



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 12:07 PM UTC

PDB ID : 8CWM / pdb_00008cwm
EMDB ID : EMD-27026
Title : Cryo-EM structure of the supercoiled *S. islandicus* REY15A archaeal flagellar filament
Authors : Kreutzberger, M.A.B.; Liu, J.; Krupovic, M.; Egelman, E.H.
Deposited on : 2022-05-19
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

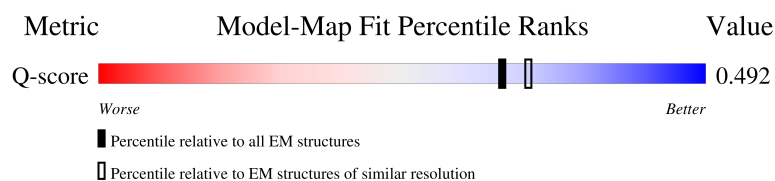
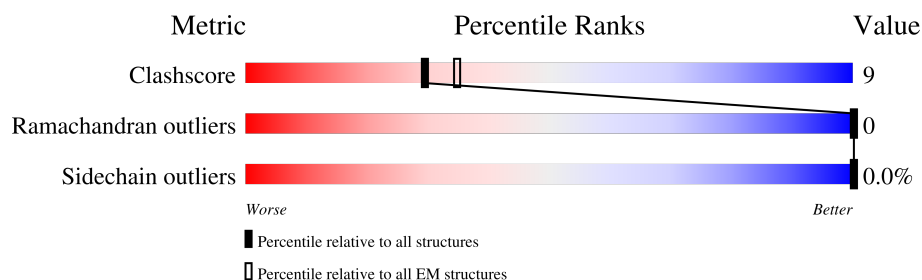
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

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



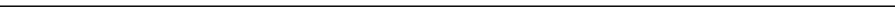
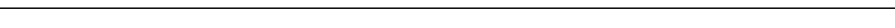
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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

Mol	Chain	Length	Quality of chain
1	0	306	 64% 29% 6%
1	1	306	 72% 22% 6%
1	2	306	 72% 22% 6%
1	3	306	 75% 19% 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	4	306	 75%18%6%
1	5	306	 75%19%6%
1	6	306	 69%25%6%
1	7	306	 70%24%6%
1	A	306	 67%27%6%
1	B	306	 72%22%6%
1	C	306	 67%26%6%
1	D	306	 71%23%6%
1	E	306	 66%27%6%
1	F	306	 70%24%6%
1	G	306	 75%19%6%
1	H	306	 76%18%6%
1	I	306	 76%17%6%
1	J	306	 80%14%6%
1	K	306	 75%19%6%
1	L	306	 76%18%6%
1	M	306	 75%19%6%
1	N	306	 68%25%6%
1	O	306	 75%19%6%
1	P	306	 70%24%6%
1	Q	306	 76%17%6%
1	R	306	 67%27%6%
1	S	306	 76%18%6%
1	T	306	 73%21%6%
1	U	306	 71%23%6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	V	306	
1	W	306	
1	X	306	
1	Y	306	
1	Z	306	
1	a	306	
1	b	306	
1	c	306	
1	d	306	
1	e	306	
1	f	306	
1	g	306	
1	h	306	
1	i	306	
1	j	306	
1	k	306	
1	l	306	
1	m	306	
1	n	306	
1	o	306	
1	p	306	
1	q	306	
1	r	306	
1	s	306	
1	t	306	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	u	306	 75% 19% 6%
1	v	306	 74% 20% 6%
1	w	306	 72% 22% 6%
1	x	306	 73% 21% 6%
1	y	306	 68% 26% 6%
1	z	306	 70% 24% 6%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 130980 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 Flagellin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	1	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	2	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	3	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	4	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	5	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	6	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	7	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	A	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	B	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	C	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	D	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	E	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	F	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	G	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	H	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	I	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	J	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	K	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	L	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	M	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	N	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	O	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	P	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	Q	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	R	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	S	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	T	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	U	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	V	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	W	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	X	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	Y	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	Z	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	a	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	b	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	c	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	d	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	e	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	f	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	g	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	h	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	i	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	j	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	k	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	l	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	m	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	n	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	o	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	p	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	q	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	r	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	s	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	t	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	u	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	v	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	w	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	x	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		
1	y	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		

Continued on next page...

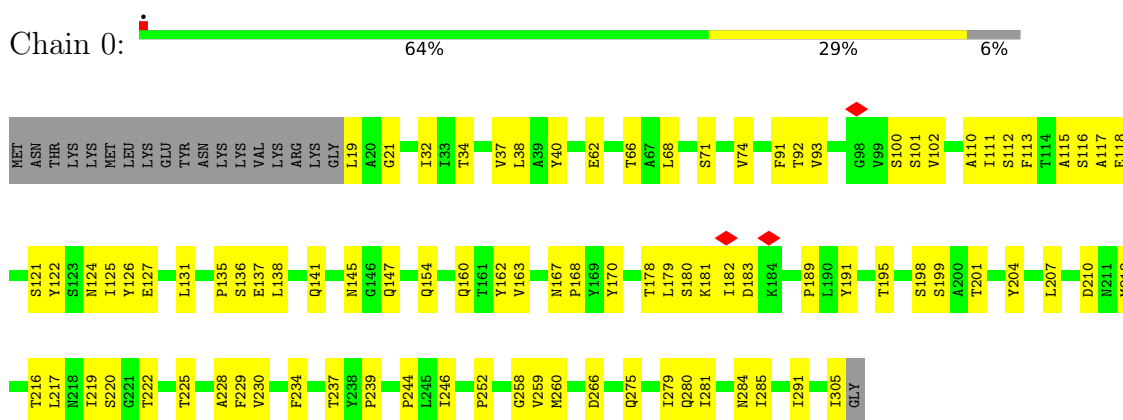
Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	z	287	Total	C	N	O	S	0	0
			2183	1422	327	431	3		

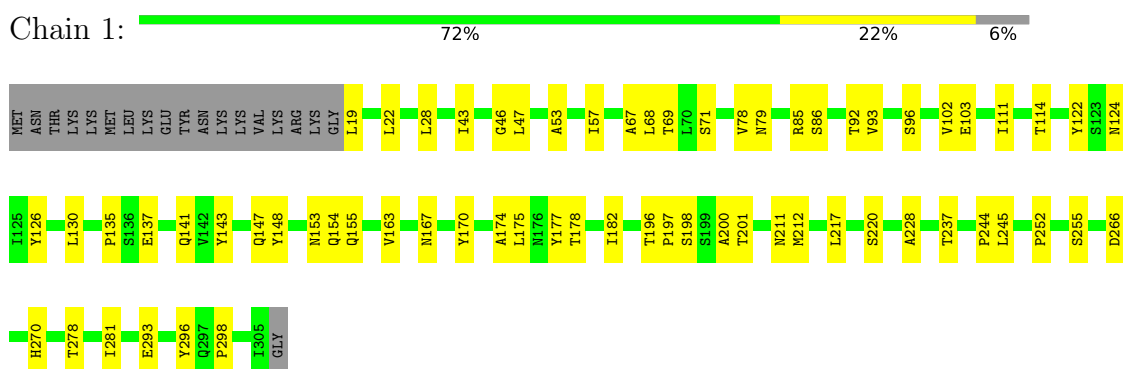
3 Residue-property plots

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.

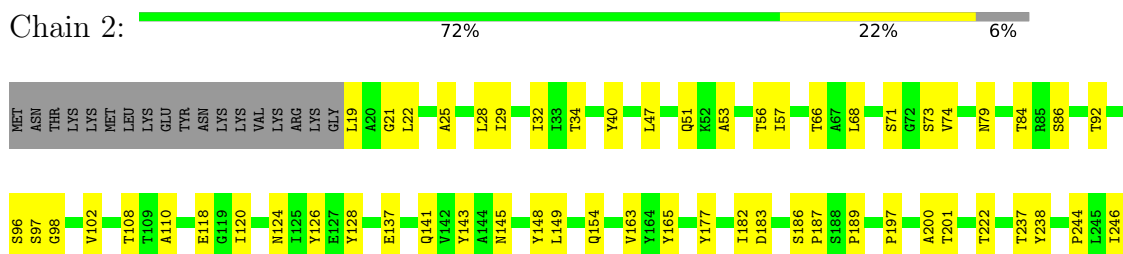
• Molecule 1: Flagellin



• Molecule 1: Flagellin



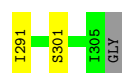
• Molecule 1: Flagellin





- Molecule 1: Flagellin

Chain 3: 



- Molecule 1: Flagellin

Chain 4: 



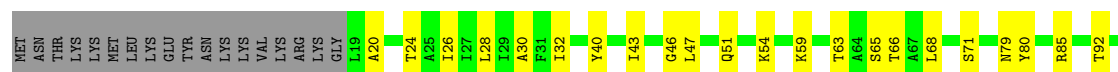
- Molecule 1: Flagellin

Chain 5: 



- Molecule 1: Flagellin

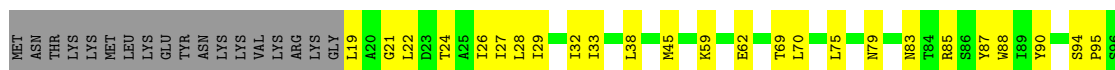
Chain 6: 





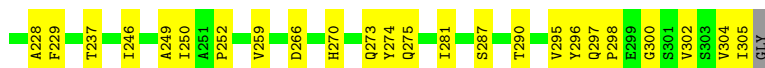
● Molecule 1: Flagellin

Chain 7: 70% 24% 6%



● Molecule 1: Flagellin

Chain A: 67% 27% 6%



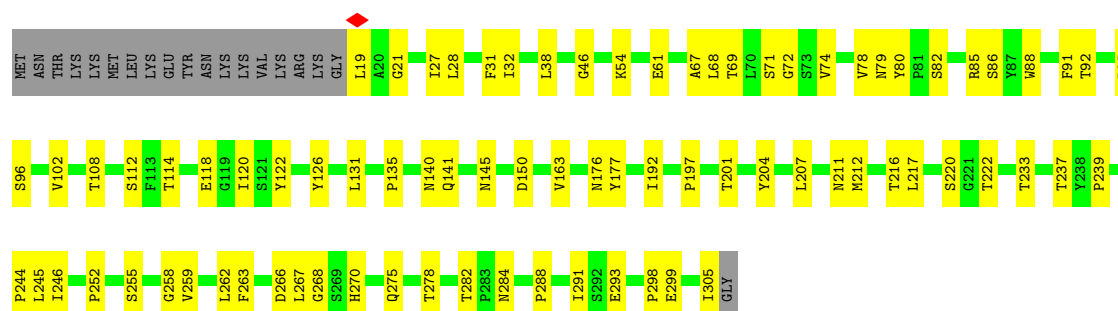
● Molecule 1: Flagellin

Chain B: 72% 22% 6%



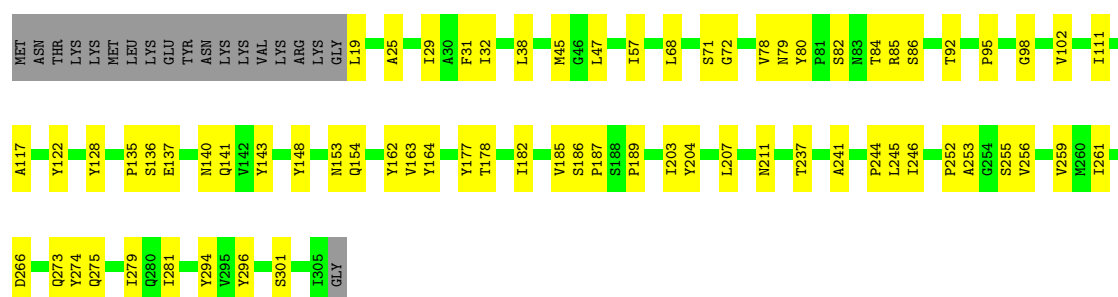
● Molecule 1: Flagellin

Chain C: 67% 26% 6%



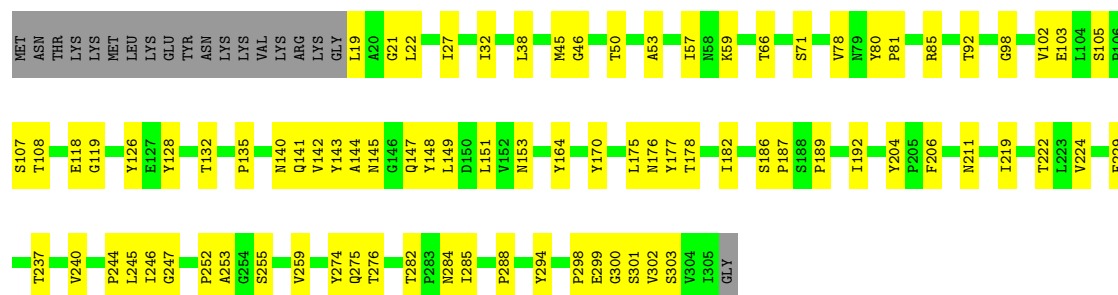
• Molecule 1: Flagellin

Chain D: 71% 23% 6%



• Molecule 1: Flagellin

Chain E: 66% 27% 6%

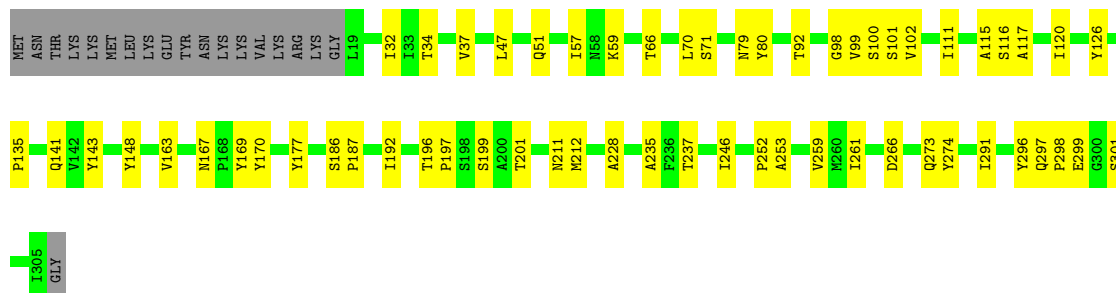


• Molecule 1: Flagellin

Chain F: 70% 24% 6%



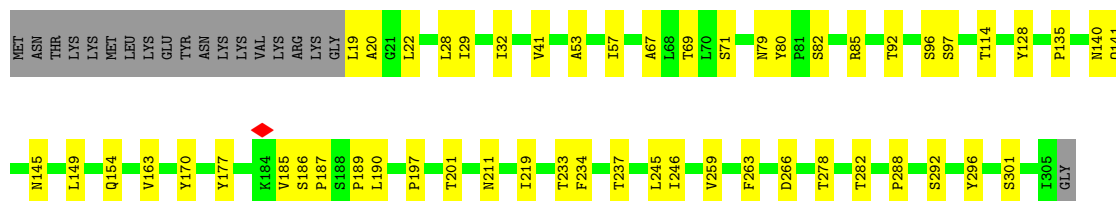
● Molecule 1: Flagellin

Chain G:  75% 19% 6%

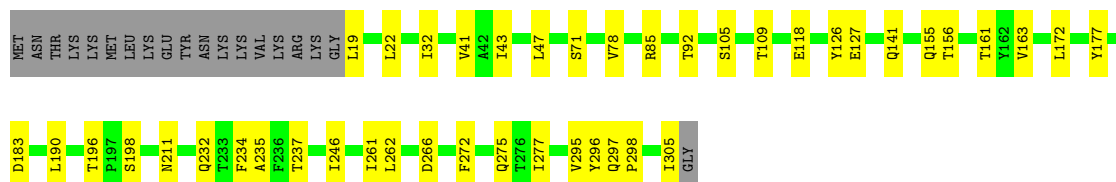
● Molecule 1: Flagellin

Chain H:  76% 18% 6%

● Molecule 1: Flagellin

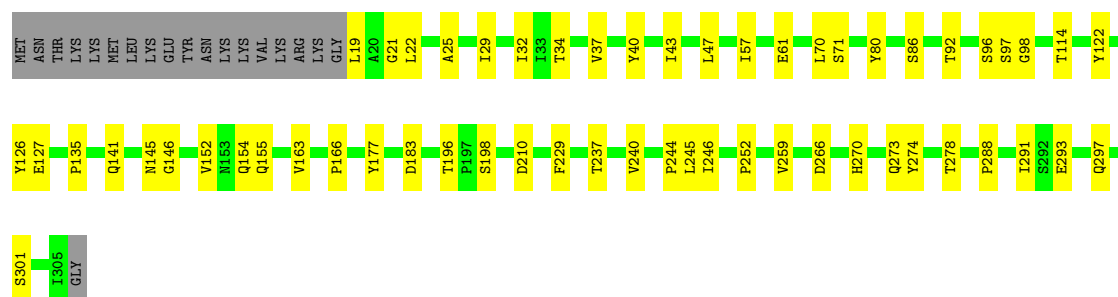
Chain I:  76% 17% 6%

● Molecule 1: Flagellin

Chain J:  80% 14% 6%

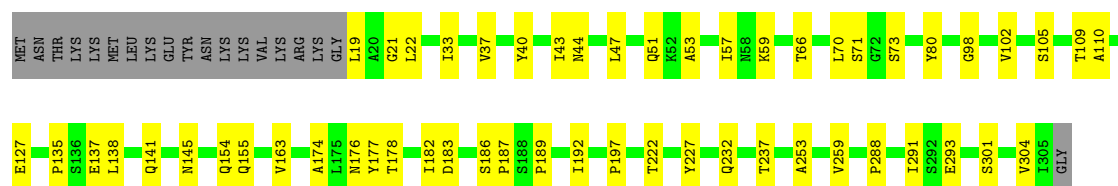
● Molecule 1: Flagellin

Chain K:  75% 19% 6%



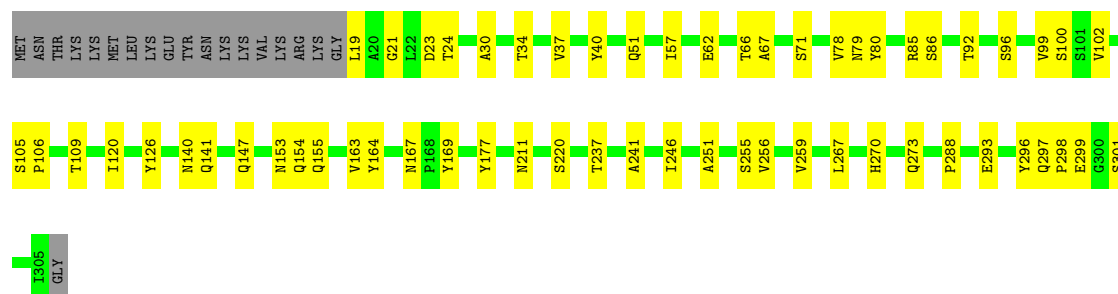
• Molecule 1: Flagellin

Chain L:  76% 18% 6%



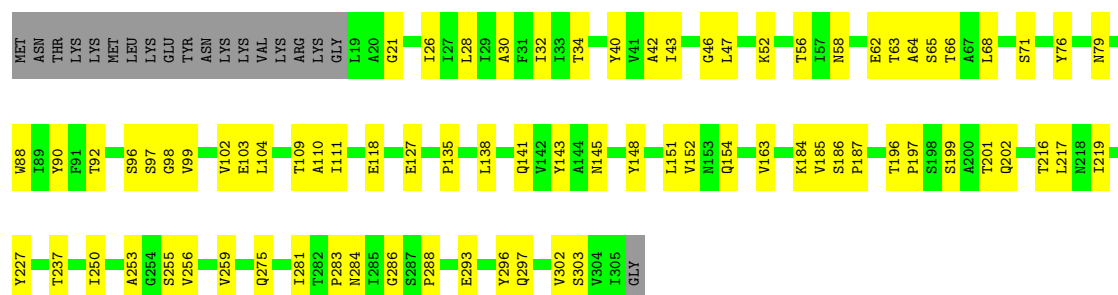
• Molecule 1: Flagellin

Chain M:  75% 19% 6%



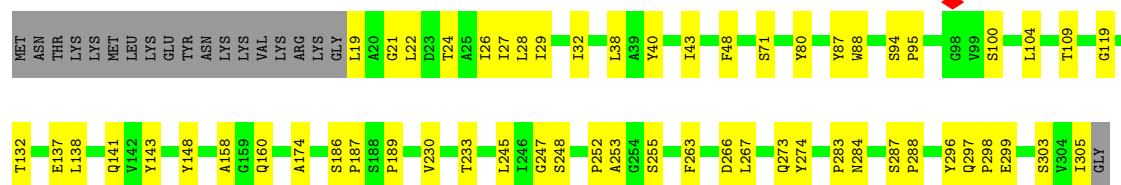
• Molecule 1: Flagellin

Chain N:  68% 25% 6%



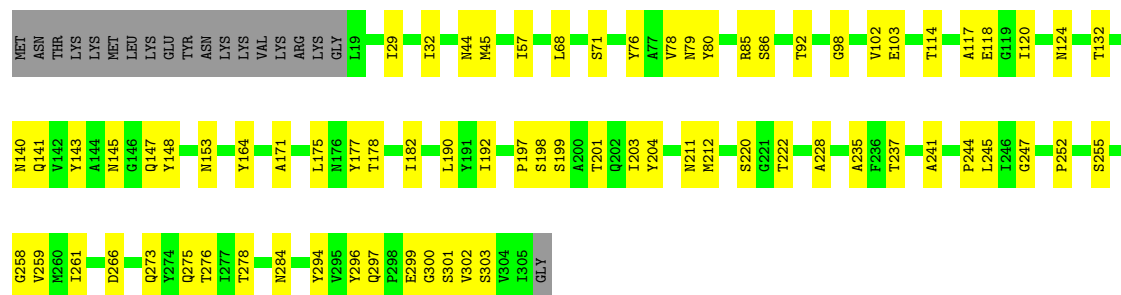
• Molecule 1: Flagellin

Chain O: 



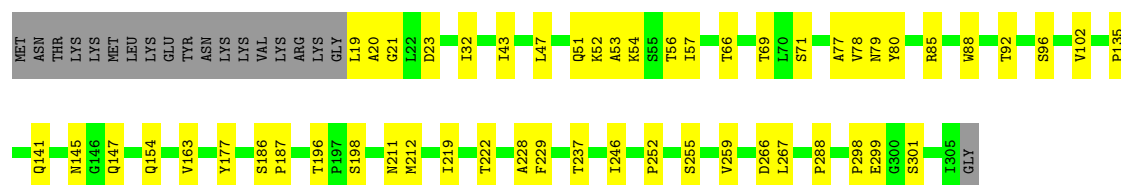
• Molecule 1: Flagellin

Chain P: 



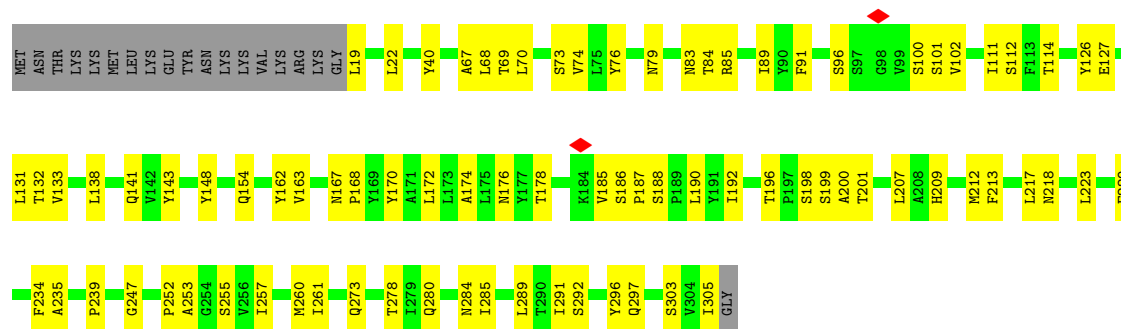
• Molecule 1: Flagellin

Chain Q: 



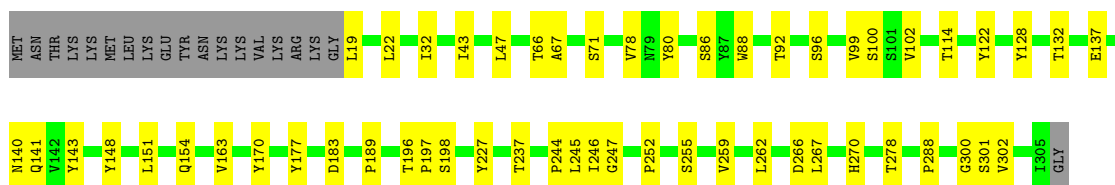
• Molecule 1: Flagellin

Chain R: 



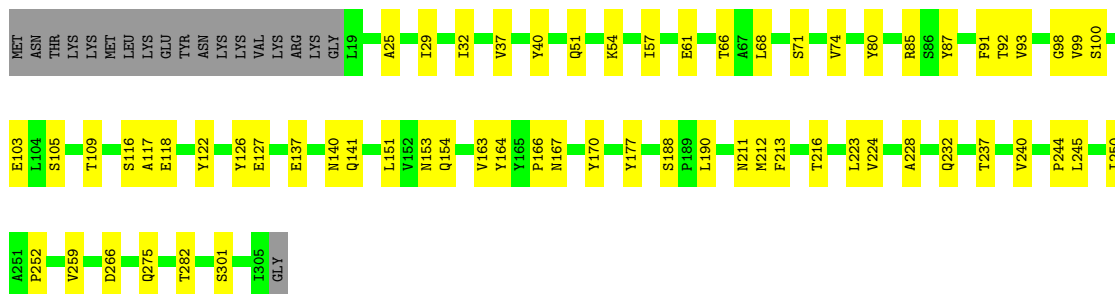
• Molecule 1: Flagellin

Chain S: 



