



Full wwPDB EM Validation Report ⓘ

Sep 17, 2025 – 01:10 PM EDT

PDB ID : 9N8M / pdb_00009n8m
EMDB ID : EMD-49131
Title : In situ sheathed flagellar FlaC filament in *Vibrio cholerae*.
Authors : Wangbiao, G.; Rajeev, K.
Deposited on : 2025-02-08
Resolution : 3.16 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.dev126
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

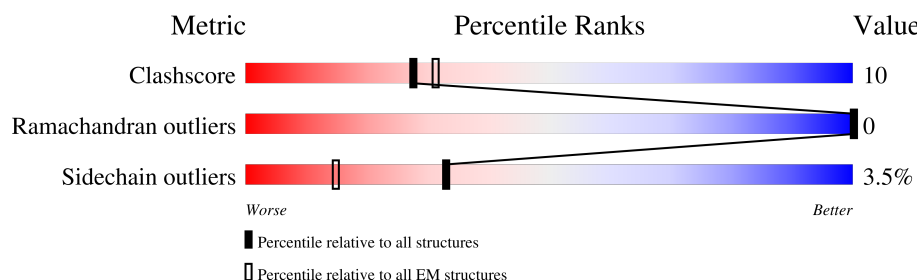
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.16 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	M1	377	<div> <div>7%</div> <div>75%</div> <div>24%</div> <div>.</div> </div>
1	M2	377	<div> <div>6%</div> <div>77%</div> <div>22%</div> <div>.</div> </div>
1	M3	377	<div> <div>5%</div> <div>79%</div> <div>19%</div> <div>.</div> </div>
1	M4	377	<div> <div>14%</div> <div>77%</div> <div>22%</div> <div>.</div> </div>
1	M5	377	<div> <div>73%</div> <div>26%</div> </div>
1	M6	377	<div> <div>6%</div> <div>74%</div> <div>25%</div> <div>.</div> </div>
1	M7	377	<div> <div>19%</div> <div>80%</div> <div>20%</div> </div>
1	M8	377	<div> <div>7%</div> <div>77%</div> <div>22%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	M9	377	
1	MA	377	
1	MB	377	
1	MC	377	
1	MD	377	
1	ME	377	
1	MF	377	
1	MG	377	
1	MH	377	
1	MI	377	
1	MJ	377	
1	MK	377	
1	ML	377	
1	MM	377	
1	MN	377	
1	MO	377	
1	MP	377	
1	MQ	377	
1	MR	377	
1	MS	377	
1	MT	377	
1	MU	377	
1	MV	377	
1	MW	377	
1	MX	377	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 92202 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 C.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	M1	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	M2	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	M3	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	M4	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	M5	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	M6	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	M7	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	M8	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	M9	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MA	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MB	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MC	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MD	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	ME	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MF	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MG	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MH	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		

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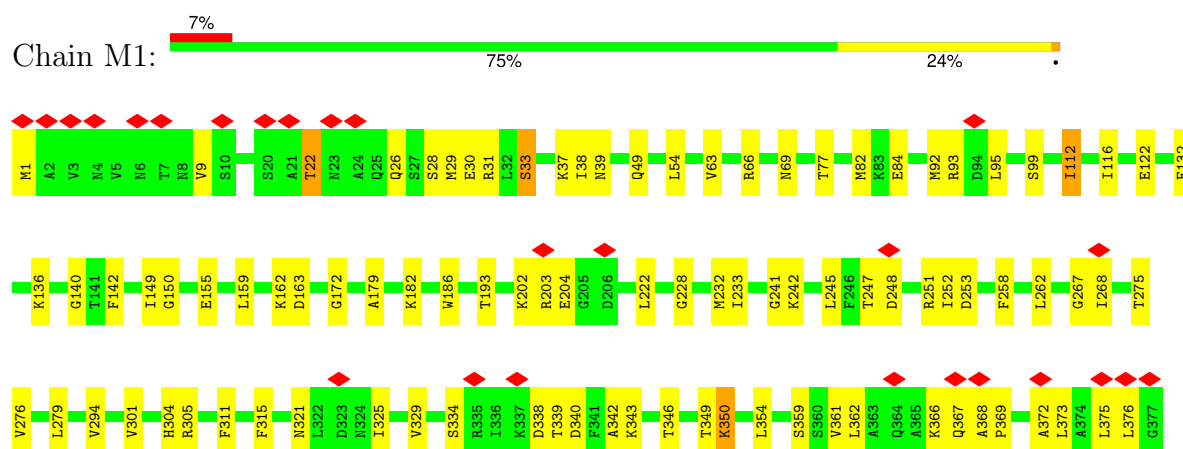
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Mol	Chain	Residues	Atoms					AltConf	Trace
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1	MJ	377	Total	C	N	O	S	0	0
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1	MK	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	ML	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MM	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MN	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MO	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MP	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MQ	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MR	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MS	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MT	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MU	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MV	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MW	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		
1	MX	377	Total	C	N	O	S	0	0
			2794	1693	503	588	10		

