C	2.62	0.42
6:U5:143:GLY:HA3	6:U5:197:TYR:OH	2.20	0.42
6:U5:173:ASN:O	6:U5:174:ALA:HB2	2.20	0.42
1:N:49:ARG:HD2	6:U3:89:PRO:O	2.20	0.42
1:O:10:ASN:HD22	6:R3:77:ARG:NH1	2.18	0.42
1:P:59:PHE:CD1	1:P:204:VAL:HG22	2.55	0.42
1:X:115:VAL:HA	1:X:124:THR:O	2.19	0.42
1:a:132:THR:HA	1:a:152:VAL:HG23	2.01	0.42
1:a:138:TRP:CE3	1:a:147:GLU:HB3	2.55	0.42
1:m:153:ASP:C	1:m:155:THR:H	2.28	0.42
1:o:209:ILE:HG13	1:o:214:ASN:O	2.20	0.42
1:q:209:ILE:HG13	1:q:214:ASN:O	2.20	0.42
1:u:30:ARG:HG3	1:u:31:PRO:HD2	2.01	0.42
1:u:59:PHE:HD1	1:u:202:LEU:HD11	1.84	0.42
1:v:83:VAL:HG23	1:v:126:THR:HG22	2.02	0.42
1:x:138:TRP:CE3	1:x:147:GLU:HB3	2.55	0.42
1:x:209:ILE:HG13	1:x:214:ASN:O	2.20	0.42
1:z:53:LEU:HD23	1:z:182:HIS:HA	2.02	0.42
1:z:78:THR:HG23	1:z:152:VAL:HG12	2.02	0.42
1:1:94:ASN:OD1	1:1:94:ASN:N	2.53	0.42
1:2:157:SER:O	1:2:158:GLU:HG2	2.20	0.42
1:B:203:THR:OG1	1:C:107:LEU:HD11	2.20	0.42
1:C:75:PHE:CE1	1:C:161:GLN:HG2	2.54	0.42
1:C:117:LEU:HD23	1:C:118:GLY:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:53:LEU:HD12	1:D:206:GLN:NE2	2.34	0.42
2:AA:95:LYS:HE3	2:AA:95:LYS:HB2	1.83	0.42
2:AD:255:GLN:O	2:AD:258:GLU:HB3	2.19	0.42
2:AE:150:LEU:HD11	2:AE:163:PHE:HB3	2.02	0.42
2:AE:170:GLY:O	2:AE:171:LYS:HD2	2.20	0.42
2:AE:172:GLU:O	2:AE:174:ILE:N	2.53	0.42
2:AE:355:GLU:OE2	2:AE:370:ILE:HA	2.19	0.42
2:AF:28:ARG:NH1	2:AF:29:ARG:HB3	2.34	0.42
2:AF:73:TRP:HH2	2:AF:113:LEU:HD22	1.85	0.42
2:AF:133:VAL:HA	2:AF:139:VAL:HA	2.02	0.42
2:AG:80:GLN:H	2:AG:80:GLN:CD	2.27	0.42
2:AG:314:GLY:O	2:AG:345:THR:HG21	2.19	0.42
2:AH:129:PHE:HB2	2:AH:194:PHE:CD2	2.55	0.42
2:AK:243:TRP:CH2	2:AL:289:MET:HG3	2.55	0.42
2:AL:129:PHE:HB2	2:AL:194:PHE:CD2	2.55	0.42
2:AL:254:GLY:C	2:AL:256:ALA:N	2.76	0.42
4:AR:25:PHE:HD1	4:AR:113:ARG:CZ	2.33	0.42
6:S3:14:GLU:O	6:T3:23:ARG:NH2	2.47	0.42
4:AT:61:ASP:OD2	4:AT:62:THR:N	2.45	0.42
6:R4:167:ARG:O	6:R4:168:ASN:C	2.62	0.42
5:AY:81:GLY:HA2	5:AY:104:VAL:HB	2.02	0.42
6:R5:137:GLU:O	6:R5:139:SER:N	2.53	0.42
6:R5:188:SER:C	6:R5:190:ALA:N	2.77	0.42
1:b:1:MET:HE2	1:b:38:MET:HG3	2.02	0.41
1:e:178:ASP:OD2	1:e:181:THR:HG22	2.19	0.41
1:f:67:THR:O	1:f:67:THR:OG1	2.32	0.41
1:h:8:PRO:HB3	1:h:43:ALA:HB1	2.01	0.41
1:j:178:ASP:OD2	1:j:181:THR:HG22	2.20	0.41
1:l:117:LEU:HD23	1:l:118:GLY:O	2.20	0.41
1:l:134:VAL:HA	1:l:151:SER:HA	2.01	0.41
1:o:71:VAL:HG13	1:o:144:ASN:HB2	2.02	0.41
1:p:157:SER:O	1:p:158:GLU:HG2	2.20	0.41
1:z:74:ALA:HB3	1:z:148:TYR:CD1	2.54	0.41
2:AB:359:SER:CB	2:AB:368:ARG:HB2	2.50	0.41
2:AC:75:VAL:H	2:AC:98:GLN:NE2	2.18	0.41
2:AD:129:PHE:HB2	2:AD:194:PHE:CD2	2.55	0.41
2:AG:220:PRO:HB2	2:AG:309:ILE:HG23	2.01	0.41
2:AI:18:PRO:O	2:AI:20:ALA:N	2.53	0.41
2:AJ:61:LEU:HD23	2:AJ:61:LEU:HA	1.78	0.41
4:AQ:50:LEU:HD13	4:AQ:51:PRO:HA	2.02	0.41
6:R3:195:PHE:O	6:R3:197:TYR:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:U3:50:PRO:HB3	6:U3:138:ASN:HB3	2.02	0.41
4:AS:12:THR:O	4:AS:13:LEU:C	2.61	0.41
6:R4:186:VAL:O	6:R4:187:ILE:C	2.62	0.41
6:U4:54:ILE:HD11	6:U4:130:TYR:CE2	2.55	0.41
5:AY:48:THR:OG1	5:AY:56:GLN:HB3	2.20	0.41
1:K:194:ALA:HB1	1:K:226:ILE:HG21	2.01	0.41
1:L:12:ALA:HB1	6:T5:51:GLU:HB3	2.02	0.41
1:V:85:GLU:OE1	1:V:124:THR:OG1	2.26	0.41
1:d:99:GLN:OE1	1:d:99:GLN:N	2.42	0.41
1:g:178:ASP:OD2	1:g:181:THR:HG22	2.20	0.41
1:l:1:MET:HE2	1:l:38:MET:HG3	2.02	0.41
1:l:25:GLU:OE1	1:l:25:GLU:N	2.47	0.41
1:l:157:SER:O	1:l:158:GLU:HG2	2.19	0.41
1:r:21:SER:HB3	1:7:49:ARG:HB3	2.02	0.41
1:t:71:VAL:HG13	1:t:144:ASN:HB2	2.02	0.41
1:x:38:MET:HG2	1:x:185:LYS:HG2	2.02	0.41
1:5:56:LYS:HB3	1:5:207:VAL:CG1	2.49	0.41
1:8:9:ARG:NH2	1:9:230:GLY:OXT	2.37	0.41
1:8:44:TRP:CH2	1:8:218:HIS:HB2	2.55	0.41
1:9:175:ARG:HE	1:9:175:ARG:HB3	1.30	0.41
1:G:24:CYS:HB3	1:G:221:CYS:HB2	1.64	0.41
2:AA:172:GLU:O	2:AA:174:ILE:N	2.53	0.41
2:AE:153:LYS:HE3	2:AE:153:LYS:HB2	1.88	0.41
2:AF:282:THR:HG22	2:AF:283:ASP:N	2.35	0.41
2:AG:359:SER:HB3	2:AG:368:ARG:HB2	2.02	0.41
2:AI:66:LEU:HD22	2:AJ:348:PRO:O	2.20	0.41
2:AI:282:THR:CG2	2:AJ:249:ARG:HD3	2.49	0.41
2:AL:133:VAL:HG13	2:AL:189:ILE:C	2.46	0.41
2:AL:217:ILE:HA	2:AL:220:PRO:HD2	2.02	0.41
4:AQ:24:ALA:O	4:AQ:25:PHE:C	2.63	0.41
6:S3:196:ARG:HE	6:S3:196:ARG:HB3	1.71	0.41
6:R4:74:ILE:CG2	6:R4:77:ARG:HB3	2.49	0.41
6:T4:15:HIS:HA	6:U5:28:LEU:HD11	2.02	0.41
6:T4:169:THR:O	6:T4:170:LEU:HD23	2.20	0.41
6:R5:94:PRO:HA	6:R5:101:LEU:HD11	2.02	0.41
6:S5:200:VAL:O	6:S5:201:LEU:HG	2.20	0.41
6:T5:132:THR:HG22	6:T5:133:GLY:N	2.32	0.41
1:K:138:TRP:CZ3	1:K:147:GLU:HB3	2.54	0.41
1:N:99:GLN:N	1:N:99:GLN:OE1	2.53	0.41
1:O:92:PHE:HB2	1:O:141:ILE:HG21	2.01	0.41
1:S:49:ARG:HD2	6:U4:89:PRO:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:12:ALA:HB1	6:R4:51:GLU:O	2.20	0.41
1:Y:92:PHE:CZ	1:Y:94:ASN:HB3	2.55	0.41
1:Z:174:ARG:CZ	1:Z:187:VAL:HG21	2.51	0.41
1:a:103:GLU:HB3	1:a:140:SER:OG	2.20	0.41
1:f:53:LEU:HD12	1:f:206:GLN:CD	2.45	0.41
1:g:30:ARG:HD2	1:g:230:GLY:H	1.85	0.41
1:n:194:ALA:HB1	1:n:226:ILE:HG21	2.02	0.41
1:o:185:LYS:HB3	1:o:185:LYS:HE3	1.87	0.41
1:q:153:ASP:HA	1:q:159:LEU:HD23	2.02	0.41
1:u:64:VAL:HG12	1:u:199:VAL:O	2.20	0.41
1:4:9:ARG:NE	1:5:33:GLU:OE2	2.53	0.41
1:4:55:ASN:OD1	1:4:177:VAL:HG22	2.21	0.41
1:B:24:CYS:HB3	1:B:221:CYS:HB2	1.26	0.41
2:AC:69:GLN:HE22	2:AD:352:THR:HG23	1.85	0.41
2:AE:95:LYS:HE3	2:AE:95:LYS:HB2	1.77	0.41
2:AF:75:VAL:H	2:AF:98:GLN:HE22	1.68	0.41
2:AF:81:ASN:ND2	2:AF:366:GLY:O	2.54	0.41
2:AG:99:GLN:NE2	2:AH:83:GLN:HB3	2.35	0.41
2:AK:83:GLN:HE21	2:AK:366:GLY:H	1.68	0.41
2:AK:382:SER:O	2:AK:386:ILE:HG12	2.21	0.41
6:R3:161:ASP:HB2	6:U3:157:ASN:ND2	2.35	0.41
6:S3:23:ARG:O	6:S3:24:VAL:HG13	2.19	0.41
6:S3:72:THR:O	6:S3:73:PRO:C	2.63	0.41
4:AS:24:ALA:O	4:AS:25:PHE:C	2.63	0.41
4:AS:93:ASP:O	4:AS:94:ARG:C	2.63	0.41
4:AT:12:THR:HG1	4:AT:15:GLU:CD	2.28	0.41
3:H:55:GLN:NE2	3:H:60:GLN:HB2	2.35	0.41
3:H:57:ASP:OD2	3:H:60:GLN:NE2	2.37	0.41
5:Aa:111:ASP:OD1	5:Aa:111:ASP:N	2.50	0.41
6:T4:141:PRO:HD2	6:T4:144:ILE:HD12	2.02	0.41
6:U4:86:LEU:HD12	6:U4:86:LEU:HA	1.79	0.41
4:AW:135:ASP:OD1	4:AX:59:GLN:HG3	2.20	0.41
6:R5:195:PHE:C	6:R5:197:TYR:H	2.28	0.41
6:S5:196:ARG:HE	6:S5:196:ARG:HB3	1.75	0.41
1:J:71:VAL:HG11	1:J:141:ILE:HB	2.02	0.41
1:R:46:ALA:HB3	1:R:47:PRO:HD3	2.02	0.41
1:R:157:SER:O	1:R:158:GLU:HG2	2.21	0.41
1:T:4:PHE:O	1:T:39:VAL:HA	2.20	0.41
1:T:73:ASN:HB3	1:T:164:PHE:CE1	2.55	0.41
1:e:85:GLU:OE1	1:e:85:GLU:N	2.53	0.41
1:g:134:VAL:HG21	1:g:162:PRO:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:g:157:SER:O	1:g:158:GLU:HG2	2.20	0.41
1:g:174:ARG:NE	1:g:187:VAL:HG21	2.35	0.41
1:i:1:MET:HE2	1:i:38:MET:HG3	2.03	0.41
1:n:138:TRP:CE3	1:n:147:GLU:HB3	2.55	0.41
1:n:167:PRO:HA	1:n:191:SER:HB3	2.02	0.41
1:o:46:ALA:HB3	1:o:47:PRO:HD3	2.02	0.41
1:o:177:VAL:O	1:o:179:PRO:HD3	2.21	0.41
1:v:8:PRO:HB2	1:v:10:ASN:OD1	2.21	0.41
1:w:90:ASP:N	1:w:90:ASP:OD1	2.53	0.41
1:4:138:TRP:CE3	1:4:147:GLU:HB3	2.55	0.41
1:B:78:THR:O	1:B:152:VAL:HA	2.20	0.41
2:AA:25:ILE:HD11	2:AL:165:TYR:CD1	2.55	0.41
2:AA:39:VAL:HG21	2:AA:147:ILE:HD11	2.02	0.41
2:AC:77:LYS:HE2	2:AC:77:LYS:HB2	1.86	0.41
2:AC:165:TYR:CD1	2:AD:25:ILE:HD11	2.54	0.41
2:AC:282:THR:N	2:AD:249:ARG:HG3	2.18	0.41
2:AE:163:PHE:CD2	2:AE:193:ALA:HB3	2.55	0.41
2:AG:63:LYS:O	2:AG:67:THR:HG22	2.21	0.41
2:AG:253:ASP:OD2	6:S4:198:ARG:HG2	2.20	0.41
2:AH:59:ARG:HB2	2:AI:312:ASN:OD1	2.20	0.41
2:AK:161:GLU:OE1	2:AK:179:LYS:HG2	2.20	0.41
2:AL:251:LEU:O	2:AL:255:GLN:HB2	2.20	0.41
3:AP:96:LEU:HD23	3:AP:96:LEU:HA	1.80	0.41
6:R4:178:ILE:O	6:R4:180:GLY:N	2.52	0.41
6:R4:183:ASN:HD22	6:R4:183:ASN:HA	1.57	0.41
6:S4:69:LEU:HB2	6:S4:99:ASN:HB2	2.02	0.41
6:T4:132:THR:HG22	6:T4:133:GLY:N	2.34	0.41
5:AY:46:THR:HG23	5:AY:60:SER:CB	2.50	0.41
6:R5:16:ALA:HB1	6:R5:156:ILE:HD11	2.02	0.41
6:R5:186:VAL:HG21	6:R5:191:GLN:NE2	2.24	0.41
6:S5:150:LYS:HD3	6:S5:189:GLY:HA3	2.02	0.41
1:J:178:ASP:OD2	1:J:181:THR:HG22	2.20	0.41
1:J:180:ARG:HH12	6:R5:124:SER:N	2.17	0.41
1:M:92:PHE:HB2	1:M:141:ILE:HG21	2.00	0.41
1:P:1:MET:HE2	1:P:38:MET:HG3	2.01	0.41
1:Q:30:ARG:NH1	1:Q:229:CYS:HA	2.36	0.41
1:V:180:ARG:HD3	1:V:180:ARG:HA	1.92	0.41
1:X:154:PRO:O	1:X:156:THR:HG23	2.20	0.41
1:d:210:ASP:OD1	1:d:214:ASN:N	2.54	0.41
1:f:116:GLU:N	1:f:116:GLU:OE2	2.53	0.41
1:n:72:SER:O	1:n:91:LEU:HD12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:195:ILE:HB	1:u:198:ASP:OD1	2.20	0.41
1:w:149:VAL:HG11	1:w:162:PRO:HG2	2.02	0.41
1:w:157:SER:O	1:w:158:GLU:HG2	2.20	0.41
1:3:9:ARG:NH2	1:4:230:GLY:OXT	2.40	0.41
1:E:172:ALA:O	1:E:175:ARG:NH1	2.53	0.41
2:AA:28:ARG:HD3	2:AL:169:ALA:HB3	2.01	0.41
2:AA:28:ARG:HD2	2:AL:169:ALA:HB3	2.02	0.41
2:AB:26:PHE:HE2	2:AB:204:ALA:HA	1.85	0.41
2:AC:63:LYS:O	2:AC:67:THR:HG22	2.20	0.41
2:AC:266:THR:HA	2:AC:273:GLY:HA2	2.02	0.41
2:AC:355:GLU:HG3	2:AC:356:ASP:N	2.36	0.41
2:AE:266:THR:OG1	2:AF:239:PRO:HB3	2.21	0.41
2:AH:368:ARG:HG3	2:AH:370:ILE:HD11	2.02	0.41
2:AL:63:LYS:HB2	2:AL:63:LYS:HE2	1.65	0.41
5:AU:48:THR:OG1	5:AU:56:GLN:HB3	2.21	0.41
5:AZ:5:LYS:O	5:AV:113:ARG:NH2	2.53	0.41
5:AZ:17:THR:OG1	5:AZ:84:GLN:HB3	2.19	0.41
6:U3:28:LEU:HD11	6:T5:15:HIS:HA	2.02	0.41
6:U3:173:ASN:O	6:U3:174:ALA:HB2	2.20	0.41
3:AN:48:SER:O	3:AN:50:ASP:N	2.54	0.41
5:AV:125:ASP:OD1	5:AV:126:GLU:N	2.53	0.41
6:S4:29:LEU:HD12	6:S4:29:LEU:HA	1.87	0.41
4:AX:86:MET:HE3	4:AX:86:MET:HB3	1.91	0.41
6:R5:7:LEU:HA	6:R5:7:LEU:HD12	1.78	0.41
6:R5:58:ILE:HD13	6:R5:58:ILE:HA	1.93	0.41
6:R5:147:GLY:HA3	6:R5:194:TRP:CE2	2.56	0.41
1:N:141:ILE:HG22	1:N:142:ASN:ND2	2.35	0.41
1:O:3:PHE:HD1	1:O:38:MET:HE2	1.85	0.41
1:R:22:CYS:SG	1:g:50:GLY:HA2	2.61	0.41
1:V:12:ALA:HB1	6:T4:51:GLU:HB3	2.03	0.41
1:V:74:ALA:HB3	1:V:148:TYR:CD1	2.56	0.41
1:X:53:LEU:HD23	1:X:182:HIS:HA	2.02	0.41
1:Y:74:ALA:HB3	1:Y:148:TYR:CD1	2.55	0.41
1:Y:126:THR:O	1:Y:126:THR:OG1	2.32	0.41
1:f:132:THR:HG21	1:f:154:PRO:HB3	2.02	0.41
1:g:25:GLU:OE1	1:g:25:GLU:N	2.46	0.41
1:h:157:SER:O	1:h:158:GLU:HG2	2.21	0.41
1:m:3:PHE:CD1	1:m:38:MET:HE2	2.56	0.41
1:m:113:GLY:HA3	1:m:125:TYR:CE2	2.56	0.41
1:n:6:VAL:HG21	1:n:218:HIS:CE1	2.55	0.41
1:r:38:MET:HG2	1:r:185:LYS:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:x:8:PRO:HB3	1:x:43:ALA:HB1	2.02	0.41
1:y:59:PHE:HE2	1:y:175:ARG:NE	2.16	0.41
1:1:1:MET:HE1	1:1:185:LYS:NZ	2.35	0.41
1:2:71:VAL:HG13	1:2:144:ASN:HB2	2.02	0.41
1:3:157:SER:OG	1:3:158:GLU:N	2.54	0.41
1:4:94:ASN:OD1	1:4:94:ASN:N	2.53	0.41
1:5:112:ASN:O	1:5:128:GLY:N	2.51	0.41
1:6:53:LEU:HD23	1:6:182:HIS:HA	2.02	0.41
1:6:167:PRO:HA	1:6:191:SER:HB3	2.03	0.41
1:D:154:PRO:O	1:D:156:THR:HG23	2.21	0.41
1:E:78:THR:HG23	1:E:152:VAL:HG12	2.01	0.41
2:AA:192:TYR:HE2	2:AA:194:PHE:HE1	1.69	0.41
2:AA:243:TRP:HB2	2:AL:276:ILE:HG22	2.03	0.41
2:AA:259:VAL:O	2:AA:263:ILE:HG13	2.20	0.41
2:AA:352:THR:HG23	2:AL:69:GLN:HE22	1.86	0.41
2:AB:293:LEU:HD12	2:AB:293:LEU:HA	1.89	0.41
2:AC:180:VAL:HG12	2:AC:182:LYS:NZ	2.36	0.41
2:AD:154:PHE:HE1	2:AD:206:ASN:HD22	1.68	0.41
2:AD:283:ASP:N	2:AD:283:ASP:OD2	2.50	0.41
2:AD:347:GLU:HB3	2:AD:348:PRO:HD3	2.02	0.41
2:AJ:182:LYS:HE3	2:AJ:182:LYS:HB2	1.89	0.41
2:AK:80:GLN:H	2:AK:80:GLN:CD	2.27	0.41
2:AL:220:PRO:HB2	2:AL:309:ILE:CG2	2.50	0.41
5:AU:41:LYS:HA	5:AZ:80:GLN:NE2	2.36	0.41
5:AZ:110:SER:OG	5:AZ:111:ASP:N	2.54	0.41
5:AZ:129:PRO:HA	5:AZ:130:PRO:HD3	1.83	0.41
6:R3:16:ALA:HB1	6:R3:156:ILE:HD11	2.02	0.41
6:U3:71:ALA:HB3	6:U3:130:TYR:HE2	1.85	0.41
4:AT:76:LEU:HD23	4:AT:76:LEU:HA	1.90	0.41
6:U4:199:ARG:HD3	6:U4:199:ARG:HA	1.92	0.41
6:S5:40:ALA:HB2	6:S5:194:TRP:CH2	2.55	0.41
1:J:92:PHE:CZ	1:J:94:ASN:HB3	2.55	0.41
1:N:46:ALA:HB3	1:N:47:PRO:HD3	2.02	0.41
1:O:12:ALA:HB1	6:R3:51:GLU:O	2.20	0.41
1:a:56:LYS:HB3	1:a:207:VAL:HG11	2.02	0.41
1:b:35:ASN:OD1	1:b:36:GLY:N	2.45	0.41
1:c:113:GLY:HA3	1:c:125:TYR:CE2	2.55	0.41
1:d:115:VAL:HA	1:d:124:THR:O	2.21	0.41
1:g:56:LYS:HB3	1:g:207:VAL:CG1	2.50	0.41
1:h:178:ASP:OD2	1:h:181:THR:HG22	2.21	0.41
1:i:52:GLY:O	1:i:209:ILE:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:k:210:ASP:HB3	1:k:216:PHE:CE2	2.50	0.41
1:l:24:CYS:HB3	1:l:221:CYS:C	2.46	0.41
1:l:56:LYS:HB3	1:l:207:VAL:HG11	2.03	0.41
1:q:47:PRO:O	1:q:49:ARG:N	2.54	0.41
1:r:157:SER:O	1:r:158:GLU:HG2	2.20	0.41
1:t:209:ILE:HG13	1:t:214:ASN:O	2.20	0.41
1:u:157:SER:O	1:u:158:GLU:HG2	2.20	0.41
1:v:1:MET:HE1	1:v:185:LYS:NZ	2.35	0.41
1:y:171:PRO:HG2	1:y:187:VAL:HB	2.02	0.41
1:1:177:VAL:O	1:1:179:PRO:HD3	2.21	0.41
1:6:101:GLU:OE1	1:6:101:GLU:N	2.54	0.41
1:7:157:SER:OG	1:7:158:GLU:N	2.53	0.41
1:A:107:LEU:HA	1:A:107:LEU:HD23	1.76	0.41
1:B:67:THR:O	1:B:67:THR:OG1	2.36	0.41
1:F:30:ARG:HD2	1:F:230:GLY:N	2.30	0.41
2:AA:355:GLU:OE2	2:AA:370:ILE:HA	2.20	0.41
2:AD:80:GLN:H	2:AD:80:GLN:CD	2.28	0.41
2:AD:131:VAL:HB	2:AD:139:VAL:HG23	2.03	0.41
2:AF:38:ASN:HB2	2:AF:151:LYS:NZ	2.34	0.41
2:AF:298:SER:HB3	2:AF:301:PRO:HG2	2.02	0.41
2:AG:223:LEU:HD23	2:AG:305:GLN:HG3	2.02	0.41
2:AH:17:ALA:HA	2:AH:18:PRO:HD3	1.94	0.41
2:AH:227:LEU:HD13	2:AH:227:LEU:HA	1.95	0.41
2:AI:338:ARG:NE	2:AJ:344:ASP:OD1	2.54	0.41
2:AK:253:ASP:OD2	6:S3:198:ARG:HG2	2.20	0.41
2:AK:350:TYR:C	2:AK:353:PRO:HD2	2.45	0.41
2:AK:351:LEU:HD23	2:AK:371:PHE:CE2	2.56	0.41
5:AZ:40:TYR:OH	5:AZ:89:VAL:HG21	2.21	0.41
6:S4:191:GLN:O	6:S4:193:GLU:N	2.54	0.41
6:T4:190:ALA:HB1	6:T4:194:TRP:CH2	2.56	0.41
4:AW:77:ARG:HD2	4:AW:150:ARG:CD	2.51	0.41
6:T5:190:ALA:HB1	6:T5:194:TRP:CH2	2.56	0.41
1:J:88:LEU:HD11	1:J:139:PHE:CG	2.56	0.41
1:L:74:ALA:HB3	1:L:148:TYR:CD1	2.55	0.41
1:Q:12:ALA:HB1	6:T3:51:GLU:HB3	2.03	0.41
1:Q:73:ASN:HB3	1:Q:164:PHE:CE1	2.55	0.41
1:T:157:SER:O	1:T:158:GLU:HG2	2.21	0.41
1:W:48:LEU:CD2	1:X:1:MET:HB2	2.51	0.41
1:a:53:LEU:HD23	1:a:182:HIS:HA	2.03	0.41
1:b:117:LEU:HD23	1:b:118:GLY:O	2.21	0.41
1:d:92:PHE:HB2	1:d:141:ILE:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:88:LEU:HD11	1:h:139:PHE:CG	2.56	0.41
1:i:74:ALA:HB3	1:i:148:TYR:CD1	2.56	0.41
1:k:53:LEU:HD23	1:k:182:HIS:HA	2.03	0.41
1:n:157:SER:OG	1:n:158:GLU:N	2.53	0.41
1:p:126:THR:O	1:p:126:THR:OG1	2.31	0.41
1:s:38:MET:HG2	1:s:185:LYS:HG2	2.02	0.41
1:t:56:LYS:HB3	1:t:207:VAL:CG1	2.50	0.41
1:v:94:ASN:OD1	1:v:94:ASN:N	2.53	0.41
1:y:87:THR:HG22	1:y:89:SER:H	1.86	0.41
1:z:177:VAL:O	1:z:179:PRO:HD3	2.21	0.41
1:3:44:TRP:CH2	1:3:218:HIS:HB2	2.56	0.41
1:3:88:LEU:HD11	1:3:139:PHE:CG	2.56	0.41
1:5:30:ARG:HD2	1:5:230:GLY:N	2.31	0.41
1:9:138:TRP:CE3	1:9:147:GLU:HB3	2.56	0.41
1:B:80:VAL:HG12	1:B:155:THR:HB	2.03	0.41
2:AB:222:ALA:HA	2:AB:225:ASP:OD2	2.20	0.41
2:AE:297:HIS:CE1	2:AE:299:LYS:HB2	2.53	0.41
2:AG:379:LEU:O	2:AG:383:ARG:HG2	2.21	0.41
2:AK:232:ILE:CD1	2:AL:219:VAL:HG13	2.48	0.41
2:AK:369:VAL:O	2:AK:370:ILE:HD13	2.21	0.41
2:AL:187:ARG:HA	2:AL:187:ARG:HD2	1.56	0.41
5:AU:46:THR:HG23	5:AU:60:SER:CB	2.51	0.41
5:AU:125:ASP:OD1	5:AU:126:GLU:N	2.54	0.41
5:AZ:33:PRO:HB3	5:AZ:69:VAL:HG23	2.02	0.41
6:T3:64:ARG:HA	6:T3:64:ARG:HD2	1.95	0.41
4:AS:135:ASP:OD1	4:AT:59:GLN:HG3	2.21	0.41
3:H:49:GLN:O	3:H:50:ASP:HB2	2.20	0.41
5:Aa:129:PRO:HA	5:Aa:130:PRO:HD3	1.84	0.41
6:R4:70:SER:HB3	6:U4:95:ARG:NH2	2.36	0.41
6:S4:158:ASN:C	6:S4:160:GLY:H	2.28	0.41
6:S4:195:PHE:O	6:S4:197:TYR:N	2.54	0.41
6:S5:93:ILE:H	6:T5:125:GLN:HE22	1.69	0.41
1:K:6:VAL:HG21	1:K:218:HIS:CE1	2.56	0.41
1:L:30:ARG:NH1	1:L:229:CYS:HA	2.36	0.41
1:L:157:SER:O	1:L:158:GLU:HG2	2.20	0.41
1:M:48:LEU:HD21	1:N:1:MET:HB2	2.03	0.41
1:O:111:SER:OG	1:O:135:ASP:OD1	2.21	0.41
1:O:167:PRO:HA	1:O:191:SER:HB3	2.02	0.41
1:Q:136:ARG:HH21	1:Q:165:THR:HG22	1.85	0.41
1:S:87:THR:O	1:S:88:LEU:HD23	2.21	0.41
1:V:75:PHE:CE1	1:V:162:PRO:HD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:149:VAL:HG11	1:V:162:PRO:HG2	2.02	0.41
1:W:46:ALA:HB3	1:W:47:PRO:HD3	2.02	0.41
1:X:200:TYR:O	1:X:224:ILE:N	2.54	0.41
1:Y:92:PHE:HB2	1:Y:141:ILE:HG21	2.02	0.41
1:e:34:VAL:HA	1:e:189:GLY:HA2	2.03	0.41
1:i:94:ASN:OD1	1:i:94:ASN:N	2.54	0.41
1:k:38:MET:SD	1:k:185:LYS:HE2	2.61	0.41
1:q:8:PRO:HB2	1:q:10:ASN:OD1	2.21	0.41
1:q:138:TRP:CH2	1:q:192:PRO:HD2	2.55	0.41
1:t:87:THR:HG22	1:t:89:SER:H	1.86	0.41
1:w:24:CYS:HB3	1:w:221:CYS:HB2	1.60	0.41
1:x:13:SER:O	1:x:13:SER:OG	2.37	0.41
1:1:174:ARG:NE	1:1:187:VAL:HG21	2.35	0.41
1:2:49:ARG:HE	1:2:49:ARG:HB2	1.61	0.41
1:6:138:TRP:CE3	1:6:147:GLU:HB3	2.55	0.41
1:8:96:GLU:OE2	1:8:96:GLU:HA	2.21	0.41
1:9:80:VAL:HG12	1:9:155:THR:HB	2.03	0.41
1:0:154:PRO:O	1:0:156:THR:HG23	2.21	0.41
1:A:53:LEU:HD23	1:A:182:HIS:HA	2.03	0.41
1:A:196:PRO:HB3	1:A:228:SER:HB3	2.02	0.41
1:C:38:MET:HE3	1:C:183:VAL:HG21	2.03	0.41
1:C:118:GLY:N	1:C:122:ALA:O	2.31	0.41
1:E:99:GLN:H	1:E:99:GLN:CD	2.29	0.41
1:E:154:PRO:O	1:E:156:THR:HG23	2.21	0.41
1:F:53:LEU:HD23	1:F:182:HIS:HA	2.03	0.41
1:G:7:ASP:N	1:G:7:ASP:OD1	2.54	0.41
1:G:108:ASN:HB3	1:G:138:TRP:CD1	2.56	0.41
2:AA:316:PRO:CD	2:AA:341:PHE:HB2	2.51	0.41
2:AA:401:LYS:HD2	2:AB:395:PHE:CD1	2.56	0.41
2:AB:31:PHE:CE1	2:AB:37:LYS:HD2	2.56	0.41
2:AC:129:PHE:HB2	2:AC:194:PHE:CD2	2.56	0.41
2:AC:223:LEU:HD23	2:AC:305:GLN:HG3	2.02	0.41
2:AC:259:VAL:HG13	6:R5:202:LEU:HD12	2.03	0.41
2:AC:291:ASN:HD22	2:AC:291:ASN:HA	1.78	0.41
2:AC:351:LEU:HB3	2:AC:371:PHE:CZ	2.56	0.41
2:AE:54:HIS:HE1	2:AE:56:VAL:HB	1.86	0.41
2:AE:390:TYR:HA	2:AE:393:VAL:HG23	2.03	0.41
2:AF:190:LYS:HG2	2:AF:191:ASN:N	2.32	0.41
2:AG:192:TYR:CE2	2:AG:194:PHE:HE1	2.35	0.41
2:AH:80:GLN:CD	2:AH:80:GLN:H	2.28	0.41
2:AH:131:VAL:HB	2:AH:139:VAL:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AH:347:GLU:HB3	2:AH:348:PRO:HD3	2.02	0.41
2:AI:276:ILE:HG22	2:AJ:243:TRP:HB2	2.02	0.41
2:AI:298:SER:HB3	2:AI:301:PRO:HG2	2.03	0.41
2:AJ:37:LYS:HE3	2:AJ:37:LYS:HB2	1.93	0.41
2:AJ:62:ASP:OD1	2:AJ:63:LYS:N	2.54	0.41
2:AK:99:GLN:NE2	2:AL:83:GLN:HB3	2.36	0.41
2:AK:286:VAL:HG11	2:AL:244:LEU:HD13	2.02	0.41
3:AM:43:LYS:HE2	3:AM:43:LYS:HB2	1.84	0.41
4:AR:34:PRO:HA	4:AR:55:VAL:O	2.21	0.41
6:U3:74:ILE:HG12	6:U3:131:VAL:HG13	2.01	0.41
4:AS:50:LEU:HD13	4:AS:51:PRO:HA	2.03	0.41
5:AV:12:ILE:HG12	5:AV:89:VAL:HG23	2.01	0.41
5:AV:108:GLU:OE1	5:AV:109:GLU:N	2.50	0.41
5:Aa:66:LEU:HD13	5:Aa:87:VAL:HG21	2.03	0.41
6:S4:187:ILE:HG21	6:S4:187:ILE:HD13	1.87	0.41
6:S4:200:VAL:O	6:S4:201:LEU:HG	2.21	0.41
6:T4:166:VAL:C	6:T4:168:ASN:N	2.79	0.41
5:AY:21:THR:OG1	5:AY:23:GLU:HG2	2.21	0.41
4:AX:95:LYS:HE3	4:AX:95:LYS:HB2	1.25	0.41
5:Ab:66:LEU:HD13	5:Ab:87:VAL:HG21	2.03	0.41
6:S5:173:ASN:HD21	6:S5:177:LEU:CB	2.27	0.41
6:S5:191:GLN:C	6:S5:193:GLU:N	2.78	0.41
6:T5:41:GLU:HB3	6:T5:48:PHE:CD2	2.55	0.41
6:U5:54:ILE:HD11	6:U5:130:TYR:CE2	2.56	0.41