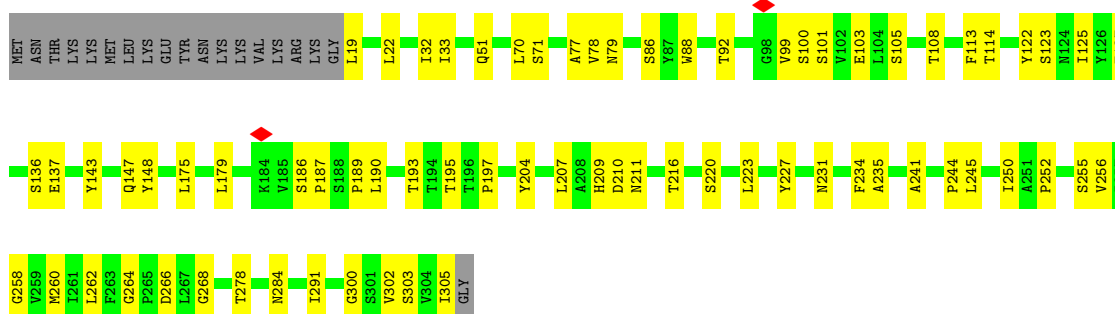
• Molecule 1: Flagellin

Chain T: 73% 21% 6%



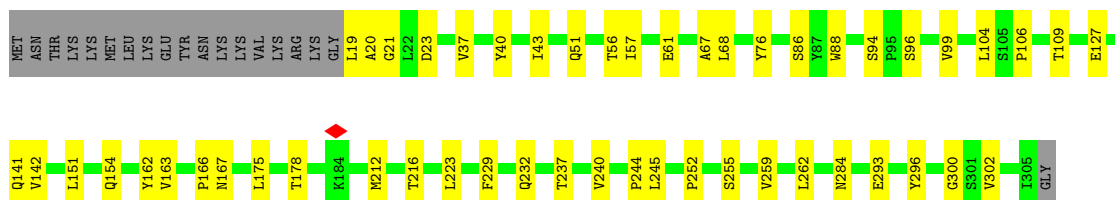
• Molecule 1: Flagellin

Chain U: 71% 23% 6%



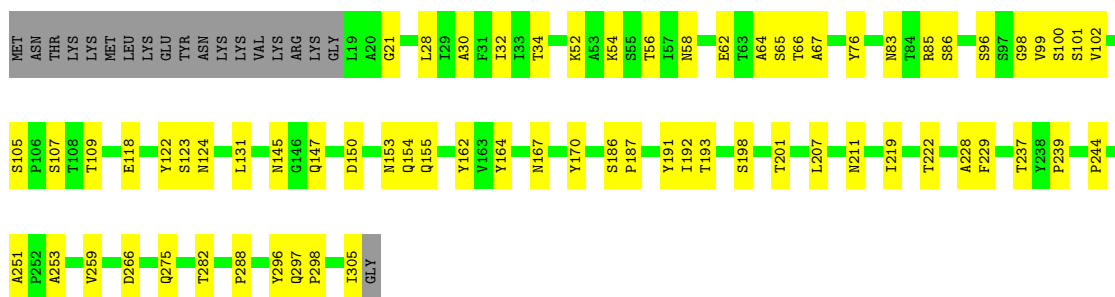
• Molecule 1: Flagellin

Chain V: 77% 17% 6%



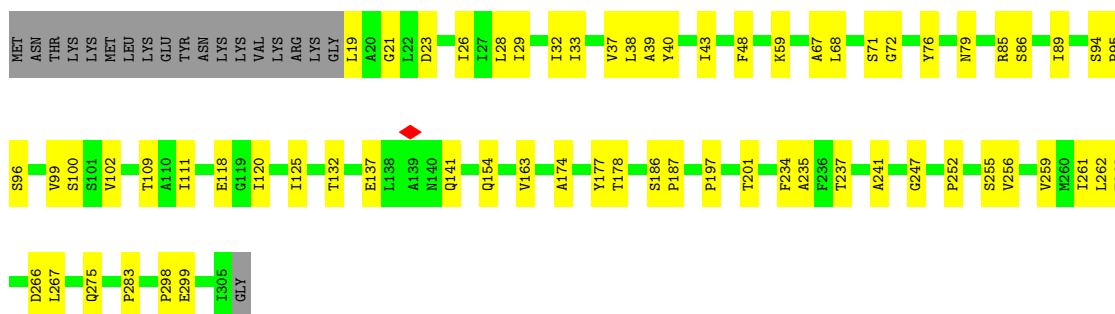
• Molecule 1: Flagellin

Chain W: 71% 23% 6%



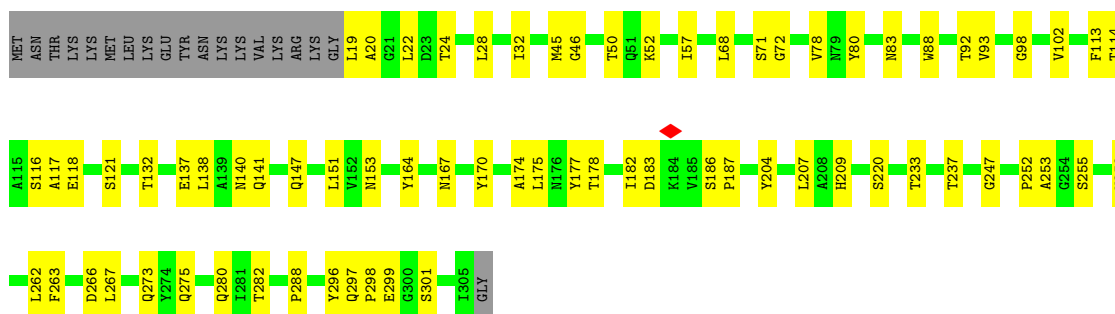
• Molecule 1: Flagellin

Chain X: 73% 21% 6%



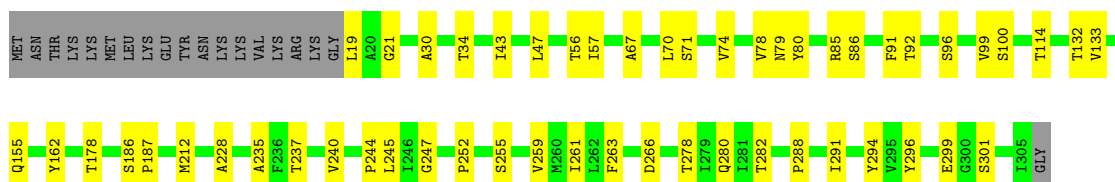
• Molecule 1: Flagellin

Chain Y: 70% 24% 6%



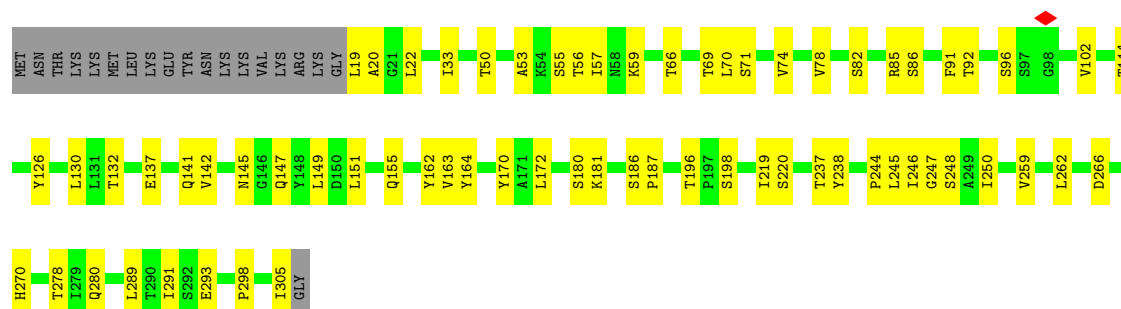
• Molecule 1: Flagellin

Chain Z: 76% 17% 6%



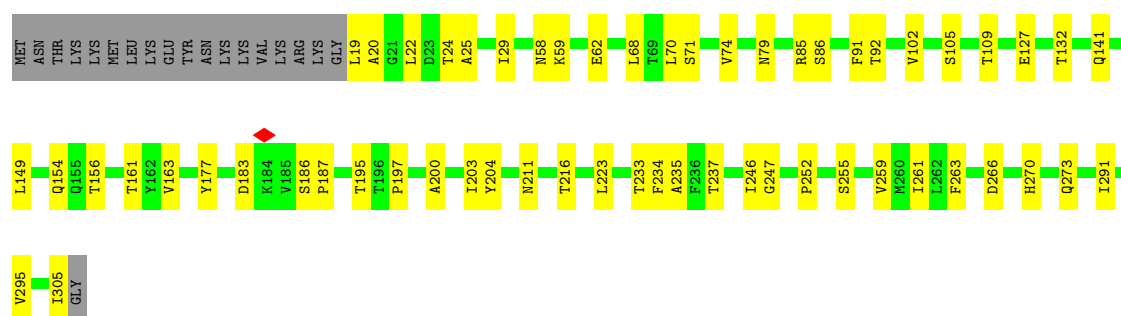
• Molecule 1: Flagellin

Chain a: 72% 22% 6%



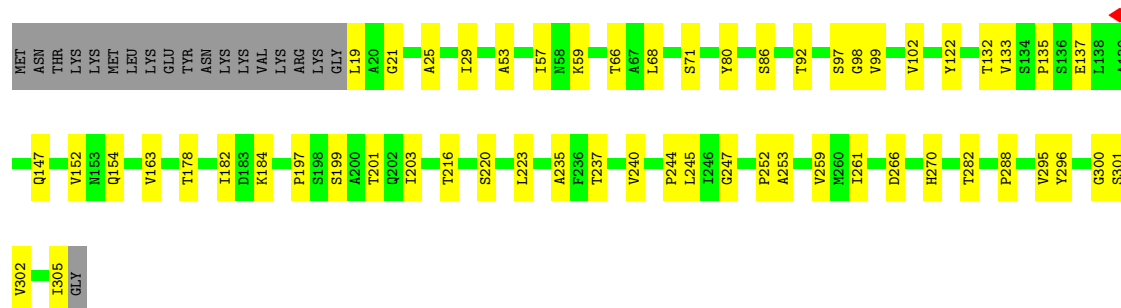
• Molecule 1: Flagellin

Chain b: 75% 19% 6%



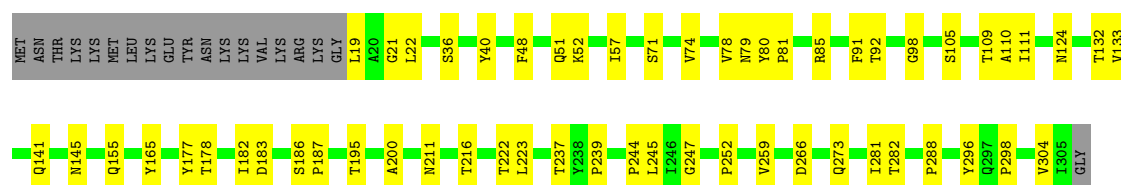
• Molecule 1: Flagellin

Chain c: 75% 18% 6%



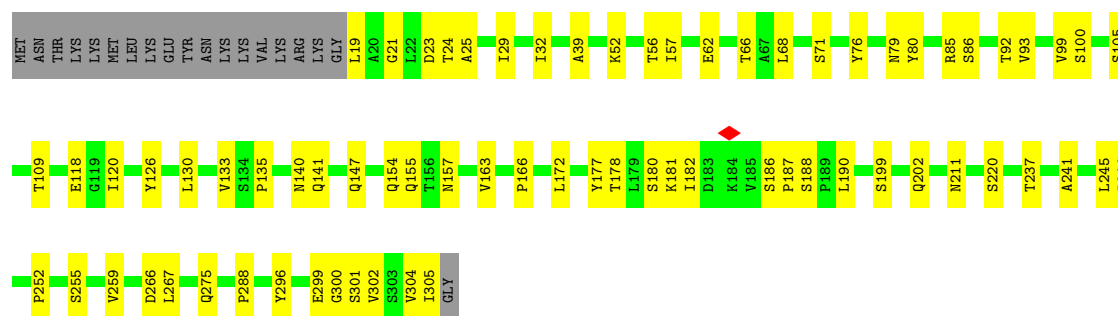
• Molecule 1: Flagellin

Chain d: 75% 19% 6%



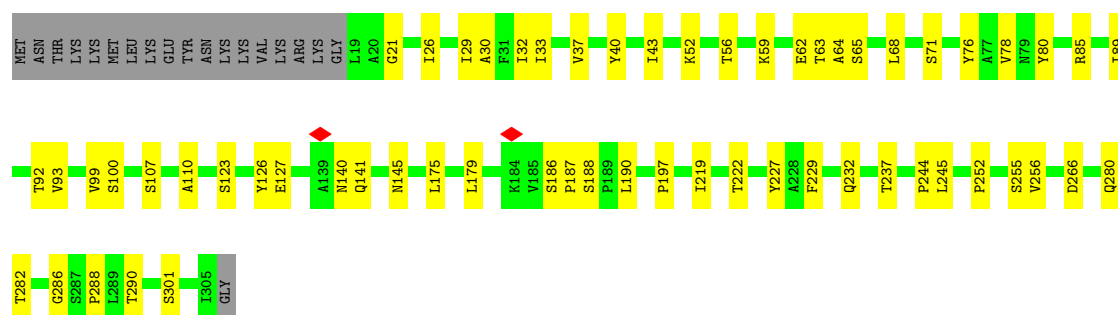
• Molecule 1: Flagellin

Chain e:  70% 24% 6%



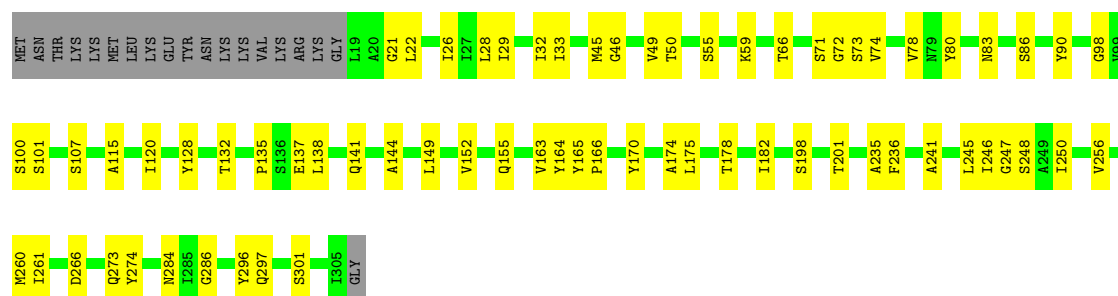
• Molecule 1: Flagellin

Chain f:  74% 20% 6%



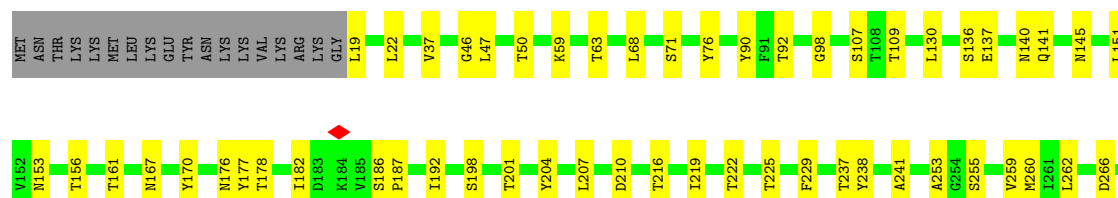
• Molecule 1: Flagellin

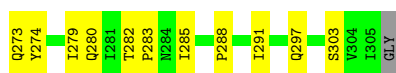
Chain g:  71% 23% 6%



• Molecule 1: Flagellin

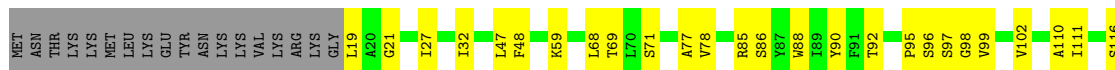
Chain h:  73% 21% 6%





● Molecule 1: Flagellin

Chain i: 73% 21% 6%



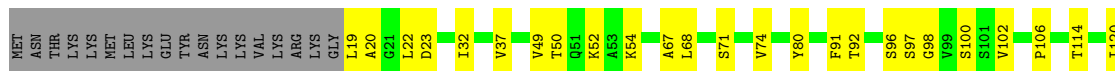
● Molecule 1: Flagellin

Chain j: 76% 18% 6%



● Molecule 1: Flagellin

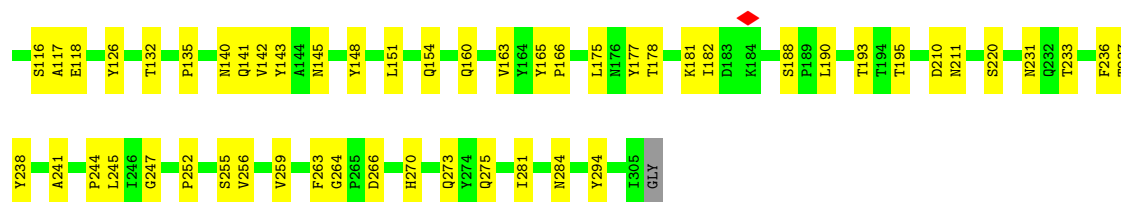
Chain k: 70% 24% 6%



● Molecule 1: Flagellin

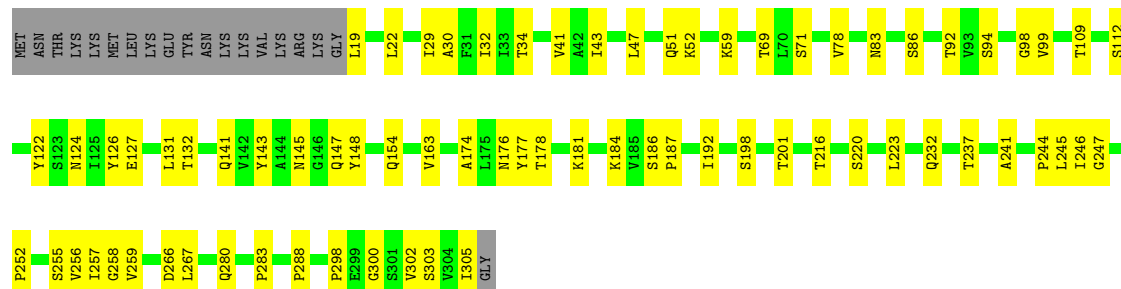
Chain l: 69% 25% 6%





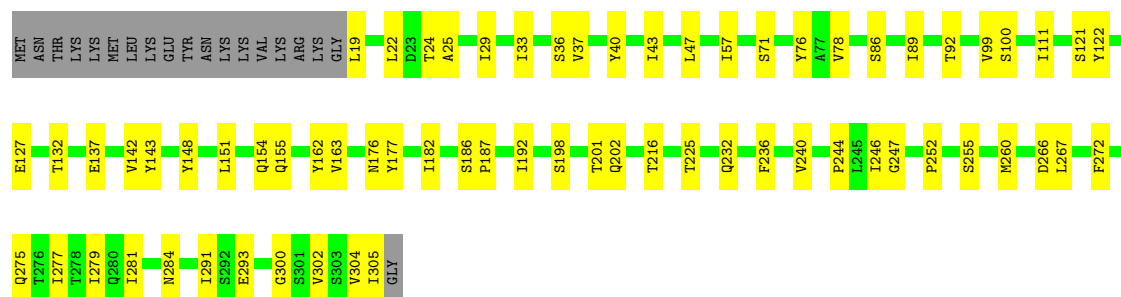
- Molecule 1: Flagellin

Chain m: 70% 24% 6%



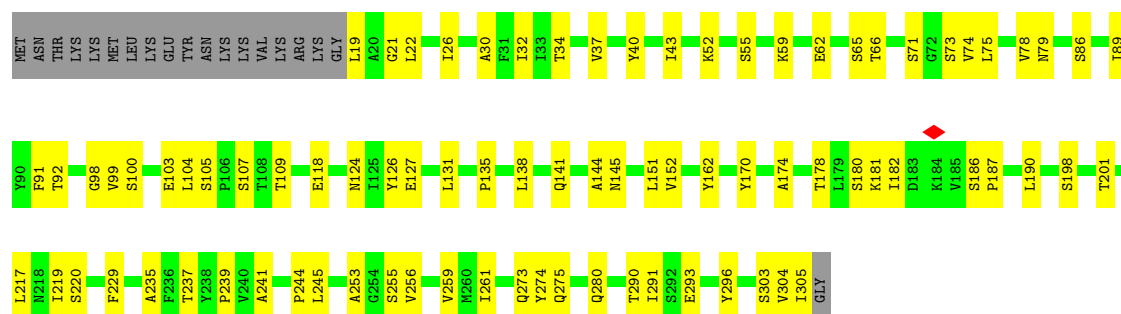
- Molecule 1: Flagellin

Chain n: 72% 22% 6%



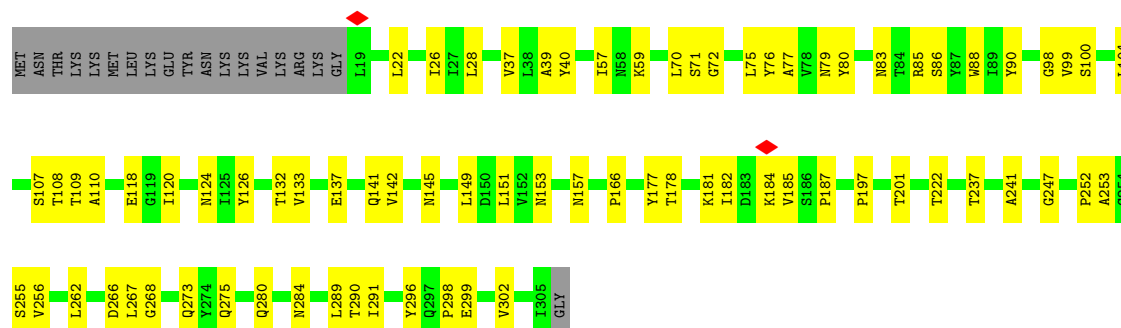
- Molecule 1: Flagellin

Chain o: 66% 27% 6%



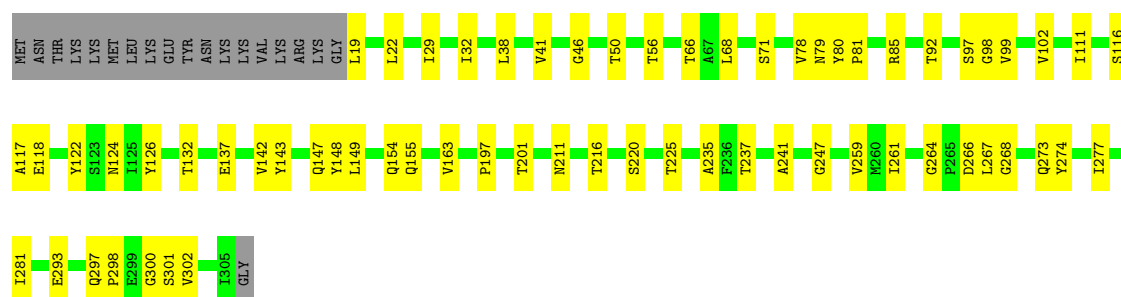
- Molecule 1: Flagellin

Chain p: 69% 25% 6%



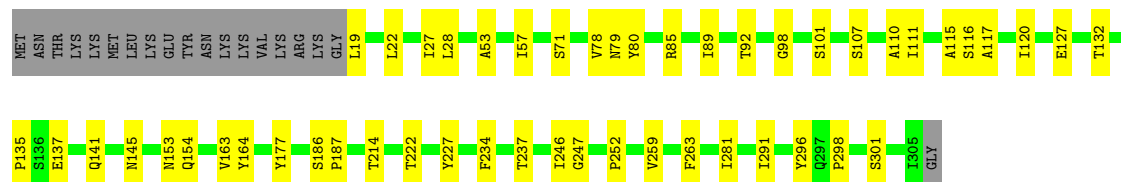
• Molecule 1: Flagellin

Chain q: 73% 21% 6%



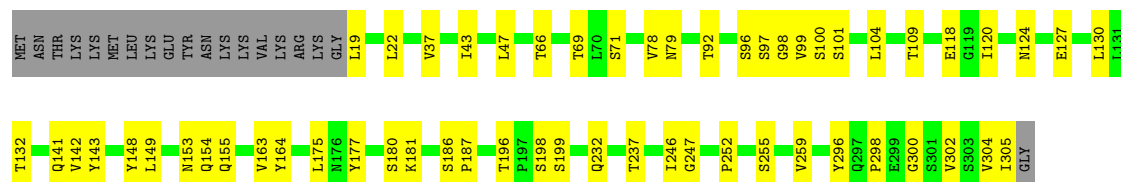
• Molecule 1: Flagellin

Chain r: 77% 16% 6%



• Molecule 1: Flagellin

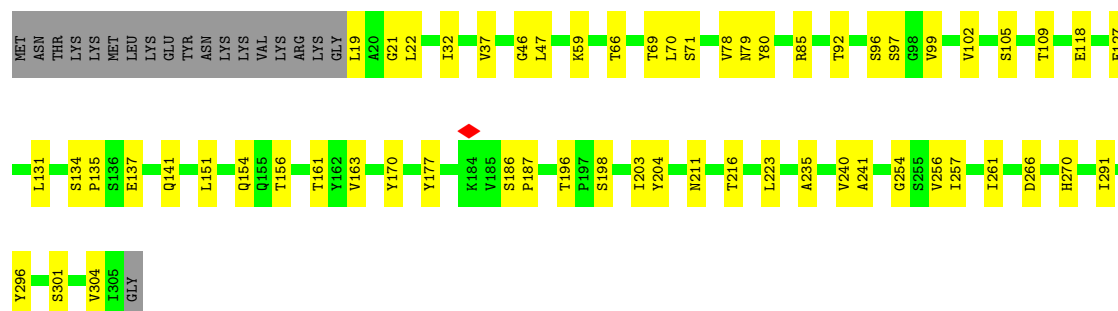
Chain s: 75% 19% 6%



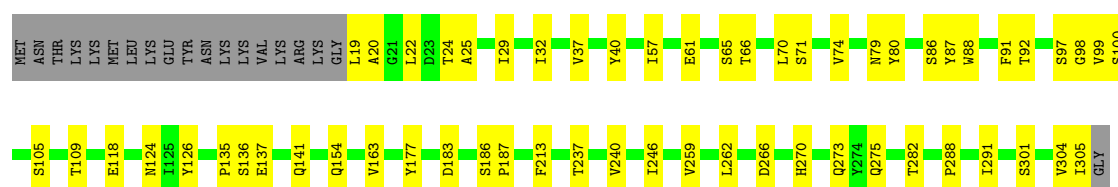
• Molecule 1: Flagellin

Chain t: 75% 19% 6%

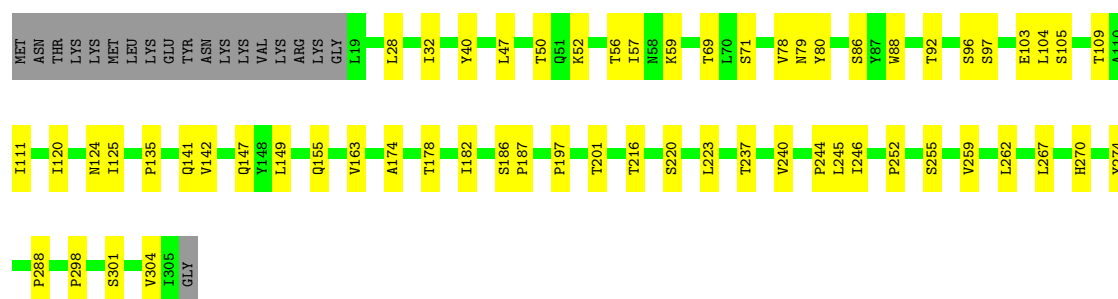




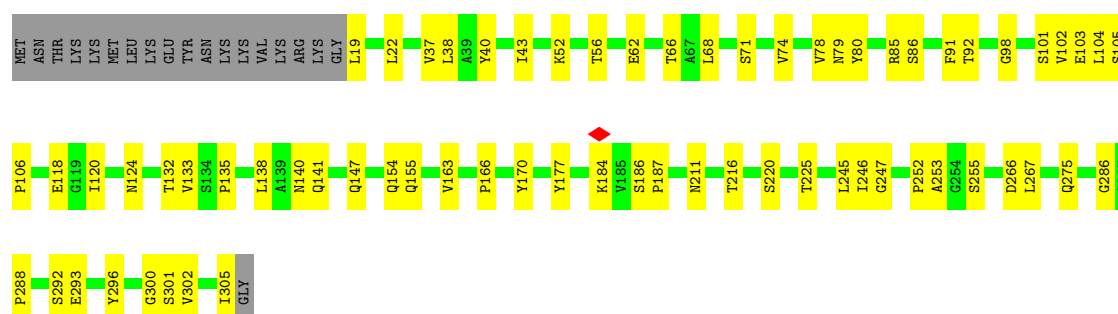
• Molecule 1: Flagellin



• Molecule 1: Flagellin



• Molecule 1: Flagellin

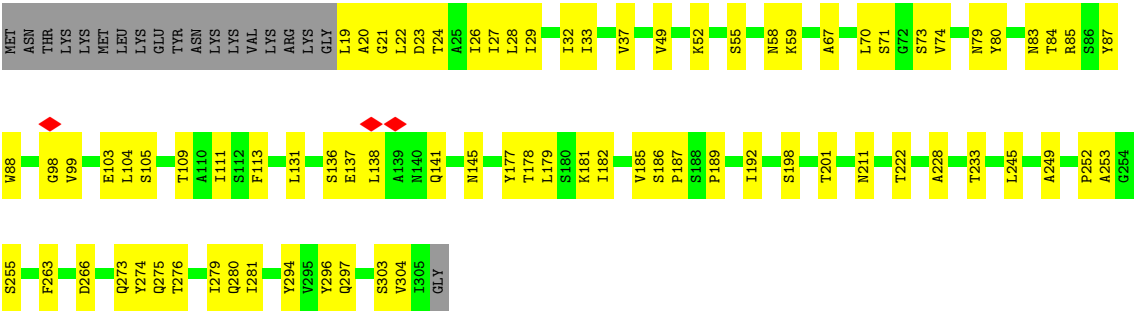


• Molecule 1: Flagellin

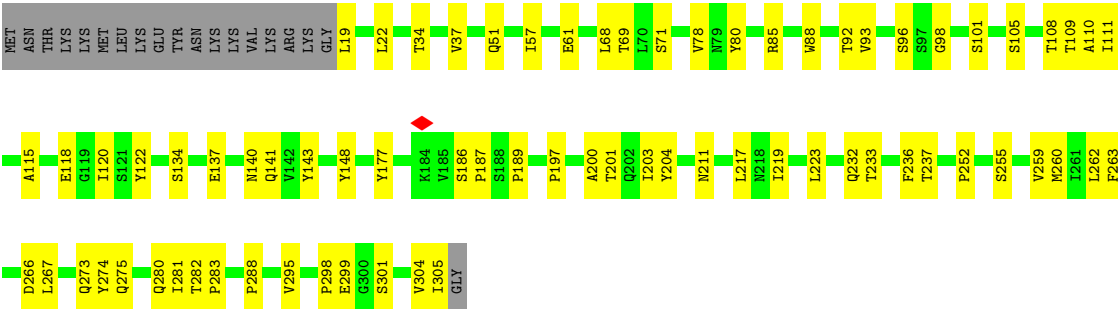




• Molecule 1: Flagellin



• Molecule 1: Flagellin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51914	Depositor
Resolution determination method	FSC 0.33 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)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.322	Depositor
Minimum map value	-0.782	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.112	Depositor
Map size ($\text{\AA}$)	673.92004, 673.92004, 673.92004	wwPDB
Map dimensions	624, 624, 624	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.12	0/2239	0.30	0/3080
1	1	0.18	0/2239	0.30	0/3080
1	2	0.19	0/2239	0.31	0/3080
1	3	0.18	0/2239	0.30	0/3080
1	4	0.18	0/2239	0.31	0/3080
1	5	0.18	0/2239	0.31	0/3080
1	6	0.17	0/2239	0.33	0/3080
1	7	0.16	0/2239	0.33	0/3080
1	A	0.16	0/2239	0.33	0/3080
1	B	0.16	0/2239	0.32	0/3080
1	C	0.14	0/2239	0.31	0/3080
1	D	0.13	0/2239	0.30	0/3080
1	E	0.15	0/2239	0.31	0/3080
1	F	0.16	0/2239	0.32	0/3080
1	G	0.18	0/2239	0.31	0/3080
1	H	0.18	0/2239	0.31	0/3080
1	I	0.17	0/2239	0.32	0/3080
1	J	0.18	0/2239	0.30	0/3080
1	K	0.18	0/2239	0.31	0/3080
1	L	0.17	0/2239	0.29	0/3080
1	M	0.18	0/2239	0.31	0/3080
1	N	0.16	0/2239	0.35	0/3080
1	O	0.15	0/2239	0.32	0/3080
1	P	0.16	0/2239	0.30	0/3080
1	Q	0.18	0/2239	0.29	0/3080
1	R	0.11	0/2239	0.30	0/3080
1	S	0.17	0/2239	0.31	0/3080
1	T	0.16	0/2239	0.31	0/3080
1	U	0.11	0/2239	0.30	0/3080
1	V	0.17	0/2239	0.33	0/3080
1	W	0.15	0/2239	0.31	0/3080
1	X	0.16	0/2239	0.30	0/3080
1	Y	0.16	0/2239	0.30	0/3080
1	Z	0.17	0/2239	0.29	0/3080

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.18	0/2239	0.31	0/3080
1	b	0.17	0/2239	0.30	0/3080
1	c	0.17	0/2239	0.30	0/3080
1	d	0.18	0/2239	0.31	0/3080
1	e	0.15	0/2239	0.30	0/3080
1	f	0.15	0/2239	0.29	0/3080
1	g	0.14	0/2239	0.30	0/3080
1	h	0.12	0/2239	0.30	0/3080
1	i	0.15	0/2239	0.30	0/3080
1	j	0.14	0/2239	0.29	0/3080
1	k	0.14	0/2239	0.31	0/3080
1	l	0.13	0/2239	0.31	0/3080
1	m	0.14	0/2239	0.29	0/3080
1	n	0.13	0/2239	0.28	0/3080
1	o	0.13	0/2239	0.31	0/3080
1	p	0.15	0/2239	0.32	0/3080
1	q	0.16	0/2239	0.30	0/3080
1	r	0.18	0/2239	0.29	0/3080
1	s	0.18	0/2239	0.30	0/3080
1	t	0.18	0/2239	0.31	0/3080
1	u	0.18	0/2239	0.32	0/3080
1	v	0.17	0/2239	0.30	0/3080
1	w	0.17	0/2239	0.31	0/3080
1	x	0.16	0/2239	0.31	0/3080
1	y	0.11	0/2239	0.31	0/3080
1	z	0.20	0/2239	0.43	0/3080
All	All	0.16	0/134340	0.31	0/184800

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	z	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	z	304	VAL	Peptide

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	2183	0	2158	60	0
1	1	2183	0	2158	43	0
1	2	2183	0	2158	48	0
1	3	2183	0	2158	39	0
1	4	2183	0	2158	42	0
1	5	2183	0	2158	42	0
1	6	2183	0	2158	54	0
1	7	2183	0	2158	49	0
1	A	2183	0	2158	58	0
1	B	2183	0	2158	48	0
1	C	2183	0	2158	56	0
1	D	2183	0	2158	52	0
1	E	2183	0	2158	57	0
1	F	2183	0	2158	48	0
1	G	2183	0	2158	40	0
1	H	2183	0	2158	36	0
1	I	2183	0	2158	39	0
1	J	2183	0	2158	27	0
1	K	2183	0	2158	40	0
1	L	2183	0	2158	38	0
1	M	2183	0	2158	39	0
1	N	2183	0	2158	52	0
1	O	2183	0	2158	43	0
1	P	2183	0	2158	49	0
1	Q	2183	0	2158	34	0
1	R	2183	0	2158	54	0
1	S	2183	0	2158	36	0
1	T	2183	0	2158	46	0
1	U	2183	0	2158	46	0
1	V	2183	0	2158	42	0
1	W	2183	0	2158	57	0
1	X	2183	0	2158	45	0
1	Y	2183	0	2158	48	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Z	2183	0	2158	34	0
1	a	2183	0	2158	42	0
1	b	2183	0	2158	34	0
1	c	2183	0	2158	36	0
1	d	2183	0	2158	39	0
1	e	2183	0	2158	51	0
1	f	2183	0	2158	46	0
1	g	2183	0	2158	53	0
1	h	2183	0	2158	42	0
1	i	2183	0	2158	41	0
1	j	2183	0	2158	37	0
1	k	2183	0	2158	49	0
1	l	2183	0	2158	53	0
1	m	2183	0	2158	46	0
1	n	2183	0	2158	46	0
1	o	2183	0	2158	58	0
1	p	2183	0	2158	55	0
1	q	2183	0	2158	43	0
1	r	2183	0	2158	33	0
1	s	2183	0	2158	40	0
1	t	2183	0	2158	39	0
1	u	2183	0	2158	39	0
1	v	2183	0	2158	41	0
1	w	2183	0	2158	48	0
1	x	2183	0	2158	47	0
1	y	2183	0	2158	56	0
1	z	2183	0	2158	47	0
All	All	130980	0	129480	2398	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 9.