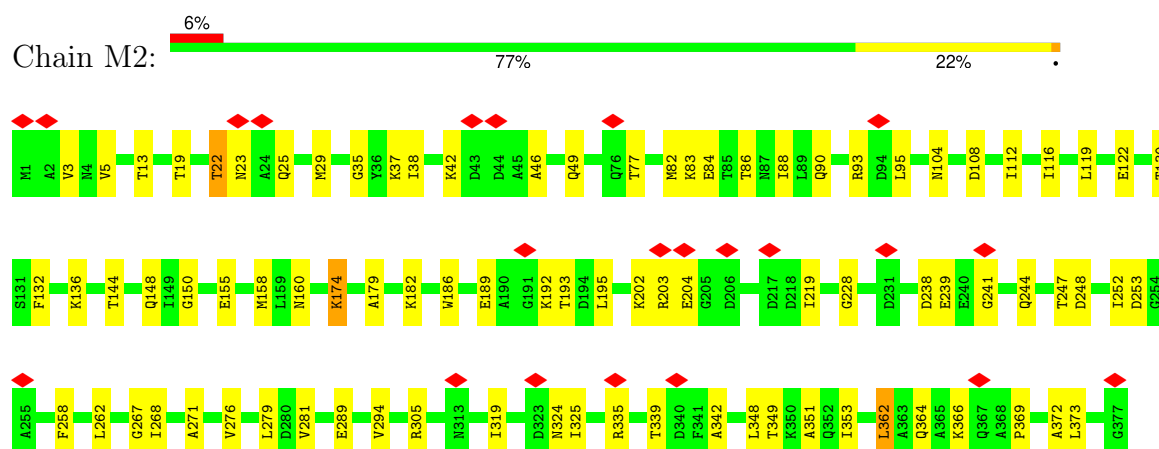
3 Residue-property plots

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.

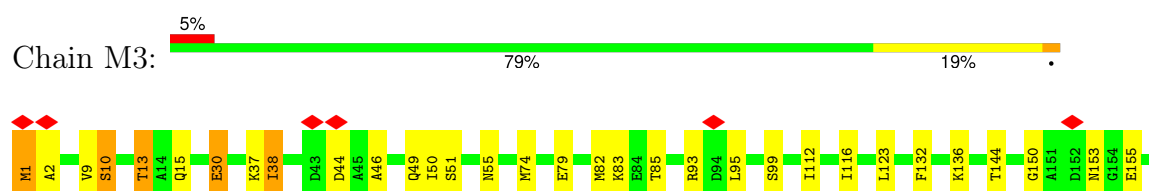
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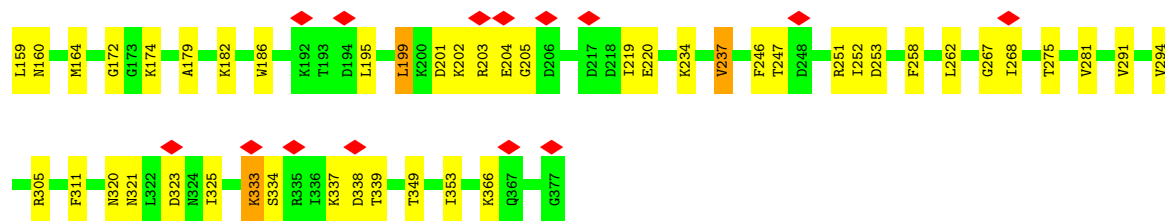


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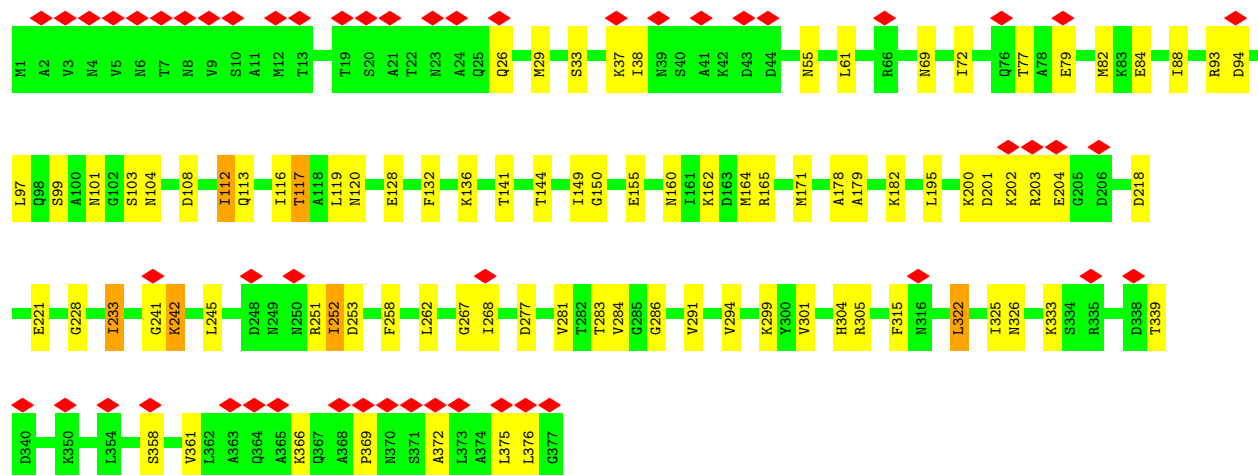
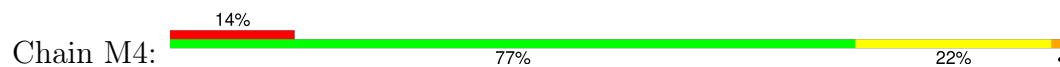