1:O:72:SER:O	1:O:91:LEU:HD12	2.21	0.41
1:O:73:ASN:HB3	1:O:164:PHE:HE1	1.86	0.41
1:T:178:ASP:OD2	1:T:181:THR:HG22	2.21	0.41
1:b:53:LEU:HD12	1:b:206:GLN:NE2	2.35	0.41
1:c:25:GLU:H	1:c:25:GLU:CD	2.26	0.41
1:e:79:LYS:HD2	1:e:153:ASP:HB2	2.02	0.41
1:j:73:ASN:HB3	1:j:164:PHE:HE1	1.86	0.41
1:j:74:ALA:HB3	1:j:148:TYR:CD1	2.56	0.41
1:j:153:ASP:HA	1:j:159:LEU:HD23	2.02	0.41
1:o:56:LYS:HB3	1:o:207:VAL:CG1	2.51	0.41
1:q:73:ASN:HB3	1:q:164:PHE:CE1	2.56	0.41
1:r:149:VAL:HG11	1:r:162:PRO:HG2	2.03	0.41
1:s:138:TRP:CE3	1:s:147:GLU:HB3	2.56	0.41
1:u:225:SER:O	1:u:225:SER:OG	2.38	0.41
1:1:47:PRO:O	1:1:49:ARG:N	2.54	0.41
1:3:1:MET:HE2	1:3:38:MET:HG3	2.03	0.41
1:3:2:TYR:CE2	1:3:27:ILE:HG23	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:38:MET:HE3	1:3:183:VAL:HG21	2.02	0.41
1:8:117:LEU:HD23	1:8:118:GLY:O	2.21	0.41
1:E:75:PHE:CZ	1:E:161:GLN:HG2	2.56	0.41
1:E:159:LEU:HD13	1:E:160:PRO:HD2	2.03	0.41
2:AA:385:ASP:O	2:AA:389:THR:HG22	2.19	0.41
2:AB:150:LEU:HD11	2:AB:163:PHE:HB3	2.03	0.41
2:AC:17:ALA:HA	2:AC:18:PRO:HD3	1.94	0.41
2:AC:253:ASP:OD2	6:S5:198:ARG:HG2	2.21	0.41
2:AC:319:LEU:O	2:AC:320:LEU:HD23	2.21	0.41
2:AD:95:LYS:HE3	2:AD:95:LYS:HB3	1.80	0.41
2:AD:264:GLU:O	2:AD:267:LYS:HG3	2.21	0.41
2:AE:362:LEU:HA	2:AE:362:LEU:HD23	1.80	0.41
2:AF:46:MET:HE2	2:AF:46:MET:HA	2.03	0.41
2:AG:180:VAL:HG12	2:AG:182:LYS:NZ	2.36	0.41
2:AH:217:ILE:HA	2:AH:220:PRO:HD2	2.02	0.41
2:AK:54:HIS:HE1	2:AK:56:VAL:HB	1.86	0.41
2:AK:379:LEU:O	2:AK:383:ARG:HG2	2.21	0.41
2:AL:77:LYS:HD2	2:AL:81:ASN:ND2	2.31	0.41
3:AP:20:ASP:OD2	3:AP:22:GLU:HB2	2.21	0.41
3:AP:45:ILE:N	3:AN:97:SER:OG	2.55	0.41
6:R3:137:GLU:O	6:R3:139:SER:N	2.54	0.41
6:S3:4:ASP:OD1	6:S3:33:ARG:NH1	2.43	0.41
6:T3:61:LYS:HE3	6:T3:61:LYS:HB2	1.72	0.41
4:AS:77:ARG:HD2	4:AS:150:ARG:CD	2.50	0.41
5:AV:128:LEU:HD13	5:AV:128:LEU:HA	1.87	0.41
6:R4:178:ILE:HD12	6:R4:178:ILE:HA	1.85	0.41
6:U4:195:PHE:O	6:U4:196:ARG:C	2.60	0.41
3:AO:49:GLN:HB3	3:I:76:SER:CB	2.51	0.41
5:AY:108:GLU:OE1	5:AY:109:GLU:N	2.50	0.41
3:I:20:ASP:OD2	3:I:22:GLU:HB2	2.20	0.41
6:R5:161:ASP:HB2	6:U5:157:ASN:ND2	2.36	0.41
6:R5:166:VAL:HG11	6:T5:177:LEU:HD13	2.03	0.41
6:U5:28:LEU:HD23	6:U5:28:LEU:HA	1.78	0.41
1:M:24:CYS:HB3	1:M:221:CYS:C	2.47	0.40
1:N:73:ASN:HB2	1:N:164:PHE:CE1	2.55	0.40
1:O:83:VAL:HG23	1:O:126:THR:HA	2.04	0.40
1:S:99:GLN:OE1	1:S:99:GLN:N	2.54	0.40
1:U:3:PHE:CD1	1:U:38:MET:HE2	2.56	0.40
1:U:27:ILE:O	1:U:224:ILE:HA	2.21	0.40
1:U:170:VAL:HG13	1:U:187:VAL:O	2.21	0.40
1:c:74:ALA:HB3	1:c:148:TYR:CD1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:d:56:LYS:HB3	1:d:207:VAL:HG11	2.03	0.40
1:f:59:PHE:HE2	1:f:175:ARG:NE	2.16	0.40
1:q:1:MET:HE2	1:q:38:MET:HG3	2.03	0.40
1:z:38:MET:HG2	1:z:185:LYS:HG2	2.02	0.40
1:3:62:ASP:OD2	1:3:62:ASP:N	2.54	0.40
1:3:75:PHE:CE1	1:3:161:GLN:HG2	2.56	0.40
1:6:174:ARG:CZ	1:6:187:VAL:HG21	2.50	0.40
1:9:166:THR:H	1:9:166:THR:HG22	1.64	0.40
1:0:75:PHE:CE1	1:0:161:GLN:HG2	2.56	0.40
1:E:75:PHE:CE1	1:E:161:GLN:HG2	2.55	0.40
1:E:210:ASP:HB3	1:E:216:PHE:CE2	2.54	0.40
2:AA:298:SER:HB3	2:AA:301:PRO:HG2	2.03	0.40
2:AA:400:GLU:H	2:AA:400:GLU:HG2	1.62	0.40
2:AB:133:VAL:HA	2:AB:139:VAL:HA	2.04	0.40
2:AC:54:HIS:HE1	2:AC:56:VAL:HB	1.85	0.40
2:AC:252:ASP:H	6:S5:198:ARG:HH12	1.69	0.40
2:AD:217:ILE:HA	2:AD:220:PRO:HD2	2.02	0.40
2:AE:264:GLU:O	2:AE:267:LYS:HG3	2.21	0.40
2:AF:99:GLN:O	2:AF:103:ARG:N	2.47	0.40
2:AF:134:MET:HG3	2:AF:138:SER:O	2.20	0.40
2:AG:129:PHE:HB2	2:AG:194:PHE:CD2	2.56	0.40
2:AG:339:LYS:HE2	2:AG:339:LYS:HB3	1.73	0.40
2:AG:355:GLU:HG3	2:AG:356:ASP:N	2.35	0.40
2:AH:276:ILE:HG22	2:AI:243:TRP:HB2	2.03	0.40
2:AH:390:TYR:O	2:AH:401:LYS:HD3	2.21	0.40
2:AI:316:PRO:HD2	2:AI:341:PHE:HB2	2.02	0.40
2:AJ:223:LEU:HD23	2:AJ:305:GLN:NE2	2.36	0.40
2:AJ:264:GLU:OE1	2:AJ:267:LYS:HD3	2.21	0.40
2:AL:249:ARG:O	2:AL:249:ARG:CG	2.63	0.40
2:AL:390:TYR:O	2:AL:401:LYS:HD3	2.21	0.40
3:AM:49:GLN:HB3	3:AP:76:SER:CB	2.50	0.40
5:AU:113:ARG:HE	5:Ab:4:ASN:ND2	2.18	0.40
6:R3:166:VAL:O	6:R3:168:ASN:N	2.54	0.40
6:S3:43:TYR:HD2	6:S3:44:THR:HG23	1.86	0.40
6:S3:200:VAL:O	6:S3:201:LEU:HG	2.21	0.40
6:T3:166:VAL:O	6:T3:168:ASN:N	2.54	0.40
3:AN:36:TRP:CD1	6:R4:17:LYS:HG2	2.56	0.40
4:AS:38:VAL:CG1	4:AS:81:ILE:HD11	2.51	0.40
4:AT:25:PHE:HD1	4:AT:113:ARG:CZ	2.34	0.40
6:R4:74:ILE:HG13	6:R4:75:ALA:N	2.36	0.40
6:T4:154:TRP:O	6:T4:158:ASN:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AW:94:ARG:O	4:AW:95:LYS:HB2	2.21	0.40
4:AX:24:ALA:O	4:AX:25:PHE:C	2.63	0.40
6:S5:74:ILE:HG23	6:S5:77:ARG:H	1.85	0.40
6:S5:74:ILE:HG13	6:S5:75:ALA:N	2.34	0.40
6:S5:158:ASN:C	6:S5:160:GLY:H	2.29	0.40
6:S5:191:GLN:O	6:S5:193:GLU:N	2.54	0.40
6:U5:71:ALA:HB3	6:U5:130:TYR:HE2	1.85	0.40
6:U5:142:ALA:O	6:U5:143:GLY:C	2.61	0.40
1:L:75:PHE:CE1	1:L:162:PRO:HD2	2.55	0.40
1:M:153:ASP:OD1	1:M:159:LEU:HB2	2.21	0.40
1:O:4:PHE:O	1:O:39:VAL:HA	2.20	0.40
1:R:107:LEU:HD23	1:R:107:LEU:HA	1.86	0.40
1:T:180:ARG:HH12	6:R4:124:SER:HA	1.86	0.40
1:b:30:ARG:HD2	1:b:230:GLY:H	1.87	0.40
1:d:85:GLU:OE1	1:d:124:THR:OG1	2.30	0.40
1:d:90:ASP:OD1	1:d:90:ASP:N	2.54	0.40
1:d:178:ASP:OD2	1:d:181:THR:HG22	2.21	0.40
1:f:56:LYS:HB3	1:f:207:VAL:HG11	2.04	0.40
1:l:174:ARG:NE	1:l:187:VAL:HG21	2.36	0.40
1:n:1:MET:HE3	1:2:48:LEU:HD23	2.04	0.40
1:o:67:THR:O	1:o:67:THR:OG1	2.35	0.40
1:p:47:PRO:O	1:p:49:ARG:N	2.54	0.40
1:s:209:ILE:HG13	1:s:214:ASN:O	2.21	0.40
1:t:177:VAL:O	1:t:179:PRO:HD3	2.22	0.40
1:u:38:MET:HG2	1:u:185:LYS:HG2	2.03	0.40
1:y:46:ALA:HB3	1:y:47:PRO:HD3	2.03	0.40
1:y:177:VAL:O	1:y:179:PRO:HD3	2.21	0.40
1:2:21:SER:HB3	1:G:49:ARG:HB3	2.02	0.40
1:2:74:ALA:HB3	1:2:148:TYR:CD1	2.57	0.40
1:5:88:LEU:HG	1:5:141:ILE:HD11	2.02	0.40
1:6:74:ALA:HB3	1:6:148:TYR:CD1	2.57	0.40
1:A:210:ASP:HB3	1:A:216:PHE:HE2	1.85	0.40
1:F:196:PRO:HB3	1:F:228:SER:HB3	2.03	0.40
2:AA:16:PRO:C	2:AL:140:ASN:HD21	2.20	0.40
2:AB:54:HIS:O	2:AB:58:PHE:HB3	2.21	0.40
2:AB:250:ASP:OD1	2:AB:250:ASP:N	2.54	0.40
2:AC:200:SER:OG	2:AC:201:ILE:N	2.55	0.40
2:AD:100:ILE:HD12	2:AD:100:ILE:HA	1.93	0.40
2:AE:18:PRO:O	2:AE:20:ALA:N	2.54	0.40
2:AE:401:LYS:HD2	2:AF:395:PHE:CD1	2.56	0.40
2:AG:97:LEU:O	2:AG:101:LEU:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AG:236:ASP:OD1	2:AG:236:ASP:N	2.54	0.40
2:AI:77:LYS:HE2	2:AI:77:LYS:HB2	1.82	0.40
2:AI:126:ARG:NH1	2:AI:197:VAL:HG23	2.36	0.40
2:AI:132:SER:OG	2:AI:140:ASN:HB3	2.20	0.40
2:AJ:251:LEU:HD12	2:AJ:251:LEU:HA	1.90	0.40
2:AK:129:PHE:HB2	2:AK:194:PHE:CD2	2.57	0.40
2:AK:255:GLN:OE1	6:R3:200:VAL:HG12	2.21	0.40
2:AK:335:ASP:OD1	2:AK:335:ASP:N	2.52	0.40
2:AL:100:ILE:HD12	2:AL:100:ILE:HA	1.93	0.40
2:AL:131:VAL:HB	2:AL:139:VAL:HG23	2.02	0.40
3:AM:77:VAL:HG23	3:I:46:ARG:HE	1.86	0.40
5:AU:29:SER:OG	5:AU:30:HIS:N	2.54	0.40
4:AR:63:SER:OG	4:AR:75:ASN:HB3	2.21	0.40
3:AP:6:ARG:HA	3:AP:38:ALA:HB2	2.03	0.40
6:R3:74:ILE:HD12	6:R3:74:ILE:HA	1.95	0.40
6:R3:200:VAL:HG22	6:R3:201:LEU:O	2.22	0.40
6:T3:150:LYS:HD3	6:T3:189:GLY:HA3	2.02	0.40
4:AS:94:ARG:O	4:AS:95:LYS:HB2	2.21	0.40
6:R4:137:GLU:O	6:R4:139:SER:N	2.54	0.40
6:S4:66:LYS:O	6:S4:67:ILE:HD13	2.21	0.40
6:S4:197:TYR:OH	6:T4:38:GLU:OE2	2.33	0.40
6:U4:103:PHE:HD1	6:U4:103:PHE:HA	1.76	0.40
4:AX:25:PHE:HD1	4:AX:113:ARG:CZ	2.34	0.40
6:R5:199:ARG:O	6:R5:201:LEU:N	2.53	0.40
6:U5:140:VAL:O	6:U5:141:PRO:C	2.64	0.40
1:U:1:MET:HE2	1:U:38:MET:HG3	2.03	0.40
1:a:56:LYS:HB3	1:a:207:VAL:CG1	2.52	0.40
1:d:56:LYS:HB3	1:d:207:VAL:CG1	2.51	0.40
1:g:7:ASP:N	1:g:7:ASP:OD1	2.53	0.40
1:i:177:VAL:O	1:i:179:PRO:HD3	2.21	0.40
1:i:178:ASP:OD2	1:i:181:THR:HG22	2.20	0.40
1:m:78:THR:HG23	1:m:152:VAL:HG12	2.03	0.40
1:m:139:PHE:CD2	1:m:141:ILE:HG13	2.57	0.40
1:v:70:LYS:HG3	1:v:144:ASN:OD1	2.21	0.40
1:2:94:ASN:OD1	1:2:94:ASN:N	2.52	0.40
1:4:4:PHE:HB2	1:4:39:VAL:HG12	2.03	0.40
1:6:118:GLY:N	1:6:122:ALA:O	2.29	0.40
1:0:159:LEU:HD13	1:0:160:PRO:HD2	2.03	0.40
1:A:25:GLU:H	1:A:25:GLU:CD	2.28	0.40
1:A:46:ALA:HB3	1:A:47:PRO:HD3	2.04	0.40
1:B:7:ASP:N	1:B:7:ASP:OD1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:170:VAL:HG13	1:F:187:VAL:O	2.21	0.40
2:AA:66:LEU:HD22	2:AB:348:PRO:O	2.20	0.40
2:AC:154:PHE:HA	2:AC:160:VAL:HA	2.03	0.40
2:AC:243:TRP:CH2	2:AD:289:MET:HG3	2.57	0.40
2:AC:285:LYS:HB3	2:AC:285:LYS:HE3	1.85	0.40
2:AC:339:LYS:O	2:AC:343:GLU:HG2	2.21	0.40
2:AD:264:GLU:C	2:AD:266:THR:H	2.28	0.40
2:AE:276:ILE:HG22	2:AF:243:TRP:HB2	2.04	0.40
2:AF:31:PHE:CE1	2:AF:37:LYS:HD2	2.57	0.40
2:AH:165:TYR:CD1	2:AI:25:ILE:HD11	2.56	0.40
2:AI:18:PRO:C	2:AI:20:ALA:N	2.79	0.40
2:AJ:229:ALA:HA	2:AJ:232:ILE:HG22	2.04	0.40
2:AJ:282:THR:HG23	2:AK:249:ARG:HD2	2.04	0.40
2:AL:131:VAL:HA	2:AL:141:ALA:O	2.21	0.40
2:AL:201:ILE:H	2:AL:201:ILE:HG13	1.75	0.40
4:AQ:156:CYS:HB3	5:AZ:3:CYS:HA	2.03	0.40
5:AU:47:ASN:HB3	5:AU:55:VAL:HG21	2.03	0.40
5:AU:84:GLN:NE2	5:AU:101:GLU:HA	2.35	0.40
5:AV:21:THR:OG1	5:AV:23:GLU:HG2	2.21	0.40
3:H:20:ASP:OD2	3:H:22:GLU:HB2	2.22	0.40
6:R4:197:TYR:HE2	6:S4:42:LEU:HD21	1.86	0.40
6:T4:150:LYS:HD3	6:T4:189:GLY:HA3	2.03	0.40
5:Ab:30:HIS:NE2	5:Ab:79:TYR:OH	2.45	0.40
6:T5:12:ILE:HG21	6:T5:29:LEU:HD21	2.04	0.40
6:T5:68:ILE:HD12	6:T5:68:ILE:HA	1.87	0.40
6:T5:166:VAL:O	6:T5:168:ASN:N	2.54	0.40
1:L:134:VAL:HG21	1:L:162:PRO:HG3	2.04	0.40
1:O:51:HIS:HB2	1:O:209:ILE:HG23	2.04	0.40
1:Q:7:ASP:N	1:Q:7:ASP:OD1	2.53	0.40
1:T:3:PHE:CD1	1:T:38:MET:HE2	2.56	0.40
1:T:180:ARG:HH12	6:R4:124:SER:N	2.20	0.40
1:X:46:ALA:HB3	1:X:47:PRO:HD3	2.02	0.40
1:b:178:ASP:OD2	1:b:181:THR:HG22	2.21	0.40
1:c:174:ARG:NH2	1:c:187:VAL:HG11	2.36	0.40
1:c:208:ALA:HB3	1:c:216:PHE:HB2	2.03	0.40
1:o:75:PHE:CE1	1:o:161:GLN:HG2	2.57	0.40
1:q:174:ARG:NE	1:q:187:VAL:HG21	2.37	0.40
1:r:49:ARG:HE	1:r:49:ARG:HB2	1.61	0.40
1:y:8:PRO:HB3	1:y:43:ALA:HB1	2.04	0.40
1:6:157:SER:O	1:6:158:GLU:HG2	2.22	0.40
1:7:88:LEU:HD11	1:7:139:PHE:CG	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:53:LEU:HD12	1:C:206:GLN:CD	2.46	0.40
1:D:94:ASN:OD1	1:D:94:ASN:N	2.53	0.40
1:F:107:LEU:HD23	1:F:107:LEU:HA	1.78	0.40
1:G:139:PHE:HE1	1:G:148:TYR:HB2	1.85	0.40
2:AA:132:SER:OG	2:AA:140:ASN:HB3	2.21	0.40
2:AC:99:GLN:NE2	2:AD:83:GLN:HB3	2.36	0.40
2:AC:298:SER:HB3	2:AC:301:PRO:CG	2.51	0.40
2:AC:359:SER:HB3	2:AC:368:ARG:HB2	2.02	0.40
2:AD:165:TYR:CD1	2:AE:25:ILE:HD11	2.57	0.40
2:AD:257:LYS:H	2:AD:257:LYS:HG2	1.47	0.40
2:AD:290:LYS:HB2	2:AD:290:LYS:HE2	1.65	0.40
2:AD:390:TYR:O	2:AD:401:LYS:HD3	2.21	0.40
2:AE:285:LYS:HB3	2:AE:285:LYS:HE3	1.90	0.40
2:AH:131:VAL:HA	2:AH:141:ALA:O	2.21	0.40
2:AH:169:ALA:HB3	2:AI:28:ARG:CD	2.51	0.40
2:AI:376:ILE:HG21	2:AI:379:LEU:HD23	2.03	0.40
2:AJ:59:ARG:HH11	2:AJ:320:LEU:HD22	1.86	0.40
2:AJ:222:ALA:HA	2:AJ:225:ASP:OD2	2.20	0.40
2:AJ:297:HIS:CE1	2:AJ:299:LYS:HB2	2.55	0.40
3:AM:57:ASP:HB3	3:AM:60:GLN:HG2	2.04	0.40
4:AQ:44:GLY:C	4:AQ:46:GLN:H	2.29	0.40
4:AQ:110:ILE:HD12	4:AQ:145:ILE:HD12	2.04	0.40
4:AR:24:ALA:O	4:AR:25:PHE:C	2.64	0.40
4:AR:87:LYS:HE3	4:AR:87:LYS:HB2	1.96	0.40
6:S3:182:ASN:OD1	6:S3:182:ASN:N	2.49	0.40
6:U3:55:VAL:HG13	6:U3:129:THR:HG22	2.02	0.40
5:Aa:4:ASN:ND2	5:AY:113:ARG:HE	2.16	0.40
6:S4:191:GLN:O	6:S4:192:ASP:C	2.64	0.40
6:U4:81:PHE:O	6:U4:89:PRO:HA	2.22	0.40
4:AW:43:SER:HB2	3:I:96:LEU:HD21	2.03	0.40
6:R5:178:ILE:O	6:R5:180:GLY:N	2.48	0.40
1:J:4:PHE:O	1:J:39:VAL:HA	2.21	0.40
1:L:49:ARG:HB3	6:T5:89:PRO:HG2	2.04	0.40
1:O:10:ASN:HD22	6:R3:77:ARG:HH12	1.68	0.40
1:O:89:SER:C	1:O:91:LEU:N	2.80	0.40
1:Q:138:TRP:CE3	1:Q:147:GLU:HB3	2.56	0.40
1:V:157:SER:O	1:V:158:GLU:HG2	2.21	0.40
1:Y:178:ASP:OD2	1:Y:181:THR:HG22	2.22	0.40
1:c:8:PRO:HB3	1:c:43:ALA:HB1	2.03	0.40
1:c:153:ASP:C	1:c:155:THR:H	2.30	0.40
1:c:157:SER:O	1:c:158:GLU:HG2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:g:107:LEU:HD23	1:g:107:LEU:HA	1.87	0.40
1:h:25:GLU:CD	1:h:25:GLU:H	2.27	0.40
1:h:80:VAL:HG12	1:h:155:THR:HB	2.04	0.40
1:j:139:PHE:HD2	1:j:141:ILE:HG13	1.86	0.40
1:q:177:VAL:O	1:q:179:PRO:HD3	2.21	0.40
1:u:177:VAL:O	1:u:179:PRO:HD3	2.21	0.40
1:v:78:THR:O	1:v:152:VAL:HA	2.21	0.40
1:2:126:THR:O	1:2:126:THR:OG1	2.26	0.40
1:3:96:GLU:HA	1:3:96:GLU:OE2	2.22	0.40
1:7:203:THR:OG1	1:8:107:LEU:HD11	2.22	0.40
1:9:70:LYS:H	1:9:70:LYS:HG2	1.73	0.40
1:B:3:PHE:CD1	1:B:38:MET:HE2	2.56	0.40
1:D:31:PRO:HD3	1:D:227:GLY:O	2.21	0.40
1:D:133:GLY:H	1:D:152:VAL:HG13	1.87	0.40
1:G:139:PHE:CE1	1:G:148:TYR:HB2	2.56	0.40
2:AC:27:ILE:HD13	2:AC:155:ASP:O	2.21	0.40
2:AD:64:LEU:HD13	2:AD:350:TYR:OH	2.22	0.40
2:AD:267:LYS:HD3	2:AE:237:GLY:HA2	2.04	0.40
2:AE:77:LYS:HE2	2:AE:77:LYS:HB2	1.82	0.40
2:AH:265:GLU:HG3	2:AH:271:ASP:H	1.87	0.40
2:AI:268:PRO:HG2	2:AJ:236:ASP:CG	2.47	0.40
2:AJ:290:LYS:HE3	2:AJ:290:LYS:HB3	1.82	0.40
2:AL:271:ASP:HB3	6:U3:66:LYS:HD2	2.03	0.40
4:AQ:77:ARG:HD2	4:AQ:150:ARG:CD	2.51	0.40
5:AZ:89:VAL:O	5:AZ:96:VAL:HG23	2.21	0.40
4:AT:24:ALA:O	4:AT:25:PHE:C	2.64	0.40
4:AT:31:ARG:NH1	4:AT:51:PRO:O	2.54	0.40
3:H:52:VAL:HG21	4:AX:141:ASP:CG	2.47	0.40
4:AX:31:ARG:NH1	4:AX:51:PRO:O	2.55	0.40
5:Ab:50:LEU:HD23	5:Ab:50:LEU:HA	1.94	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
1	1	219/230 (95%)	196 (90%)	23 (10%)	0	100	100
1	2	219/230 (95%)	195 (89%)	24 (11%)	0	100	100
1	3	219/230 (95%)	201 (92%)	18 (8%)	0	100	100
1	4	219/230 (95%)	196 (90%)	21 (10%)	2 (1%)	14	46
1	5	219/230 (95%)	200 (91%)	19 (9%)	0	100	100
1	6	219/230 (95%)	197 (90%)	22 (10%)	0	100	100
1	7	219/230 (95%)	202 (92%)	17 (8%)	0	100	100
1	8	219/230 (95%)	202 (92%)	17 (8%)	0	100	100
1	9	219/230 (95%)	195 (89%)	23 (10%)	1 (0%)	24	57
1	A	219/230 (95%)	196 (90%)	23 (10%)	0	100	100
1	B	219/230 (95%)	204 (93%)	15 (7%)	0	100	100
1	C	219/230 (95%)	202 (92%)	17 (8%)	0	100	100
1	D	219/230 (95%)	198 (90%)	20 (9%)	1 (0%)	24	57
1	E	219/230 (95%)	200 (91%)	19 (9%)	0	100	100
1	F	219/230 (95%)	196 (90%)	23 (10%)	0	100	100
1	G	219/230 (95%)	201 (92%)	18 (8%)	0	100	100
1	J	219/230 (95%)	194 (89%)	25 (11%)	0	100	100
1	K	219/230 (95%)	193 (88%)	26 (12%)	0	100	100
1	L	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	M	219/230 (95%)	196 (90%)	23 (10%)	0	100	100
1	N	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	O	219/230 (95%)	193 (88%)	25 (11%)	1 (0%)	24	57
1	P	219/230 (95%)	192 (88%)	27 (12%)	0	100	100
1	Q	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	R	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	S	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	T	219/230 (95%)	191 (87%)	28 (13%)	0	100	100
1	U	219/230 (95%)	195 (89%)	24 (11%)	0	100	100
1	V	219/230 (95%)	201 (92%)	18 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	W	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	X	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	Y	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	Z	219/230 (95%)	197 (90%)	22 (10%)	0	100	100
1	a	219/230 (95%)	196 (90%)	23 (10%)	0	100	100
1	b	219/230 (95%)	200 (91%)	19 (9%)	0	100	100
1	c	219/230 (95%)	196 (90%)	23 (10%)	0	100	100
1	d	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
1	e	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
1	f	219/230 (95%)	197 (90%)	22 (10%)	0	100	100
1	g	219/230 (95%)	200 (91%)	19 (9%)	0	100	100
1	h	219/230 (95%)	201 (92%)	18 (8%)	0	100	100
1	i	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	j	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	k	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	l	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
1	m	219/230 (95%)	197 (90%)	22 (10%)	0	100	100
1	n	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	o	219/230 (95%)	197 (90%)	22 (10%)	0	100	100
1	p	219/230 (95%)	194 (89%)	25 (11%)	0	100	100
1	q	219/230 (95%)	196 (90%)	23 (10%)	0	100	100
1	r	219/230 (95%)	194 (89%)	25 (11%)	0	100	100
1	s	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	t	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	u	219/230 (95%)	195 (89%)	24 (11%)	0	100	100
1	v	219/230 (95%)	196 (90%)	23 (10%)	0	100	100
1	w	219/230 (95%)	195 (89%)	24 (11%)	0	100	100
1	x	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	y	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
1	z	219/230 (95%)	194 (89%)	25 (11%)	0	100	100
2	AA	377/420 (90%)	323 (86%)	54 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	377/420 (90%)	324 (86%)	53 (14%)	0	100	100
2	AC	377/420 (90%)	324 (86%)	53 (14%)	0	100	100
2	AD	377/420 (90%)	323 (86%)	54 (14%)	0	100	100
2	AE	377/420 (90%)	322 (85%)	53 (14%)	2 (0%)	24	57
2	AF	377/420 (90%)	324 (86%)	52 (14%)	1 (0%)	36	67
2	AG	377/420 (90%)	323 (86%)	54 (14%)	0	100	100
2	AH	377/420 (90%)	321 (85%)	55 (15%)	1 (0%)	36	67
2	AI	377/420 (90%)	323 (86%)	52 (14%)	2 (0%)	24	57
2	AJ	377/420 (90%)	323 (86%)	54 (14%)	0	100	100
2	AK	377/420 (90%)	323 (86%)	54 (14%)	0	100	100
2	AL	377/420 (90%)	315 (84%)	62 (16%)	0	100	100
3	AM	123/141 (87%)	107 (87%)	16 (13%)	0	100	100
3	AN	123/141 (87%)	107 (87%)	14 (11%)	2 (2%)	7	36
3	AO	123/141 (87%)	108 (88%)	15 (12%)	0	100	100
3	AP	123/141 (87%)	110 (89%)	11 (9%)	2 (2%)	7	36
3	H	123/141 (87%)	109 (89%)	11 (9%)	3 (2%)	4	29
3	I	123/141 (87%)	108 (88%)	13 (11%)	2 (2%)	7	36
4	AQ	153/178 (86%)	136 (89%)	15 (10%)	2 (1%)	9	39
4	AR	153/178 (86%)	137 (90%)	15 (10%)	1 (1%)	18	51
4	AS	153/178 (86%)	132 (86%)	18 (12%)	3 (2%)	6	32
4	AT	153/178 (86%)	137 (90%)	15 (10%)	1 (1%)	18	51
4	AW	153/178 (86%)	134 (88%)	16 (10%)	3 (2%)	6	32
4	AX	153/178 (86%)	135 (88%)	15 (10%)	3 (2%)	6	32
5	AU	126/136 (93%)	112 (89%)	13 (10%)	1 (1%)	16	49
5	AV	126/136 (93%)	114 (90%)	11 (9%)	1 (1%)	16	49
5	AY	126/136 (93%)	113 (90%)	12 (10%)	1 (1%)	16	49
5	AZ	126/136 (93%)	115 (91%)	11 (9%)	0	100	100
5	Aa	126/136 (93%)	115 (91%)	11 (9%)	0	100	100
5	Ab	126/136 (93%)	115 (91%)	11 (9%)	0	100	100
6	R3	177/202 (88%)	142 (80%)	30 (17%)	5 (3%)	4	26
6	R4	177/202 (88%)	142 (80%)	29 (16%)	6 (3%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	R5	177/202 (88%)	141 (80%)	31 (18%)	5 (3%)	4	26
6	S3	176/202 (87%)	142 (81%)	30 (17%)	4 (2%)	5	30
6	S4	176/202 (87%)	143 (81%)	28 (16%)	5 (3%)	4	26
6	S5	176/202 (87%)	142 (81%)	30 (17%)	4 (2%)	5	30
6	T3	175/202 (87%)	143 (82%)	30 (17%)	2 (1%)	11	42
6	T4	175/202 (87%)	146 (83%)	27 (15%)	2 (1%)	11	42
6	T5	175/202 (87%)	143 (82%)	30 (17%)	2 (1%)	11	42
6	U3	176/202 (87%)	143 (81%)	27 (15%)	6 (3%)	3	23
6	U4	176/202 (87%)	139 (79%)	32 (18%)	5 (3%)	4	26
6	U5	176/202 (87%)	142 (81%)	29 (16%)	5 (3%)	4	26
All	All	22188/23994 (92%)	19565 (88%)	2536 (11%)	87 (0%)	31	62