All (2398) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:163:VAL:HG21	1:C:246:ILE:HD12	1.60	0.83
1:e:19:LEU:HD12	1:e:21:GLY:H	1.45	0.81
1:l:178:THR:HA	1:l:182:ILE:HD13	1.63	0.81
1:v:216:THR:HB	1:v:223:LEU:HD11	1.63	0.80
1:f:65:SER:HB2	1:f:99:VAL:HB	1.63	0.80
1:u:154:GLN:HB3	1:u:163:VAL:HG12	1.64	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:19:LEU:HD21	1:1:22:LEU:HD23	1.65	0.77
1:B:38:LEU:HD21	1:W:21:GLY:HA3	1.66	0.77
1:o:65:SER:HB2	1:o:99:VAL:HB	1.68	0.76
1:k:114:THR:HG1	1:k:278:THR:HG1	1.33	0.76
1:m:147:GLN:HE22	1:m:220:SER:HB3	1.49	0.75
1:R:84:THR:HG23	1:R:85:ARG:HG2	1.68	0.75
1:x:163:VAL:HG21	1:x:246:ILE:HD12	1.67	0.75
1:F:78:VAL:HG11	1:F:298:PRO:HB2	1.68	0.75
1:o:78:VAL:HG12	1:o:86:SER:HA	1.68	0.75
1:A:19:LEU:HG	1:A:21:GLY:H	1.49	0.75
1:6:65:SER:HB2	1:6:99:VAL:HB	1.69	0.74
1:m:244:PRO:HD2	1:m:252:PRO:HG3	1.69	0.74
1:y:274:TYR:H	1:y:296:TYR:HA	1.52	0.74
1:j:19:LEU:HD21	1:j:22:LEU:HD23	1.70	0.74
1:l:233:THR:HG23	1:l:263:PHE:HA	1.70	0.73
1:V:216:THR:HB	1:V:223:LEU:HD11	1.71	0.72
1:D:135:PRO:HD3	1:D:246:ILE:HD13	1.69	0.72
1:R:218:ASN:HD22	1:R:223:LEU:HD22	1.53	0.72
1:D:163:VAL:HG21	1:D:246:ILE:HD12	1.71	0.72
1:h:237:THR:HG22	1:h:259:VAL:HG22	1.69	0.72
1:n:176:ASN:HB2	1:n:192:ILE:HD12	1.71	0.72
1:n:240:VAL:O	1:o:124:ASN:ND2	2.23	0.72
1:m:141:GLN:NE2	1:m:177:TYR:OH	2.23	0.72
1:o:40:TYR:HA	1:o:43:ILE:HD12	1.72	0.72
1:J:141:GLN:NE2	1:J:177:TYR:OH	2.23	0.72
1:x:65:SER:HB2	1:x:99:VAL:HB	1.72	0.72
1:A:38:LEU:HD21	1:N:21:GLY:HA3	1.71	0.71
1:D:136:SER:O	1:D:140:ASN:ND2	2.23	0.71
1:g:78:VAL:HG12	1:g:86:SER:HA	1.71	0.71
1:Y:141:GLN:NE2	1:Y:177:TYR:OH	2.23	0.71
1:E:141:GLN:NE2	1:E:177:TYR:OH	2.24	0.71
1:M:155:GLN:NE2	1:N:127:GLU:O	2.24	0.71
1:z:189:PRO:HB3	1:z:232:GLN:HE21	1.56	0.71
1:k:120:ILE:HG12	1:k:267:LEU:HD12	1.71	0.70
1:m:19:LEU:HD21	1:m:22:LEU:HD13	1.72	0.70
1:U:92:THR:HA	1:U:258:GLY:HA2	1.73	0.70
1:K:154:GLN:HB3	1:K:163:VAL:HG12	1.73	0.70
1:6:40:TYR:HA	1:6:43:ILE:HD12	1.72	0.70
1:H:135:PRO:HG3	1:H:163:VAL:HG11	1.74	0.70
1:u:141:GLN:NE2	1:u:177:TYR:OH	2.24	0.70
1:C:72:GLY:HA2	1:Y:280:GLN:HE22	1.56	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:145:ASN:ND2	1:Q:222:THR:OG1	2.25	0.70
1:U:103:GLU:HG2	1:U:250:ILE:HG12	1.74	0.70
1:m:145:ASN:ND2	1:m:220:SER:OG	2.23	0.70
1:u:71:SER:O	1:u:92:THR:OG1	2.10	0.70
1:K:80:TYR:HB2	1:K:301:SER:HB3	1.73	0.69
1:R:273:GLN:NE2	1:R:296:TYR:O	2.25	0.69
1:S:80:TYR:HB2	1:S:301:SER:HB3	1.73	0.69
1:A:192:ILE:HG22	1:A:228:ALA:HA	1.74	0.69
1:2:47:LEU:HD23	1:3:37:VAL:HG21	1.75	0.69
1:2:98:GLY:O	1:4:296:TYR:OH	2.11	0.69
1:j:72:GLY:HA2	1:k:280:GLN:HE22	1.58	0.69
1:k:74:VAL:HG23	1:k:91:PHE:HB3	1.74	0.69
1:N:65:SER:HB2	1:N:99:VAL:HB	1.73	0.69
1:Y:71:SER:O	1:Y:92:THR:OG1	2.11	0.69
1:2:126:TYR:HH	1:2:237:THR:HG1	1.32	0.69
1:C:126:TYR:HH	1:C:237:THR:HG1	1.40	0.69
1:y:98:GLY:HA2	1:y:253:ALA:HB1	1.73	0.69
1:N:98:GLY:HA2	1:N:253:ALA:HB1	1.74	0.69
1:V:240:VAL:O	1:W:124:ASN:ND2	2.26	0.69
1:6:178:THR:HA	1:6:182:ILE:HD12	1.74	0.68
1:M:19:LEU:HG	1:M:21:GLY:H	1.56	0.68
1:R:79:ASN:O	1:R:83:ASN:ND2	2.26	0.68
1:l:244:PRO:HD2	1:l:252:PRO:HG3	1.75	0.68
1:t:141:GLN:NE2	1:t:177:TYR:OH	2.27	0.68
1:I:79:ASN:ND2	1:I:82:SER:O	2.26	0.68
1:6:40:TYR:HB2	1:O:287:SER:HB2	1.74	0.68
1:A:141:GLN:NE2	1:A:177:TYR:OH	2.26	0.68
1:A:156:THR:HG22	1:A:161:THR:HG23	1.76	0.68
1:z:141:GLN:NE2	1:z:177:TYR:OH	2.25	0.68
1:R:19:LEU:HD21	1:R:22:LEU:HD23	1.76	0.68
1:1:178:THR:HG22	1:1:182:ILE:HD12	1.75	0.68
1:O:138:LEU:HD21	1:O:174:ALA:HB1	1.76	0.68
1:U:193:THR:HG22	1:U:195:THR:H	1.59	0.68
1:U:244:PRO:HD2	1:U:252:PRO:HG3	1.76	0.68
1:P:80:TYR:HB2	1:P:301:SER:HB2	1.75	0.67
1:q:71:SER:O	1:q:92:THR:OG1	2.12	0.67
1:1:85:ARG:NH2	1:1:211:ASN:OD1	2.28	0.67
1:D:143:TYR:HB3	1:D:148:TYR:HA	1.76	0.67
1:q:273:GLN:NE2	1:q:297:GLN:OE1	2.27	0.67
1:i:69:THR:HG23	1:i:96:SER:HA	1.76	0.67
1:W:65:SER:HB2	1:W:99:VAL:HB	1.76	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:d:244:PRO:HD2	1:d:252:PRO:HG3	1.77	0.67
1:B:19:LEU:HG	1:B:21:GLY:H	1.60	0.67
1:N:40:TYR:HA	1:N:43:ILE:HD12	1.77	0.67
1:H:80:TYR:HB2	1:H:301:SER:HB2	1.76	0.67
1:O:204:TYR:HB3	1:O:207:LEU:HD13	1.77	0.67
1:X:237:THR:HG22	1:X:259:VAL:HG22	1.76	0.67
1:6:216:THR:HG22	1:6:225:THR:HG22	1.78	0.66
1:r:98:GLY:O	1:t:296:TYR:OH	2.13	0.66
1:B:19:LEU:HD21	1:B:22:LEU:HD13	1.75	0.66
1:k:19:LEU:HD21	1:k:22:LEU:HD23	1.78	0.66
1:D:80:TYR:HB2	1:D:301:SER:HB3	1.76	0.66
1:H:293:GLU:OE2	1:z:51:GLN:NE2	2.28	0.66
1:M:51:GLN:NE2	1:x:293:GLU:OE1	2.27	0.66
1:A:78:VAL:HG11	1:A:298:PRO:HB2	1.76	0.66
1:J:85:ARG:NH2	1:J:211:ASN:OD1	2.28	0.66
1:G:66:THR:HB	1:G:102:VAL:HG12	1.76	0.66
1:Z:282:THR:HG22	1:Z:288:PRO:HB3	1.78	0.66
1:I:69:THR:HG23	1:I:96:SER:HA	1.78	0.66
1:6:71:SER:O	1:6:92:THR:OG1	2.14	0.66
1:F:122:TYR:OH	1:F:266:ASP:OD2	2.14	0.66
1:G:71:SER:O	1:G:92:THR:OG1	2.13	0.66
1:I:141:GLN:NE2	1:I:177:TYR:OH	2.29	0.65
1:r:19:LEU:HD21	1:r:22:LEU:HD23	1.78	0.65
1:t:85:ARG:NH2	1:t:211:ASN:OD1	2.28	0.65
1:H:71:SER:O	1:H:92:THR:OG1	2.15	0.65
1:w:74:VAL:HG12	1:w:91:PHE:HB3	1.77	0.65
1:x:71:SER:O	1:x:92:THR:OG1	2.15	0.65
1:C:204:TYR:HB3	1:C:207:LEU:HD13	1.77	0.65
1:2:154:GLN:HB3	1:2:163:VAL:HG12	1.78	0.65
1:A:71:SER:O	1:A:92:THR:OG1	2.14	0.65
1:c:98:GLY:O	1:e:296:TYR:OH	2.15	0.65
1:U:147:GLN:HE22	1:U:220:SER:HB3	1.62	0.65
1:h:178:THR:HA	1:h:182:ILE:HD12	1.78	0.65
1:p:120:ILE:HG21	1:p:267:LEU:HD13	1.77	0.65
1:c:80:TYR:HB2	1:c:301:SER:HB3	1.79	0.65
1:l:241:ALA:HB3	1:l:256:VAL:HB	1.78	0.65
1:F:282:THR:HG23	1:F:288:PRO:HG3	1.78	0.65
1:e:71:SER:O	1:e:92:THR:OG1	2.14	0.65
1:N:28:LEU:HD11	1:O:22:LEU:HB2	1.79	0.65
1:4:71:SER:O	1:4:92:THR:OG1	2.15	0.64
1:2:71:SER:O	1:2:92:THR:OG1	2.14	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:38:LEU:HD21	1:x:21:GLY:HA3	1.78	0.64
1:J:47:LEU:HD23	1:K:37:VAL:HG21	1.77	0.64
1:e:135:PRO:HG3	1:e:163:VAL:HG11	1.77	0.64
1:e:141:GLN:NE2	1:e:177:TYR:OH	2.31	0.64
1:7:97:SER:OG	1:A:59:LYS:NZ	2.31	0.64
1:R:273:GLN:NE2	1:R:297:GLN:OE1	2.30	0.64
1:h:151:LEU:HA	1:h:170:TYR:HD2	1.61	0.64
1:7:137:GLU:O	1:7:141:GLN:NE2	2.31	0.64
1:L:19:LEU:HD21	1:L:22:LEU:HD13	1.79	0.64
1:e:147:GLN:NE2	1:e:220:SER:OG	2.29	0.64
1:O:252:PRO:O	1:O:255:SER:OG	2.16	0.64
1:2:79:ASN:ND2	1:2:84:THR:OG1	2.30	0.64
1:3:145:ASN:ND2	1:3:222:THR:OG1	2.30	0.64
1:B:32:ILE:HD13	1:z:57:ILE:HG12	1.80	0.64
1:H:32:ILE:HD13	1:a:57:ILE:HG12	1.80	0.64
1:p:137:GLU:O	1:p:141:GLN:NE2	2.30	0.64
1:k:237:THR:HG22	1:k:259:VAL:HG22	1.80	0.64
1:4:51:GLN:NE2	1:M:293:GLU:OE1	2.31	0.63
1:B:126:TYR:HH	1:B:237:THR:HG1	1.41	0.63
1:C:54:LYS:HG3	1:Y:45:MET:HE3	1.80	0.63
1:F:143:TYR:HB3	1:F:148:TYR:HA	1.80	0.63
1:L:189:PRO:HB3	1:L:232:GLN:HE21	1.62	0.63
1:Y:204:TYR:HB3	1:Y:207:LEU:HD13	1.80	0.63
1:m:154:GLN:HB3	1:m:163:VAL:HG12	1.80	0.63
1:y:185:VAL:HG22	1:y:187:PRO:HD2	1.80	0.63
1:D:273:GLN:H	1:D:275:GLN:HE21	1.46	0.63
1:b:132:THR:HA	1:b:247:GLY:HA2	1.80	0.63
1:c:57:ILE:HG12	1:t:32:ILE:HD13	1.81	0.63
1:e:304:VAL:HG12	1:e:305:ILE:HG12	1.80	0.63
1:n:71:SER:O	1:n:92:THR:OG1	2.16	0.63
1:3:57:ILE:HG12	1:S:32:ILE:HD13	1.80	0.63
1:C:86:SER:HB2	1:C:268:GLY:HA2	1.80	0.63
1:T:141:GLN:NE2	1:T:177:TYR:OH	2.32	0.63
1:T:154:GLN:HB3	1:T:163:VAL:HG12	1.81	0.63
1:a:145:ASN:ND2	1:a:219:ILE:O	2.31	0.63
1:v:71:SER:O	1:v:92:THR:OG1	2.17	0.63
1:e:180:SER:HB3	1:e:181:LYS:HZ3	1.64	0.63
1:l:78:VAL:HG12	1:l:86:SER:HA	1.80	0.63
1:s:19:LEU:HD21	1:s:22:LEU:HD13	1.81	0.63
1:M:106:PRO:O	1:d:155:GLN:NE2	2.32	0.63
1:i:97:SER:HB2	1:i:99:VAL:HG13	1.81	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:k:141:GLN:NE2	1:k:177:TYR:OH	2.32	0.63
1:u:70:LEU:HD22	1:u:291:ILE:HD12	1.81	0.63
1:H:51:GLN:NE2	1:a:293:GLU:OE2	2.31	0.63
1:N:135:PRO:HB3	1:N:152:VAL:HG11	1.81	0.63
1:R:131:LEU:HD21	1:R:257:ILE:HD11	1.80	0.63
1:f:80:TYR:HB2	1:f:301:SER:HB2	1.81	0.63
1:g:137:GLU:O	1:g:141:GLN:NE2	2.31	0.63
1:7:118:GLU:HG3	1:7:120:ILE:HG12	1.81	0.63
1:A:143:TYR:HB3	1:A:148:TYR:HA	1.81	0.63
1:D:38:LEU:HD21	1:o:21:GLY:HA3	1.79	0.63
1:f:127:GLU:OE2	1:f:232:GLN:NE2	2.32	0.63
1:g:135:PRO:HB3	1:g:152:VAL:HG11	1.81	0.63
1:R:74:VAL:HG23	1:R:91:PHE:HB3	1.81	0.62
1:r:145:ASN:ND2	1:r:222:THR:OG1	2.31	0.62
1:h:98:GLY:HA2	1:h:253:ALA:HB1	1.80	0.62
1:H:29:ILE:HG23	1:a:56:THR:HG21	1.80	0.62
1:l:145:ASN:ND2	1:l:220:SER:OG	2.32	0.62
1:0:71:SER:O	1:0:92:THR:OG1	2.17	0.62
1:J:156:THR:HG22	1:J:161:THR:HG22	1.82	0.62
1:i:71:SER:O	1:i:92:THR:OG1	2.14	0.62
1:G:135:PRO:HG3	1:G:163:VAL:HG11	1.82	0.62
1:c:132:THR:HA	1:c:247:GLY:HA2	1.80	0.62
1:g:296:TYR:HD2	1:g:297:GLN:HG2	1.64	0.62
1:j:71:SER:O	1:j:92:THR:OG1	2.18	0.62
1:p:132:THR:HA	1:p:247:GLY:HA2	1.79	0.62
1:S:163:VAL:HG22	1:S:246:ILE:HG13	1.81	0.62
1:f:71:SER:O	1:f:92:THR:OG1	2.16	0.62
1:y:145:ASN:ND2	1:y:222:THR:OG1	2.32	0.62
1:O:19:LEU:HG	1:O:21:GLY:H	1.65	0.62
1:n:154:GLN:HB3	1:n:163:VAL:HG12	1.82	0.62
1:p:145:ASN:ND2	1:p:222:THR:OG1	2.32	0.62
1:V:99:VAL:HG11	1:n:33:ILE:HD11	1.81	0.62
1:h:260:MET:HE3	1:h:262:LEU:HD21	1.80	0.62
1:v:240:VAL:O	1:w:124:ASN:ND2	2.33	0.62
1:3:155:GLN:NE2	1:L:127:GLU:O	2.33	0.62
1:p:110:ALA:HA	1:p:124:ASN:HD22	1.65	0.62
1:s:78:VAL:HG11	1:s:298:PRO:HB2	1.81	0.62
1:0:92:THR:HA	1:0:258:GLY:HA2	1.81	0.61
1:6:80:TYR:HB2	1:6:301:SER:HB2	1.82	0.61
1:m:181:LYS:O	1:m:184:LYS:NZ	2.26	0.61
1:5:71:SER:O	1:5:92:THR:OG1	2.18	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:237:THR:HG22	1:G:259:VAL:HG22	1.81	0.61
1:i:98:GLY:HA2	1:i:253:ALA:HB1	1.83	0.61
1:6:141:GLN:NE2	1:6:177:TYR:OH	2.33	0.61
1:C:68:LEU:HD21	1:C:102:VAL:HG11	1.80	0.61
1:L:145:ASN:ND2	1:L:222:THR:OG1	2.33	0.61
1:C:291:ILE:HG22	1:C:293:GLU:OE1	2.01	0.61
1:0:74:VAL:HG23	1:0:91:PHE:HB3	1.83	0.61
1:A:29:ILE:HG23	1:q:56:THR:HG21	1.81	0.61
1:D:85:ARG:NH2	1:D:211:ASN:OD1	2.33	0.61
1:P:78:VAL:HG12	1:P:86:SER:HA	1.81	0.61
1:Q:154:GLN:HB3	1:Q:163:VAL:HG12	1.83	0.61
1:R:172:LEU:HD21	1:R:260:MET:HE1	1.82	0.61
1:W:32:ILE:HD12	1:g:26:ILE:HB	1.83	0.61
1:w:141:GLN:OE1	1:w:141:GLN:N	2.32	0.61
1:5:142:VAL:HG21	1:5:151:LEU:HD11	1.82	0.61
1:D:98:GLY:O	1:i:296:TYR:OH	2.17	0.61
1:j:23:ASP:OD1	1:j:23:ASP:N	2.34	0.61
1:l:143:TYR:HB3	1:l:148:TYR:HA	1.82	0.61
1:U:32:ILE:HD13	1:n:57:ILE:HG12	1.82	0.61
1:0:127:GLU:OE2	1:h:153:ASN:ND2	2.30	0.61
1:F:153:ASN:ND2	1:F:164:TYR:OH	2.34	0.61
1:P:153:ASN:ND2	1:P:164:TYR:OH	2.34	0.61
1:X:67:ALA:HB3	1:X:99:VAL:HG21	1.82	0.61
1:k:211:ASN:ND2	1:k:263:PHE:O	2.34	0.61
1:k:235:ALA:HB2	1:k:261:ILE:HG22	1.83	0.61
1:n:155:GLN:NE2	1:o:127:GLU:O	2.33	0.61
1:7:237:THR:HG22	1:7:259:VAL:HG22	1.81	0.61
1:A:178:THR:HA	1:A:182:ILE:HG12	1.83	0.61
1:D:68:LEU:HD21	1:D:102:VAL:HG11	1.83	0.61
1:l:71:SER:O	1:l:92:THR:OG1	2.18	0.61
1:n:304:VAL:HG12	1:n:305:ILE:HG12	1.83	0.61
1:N:185:VAL:HG22	1:N:187:PRO:HD2	1.82	0.60
1:A:147:GLN:NE2	1:A:220:SER:OG	2.34	0.60
1:M:154:GLN:HB3	1:M:163:VAL:HG12	1.83	0.60
1:7:147:GLN:NE2	1:7:220:SER:OG	2.34	0.60
1:I:28:LEU:HD11	1:S:22:LEU:HD12	1.82	0.60
1:n:137:GLU:HG2	1:n:182:ILE:HD11	1.83	0.60
1:z:233:THR:HG23	1:z:263:PHE:HA	1.83	0.60
1:6:98:GLY:HA2	1:6:253:ALA:HB1	1.81	0.60
1:F:71:SER:O	1:F:92:THR:OG1	2.16	0.60
1:k:126:TYR:OH	1:k:237:THR:OG1	2.19	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:t:47:LEU:HD23	1:u:37:VAL:HG21	1.83	0.60
1:I:85:ARG:NH2	1:I:211:ASN:OD1	2.34	0.60
1:L:154:GLN:HB3	1:L:163:VAL:HG12	1.83	0.60
1:S:237:THR:HG22	1:S:259:VAL:HG22	1.83	0.60
1:h:19:LEU:HD21	1:h:22:LEU:HD13	1.83	0.60
1:k:147:GLN:HE22	1:k:220:SER:HB3	1.65	0.60
1:J:19:LEU:HD21	1:J:22:LEU:HD13	1.83	0.60
1:6:248:SER:OG	1:O:80:TYR:OH	2.18	0.60
1:b:154:GLN:HB3	1:b:163:VAL:HG12	1.83	0.60
1:y:19:LEU:HD23	1:y:21:GLY:H	1.67	0.60
1:z:80:TYR:HB2	1:z:301:SER:HB2	1.83	0.60
1:U:113:PHE:HB3	1:U:122:TYR:HB2	1.84	0.60
1:W:98:GLY:HA2	1:W:253:ALA:HB1	1.83	0.60
1:4:237:THR:HG22	1:4:259:VAL:HG22	1.83	0.60
1:E:118:GLU:OE1	1:E:275:GLN:NE2	2.32	0.60
1:Y:153:ASN:ND2	1:Y:164:TYR:OH	2.35	0.60
1:m:237:THR:HG22	1:m:259:VAL:HG22	1.84	0.60
1:C:71:SER:O	1:C:92:THR:OG1	2.19	0.60
1:L:80:TYR:HB2	1:L:301:SER:HB2	1.83	0.60
1:s:71:SER:O	1:s:92:THR:OG1	2.20	0.60
1:w:147:GLN:NE2	1:w:220:SER:OG	2.34	0.60
1:C:145:ASN:ND2	1:C:222:THR:OG1	2.32	0.59
1:i:154:GLN:HB3	1:i:163:VAL:HG12	1.83	0.59
1:2:163:VAL:HG22	1:2:246:ILE:HG13	1.84	0.59
1:C:141:GLN:NE2	1:C:177:TYR:OH	2.34	0.59
1:Y:296:TYR:HE2	1:p:98:GLY:HA3	1.67	0.59
1:c:296:TYR:OH	1:s:98:GLY:O	2.21	0.59
1:w:155:GLN:HE21	1:x:107:SER:HA	1.65	0.59
1:B:85:ARG:NH2	1:B:211:ASN:OD1	2.35	0.59
1:C:244:PRO:HD2	1:C:252:PRO:HG3	1.84	0.59
1:D:178:THR:HA	1:D:182:ILE:HG12	1.83	0.59
1:N:103:GLU:HG2	1:N:250:ILE:HG12	1.83	0.59
1:k:154:GLN:HB3	1:k:163:VAL:HG12	1.84	0.59
1:w:141:GLN:NE2	1:w:177:TYR:OH	2.35	0.59
1:5:141:GLN:OE1	1:5:141:GLN:N	2.34	0.59
1:D:80:TYR:HE2	1:y:245:LEU:HD23	1.67	0.59
1:F:57:ILE:HG12	1:X:32:ILE:HG21	1.84	0.59
1:F:287:SER:HA	1:X:40:TYR:HE1	1.67	0.59
1:y:178:THR:HA	1:y:182:ILE:HG12	1.84	0.59
1:Q:196:THR:HG22	1:Q:198:SER:H	1.67	0.59
1:6:66:THR:HB	1:6:102:VAL:HG12	1.84	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:198:SER:O	1:B:201:THR:OG1	2.20	0.59
1:M:71:SER:O	1:M:92:THR:OG1	2.21	0.59
1:N:71:SER:O	1:N:92:THR:OG1	2.20	0.59
1:y:58:ASN:HD22	1:y:59:LYS:HD3	1.68	0.59
1:C:78:VAL:HG11	1:C:298:PRO:HB2	1.85	0.59
1:7:29:ILE:HD12	1:E:53:ALA:HA	1.85	0.59
1:k:126:TYR:HH	1:k:237:THR:HG1	1.50	0.59
1:U:216:THR:HB	1:U:223:LEU:HD11	1.84	0.59
1:Y:132:THR:HA	1:Y:247:GLY:HA2	1.85	0.59
1:n:19:LEU:HD21	1:n:22:LEU:HD13	1.85	0.59
1:4:32:ILE:HD13	1:M:57:ILE:HG12	1.83	0.59
1:4:244:PRO:HD2	1:4:252:PRO:HG3	1.85	0.59
1:E:153:ASN:ND2	1:E:164:TYR:OH	2.35	0.59
1:G:32:ILE:HD13	1:r:57:ILE:HG12	1.83	0.59
1:G:273:GLN:NE2	1:G:297:GLN:OE1	2.36	0.59
1:y:179:LEU:HD21	1:y:189:PRO:HD2	1.85	0.59
1:0:191:TYR:HB3	1:0:229:PHE:HB2	1.83	0.58
1:A:98:GLY:O	1:r:296:TYR:OH	2.21	0.58
1:P:44:ASN:HB2	1:Q:288:PRO:HD2	1.85	0.58
1:V:61:GLU:OE2	1:W:52:LYS:NZ	2.34	0.58
1:7:94:SER:HB3	1:7:256:VAL:HA	1.84	0.58
1:E:78:VAL:HG11	1:E:298:PRO:HB2	1.85	0.58
1:F:145:ASN:HD21	1:F:222:THR:HB	1.68	0.58
1:h:241:ALA:O	1:h:255:SER:OG	2.20	0.58
1:i:237:THR:HG22	1:i:259:VAL:HG22	1.84	0.58
1:j:85:ARG:NH2	1:j:211:ASN:OD1	2.36	0.58
1:m:92:THR:HA	1:m:258:GLY:HA2	1.84	0.58
1:s:132:THR:HA	1:s:247:GLY:HA2	1.85	0.58
1:4:19:LEU:HD21	1:4:22:LEU:HD13	1.86	0.58
1:W:32:ILE:HG23	1:g:26:ILE:HG21	1.85	0.58
1:0:145:ASN:ND2	1:0:222:THR:OG1	2.30	0.58
1:1:196:THR:HG22	1:1:198:SER:H	1.67	0.58
1:4:127:GLU:O	1:K:155:GLN:NE2	2.36	0.58
1:B:118:GLU:OE1	1:B:275:GLN:NE2	2.34	0.58
1:E:27:ILE:HD13	1:p:39:ALA:HB2	1.86	0.58
1:b:86:SER:OG	1:b:270:HIS:O	2.21	0.58
1:o:71:SER:O	1:o:92:THR:OG1	2.21	0.58
1:v:163:VAL:HG22	1:v:246:ILE:HG13	1.83	0.58
1:w:78:VAL:HG12	1:w:86:SER:HA	1.83	0.58
1:F:151:LEU:HA	1:F:170:TYR:HD2	1.67	0.58
1:I:282:THR:HG22	1:I:288:PRO:HB3	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:154:GLN:HB3	1:S:163:VAL:HG12	1.85	0.58
1:Y:80:TYR:HB2	1:Y:301:SER:HB2	1.85	0.58
1:c:178:THR:HG22	1:c:182:ILE:HG13	1.86	0.58
1:w:135:PRO:HG3	1:w:163:VAL:HG11	1.85	0.58
1:3:85:ARG:NH2	1:3:211:ASN:OD1	2.36	0.58
1:P:76:TYR:HB3	1:P:303:SER:HB2	1.86	0.58
1:k:71:SER:O	1:k:92:THR:OG1	2.22	0.58
1:f:244:PRO:HD2	1:f:252:PRO:HG3	1.84	0.58
1:w:163:VAL:HG22	1:w:246:ILE:HG13	1.86	0.58
1:E:66:THR:HB	1:E:102:VAL:HG12	1.86	0.58
1:g:248:SER:HB3	1:g:250:ILE:HG12	1.86	0.58
1:i:111:ILE:HG12	1:i:281:ILE:HG12	1.86	0.58
1:3:70:LEU:HD22	1:3:291:ILE:HD12	1.86	0.58
1:6:109:THR:HG22	1:6:283:PRO:HA	1.86	0.58
1:E:98:GLY:HA2	1:E:253:ALA:HB1	1.85	0.58
1:T:74:VAL:HG23	1:T:91:PHE:HB3	1.85	0.58
1:r:71:SER:O	1:r:92:THR:OG1	2.21	0.58
1:w:71:SER:O	1:w:92:THR:OG1	2.20	0.58
1:S:141:GLN:NE2	1:S:177:TYR:OH	2.37	0.57
1:U:33:ILE:HD11	1:m:99:VAL:HG11	1.86	0.57
1:1:137:GLU:O	1:1:141:GLN:NE2	2.37	0.57
1:5:19:LEU:HD21	1:5:22:LEU:HD13	1.85	0.57
1:f:145:ASN:ND2	1:f:222:THR:OG1	2.37	0.57
1:h:98:GLY:O	1:j:296:TYR:OH	2.20	0.57
1:q:216:THR:HG22	1:q:225:THR:HG22	1.85	0.57
1:2:86:SER:OG	1:2:270:HIS:O	2.18	0.57
1:4:80:TYR:HB2	1:4:301:SER:HB2	1.86	0.57
1:F:85:ARG:NH2	1:F:211:ASN:OD1	2.37	0.57
1:Q:147:GLN:HE21	1:Q:219:ILE:HG23	1.70	0.57
1:U:143:TYR:HB3	1:U:148:TYR:HA	1.86	0.57
1:q:19:LEU:HD21	1:q:22:LEU:HD23	1.85	0.57
1:5:51:GLN:NE2	1:N:293:GLU:OE2	2.38	0.57
1:C:88:TRP:HB3	1:C:262:LEU:HD23	1.86	0.57
1:R:185:VAL:HG22	1:R:187:PRO:HD2	1.85	0.57
1:c:237:THR:HG22	1:c:259:VAL:HG22	1.86	0.57
1:j:19:LEU:HG	1:j:21:GLY:H	1.69	0.57
1:l:211:ASN:ND2	1:l:264:GLY:O	2.36	0.57
1:v:244:PRO:HD2	1:v:252:PRO:HG3	1.86	0.57
1:1:293:GLU:OE2	1:Q:51:GLN:NE2	2.36	0.57
1:E:71:SER:O	1:E:92:THR:OG1	2.22	0.57
1:R:154:GLN:HB3	1:R:163:VAL:HG12	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:33:ILE:HD11	1:s:99:VAL:HG11	1.87	0.57
1:f:43:ILE:HG23	1:p:37:VAL:HG21	1.86	0.57
1:5:154:GLN:HB3	1:5:163:VAL:HG12	1.87	0.57
1:7:132:THR:HA	1:7:247:GLY:HA2	1.85	0.57
1:U:211:ASN:HD21	1:U:268:GLY:HA3	1.69	0.57
1:1:154:GLN:HB3	1:1:163:VAL:HG12	1.85	0.57
1:3:134:SER:OG	1:3:137:GLU:OE1	2.22	0.57
1:B:296:TYR:CZ	1:g:59:LYS:HD2	2.40	0.57
1:D:137:GLU:N	1:D:137:GLU:OE2	2.37	0.57
1:P:276:THR:HG22	1:P:294:TYR:HD1	1.70	0.57
1:w:103:GLU:OE2	1:w:105:SER:N	2.38	0.57
1:1:28:LEU:HD11	1:2:22:LEU:HD12	1.87	0.57
1:R:67:ALA:O	1:R:96:SER:N	2.38	0.57
1:X:174:ALA:O	1:X:178:THR:OG1	2.22	0.57
1:w:252:PRO:O	1:w:255:SER:OG	2.23	0.57
1:1:147:GLN:HE21	1:1:220:SER:HB3	1.69	0.57
1:6:237:THR:HG22	1:6:259:VAL:HG22	1.87	0.57
1:D:153:ASN:OD1	1:D:154:GLN:N	2.38	0.57
1:M:78:VAL:HG12	1:M:86:SER:HA	1.87	0.57
1:0:111:ILE:O	1:0:124:ASN:N	2.37	0.57
1:0:111:ILE:HG12	1:0:126:TYR:HB2	1.87	0.57
1:D:111:ILE:HG12	1:D:281:ILE:HG12	1.86	0.57
1:O:158:ALA:O	1:O:160:GLN:NE2	2.38	0.57
1:V:244:PRO:HD2	1:V:252:PRO:HG3	1.87	0.57
1:A:101:SER:HB2	1:A:252:PRO:HA	1.86	0.56
1:I:296:TYR:OH	1:P:98:GLY:O	2.22	0.56
1:P:147:GLN:HE21	1:P:220:SER:HB3	1.70	0.56
1:h:198:SER:O	1:h:201:THR:OG1	2.23	0.56
1:s:101:SER:HB3	1:s:252:PRO:HA	1.86	0.56
1:6:153:ASN:ND2	1:6:164:TYR:OH	2.37	0.56
1:7:241:ALA:HB3	1:7:256:VAL:HB	1.87	0.56
1:I:154:GLN:HB3	1:I:163:VAL:HG12	1.87	0.56
1:M:141:GLN:NE2	1:M:177:TYR:OH	2.37	0.56
1:Q:237:THR:HG22	1:Q:259:VAL:HG22	1.88	0.56
1:f:244:PRO:HG2	1:f:245:LEU:HD12	1.87	0.56
1:z:274:TYR:N	1:z:295:VAL:O	2.38	0.56
1:3:216:THR:HB	1:3:223:LEU:HD11	1.86	0.56
1:B:143:TYR:HB3	1:B:148:TYR:HA	1.88	0.56
1:D:31:PHE:HE2	1:n:24:THR:HG21	1.70	0.56
1:E:145:ASN:HD21	1:E:222:THR:HB	1.70	0.56
1:L:141:GLN:HG3	1:L:177:TYR:CZ	2.40	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:233:THR:HG23	1:O:263:PHE:HA	1.85	0.56
1:T:54:LYS:HB2	1:m:41:VAL:HG21	1.88	0.56
1:W:85:ARG:NH2	1:W:211:ASN:OD1	2.38	0.56
1:a:186:SER:OG	1:a:187:PRO:HD3	2.06	0.56
1:b:295:VAL:HG22	1:b:305:ILE:HG23	1.86	0.56
1:o:273:GLN:HG2	1:o:274:TYR:CD1	2.40	0.56
1:w:74:VAL:HG23	1:w:305:ILE:HA	1.86	0.56
1:x:85:ARG:NH2	1:x:211:ASN:OD1	2.36	0.56
1:C:237:THR:HG22	1:C:259:VAL:HG22	1.88	0.56
1:U:303:SER:HB3	1:U:305:ILE:HG22	1.87	0.56
1:w:68:LEU:HD21	1:w:102:VAL:HG11	1.86	0.56
1:7:26:ILE:HA	1:7:29:ILE:HG22	1.88	0.56
1:D:237:THR:HG22	1:D:259:VAL:HG22	1.88	0.56
1:d:145:ASN:OD1	1:d:222:THR:OG1	2.23	0.56
1:e:163:VAL:HG22	1:e:246:ILE:HG13	1.87	0.56
1:Q:71:SER:O	1:Q:92:THR:OG1	2.16	0.56
1:Z:71:SER:O	1:Z:92:THR:OG1	2.19	0.56
1:h:109:THR:HG23	1:h:283:PRO:HA	1.88	0.56
1:j:233:THR:HG23	1:j:263:PHE:HA	1.87	0.56
1:u:237:THR:HG22	1:u:259:VAL:HG22	1.88	0.56
1:F:296:TYR:OH	1:X:59:LYS:NZ	2.38	0.56
1:e:266:ASP:N	1:e:266:ASP:OD1	2.39	0.56
1:j:244:PRO:HG2	1:j:245:LEU:HD12	1.86	0.56
1:p:79:ASN:O	1:p:83:ASN:ND2	2.38	0.56
1:y:186:SER:OG	1:y:187:PRO:HD3	2.06	0.56
1:C:252:PRO:O	1:C:255:SER:OG	2.22	0.56
1:O:137:GLU:O	1:O:141:GLN:NE2	2.39	0.56
1:U:114:THR:OG1	1:U:278:THR:OG1	2.21	0.56
1:r:154:GLN:HB3	1:r:163:VAL:HG12	1.88	0.56
1:1:141:GLN:HG3	1:1:177:TYR:CZ	2.40	0.56
1:2:57:ILE:HG12	1:I:32:ILE:HD13	1.88	0.56
1:6:145:ASN:HD22	1:6:219:ILE:HB	1.69	0.56
1:6:154:GLN:HB3	1:6:163:VAL:HG12	1.87	0.56
1:B:237:THR:HG22	1:B:259:VAL:HG22	1.87	0.56
1:N:154:GLN:HB3	1:N:163:VAL:HG12	1.86	0.56
1:3:244:PRO:HD2	1:3:252:PRO:HG3	1.88	0.56
1:E:178:THR:HA	1:E:182:ILE:HG12	1.88	0.56
1:Q:135:PRO:HG3	1:Q:163:VAL:HG11	1.87	0.56
1:W:64:ALA:HB2	1:o:26:ILE:HG23	1.88	0.56
1:a:237:THR:HG22	1:a:259:VAL:HG22	1.88	0.56
1:b:141:GLN:NE2	1:b:177:TYR:OH	2.30	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i:143:TYR:HB3	1:i:148:TYR:HA	1.88	0.56
1:0:111:ILE:HD12	1:0:281:ILE:HG12	1.86	0.55
1:4:240:VAL:O	1:5:124:ASN:ND2	2.36	0.55
1:M:147:GLN:HE21	1:M:220:SER:HB3	1.71	0.55
1:Q:66:THR:HG23	1:Q:102:VAL:HG22	1.87	0.55
1:W:118:GLU:OE1	1:W:275:GLN:NE2	2.39	0.55
1:y:80:TYR:O	1:y:83:ASN:ND2	2.38	0.55
1:5:293:GLU:OE1	1:L:51:GLN:NE2	2.39	0.55
1:6:63:THR:HA	1:6:286:GLY:HA2	1.88	0.55
1:B:296:TYR:CE1	1:W:98:GLY:HA3	2.41	0.55
1:E:85:ARG:NH2	1:E:211:ASN:OD1	2.39	0.55
1:P:178:THR:HA	1:P:182:ILE:HG12	1.87	0.55
1:x:80:TYR:HB2	1:x:301:SER:HB2	1.88	0.55
1:z:186:SER:OG	1:z:187:PRO:HD3	2.06	0.55
1:N:109:THR:HG23	1:N:283:PRO:HA	1.89	0.55
1:a:74:VAL:HG23	1:a:91:PHE:HB3	1.87	0.55
1:0:179:LEU:HA	1:0:183:ASP:HB3	1.88	0.55
1:A:57:ILE:HG12	1:O:32:ILE:HG21	1.88	0.55
1:C:69:THR:HG23	1:C:96:SER:HA	1.87	0.55
1:W:153:ASN:ND2	1:W:164:TYR:OH	2.40	0.55
1:g:132:THR:HA	1:g:247:GLY:HA2	1.87	0.55
1:n:198:SER:O	1:n:201:THR:OG1	2.23	0.55
1:t:196:THR:HG22	1:t:198:SER:H	1.70	0.55
1:K:70:LEU:HD22	1:K:291:ILE:HD12	1.87	0.55
1:P:145:ASN:OD1	1:P:222:THR:OG1	2.21	0.55
1:l:118:GLU:OE2	1:l:270:HIS:ND1	2.36	0.55
1:6:140:ASN:HB2	1:6:141:GLN:OE1	2.06	0.55
1:A:295:VAL:HG12	1:A:305:ILE:HG23	1.89	0.55
1:D:294:TYR:O	1:y:59:LYS:NZ	2.30	0.55
1:Q:186:SER:HB3	1:Q:187:PRO:HD3	1.88	0.55
1:Z:186:SER:OG	1:Z:187:PRO:HD3	2.06	0.55
1:b:237:THR:HG22	1:b:259:VAL:HG22	1.89	0.55
1:d:52:LYS:NZ	1:u:61:GLU:OE2	2.38	0.55
1:A:274:TYR:OH	1:O:284:ASN:ND2	2.40	0.55
1:K:273:GLN:NE2	1:K:297:GLN:OE1	2.40	0.55
1:U:252:PRO:O	1:U:255:SER:OG	2.25	0.55
1:Z:155:GLN:NE2	1:s:127:GLU:O	2.40	0.55
1:d:51:GLN:NE2	1:w:293:GLU:OE1	2.40	0.55
1:e:141:GLN:OE1	1:e:141:GLN:N	2.38	0.55
1:j:143:TYR:HB3	1:j:148:TYR:HA	1.89	0.55
1:t:69:THR:HB	1:t:96:SER:HA	1.88	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:74:VAL:HG23	1:C:91:PHE:HB3	1.89	0.55
1:s:127:GLU:OE2	1:s:232:GLN:NE2	2.39	0.55
1:2:32:ILE:HD13	1:K:57:ILE:HG12	1.89	0.55
1:C:85:ARG:NH2	1:C:211:ASN:OD1	2.39	0.55
1:e:237:THR:HG22	1:e:259:VAL:HG22	1.89	0.55
1:h:141:GLN:NE2	1:h:177:TYR:OH	2.40	0.55
1:s:141:GLN:NE2	1:s:177:TYR:OH	2.31	0.55
1:D:153:ASN:ND2	1:D:164:TYR:OH	2.40	0.55
1:J:127:GLU:OE2	1:J:232:GLN:NE2	2.40	0.55
1:P:141:GLN:NE2	1:P:177:TYR:OH	2.40	0.55
1:W:145:ASN:ND2	1:W:222:THR:OG1	2.40	0.55
1:c:295:VAL:HG12	1:c:305:ILE:HG23	1.89	0.55
1:e:155:GLN:HE22	1:f:127:GLU:HA	1.72	0.55
1:m:127:GLU:OE2	1:m:232:GLN:NE2	2.40	0.55
1:x:68:LEU:HD21	1:x:102:VAL:HG11	1.88	0.55
1:z:105:SER:HB3	1:z:108:THR:HG22	1.89	0.55
1:B:240:VAL:O	1:P:124:ASN:ND2	2.38	0.54