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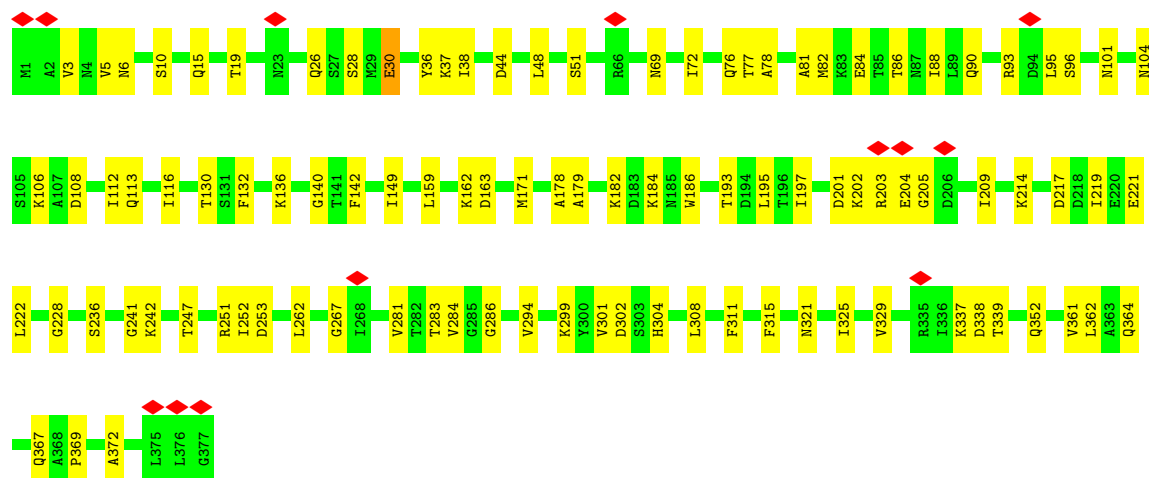
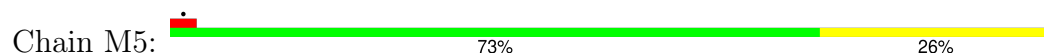




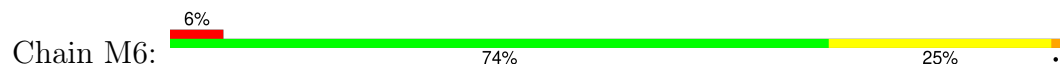
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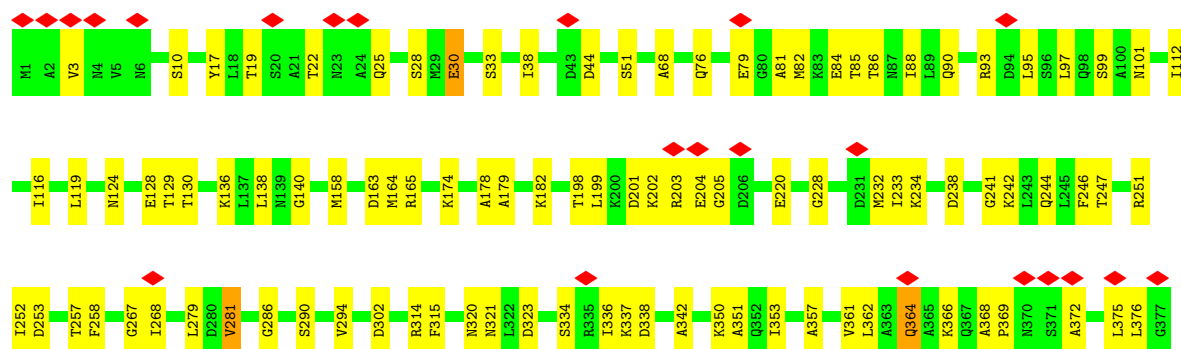