All (87) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AP	50	ASP
6	R3	168	ASN
6	S3	73	PRO
6	U3	141	PRO
6	U3	174	ALA
3	AN	50	ASP
4	AS	95	LYS
3	H	50	ASP
6	R4	174	ALA
6	S4	73	PRO
6	U4	174	ALA
6	U4	181	THR
4	AW	95	LYS
4	AX	95	LYS
3	I	50	ASP
6	S5	73	PRO
6	S5	75	ALA
6	U5	171	ASN
6	U5	174	ALA
1	4	158	GLU
1	9	158	GLU
2	AE	19	SER
2	AI	19	SER

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Mol	Chain	Res	Type
6	S3	63	ARG
6	S3	75	ALA
6	U3	176	GLY
3	H	48	SER
3	H	49	GLN
6	S4	63	ARG
6	S4	75	ALA
4	AX	94	ARG
6	R5	167	ARG
6	R5	196	ARG
6	S5	63	ARG
6	U5	176	GLY
1	O	90	ASP
1	4	160	PRO
2	AI	17	ALA
4	AQ	95	LYS
3	AP	49	GLN
6	S3	141	PRO
6	T3	50	PRO
6	T3	167	ARG
4	AS	94	ARG
5	AV	128	LEU
6	R4	167	ARG
6	R4	186	VAL
6	R4	189	GLY
6	T4	50	PRO
6	U4	179	GLY
4	AW	94	ARG
3	I	49	GLN
6	R5	201	LEU
6	T5	50	PRO
2	AE	17	ALA
2	AF	30	PHE
4	AQ	24	ALA
5	AU	128	LEU
6	U3	21	ASN
6	U3	23	ARG
3	AN	48	SER
4	AS	24	ALA
4	AT	24	ALA
6	S4	141	PRO
6	U4	191	GLN