1:D:122:TYR:OH	1:D:266:ASP:OD2	2.25	0.54
1:W:153:ASN:OD1	1:W:154:GLN:N	2.40	0.54
1:Z:57:ILE:HG12	1:q:32:ILE:HD13	1.88	0.54
1:j:47:LEU:HD23	1:k:37:VAL:HG11	1.90	0.54
1:I:237:THR:HG22	1:I:259:VAL:HG22	1.88	0.54
1:L:137:GLU:O	1:L:141:GLN:NE2	2.41	0.54
1:P:32:ILE:HD13	1:Q:57:ILE:HG12	1.89	0.54
1:Q:141:GLN:NE2	1:Q:177:TYR:OH	2.29	0.54
1:T:244:PRO:HD2	1:T:252:PRO:HG3	1.88	0.54
1:l:237:THR:HG22	1:l:259:VAL:HG22	1.89	0.54
1:p:241:ALA:HB3	1:p:256:VAL:HB	1.88	0.54
1:y:296:TYR:HD1	1:y:297:GLN:HG2	1.72	0.54
1:0:195:THR:HG1	1:0:199:SER:HG	1.51	0.54
1:4:124:ASN:ND2	1:K:240:VAL:O	2.37	0.54
1:A:273:GLN:NE2	1:A:297:GLN:OE1	2.41	0.54
1:b:186:SER:OG	1:b:187:PRO:HD3	2.07	0.54
1:i:197:PRO:HB3	1:i:212:MET:HE1	1.89	0.54
1:p:142:VAL:HG21	1:p:151:LEU:HD11	1.89	0.54
1:r:141:GLN:NE2	1:r:177:TYR:OH	2.38	0.54
1:v:155:GLN:NE2	1:w:106:PRO:O	2.40	0.54
1:x:166:PRO:HG2	1:x:170:TYR:HD1	1.72	0.54
1:7:22:LEU:HD21	1:E:46:GLY:HA2	1.89	0.54
1:A:66:THR:HG22	1:A:100:SER:HB2	1.90	0.54
1:A:103:GLU:OE2	1:q:297:GLN:NE2	2.40	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:32:ILE:HG13	1:P:57:ILE:HG12	1.88	0.54
1:I:185:VAL:HG22	1:I:187:PRO:HD2	1.89	0.54
1:I:190:LEU:HD23	1:I:234:PHE:HZ	1.72	0.54
1:K:71:SER:O	1:K:92:THR:OG1	2.25	0.54
1:N:196:THR:HB	1:N:199:SER:HB2	1.90	0.54
1:O:274:TYR:H	1:O:296:TYR:HB3	1.73	0.54
1:X:186:SER:OG	1:X:187:PRO:HD3	2.07	0.54
1:q:154:GLN:HB3	1:q:163:VAL:HG12	1.88	0.54
1:H:237:THR:HG22	1:H:259:VAL:HG22	1.90	0.54
1:T:71:SER:O	1:T:92:THR:OG1	2.21	0.54
1:V:76:TYR:HH	1:V:86:SER:HG	1.55	0.54
1:i:47:LEU:HD23	1:j:37:VAL:HG11	1.90	0.54
1:r:135:PRO:HG3	1:r:163:VAL:HG11	1.89	0.54
1:y:137:GLU:O	1:y:141:GLN:NE2	2.34	0.54
1:B:70:LEU:HD22	1:B:291:ILE:HD12	1.89	0.54
1:E:140:ASN:HB3	1:E:141:GLN:OE1	2.08	0.54
1:a:147:GLN:NE2	1:a:220:SER:OG	2.40	0.54
1:n:78:VAL:HG12	1:n:86:SER:HA	1.90	0.54
1:t:70:LEU:HD22	1:t:291:ILE:HD12	1.89	0.54
1:u:137:GLU:OE1	1:u:137:GLU:N	2.40	0.54
1:y:67:ALA:HB3	1:y:99:VAL:HG21	1.88	0.54
1:z:134:SER:OG	1:z:137:GLU:OE1	2.26	0.54
1:O:122:TYR:OH	1:O:266:ASP:OD2	2.26	0.54
1:7:45:MET:HG3	1:x:54:LYS:HD3	1.89	0.54
1:7:284:ASN:ND2	1:E:274:TYR:OH	2.39	0.54
1:C:38:LEU:HD11	1:f:21:GLY:HA3	1.90	0.54
1:D:71:SER:O	1:D:92:THR:OG1	2.19	0.54
1:G:98:GLY:HA2	1:G:253:ALA:HB1	1.89	0.54
1:X:79:ASN:HD21	1:X:85:ARG:H	1.55	0.54
1:c:19:LEU:HG	1:c:21:GLY:H	1.73	0.54
1:c:71:SER:O	1:c:92:THR:OG1	2.21	0.54
1:w:80:TYR:HB2	1:w:301:SER:HB3	1.90	0.54
1:3:71:SER:O	1:3:92:THR:OG1	2.24	0.54
1:K:135:PRO:HG3	1:K:163:VAL:HG11	1.88	0.54
1:P:85:ARG:NH2	1:P:211:ASN:OD1	2.40	0.54
1:T:85:ARG:NH2	1:T:211:ASN:OD1	2.41	0.54
1:Z:252:PRO:HG2	1:Z:255:SER:HB3	1.90	0.54
1:1:71:SER:O	1:1:92:THR:OG1	2.25	0.54
1:7:79:ASN:HD21	1:7:85:ARG:H	1.55	0.54
1:A:145:ASN:HD21	1:A:222:THR:HB	1.72	0.54
1:H:196:THR:HG22	1:H:198:SER:H	1.73	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:32:ILE:HD13	1:d:57:ILE:HG12	1.88	0.54
1:U:204:TYR:HB3	1:U:207:LEU:HD13	1.89	0.54
1:U:209:HIS:HB3	1:l:220:SER:HA	1.89	0.54
1:l:154:GLN:HB3	1:l:163:VAL:HG12	1.89	0.54
1:6:131:LEU:HG	1:6:239:PRO:HD3	1.90	0.54
1:G:80:TYR:CE1	1:G:299:GLU:HA	2.42	0.54
1:T:80:TYR:HB2	1:T:301:SER:HB3	1.90	0.54
1:W:167:ASN:OD1	1:W:170:TYR:N	2.41	0.54
1:6:201:THR:OG1	1:6:202:GLN:NE2	2.42	0.53
1:A:85:ARG:NH2	1:A:211:ASN:OD1	2.41	0.53
1:C:61:GLU:OE2	1:Y:52:LYS:NZ	2.34	0.53
1:F:34:THR:HG22	1:O:43:ILE:HG13	1.89	0.53
1:R:76:TYR:HB3	1:R:303:SER:HB3	1.90	0.53
1:V:99:VAL:HG12	1:W:56:THR:HG22	1.89	0.53
1:j:252:PRO:O	1:j:255:SER:OG	2.24	0.53
1:r:78:VAL:HG11	1:r:298:PRO:HB2	1.89	0.53
1:4:266:ASP:N	1:4:266:ASP:OD1	2.41	0.53
1:6:26:ILE:HG23	1:N:64:ALA:HB2	1.89	0.53
1:M:102:VAL:HG13	1:M:251:ALA:HB3	1.90	0.53
1:Q:163:VAL:HG22	1:Q:246:ILE:HG13	1.89	0.53
1:R:235:ALA:HB2	1:R:261:ILE:HG23	1.91	0.53
1:X:94:SER:HB3	1:X:256:VAL:HA	1.91	0.53
1:a:126:TYR:HH	1:a:237:THR:HG1	1.55	0.53
1:i:211:ASN:ND2	1:i:263:PHE:O	2.42	0.53
1:j:110:ALA:HA	1:j:124:ASN:OD1	2.08	0.53
1:r:101:SER:HB3	1:r:252:PRO:HA	1.91	0.53
1:I:67:ALA:O	1:I:96:SER:N	2.42	0.53
1:W:83:ASN:HD22	1:W:298:PRO:HG2	1.72	0.53
1:A:237:THR:HG22	1:A:259:VAL:HG22	1.89	0.53
1:E:151:LEU:HA	1:E:170:TYR:HD2	1.73	0.53
1:J:71:SER:O	1:J:92:THR:OG1	2.25	0.53
1:d:111:ILE:HG12	1:d:281:ILE:HG12	1.89	0.53
1:g:241:ALA:HB3	1:g:256:VAL:HB	1.90	0.53
1:l:19:LEU:HD21	1:l:22:LEU:HD23	1.90	0.53
1:n:142:VAL:HG11	1:n:151:LEU:HD21	1.91	0.53
1:t:19:LEU:HD21	1:t:22:LEU:HD13	1.91	0.53
1:E:119:GLY:HA2	1:p:302:VAL:HG11	1.90	0.53
1:Y:68:LEU:HD21	1:Y:102:VAL:HG21	1.90	0.53
1:d:183:ASP:OD1	1:d:183:ASP:N	2.42	0.53
1:l:252:PRO:HG2	1:l:255:SER:HB3	1.90	0.53
1:u:163:VAL:HG22	1:u:246:ILE:HG13	1.91	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:266:ASP:N	1:u:266:ASP:OD1	2.42	0.53
1:F:245:LEU:HD23	1:F:245:LEU:H	1.74	0.53
1:V:76:TYR:OH	1:V:86:SER:OG	2.23	0.53
1:e:85:ARG:NH2	1:e:211:ASN:OD1	2.41	0.53
1:e:154:GLN:HB3	1:e:163:VAL:HG12	1.91	0.53
1:H:235:ALA:HB2	1:H:261:ILE:HG12	1.91	0.53
1:T:118:GLU:OE1	1:T:275:GLN:NE2	2.42	0.53
1:a:162:TYR:OH	1:u:273:GLN:NE2	2.39	0.53
1:j:295:VAL:HG12	1:j:305:ILE:HG23	1.90	0.53
1:r:186:SER:OG	1:r:187:PRO:HD3	2.08	0.53
1:z:118:GLU:OE1	1:z:275:GLN:NE2	2.41	0.53
1:C:92:THR:HA	1:C:258:GLY:HA2	1.90	0.53
1:E:107:SER:OG	1:p:157:ASN:ND2	2.41	0.53
1:Y:296:TYR:CE2	1:p:98:GLY:HA3	2.44	0.53
1:d:178:THR:HG22	1:d:182:ILE:HG13	1.90	0.53
1:h:76:TYR:HB3	1:h:303:SER:HB2	1.90	0.53
1:w:19:LEU:HD21	1:w:22:LEU:HD13	1.91	0.53
1:B:178:THR:HA	1:B:182:ILE:HG12	1.89	0.53
1:G:163:VAL:HG22	1:G:246:ILE:HG13	1.90	0.53
1:K:244:PRO:HD2	1:K:252:PRO:HG3	1.89	0.53
1:U:51:GLN:NE2	1:n:293:GLU:OE2	2.41	0.53
1:W:131:LEU:HG	1:W:239:PRO:HD3	1.91	0.53
1:k:181:LYS:O	1:k:184:LYS:NZ	2.32	0.53
1:m:71:SER:O	1:m:92:THR:OG1	2.25	0.53
1:n:132:THR:HA	1:n:247:GLY:HA2	1.89	0.53
1:q:273:GLN:HG2	1:q:274:TYR:HD1	1.74	0.53
1:w:186:SER:OG	1:w:187:PRO:HD3	2.09	0.53
1:A:173:LEU:HD23	1:A:192:ILE:HD12	1.90	0.53
1:R:101:SER:HB2	1:R:252:PRO:HA	1.90	0.53
1:Z:74:VAL:HG23	1:Z:91:PHE:HB3	1.91	0.53
1:m:122:TYR:OH	1:m:266:ASP:OD2	2.26	0.53
1:q:68:LEU:HD21	1:q:102:VAL:HG21	1.91	0.53
1:t:134:SER:OG	1:t:137:GLU:OE1	2.25	0.53
1:3:154:GLN:HB3	1:3:163:VAL:HG12	1.90	0.52
1:G:70:LEU:HD22	1:G:291:ILE:HD12	1.91	0.52
1:I:114:THR:HG23	1:I:278:THR:HB	1.91	0.52
1:M:237:THR:HG22	1:M:259:VAL:HG22	1.90	0.52
1:W:162:TYR:CE2	1:g:107:SER:HB3	2.45	0.52
1:t:71:SER:O	1:t:92:THR:OG1	2.26	0.52
1:v:103:GLU:OE1	1:v:105:SER:N	2.41	0.52
1:w:118:GLU:HG3	1:w:275:GLN:HE22	1.73	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:z:80:TYR:HE1	1:z:299:GLU:HA	1.74	0.52
1:1:114:THR:HG23	1:1:278:THR:HB	1.91	0.52
1:D:245:LEU:HD23	1:D:245:LEU:H	1.73	0.52
1:H:59:LYS:NZ	1:H:62:GLU:OE2	2.39	0.52
1:a:71:SER:O	1:a:92:THR:OG1	2.26	0.52
1:i:145:ASN:ND2	1:i:219:ILE:O	2.42	0.52
1:n:162:TYR:CE1	1:n:244:PRO:HB3	2.44	0.52
1:o:98:GLY:HA2	1:o:253:ALA:HB1	1.92	0.52
1:R:143:TYR:HB3	1:R:148:TYR:HA	1.91	0.52
1:b:156:THR:HG22	1:b:161:THR:HG22	1.92	0.52
1:4:154:GLN:HB3	1:4:163:VAL:HG12	1.91	0.52
1:R:188:SER:OG	1:R:190:LEU:O	2.26	0.52
1:U:175:LEU:HD22	1:U:190:LEU:HD13	1.92	0.52
1:V:19:LEU:HD11	1:X:38:LEU:HD12	1.91	0.52
1:W:162:TYR:CE1	1:W:244:PRO:HB3	2.45	0.52
1:X:118:GLU:OE2	1:X:275:GLN:NE2	2.38	0.52
1:b:266:ASP:N	1:b:266:ASP:OD1	2.42	0.52
1:f:140:ASN:HB3	1:f:141:GLN:OE1	2.09	0.52
1:z:101:SER:HB3	1:z:252:PRO:HA	1.90	0.52
1:K:86:SER:OG	1:K:270:HIS:O	2.26	0.52
1:W:155:GLN:HE21	1:g:107:SER:HA	1.73	0.52
1:Y:140:ASN:HB3	1:Y:141:GLN:OE1	2.09	0.52
1:b:70:LEU:HD22	1:b:291:ILE:HD12	1.92	0.52
1:e:199:SER:HA	1:e:202:GLN:HE22	1.75	0.52
1:f:40:TYR:HA	1:f:43:ILE:HD12	1.92	0.52
1:v:237:THR:HG22	1:v:259:VAL:HG22	1.92	0.52
1:J:41:VAL:HG21	1:a:50:THR:HG23	1.91	0.52
1:L:186:SER:OG	1:L:187:PRO:HD3	2.09	0.52
1:V:67:ALA:HB3	1:V:96:SER:HB3	1.90	0.52
1:a:180:SER:OG	1:a:181:LYS:HG2	2.10	0.52
1:b:74:VAL:HG12	1:b:91:PHE:HB3	1.90	0.52
1:o:241:ALA:HB3	1:o:256:VAL:HB	1.91	0.52
1:r:163:VAL:HG22	1:r:246:ILE:HG13	1.92	0.52
1:x:54:LYS:O	1:x:58:ASN:ND2	2.42	0.52
1:y:198:SER:O	1:y:201:THR:OG1	2.23	0.52
1:4:189:PRO:HB3	1:4:232:GLN:HE21	1.74	0.52
1:7:284:ASN:N	1:7:284:ASN:OD1	2.43	0.52
1:G:116:SER:OG	1:G:117:ALA:N	2.43	0.52
1:P:190:LEU:HD21	1:P:192:ILE:HG13	1.92	0.52
1:a:114:THR:HG23	1:a:278:THR:HB	1.92	0.52
1:p:76:TYR:OH	1:p:86:SER:OG	2.17	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:q:126:TYR:OH	1:q:237:THR:OG1	2.24	0.52
1:s:196:THR:HG22	1:s:198:SER:H	1.75	0.52
1:D:98:GLY:HA2	1:D:253:ALA:HB1	1.92	0.52
1:E:245:LEU:HD23	1:E:245:LEU:H	1.74	0.52
1:H:163:VAL:HG22	1:H:246:ILE:HG13	1.91	0.52
1:O:273:GLN:HA	1:O:296:TYR:HA	1.91	0.52
1:S:140:ASN:OD1	1:S:141:GLN:N	2.42	0.52
1:U:137:GLU:OE1	1:U:137:GLU:N	2.38	0.52
1:Y:175:LEU:HA	1:Y:178:THR:HG22	1.92	0.52
1:d:71:SER:O	1:d:92:THR:OG1	2.26	0.52
1:n:198:SER:O	1:n:202:GLN:NE2	2.41	0.52
1:1:126:TYR:OH	1:1:237:THR:OG1	2.20	0.52
1:3:153:ASN:ND2	1:3:164:TYR:OH	2.43	0.52
1:I:71:SER:O	1:I:92:THR:OG1	2.26	0.52
1:J:126:TYR:HH	1:J:237:THR:HG1	1.55	0.52
1:5:237:THR:HG22	1:5:259:VAL:HG22	1.92	0.52
1:f:282:THR:HG22	1:f:288:PRO:HB3	1.91	0.52
1:o:237:THR:HG22	1:o:259:VAL:HG22	1.91	0.52
1:t:216:THR:HB	1:t:223:LEU:HD11	1.90	0.52
1:K:237:THR:HG22	1:K:259:VAL:HG22	1.92	0.51
1:Y:98:GLY:HA2	1:Y:253:ALA:HB1	1.92	0.51
1:g:138:LEU:HD11	1:g:174:ALA:HB1	1.92	0.51
1:n:244:PRO:HD2	1:n:252:PRO:HG3	1.92	0.51
1:p:252:PRO:O	1:p:255:SER:OG	2.21	0.51
1:y:233:THR:HG23	1:y:263:PHE:HA	1.92	0.51
1:2:110:ALA:HB3	1:2:282:THR:HG23	1.92	0.51
1:3:80:TYR:HB2	1:3:301:SER:HB3	1.92	0.51
1:6:99:VAL:HG23	1:6:100:SER:H	1.75	0.51
1:F:32:ILE:HD13	1:G:57:ILE:HG12	1.92	0.51
1:S:143:TYR:HB3	1:S:148:TYR:HA	1.92	0.51
1:W:186:SER:OG	1:W:187:PRO:HD3	2.10	0.51
1:X:68:LEU:HD12	1:X:102:VAL:HG11	1.92	0.51
1:c:147:GLN:HE21	1:c:220:SER:HB3	1.74	0.51
1:f:26:ILE:H	1:f:26:ILE:HD12	1.76	0.51
1:v:103:GLU:OE1	1:v:104:LEU:N	2.43	0.51
1:1:124:ASN:ND2	1:H:240:VAL:O	2.42	0.51
1:4:142:VAL:HG22	1:4:149:LEU:HD21	1.92	0.51
1:A:53:ALA:HA	1:O:29:ILE:HD12	1.93	0.51
1:Y:20:ALA:O	1:Y:24:THR:OG1	2.20	0.51
1:Z:47:LEU:HD22	1:s:37:VAL:HG11	1.92	0.51
1:n:111:ILE:HG12	1:n:281:ILE:HG12	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:v:245:LEU:HD23	1:v:245:LEU:H	1.75	0.51
1:4:186:SER:OG	1:4:187:PRO:HD3	2.10	0.51
1:K:122:TYR:OH	1:K:266:ASP:OD2	2.29	0.51
1:Z:19:LEU:HG	1:Z:21:GLY:H	1.76	0.51
1:a:196:THR:HG22	1:a:198:SER:H	1.76	0.51
1:k:141:GLN:HG2	1:k:141:GLN:O	2.10	0.51
1:q:66:THR:HB	1:q:102:VAL:HG12	1.92	0.51
1:q:116:SER:OG	1:q:117:ALA:N	2.43	0.51
1:q:155:GLN:HE21	1:r:107:SER:HA	1.75	0.51
1:r:137:GLU:OE1	1:r:137:GLU:N	2.42	0.51
1:z:88:TRP:HB3	1:z:262:LEU:HD23	1.93	0.51
1:5:126:TYR:HH	1:5:237:THR:HG1	1.59	0.51
1:D:128:TYR:HE2	1:D:189:PRO:HG3	1.76	0.51
1:I:186:SER:OG	1:I:187:PRO:HD3	2.10	0.51
1:J:78:VAL:HG11	1:J:298:PRO:HB2	1.93	0.51
1:M:297:GLN:HE21	1:M:298:PRO:HD2	1.76	0.51
1:W:76:TYR:OH	1:W:86:SER:OG	2.20	0.51
1:X:137:GLU:O	1:X:141:GLN:NE2	2.44	0.51
1:i:186:SER:OG	1:i:187:PRO:HD3	2.11	0.51
1:p:185:VAL:HG22	1:p:187:PRO:HD2	1.92	0.51
1:y:26:ILE:HA	1:y:29:ILE:HG22	1.92	0.51
1:y:73:SER:OG	1:y:74:VAL:N	2.43	0.51
1:E:141:GLN:HG2	1:E:141:GLN:O	2.10	0.51
1:G:80:TYR:HE1	1:G:299:GLU:HA	1.76	0.51
1:G:143:TYR:HB3	1:G:148:TYR:HA	1.93	0.51
1:U:19:LEU:HD21	1:U:22:LEU:HD13	1.92	0.51
1:q:85:ARG:NH2	1:q:211:ASN:OD1	2.44	0.51
1:v:147:GLN:NE2	1:v:220:SER:OG	2.41	0.51
1:v:174:ALA:O	1:v:178:THR:HG23	2.11	0.51
1:6:118:GLU:OE2	1:6:275:GLN:NE2	2.35	0.51
1:6:245:LEU:HB3	1:O:80:TYR:OH	2.10	0.51
1:A:135:PRO:HD3	1:A:246:ILE:HD13	1.92	0.51
1:C:67:ALA:HB3	1:C:96:SER:HB3	1.93	0.51
1:S:128:TYR:HE1	1:S:189:PRO:HG3	1.75	0.51
1:Z:162:TYR:OH	1:b:273:GLN:NE2	2.37	0.51
1:s:143:TYR:HB3	1:s:148:TYR:CD2	2.46	0.51
1:H:141:GLN:OE1	1:H:141:GLN:N	2.42	0.51
1:S:67:ALA:O	1:S:96:SER:N	2.36	0.51
1:U:100:SER:OG	1:U:101:SER:N	2.44	0.51
1:y:141:GLN:H	1:y:141:GLN:CD	2.19	0.51
1:1:245:LEU:HD13	1:1:252:PRO:HB3	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:296:TYR:OH	1:z:98:GLY:O	2.28	0.51
1:3:74:VAL:HG23	1:3:91:PHE:HB3	1.93	0.51
1:g:80:TYR:O	1:g:83:ASN:ND2	2.44	0.51
1:h:273:GLN:HG3	1:h:274:TYR:CD1	2.46	0.51
1:m:78:VAL:HG12	1:m:86:SER:HA	1.93	0.51
1:0:37:VAL:HG11	1:h:47:LEU:HD23	1.93	0.51
1:E:252:PRO:O	1:E:255:SER:OG	2.23	0.51
1:K:141:GLN:HG3	1:K:177:TYR:CZ	2.46	0.51
1:L:70:LEU:HD22	1:L:291:ILE:HD12	1.93	0.51
1:L:237:THR:HG22	1:L:259:VAL:HG22	1.92	0.51
1:P:141:GLN:HG2	1:P:141:GLN:O	2.11	0.51
1:T:98:GLY:O	1:V:296:TYR:OH	2.20	0.51
1:U:78:VAL:HG22	1:U:86:SER:HA	1.92	0.51
1:a:172:LEU:HD21	1:a:262:LEU:HD11	1.93	0.51
1:m:303:SER:HB3	1:m:305:ILE:HG22	1.93	0.51
1:0:68:LEU:HD12	1:0:93:VAL:HG22	1.93	0.50
1:0:138:LEU:HD21	1:0:178:THR:HG23	1.93	0.50
1:I:149:LEU:HD12	1:I:170:TYR:HE2	1.77	0.50
1:R:198:SER:O	1:R:201:THR:OG1	2.22	0.50
1:i:163:VAL:HG22	1:i:246:ILE:HG13	1.92	0.50
1:i:178:THR:HA	1:i:182:ILE:HD13	1.93	0.50
1:l:177:TYR:CZ	1:l:181:LYS:HD3	2.46	0.50
1:l:245:LEU:HD23	1:l:245:LEU:H	1.76	0.50
1:o:55:SER:O	1:o:59:LYS:HG2	2.10	0.50
1:o:178:THR:HA	1:o:182:ILE:HG12	1.93	0.50
1:x:99:VAL:HG23	1:x:100:SER:H	1.76	0.50
1:5:74:VAL:HG22	1:5:305:ILE:HD13	1.93	0.50
1:D:79:ASN:ND2	1:D:82:SER:O	2.44	0.50
1:D:84:THR:HG23	1:D:85:ARG:HG2	1.92	0.50
1:N:68:LEU:HD21	1:N:102:VAL:HG21	1.93	0.50
1:T:122:TYR:OH	1:T:266:ASP:OD2	2.28	0.50
1:a:22:LEU:HD12	1:r:28:LEU:HD11	1.93	0.50
1:e:57:ILE:HG12	1:v:32:ILE:HD13	1.93	0.50
1:n:266:ASP:OD1	1:n:267:LEU:N	2.43	0.50
1:u:80:TYR:HB2	1:u:301:SER:HB2	1.93	0.50
1:4:153:ASN:ND2	1:4:164:TYR:OH	2.45	0.50
1:4:245:LEU:HD23	1:4:245:LEU:H	1.76	0.50
1:E:135:PRO:HD3	1:E:246:ILE:HD13	1.94	0.50
1:E:240:VAL:O	1:q:124:ASN:ND2	2.35	0.50
1:c:86:SER:OG	1:c:270:HIS:O	2.20	0.50
1:k:197:PRO:HD3	1:k:227:TYR:CZ	2.46	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:m:176:ASN:HB2	1:m:192:ILE:HD12	1.91	0.50
1:n:127:GLU:OE2	1:n:232:GLN:NE2	2.45	0.50
1:C:122:TYR:OH	1:C:266:ASP:OD2	2.30	0.50
1:E:80:TYR:HB2	1:E:301:SER:HB3	1.93	0.50
1:E:299:GLU:O	1:E:303:SER:OG	2.26	0.50
1:G:141:GLN:NE2	1:G:177:TYR:OH	2.34	0.50
1:H:122:TYR:OH	1:H:266:ASP:OD2	2.28	0.50
1:N:58:ASN:O	1:N:62:GLU:HG3	2.12	0.50
1:P:80:TYR:CE1	1:P:299:GLU:HA	2.47	0.50
1:R:70:LEU:HD22	1:R:291:ILE:HG13	1.93	0.50
1:i:77:ALA:HB3	1:i:88:TRP:H	1.76	0.50
1:z:266:ASP:N	1:z:266:ASP:OD1	2.41	0.50
1:0:135:PRO:HG3	1:0:163:VAL:HG11	1.93	0.50
1:0:279:ILE:HD12	1:0:291:ILE:HD11	1.93	0.50
1:6:85:ARG:NH2	1:6:211:ASN:OD1	2.45	0.50
1:B:54:LYS:HG3	1:P:45:MET:HE3	1.92	0.50
1:E:175:LEU:HA	1:E:178:THR:HG22	1.93	0.50
1:L:19:LEU:HG	1:L:21:GLY:H	1.76	0.50
1:N:76:TYR:HB3	1:N:303:SER:HB2	1.93	0.50
1:e:76:TYR:OH	1:e:86:SER:OG	2.27	0.50
1:e:157:ASN:HD21	1:f:107:SER:HB2	1.76	0.50
1:g:178:THR:HA	1:g:182:ILE:HG12	1.93	0.50
1:m:143:TYR:HB3	1:m:148:TYR:HA	1.94	0.50
1:n:47:LEU:HD22	1:o:37:VAL:HG11	1.94	0.50
1:0:111:ILE:HB	1:0:125:ILE:HG12	1.93	0.50
1:L:138:LEU:HD13	1:L:174:ALA:HB1	1.94	0.50
1:L:155:GLN:NE2	1:V:106:PRO:O	2.45	0.50
1:P:76:TYR:O	1:P:303:SER:N	2.39	0.50
1:T:266:ASP:N	1:T:266:ASP:OD1	2.41	0.50
1:X:26:ILE:HA	1:X:29:ILE:HG22	1.93	0.50
1:e:62:GLU:O	1:e:66:THR:HG22	2.11	0.50
1:i:126:TYR:OH	1:i:237:THR:OG1	2.22	0.50
1:o:174:ALA:O	1:o:178:THR:OG1	2.26	0.50
1:t:97:SER:O	1:t:99:VAL:N	2.45	0.50
1:w:166:PRO:HG2	1:w:170:TYR:HD2	1.76	0.50
1:z:80:TYR:CE1	1:z:299:GLU:HA	2.46	0.50
1:0:198:SER:O	1:0:201:THR:OG1	2.23	0.50
1:B:296:TYR:HE1	1:W:98:GLY:HA3	1.75	0.50
1:G:115:ALA:HB3	1:G:120:ILE:HG22	1.93	0.50
1:N:118:GLU:OE1	1:N:275:GLN:NE2	2.37	0.50
1:T:216:THR:HB	1:T:223:LEU:HD11	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:105:SER:HB3	1:U:108:THR:HG22	1.94	0.50
1:Z:244:PRO:HD2	1:Z:252:PRO:HG3	1.93	0.50
1:e:252:PRO:O	1:e:255:SER:OG	2.24	0.50
1:f:32:ILE:HD13	1:p:26:ILE:HD12	1.94	0.50
1:l:75:LEU:HD22	1:l:90:TYR:HD2	1.77	0.50
1:z:69:THR:HG22	1:z:96:SER:HA	1.93	0.50
1:2:110:ALA:HA	1:2:124:ASN:OD1	2.12	0.50
1:4:122:TYR:OH	1:4:266:ASP:OD2	2.29	0.50
1:B:71:SER:O	1:B:92:THR:OG1	2.21	0.50
1:F:20:ALA:HA	1:F:23:ASP:HB2	1.93	0.50
1:T:66:THR:HG22	1:T:100:SER:OG	2.12	0.50
1:W:62:GLU:O	1:W:66:THR:OG1	2.15	0.50
1:c:122:TYR:OH	1:c:266:ASP:OD2	2.29	0.50
1:d:273:GLN:HG3	1:d:296:TYR:O	2.12	0.50
1:v:50:THR:HG22	1:w:38:LEU:HD13	1.93	0.50
1:F:83:ASN:ND2	1:F:298:PRO:O	2.45	0.50
1:T:103:GLU:HG3	1:T:250:ILE:HG12	1.93	0.50
1:T:141:GLN:N	1:T:141:GLN:OE1	2.44	0.50
1:T:167:ASN:HB2	1:T:170:TYR:HD1	1.76	0.50
1:h:266:ASP:OD1	1:h:266:ASP:N	2.45	0.50
1:r:79:ASN:OD1	1:r:79:ASN:N	2.45	0.50
1:y:192:ILE:HD12	1:y:228:ALA:HB2	1.94	0.50
1:0:19:LEU:HG	1:0:21:GLY:H	1.77	0.49
1:A:86:SER:OG	1:A:270:HIS:O	2.26	0.49
1:Y:233:THR:HG23	1:Y:263:PHE:HA	1.93	0.49
1:d:98:GLY:O	1:x:296:TYR:OH	2.29	0.49
1:i:137:GLU:OE1	1:i:137:GLU:N	2.42	0.49
1:o:138:LEU:HD21	1:o:151:LEU:HB2	1.93	0.49
1:q:132:THR:HA	1:q:247:GLY:HA2	1.93	0.49
1:v:178:THR:HA	1:v:182:ILE:HG12	1.94	0.49
1:7:142:VAL:HG21	1:7:151:LEU:HD11	1.94	0.49
1:A:266:ASP:N	1:A:266:ASP:OD1	2.43	0.49
1:J:196:THR:HG22	1:J:198:SER:H	1.77	0.49
1:V:141:GLN:HG2	1:V:141:GLN:O	2.11	0.49
1:g:198:SER:O	1:g:201:THR:OG1	2.28	0.49
1:n:36:SER:O	1:n:40:TYR:N	2.44	0.49
1:o:273:GLN:HG3	1:o:296:TYR:O	2.12	0.49
1:q:277:ILE:N	1:q:293:GLU:O	2.38	0.49
1:y:177:TYR:CE2	1:y:181:LYS:HG3	2.47	0.49
1:z:68:LEU:HD22	1:z:93:VAL:HG12	1.95	0.49
1:P:71:SER:O	1:P:92:THR:OG1	2.22	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:237:THR:HG22	1:P:259:VAL:HG22	1.93	0.49
1:Z:244:PRO:HG2	1:Z:245:LEU:HD12	1.95	0.49
1:d:237:THR:HG22	1:d:259:VAL:HG22	1.93	0.49
1:o:73:SER:OG	1:o:74:VAL:N	2.44	0.49
1:p:80:TYR:OH	1:x:245:LEU:HB3	2.12	0.49
1:q:237:THR:HG22	1:q:259:VAL:HG22	1.93	0.49
1:u:118:GLU:OE2	1:u:275:GLN:NE2	2.46	0.49
1:v:197:PRO:O	1:v:201:THR:OG1	2.26	0.49
1:y:23:ASP:N	1:y:23:ASP:OD1	2.44	0.49
1:B:153:ASN:ND2	1:B:164:TYR:OH	2.45	0.49
1:S:71:SER:O	1:S:92:THR:OG1	2.31	0.49
1:U:71:SER:O	1:U:92:THR:OG1	2.29	0.49
1:U:77:ALA:HB3	1:U:88:TRP:H	1.77	0.49
1:r:115:ALA:HB3	1:r:120:ILE:HG22	1.94	0.49
1:l:153:ASN:HD21	1:l:155:GLN:HE22	1.60	0.49
1:N:26:ILE:H	1:N:26:ILE:HD12	1.78	0.49
1:W:100:SER:OG	1:W:101:SER:N	2.45	0.49
1:Y:116:SER:OG	1:Y:117:ALA:N	2.45	0.49
1:g:90:TYR:HB2	1:g:260:MET:HG3	1.94	0.49
1:j:61:GLU:OE1	1:k:52:LYS:NZ	2.45	0.49
1:o:99:VAL:HG23	1:o:100:SER:H	1.77	0.49
1:t:266:ASP:N	1:t:266:ASP:OD1	2.43	0.49
1:z:115:ALA:HB3	1:z:120:ILE:HG22	1.95	0.49
1:0:121:SER:O	1:h:167:ASN:ND2	2.46	0.49
1:3:65:SER:O	1:3:100:SER:OG	2.29	0.49
1:5:85:ARG:NH2	1:5:211:ASN:OD1	2.45	0.49
1:B:108:THR:HB	1:B:284:ASN:HB3	1.95	0.49
1:D:162:TYR:CE1	1:D:244:PRO:HB3	2.48	0.49
1:G:186:SER:OG	1:G:187:PRO:HD3	2.13	0.49
1:P:266:ASP:OD1	1:P:266:ASP:N	2.45	0.49
1:a:155:GLN:HE22	1:a:164:TYR:HE2	1.60	0.49
1:l:66:THR:HB	1:l:102:VAL:HG12	1.94	0.49
1:n:162:TYR:CE2	1:o:107:SER:HB2	2.47	0.49
1:w:266:ASP:N	1:w:266:ASP:OD1	2.45	0.49
1:0:113:PHE:O	1:0:122:TYR:N	2.45	0.49
1:6:296:TYR:OH	1:L:98:GLY:O	2.29	0.49
1:D:294:TYR:H	1:y:59:LYS:HZ2	1.60	0.49
1:J:235:ALA:HB2	1:J:261:ILE:HG12	1.95	0.49
1:L:73:SER:HB2	1:L:304:VAL:HG23	1.94	0.49
1:Q:252:PRO:O	1:Q:255:SER:OG	2.26	0.49
1:R:112:SER:HB2	1:R:280:GLN:HE21	1.76	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:39:ALA:O	1:X:43:ILE:HG22	2.13	0.49
1:c:240:VAL:O	1:v:124:ASN:ND2	2.42	0.49
1:y:20:ALA:O	1:y:24:THR:OG1	2.19	0.49
1:y:252:PRO:HG2	1:y:255:SER:HB3	1.93	0.49
1:B:78:VAL:HG22	1:B:86:SER:HA	1.93	0.49
1:G:273:GLN:HG2	1:G:274:TYR:CD1	2.48	0.49
1:H:98:GLY:O	1:J:296:TYR:OH	2.28	0.49
1:K:196:THR:HG22	1:K:198:SER:H	1.76	0.49
1:U:136:SER:OG	1:U:137:GLU:OE1	2.23	0.49
1:b:71:SER:O	1:b:92:THR:OG1	2.25	0.49
1:c:244:PRO:HD2	1:c:252:PRO:HG3	1.95	0.49
1:n:76:TYR:HD1	1:n:89:ILE:HG12	1.77	0.49
1:o:138:LEU:HD22	1:o:152:VAL:HG23	1.93	0.49
1:t:118:GLU:HG2	1:t:270:HIS:ND1	2.28	0.49
1:0:217:LEU:HG	1:0:219:ILE:HD11	1.95	0.49
1:4:49:VAL:HG23	1:K:61:GLU:HG3	1.94	0.49
1:4:183:ASP:OD1	1:4:183:ASP:N	2.42	0.49
1:B:96:SER:OG	1:B:97:SER:N	2.46	0.49
1:S:114:THR:HG23	1:S:278:THR:HB	1.95	0.49
1:X:67:ALA:HB1	1:X:96:SER:OG	2.12	0.49
1:Y:186:SER:OG	1:Y:187:PRO:HD3	2.13	0.49
1:h:273:GLN:HE22	1:h:297:GLN:HA	1.77	0.49
1:i:141:GLN:NE2	1:i:177:TYR:OH	2.45	0.49
1:p:88:TRP:HB3	1:p:262:LEU:HD23	1.93	0.49
1:r:214:THR:HG22	1:r:227:TYR:HD2	1.78	0.49
1:w:62:GLU:O	1:w:66:THR:HG22	2.13	0.49
1:0:68:LEU:HD21	1:0:102:VAL:HG21	1.94	0.49
1:0:178:THR:HA	1:0:182:ILE:HG12	1.94	0.49
1:D:78:VAL:HG22	1:D:86:SER:HA	1.95	0.49
1:F:285:ILE:HD13	1:G:296:TYR:HE2	1.78	0.49
1:h:145:ASN:OD1	1:h:222:THR:OG1	2.30	0.49
1:0:160:GLN:NE2	1:0:162:TYR:OH	2.40	0.48
1:4:79:ASN:OD1	1:4:79:ASN:N	2.44	0.48
1:I:141:GLN:OE1	1:I:141:GLN:N	2.46	0.48
1:N:52:LYS:O	1:N:56:THR:OG1	2.23	0.48
1:S:137:GLU:OE1	1:S:137:GLU:N	2.46	0.48
1:S:245:LEU:HD23	1:S:245:LEU:H	1.77	0.48
1:V:162:TYR:CD2	1:W:107:SER:HB2	2.48	0.48
1:W:28:LEU:O	1:W:32:ILE:HG12	2.13	0.48
1:b:19:LEU:HD21	1:b:22:LEU:HG	1.95	0.48
1:e:126:TYR:OH	1:e:237:THR:OG1	2.22	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:32:ILE:HD13	1:p:26:ILE:HB	1.95	0.48
1:f:99:VAL:HG23	1:f:100:SER:H	1.78	0.48
1:o:186:SER:OG	1:o:187:PRO:HD3	2.13	0.48
1:p:118:GLU:OE2	1:p:275:GLN:NE2	2.46	0.48
1:u:66:THR:HG22	1:u:100:SER:OG	2.13	0.48
1:v:141:GLN:OE1	1:v:141:GLN:N	2.45	0.48
1:2:273:GLN:OE1	1:2:297:GLN:NE2	2.46	0.48
1:J:266:ASP:N	1:J:266:ASP:OD1	2.45	0.48
1:M:140:ASN:HB3	1:M:141:GLN:OE1	2.13	0.48
1:V:43:ILE:HA	1:W:34:THR:HG22	1.95	0.48
1:W:282:THR:HA	1:W:288:PRO:HB3	1.95	0.48
1:c:282:THR:HG22	1:c:288:PRO:HB3	1.96	0.48
1:e:118:GLU:OE2	1:e:275:GLN:NE2	2.42	0.48
1:k:68:LEU:HD21	1:k:102:VAL:HG11	1.95	0.48
1:m:216:THR:HB	1:m:223:LEU:HD11	1.95	0.48
1:s:43:ILE:O	1:s:47:LEU:HG	2.13	0.48
1:s:153:ASN:ND2	1:s:164:TYR:OH	2.45	0.48
1:0:212:MET:HE1	1:0:228:ALA:H	1.78	0.48
1:2:96:SER:OG	1:2:97:SER:N	2.45	0.48
1:G:111:ILE:HG13	1:G:126:TYR:HB2	1.94	0.48
1:P:143:TYR:HB3	1:P:148:TYR:HA	1.94	0.48
1:T:137:GLU:OE1	1:T:137:GLU:N	2.43	0.48
1:Z:86:SER:HB3	1:Z:263:PHE:HD2	1.79	0.48
1:k:252:PRO:O	1:k:255:SER:OG	2.28	0.48
1:n:162:TYR:HE2	1:o:107:SER:HB2	1.78	0.48
1:0:244:PRO:HD2	1:0:252:PRO:HG3	1.94	0.48
1:R:114:THR:OG1	1:R:278:THR:OG1	2.28	0.48
1:c:154:GLN:HB3	1:c:163:VAL:HG12	1.95	0.48
1:o:280:GLN:OE1	1:o:290:THR:OG1	2.27	0.48
1:0:116:SER:OG	1:0:275:GLN:OE1	2.30	0.48
1:E:144:ALA:HB1	1:E:224:VAL:HG11	1.94	0.48
1:U:234:PHE:O	1:U:262:LEU:N	2.46	0.48
1:Y:138:LEU:HD13	1:Y:174:ALA:HB1	1.96	0.48
1:b:163:VAL:HG22	1:b:246:ILE:HG13	1.95	0.48
1:d:266:ASP:N	1:d:266:ASP:OD1	2.46	0.48
1:m:186:SER:OG	1:m:187:PRO:HD3	2.13	0.48
1:n:137:GLU:OE1	1:n:177:TYR:OH	2.31	0.48
1:t:19:LEU:HG	1:t:21:GLY:H	1.78	0.48
1:x:145:ASN:ND2	1:x:220:SER:OG	2.47	0.48
1:2:252:PRO:HG2	1:2:255:SER:HB3	1.94	0.48
1:6:54:LYS:HE2	1:X:48:PHE:CD2	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:GLU:OE1	1:A:118:GLU:N	2.46	0.48
1:A:296:TYR:CE1	1:N:98:GLY:HA3	2.47	0.48
1:B:212:MET:HA	1:B:228:ALA:O	2.13	0.48
1:D:162:TYR:CE2	1:h:107:SER:HB2	2.49	0.48
1:M:85:ARG:NH2	1:M:211:ASN:OD1	2.43	0.48