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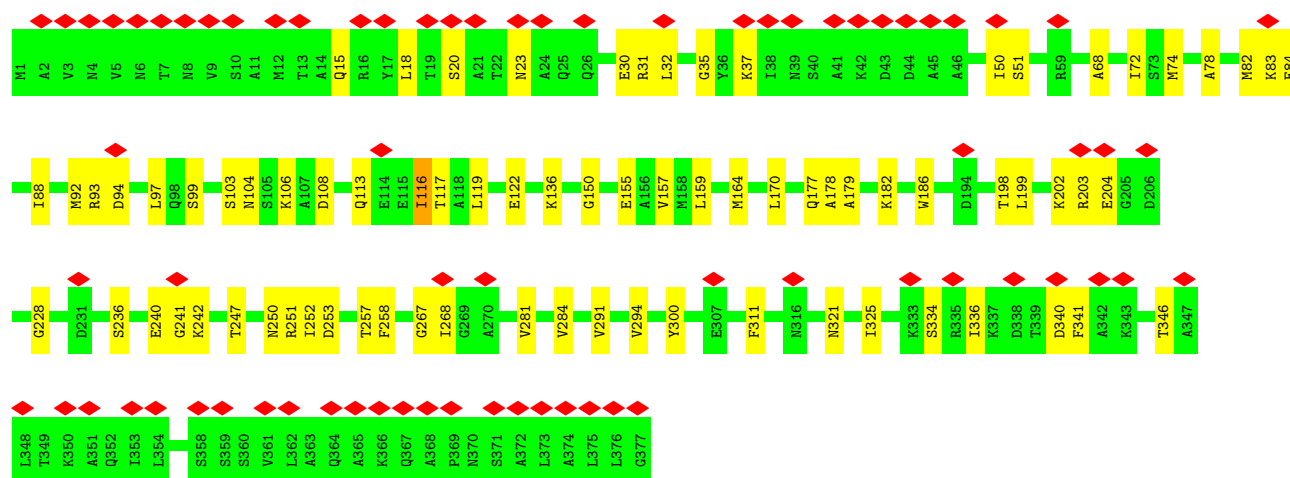
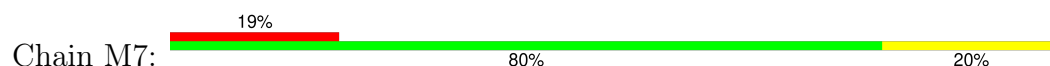


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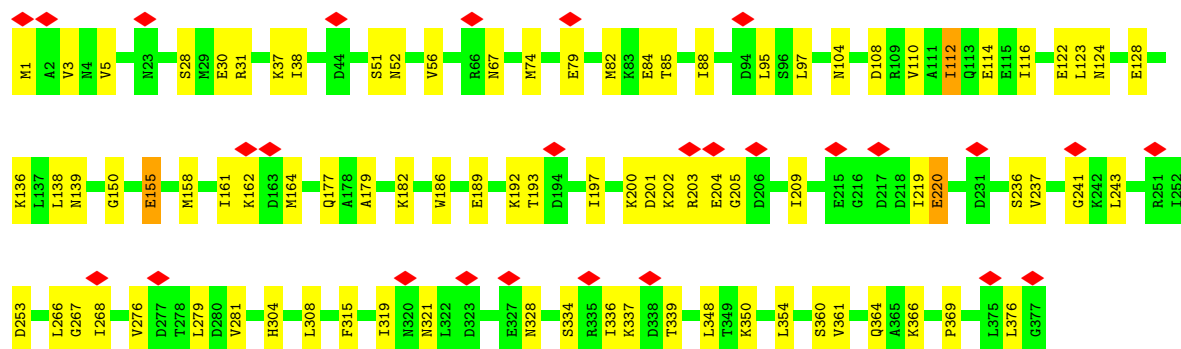
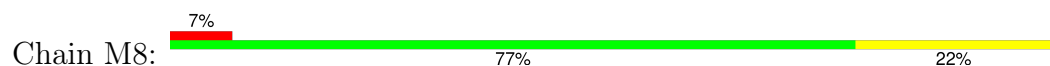




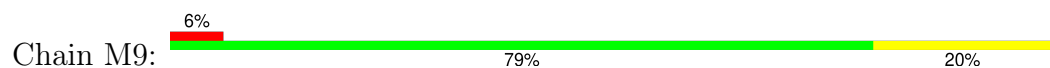
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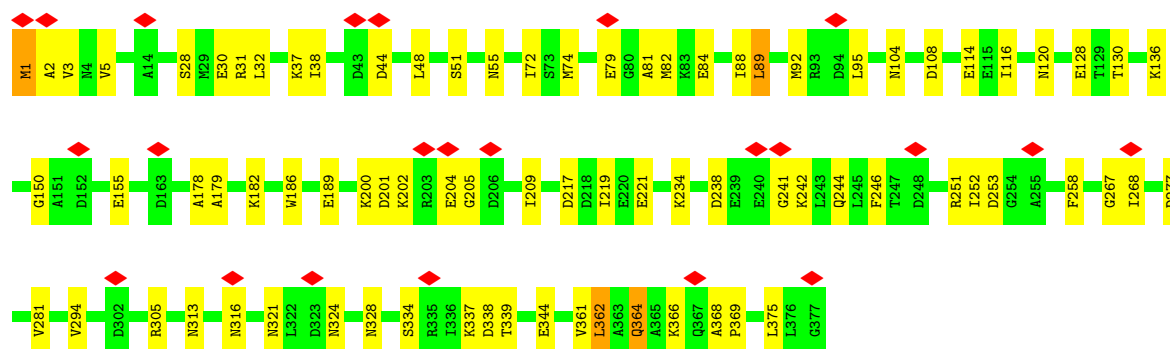