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Mol	Chain	Res	Type
4	AW	24	ALA
5	AY	128	LEU
6	R5	200	VAL
6	S5	141	PRO
6	T5	167	ARG
2	AH	67	THR
4	AR	24	ALA
6	R3	73	PRO
6	R3	167	ARG
6	R4	73	PRO
6	R4	199	ARG
6	T4	167	ARG
6	U4	63	ARG
4	AX	24	ALA
6	R5	73	PRO
6	U5	23	ARG
6	R3	166	VAL
6	R3	174	ALA
6	U3	63	ARG
6	U5	63	ARG
1	D	160	PRO
6	S4	74	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	0	186/191 (97%)	184 (99%)	2 (1%)	65	75
1	1	186/191 (97%)	184 (99%)	2 (1%)	65	75
1	2	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	3	186/191 (97%)	186 (100%)	0	100	100
1	4	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	5	186/191 (97%)	184 (99%)	2 (1%)	65	75
1	6	186/191 (97%)	186 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	7	186/191 (97%)	183 (98%)	3 (2%)	55	71
1	8	186/191 (97%)	186 (100%)	0	100	100
1	9	186/191 (97%)	184 (99%)	2 (1%)	65	75
1	A	186/191 (97%)	186 (100%)	0	100	100
1	B	186/191 (97%)	184 (99%)	2 (1%)	65	75
1	C	186/191 (97%)	186 (100%)	0	100	100
1	D	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	E	186/191 (97%)	184 (99%)	2 (1%)	65	75
1	F	186/191 (97%)	186 (100%)	0	100	100
1	G	186/191 (97%)	183 (98%)	3 (2%)	55	71
1	J	186/191 (97%)	186 (100%)	0	100	100
1	K	186/191 (97%)	186 (100%)	0	100	100
1	L	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	M	186/191 (97%)	186 (100%)	0	100	100
1	N	186/191 (97%)	186 (100%)	0	100	100
1	O	186/191 (97%)	184 (99%)	2 (1%)	65	75
1	P	186/191 (97%)	186 (100%)	0	100	100
1	Q	186/191 (97%)	184 (99%)	2 (1%)	65	75
1	R	186/191 (97%)	186 (100%)	0	100	100
1	S	186/191 (97%)	186 (100%)	0	100	100
1	T	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	U	186/191 (97%)	186 (100%)	0	100	100
1	V	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	W	186/191 (97%)	186 (100%)	0	100	100
1	X	186/191 (97%)	186 (100%)	0	100	100
1	Y	186/191 (97%)	186 (100%)	0	100	100
1	Z	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	a	186/191 (97%)	186 (100%)	0	100	100
1	b	186/191 (97%)	186 (100%)	0	100	100
1	c	186/191 (97%)	186 (100%)	0	100	100
1	d	186/191 (97%)	186 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	e	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	f	186/191 (97%)	186 (100%)	0	100	100
1	g	186/191 (97%)	186 (100%)	0	100	100
1	h	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	i	186/191 (97%)	186 (100%)	0	100	100
1	j	186/191 (97%)	184 (99%)	2 (1%)	65	75
1	k	186/191 (97%)	186 (100%)	0	100	100
1	l	186/191 (97%)	186 (100%)	0	100	100
1	m	186/191 (97%)	186 (100%)	0	100	100
1	n	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	o	186/191 (97%)	186 (100%)	0	100	100
1	p	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	q	186/191 (97%)	184 (99%)	2 (1%)	65	75
1	r	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	s	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	t	186/191 (97%)	186 (100%)	0	100	100
1	u	186/191 (97%)	184 (99%)	2 (1%)	65	75
1	v	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	w	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	x	186/191 (97%)	185 (100%)	1 (0%)	81	81
1	y	186/191 (97%)	186 (100%)	0	100	100
1	z	186/191 (97%)	185 (100%)	1 (0%)	81	81
2	AA	311/339 (92%)	310 (100%)	1 (0%)	86	83
2	AB	311/339 (92%)	311 (100%)	0	100	100
2	AC	311/339 (92%)	310 (100%)	1 (0%)	86	83
2	AD	311/339 (92%)	304 (98%)	7 (2%)	44	65
2	AE	311/339 (92%)	311 (100%)	0	100	100
2	AF	311/339 (92%)	307 (99%)	4 (1%)	61	73
2	AG	311/339 (92%)	310 (100%)	1 (0%)	86	83
2	AH	311/339 (92%)	305 (98%)	6 (2%)	50	68
2	AI	311/339 (92%)	309 (99%)	2 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AJ	311/339 (92%)	309 (99%)	2 (1%)	78	80
2	AK	311/339 (92%)	310 (100%)	1 (0%)	86	83
2	AL	311/339 (92%)	306 (98%)	5 (2%)	55	71
3	AM	114/128 (89%)	114 (100%)	0	100	100
3	AN	114/128 (89%)	111 (97%)	3 (3%)	40	64
3	AO	114/128 (89%)	114 (100%)	0	100	100
3	AP	114/128 (89%)	112 (98%)	2 (2%)	51	70
3	H	114/128 (89%)	112 (98%)	2 (2%)	51	70
3	I	114/128 (89%)	112 (98%)	2 (2%)	51	70
4	AQ	134/153 (88%)	131 (98%)	3 (2%)	45	66
4	AR	134/153 (88%)	129 (96%)	5 (4%)	30	57
4	AS	134/153 (88%)	131 (98%)	3 (2%)	45	66
4	AT	134/153 (88%)	132 (98%)	2 (2%)	57	72
4	AW	134/153 (88%)	131 (98%)	3 (2%)	45	66
4	AX	134/153 (88%)	132 (98%)	2 (2%)	57	72
5	AU	113/116 (97%)	111 (98%)	2 (2%)	51	70
5	AV	113/116 (97%)	111 (98%)	2 (2%)	51	70
5	AY	113/116 (97%)	112 (99%)	1 (1%)	70	76
5	AZ	113/116 (97%)	111 (98%)	2 (2%)	51	70
5	Aa	113/116 (97%)	111 (98%)	2 (2%)	51	70
5	Ab	113/116 (97%)	110 (97%)	3 (3%)	39	63
6	R3	149/168 (89%)	142 (95%)	7 (5%)	23	51
6	R4	149/168 (89%)	140 (94%)	9 (6%)	17	45
6	R5	149/168 (89%)	147 (99%)	2 (1%)	61	73
6	S3	148/168 (88%)	145 (98%)	3 (2%)	48	67
6	S4	148/168 (88%)	145 (98%)	3 (2%)	48	67
6	S5	148/168 (88%)	146 (99%)	2 (1%)	59	72
6	T3	147/168 (88%)	144 (98%)	3 (2%)	48	67
6	T4	147/168 (88%)	141 (96%)	6 (4%)	27	54
6	T5	147/168 (88%)	142 (97%)	5 (3%)	32	59
6	U3	148/168 (88%)	140 (95%)	8 (5%)	20	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	U4	148/168 (88%)	133 (90%)	15 (10%)	7	29
6	U5	148/168 (88%)	143 (97%)	5 (3%)	32	59
All	All	18834/19926 (94%)	18652 (99%)	182 (1%)	65	76