1:R:111:ILE:HG22	1:R:126:TYR:HB2	1.95	0.48
1:R:167:ASN:HB3	1:R:170:TYR:CD1	2.49	0.48
1:e:52:LYS:O	1:e:56:THR:HG23	2.13	0.48
1:l:175:LEU:HD22	1:l:190:LEU:HD13	1.95	0.48
1:l:181:LYS:HG3	1:l:182:ILE:HD12	1.94	0.48
1:w:103:GLU:OE2	1:w:104:LEU:N	2.46	0.48
1:3:51:GLN:NE2	1:4:293:GLU:OE2	2.43	0.48
1:M:62:GLU:O	1:M:66:THR:HG22	2.13	0.48
1:P:68:LEU:HD21	1:P:102:VAL:HG21	1.96	0.48
1:T:188:SER:OG	1:T:190:LEU:O	2.29	0.48
1:Z:114:THR:HG23	1:Z:278:THR:HB	1.96	0.48
1:d:124:ASN:ND2	1:u:240:VAL:O	2.46	0.48
1:m:126:TYR:HH	1:m:237:THR:HG1	1.57	0.48
1:6:68:LEU:HD21	1:6:102:VAL:HG21	1.95	0.48
1:C:135:PRO:HD3	1:C:246:ILE:HD13	1.96	0.48
1:I:140:ASN:HB2	1:I:141:GLN:OE1	2.14	0.48
1:K:98:GLY:O	1:M:296:TYR:OH	2.23	0.48
1:P:171:ALA:O	1:P:175:LEU:N	2.44	0.48
1:S:132:THR:HA	1:S:247:GLY:HA2	1.96	0.48
1:V:19:LEU:HG	1:V:21:GLY:H	1.79	0.48
1:g:73:SER:OG	1:g:74:VAL:N	2.47	0.48
1:o:291:ILE:HG22	1:o:293:GLU:OE2	2.13	0.48
1:o:303:SER:OG	1:o:304:VAL:N	2.46	0.48
1:z:19:LEU:HD21	1:z:22:LEU:HD23	1.96	0.48
1:g:28:LEU:O	1:g:32:ILE:HG12	2.14	0.48
1:p:71:SER:OG	1:p:72:GLY:N	2.47	0.48
1:u:19:LEU:HD21	1:u:22:LEU:HG	1.96	0.48
1:5:73:SER:HB3	1:5:304:VAL:HG13	1.96	0.48
1:L:71:SER:O	1:L:71:SER:OG	2.32	0.48
1:S:252:PRO:O	1:S:255:SER:OG	2.29	0.48
1:V:104:LEU:HA	1:V:109:THR:HG21	1.96	0.48
1:X:76:TYR:OH	1:X:86:SER:OG	2.28	0.48
1:b:68:LEU:HD21	1:b:102:VAL:HG21	1.96	0.48
1:c:216:THR:HB	1:c:223:LEU:HD21	1.95	0.48
1:i:90:TYR:HD1	1:i:260:MET:HB2	1.78	0.48
1:l:266:ASP:N	1:l:266:ASP:OD1	2.46	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:w:98:GLY:HA2	1:w:253:ALA:HB1	1.94	0.48
1:x:197:PRO:HD3	1:x:227:TYR:CZ	2.49	0.48
1:1:68:LEU:HD21	1:1:102:VAL:HG11	1.96	0.47
1:J:32:ILE:HD13	1:u:57:ILE:HG12	1.96	0.47
1:N:255:SER:OG	1:N:256:VAL:N	2.46	0.47
1:V:293:GLU:OE1	1:m:51:GLN:NE2	2.42	0.47
1:e:80:TYR:HB2	1:e:301:SER:HB3	1.95	0.47
1:y:266:ASP:OD1	1:y:266:ASP:N	2.45	0.47
1:z:111:ILE:HG12	1:z:281:ILE:HG12	1.96	0.47
1:2:66:THR:HB	1:2:102:VAL:HG12	1.96	0.47
1:B:19:LEU:HA	1:I:20:ALA:HB2	1.95	0.47
1:E:143:TYR:HB3	1:E:148:TYR:HA	1.96	0.47
1:H:273:GLN:NE2	1:H:297:GLN:OE1	2.47	0.47
1:T:57:ILE:HG12	1:k:32:ILE:HG13	1.96	0.47
1:e:80:TYR:CE1	1:e:299:GLU:HA	2.49	0.47
1:h:71:SER:O	1:h:92:THR:OG1	2.23	0.47
1:h:140:ASN:HB2	1:h:141:GLN:OE1	2.14	0.47
1:l:126:TYR:CE1	1:l:237:THR:HG23	2.48	0.47
1:t:235:ALA:HB2	1:t:261:ILE:HG12	1.96	0.47
1:0:111:ILE:H	1:0:124:ASN:HA	1.79	0.47
1:0:131:LEU:HD22	1:0:239:PRO:HD3	1.95	0.47
1:4:273:GLN:HG3	1:4:296:TYR:O	2.14	0.47
1:B:136:SER:OG	1:B:137:GLU:OE2	2.32	0.47
1:H:266:ASP:OD1	1:H:266:ASP:N	2.45	0.47
1:W:67:ALA:O	1:W:96:SER:N	2.46	0.47
1:X:71:SER:OG	1:X:72:GLY:N	2.46	0.47
1:Y:118:GLU:OE2	1:Y:275:GLN:NE2	2.43	0.47
1:d:40:TYR:CZ	1:w:288:PRO:HD3	2.50	0.47
1:h:279:ILE:HB	1:h:291:ILE:HD12	1.95	0.47
1:r:53:ALA:O	1:r:57:ILE:HG13	2.14	0.47
1:s:155:GLN:NE2	1:t:127:GLU:O	2.47	0.47
1:w:245:LEU:HD23	1:w:245:LEU:H	1.78	0.47
1:A:122:TYR:OH	1:A:266:ASP:OD2	2.32	0.47
1:J:155:GLN:NE2	1:K:127:GLU:O	2.47	0.47
1:i:235:ALA:HB2	1:i:261:ILE:HG12	1.97	0.47
1:v:28:LEU:O	1:v:32:ILE:HG13	2.15	0.47
1:w:52:LYS:O	1:w:56:THR:HG23	2.15	0.47
1:x:52:LYS:O	1:x:56:THR:HG23	2.14	0.47
1:z:197:PRO:O	1:z:201:THR:HG23	2.15	0.47
1:1:122:TYR:OH	1:1:266:ASP:OD2	2.32	0.47
1:2:183:ASP:OD1	1:2:183:ASP:N	2.41	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:VAL:O	1:B:301:SER:HA	2.15	0.47
1:E:32:ILE:HG13	1:Y:57:ILE:HG12	1.96	0.47
1:F:220:SER:O	1:F:220:SER:OG	2.30	0.47
1:J:295:VAL:HG12	1:J:305:ILE:HG23	1.95	0.47
1:L:137:GLU:OE1	1:L:137:GLU:N	2.45	0.47
1:M:167:ASN:OD1	1:M:169:TYR:N	2.44	0.47
1:O:71:SER:OG	1:O:94:SER:OG	2.19	0.47
1:P:241:ALA:HB2	1:i:110:ALA:HB2	1.97	0.47
1:S:266:ASP:OD1	1:S:266:ASP:N	2.48	0.47
1:T:166:PRO:O	1:T:167:ASN:ND2	2.48	0.47
1:U:125:ILE:O	1:U:235:ALA:N	2.48	0.47
1:f:99:VAL:HG23	1:f:100:SER:N	2.29	0.47
1:f:188:SER:OG	1:f:190:LEU:O	2.32	0.47
1:v:142:VAL:HG22	1:v:149:LEU:HD21	1.97	0.47
1:0:154:GLN:HB3	1:0:163:VAL:HG12	1.94	0.47
1:2:120:ILE:HG12	1:2:267:LEU:HD13	1.94	0.47
1:5:62:GLU:O	1:5:66:THR:HG22	2.14	0.47
1:7:235:ALA:HB2	1:7:261:ILE:HG12	1.96	0.47
1:A:68:LEU:HD11	1:A:104:LEU:HD21	1.96	0.47
1:F:197:PRO:O	1:F:201:THR:HG23	2.15	0.47
1:W:297:GLN:HE22	1:n:284:ASN:HD22	1.63	0.47
1:Y:114:THR:HG22	1:Y:121:SER:HA	1.96	0.47
1:g:155:GLN:HE22	1:g:164:TYR:HE2	1.61	0.47
1:k:186:SER:OG	1:k:187:PRO:HD3	2.15	0.47
1:u:97:SER:O	1:u:99:VAL:N	2.41	0.47
1:z:217:LEU:HD23	1:z:219:ILE:HD11	1.96	0.47
1:0:136:SER:OG	1:0:137:GLU:OE2	2.29	0.47
1:0:179:LEU:HD21	1:0:189:PRO:HD2	1.97	0.47
1:1:78:VAL:HG11	1:1:298:PRO:HB2	1.96	0.47
1:3:43:ILE:O	1:3:47:LEU:HG	2.14	0.47
1:4:99:VAL:HG23	1:4:100:SER:H	1.80	0.47
1:5:288:PRO:HD2	1:L:44:ASN:HB2	1.96	0.47
1:A:212:MET:HE3	1:A:212:MET:HB3	1.82	0.47
1:B:296:TYR:CE2	1:g:59:LYS:HD2	2.50	0.47
1:C:233:THR:HG23	1:C:263:PHE:HA	1.97	0.47
1:F:128:TYR:CE1	1:F:189:PRO:HG3	2.50	0.47
1:H:147:GLN:HE21	1:H:219:ILE:HG23	1.79	0.47
1:J:272:PHE:CG	1:J:277:ILE:HD11	2.50	0.47
1:N:184:LYS:H	1:N:184:LYS:HD2	1.79	0.47
1:U:123:SER:OG	1:l:166:PRO:O	2.24	0.47
1:U:211:ASN:HD22	1:U:264:GLY:C	2.23	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:166:PRO:O	1:W:123:SER:OG	2.27	0.47
1:W:266:ASP:OD1	1:W:266:ASP:N	2.48	0.47
1:X:99:VAL:HG23	1:X:100:SER:N	2.30	0.47
1:Y:296:TYR:OH	1:p:98:GLY:O	2.21	0.47
1:b:183:ASP:OD2	1:b:183:ASP:N	2.43	0.47
1:e:245:LEU:HD23	1:e:245:LEU:H	1.78	0.47
1:g:138:LEU:O	1:g:138:LEU:HD23	2.14	0.47
1:h:210:ASP:HB2	1:h:229:PHE:HB3	1.96	0.47
1:l:210:ASP:OD2	1:l:231:ASN:HB3	2.14	0.47
1:o:105:SER:O	1:o:109:THR:HG22	2.14	0.47
1:q:118:GLU:N	1:q:118:GLU:OE2	2.47	0.47
1:u:40:TYR:CZ	1:v:288:PRO:HD3	2.50	0.47
1:v:135:PRO:HG3	1:v:163:VAL:HG11	1.96	0.47
1:v:252:PRO:O	1:v:255:SER:OG	2.27	0.47
1:y:49:VAL:HA	1:y:52:LYS:HB3	1.97	0.47
1:1:252:PRO:HG2	1:1:255:SER:HB3	1.97	0.47
1:7:32:ILE:HG21	1:E:57:ILE:HG12	1.96	0.47
1:A:212:MET:HA	1:A:228:ALA:O	2.15	0.47
1:S:196:THR:HG22	1:S:198:SER:H	1.79	0.47
1:W:296:TYR:OH	1:m:98:GLY:O	2.29	0.47
1:h:130:LEU:HD12	1:h:238:TYR:HB3	1.97	0.47
1:l:103:GLU:OE2	1:l:284:ASN:ND2	2.45	0.47
1:w:154:GLN:HB3	1:w:163:VAL:HG12	1.97	0.47
1:2:51:GLN:NE2	1:K:293:GLU:OE2	2.31	0.47
1:e:140:ASN:HB2	1:e:141:GLN:OE1	2.15	0.47
1:g:166:PRO:HG2	1:g:170:TYR:HD2	1.79	0.47
1:k:80:TYR:HB2	1:k:301:SER:HB2	1.96	0.47
1:o:170:TYR:HE1	1:o:217:LEU:HD21	1.79	0.47
1:x:237:THR:HG22	1:x:259:VAL:HG22	1.97	0.47
1:y:70:LEU:HD23	1:y:71:SER:N	2.30	0.47
1:0:220:SER:HA	1:R:209:HIS:HB3	1.96	0.47
1:2:19:LEU:HG	1:2:21:GLY:H	1.80	0.47
1:6:96:SER:OG	1:6:97:SER:N	2.47	0.47
1:C:108:THR:HG22	1:C:284:ASN:HB3	1.97	0.47
1:D:19:LEU:HB2	1:j:23:ASP:OD2	2.15	0.47
1:Q:77:ALA:HB3	1:Q:88:TRP:H	1.79	0.47
1:R:73:SER:OG	1:R:74:VAL:N	2.48	0.47
1:c:266:ASP:OD1	1:c:266:ASP:N	2.45	0.47
1:e:241:ALA:HB2	1:f:110:ALA:HB2	1.96	0.47
1:g:274:TYR:H	1:g:296:TYR:HA	1.80	0.47
1:o:19:LEU:HD12	1:o:22:LEU:HD13	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:t:254:GLY:O	1:v:274:TYR:OH	2.28	0.47
1:w:140:ASN:HB3	1:w:141:GLN:OE1	2.15	0.47
1:4:135:PRO:HG3	1:4:163:VAL:HG11	1.97	0.46
1:C:68:LEU:HD23	1:C:95:PRO:HA	1.97	0.46
1:L:57:ILE:HG12	1:T:32:ILE:HD13	1.97	0.46
1:N:88:TRP:HZ3	1:N:90:TYR:HB3	1.80	0.46
1:R:162:TYR:OH	1:l:273:GLN:NE2	2.48	0.46
1:T:25:ALA:O	1:T:29:ILE:HG13	2.15	0.46
1:U:108:THR:OG1	1:U:284:ASN:ND2	2.48	0.46
1:Y:80:TYR:CE1	1:Y:299:GLU:HA	2.50	0.46
1:f:59:LYS:O	1:f:63:THR:HG23	2.15	0.46
1:o:75:LEU:O	1:o:89:ILE:HG13	2.15	0.46
1:u:88:TRP:HB3	1:u:262:LEU:HD23	1.97	0.46
1:6:51:GLN:NE2	1:O:305:ILE:HD11	2.29	0.46
1:7:79:ASN:O	1:7:83:ASN:ND2	2.48	0.46
1:7:105:SER:O	1:7:109:THR:HG22	2.15	0.46
1:D:294:TYR:H	1:y:59:LYS:NZ	2.13	0.46
1:G:167:ASN:HB3	1:G:170:TYR:HD2	1.79	0.46
1:G:211:ASN:OD1	1:G:212:MET:N	2.43	0.46
1:L:135:PRO:HG3	1:L:163:VAL:HG11	1.97	0.46
1:N:138:LEU:HD12	1:N:151:LEU:HD12	1.96	0.46
1:P:252:PRO:O	1:P:255:SER:OG	2.19	0.46
1:R:280:GLN:HA	1:R:289:LEU:O	2.16	0.46
1:V:56:THR:HG21	1:m:29:ILE:HG23	1.98	0.46
1:X:252:PRO:O	1:X:255:SER:OG	2.22	0.46
1:a:137:GLU:O	1:a:141:GLN:NE2	2.49	0.46
1:f:52:LYS:O	1:f:56:THR:HG23	2.15	0.46
1:g:144:ALA:HB2	1:g:149:LEU:HD22	1.97	0.46
1:j:188:SER:OG	1:j:190:LEU:O	2.32	0.46
1:p:149:LEU:HD23	1:p:149:LEU:H	1.80	0.46
1:q:264:GLY:O	1:q:268:GLY:N	2.42	0.46
1:s:118:GLU:HB2	1:s:120:ILE:HG22	1.96	0.46
1:0:147:GLN:HE22	1:0:220:SER:HB3	1.80	0.46
1:2:244:PRO:HD2	1:2:252:PRO:HG3	1.98	0.46
1:A:62:GLU:O	1:A:66:THR:HG23	2.16	0.46
1:C:216:THR:O	1:C:217:LEU:HD23	2.15	0.46
1:K:40:TYR:CZ	1:d:288:PRO:HD3	2.50	0.46
1:N:216:THR:O	1:N:217:LEU:HD23	2.16	0.46
1:O:186:SER:OG	1:O:187:PRO:HD3	2.16	0.46
1:X:111:ILE:O	1:X:125:ILE:HG12	2.15	0.46
1:d:282:THR:HB	1:d:288:PRO:HB3	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:g:152:VAL:HG22	1:g:165:TYR:CZ	2.50	0.46
1:o:145:ASN:ND2	1:o:220:SER:OG	2.49	0.46
1:q:197:PRO:O	1:q:201:THR:HG23	2.16	0.46
1:s:180:SER:OG	1:s:181:LYS:HG2	2.15	0.46
1:x:99:VAL:HG23	1:x:100:SER:N	2.30	0.46
1:2:128:TYR:CE2	1:2:189:PRO:HG3	2.50	0.46
1:C:31:PHE:HZ	1:e:24:THR:HG21	1.80	0.46
1:C:197:PRO:HB3	1:C:212:MET:HE1	1.97	0.46
1:F:212:MET:HA	1:F:228:ALA:O	2.15	0.46
1:G:47:LEU:HD23	1:H:37:VAL:HG11	1.97	0.46
1:J:163:VAL:HG22	1:J:246:ILE:HG13	1.97	0.46
1:R:133:VAL:HG11	1:R:178:THR:HG21	1.97	0.46
1:W:54:LYS:NZ	1:W:58:ASN:HD21	2.13	0.46
1:a:66:THR:HB	1:a:102:VAL:HG12	1.98	0.46
1:q:78:VAL:HG11	1:q:298:PRO:HB2	1.97	0.46
1:q:111:ILE:HG12	1:q:281:ILE:HG12	1.98	0.46
1:u:186:SER:OG	1:u:187:PRO:HD3	2.15	0.46
1:v:88:TRP:HB3	1:v:262:LEU:HD23	1.98	0.46
1:w:79:ASN:OD1	1:w:79:ASN:N	2.45	0.46
1:y:23:ASP:O	1:y:27:ILE:HG13	2.15	0.46
1:A:73:SER:HB3	1:A:304:VAL:HG13	1.97	0.46
1:B:105:SER:O	1:B:109:THR:HG22	2.16	0.46
1:G:80:TYR:HB2	1:G:301:SER:HB2	1.98	0.46
1:G:197:PRO:O	1:G:201:THR:HG23	2.15	0.46
1:I:19:LEU:HD21	1:I:22:LEU:HG	1.98	0.46
1:a:70:LEU:HD22	1:a:291:ILE:HD12	1.97	0.46
1:a:244:PRO:HG2	1:a:245:LEU:HD12	1.97	0.46
1:d:19:LEU:HD21	1:d:22:LEU:HD13	1.98	0.46
1:d:245:LEU:HD23	1:d:245:LEU:H	1.80	0.46
1:e:186:SER:OG	1:e:187:PRO:HD3	2.15	0.46
1:t:66:THR:HB	1:t:102:VAL:HG12	1.97	0.46
1:2:73:SER:OG	1:2:74:VAL:N	2.49	0.46
1:4:40:TYR:CZ	1:M:288:PRO:HD3	2.51	0.46
1:M:80:TYR:CE1	1:M:299:GLU:HA	2.51	0.46
1:Q:80:TYR:HB2	1:Q:301:SER:HB2	1.97	0.46
1:S:88:TRP:HB3	1:S:262:LEU:HD23	1.97	0.46
1:V:252:PRO:O	1:V:255:SER:OG	2.31	0.46
1:W:207:LEU:HD22	1:W:229:PHE:HD2	1.80	0.46
1:X:132:THR:HA	1:X:247:GLY:HA2	1.97	0.46
1:a:86:SER:OG	1:a:270:HIS:O	2.22	0.46
1:d:141:GLN:HG3	1:d:177:TYR:CZ	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:288:PRO:HD3	1:w:40:TYR:CZ	2.51	0.46
1:g:273:GLN:HA	1:g:296:TYR:HA	1.98	0.46
1:h:136:SER:OG	1:h:137:GLU:OE1	2.27	0.46
1:j:110:ALA:HB3	1:j:282:THR:HG23	1.97	0.46
1:y:19:LEU:HD22	1:y:22:LEU:H	1.80	0.46
1:1:167:ASN:N	1:1:167:ASN:OD1	2.48	0.46
1:1:174:ALA:O	1:1:178:THR:HG23	2.16	0.46
1:3:62:GLU:O	1:3:66:THR:OG1	2.25	0.46
1:C:131:LEU:HD23	1:C:239:PRO:HD3	1.98	0.46
1:H:78:VAL:HG23	1:H:85:ARG:O	2.15	0.46
1:I:163:VAL:HG22	1:I:246:ILE:HG13	1.96	0.46
1:R:131:LEU:HD22	1:R:239:PRO:HD3	1.98	0.46
1:f:266:ASP:OD1	1:f:266:ASP:N	2.48	0.46
1:i:252:PRO:O	1:i:255:SER:OG	2.30	0.46
1:r:237:THR:HG22	1:r:259:VAL:HG22	1.96	0.46
1:t:154:GLN:HB3	1:t:163:VAL:HG12	1.97	0.46
1:x:40:TYR:HA	1:x:43:ILE:HD12	1.98	0.46
1:3:69:THR:HB	1:3:96:SER:HA	1.97	0.46
1:7:87:TYR:HB3	1:7:88:TRP:CD1	2.51	0.46
1:7:279:ILE:HB	1:7:291:ILE:HB	1.98	0.46
1:E:176:ASN:HB2	1:E:192:ILE:HD12	1.98	0.46
1:E:186:SER:OG	1:E:187:PRO:HD3	2.16	0.46
1:N:197:PRO:O	1:N:201:THR:HG23	2.15	0.46
1:R:40:TYR:CE2	1:k:288:PRO:HD3	2.51	0.46
1:Y:147:GLN:HE21	1:Y:220:SER:HB2	1.81	0.46
1:b:233:THR:HG23	1:b:263:PHE:HA	1.97	0.46
1:c:245:LEU:HD23	1:c:245:LEU:H	1.80	0.46
1:l:132:THR:HA	1:l:247:GLY:HA2	1.97	0.46
1:t:241:ALA:HB3	1:t:256:VAL:HB	1.98	0.46
1:C:28:LEU:O	1:C:32:ILE:HG13	2.16	0.46
1:F:178:THR:HA	1:F:182:ILE:HG12	1.97	0.46
1:G:196:THR:HG23	1:G:199:SER:H	1.80	0.46
1:V:142:VAL:HG21	1:V:151:LEU:HD11	1.97	0.46
1:Z:266:ASP:N	1:Z:266:ASP:OD1	2.47	0.46
1:i:266:ASP:OD1	1:i:266:ASP:N	2.47	0.46
1:p:77:ALA:HA	1:p:302:VAL:HA	1.97	0.46
1:p:141:GLN:HG3	1:p:177:TYR:CE2	2.51	0.46
1:x:78:VAL:HG23	1:x:85:ARG:O	2.16	0.46
1:1:67:ALA:O	1:1:96:SER:OG	2.27	0.46
1:2:149:LEU:HD23	1:2:149:LEU:H	1.80	0.46
1:3:47:LEU:HD22	1:L:37:VAL:HG11	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:7:186:SER:OG	1:7:187:PRO:HD3	2.16	0.46
1:E:126:TYR:OH	1:E:237:THR:OG1	2.22	0.46
1:E:142:VAL:HG22	1:E:149:LEU:HD21	1.96	0.46
1:O:143:TYR:HB2	1:O:148:TYR:CE2	2.51	0.46
1:Q:53:ALA:O	1:Q:57:ILE:HG13	2.15	0.46
1:R:186:SER:OG	1:R:187:PRO:HD3	2.15	0.46
1:T:141:GLN:O	1:T:141:GLN:HG2	2.16	0.46
1:Y:78:VAL:HG11	1:Y:298:PRO:HB2	1.98	0.46
1:Y:178:THR:HA	1:Y:182:ILE:HG12	1.99	0.46
1:d:132:THR:HA	1:d:247:GLY:HA2	1.98	0.46
1:e:23:ASP:OD1	1:e:24:THR:N	2.49	0.46
1:j:67:ALA:O	1:j:96:SER:N	2.41	0.46
1:m:241:ALA:HB3	1:m:256:VAL:HB	1.97	0.46
1:v:80:TYR:HB2	1:v:301:SER:HB2	1.97	0.46
1:z:143:TYR:HB3	1:z:148:TYR:HA	1.98	0.46
1:2:79:ASN:OD1	1:2:79:ASN:N	2.49	0.45
1:7:85:ARG:HA	1:7:268:GLY:O	2.15	0.45
1:A:196:THR:HG22	1:A:198:SER:H	1.82	0.45
1:D:252:PRO:O	1:D:255:SER:OG	2.30	0.45
1:F:68:LEU:HD21	1:F:102:VAL:HG21	1.98	0.45
1:L:53:ALA:O	1:L:57:ILE:HG13	2.16	0.45
1:R:89:ILE:HD11	1:R:261:ILE:HD12	1.98	0.45
1:Z:235:ALA:HB2	1:Z:261:ILE:HG12	1.96	0.45
1:b:216:THR:HB	1:b:223:LEU:HD21	1.98	0.45
1:d:36:SER:HG	1:v:97:SER:HG	1.63	0.45
1:h:59:LYS:HE3	1:i:296:TYR:CZ	2.51	0.45
1:h:282:THR:HB	1:h:288:PRO:HB3	1.97	0.45
1:p:133:VAL:HG21	1:p:178:THR:HG21	1.98	0.45
1:t:78:VAL:HG23	1:t:85:ARG:O	2.17	0.45
1:u:86:SER:OG	1:u:270:HIS:O	2.31	0.45
1:1:86:SER:OG	1:1:270:HIS:O	2.30	0.45
1:2:272:PHE:CG	1:2:277:ILE:HD11	2.51	0.45
1:B:46:GLY:HA2	1:g:22:LEU:HD13	1.99	0.45
1:E:50:THR:HG23	1:q:41:VAL:HG11	1.97	0.45
1:P:140:ASN:HB3	1:P:141:GLN:OE1	2.15	0.45
1:V:127:GLU:OE2	1:V:232:GLN:NE2	2.49	0.45
1:V:237:THR:HG22	1:V:259:VAL:HG22	1.99	0.45
1:Y:137:GLU:N	1:Y:137:GLU:OE1	2.50	0.45
1:b:197:PRO:HA	1:b:200:ALA:HB3	1.98	0.45
1:n:143:TYR:HB3	1:n:148:TYR:HA	1.98	0.45
1:o:37:VAL:HA	1:o:40:TYR:CZ	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:o:126:TYR:CE1	1:o:237:THR:HG23	2.51	0.45
1:v:69:THR:HB	1:v:96:SER:HA	1.97	0.45
1:0:167:ASN:HB2	1:0:170:TYR:CG	2.51	0.45
1:2:141:GLN:HG3	1:2:177:TYR:CZ	2.52	0.45
1:6:59:LYS:O	1:6:63:THR:HG23	2.17	0.45
1:7:24:THR:HA	1:7:27:ILE:HB	1.97	0.45
1:7:28:LEU:O	1:7:32:ILE:HG12	2.16	0.45
1:F:252:PRO:O	1:F:255:SER:OG	2.30	0.45
1:F:266:ASP:OD1	1:F:267:LEU:N	2.44	0.45
1:M:86:SER:OG	1:M:270:HIS:O	2.28	0.45
1:S:288:PRO:HD3	1:j:40:TYR:CE1	2.52	0.45
1:U:266:ASP:OD1	1:U:266:ASP:N	2.48	0.45
1:b:252:PRO:O	1:b:255:SER:OG	2.32	0.45
1:c:53:ALA:O	1:c:57:ILE:HG13	2.16	0.45
1:i:197:PRO:HD3	1:i:227:TYR:CE1	2.50	0.45
1:j:77:ALA:HB3	1:j:88:TRP:H	1.82	0.45
1:r:80:TYR:HB2	1:r:301:SER:HB3	1.98	0.45
1:s:154:GLN:HB3	1:s:163:VAL:HG12	1.98	0.45
1:0:100:SER:OG	1:0:101:SER:N	2.48	0.45
1:1:43:ILE:O	1:1:47:LEU:HG	2.16	0.45
1:5:88:TRP:HB3	1:5:262:LEU:HD23	1.98	0.45
1:B:134:SER:HB3	1:B:137:GLU:HG2	1.98	0.45
1:D:204:TYR:HB3	1:D:207:LEU:HD13	1.97	0.45
1:E:237:THR:HG22	1:E:259:VAL:HG22	1.98	0.45
1:F:72:GLY:HA2	1:z:280:GLN:HE22	1.81	0.45
1:G:66:THR:HG22	1:G:100:SER:OG	2.16	0.45
1:G:297:GLN:HE21	1:G:298:PRO:HD2	1.81	0.45
1:M:153:ASN:ND2	1:M:164:TYR:OH	2.50	0.45
1:N:32:ILE:HG23	1:O:26:ILE:HG21	1.97	0.45
1:N:135:PRO:HG3	1:N:163:VAL:HG11	1.98	0.45
1:R:168:PRO:HB3	1:R:260:MET:SD	2.56	0.45
1:Y:273:GLN:HE21	1:Y:297:GLN:HE22	1.63	0.45
1:a:78:VAL:HG23	1:a:85:ARG:O	2.15	0.45
1:c:197:PRO:O	1:c:201:THR:HG23	2.16	0.45
1:c:235:ALA:HB2	1:c:261:ILE:HG12	1.98	0.45
1:k:273:GLN:NE2	1:k:298:PRO:HD3	2.31	0.45
1:p:266:ASP:OD1	1:p:266:ASP:N	2.49	0.45
1:x:28:LEU:O	1:x:32:ILE:HG12	2.16	0.45
1:x:55:SER:HA	1:x:58:ASN:HD22	1.81	0.45
1:y:79:ASN:HD21	1:y:85:ARG:HB2	1.82	0.45
1:z:85:ARG:NH2	1:z:211:ASN:OD1	2.50	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:z:217:LEU:O	1:z:223:LEU:HD12	2.16	0.45
1:0:266:ASP:OD1	1:0:266:ASP:N	2.50	0.45
1:6:43:ILE:O	1:6:47:LEU:HG	2.16	0.45
1:7:38:LEU:HD11	1:x:46:GLY:HA3	1.99	0.45
1:7:274:TYR:H	1:7:296:TYR:HB3	1.81	0.45
1:B:40:TYR:CZ	1:z:288:PRO:HD3	2.52	0.45
1:F:70:LEU:HD22	1:F:291:ILE:HD12	1.98	0.45
1:I:197:PRO:O	1:I:201:THR:HG23	2.17	0.45
1:N:284:ASN:OD1	1:N:284:ASN:N	2.49	0.45
1:P:296:TYR:CE1	1:g:98:GLY:HA3	2.51	0.45
1:W:122:TYR:OH	1:W:266:ASP:OD2	2.34	0.45
1:Z:70:LEU:HD13	1:Z:291:ILE:HG21	1.98	0.45
1:a:22:LEU:HD21	1:t:46:GLY:HA2	1.99	0.45
1:g:100:SER:OG	1:g:101:SER:N	2.49	0.45
1:i:78:VAL:HG23	1:i:85:ARG:O	2.17	0.45
1:k:266:ASP:OD1	1:k:266:ASP:N	2.48	0.45
1:o:162:TYR:CZ	1:o:244:PRO:HB3	2.52	0.45
1:q:122:TYR:OH	1:q:266:ASP:OD2	2.35	0.45
1:y:87:TYR:HB3	1:y:88:TRP:CD1	2.52	0.45
1:0:32:ILE:HD11	1:R:22:LEU:HB3	1.99	0.45
1:1:69:THR:HG23	1:1:96:SER:HA	1.97	0.45
1:5:99:VAL:HG23	1:5:100:SER:H	1.82	0.45
1:7:138:LEU:HD11	1:7:151:LEU:HD12	1.98	0.45
1:O:28:LEU:O	1:O:32:ILE:HG12	2.16	0.45
1:O:252:PRO:HG2	1:O:255:SER:HB3	1.97	0.45
1:O:297:GLN:O	1:O:297:GLN:HG3	2.15	0.45
1:S:99:VAL:HG23	1:S:100:SER:H	1.82	0.45
1:U:186:SER:OG	1:U:187:PRO:HD3	2.17	0.45
1:V:245:LEU:HD23	1:V:245:LEU:H	1.82	0.45
1:Y:273:GLN:HE21	1:Y:297:GLN:NE2	2.15	0.45
1:k:20:ALA:HA	1:k:23:ASP:HB2	1.98	0.45
1:o:62:GLU:O	1:o:66:THR:HG22	2.16	0.45
1:o:99:VAL:HG23	1:o:100:SER:N	2.31	0.45
1:p:273:GLN:HA	1:p:296:TYR:HA	1.98	0.45
1:t:79:ASN:OD1	1:t:79:ASN:N	2.50	0.45
1:v:105:SER:O	1:v:109:THR:HG22	2.17	0.45
1:3:86:SER:OG	1:3:270:HIS:O	2.25	0.45
1:7:149:LEU:HD23	1:7:149:LEU:H	1.82	0.45
1:D:57:ILE:HG12	1:y:32:ILE:HG21	1.99	0.45
1:D:141:GLN:N	1:D:141:GLN:OE1	2.50	0.45
1:I:96:SER:OG	1:I:97:SER:N	2.49	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:273:GLN:NE2	1:M:297:GLN:OE1	2.50	0.45
1:R:284:ASN:CG	1:R:285:ILE:HD12	2.42	0.45
1:V:162:TYR:CE2	1:W:107:SER:HB2	2.52	0.45
1:a:69:THR:HG23	1:a:96:SER:HA	1.98	0.45
1:b:85:ARG:NH2	1:b:211:ASN:OD1	2.49	0.45
1:c:182:ILE:O	1:c:184:LYS:NZ	2.46	0.45
1:f:227:TYR:HB3	1:f:229:PHE:HE1	1.82	0.45
1:i:78:VAL:HG11	1:i:298:PRO:HB2	1.97	0.45
1:n:122:TYR:OH	1:n:266:ASP:OD2	2.34	0.45
1:o:144:ALA:HB3	1:o:219:ILE:HD11	1.99	0.45
1:7:266:ASP:N	1:7:266:ASP:OD1	2.50	0.45
1:F:141:GLN:O	1:F:141:GLN:HG2	2.16	0.45
1:G:273:GLN:HG2	1:G:274:TYR:HD1	1.82	0.45
1:M:141:GLN:HG2	1:M:141:GLN:O	2.16	0.45
1:U:70:LEU:HD13	1:U:291:ILE:HD13	1.99	0.45
1:V:162:TYR:HE1	1:V:244:PRO:HB3	1.81	0.45
1:Y:252:PRO:O	1:Y:255:SER:OG	2.30	0.45
1:e:25:ALA:O	1:e:29:ILE:HG12	2.17	0.45
1:i:116:SER:OG	1:i:117:ALA:N	2.50	0.45
1:l:141:GLN:OE1	1:l:141:GLN:N	2.50	0.45
1:p:126:TYR:CE1	1:p:237:THR:HG23	2.52	0.45
1:r:116:SER:OG	1:r:117:ALA:N	2.49	0.45
1:v:186:SER:OG	1:v:187:PRO:HD3	2.16	0.45
1:3:201:THR:HB	1:3:208:ALA:HB2	1.98	0.45
1:4:123:SER:OG	1:K:166:PRO:O	2.29	0.45
1:6:293:GLU:OE2	1:V:51:GLN:NE2	2.46	0.45
1:7:95:PRO:HB2	1:7:254:GLY:H	1.82	0.45
1:B:293:GLU:OE1	1:g:55:SER:OG	2.35	0.45
1:E:98:GLY:O	1:Z:296:TYR:OH	2.29	0.45
1:E:282:THR:HA	1:E:288:PRO:HB3	1.98	0.45
1:H:280:GLN:HE21	1:H:288:PRO:HB2	1.82	0.45
1:I:57:ILE:HG12	1:i:32:ILE:HD12	1.98	0.45
1:Q:78:VAL:HG23	1:Q:85:ARG:O	2.17	0.45
1:U:88:TRP:CD2	1:U:260:MET:HE3	2.52	0.45
1:V:68:LEU:HD11	1:V:104:LEU:HD21	1.98	0.45
1:c:137:GLU:OE1	1:c:137:GLU:N	2.49	0.45
1:d:133:VAL:HG21	1:d:178:THR:HG21	1.97	0.45
1:e:79:ASN:OD1	1:e:79:ASN:N	2.48	0.45
1:m:132:THR:HA	1:m:247:GLY:HA2	1.99	0.45
1:p:290:THR:N	1:x:44:ASN:OD1	2.48	0.45
1:q:147:GLN:HE21	1:q:220:SER:HB2	1.82	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:25:ALA:O	1:u:29:ILE:HG13	2.17	0.45
1:z:71:SER:O	1:z:71:SER:OG	2.31	0.45
1:0:284:ASN:OD1	1:0:285:ILE:N	2.50	0.45
1:A:97:SER:O	1:A:99:VAL:N	2.46	0.45
1:B:76:TYR:O	1:B:303:SER:N	2.35	0.45
1:N:197:PRO:HD3	1:N:227:TYR:CZ	2.52	0.45
1:P:114:THR:HG23	1:P:278:THR:HB	1.99	0.45
1:R:132:THR:HA	1:R:247:GLY:HA2	1.97	0.45
1:X:298:PRO:O	1:X:299:GLU:HG3	2.17	0.45
1:a:19:LEU:HD21	1:a:22:LEU:HG	1.98	0.45
1:k:241:ALA:HB3	1:k:256:VAL:HB	1.99	0.45
1:n:186:SER:OG	1:n:187:PRO:HD3	2.16	0.45
1:p:98:GLY:HA2	1:p:253:ALA:HB1	1.98	0.45
1:z:34:THR:O	1:z:37:VAL:HG12	2.17	0.45
1:z:78:VAL:HG11	1:z:298:PRO:HB2	1.98	0.45
1:z:122:TYR:HE2	1:z:267:LEU:HD22	1.82	0.45
1:2:118:GLU:OE2	1:2:275:GLN:NE2	2.42	0.44
1:3:53:ALA:O	1:3:57:ILE:HG13	2.18	0.44
1:5:203:ILE:H	1:5:203:ILE:HD12	1.81	0.44
1:E:108:THR:HG22	1:E:284:ASN:HB3	2.00	0.44
1:J:190:LEU:HD23	1:J:234:PHE:HZ	1.82	0.44
1:T:240:VAL:O	1:m:124:ASN:ND2	2.48	0.44
1:U:179:LEU:HD21	1:U:189:PRO:HG2	1.99	0.44
1:Y:72:GLY:HA2	1:Z:280:GLN:HE22	1.82	0.44
1:Z:79:ASN:OD1	1:Z:79:ASN:N	2.50	0.44
1:d:19:LEU:HG	1:d:21:GLY:H	1.82	0.44
1:l:188:SER:OG	1:l:190:LEU:O	2.31	0.44
1:x:141:GLN:HG2	1:x:141:GLN:O	2.17	0.44
1:y:296:TYR:CD1	1:y:297:GLN:HG2	2.52	0.44
1:0:40:TYR:CE1	1:j:288:PRO:HD3	2.52	0.44
1:3:59:LYS:HA	1:3:59:LYS:HD3	1.75	0.44
1:5:78:VAL:HG12	1:5:86:SER:HA	1.99	0.44
1:B:68:LEU:HD21	1:B:102:VAL:HG21	1.99	0.44
1:F:73:SER:OG	1:F:74:VAL:N	2.49	0.44
1:F:74:VAL:HA	1:F:91:PHE:HB3	1.98	0.44
1:H:154:GLN:HB3	1:H:163:VAL:HG12	1.98	0.44
1:H:186:SER:OG	1:H:187:PRO:HD3	2.17	0.44
1:I:135:PRO:HG3	1:I:163:VAL:HG11	1.97	0.44
1:R:68:LEU:HD11	1:R:102:VAL:HG21	1.99	0.44
1:W:30:ALA:O	1:W:34:THR:HG23	2.17	0.44
1:W:145:ASN:HD22	1:W:219:ILE:HG13	1.81	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:219:ILE:O	1:W:222:THR:OG1	2.32	0.44
1:Y:183:ASP:OD1	1:Y:183:ASP:N	2.51	0.44
1:Z:132:THR:HA	1:Z:247:GLY:HA2	1.98	0.44
1:a:151:LEU:HA	1:a:170:TYR:HD2	1.82	0.44
1:c:66:THR:HB	1:c:102:VAL:HG12	1.99	0.44
1:g:71:SER:OG	1:g:72:GLY:N	2.51	0.44
1:g:115:ALA:H	1:g:120:ILE:HG13	1.81	0.44
1:g:163:VAL:HG11	1:g:246:ILE:HD13	1.98	0.44
1:p:280:GLN:HA	1:p:289:LEU:O	2.17	0.44
1:s:97:SER:O	1:s:99:VAL:N	2.48	0.44
1:1:266:ASP:N	1:1:266:ASP:OD1	2.48	0.44
1:4:52:LYS:O	1:4:56:THR:HG23	2.17	0.44
1:6:252:PRO:O	1:6:255:SER:OG	2.32	0.44
1:E:103:GLU:OE1	1:E:105:SER:OG	2.31	0.44
1:G:192:ILE:HG12	1:G:228:ALA:HA	1.99	0.44
1:I:79:ASN:OD1	1:I:79:ASN:N	2.49	0.44
1:Q:78:VAL:HG11	1:Q:298:PRO:HB2	1.99	0.44
1:S:86:SER:OG	1:S:270:HIS:O	2.27	0.44
1:S:151:LEU:HA	1:S:170:TYR:HD2	1.81	0.44
1:a:266:ASP:OD1	1:a:266:ASP:N	2.51	0.44
1:c:135:PRO:HB3	1:c:152:VAL:HG11	1.99	0.44
1:j:126:TYR:CE1	1:j:237:THR:HG23	2.53	0.44
1:n:33:ILE:O	1:n:37:VAL:HG23	2.18	0.44
1:p:298:PRO:C	1:p:299:GLU:HG3	2.42	0.44
1:u:79:ASN:OD1	1:u:79:ASN:N	2.50	0.44
1:w:132:THR:HA	1:w:247:GLY:HA2	1.99	0.44
1:7:287:SER:OG	1:7:288:PRO:O	2.31	0.44
1:7:298:PRO:O	1:7:299:GLU:HG3	2.18	0.44
1:C:79:ASN:OD1	1:C:79:ASN:N	2.51	0.44
1:C:82:SER:O	1:C:82:SER:OG	2.35	0.44
1:I:67:ALA:HB3	1:I:96:SER:HB3	1.99	0.44
1:K:19:LEU:HD21	1:K:22:LEU:HG	1.99	0.44
1:O:298:PRO:O	1:O:299:GLU:HG3	2.18	0.44
1:P:118:GLU:CD	1:P:275:GLN:HE22	2.26	0.44
1:Y:167:ASN:HB3	1:Y:170:TYR:HD2	1.81	0.44
1:g:66:THR:HG21	1:g:286:GLY:HA3	2.00	0.44
1:i:59:LYS:HD3	1:i:59:LYS:HA	1.78	0.44
1:j:186:SER:OG	1:j:187:PRO:HD3	2.17	0.44