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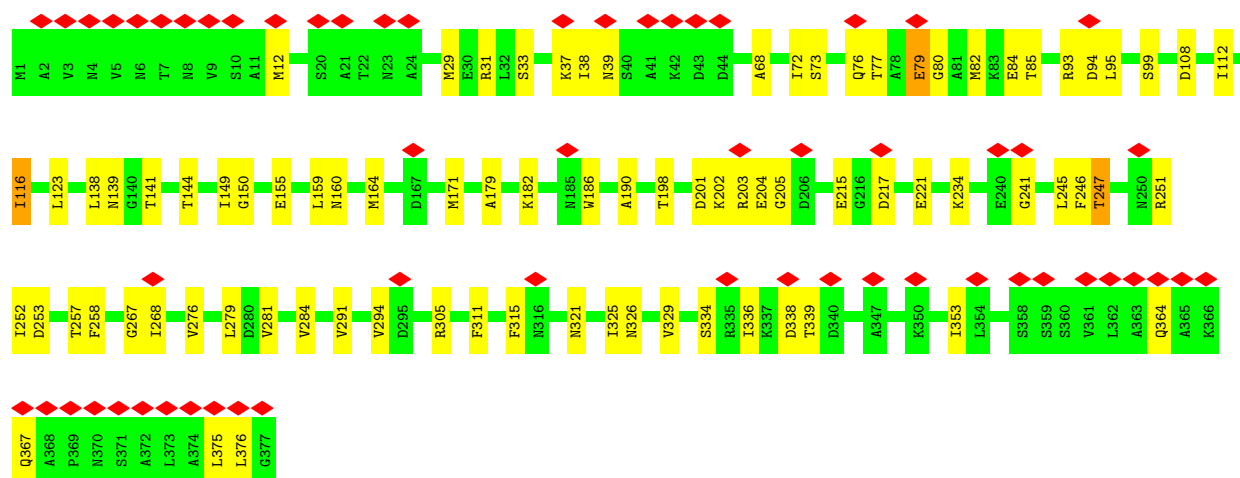
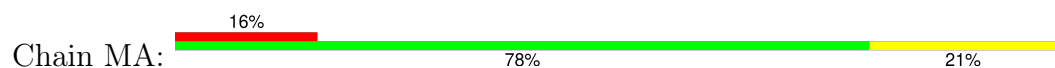


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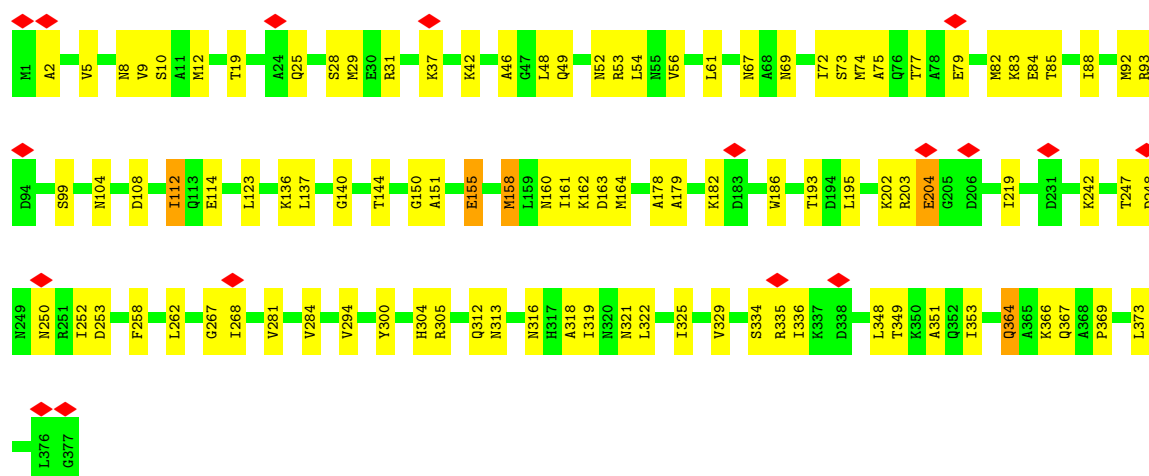
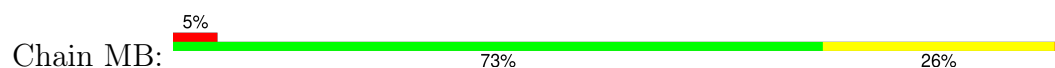