All (182) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	181	THR
1	O	88	LEU
1	O	89	SER
1	Q	136	ARG
1	Q	181	THR
1	T	88	LEU
1	V	181	THR
1	Z	77	ARG
1	e	156	THR
1	h	132	THR
1	j	144	ASN
1	j	156	THR
1	n	156	THR
1	p	156	THR
1	q	220	SER
1	q	221	CYS
1	r	221	CYS
1	s	156	THR
1	u	156	THR
1	u	207	VAL
1	v	221	CYS
1	w	221	CYS
1	x	156	THR
1	z	156	THR
1	1	220	SER
1	1	221	CYS
1	2	221	CYS
1	4	159	LEU
1	5	23	CYS
1	5	229	CYS
1	7	114	VAL
1	7	177	VAL
1	7	221	CYS
1	9	77	ARG

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Mol	Chain	Res	Type
1	9	175	ARG
1	0	23	CYS
1	0	229	CYS
1	B	180	ARG
1	B	221	CYS
1	D	175	ARG
1	E	23	CYS
1	E	229	CYS
1	G	114	VAL
1	G	177	VAL
1	G	221	CYS
2	AA	391	ASP
2	AC	346	ILE
2	AD	71	VAL
2	AD	182	LYS
2	AD	183	ASN
2	AD	184	ASP
2	AD	245	VAL
2	AD	257	LYS
2	AD	397	THR
2	AF	27	ILE
2	AF	28	ARG
2	AF	29	ARG
2	AF	285	LYS
2	AG	346	ILE
2	AH	66	LEU
2	AH	67	THR
2	AH	68	VAL
2	AH	71	VAL
2	AH	187	ARG
2	AH	397	THR
2	AI	249	ARG
2	AI	391	ASP
2	AJ	374	ASP
2	AJ	376	ILE
2	AK	346	ILE
2	AL	66	LEU
2	AL	68	VAL
2	AL	71	VAL
2	AL	187	ARG
2	AL	397	THR
4	AQ	93	ASP

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Mol	Chain	Res	Type
4	AQ	94	ARG
4	AQ	95	LYS
5	AU	66	LEU
5	AU	128	LEU
4	AR	49	LYS
4	AR	50	LEU
4	AR	93	ASP
4	AR	94	ARG
4	AR	95	LYS
3	AP	47	PHE
3	AP	49	GLN
5	AZ	39	THR
5	AZ	96	VAL
6	R3	144	ILE
6	R3	166	VAL
6	R3	168	ASN
6	R3	169	THR
6	R3	173	ASN
6	R3	201	LEU
6	R3	202	LEU
6	S3	72	THR
6	S3	77	ARG
6	S3	196	ARG
6	T3	55	VAL
6	T3	166	VAL
6	T3	167	ARG
6	U3	20	ASP
6	U3	23	ARG
6	U3	79	VAL
6	U3	134	ARG
6	U3	135	ARG
6	U3	136	CYS
6	U3	175	GLN
6	U3	186	VAL
3	AN	48	SER
3	AN	49	GLN
3	AN	50	ASP
4	AS	11	VAL
4	AS	94	ARG
4	AS	95	LYS
5	AV	66	LEU
5	AV	128	LEU

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Mol	Chain	Res	Type
4	AT	94	ARG
4	AT	95	LYS
3	H	47	PHE
3	H	49	GLN
5	Aa	39	THR
5	Aa	82	CYS
6	R4	144	ILE
6	R4	169	THR
6	R4	173	ASN
6	R4	178	ILE
6	R4	182	ASN
6	R4	183	ASN
6	R4	186	VAL
6	R4	198	ARG
6	R4	200	VAL
6	S4	72	THR
6	S4	74	ILE
6	S4	77	ARG
6	T4	20	ASP
6	T4	166	VAL
6	T4	167	ARG
6	T4	170	LEU
6	T4	199	ARG
6	T4	200	VAL
6	U4	17	LYS
6	U4	19	ASP
6	U4	20	ASP
6	U4	79	VAL
6	U4	140	VAL
6	U4	144	ILE
6	U4	150	LYS
6	U4	152	ILE
6	U4	157	ASN
6	U4	163	VAL
6	U4	164	MET
6	U4	166	VAL
6	U4	177	LEU
6	U4	182	ASN
6	U4	192	ASP
4	AW	15	GLU
4	AW	94	ARG
4	AW	95	LYS

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Mol	Chain	Res	Type
5	AY	128	LEU
4	AX	94	ARG
4	AX	95	LYS
3	I	47	PHE
3	I	49	GLN
5	Ab	39	THR
5	Ab	82	CYS
5	Ab	96	VAL
6	R5	144	ILE
6	R5	169	THR
6	S5	72	THR
6	S5	74	ILE
6	T5	20	ASP
6	T5	55	VAL
6	T5	166	VAL
6	T5	167	ARG
6	T5	170	LEU
6	U5	19	ASP
6	U5	20	ASP
6	U5	79	VAL
6	U5	140	VAL
6	U5	144	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (219) such sidechains are listed below:

Mol	Chain	Res	Type
1	J	112	ASN
1	K	112	ASN
1	M	55	ASN
1	M	218	HIS
1	N	142	ASN
1	O	112	ASN
1	P	112	ASN
1	R	55	ASN
1	R	218	HIS
1	S	142	ASN
1	T	112	ASN
1	U	112	ASN
1	W	55	ASN
1	X	142	ASN
1	Y	182	HIS
1	Z	182	HIS

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Mol	Chain	Res	Type
1	a	120	ASN
1	e	55	ASN
1	e	182	HIS
1	f	120	ASN
1	g	55	ASN
1	j	182	HIS
1	k	120	ASN
1	q	51	HIS
1	r	10	ASN
1	r	55	ASN
1	r	99	GLN
1	u	112	ASN
1	v	51	HIS
1	w	10	ASN
1	w	55	ASN
1	w	99	GLN
1	w	112	ASN
1	x	112	ASN
1	z	144	ASN
1	1	51	HIS
1	2	10	ASN
1	2	55	ASN
1	2	99	GLN
1	3	55	ASN
1	3	112	ASN
1	5	112	ASN
1	6	218	HIS
1	7	55	ASN
1	7	112	ASN
1	7	120	ASN
1	8	55	ASN
1	8	112	ASN
1	0	112	ASN
1	B	55	ASN
1	B	112	ASN
1	B	120	ASN
1	C	55	ASN
1	C	112	ASN
1	D	99	GLN
1	E	112	ASN
1	F	218	HIS
1	G	55	ASN