1:o:103:GLU:O	1:o:104:LEU:HD23	2.17	0.44
1:E:244:PRO:HD2	1:E:252:PRO:HG3	1.99	0.44
1:L:66:THR:HG23	1:L:102:VAL:HG22	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:245:LEU:O	1:O:248:SER:OG	2.28	0.44
1:X:154:GLN:HB3	1:X:163:VAL:HG12	1.99	0.44
1:h:204:TYR:HB3	1:h:207:LEU:HD13	2.00	0.44
1:p:22:LEU:O	1:p:26:ILE:HG12	2.17	0.44
1:r:78:VAL:HG23	1:r:85:ARG:O	2.17	0.44
1:s:130:LEU:HD11	1:s:175:LEU:HD13	2.00	0.44
1:y:55:SER:O	1:y:59:LYS:HG2	2.17	0.44
1:2:108:THR:OG1	1:K:274:TYR:OH	2.25	0.44
1:5:140:ASN:HB3	1:5:141:GLN:OE1	2.17	0.44
1:7:110:ALA:HB2	1:x:241:ALA:HB2	2.00	0.44
1:A:167:ASN:HB3	1:A:170:TYR:HB2	2.00	0.44
1:B:98:GLY:HA2	1:B:253:ALA:HB1	2.00	0.44
1:C:141:GLN:HG2	1:C:141:GLN:O	2.17	0.44
1:C:220:SER:HA	1:Y:209:HIS:HB3	2.00	0.44
1:F:33:ILE:O	1:F:37:VAL:HG23	2.18	0.44
1:J:183:ASP:OD1	1:J:183:ASP:N	2.45	0.44
1:L:43:ILE:O	1:L:47:LEU:HG	2.17	0.44
1:R:138:LEU:HD11	1:R:174:ALA:HA	1.98	0.44
1:V:57:ILE:HG12	1:m:32:ILE:HD13	2.00	0.44
1:V:88:TRP:HB3	1:V:262:LEU:HD23	1.99	0.44
1:b:79:ASN:N	1:b:79:ASN:OD1	2.51	0.44
1:c:71:SER:O	1:c:71:SER:OG	2.30	0.44
1:g:26:ILE:HA	1:g:29:ILE:HG22	1.99	0.44
1:k:32:ILE:HD11	1:l:22:LEU:HB3	2.00	0.44
1:k:50:THR:HG21	1:l:37:VAL:HG12	1.99	0.44
1:p:107:SER:OG	1:p:108:THR:N	2.50	0.44
1:v:52:LYS:O	1:v:56:THR:HG23	2.18	0.44
1:x:63:THR:HA	1:x:286:GLY:HA2	2.00	0.44
1:2:145:ASN:ND2	1:2:222:THR:OG1	2.50	0.44
1:5:147:GLN:HE21	1:5:220:SER:HB3	1.83	0.44
1:M:141:GLN:OE1	1:M:141:GLN:N	2.50	0.44
1:Q:19:LEU:HG	1:Q:21:GLY:H	1.82	0.44
1:d:110:ALA:HB3	1:d:282:THR:HG23	2.00	0.44
1:e:188:SER:OG	1:e:190:LEU:O	2.36	0.44
1:j:211:ASN:ND2	1:j:264:GLY:O	2.51	0.44
1:q:98:GLY:HA3	1:s:296:TYR:OH	2.18	0.44
1:u:282:THR:HG22	1:u:288:PRO:HB3	1.99	0.44
1:y:137:GLU:HG2	1:y:138:LEU:HD22	1.99	0.44
1:0:180:SER:HB2	1:0:181:LYS:NZ	2.32	0.44
1:1:79:ASN:OD1	1:1:79:ASN:N	2.51	0.44
1:3:137:GLU:OE1	1:3:137:GLU:N	2.50	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:ASP:OD1	1:A:24:THR:N	2.51	0.44
1:I:80:TYR:HB2	1:I:301:SER:HB3	1.99	0.44
1:K:135:PRO:HB3	1:K:152:VAL:HG11	2.00	0.44
1:K:210:ASP:HB2	1:K:229:PHE:HB3	1.99	0.44
1:L:288:PRO:HD3	1:T:40:TYR:CZ	2.52	0.44
1:R:252:PRO:O	1:R:255:SER:OG	2.24	0.44
1:S:47:LEU:HD22	1:T:37:VAL:HG11	1.99	0.44
1:V:252:PRO:HG2	1:V:255:SER:HB3	1.99	0.44
1:Y:88:TRP:HB3	1:Y:262:LEU:HD23	2.00	0.44
1:c:68:LEU:HD21	1:c:102:VAL:HG21	2.00	0.44
1:e:178:THR:HA	1:e:182:ILE:HG12	2.00	0.44
1:g:46:GLY:O	1:g:50:THR:HG23	2.18	0.44
1:h:156:THR:HA	1:h:161:THR:HA	2.00	0.44
1:l:65:SER:O	1:l:100:SER:OG	2.34	0.44
1:m:252:PRO:HG2	1:m:255:SER:HB3	2.00	0.44
1:o:255:SER:OG	1:o:256:VAL:N	2.51	0.44
1:q:80:TYR:HB2	1:q:301:SER:HB2	2.00	0.44
1:s:186:SER:OG	1:s:187:PRO:HD3	2.18	0.44
1:B:66:THR:HG22	1:B:100:SER:HB2	1.99	0.44
1:B:79:ASN:OD1	1:B:79:ASN:N	2.51	0.44
1:J:105:SER:O	1:J:109:THR:HG22	2.17	0.44
1:M:37:VAL:HA	1:M:40:TYR:HB3	1.99	0.44
1:Q:212:MET:HA	1:Q:228:ALA:O	2.18	0.44
1:U:241:ALA:HB3	1:U:256:VAL:HB	2.00	0.44
1:j:140:ASN:HB3	1:j:141:GLN:OE1	2.17	0.44
1:m:131:LEU:HD21	1:m:257:ILE:HD12	2.00	0.44
1:n:252:PRO:O	1:n:255:SER:OG	2.32	0.44
1:p:177:TYR:HE2	1:p:181:LYS:HD2	1.82	0.44
1:s:142:VAL:HG22	1:s:149:LEU:HD21	1.99	0.44
1:s:153:ASN:OD1	1:s:154:GLN:N	2.51	0.44
1:y:33:ILE:O	1:y:37:VAL:HG23	2.18	0.44
1:0:141:GLN:OE1	1:0:141:GLN:N	2.51	0.43
1:1:212:MET:HA	1:1:228:ALA:O	2.18	0.43
1:3:111:ILE:O	1:3:125:ILE:HG12	2.17	0.43
1:6:99:VAL:HG23	1:6:100:SER:N	2.33	0.43
1:B:145:ASN:ND2	1:B:220:SER:OG	2.51	0.43
1:E:22:LEU:HD12	1:p:28:LEU:HD11	2.00	0.43
1:G:101:SER:HB3	1:G:252:PRO:HA	2.00	0.43
1:H:49:VAL:HG21	1:z:22:LEU:HD13	2.00	0.43
1:M:30:ALA:O	1:M:34:THR:HG23	2.17	0.43
1:N:143:TYR:HB3	1:N:148:TYR:HA	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:127:GLU:OE2	1:T:232:GLN:NE2	2.50	0.43
1:T:275:GLN:HE21	1:j:160:GLN:NE2	2.16	0.43
1:U:197:PRO:HD3	1:U:227:TYR:CZ	2.53	0.43
1:W:102:VAL:HG23	1:W:251:ALA:HB3	2.00	0.43
1:W:237:THR:HG22	1:W:259:VAL:HG22	2.00	0.43
1:X:79:ASN:HD21	1:X:85:ARG:N	2.16	0.43
1:d:216:THR:HB	1:d:223:LEU:HD11	2.00	0.43
1:k:32:ILE:HD13	1:k:32:ILE:HA	1.88	0.43
1:p:79:ASN:HD21	1:p:85:ARG:H	1.64	0.43
1:p:104:LEU:HA	1:p:109:THR:HG21	2.00	0.43
1:q:79:ASN:OD1	1:q:79:ASN:N	2.51	0.43
1:t:105:SER:O	1:t:109:THR:HG22	2.18	0.43
1:v:78:VAL:HG11	1:v:298:PRO:HB2	1.99	0.43
1:z:203:ILE:HG23	1:z:204:TYR:CD2	2.53	0.43
1:0:110:ALA:HB2	1:h:241:ALA:HB2	1.99	0.43
1:B:80:TYR:N	1:B:81:PRO:HD2	2.32	0.43
1:C:19:LEU:HD12	1:C:21:GLY:H	1.83	0.43
1:F:66:THR:HB	1:F:102:VAL:HG12	2.00	0.43
1:H:274:TYR:N	1:H:295:VAL:O	2.48	0.43
1:O:132:THR:HA	1:O:247:GLY:HA2	2.01	0.43
1:X:197:PRO:O	1:X:201:THR:HG23	2.18	0.43
1:b:105:SER:O	1:b:109:THR:HG22	2.18	0.43
1:f:197:PRO:HD3	1:f:227:TYR:CZ	2.54	0.43
1:h:219:ILE:O	1:h:222:THR:OG1	2.36	0.43
1:q:142:VAL:HG22	1:q:149:LEU:HD21	1.99	0.43
1:t:97:SER:O	1:t:99:VAL:HG22	2.18	0.43
1:0:168:PRO:HB3	1:0:260:MET:SD	2.58	0.43
1:2:197:PRO:O	1:2:201:THR:HG23	2.18	0.43
1:4:135:PRO:HB3	1:4:152:VAL:HG11	1.99	0.43
1:6:147:GLN:HE21	1:6:219:ILE:HG23	1.83	0.43
1:I:145:ASN:ND2	1:I:219:ILE:O	2.52	0.43
1:J:43:ILE:HA	1:K:34:THR:HG22	2.00	0.43
1:P:245:LEU:HD23	1:Q:80:TYR:OH	2.18	0.43
1:T:105:SER:O	1:T:109:THR:HG22	2.18	0.43
1:Y:80:TYR:O	1:Y:83:ASN:ND2	2.51	0.43
1:b:246:ILE:HD13	1:b:246:ILE:HA	1.89	0.43
1:e:172:LEU:HD23	1:e:172:LEU:HA	1.85	0.43
1:f:126:TYR:CE1	1:f:237:THR:HG23	2.53	0.43
1:f:186:SER:HB3	1:f:187:PRO:HD3	2.00	0.43
1:f:280:GLN:HG3	1:f:290:THR:HG22	2.00	0.43
1:j:131:LEU:HD21	1:j:257:ILE:HD12	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:74:VAL:HG12	1:l:91:PHE:HB3	2.00	0.43
1:m:198:SER:O	1:m:201:THR:OG1	2.36	0.43
1:r:71:SER:O	1:r:71:SER:OG	2.36	0.43
1:t:240:VAL:O	1:u:124:ASN:ND2	2.51	0.43
1:v:79:ASN:N	1:v:79:ASN:OD1	2.50	0.43
1:v:86:SER:OG	1:v:270:HIS:O	2.35	0.43
1:2:53:ALA:O	1:2:57:ILE:HG13	2.18	0.43
1:5:141:GLN:HG2	1:5:141:GLN:O	2.18	0.43
1:5:244:PRO:HD2	1:5:252:PRO:HG3	2.01	0.43
1:C:46:GLY:HA2	1:p:22:LEU:HD21	2.00	0.43
1:H:80:TYR:HE1	1:H:299:GLU:HA	1.83	0.43
1:O:95:PRO:HG2	1:O:253:ALA:HA	2.01	0.43
1:O:104:LEU:HA	1:O:109:THR:HG21	2.00	0.43
1:P:197:PRO:O	1:P:201:THR:OG1	2.31	0.43
1:Q:80:TYR:CE1	1:Q:299:GLU:HA	2.53	0.43
1:R:127:GLU:HG2	1:R:234:PHE:HB2	2.00	0.43
1:U:245:LEU:HD23	1:U:245:LEU:H	1.84	0.43
1:W:54:LYS:HD3	1:g:45:MET:HG3	2.01	0.43
1:f:29:ILE:O	1:f:33:ILE:HG12	2.19	0.43
1:f:32:ILE:HB	1:p:26:ILE:HD12	2.00	0.43
1:i:86:SER:OG	1:i:268:GLY:HA2	2.18	0.43
1:n:25:ALA:O	1:n:29:ILE:HG13	2.17	0.43
1:s:69:THR:HB	1:s:96:SER:HA	1.99	0.43
1:s:79:ASN:N	1:s:79:ASN:OD1	2.51	0.43
1:s:149:LEU:H	1:s:149:LEU:HD23	1.84	0.43
1:w:133:VAL:HG21	1:w:138:LEU:HD21	2.00	0.43
1:y:131:LEU:HB3	1:y:249:ALA:HA	1.99	0.43
1:3:105:SER:O	1:3:109:THR:HG22	2.18	0.43
1:3:233:THR:HG23	1:3:263:PHE:HA	2.01	0.43
1:5:37:VAL:HA	1:5:40:TYR:HB3	1.99	0.43
1:D:185:VAL:HG22	1:D:187:PRO:HD2	2.00	0.43
1:D:203:ILE:HG23	1:D:204:TYR:HD2	1.83	0.43
1:F:96:SER:OG	1:F:97:SER:N	2.51	0.43
1:L:98:GLY:HA2	1:L:253:ALA:HB1	2.00	0.43
1:O:287:SER:OG	1:O:288:PRO:O	2.34	0.43
1:T:126:TYR:OH	1:T:237:THR:OG1	2.29	0.43
1:T:237:THR:HG22	1:T:259:VAL:HG22	2.00	0.43
1:b:25:ALA:O	1:b:29:ILE:HG13	2.19	0.43
1:k:106:PRO:HA	1:k:126:TYR:CE2	2.53	0.43
1:k:217:LEU:HB2	1:k:219:ILE:HD11	2.00	0.43
1:n:272:PHE:CD1	1:n:277:ILE:HD11	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:40:TYR:CZ	1:4:288:PRO:HD3	2.54	0.43
1:3:145:ASN:ND2	1:3:222:THR:HG1	2.17	0.43
1:6:51:GLN:HE22	1:O:305:ILE:HD11	1.82	0.43
1:C:118:GLU:CD	1:C:275:GLN:HE22	2.27	0.43
1:C:122:TYR:HE1	1:C:267:LEU:HD21	1.84	0.43
1:E:285:ILE:HD12	1:E:285:ILE:HA	1.87	0.43
1:L:105:SER:O	1:L:109:THR:HG22	2.19	0.43
1:M:80:TYR:HB2	1:M:301:SER:HB2	1.99	0.43
1:O:266:ASP:N	1:O:266:ASP:OD1	2.51	0.43
1:P:237:THR:HA	1:P:258:GLY:O	2.19	0.43
1:Q:69:THR:HB	1:Q:96:SER:HA	2.00	0.43
1:d:48:PHE:HE2	1:w:292:SER:HB3	1.83	0.43
1:e:19:LEU:HD12	1:e:21:GLY:N	2.25	0.43
1:e:300:GLY:C	1:e:302:VAL:H	2.27	0.43
1:f:175:LEU:O	1:f:179:LEU:HG	2.18	0.43
1:g:22:LEU:HD12	1:g:22:LEU:HA	1.89	0.43
1:l:69:THR:N	1:l:94:SER:O	2.48	0.43
1:l:105:SER:O	1:l:109:THR:HG22	2.19	0.43
1:t:151:LEU:HA	1:t:170:TYR:HD2	1.84	0.43
1:u:98:GLY:O	1:w:296:TYR:OH	2.22	0.43
1:x:230:VAL:HG12	1:x:232:GLN:H	1.84	0.43
1:3:88:TRP:HB3	1:3:262:LEU:HD23	2.01	0.43
1:6:297:GLN:HE22	1:V:284:ASN:HD22	1.66	0.43
1:A:103:GLU:HG3	1:A:250:ILE:HG12	2.00	0.43
1:E:149:LEU:HD23	1:E:149:LEU:H	1.82	0.43
1:N:46:GLY:HA3	1:O:38:LEU:HD21	2.00	0.43
1:T:68:LEU:HD22	1:T:93:VAL:HG12	2.01	0.43
1:U:79:ASN:N	1:U:79:ASN:OD1	2.52	0.43
1:V:154:GLN:HB3	1:V:163:VAL:HG12	2.00	0.43
1:V:167:ASN:ND2	1:W:122:TYR:HA	2.34	0.43
1:X:33:ILE:O	1:X:37:VAL:HG23	2.19	0.43
1:e:120:ILE:HG12	1:e:267:LEU:HD13	2.00	0.43
1:g:80:TYR:HB2	1:g:301:SER:HA	2.01	0.43
1:j:137:GLU:OE1	1:j:137:GLU:N	2.49	0.43
1:l:140:ASN:HD22	1:l:141:GLN:CD	2.27	0.43
1:t:186:SER:OG	1:t:187:PRO:HD3	2.18	0.43
1:z:236:PHE:CE1	1:z:260:MET:HB3	2.53	0.43
1:1:135:PRO:HG3	1:1:163:VAL:HG11	2.01	0.43
1:4:114:THR:HG23	1:4:278:THR:HB	2.01	0.43
1:7:87:TYR:HB3	1:7:88:TRP:HD1	1.82	0.43
1:7:149:LEU:HD13	1:7:219:ILE:HG12	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:27:ILE:HD11	1:e:19:LEU:HD13	2.00	0.43
1:G:99:VAL:HG23	1:G:100:SER:H	1.84	0.43
1:I:266:ASP:N	1:I:266:ASP:OD1	2.51	0.43
1:K:96:SER:OG	1:K:97:SER:N	2.51	0.43
1:L:197:PRO:HD3	1:L:227:TYR:CZ	2.54	0.43
1:M:23:ASP:OD2	1:M:24:THR:N	2.52	0.43
1:P:79:ASN:N	1:P:79:ASN:OD1	2.51	0.43
1:Q:79:ASN:OD1	1:Q:79:ASN:N	2.51	0.43
1:R:212:MET:SD	1:R:213:PHE:N	2.92	0.43
1:V:162:TYR:CE1	1:V:244:PRO:HB3	2.53	0.43
1:W:99:VAL:HG23	1:W:100:SER:H	1.84	0.43
1:W:162:TYR:CD2	1:g:107:SER:HB3	2.54	0.43
1:d:74:VAL:HG12	1:d:91:PHE:HB3	2.00	0.43
1:f:63:THR:HA	1:f:286:GLY:HA2	2.01	0.43
1:f:78:VAL:HG23	1:f:85:ARG:O	2.18	0.43
1:g:175:LEU:HA	1:g:178:THR:HG22	2.00	0.43
1:l:193:THR:HG22	1:l:195:THR:HG22	2.01	0.43
1:0:62:GLU:O	1:0:66:THR:HG22	2.19	0.43
1:0:182:ILE:HG13	1:0:183:ASP:N	2.34	0.43
1:4:189:PRO:HA	1:4:231:ASN:ND2	2.33	0.43
1:5:36:SER:HA	1:6:26:ILE:HG21	2.00	0.43
1:5:299:GLU:N	1:5:299:GLU:OE1	2.52	0.43
1:A:211:ASN:O	1:A:229:PHE:HA	2.19	0.43
1:A:287:SER:HA	1:O:40:TYR:HE1	1.83	0.43
1:K:163:VAL:HG22	1:K:246:ILE:HG13	2.01	0.43
1:M:79:ASN:OD1	1:M:79:ASN:N	2.51	0.43
1:P:273:GLN:NE2	1:P:297:GLN:OE1	2.52	0.43
1:Q:43:ILE:O	1:Q:47:LEU:HG	2.19	0.43
1:d:304:VAL:HG13	1:d:304:VAL:O	2.19	0.43
1:f:37:VAL:HA	1:f:40:TYR:CE1	2.54	0.43
1:f:219:ILE:O	1:f:222:THR:OG1	2.31	0.43
1:j:141:GLN:HG3	1:j:177:TYR:CZ	2.54	0.43
1:j:273:GLN:NE2	1:j:297:GLN:OE1	2.52	0.43
1:k:100:SER:C	1:k:253:ALA:HB2	2.44	0.43
1:o:198:SER:O	1:o:201:THR:OG1	2.35	0.43
1:u:183:ASP:OD1	1:u:183:ASP:N	2.45	0.43
1:z:140:ASN:HB2	1:z:141:GLN:OE1	2.19	0.43
1:3:118:GLU:HG2	1:3:270:HIS:ND1	2.34	0.43
1:3:186:SER:OG	1:3:187:PRO:HD3	2.18	0.43
1:6:28:LEU:HD13	1:X:23:ASP:HB3	2.00	0.43
1:A:184:LYS:HA	1:A:184:LYS:HD3	1.87	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:176:ASN:HB2	1:C:192:ILE:HD13	2.01	0.43
1:E:128:TYR:CE2	1:E:189:PRO:HG3	2.54	0.43
1:F:68:LEU:HD11	1:F:104:LEU:HD21	2.00	0.43
1:F:179:LEU:HD23	1:F:179:LEU:HA	1.89	0.43
1:G:51:GLN:HG3	1:r:291:ILE:HG22	2.01	0.43
1:N:302:VAL:HG21	1:O:119:GLY:HA2	1.99	0.43
1:R:217:LEU:HD12	1:R:218:ASN:H	1.84	0.43
1:S:78:VAL:HG12	1:S:86:SER:HA	2.00	0.43
1:X:252:PRO:HG2	1:X:255:SER:HB3	2.00	0.43
1:Y:113:PHE:CD2	1:Y:267:LEU:HD21	2.54	0.43
1:Z:99:VAL:HG23	1:Z:100:SER:N	2.34	0.43
1:a:132:THR:HA	1:a:247:GLY:HA2	2.01	0.43
1:k:67:ALA:O	1:k:96:SER:N	2.43	0.43
1:o:141:GLN:N	1:o:141:GLN:OE1	2.52	0.43
1:t:141:GLN:O	1:t:141:GLN:HG2	2.19	0.43
1:v:120:ILE:HG21	1:v:267:LEU:HD13	2.01	0.43
1:x:111:ILE:HG12	1:x:281:ILE:HG12	2.01	0.43
1:4:43:ILE:O	1:4:47:LEU:HG	2.19	0.42
1:6:32:ILE:HG23	1:X:26:ILE:HG21	2.01	0.42
1:7:156:THR:HA	1:7:161:THR:HA	2.01	0.42
1:A:47:LEU:HD23	1:G:37:VAL:HG21	2.00	0.42
1:B:97:SER:O	1:B:99:VAL:N	2.42	0.42
1:C:120:ILE:HG12	1:C:267:LEU:HD21	2.01	0.42
1:D:45:MET:HG2	1:y:22:LEU:HD21	2.00	0.42
1:E:45:MET:HE2	1:p:57:ILE:HG22	2.01	0.42
1:F:25:ALA:O	1:F:29:ILE:HG13	2.19	0.42
1:F:104:LEU:HA	1:F:109:THR:HG21	2.00	0.42
1:N:186:SER:OG	1:N:187:PRO:HD3	2.18	0.42
1:O:100:SER:O	1:O:253:ALA:HB2	2.19	0.42
1:P:244:PRO:HG2	1:P:245:LEU:HD12	2.01	0.42
1:R:253:ALA:HB3	1:l:294:TYR:CE2	2.54	0.42
1:T:167:ASN:HB2	1:T:170:TYR:CD1	2.54	0.42
1:T:223:LEU:HD12	1:T:224:VAL:H	1.84	0.42
1:U:127:GLU:OE2	1:U:234:PHE:HB2	2.19	0.42
1:X:266:ASP:OD1	1:X:266:ASP:N	2.47	0.42
1:Z:133:VAL:HG21	1:Z:178:THR:HG21	2.00	0.42
1:a:78:VAL:HG11	1:a:298:PRO:HB2	2.00	0.42
1:c:98:GLY:HA2	1:c:253:ALA:HB1	2.01	0.42
1:h:216:THR:HB	1:h:225:THR:HG22	2.01	0.42
1:l:116:SER:OG	1:l:117:ALA:N	2.51	0.42
1:o:79:ASN:OD1	1:o:79:ASN:N	2.50	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:o:138:LEU:HD11	1:o:174:ALA:HB1	2.00	0.42
1:s:104:LEU:HA	1:s:109:THR:HG21	2.01	0.42
1:v:59:LYS:HA	1:v:59:LYS:HD3	1.73	0.42
1:v:304:VAL:O	1:v:304:VAL:HG13	2.19	0.42
1:4:138:LEU:HD21	1:4:174:ALA:HB1	2.01	0.42
1:7:130:LEU:HD12	1:7:238:TYR:HB3	2.01	0.42
1:7:298:PRO:O	1:7:303:SER:OG	2.33	0.42
1:D:95:PRO:HG2	1:D:253:ALA:HA	2.01	0.42
1:I:41:VAL:HG21	1:Q:54:LYS:HB2	2.01	0.42
1:N:145:ASN:HD22	1:N:219:ILE:HB	1.83	0.42
1:R:100:SER:OG	1:R:101:SER:N	2.51	0.42
1:V:94:SER:HB2	1:V:255:SER:O	2.18	0.42
1:a:55:SER:O	1:a:59:LYS:HG2	2.20	0.42
1:b:203:ILE:HG23	1:b:204:TYR:CD2	2.55	0.42
1:m:30:ALA:O	1:m:34:THR:HG23	2.20	0.42
1:t:131:LEU:HD21	1:t:257:ILE:HD12	2.00	0.42
1:t:156:THR:HG22	1:t:161:THR:HG22	2.01	0.42
1:u:20:ALA:O	1:u:24:THR:HG22	2.19	0.42
1:w:101:SER:HB3	1:w:252:PRO:HA	2.00	0.42
1:4:47:LEU:HD22	1:5:37:VAL:HG11	2.01	0.42
1:A:179:LEU:HD13	1:A:189:PRO:HD2	2.01	0.42
1:C:86:SER:OG	1:C:270:HIS:O	2.24	0.42
1:D:47:LEU:HD23	1:h:37:VAL:HG11	2.01	0.42
1:G:266:ASP:N	1:G:266:ASP:OD1	2.52	0.42
1:I:53:ALA:O	1:I:57:ILE:HG13	2.19	0.42
1:M:255:SER:OG	1:M:256:VAL:N	2.52	0.42
1:Q:266:ASP:OD1	1:Q:267:LEU:N	2.52	0.42
1:S:66:THR:HB	1:S:102:VAL:HG12	2.00	0.42
1:S:71:SER:O	1:S:71:SER:OG	2.32	0.42
1:W:147:GLN:HE21	1:W:219:ILE:HB	1.84	0.42
1:W:192:ILE:HG23	1:W:228:ALA:HB2	2.01	0.42
1:W:305:ILE:HD12	1:W:305:ILE:HA	1.93	0.42
1:X:141:GLN:HG3	1:X:177:TYR:CZ	2.53	0.42
1:a:130:LEU:HD12	1:a:238:TYR:HB3	2.01	0.42
1:l:165:TYR:HD1	1:l:238:TYR:HD2	1.67	0.42
1:o:74:VAL:HG12	1:o:91:PHE:HB3	2.01	0.42
1:q:266:ASP:OD1	1:q:267:LEU:N	2.53	0.42
1:x:26:ILE:HD12	1:x:26:ILE:H	1.84	0.42
1:0:237:THR:HG22	1:0:259:VAL:HG22	2.01	0.42
1:1:197:PRO:HA	1:1:200:ALA:HB3	2.01	0.42
1:5:273:GLN:HG3	1:5:296:TYR:O	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:212:MET:HG3	1:R:229:PHE:CZ	2.54	0.42
1:b:58:ASN:O	1:b:62:GLU:HG2	2.19	0.42
1:u:32:ILE:HD13	1:v:57:ILE:HG12	2.01	0.42
1:w:135:PRO:HA	1:w:138:LEU:HD12	2.00	0.42
1:y:303:SER:OG	1:y:304:VAL:N	2.52	0.42
1:2:137:GLU:O	1:2:141:GLN:NE2	2.52	0.42
1:3:266:ASP:OD1	1:3:266:ASP:N	2.50	0.42
1:4:191:TYR:HE2	1:4:193:THR:HB	1.84	0.42
1:7:252:PRO:O	1:7:255:SER:OG	2.23	0.42
1:A:305:ILE:HD12	1:A:305:ILE:HA	1.89	0.42
1:E:147:GLN:HE21	1:E:219:ILE:HG23	1.84	0.42
1:J:172:LEU:HD21	1:J:262:LEU:HD11	2.02	0.42
1:N:43:ILE:O	1:N:47:LEU:HG	2.19	0.42
1:O:263:PHE:CD2	1:O:267:LEU:HD23	2.54	0.42
1:P:103:GLU:OE1	1:P:284:ASN:ND2	2.50	0.42
1:b:149:LEU:HD23	1:b:149:LEU:H	1.84	0.42
1:d:85:ARG:NH2	1:d:211:ASN:OD1	2.53	0.42
1:f:68:LEU:HB3	1:f:93:VAL:HG13	2.00	0.42
1:o:135:PRO:HB3	1:o:152:VAL:HG21	2.02	0.42
1:s:66:THR:HG22	1:s:100:SER:OG	2.19	0.42
1:u:118:GLU:N	1:u:118:GLU:OE1	2.53	0.42
1:2:197:PRO:HA	1:2:200:ALA:HB3	2.01	0.42
1:5:141:GLN:NE2	1:5:177:TYR:OH	2.53	0.42
1:6:141:GLN:O	1:6:141:GLN:HG2	2.18	0.42
1:6:240:VAL:HG12	1:6:256:VAL:O	2.19	0.42
1:J:78:VAL:HG23	1:J:85:ARG:O	2.20	0.42
1:P:29:ILE:HG23	1:Q:56:THR:HG21	2.00	0.42
1:S:122:TYR:HE2	1:S:267:LEU:HD22	1.84	0.42
1:T:116:SER:OG	1:T:117:ALA:N	2.52	0.42
1:U:210:ASP:OD2	1:U:231:ASN:HB3	2.20	0.42
1:V:175:LEU:HA	1:V:178:THR:HG22	2.01	0.42
1:X:235:ALA:HB2	1:X:261:ILE:HG12	2.01	0.42
1:Y:46:GLY:O	1:Y:50:THR:HG23	2.20	0.42
1:a:53:ALA:O	1:a:57:ILE:HG13	2.20	0.42
1:h:68:LEU:HD23	1:h:68:LEU:HA	1.89	0.42
1:k:97:SER:OG	1:k:98:GLY:N	2.53	0.42
1:l:40:TYR:CZ	1:m:288:PRO:HD3	2.55	0.42
1:l:142:VAL:HG11	1:l:151:LEU:HD21	2.02	0.42
1:m:109:THR:HG22	1:m:283:PRO:HA	2.02	0.42
1:o:32:ILE:HD13	1:y:26:ILE:HD12	2.01	0.42
1:q:137:GLU:OE1	1:q:137:GLU:N	2.52	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:s:47:LEU:HD22	1:t:37:VAL:HG11	2.02	0.42
1:s:237:THR:HG22	1:s:259:VAL:HG22	2.02	0.42
1:u:304:VAL:O	1:u:305:ILE:HB	2.19	0.42
1:y:276:THR:HG1	1:y:294:TYR:HD1	1.67	0.42
1:1:170:TYR:HE1	1:1:217:LEU:HD21	1.85	0.42
1:2:165:TYR:HB2	1:2:238:TYR:CD1	2.55	0.42
1:N:30:ALA:O	1:N:34:THR:HG23	2.20	0.42
1:N:111:ILE:HG12	1:N:281:ILE:HG12	2.02	0.42
1:Y:138:LEU:HB3	1:Y:151:LEU:HD12	2.01	0.42
1:a:142:VAL:HG22	1:a:149:LEU:HD21	2.02	0.42
1:c:97:SER:O	1:c:99:VAL:N	2.51	0.42
1:g:45:MET:O	1:g:49:VAL:HG23	2.19	0.42
1:k:295:VAL:HG12	1:k:305:ILE:HG23	2.02	0.42
1:l:135:PRO:HG3	1:l:163:VAL:HG11	2.02	0.42
1:l:160:GLN:NE2	1:n:275:GLN:HE21	2.18	0.42
1:s:300:GLY:C	1:s:302:VAL:H	2.28	0.42
1:t:135:PRO:HG3	1:t:163:VAL:HG11	2.01	0.42
1:t:203:ILE:HG23	1:t:204:TYR:CD2	2.54	0.42
1:x:137:GLU:OE1	1:x:137:GLU:N	2.44	0.42
1:x:197:PRO:O	1:x:201:THR:HG23	2.20	0.42
1:x:212:MET:HE2	1:x:229:PHE:CE2	2.54	0.42
1:z:200:ALA:HA	1:z:203:ILE:HG22	2.01	0.42
1:z:273:GLN:HG2	1:z:274:TYR:CD1	2.55	0.42
1:0:34:THR:HG23	1:h:46:GLY:HA3	2.01	0.42
1:2:143:TYR:HB3	1:2:148:TYR:CD2	2.55	0.42
1:3:252:PRO:HG2	1:3:255:SER:HB3	2.00	0.42
1:B:216:THR:C	1:B:217:LEU:HD12	2.45	0.42
1:C:305:ILE:HD12	1:C:305:ILE:HA	1.90	0.42
1:F:111:ILE:HA	1:F:280:GLN:O	2.19	0.42
1:F:130:LEU:HD12	1:F:238:TYR:HB3	2.01	0.42
1:F:132:THR:HG22	1:F:249:ALA:HB2	2.02	0.42
1:T:153:ASN:ND2	1:T:164:TYR:OH	2.52	0.42
1:X:59:LYS:HA	1:X:59:LYS:HD2	1.84	0.42
1:Z:67:ALA:O	1:Z:96:SER:N	2.45	0.42
1:Z:240:VAL:O	1:s:124:ASN:ND2	2.52	0.42
1:e:141:GLN:O	1:e:141:GLN:HG2	2.19	0.42
1:g:59:LYS:HD3	1:g:59:LYS:HA	1.75	0.42
1:g:80:TYR:OH	1:o:245:LEU:HD23	2.20	0.42
1:j:167:ASN:OD1	1:j:170:TYR:N	2.40	0.42
1:l:126:TYR:HE1	1:l:236:PHE:HA	1.85	0.42
1:l:252:PRO:O	1:l:255:SER:OG	2.31	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:n:43:ILE:O	1:n:47:LEU:HG	2.20	0.42
1:p:85:ARG:HA	1:p:268:GLY:O	2.18	0.42
1:y:28:LEU:O	1:y:32:ILE:HG12	2.20	0.42
1:y:113:PHE:HD2	1:y:279:ILE:HG12	1.84	0.42
1:0:125:ILE:HB	1:0:234:PHE:HA	2.00	0.42
1:B:110:ALA:HB2	1:X:241:ALA:HB2	2.02	0.42
1:B:132:THR:HG22	1:B:249:ALA:HB2	2.01	0.42
1:H:98:GLY:HA2	1:H:253:ALA:HB1	2.01	0.42
1:H:131:LEU:HD21	1:H:257:ILE:HD12	2.01	0.42
1:H:141:GLN:NE2	1:H:177:TYR:OH	2.51	0.42
1:I:245:LEU:HD12	1:I:245:LEU:O	2.20	0.42
1:N:96:SER:OG	1:N:97:SER:N	2.52	0.42
1:O:24:THR:HA	1:O:27:ILE:HB	2.02	0.42
1:P:198:SER:OG	1:P:199:SER:N	2.53	0.42
1:S:244:PRO:HD2	1:S:252:PRO:HG3	2.02	0.42
1:V:212:MET:HB2	1:V:229:PHE:CE2	2.54	0.42
1:a:163:VAL:HG22	1:a:246:ILE:HG13	2.02	0.42
1:b:235:ALA:HB2	1:b:261:ILE:HG12	2.01	0.42
1:e:166:PRO:HA	1:f:123:SER:O	2.19	0.42
1:f:255:SER:OG	1:f:256:VAL:N	2.52	0.42
1:g:29:ILE:O	1:g:33:ILE:HG12	2.19	0.42
1:g:235:ALA:HB2	1:g:261:ILE:HG12	2.02	0.42
1:o:190:LEU:HD12	1:o:229:PHE:O	2.20	0.42
1:u:87:TYR:CD1	1:u:213:PHE:HB3	2.55	0.42
1:y:211:ASN:OD1	1:y:211:ASN:N	2.52	0.42
1:y:273:GLN:O	1:y:275:GLN:NE2	2.53	0.42
1:1:68:LEU:HD13	1:1:93:VAL:HG11	2.01	0.42
1:1:103:GLU:OE2	1:J:297:GLN:HG3	2.20	0.42
1:3:135:PRO:HB3	1:3:152:VAL:HG11	2.02	0.42
1:D:141:GLN:NE2	1:D:177:TYR:OH	2.53	0.42
1:E:204:TYR:HB3	1:E:206:PHE:CZ	2.55	0.42
1:L:176:ASN:HB2	1:L:192:ILE:HD12	2.01	0.42
1:N:63:THR:HA	1:N:286:GLY:HA2	2.01	0.42
1:N:68:LEU:HD11	1:N:104:LEU:HD21	2.02	0.42
1:N:296:TYR:HB3	1:N:297:GLN:OE1	2.20	0.42
1:Q:52:LYS:NZ	1:z:61:GLU:OE1	2.53	0.42
1:Q:211:ASN:O	1:Q:229:PHE:HA	2.20	0.42
1:R:200:ALA:HB1	1:R:207:LEU:HD23	2.01	0.42
1:S:43:ILE:O	1:S:47:LEU:HG	2.19	0.42
1:W:191:TYR:HE2	1:W:193:THR:HB	1.85	0.42
1:X:109:THR:HG22	1:X:283:PRO:HA	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:78:VAL:HG23	1:Z:85:ARG:O	2.20	0.42
1:d:79:ASN:OD1	1:d:79:ASN:N	2.52	0.42
1:f:99:VAL:HA	1:p:59:LYS:HE3	2.00	0.42
1:i:68:LEU:HD23	1:i:95:PRO:HA	2.02	0.42
1:o:151:LEU:HA	1:o:170:TYR:HD2	1.84	0.42
1:o:305:ILE:HD12	1:o:305:ILE:HA	1.89	0.42
1:q:97:SER:O	1:q:99:VAL:N	2.42	0.42
1:x:65:SER:O	1:x:99:VAL:HG21	2.20	0.42
1:0:38:LEU:HD13	1:h:50:THR:HG22	2.01	0.41
1:0:163:VAL:HG22	1:0:246:ILE:HG13	2.01	0.41
1:A:290:THR:HG21	1:O:48:PHE:CD1	2.55	0.41
1:C:150:ASP:OD2	1:C:150:ASP:N	2.51	0.41
1:H:66:THR:HG23	1:H:102:VAL:HG22	2.01	0.41
1:J:118:GLU:OE1	1:J:275:GLN:NE2	2.53	0.41
1:K:43:ILE:O	1:K:47:LEU:HG	2.20	0.41
1:N:237:THR:HG22	1:N:259:VAL:HG22	2.01	0.41
1:P:212:MET:HA	1:P:228:ALA:O	2.20	0.41
1:S:300:GLY:C	1:S:302:VAL:H	2.28	0.41
1:T:282:THR:O	1:T:282:THR:OG1	2.36	0.41
1:Y:237:THR:HG22	1:Y:259:VAL:HG22	2.02	0.41
1:Y:266:ASP:OD1	1:Y:266:ASP:N	2.53	0.41
1:Y:282:THR:HG22	1:Y:288:PRO:HB3	2.01	0.41
1:e:68:LEU:HD13	1:e:93:VAL:HG11	2.00	0.41
1:k:300:GLY:C	1:k:302:VAL:H	2.28	0.41
1:m:43:ILE:O	1:m:47:LEU:HG	2.20	0.41
1:m:83:ASN:ND2	1:m:298:PRO:HG2	2.35	0.41
1:m:174:ALA:O	1:m:178:THR:OG1	2.25	0.41
1:n:99:VAL:HG23	1:n:100:SER:N	2.35	0.41
1:n:300:GLY:C	1:n:302:VAL:H	2.26	0.41
1:o:118:GLU:HG2	1:o:275:GLN:OE1	2.19	0.41
1:p:75:LEU:HD12	1:p:90:TYR:HD2	1.85	0.41
1:p:284:ASN:OD1	1:p:284:ASN:N	2.52	0.41
1:q:300:GLY:C	1:q:302:VAL:H	2.28	0.41
1:u:136:SER:OG	1:u:137:GLU:OE1	2.29	0.41
1:w:66:THR:HG23	1:w:286:GLY:HA3	2.01	0.41
1:w:300:GLY:C	1:w:302:VAL:H	2.28	0.41
1:2:40:TYR:CE2	1:K:288:PRO:HD3	2.56	0.41
1:4:193:THR:OG1	1:4:195:THR:HG22	2.19	0.41
1:6:186:SER:OG	1:6:187:PRO:HD3	2.20	0.41
1:7:107:SER:OG	1:x:157:ASN:ND2	2.48	0.41
1:A:78:VAL:HG23	1:A:85:ARG:O	2.19	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:GLU:CD	1:A:275:GLN:HE22	2.26	0.41
1:B:211:ASN:OD1	1:B:212:MET:N	2.53	0.41
1:D:25:ALA:O	1:D:29:ILE:HG13	2.20	0.41
1:D:117:ALA:HB2	1:D:275:GLN:HB3	2.02	0.41
1:N:42:ALA:O	1:N:46:GLY:N	2.53	0.41
1:P:117:ALA:HB3	1:P:275:GLN:HG2	2.02	0.41
1:R:141:GLN:HB2	1:R:148:TYR:HE2	1.86	0.41
1:d:80:TYR:N	1:d:81:PRO:HD2	2.35	0.41
1:d:195:THR:HG23	1:d:200:ALA:HB2	2.01	0.41
1:e:32:ILE:HD12	1:e:32:ILE:HA	1.93	0.41
1:g:21:GLY:HA2	1:i:27:ILE:HD11	2.02	0.41
1:i:121:SER:OG	1:i:122:TYR:N	2.53	0.41
1:i:300:GLY:C	1:i:302:VAL:H	2.28	0.41
1:k:147:GLN:OE1	1:k:147:GLN:N	2.52	0.41
1:n:236:PHE:CE1	1:n:260:MET:HB3	2.55	0.41
1:q:38:LEU:HD23	1:r:27:ILE:HD12	2.03	0.41
1:q:143:TYR:HB3	1:q:148:TYR:CD2	2.54	0.41
1:x:165:TYR:HE1	1:x:239:PRO:HD2	1.85	0.41
1:y:136:SER:OG	1:y:137:GLU:OE1	2.39	0.41
1:5:40:TYR:CE1	1:N:288:PRO:HD3	2.56	0.41
1:5:79:ASN:OD1	1:5:79:ASN:N	2.53	0.41
1:5:240:VAL:O	1:6:124:ASN:ND2	2.51	0.41
1:7:130:LEU:HD13	1:7:165:TYR:HE2	1.85	0.41
1:C:114:THR:HG23	1:C:278:THR:HB	2.01	0.41
1:C:282:THR:HG22	1:C:288:PRO:HB3	2.02	0.41
1:F:175:LEU:HA	1:F:178:THR:HG22	2.02	0.41
1:F:303:SER:HB3	1:F:305:ILE:HG22	2.03	0.41
1:H:86:SER:OG	1:H:268:GLY:HA2	2.19	0.41