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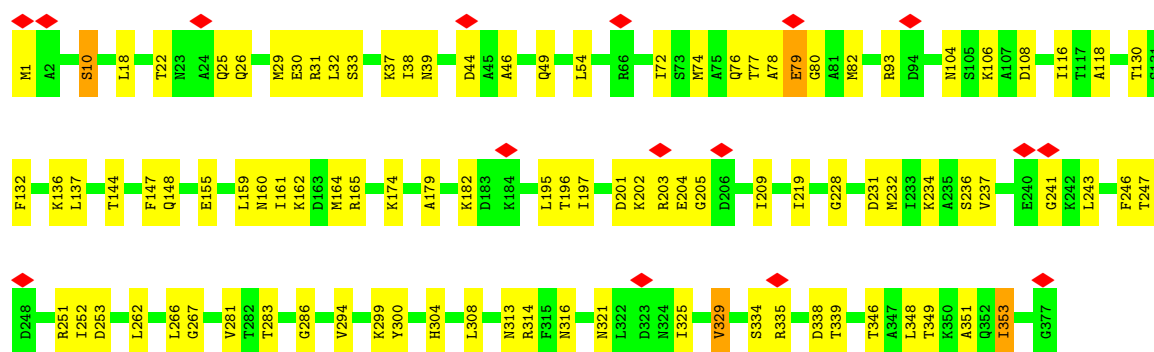


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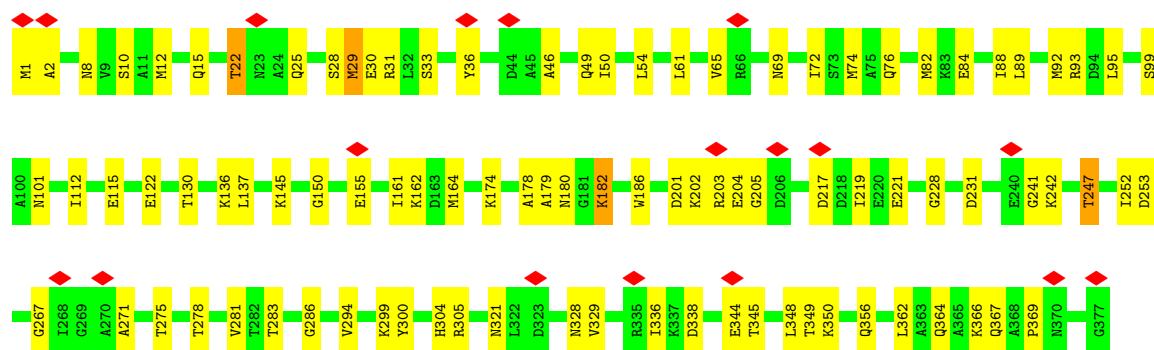
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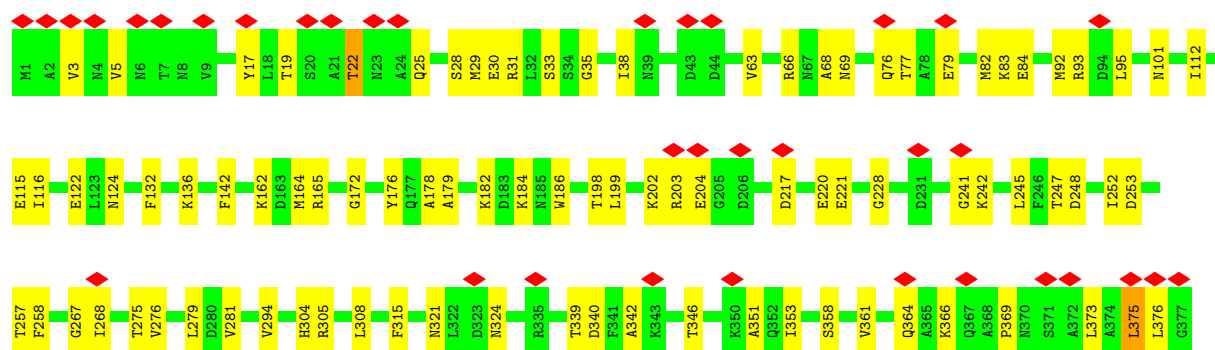
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Chain MD: 