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Mol	Chain	Res	Type
1	G	112	ASN
1	G	120	ASN
2	AA	38	ASN
2	AA	69	GLN
2	AA	191	ASN
2	AA	240	ASN
2	AA	291	ASN
2	AA	297	HIS
2	AA	312	ASN
2	AB	49	GLN
2	AB	69	GLN
2	AB	81	ASN
2	AB	112	GLN
2	AB	191	ASN
2	AB	255	GLN
2	AB	291	ASN
2	AB	312	ASN
2	AC	69	GLN
2	AC	81	ASN
2	AC	99	GLN
2	AC	102	GLN
2	AC	112	GLN
2	AC	164	GLN
2	AC	191	ASN
2	AC	202	ASN
2	AC	240	ASN
2	AC	291	ASN
2	AC	297	HIS
2	AD	44	ASN
2	AD	81	ASN
2	AD	112	GLN
2	AD	140	ASN
2	AD	164	GLN
2	AD	183	ASN
2	AD	191	ASN
2	AD	272	ASN
2	AD	291	ASN
2	AD	297	HIS
2	AE	191	ASN
2	AE	240	ASN
2	AE	291	ASN
2	AF	69	GLN

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Mol	Chain	Res	Type
2	AF	81	ASN
2	AF	112	GLN
2	AF	191	ASN
2	AF	202	ASN
2	AF	206	ASN
2	AF	215	GLN
2	AF	291	ASN
2	AF	312	ASN
2	AG	69	GLN
2	AG	81	ASN
2	AG	99	GLN
2	AG	102	GLN
2	AG	112	GLN
2	AG	164	GLN
2	AG	191	ASN
2	AG	202	ASN
2	AG	211	ASN
2	AG	240	ASN
2	AG	291	ASN
2	AH	44	ASN
2	AH	81	ASN
2	AH	112	GLN
2	AH	140	ASN
2	AH	164	GLN
2	AH	191	ASN
2	AH	272	ASN
2	AH	291	ASN
2	AH	297	HIS
2	AI	69	GLN
2	AI	81	ASN
2	AI	191	ASN
2	AI	240	ASN
2	AJ	69	GLN
2	AJ	81	ASN
2	AJ	112	GLN
2	AJ	191	ASN
2	AJ	206	ASN
2	AJ	255	GLN
2	AJ	291	ASN
2	AJ	312	ASN
2	AK	69	GLN
2	AK	81	ASN

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Mol	Chain	Res	Type
2	AK	99	GLN
2	AK	102	GLN
2	AK	112	GLN
2	AK	152	GLN
2	AK	164	GLN
2	AK	183	ASN
2	AK	191	ASN
2	AK	202	ASN
2	AK	206	ASN
2	AK	240	ASN
2	AK	291	ASN
2	AL	69	GLN
2	AL	81	ASN
2	AL	112	GLN
2	AL	164	GLN
2	AL	191	ASN
2	AL	291	ASN
2	AL	297	HIS
5	AU	6	GLN
5	AU	42	ASN
5	AU	88	GLN
4	AR	75	ASN
4	AR	125	HIS
4	AR	151	GLN
3	AP	8	HIS
5	AZ	6	GLN
6	R3	125	GLN
6	R3	155	ASN
6	R3	168	ASN
6	R3	182	ASN
6	R3	191	GLN
6	S3	125	GLN
6	S3	155	ASN
6	S3	158	ASN
6	T3	138	ASN
6	U3	2	ASN
6	U3	155	ASN
3	AN	49	GLN
5	AV	6	GLN
5	AV	42	ASN
5	AV	88	GLN
4	AT	75	ASN

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Mol	Chain	Res	Type
4	AT	125	HIS
4	AT	151	GLN
3	H	8	HIS
5	Aa	6	GLN
6	R4	125	GLN
6	R4	155	ASN
6	R4	173	ASN
6	R4	183	ASN
6	R4	191	GLN
6	S4	125	GLN
6	S4	155	ASN
6	S4	158	ASN
6	S4	191	GLN
6	T4	138	ASN
6	U4	2	ASN
6	U4	155	ASN
6	U4	168	ASN
5	AY	6	GLN
5	AY	42	ASN
5	AY	88	GLN
4	AX	75	ASN
4	AX	125	HIS
4	AX	151	GLN
4	AX	152	ASN
3	I	8	HIS
5	Ab	6	GLN
6	R5	125	GLN
6	R5	155	ASN
6	R5	191	GLN
6	S5	125	GLN
6	S5	155	ASN
6	S5	158	ASN
6	U5	2	ASN
6	U5	138	ASN
6	U5	155	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

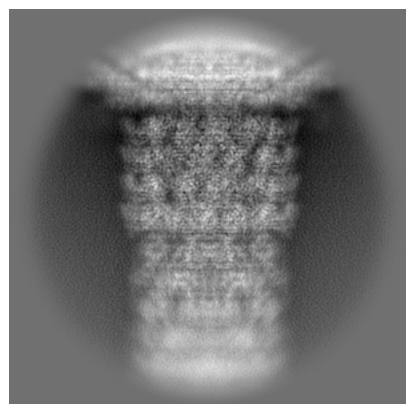
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29503. These allow visual inspection of the internal detail of the map and identification of artifacts.

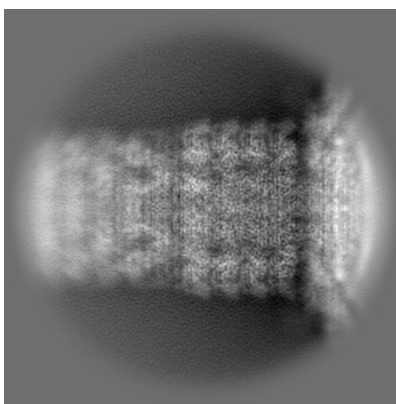
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

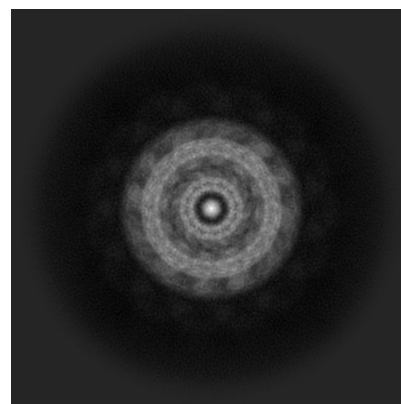
6.1.1 Primary map



X

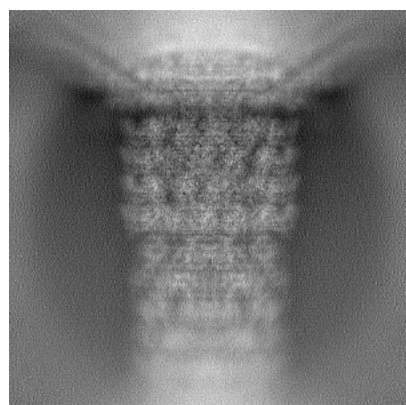


Y

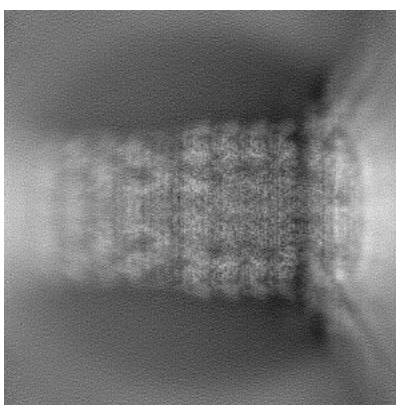


Z

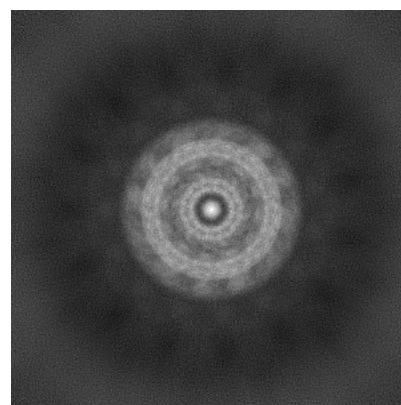
6.1.2 Raw map



X



Y

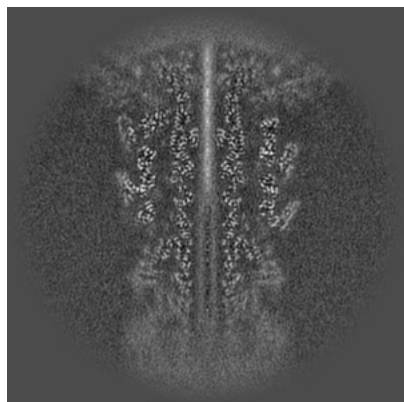


Z

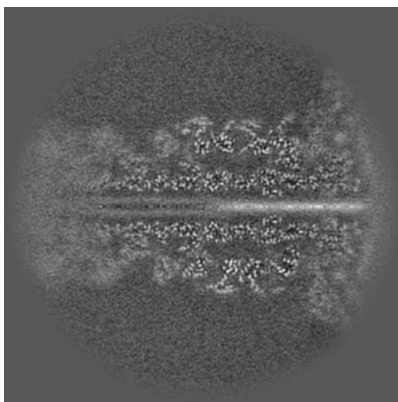
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

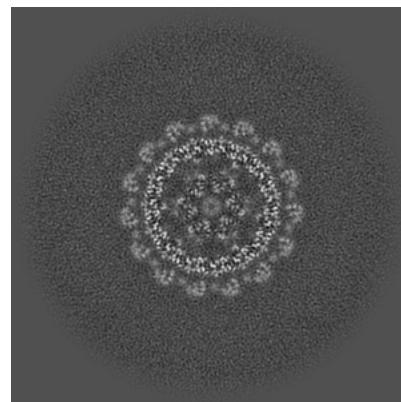
6.2.1 Primary map



X Index: 224

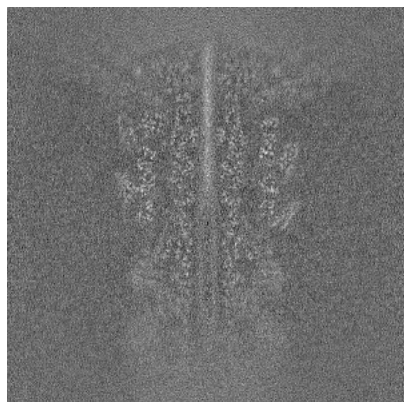


Y Index: 224

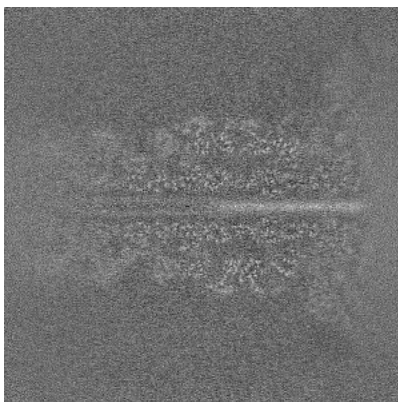


Z Index: 224

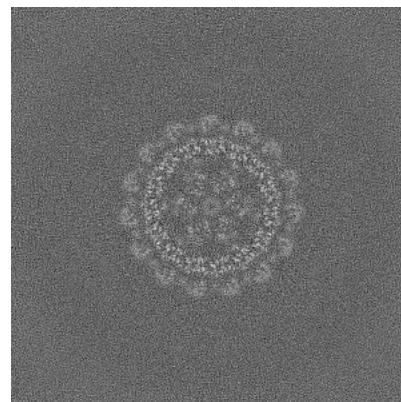
6.2.2 Raw map



X Index: 224



Y Index: 224

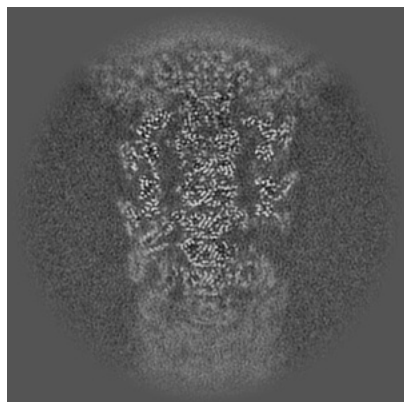


Z Index: 224

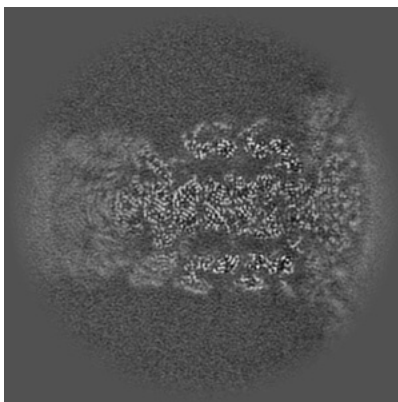
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

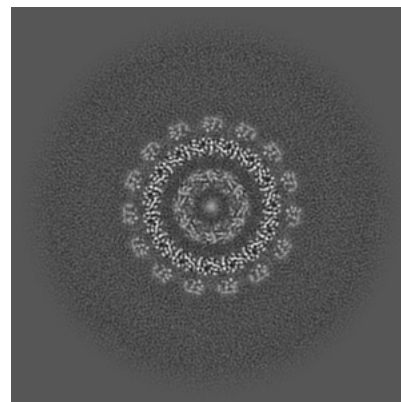
6.3.1 Primary map



X Index: 246

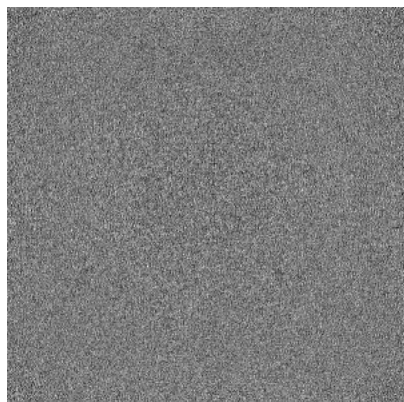


Y Index: 246

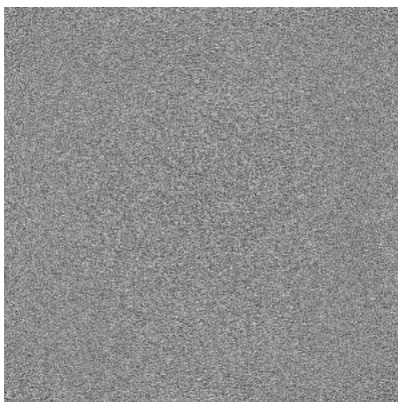


Z Index: 284

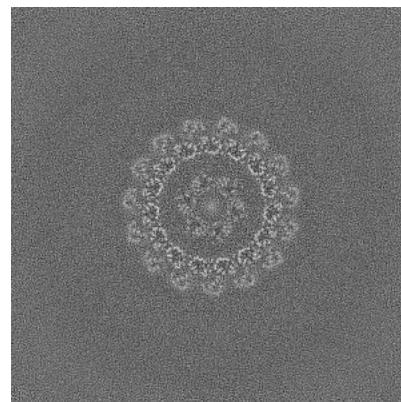
6.3.2 Raw map



X Index: 0



Y Index: 0

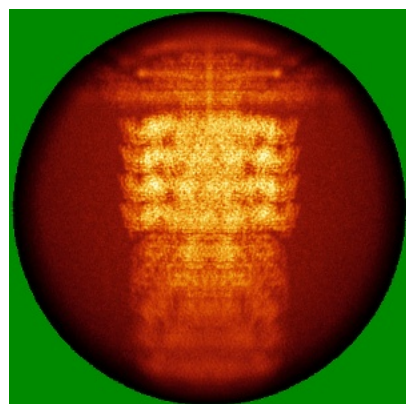


Z Index: 249

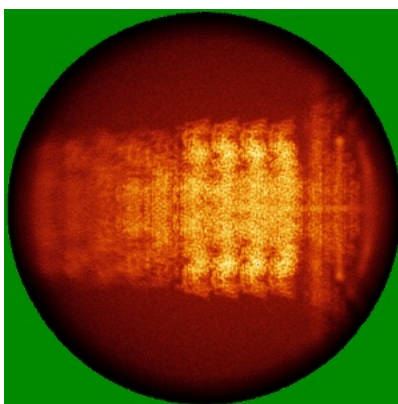
The images above show the largest variance slices of the map in three orthogonal directions.