1:K:114:THR:HG23	1:K:278:THR:HB	2.02	0.41
1:N:141:GLN:O	1:N:141:GLN:HG2	2.20	0.41
1:T:212:MET:HA	1:T:228:ALA:O	2.20	0.41
1:Z:43:ILE:O	1:Z:47:LEU:HG	2.20	0.41
1:b:195:THR:HG23	1:b:200:ALA:HB2	2.01	0.41
1:c:25:ALA:O	1:c:29:ILE:HG13	2.20	0.41
1:d:186:SER:OG	1:d:187:PRO:HD3	2.20	0.41
1:e:105:SER:O	1:e:109:THR:HG22	2.20	0.41
1:e:288:PRO:HD3	1:v:40:TYR:CZ	2.55	0.41
1:h:63:THR:OG1	1:h:285:ILE:HD11	2.19	0.41
1:i:19:LEU:HG	1:i:21:GLY:H	1.84	0.41
1:i:141:GLN:O	1:i:141:GLN:HG2	2.20	0.41
1:n:163:VAL:HG22	1:n:246:ILE:HD11	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:o:131:LEU:HG	1:o:239:PRO:HD3	2.01	0.41
1:p:70:LEU:HD13	1:p:291:ILE:HD11	2.01	0.41
1:q:78:VAL:HG23	1:q:85:ARG:O	2.21	0.41
1:q:235:ALA:HB2	1:q:261:ILE:HG12	2.02	0.41
1:r:153:ASN:ND2	1:r:164:TYR:OH	2.47	0.41
1:z:252:PRO:O	1:z:255:SER:OG	2.33	0.41
1:1:46:GLY:HA3	1:2:34:THR:HG23	2.02	0.41
1:2:56:THR:HG21	1:I:29:ILE:HG23	2.02	0.41
1:2:68:LEU:HD21	1:2:102:VAL:HG21	2.02	0.41
1:2:266:ASP:OD1	1:2:266:ASP:N	2.51	0.41
1:A:46:GLY:O	1:A:50:THR:HG22	2.20	0.41
1:A:300:GLY:C	1:A:302:VAL:H	2.29	0.41
1:D:241:ALA:HB3	1:D:256:VAL:HB	2.02	0.41
1:H:145:ASN:ND2	1:H:222:THR:HB	2.35	0.41
1:K:126:TYR:HH	1:K:237:THR:HG1	1.57	0.41
1:R:305:ILE:HD12	1:R:305:ILE:HA	1.93	0.41
1:W:150:ASP:OD1	1:W:150:ASP:N	2.49	0.41
1:W:198:SER:O	1:W:201:THR:OG1	2.31	0.41
1:b:59:LYS:HD3	1:b:59:LYS:HA	1.59	0.41
1:l:177:TYR:CE2	1:l:181:LYS:HD3	2.55	0.41
1:o:30:ALA:O	1:o:34:THR:HG23	2.20	0.41
1:p:37:VAL:HA	1:p:40:TYR:HB3	2.03	0.41
1:w:43:ILE:HG23	1:x:30:ALA:HB1	2.02	0.41
1:x:37:VAL:HA	1:x:40:TYR:CZ	2.55	0.41
1:x:154:GLN:HB3	1:x:163:VAL:HG12	2.02	0.41
1:z:109:THR:HG22	1:z:283:PRO:HA	2.03	0.41
1:0:115:ALA:HB1	1:0:118:GLU:OE2	2.21	0.41
1:2:141:GLN:HG3	1:2:177:TYR:CE2	2.56	0.41
1:4:99:VAL:HG11	1:L:33:ILE:HD11	2.01	0.41
1:7:150:ASP:OD1	1:7:150:ASP:N	2.50	0.41
1:A:111:ILE:HG12	1:A:281:ILE:HG12	2.02	0.41
1:A:151:LEU:HD23	1:A:174:ALA:HB2	2.02	0.41
1:D:261:ILE:HD12	1:D:279:ILE:HD13	2.03	0.41
1:E:19:LEU:HG	1:E:21:GLY:H	1.85	0.41
1:E:59:LYS:HD2	1:E:59:LYS:HA	1.84	0.41
1:G:235:ALA:HB2	1:G:261:ILE:HG12	2.03	0.41
1:O:109:THR:HG22	1:O:283:PRO:HA	2.02	0.41
1:R:22:LEU:HD13	1:k:49:VAL:HG11	2.02	0.41
1:R:176:ASN:HD21	1:R:192:ILE:H	1.67	0.41
1:R:285:ILE:HD11	1:k:296:TYR:CE2	2.55	0.41
1:X:120:ILE:HG21	1:X:267:LEU:HD13	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:30:ALA:O	1:Z:34:THR:HG23	2.21	0.41
1:Z:80:TYR:CE1	1:Z:299:GLU:HA	2.55	0.41
1:e:199:SER:HA	1:e:202:GLN:NE2	2.33	0.41
1:g:266:ASP:N	1:g:266:ASP:OD1	2.53	0.41
1:n:279:ILE:O	1:n:291:ILE:N	2.49	0.41
1:p:273:GLN:HE21	1:p:298:PRO:HD3	1.85	0.41
1:r:111:ILE:HG12	1:r:281:ILE:HG23	2.02	0.41
1:s:141:GLN:HG3	1:s:177:TYR:CE2	2.55	0.41
1:x:79:ASN:OD1	1:x:79:ASN:N	2.52	0.41
1:0:112:SER:OG	1:0:280:GLN:HB3	2.20	0.41
1:1:111:ILE:HG12	1:1:281:ILE:HG12	2.03	0.41
1:6:113:PHE:CE1	1:6:267:LEU:HD21	2.56	0.41
1:A:46:GLY:HA3	1:G:34:THR:HG23	2.03	0.41
1:B:80:TYR:CE2	1:g:245:LEU:HD11	2.55	0.41
1:C:78:VAL:HG23	1:C:85:ARG:O	2.21	0.41
1:C:112:SER:O	1:C:112:SER:OG	2.34	0.41
1:C:140:ASN:HB3	1:C:141:GLN:OE1	2.20	0.41
1:D:80:TYR:CE2	1:y:245:LEU:HD23	2.51	0.41
1:H:149:LEU:H	1:H:149:LEU:HD23	1.86	0.41
1:N:79:ASN:N	1:N:79:ASN:OD1	2.53	0.41
1:S:197:PRO:HD3	1:S:227:TYR:CZ	2.56	0.41
1:V:20:ALA:HA	1:V:23:ASP:OD1	2.20	0.41
1:Z:237:THR:HG22	1:Z:259:VAL:HG22	2.02	0.41
1:a:82:SER:O	1:a:82:SER:OG	2.39	0.41
1:c:59:LYS:HD3	1:c:59:LYS:HA	1.89	0.41
1:c:300:GLY:C	1:c:302:VAL:H	2.29	0.41
1:d:78:VAL:HG11	1:d:298:PRO:HB2	2.03	0.41
1:e:130:LEU:O	1:e:133:VAL:HG12	2.20	0.41
1:f:71:SER:O	1:f:71:SER:OG	2.35	0.41
1:h:186:SER:OG	1:h:187:PRO:HD3	2.21	0.41
1:j:86:SER:OG	1:j:268:GLY:HA2	2.20	0.41
1:j:300:GLY:C	1:j:302:VAL:H	2.29	0.41
1:m:300:GLY:C	1:m:302:VAL:H	2.28	0.41
1:q:80:TYR:N	1:q:81:PRO:HD2	2.35	0.41
1:r:127:GLU:HG3	1:r:234:PHE:HB2	2.01	0.41
1:s:163:VAL:HG22	1:s:246:ILE:HG13	2.03	0.41
1:s:252:PRO:O	1:s:255:SER:OG	2.28	0.41
1:u:135:PRO:HG3	1:u:163:VAL:HG11	2.02	0.41
1:z:237:THR:HG22	1:z:259:VAL:HG13	2.02	0.41
1:0:305:ILE:HD12	1:0:305:ILE:HA	1.88	0.41
1:2:28:LEU:HD11	1:3:22:LEU:HD12	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:199:SER:HA	1:6:202:GLN:HG2	2.02	0.41
1:B:59:LYS:HD2	1:B:59:LYS:HA	1.83	0.41
1:D:186:SER:OG	1:D:187:PRO:HD3	2.21	0.41
1:F:30:ALA:O	1:F:34:THR:HG23	2.21	0.41
1:H:212:MET:HA	1:H:228:ALA:O	2.21	0.41
1:K:40:TYR:CE2	1:d:288:PRO:HD3	2.55	0.41
1:L:293:GLU:OE1	1:T:51:GLN:NE2	2.35	0.41
1:M:99:VAL:HG23	1:M:100:SER:H	1.85	0.41
1:M:120:ILE:HG21	1:M:267:LEU:HD11	2.03	0.41
1:P:300:GLY:C	1:P:302:VAL:H	2.28	0.41
1:S:183:ASP:OD1	1:S:183:ASP:N	2.46	0.41
1:T:140:ASN:HB3	1:T:141:GLN:OE1	2.21	0.41
1:U:99:VAL:HG23	1:U:100:SER:N	2.35	0.41
1:W:83:ASN:ND2	1:W:298:PRO:HG2	2.35	0.41
1:X:28:LEU:O	1:X:32:ILE:HG12	2.21	0.41
1:X:89:ILE:HG13	1:X:263:PHE:HE1	1.84	0.41
1:Y:28:LEU:O	1:Y:32:ILE:HG12	2.21	0.41
1:a:280:GLN:HA	1:a:289:LEU:O	2.21	0.41
1:h:90:TYR:HB2	1:h:260:MET:HG3	2.02	0.41
1:n:121:SER:O	1:n:121:SER:OG	2.38	0.41
1:p:153:ASN:OD1	1:p:166:PRO:HG3	2.20	0.41
1:y:103:GLU:OE2	1:y:105:SER:N	2.54	0.41
1:z:305:ILE:HD12	1:z:305:ILE:HA	1.90	0.41
1:0:210:ASP:HB2	1:0:230:VAL:O	2.21	0.41
1:4:59:LYS:HD3	1:4:59:LYS:HA	1.85	0.41
1:5:80:TYR:CE1	1:5:299:GLU:HA	2.56	0.41
1:7:29:ILE:O	1:7:33:ILE:HG12	2.21	0.41
1:F:72:GLY:HA2	1:z:280:GLN:NE2	2.36	0.41
1:F:118:GLU:OE1	1:F:275:GLN:NE2	2.53	0.41
1:I:128:TYR:HE1	1:I:189:PRO:HG3	1.86	0.41
1:I:292:SER:HB3	1:i:48:PHE:HE1	1.86	0.41
1:K:25:ALA:O	1:K:29:ILE:HG13	2.21	0.41
1:K:183:ASP:OD1	1:K:183:ASP:N	2.45	0.41
1:L:109:THR:OG1	1:L:110:ALA:N	2.53	0.41
1:R:196:THR:O	1:R:199:SER:OG	2.39	0.41
1:Y:68:LEU:HD13	1:Y:93:VAL:HG11	2.03	0.41
1:Z:212:MET:HA	1:Z:228:ALA:O	2.20	0.41
1:a:305:ILE:HD12	1:a:305:ILE:HA	1.96	0.41
1:e:99:VAL:HG23	1:e:100:SER:H	1.85	0.41
1:j:302:VAL:O	1:j:302:VAL:HG23	2.21	0.41
1:k:137:GLU:OE1	1:k:137:GLU:N	2.53	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:k:172:LEU:HD21	1:k:262:LEU:HD11	2.03	0.41
1:k:210:ASP:HB2	1:k:230:VAL:O	2.20	0.41
1:o:235:ALA:HB2	1:o:261:ILE:HG12	2.03	0.41
1:t:59:LYS:HA	1:t:59:LYS:HD3	1.85	0.41
1:y:84:THR:HG23	1:y:85:ARG:HD3	2.01	0.41
1:2:182:ILE:HD13	1:2:182:ILE:HA	1.94	0.41
1:2:186:SER:OG	1:2:187:PRO:HD3	2.21	0.41
1:4:86:SER:OG	1:4:270:HIS:O	2.29	0.41
1:5:96:SER:OG	1:5:97:SER:N	2.54	0.41
1:5:288:PRO:HD3	1:L:40:TYR:CZ	2.56	0.41
1:6:155:GLN:HE22	1:6:164:TYR:HE2	1.69	0.41
1:7:59:LYS:O	1:7:62:GLU:HG3	2.20	0.41
1:C:266:ASP:OD1	1:C:267:LEU:N	2.52	0.41
1:D:72:GLY:HA2	1:h:280:GLN:NE2	2.36	0.41
1:E:80:TYR:N	1:E:81:PRO:HD2	2.35	0.41
1:E:300:GLY:C	1:E:302:VAL:H	2.28	0.41
1:I:149:LEU:HD23	1:I:149:LEU:H	1.86	0.41
1:R:69:THR:HG23	1:R:96:SER:HA	2.03	0.41
1:S:128:TYR:CE1	1:S:189:PRO:HG3	2.55	0.41
1:V:300:GLY:C	1:V:302:VAL:H	2.29	0.41
1:X:234:PHE:CZ	1:X:262:LEU:HD12	2.56	0.41
1:X:298:PRO:C	1:X:299:GLU:HG3	2.46	0.41
1:Z:80:TYR:HB2	1:Z:301:SER:HB2	2.02	0.41
1:c:133:VAL:HG11	1:c:178:THR:HG21	2.03	0.41
1:f:64:ALA:HB2	1:x:26:ILE:HG23	2.03	0.41
1:f:76:TYR:HD1	1:f:89:ILE:HG12	1.86	0.41
1:g:284:ASN:OD1	1:g:284:ASN:N	2.54	0.41
1:l:117:ALA:HB3	1:l:275:GLN:CD	2.46	0.41
1:m:112:SER:HG	1:m:280:GLN:HB3	1.86	0.41
1:m:266:ASP:OD1	1:m:267:LEU:N	2.54	0.41
1:r:89:ILE:HG13	1:r:263:PHE:CE2	2.56	0.41
1:s:304:VAL:O	1:s:305:ILE:HB	2.21	0.41
1:t:304:VAL:HG23	1:t:304:VAL:O	2.21	0.41
1:u:126:TYR:OH	1:u:237:THR:OG1	2.25	0.41
1:y:111:ILE:HA	1:y:280:GLN:O	2.21	0.41
1:z:110:ALA:HB3	1:z:282:THR:HG23	2.03	0.41
1:1:53:ALA:O	1:1:57:ILE:HG13	2.21	0.41
1:B:74:VAL:HA	1:B:91:PHE:HB3	2.03	0.41
1:C:245:LEU:HD12	1:C:245:LEU:O	2.22	0.41
1:D:296:TYR:CE1	1:o:98:GLY:HA3	2.56	0.41
1:E:211:ASN:O	1:E:229:PHE:HA	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:79:ASN:OD1	1:F:79:ASN:N	2.53	0.41
1:G:59:LYS:HD3	1:G:59:LYS:HA	1.85	0.41
1:G:167:ASN:ND2	1:G:169:TYR:HB2	2.36	0.41
1:K:245:LEU:HD12	1:K:245:LEU:O	2.21	0.41
1:M:241:ALA:HB2	1:N:110:ALA:HB2	2.03	0.41
1:O:87:TYR:HB3	1:O:88:TRP:CD1	2.56	0.41
1:P:235:ALA:HB2	1:P:261:ILE:HG12	2.02	0.41
1:P:300:GLY:O	1:P:301:SER:HB3	2.21	0.41
1:R:278:THR:HG22	1:R:292:SER:HB2	2.03	0.41
1:T:61:GLU:CD	1:m:52:LYS:HD3	2.46	0.41
1:T:245:LEU:O	1:T:245:LEU:HD12	2.21	0.41
1:U:71:SER:OG	1:U:92:THR:OG1	2.28	0.41
1:U:300:GLY:C	1:U:302:VAL:H	2.29	0.41
1:X:68:LEU:HA	1:X:95:PRO:HA	2.03	0.41
1:Y:19:LEU:HD21	1:Y:22:LEU:HB2	2.03	0.41
1:Y:267:LEU:HD12	1:Y:267:LEU:HA	1.95	0.41
1:d:165:TYR:HE1	1:d:239:PRO:HD2	1.85	0.41
1:g:128:TYR:O	1:g:236:PHE:HA	2.21	0.41
1:i:68:LEU:HD21	1:i:102:VAL:HG21	2.03	0.41
1:m:47:LEU:HD22	1:m:37:VAL:HG11	2.03	0.41
1:o:52:LYS:O	1:o:55:SER:OG	2.34	0.41
1:u:74:VAL:HG12	1:u:91:PHE:HB3	2.02	0.41
1:1:143:TYR:HB3	1:1:148:TYR:HA	2.03	0.40
1:5:114:THR:HG23	1:5:278:THR:HB	2.04	0.40
1:A:132:THR:HG23	1:A:249:ALA:HB2	2.04	0.40
1:B:68:LEU:HD23	1:B:95:PRO:HA	2.04	0.40
1:C:197:PRO:O	1:C:201:THR:HG23	2.21	0.40
1:D:273:GLN:HG2	1:D:274:TYR:CD1	2.56	0.40
1:H:273:GLN:O	1:H:275:GLN:HG3	2.20	0.40
1:L:59:LYS:HD3	1:L:59:LYS:HA	1.93	0.40
1:P:203:ILE:HG23	1:P:204:TYR:CD1	2.56	0.40
1:T:151:LEU:HA	1:T:170:TYR:HD2	1.86	0.40
1:a:248:SER:OG	1:a:250:ILE:HG22	2.21	0.40
1:b:20:ALA:O	1:b:24:THR:HG23	2.20	0.40
1:g:274:TYR:H	1:g:296:TYR:HB3	1.86	0.40
1:k:302:VAL:HG23	1:k:302:VAL:O	2.21	0.40
1:l:141:GLN:NE2	1:l:177:TYR:OH	2.54	0.40
1:m:59:LYS:HD3	1:m:59:LYS:HA	1.83	0.40
1:q:46:GLY:O	1:q:50:THR:HG23	2.22	0.40
1:q:241:ALA:HB2	1:r:110:ALA:HB2	2.03	0.40
1:t:80:TYR:HB2	1:t:301:SER:HB3	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:x:80:TYR:CE1	1:x:299:GLU:HA	2.56	0.40
1:x:98:GLY:HA2	1:x:253:ALA:HB1	2.03	0.40
1:y:252:PRO:O	1:y:255:SER:OG	2.32	0.40
1:y:280:GLN:O	1:y:281:ILE:HD13	2.21	0.40
1:2:120:ILE:HD12	1:2:120:ILE:HA	1.96	0.40
1:3:118:GLU:OE1	1:3:118:GLU:N	2.45	0.40
1:4:240:VAL:HG12	1:4:256:VAL:O	2.21	0.40
1:5:177:TYR:CE2	1:5:181:LYS:HD2	2.56	0.40
1:5:296:TYR:O	1:5:297:GLN:HG2	2.22	0.40
1:7:19:LEU:HG	1:7:21:GLY:H	1.86	0.40
1:A:19:LEU:HA	1:a:20:ALA:HB2	2.02	0.40
1:L:178:THR:HG22	1:L:182:ILE:HG13	2.03	0.40
1:M:246:ILE:HD13	1:M:246:ILE:HA	1.95	0.40
1:N:66:THR:HB	1:N:102:VAL:HG12	2.03	0.40
1:N:199:SER:HA	1:N:202:GLN:CD	2.45	0.40
1:O:298:PRO:O	1:O:303:SER:OG	2.31	0.40
1:T:87:TYR:CD1	1:T:213:PHE:HB3	2.56	0.40
1:b:127:GLU:HG3	1:b:234:PHE:HB2	2.03	0.40
1:d:105:SER:O	1:d:109:THR:HG22	2.20	0.40
1:k:114:THR:HG22	1:k:121:SER:HA	2.03	0.40
1:k:151:LEU:HD13	1:k:174:ALA:HB2	2.03	0.40
1:n:216:THR:HA	1:n:225:THR:HA	2.02	0.40
1:p:182:ILE:O	1:p:184:LYS:NZ	2.43	0.40
1:r:132:THR:HA	1:r:247:GLY:HA2	2.02	0.40
1:v:111:ILE:O	1:v:125:ILE:HG12	2.21	0.40
1:w:184:LYS:HA	1:w:184:LYS:HD3	1.95	0.40
1:y:104:LEU:HA	1:y:109:THR:HG21	2.03	0.40
1:0:216:THR:HA	1:0:225:THR:HA	2.04	0.40
1:3:245:LEU:HD12	1:3:245:LEU:O	2.21	0.40
1:5:284:ASN:OD1	1:5:285:ILE:N	2.53	0.40
1:6:20:ALA:O	1:6:24:THR:HG23	2.22	0.40
1:6:46:GLY:HA3	1:X:38:LEU:HD22	2.03	0.40
1:6:79:ASN:N	1:6:79:ASN:OD1	2.54	0.40
1:6:112:SER:OG	1:6:280:GLN:HB3	2.21	0.40
1:6:185:VAL:HG22	1:6:187:PRO:HD2	2.02	0.40
1:7:75:LEU:HD12	1:7:90:TYR:HD2	1.86	0.40
1:A:57:ILE:HG21	1:F:22:LEU:HD21	2.01	0.40
1:E:276:THR:HG22	1:E:294:TYR:HD1	1.86	0.40
1:G:79:ASN:OD1	1:G:79:ASN:N	2.54	0.40
1:I:233:THR:HG23	1:I:263:PHE:HA	2.04	0.40
1:M:67:ALA:O	1:M:96:SER:OG	2.24	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:189:PRO:O	1:O:230:VAL:HA	2.22	0.40
1:P:120:ILE:HD12	1:P:120:ILE:HA	1.95	0.40
1:Q:20:ALA:HA	1:Q:23:ASP:OD1	2.22	0.40
1:W:105:SER:O	1:W:109:THR:HG22	2.21	0.40
1:X:19:LEU:HG	1:X:21:GLY:H	1.86	0.40
1:f:59:LYS:HA	1:f:62:GLU:OE2	2.21	0.40
1:h:176:ASN:ND2	1:h:192:ILE:HB	2.36	0.40
1:v:47:LEU:HD23	1:w:37:VAL:HG11	2.04	0.40
1:w:85:ARG:NH2	1:w:211:ASN:OD1	2.49	0.40
1:w:120:ILE:HD13	1:w:267:LEU:HD13	2.02	0.40
1:w:216:THR:HG22	1:w:225:THR:HG22	2.02	0.40
1:1:130:LEU:HD11	1:1:175:LEU:HD13	2.04	0.40
1:1:244:PRO:HG2	1:1:245:LEU:HD12	2.03	0.40
1:5:304:VAL:HG12	1:5:305:ILE:HG12	2.04	0.40
1:7:69:THR:OG1	1:7:70:LEU:N	2.49	0.40
1:C:80:TYR:CE1	1:C:299:GLU:HA	2.56	0.40
1:E:132:THR:HA	1:E:247:GLY:HA2	2.03	0.40
1:E:253:ALA:HB3	1:Z:294:TYR:HE2	1.87	0.40
1:K:19:LEU:HG	1:K:21:GLY:H	1.86	0.40
1:K:145:ASN:OD1	1:K:146:GLY:N	2.48	0.40
1:L:183:ASP:OD1	1:L:183:ASP:N	2.45	0.40
1:M:109:THR:HG23	1:M:126:TYR:HD2	1.86	0.40
1:Z:56:THR:HG21	1:q:29:ILE:HG23	2.02	0.40
1:c:199:SER:O	1:c:203:ILE:HG22	2.21	0.40
1:e:39:ALA:HB1	1:f:30:ALA:HB2	2.02	0.40
1:l:111:ILE:HG12	1:l:281:ILE:HG12	2.03	0.40
1:s:198:SER:OG	1:s:199:SER:N	2.54	0.40
1:s:246:ILE:HD13	1:s:246:ILE:HA	1.94	0.40
1:u:65:SER:O	1:u:65:SER:OG	2.35	0.40
1:u:105:SER:O	1:u:109:THR:HG22	2.21	0.40
1:w:118:GLU:HG3	1:w:275:GLN:NE2	2.37	0.40
1:x:162:TYR:HD2	1:x:242:GLY:HA2	1.86	0.40
1:0:116:SER:OG	1:0:117:ALA:N	2.55	0.40
1:1:57:ILE:HG12	1:Q:32:ILE:HD13	2.04	0.40
1:1:197:PRO:O	1:1:201:THR:HG23	2.21	0.40
1:2:25:ALA:O	1:2:29:ILE:HG13	2.22	0.40
1:5:39:ALA:HB1	1:6:30:ALA:HB2	2.04	0.40
1:5:167:ASN:OD1	1:5:168:PRO:HD2	2.21	0.40
1:M:105:SER:O	1:M:109:THR:HG22	2.21	0.40
1:P:132:THR:O	1:P:247:GLY:HA2	2.22	0.40
1:S:19:LEU:HD21	1:S:22:LEU:HG	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:99:VAL:HG11	1:l:33:ILE:HD11	2.04	0.40
1:U:147:GLN:OE1	1:U:147:GLN:N	2.55	0.40
1:V:37:VAL:HA	1:V:40:TYR:HB3	2.03	0.40
1:W:191:TYR:CE2	1:W:193:THR:HB	2.55	0.40
1:j:266:ASP:OD1	1:j:266:ASP:N	2.54	0.40
1:k:54:LYS:HG3	1:l:45:MET:HG3	2.04	0.40
1:m:69:THR:N	1:m:94:SER:O	2.54	0.40
1:m:245:LEU:HD23	1:m:245:LEU:H	1.85	0.40
1:m:246:ILE:HD13	1:m:246:ILE:HA	1.87	0.40
1:o:180:SER:C	1:o:181:LYS:HD3	2.46	0.40
1:p:99:VAL:HG23	1:p:100:SER:N	2.36	0.40
1:p:197:PRO:O	1:p:201:THR:HG23	2.21	0.40
1:x:20:ALA:O	1:x:24:THR:HG23	2.21	0.40
1:z:71:SER:O	1:z:92:THR:OG1	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	285/306 (93%)	272 (95%)	13 (5%)	0	100	100
1	1	285/306 (93%)	270 (95%)	15 (5%)	0	100	100
1	2	285/306 (93%)	267 (94%)	18 (6%)	0	100	100
1	3	285/306 (93%)	264 (93%)	21 (7%)	0	100	100
1	4	285/306 (93%)	266 (93%)	19 (7%)	0	100	100
1	5	285/306 (93%)	267 (94%)	18 (6%)	0	100	100
1	6	285/306 (93%)	264 (93%)	21 (7%)	0	100	100
1	7	285/306 (93%)	260 (91%)	25 (9%)	0	100	100
1	A	285/306 (93%)	271 (95%)	14 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	285/306 (93%)	265 (93%)	20 (7%)	0	100	100
1	C	285/306 (93%)	265 (93%)	20 (7%)	0	100	100
1	D	285/306 (93%)	271 (95%)	14 (5%)	0	100	100
1	E	285/306 (93%)	261 (92%)	24 (8%)	0	100	100
1	F	285/306 (93%)	268 (94%)	17 (6%)	0	100	100
1	G	285/306 (93%)	267 (94%)	18 (6%)	0	100	100
1	H	285/306 (93%)	270 (95%)	15 (5%)	0	100	100
1	I	285/306 (93%)	270 (95%)	15 (5%)	0	100	100
1	J	285/306 (93%)	268 (94%)	17 (6%)	0	100	100
1	K	285/306 (93%)	271 (95%)	14 (5%)	0	100	100
1	L	285/306 (93%)	265 (93%)	20 (7%)	0	100	100
1	M	285/306 (93%)	269 (94%)	16 (6%)	0	100	100
1	N	285/306 (93%)	262 (92%)	23 (8%)	0	100	100
1	O	285/306 (93%)	266 (93%)	19 (7%)	0	100	100
1	P	285/306 (93%)	264 (93%)	21 (7%)	0	100	100
1	Q	285/306 (93%)	270 (95%)	15 (5%)	0	100	100
1	R	285/306 (93%)	270 (95%)	15 (5%)	0	100	100
1	S	285/306 (93%)	270 (95%)	15 (5%)	0	100	100
1	T	285/306 (93%)	266 (93%)	19 (7%)	0	100	100
1	U	285/306 (93%)	272 (95%)	13 (5%)	0	100	100
1	V	285/306 (93%)	264 (93%)	21 (7%)	0	100	100
1	W	285/306 (93%)	271 (95%)	14 (5%)	0	100	100
1	X	285/306 (93%)	268 (94%)	17 (6%)	0	100	100
1	Y	285/306 (93%)	267 (94%)	18 (6%)	0	100	100
1	Z	285/306 (93%)	270 (95%)	15 (5%)	0	100	100
1	a	285/306 (93%)	265 (93%)	20 (7%)	0	100	100
1	b	285/306 (93%)	271 (95%)	14 (5%)	0	100	100
1	c	285/306 (93%)	264 (93%)	21 (7%)	0	100	100
1	d	285/306 (93%)	264 (93%)	21 (7%)	0	100	100
1	e	285/306 (93%)	266 (93%)	19 (7%)	0	100	100
1	f	285/306 (93%)	259 (91%)	26 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	g	285/306 (93%)	264 (93%)	21 (7%)	0	100	100
1	h	285/306 (93%)	268 (94%)	17 (6%)	0	100	100
1	i	285/306 (93%)	267 (94%)	18 (6%)	0	100	100
1	j	285/306 (93%)	264 (93%)	21 (7%)	0	100	100
1	k	285/306 (93%)	267 (94%)	18 (6%)	0	100	100
1	l	285/306 (93%)	269 (94%)	16 (6%)	0	100	100
1	m	285/306 (93%)	269 (94%)	16 (6%)	0	100	100
1	n	285/306 (93%)	267 (94%)	18 (6%)	0	100	100
1	o	285/306 (93%)	266 (93%)	19 (7%)	0	100	100
1	p	285/306 (93%)	264 (93%)	21 (7%)	0	100	100
1	q	285/306 (93%)	268 (94%)	17 (6%)	0	100	100
1	r	285/306 (93%)	268 (94%)	17 (6%)	0	100	100
1	s	285/306 (93%)	265 (93%)	20 (7%)	0	100	100
1	t	285/306 (93%)	267 (94%)	18 (6%)	0	100	100
1	u	285/306 (93%)	265 (93%)	20 (7%)	0	100	100
1	v	285/306 (93%)	261 (92%)	24 (8%)	0	100	100
1	w	285/306 (93%)	270 (95%)	15 (5%)	0	100	100
1	x	285/306 (93%)	266 (93%)	19 (7%)	0	100	100
1	y	285/306 (93%)	267 (94%)	18 (6%)	0	100	100
1	z	285/306 (93%)	263 (92%)	22 (8%)	0	100	100
All	All	17100/18360 (93%)	16005 (94%)	1095 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	244/261 (94%)	244 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	244/261 (94%)	244 (100%)	0	100	100
1	2	244/261 (94%)	243 (100%)	1 (0%)	84	83
1	3	244/261 (94%)	244 (100%)	0	100	100
1	4	244/261 (94%)	243 (100%)	1 (0%)	84	83
1	5	244/261 (94%)	244 (100%)	0	100	100
1	6	244/261 (94%)	244 (100%)	0	100	100
1	7	244/261 (94%)	244 (100%)	0	100	100
1	A	244/261 (94%)	244 (100%)	0	100	100
1	B	244/261 (94%)	244 (100%)	0	100	100
1	C	244/261 (94%)	244 (100%)	0	100	100
1	D	244/261 (94%)	244 (100%)	0	100	100
1	E	244/261 (94%)	244 (100%)	0	100	100
1	F	244/261 (94%)	244 (100%)	0	100	100
1	G	244/261 (94%)	244 (100%)	0	100	100
1	H	244/261 (94%)	244 (100%)	0	100	100
1	I	244/261 (94%)	244 (100%)	0	100	100
1	J	244/261 (94%)	244 (100%)	0	100	100
1	K	244/261 (94%)	244 (100%)	0	100	100
1	L	244/261 (94%)	244 (100%)	0	100	100
1	M	244/261 (94%)	244 (100%)	0	100	100
1	N	244/261 (94%)	244 (100%)	0	100	100
1	O	244/261 (94%)	244 (100%)	0	100	100
1	P	244/261 (94%)	244 (100%)	0	100	100
1	Q	244/261 (94%)	244 (100%)	0	100	100
1	R	244/261 (94%)	244 (100%)	0	100	100
1	S	244/261 (94%)	244 (100%)	0	100	100
1	T	244/261 (94%)	244 (100%)	0	100	100
1	U	244/261 (94%)	244 (100%)	0	100	100
1	V	244/261 (94%)	244 (100%)	0	100	100
1	W	244/261 (94%)	244 (100%)	0	100	100
1	X	244/261 (94%)	244 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Y	244/261 (94%)	244 (100%)	0	100	100
1	Z	244/261 (94%)	244 (100%)	0	100	100
1	a	244/261 (94%)	244 (100%)	0	100	100
1	b	244/261 (94%)	244 (100%)	0	100	100
1	c	244/261 (94%)	244 (100%)	0	100	100
1	d	244/261 (94%)	244 (100%)	0	100	100
1	e	244/261 (94%)	244 (100%)	0	100	100
1	f	244/261 (94%)	244 (100%)	0	100	100
1	g	244/261 (94%)	244 (100%)	0	100	100
1	h	244/261 (94%)	244 (100%)	0	100	100
1	i	244/261 (94%)	244 (100%)	0	100	100
1	j	244/261 (94%)	244 (100%)	0	100	100
1	k	244/261 (94%)	244 (100%)	0	100	100
1	l	244/261 (94%)	244 (100%)	0	100	100
1	m	244/261 (94%)	244 (100%)	0	100	100
1	n	244/261 (94%)	244 (100%)	0	100	100
1	o	244/261 (94%)	244 (100%)	0	100	100
1	p	244/261 (94%)	244 (100%)	0	100	100
1	q	244/261 (94%)	244 (100%)	0	100	100
1	r	244/261 (94%)	244 (100%)	0	100	100
1	s	244/261 (94%)	244 (100%)	0	100	100
1	t	244/261 (94%)	244 (100%)	0	100	100
1	u	244/261 (94%)	244 (100%)	0	100	100
1	v	244/261 (94%)	244 (100%)	0	100	100
1	w	244/261 (94%)	244 (100%)	0	100	100
1	x	244/261 (94%)	244 (100%)	0	100	100
1	y	244/261 (94%)	244 (100%)	0	100	100
1	z	244/261 (94%)	244 (100%)	0	100	100
All	All	14640/15660 (94%)	14638 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	2	282	THR
1	4	79	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (247) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	160	GLN
1	0	167	ASN
1	0	202	GLN
1	1	83	ASN
1	1	141	GLN
1	1	147	GLN
1	1	153	ASN
1	2	83	ASN
1	2	153	ASN
1	2	273	GLN
1	2	297	GLN
1	3	153	ASN
1	4	153	ASN
1	4	155	GLN
1	4	231	ASN
1	4	232	GLN
1	5	83	ASN
1	5	147	GLN
1	6	145	ASN
1	6	147	GLN
1	6	153	ASN
1	6	157	ASN
1	6	202	GLN
1	6	280	GLN
1	6	297	GLN
1	7	124	ASN
1	7	147	GLN
1	A	51	GLN
1	A	141	GLN
1	A	145	ASN
1	A	202	GLN
1	A	209	HIS
1	A	273	GLN
1	A	297	GLN
1	B	51	GLN
1	B	145	ASN
1	B	209	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	270	HIS
1	C	140	ASN
1	C	145	ASN
1	C	167	ASN
1	C	275	GLN
1	D	51	GLN
1	D	124	ASN
1	D	155	GLN
1	D	160	GLN
1	D	167	ASN
1	D	273	GLN
1	D	275	GLN
1	E	83	ASN
1	E	141	GLN
1	E	153	ASN
1	E	270	HIS
1	E	297	GLN
1	F	145	ASN
1	F	153	ASN
1	F	209	HIS
1	G	145	ASN
1	G	153	ASN
1	G	273	GLN
1	G	297	GLN
1	H	202	GLN
1	H	273	GLN
1	H	297	GLN
1	I	51	GLN
1	I	83	ASN
1	I	209	HIS
1	J	51	GLN
1	J	83	ASN
1	J	141	GLN
1	J	145	ASN
1	J	209	HIS
1	J	232	GLN
1	K	51	GLN
1	K	83	ASN
1	K	273	GLN
1	K	297	GLN
1	L	83	ASN
1	L	145	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	L	232	GLN
1	M	83	ASN
1	M	147	GLN
1	M	153	ASN
1	M	160	GLN
1	M	273	GLN
1	M	297	GLN
1	N	51	GLN
1	N	140	ASN
1	N	157	ASN
1	N	218	ASN
1	N	232	GLN
1	O	157	ASN
1	P	140	ASN
1	P	147	GLN
1	P	153	ASN
1	P	273	GLN
1	Q	83	ASN
1	Q	145	ASN
1	Q	147	GLN
1	Q	297	GLN
1	R	58	ASN
1	R	124	ASN
1	R	218	ASN
1	R	275	GLN
1	R	280	GLN
1	S	51	GLN
1	S	153	ASN
1	S	218	ASN
1	T	140	ASN
1	T	145	ASN
1	T	155	GLN
1	T	167	ASN
1	T	232	GLN
1	T	273	GLN
1	U	44	ASN
1	U	176	ASN
1	U	209	HIS
1	U	275	GLN
1	V	167	ASN
1	V	232	GLN
1	W	51	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	W	58	ASN
1	W	83	ASN
1	W	140	ASN
1	W	145	ASN
1	W	147	GLN
1	W	232	GLN
1	W	297	GLN
1	X	83	ASN
1	X	124	ASN
1	Y	145	ASN
1	Y	147	GLN
1	Y	209	HIS
1	Y	273	GLN
1	Y	280	GLN
1	a	83	ASN
1	a	147	GLN
1	a	154	GLN
1	b	83	ASN
1	b	140	ASN
1	b	202	GLN
1	c	51	GLN
1	c	83	ASN
1	c	147	GLN
1	c	155	GLN
1	c	297	GLN
1	d	140	ASN
1	d	154	GLN
1	d	232	GLN
1	e	83	ASN
1	e	147	GLN
1	e	155	GLN
1	e	157	ASN
1	e	273	GLN
1	f	51	GLN
1	f	58	ASN
1	f	83	ASN
1	f	147	GLN
1	f	157	ASN
1	f	232	GLN
1	g	51	GLN
1	g	141	GLN
1	h	83	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	h	155	GLN
1	h	176	ASN
1	i	83	ASN
1	i	140	ASN
1	i	273	GLN
1	j	157	ASN
1	j	160	GLN
1	j	273	GLN
1	j	297	GLN
1	k	140	ASN
1	k	141	GLN
1	k	157	ASN
1	k	176	ASN
1	k	202	GLN
1	k	275	GLN
1	k	280	GLN
1	l	140	ASN
1	l	145	ASN
1	l	167	ASN
1	l	273	GLN
1	l	297	GLN
1	m	141	GLN
1	m	160	GLN
1	n	44	ASN
1	n	51	GLN
1	n	83	ASN
1	n	270	HIS
1	n	273	GLN
1	n	275	GLN
1	n	297	GLN
1	o	44	ASN
1	o	140	ASN
1	o	145	ASN
1	o	153	ASN
1	o	270	HIS
1	p	51	GLN
1	p	124	ASN
1	p	145	ASN
1	p	157	ASN
1	p	176	ASN
1	p	273	GLN
1	p	280	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	q	145	ASN
1	q	147	GLN
1	q	153	ASN
1	q	155	GLN
1	q	160	GLN
1	q	275	GLN
1	q	280	GLN
1	r	145	ASN
1	r	160	GLN
1	s	51	GLN
1	s	83	ASN
1	s	145	ASN
1	s	218	ASN
1	s	232	GLN
1	t	83	ASN
1	t	141	GLN
1	t	154	GLN
1	t	273	GLN
1	u	140	ASN
1	u	141	GLN
1	u	160	GLN
1	u	273	GLN
1	v	147	GLN
1	w	83	ASN
1	w	147	GLN
1	w	209	HIS
1	w	275	GLN
1	x	140	ASN
1	x	145	ASN
1	x	153	ASN
1	y	58	ASN
1	y	145	ASN
1	y	154	GLN
1	y	176	ASN
1	y	202	GLN
1	y	297	GLN
1	z	44	ASN
1	z	141	GLN
1	z	145	ASN
1	z	160	GLN
1	z	232	GLN
1	z	273	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