• Molecule 1: Flagellin C

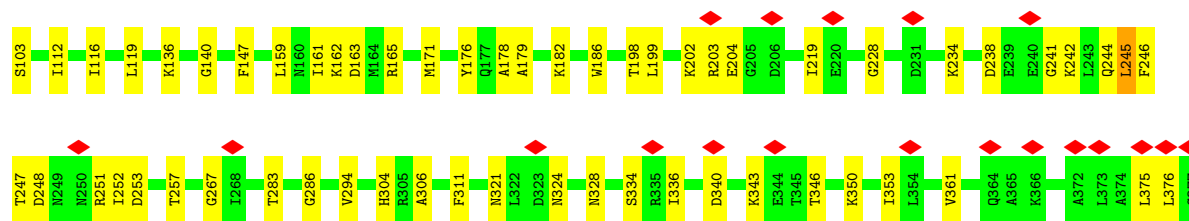
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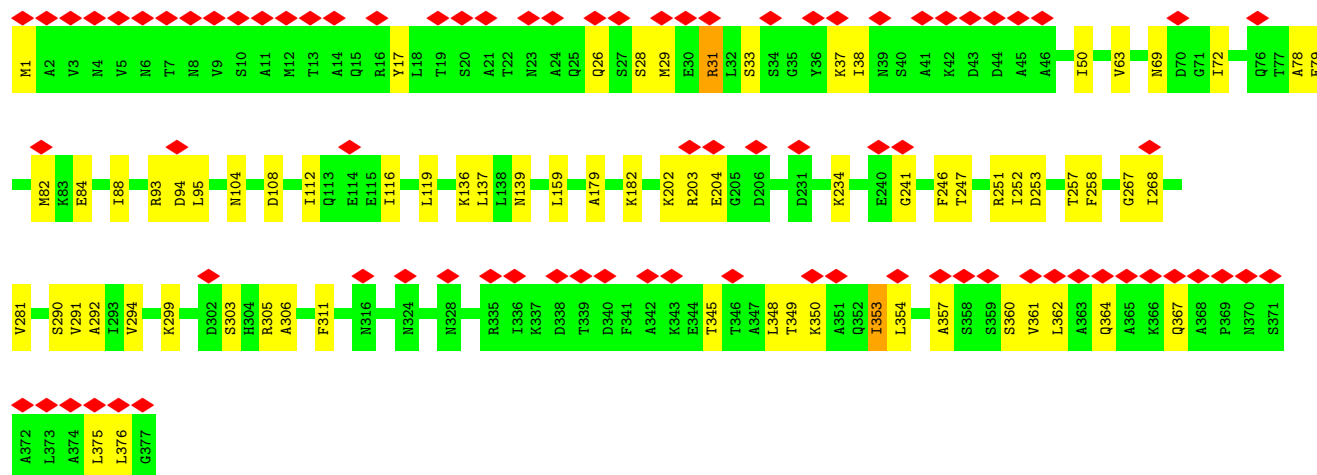
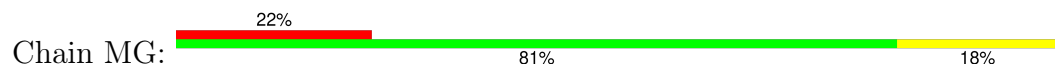
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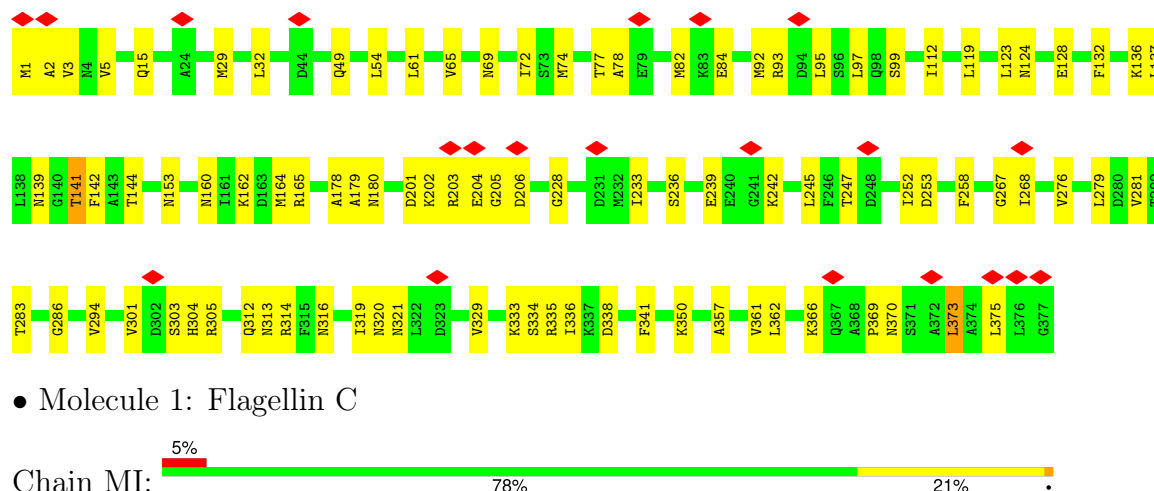
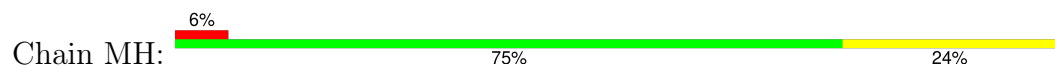