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

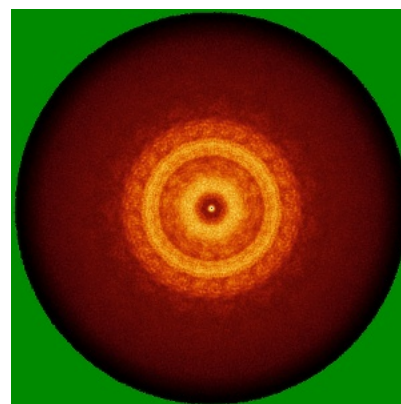
6.4.1 Primary map



X

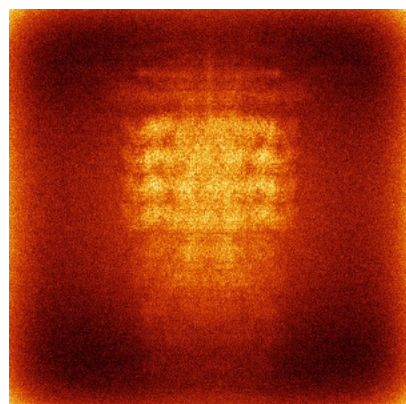


Y

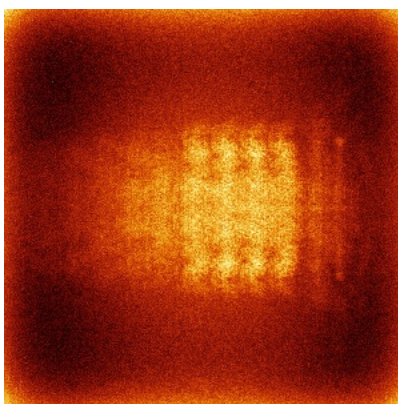


Z

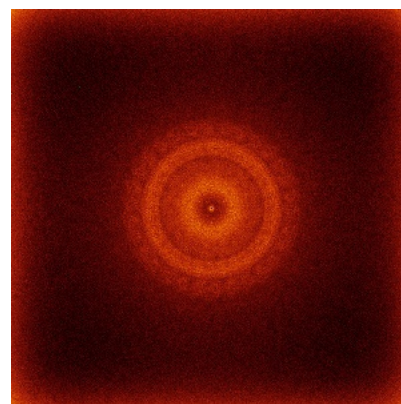
6.4.2 Raw map



X



Y

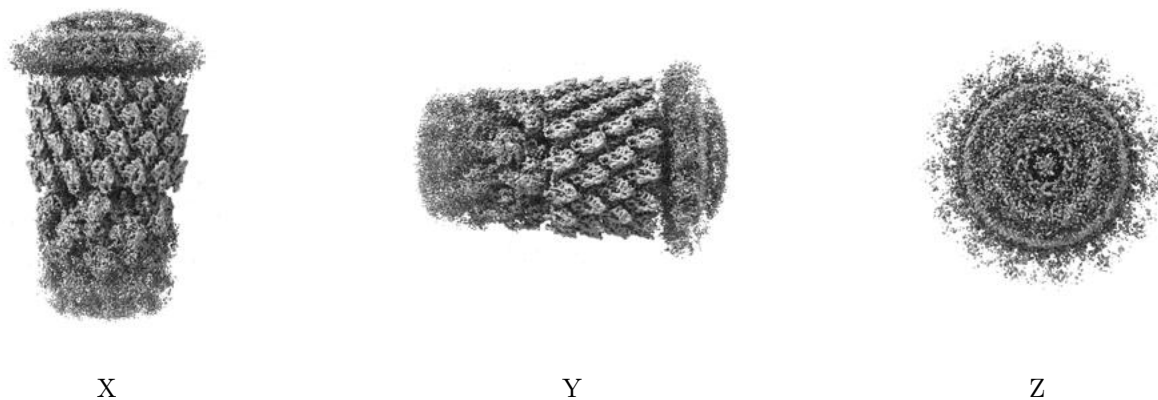


Z

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

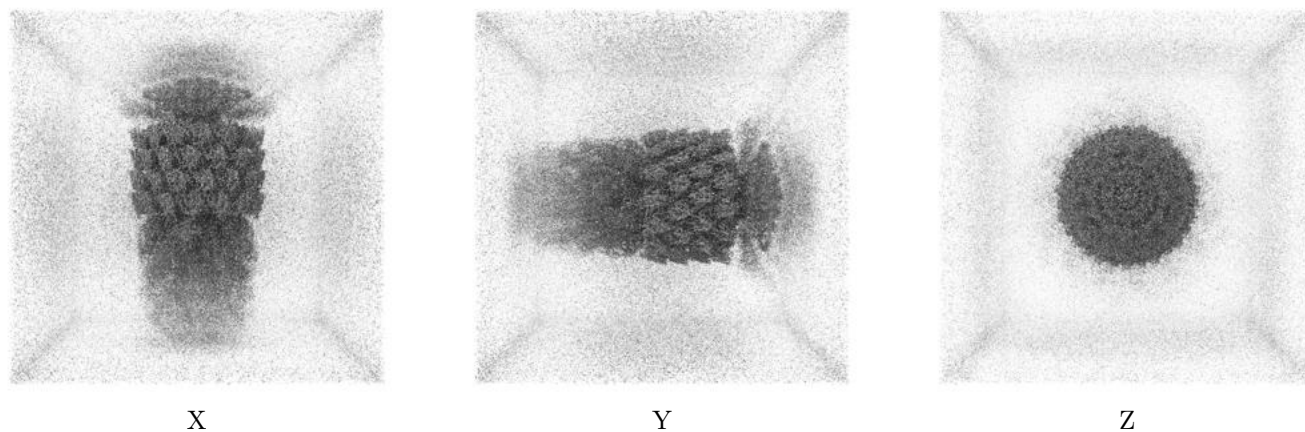
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

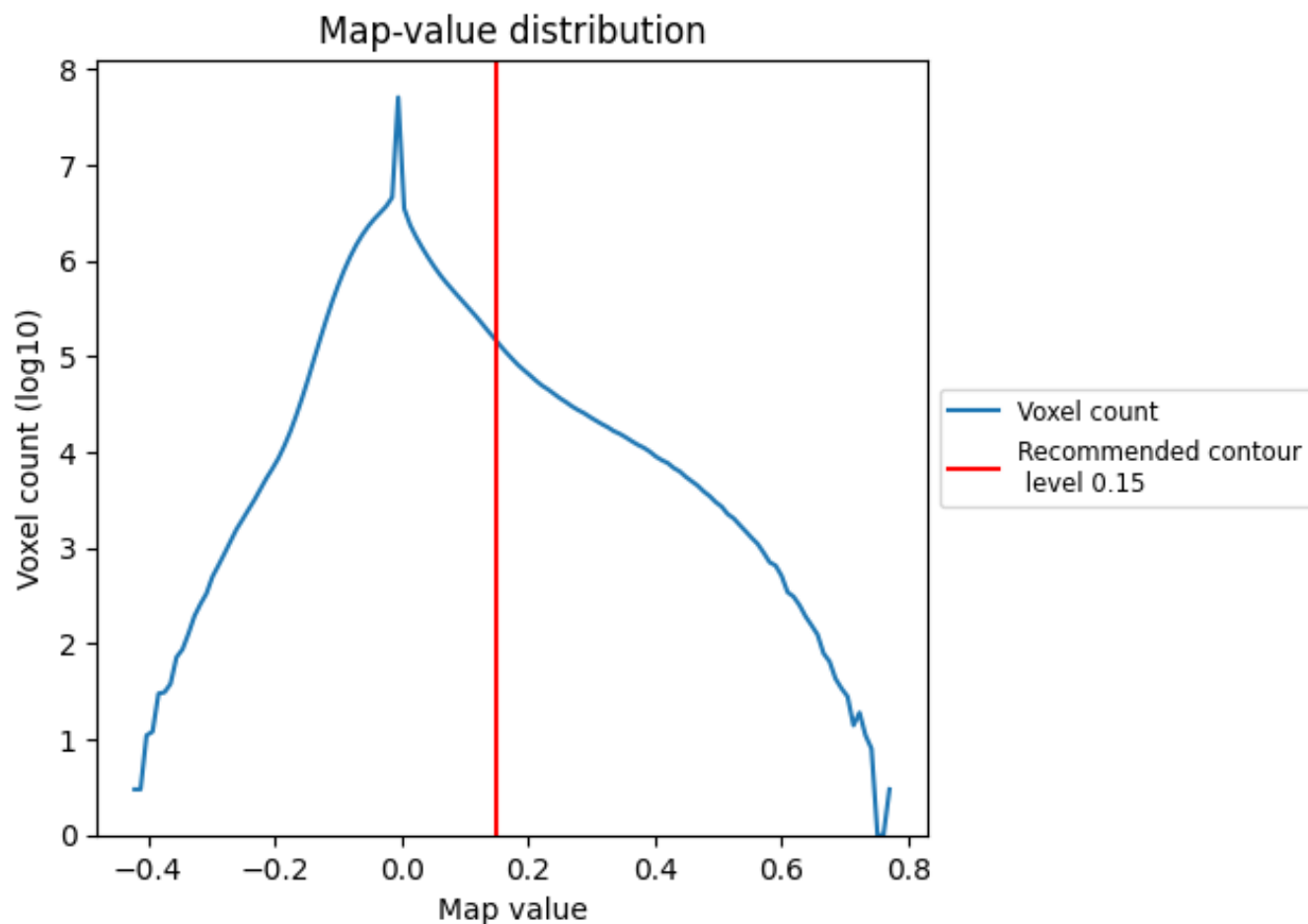
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

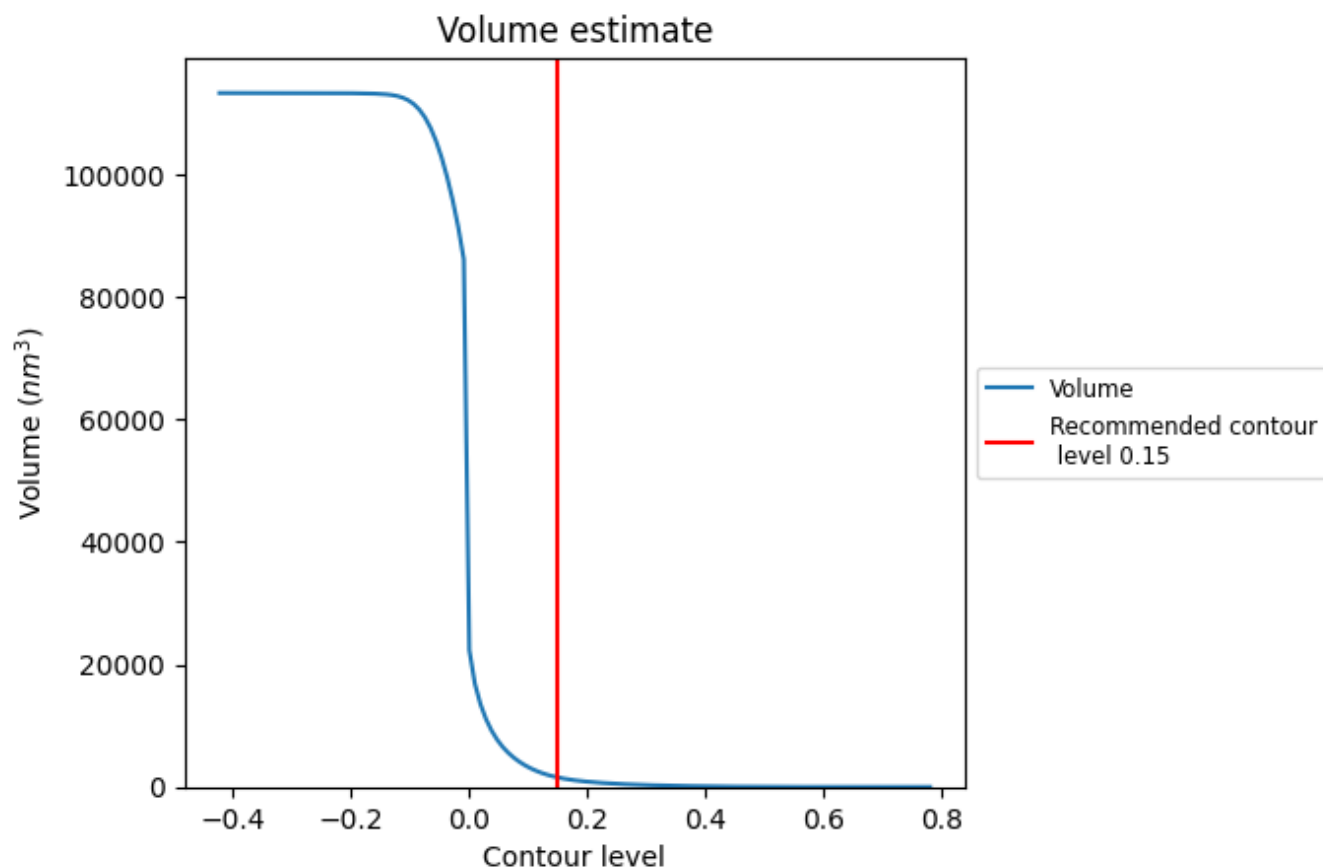
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

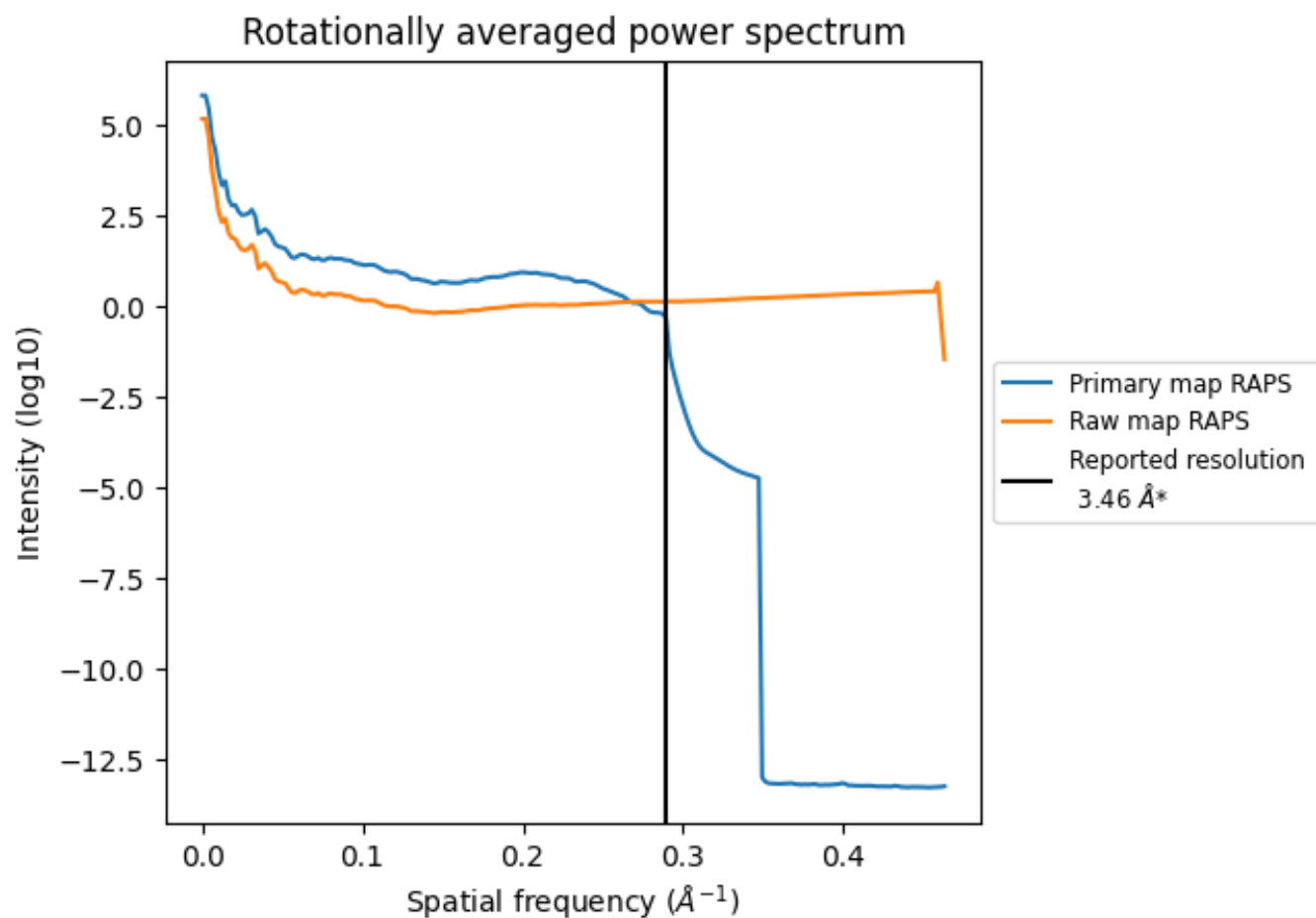
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1570 nm³; this corresponds to an approximate mass of 1418 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