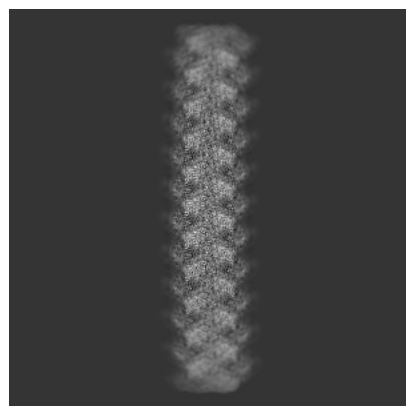
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27026. These allow visual inspection of the internal detail of the map and identification of artifacts.

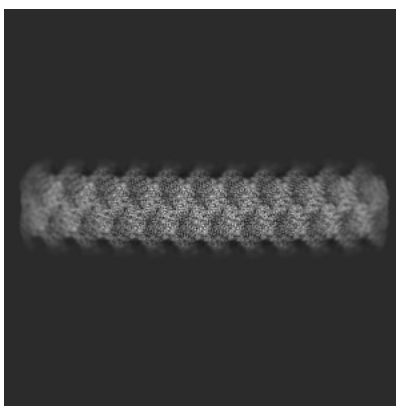
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

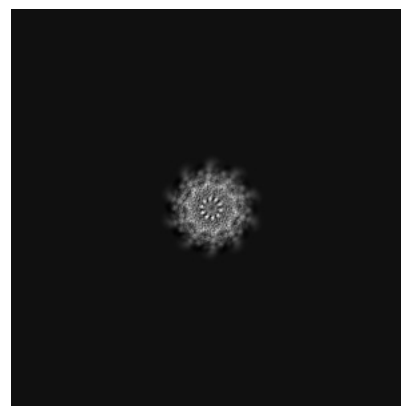
6.1.1 Primary map



X

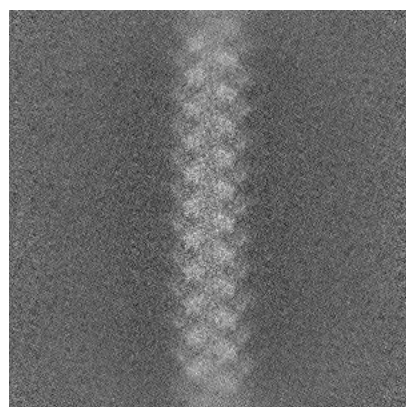


Y

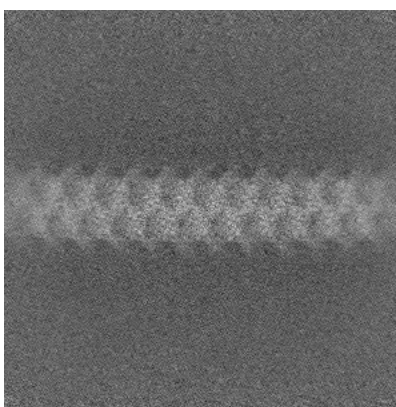


Z

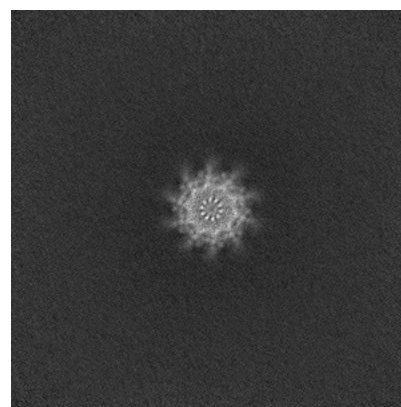
6.1.2 Raw map



X



Y

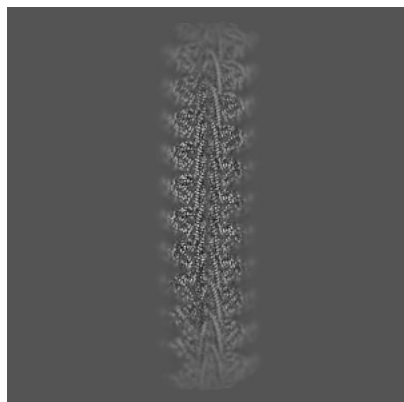


Z

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

6.2 Central slices [i](#)

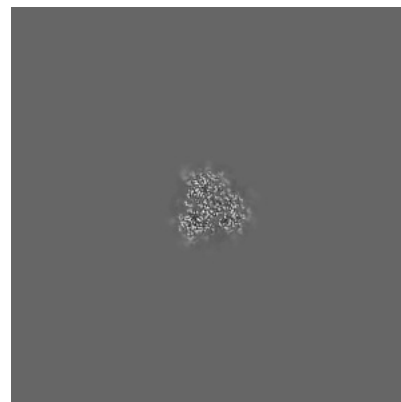
6.2.1 Primary map



X Index: 312

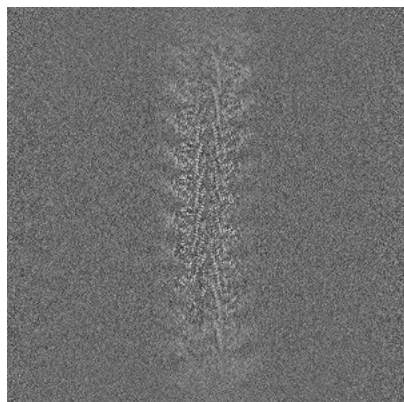


Y Index: 312

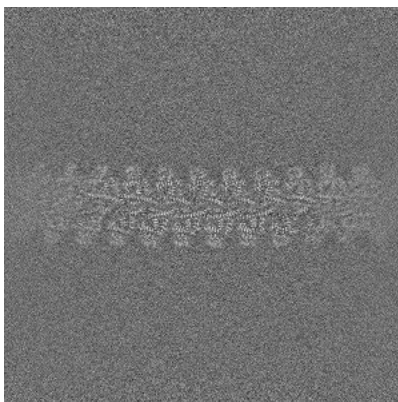


Z Index: 312

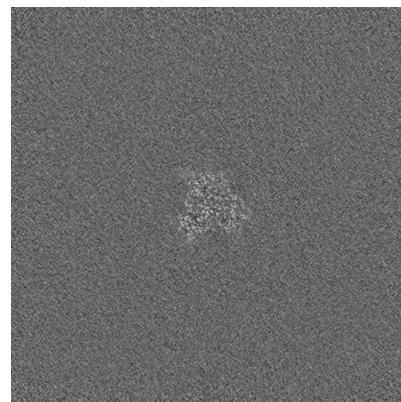
6.2.2 Raw map



X Index: 312



Y Index: 312



Z Index: 312

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

6.3 Largest variance slices [i](#)

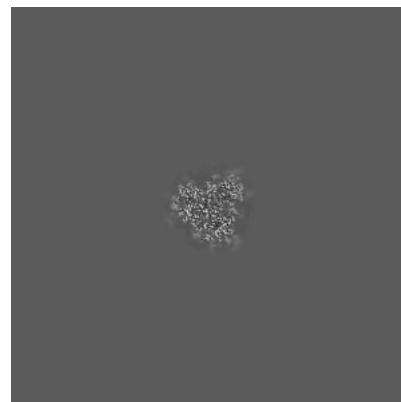
6.3.1 Primary map



X Index: 304

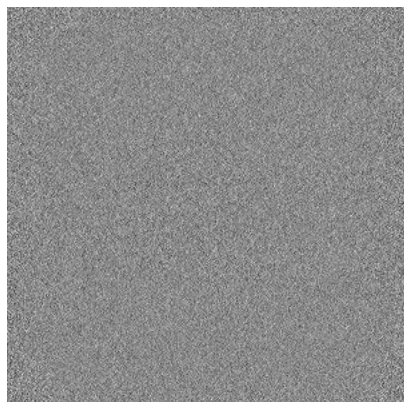


Y Index: 307

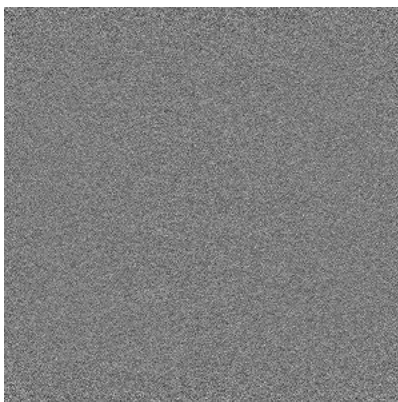


Z Index: 286

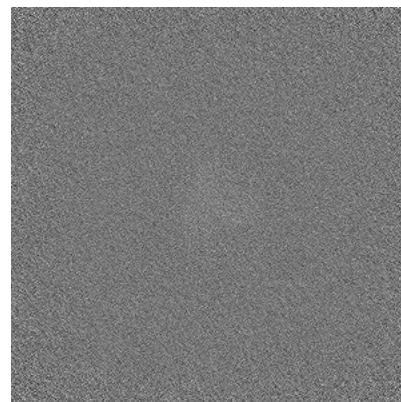
6.3.2 Raw map



X Index: 0



Y Index: 0

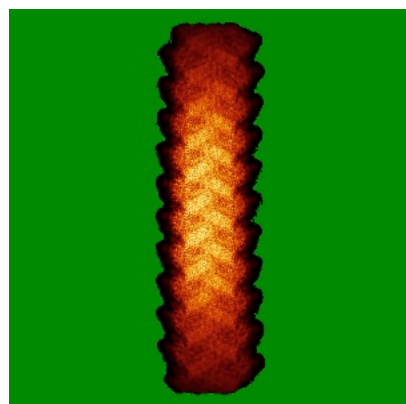


Z Index: 0

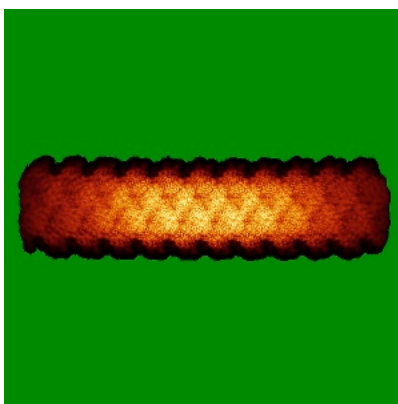
The images above show the largest variance slices of the map in three orthogonal directions.

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

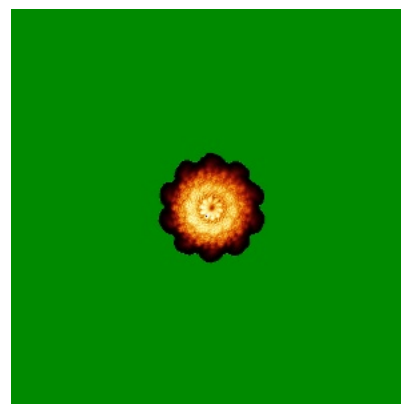
6.4.1 Primary map



X

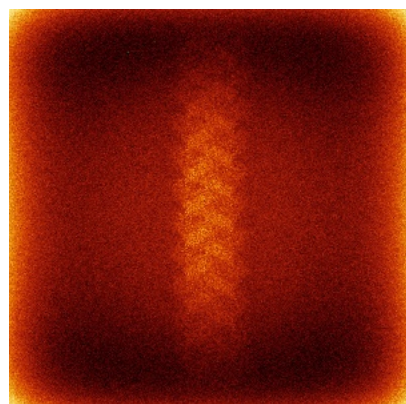


Y

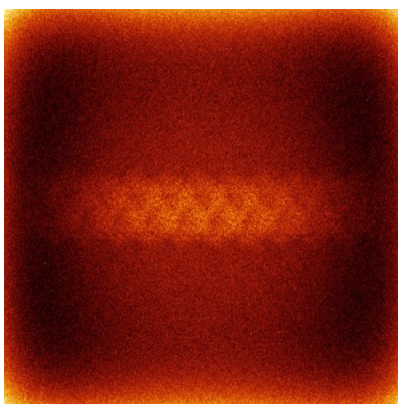


Z

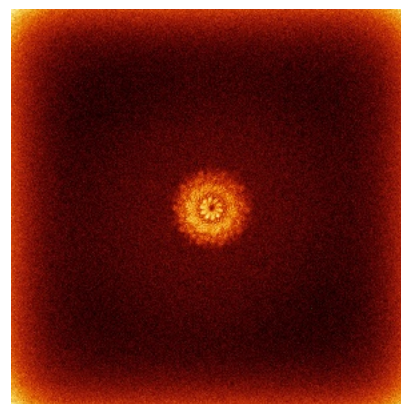
6.4.2 Raw map



X



Y

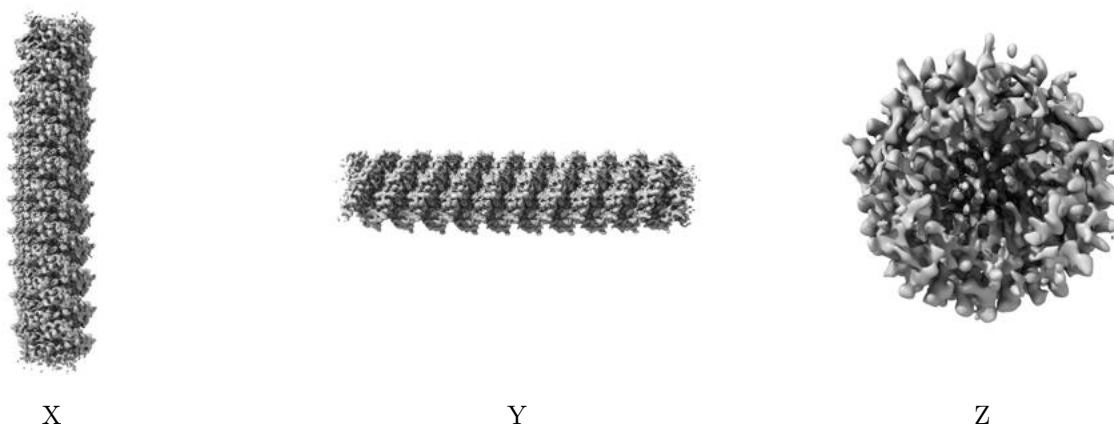


Z

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.

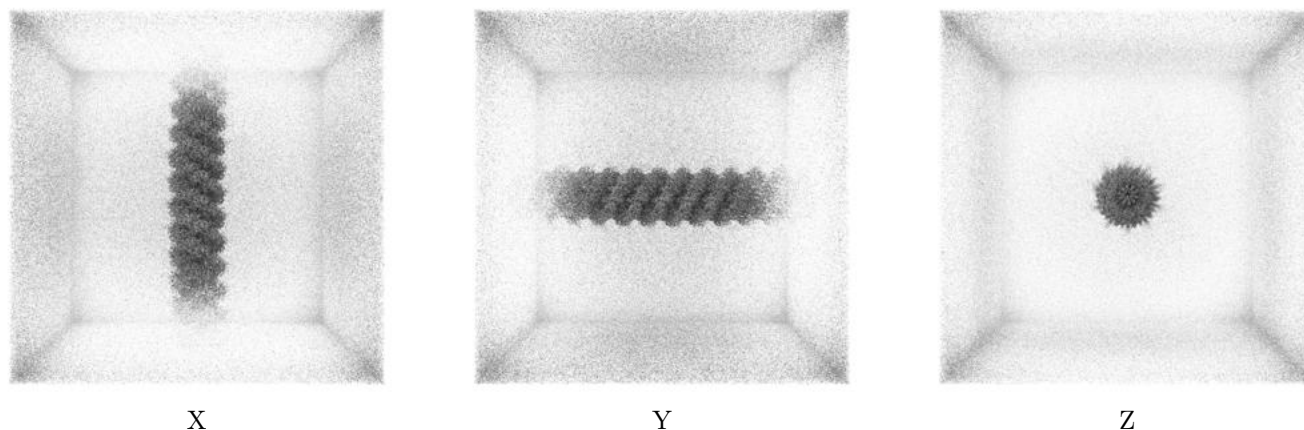
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.112. 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.

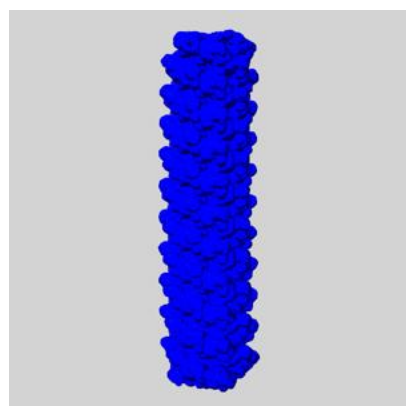
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

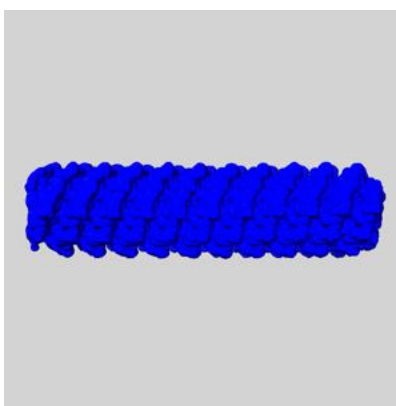
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

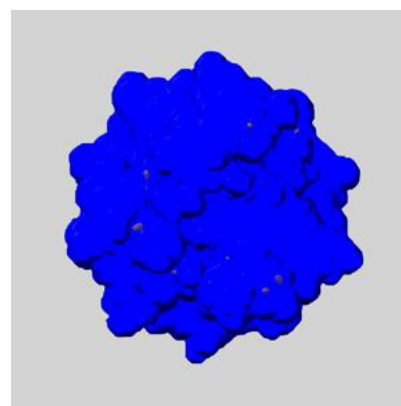
6.6.1 emd_27026_msk_1.map [i](#)



X



Y

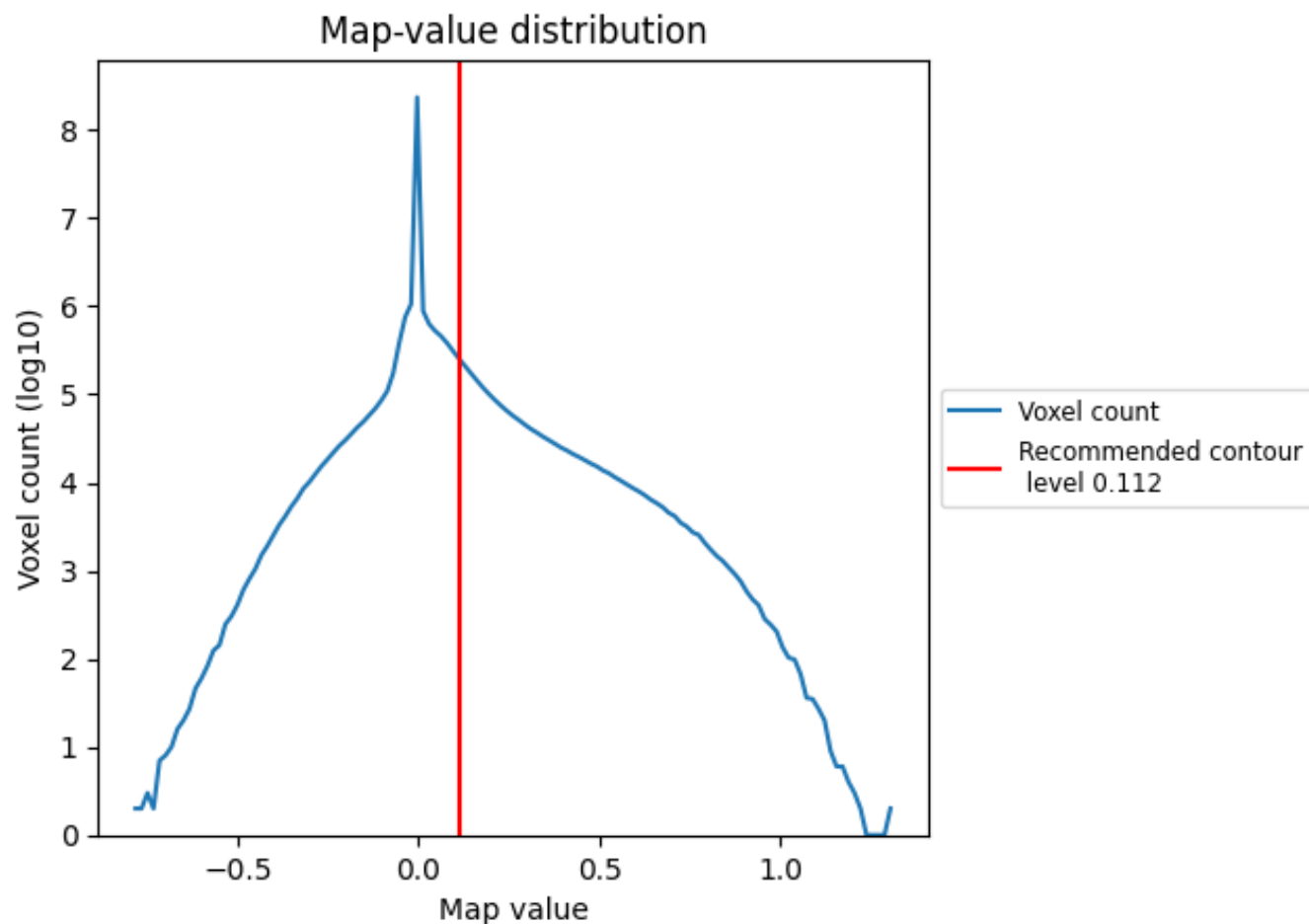


Z

7 Map analysis [i](#)

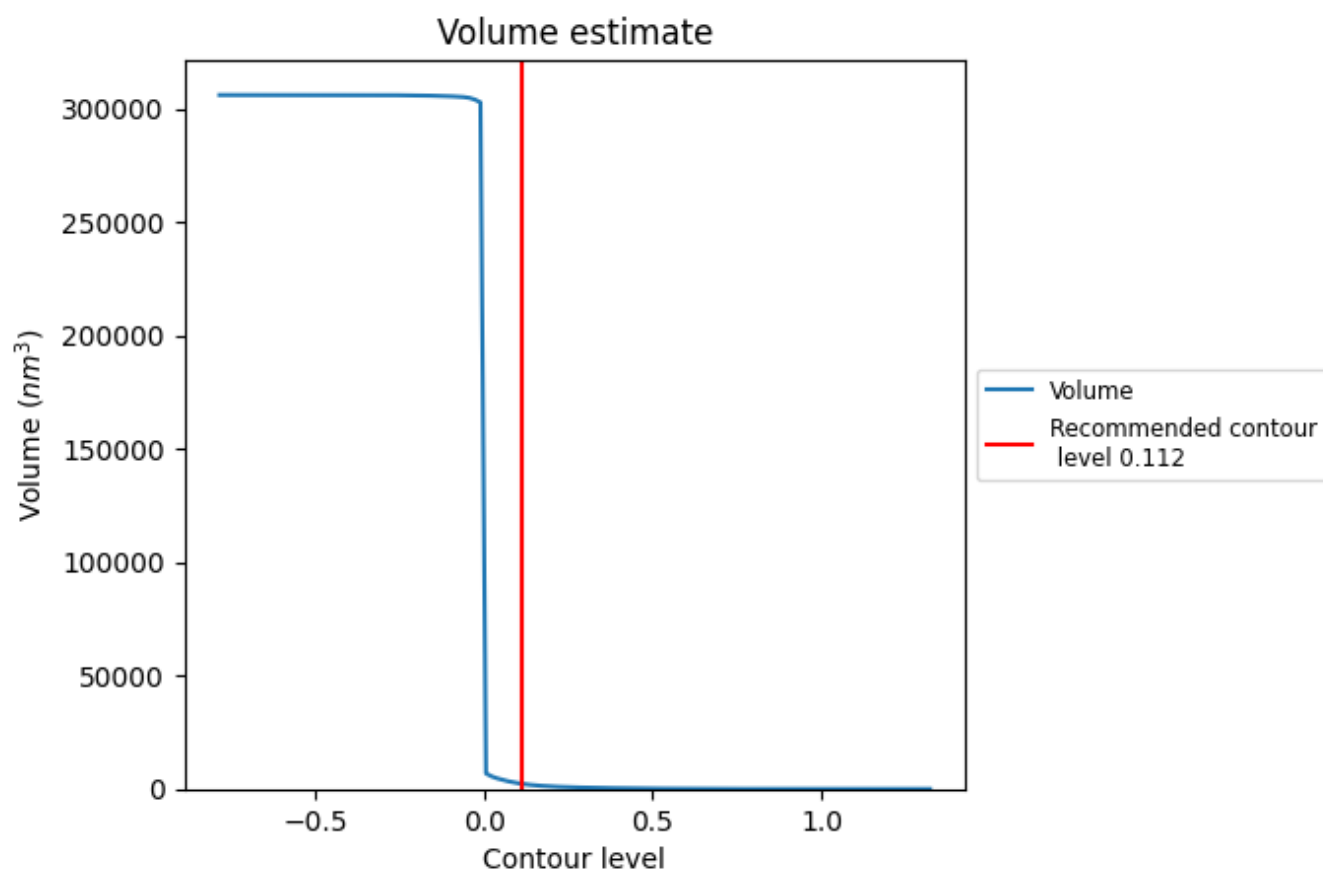
This section contains the results of statistical analysis of the map.

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.

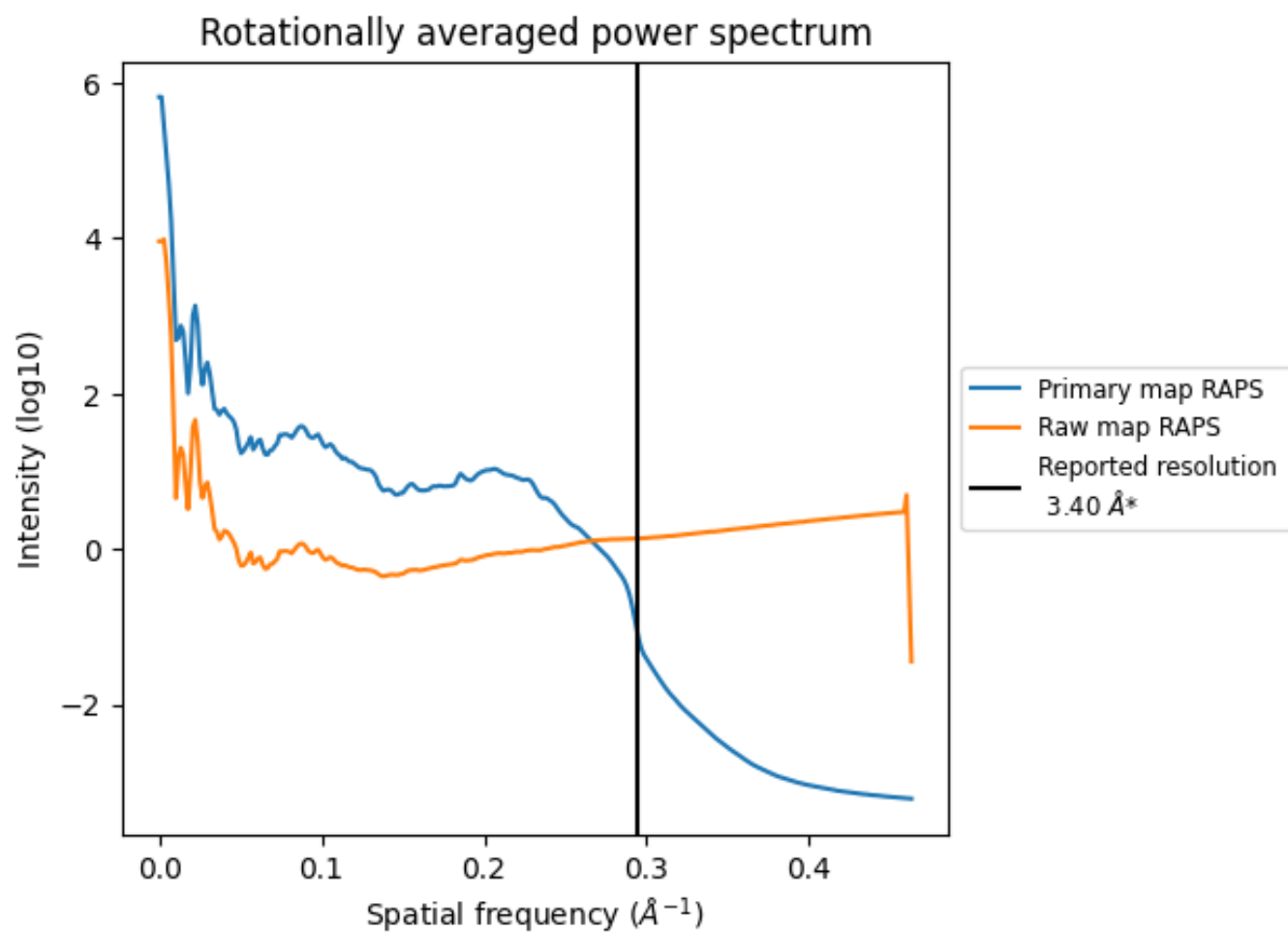
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2306 nm^3 ; this corresponds to an approximate mass of 2083 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

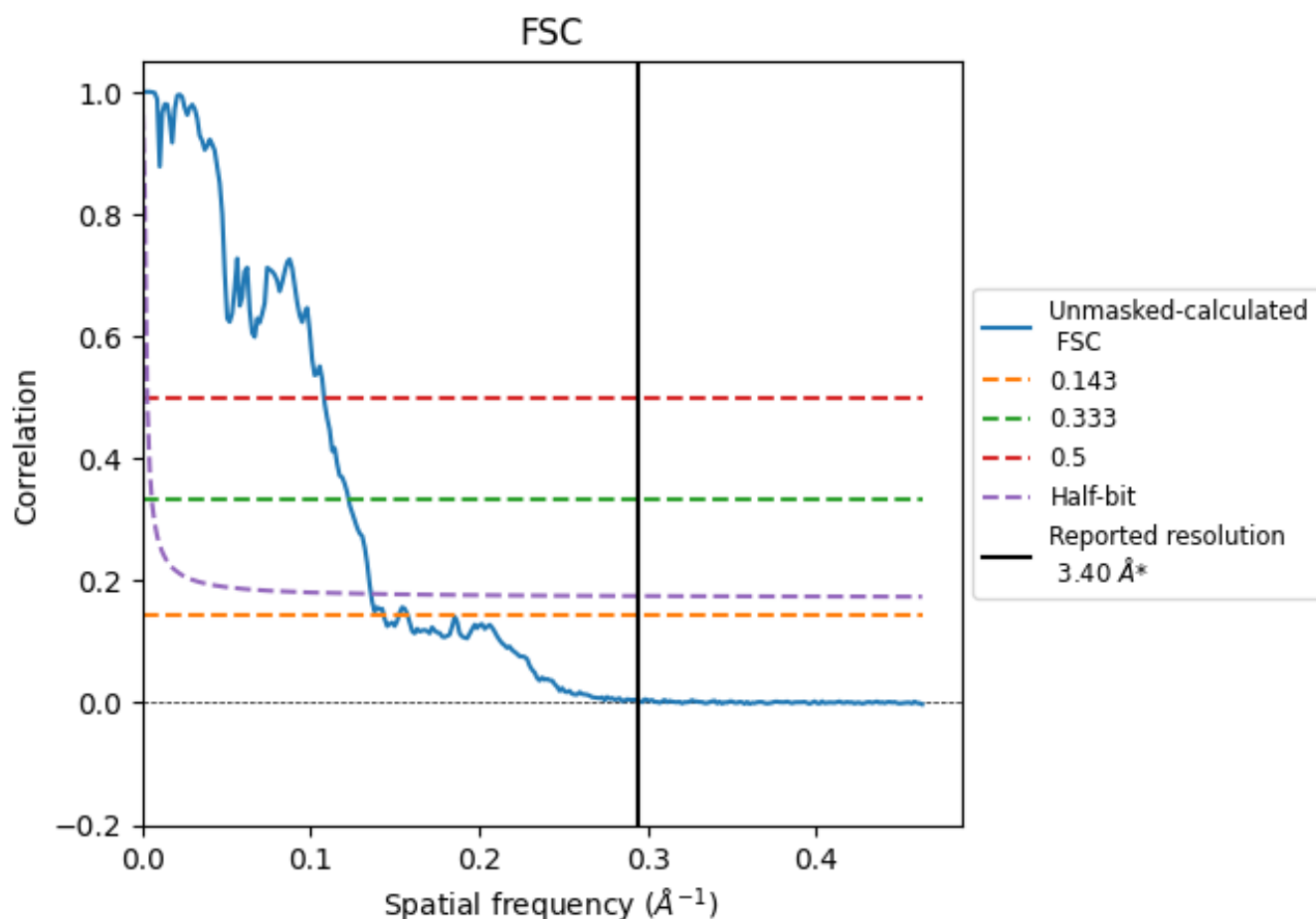


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [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 $0.294 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

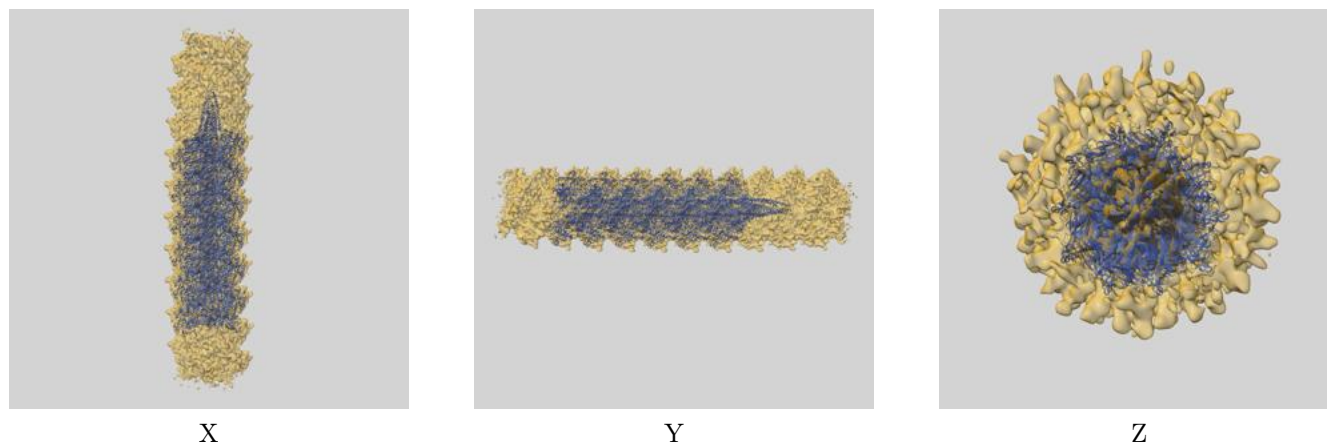
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	0.333
Reported by author	-	-	-	3.40
Author-provided FSC curve	-	-	-	-
Unmasked-calculated*	6.97	9.26	7.36	8.16

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.33 CUT-OFF 8.16 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

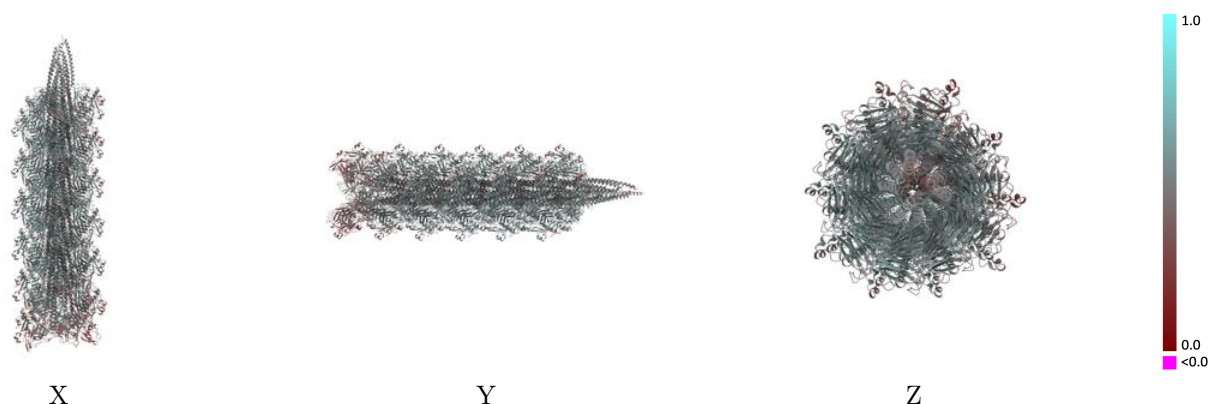
This section contains information regarding the fit between EMDB map EMD-27026 and PDB model 8CWM. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



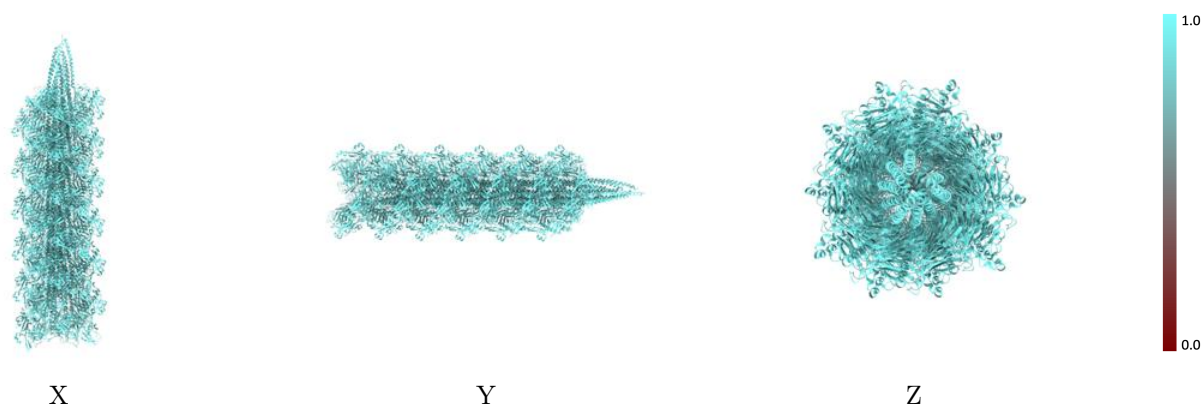
The images above show the 3D surface view of the map at the recommended contour level 0.112 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



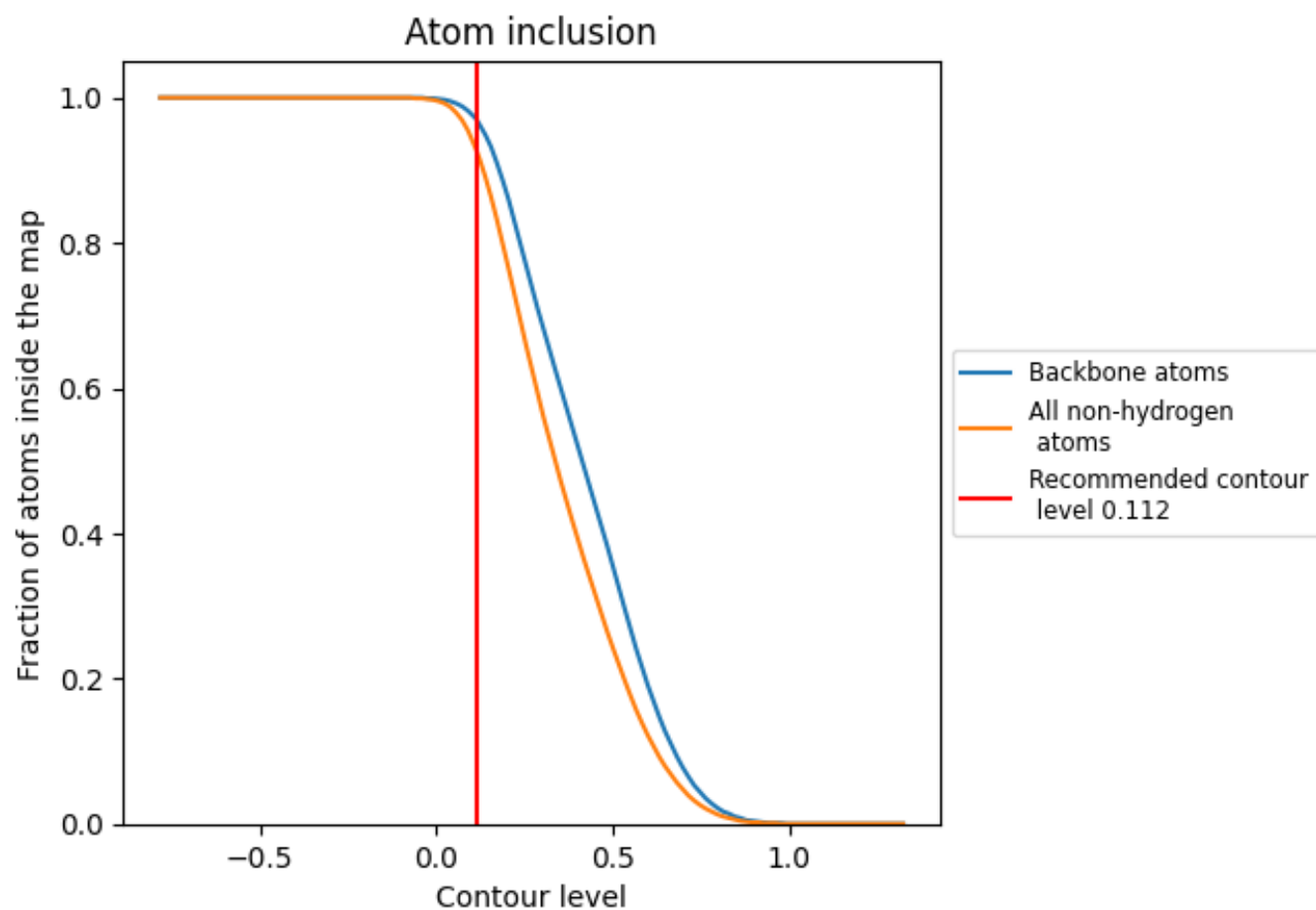
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.112).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 93% 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 (0.112) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9290	 0.4920
0	 0.8590	 0.3970
1	 0.9520	 0.5330
2	 0.9630	 0.5310
3	 0.9550	 0.5310
4	 0.9530	 0.5290
5	 0.9490	 0.5200
6	 0.9340	 0.4970
7	 0.9180	 0.4720
A	 0.9400	 0.4930
B	 0.9320	 0.4900
C	 0.9050	 0.4630
D	 0.8940	 0.4480
E	 0.9330	 0.4810
F	 0.9350	 0.4980
G	 0.9540	 0.5200
H	 0.9600	 0.5300
I	 0.9400	 0.5210
J	 0.9610	 0.5300
K	 0.9520	 0.5290
L	 0.9410	 0.5220
M	 0.9450	 0.5170
N	 0.9430	 0.4960
O	 0.9250	 0.4770
P	 0.9350	 0.4920
Q	 0.9580	 0.5240
R	 0.8480	 0.3820
S	 0.9480	 0.5200
T	 0.9400	 0.5140
U	 0.8480	 0.3890
V	 0.9270	 0.5020
W	 0.9220	 0.4850
X	 0.9190	 0.4770
Y	 0.9310	 0.4950
Z	 0.9480	 0.5210



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
a	 0.9560	 0.5330
b	 0.9350	 0.5170
c	 0.9490	 0.5200
d	 0.9560	 0.5270
e	 0.9230	 0.4870
f	 0.9140	 0.4800
g	 0.8990	 0.4570
h	 0.8850	 0.4270
i	 0.9310	 0.4870
j	 0.9260	 0.4870
k	 0.9120	 0.4740
l	 0.8930	 0.4480
m	 0.9240	 0.4900
n	 0.9080	 0.4590
o	 0.8740	 0.4240
p	 0.9000	 0.4610
q	 0.9530	 0.5180
r	 0.9600	 0.5290
s	 0.9520	 0.5290
t	 0.9570	 0.5290
u	 0.9570	 0.5300
v	 0.9430	 0.5190
w	 0.9460	 0.5130
x	 0.9420	 0.4920
y	 0.8420	 0.3700
z	 0.9430	 0.5110