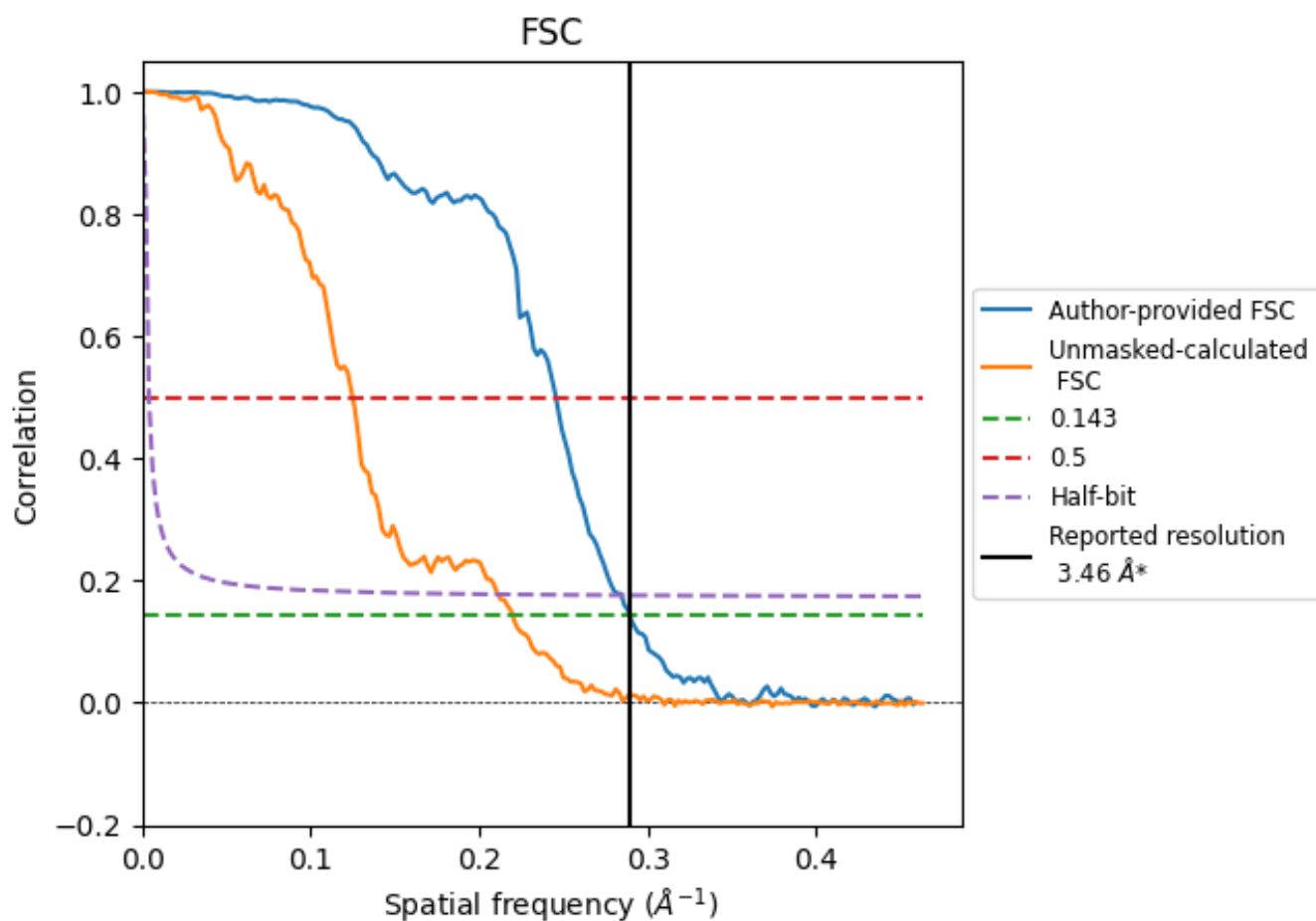


*Reported resolution corresponds to spatial frequency of 0.289 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.289 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

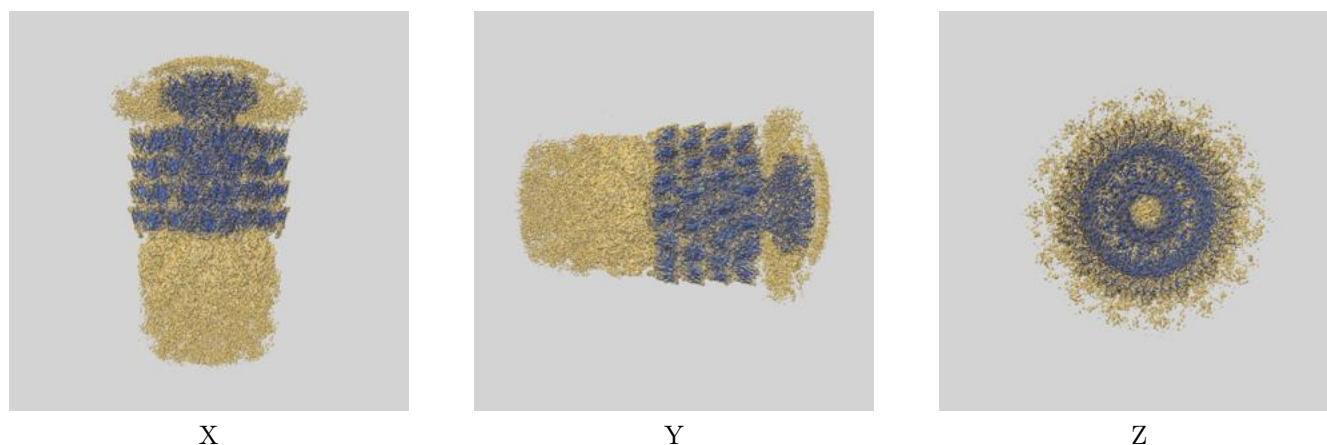
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.46	-	-
Author-provided FSC curve	3.46	4.07	3.51
Unmasked-calculated*	4.55	8.01	4.74

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.55 differs from the reported value 3.46 by more than 10 %

9 Map-model fit [i](#)

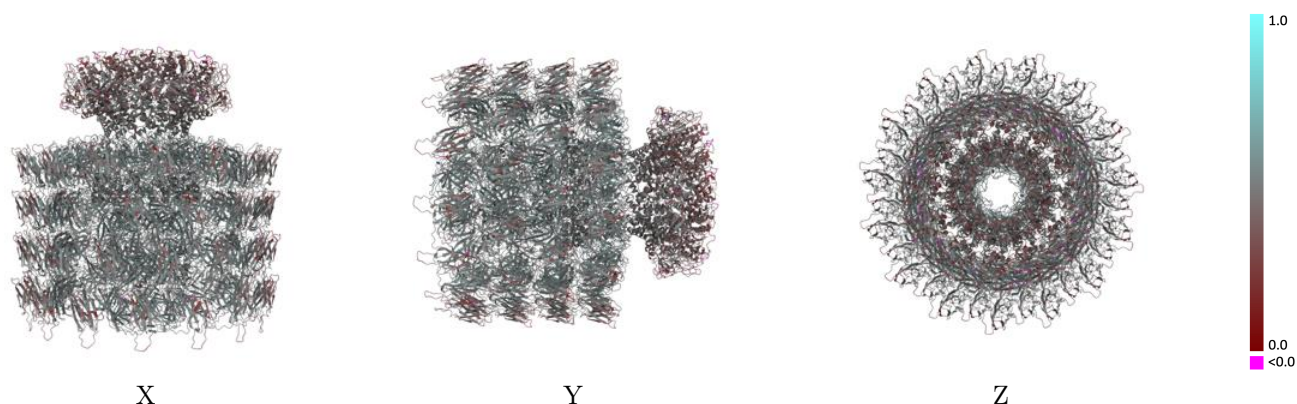
This section contains information regarding the fit between EMDB map EMD-29503 and PDB model 8FWE. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



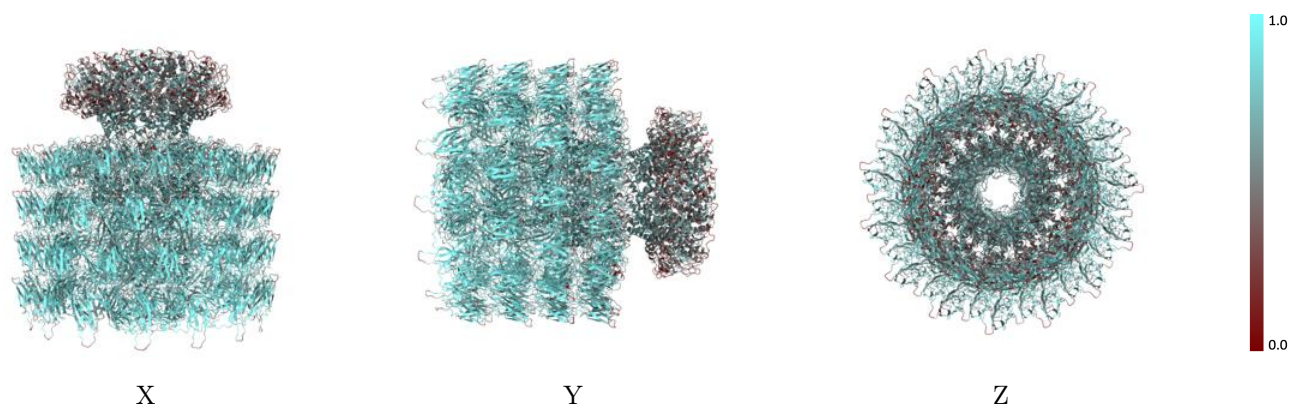
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



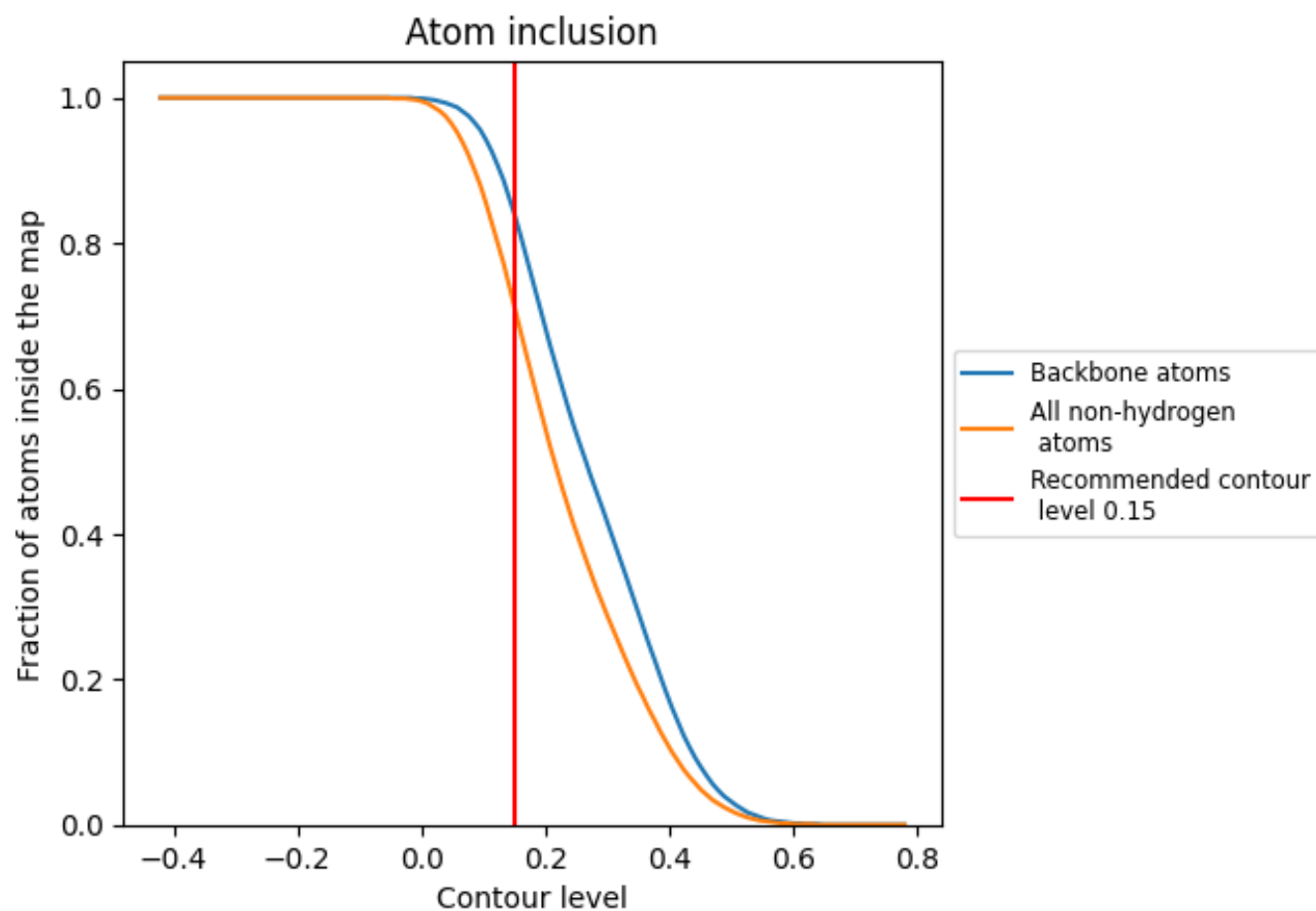
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 71% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7140	 0.4750
0	 0.7990	 0.4700
1	 0.8180	 0.4950
2	 0.8130	 0.4880
3	 0.7890	 0.4700
4	 0.7910	 0.4670
5	 0.7960	 0.4710
6	 0.7940	 0.4650
7	 0.7830	 0.4660
8	 0.7880	 0.4720
9	 0.7860	 0.4660
A	 0.8000	 0.4650
AA	 0.5160	 0.4230
AB	 0.4750	 0.3970
AC	 0.4810	 0.4030
AD	 0.5070	 0.4190
AE	 0.5210	 0.4250
AF	 0.4770	 0.4000
AG	 0.4870	 0.4030
AH	 0.5080	 0.4200
AI	 0.5170	 0.4240
AJ	 0.4730	 0.3980
AK	 0.4860	 0.4020
AL	 0.5120	 0.4200
AM	 0.7670	 0.5320
AN	 0.7700	 0.5300
AO	 0.7740	 0.5260
AP	 0.7530	 0.5310
AQ	 0.7740	 0.5200
AR	 0.7680	 0.5160
AS	 0.7750	 0.5200
AT	 0.7660	 0.5180
AU	 0.7650	 0.5150
AV	 0.7680	 0.5180
AW	 0.7660	 0.5220



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Chain	Atom inclusion	Q-score
AX	 0.7620	 0.5180
AY	 0.7630	 0.5180
AZ	 0.7570	 0.5220
Aa	 0.7570	 0.5220
Ab	 0.7580	 0.5210
B	 0.7850	 0.4660
C	 0.7910	 0.4700
D	 0.7800	 0.4620
E	 0.7980	 0.4720
F	 0.7940	 0.4650
G	 0.7800	 0.4670
H	 0.7550	 0.5280
I	 0.7530	 0.5280
J	 0.7510	 0.4910
K	 0.7490	 0.4920
L	 0.7520	 0.4840
M	 0.7250	 0.4830
N	 0.7210	 0.4810
O	 0.7580	 0.4920
P	 0.7450	 0.4900
Q	 0.7510	 0.4830
R	 0.7240	 0.4830
R3	 0.7010	 0.5040
R4	 0.6930	 0.5070
R5	 0.6940	 0.5030
S	 0.7250	 0.4810
S3	 0.6950	 0.5080
S4	 0.6940	 0.5100
S5	 0.6880	 0.5100
T	 0.7570	 0.4890
T3	 0.6420	 0.5120
T4	 0.6410	 0.5090
T5	 0.6440	 0.5110
U	 0.7530	 0.4920
U3	 0.6420	 0.4980
U4	 0.6400	 0.5010
U5	 0.6430	 0.5000
V	 0.7550	 0.4880
W	 0.7260	 0.4840
X	 0.7240	 0.4820
Y	 0.8100	 0.4960
Z	 0.7940	 0.4910

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Chain	Atom inclusion	Q-score
a	 0.8080	 0.4890
b	 0.7970	 0.4830
c	 0.7940	 0.4890
d	 0.8080	 0.4920
e	 0.7930	 0.4910
f	 0.8060	 0.4890
g	 0.7990	 0.4830
h	 0.7930	 0.4900
i	 0.8090	 0.4930
j	 0.7910	 0.4900
k	 0.8110	 0.4910
l	 0.7950	 0.4850
m	 0.7920	 0.4910
n	 0.8290	 0.4920
o	 0.8260	 0.4980
p	 0.8170	 0.4910
q	 0.8240	 0.4930
r	 0.8110	 0.4880
s	 0.8260	 0.4900
t	 0.8280	 0.4980
u	 0.8180	 0.4930
v	 0.8190	 0.4930
w	 0.8180	 0.4880
x	 0.8250	 0.4910
y	 0.8210	 0.4980
z	 0.8210	 0.4930