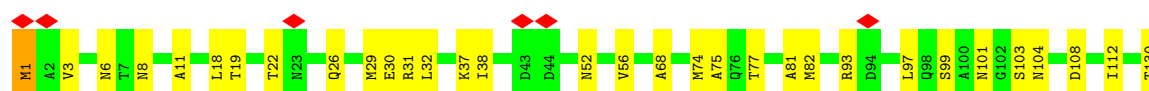
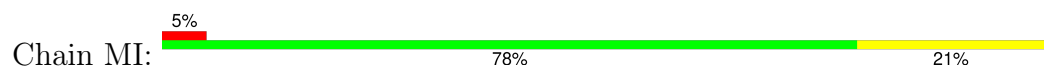
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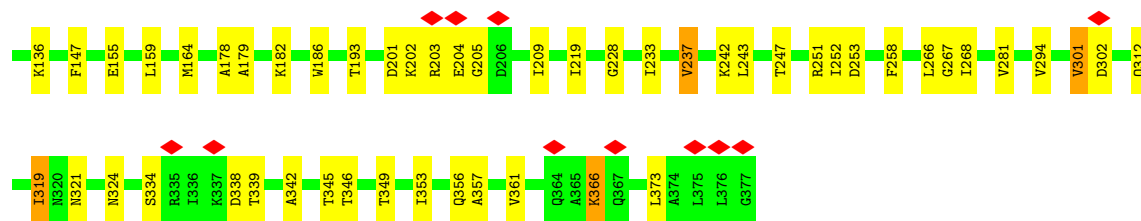


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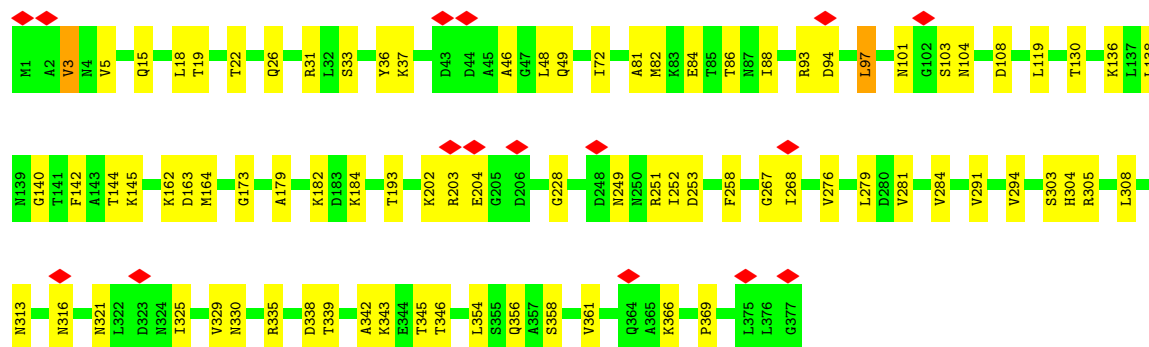
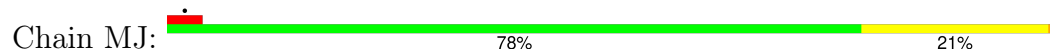


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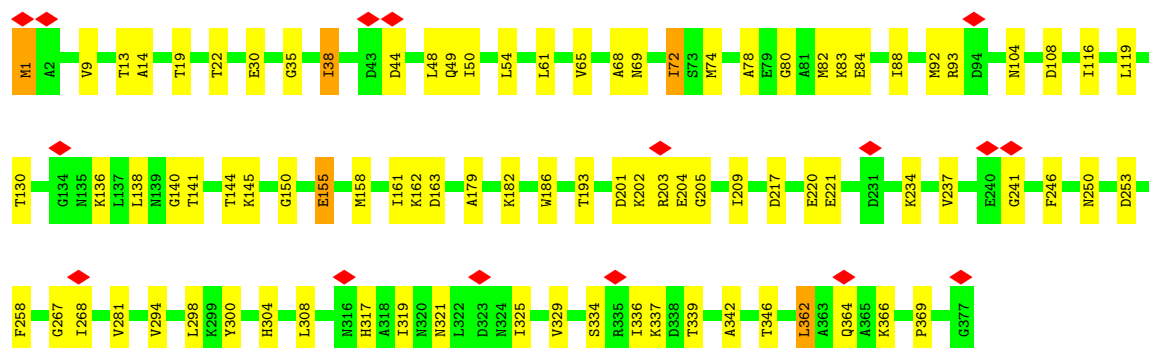
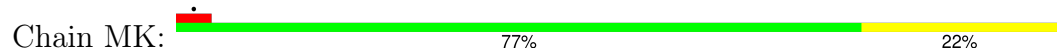




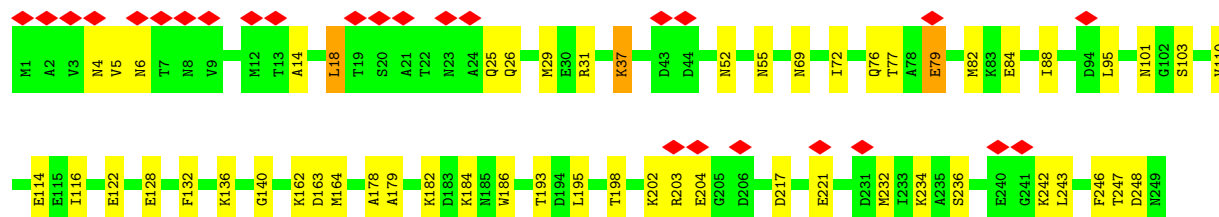
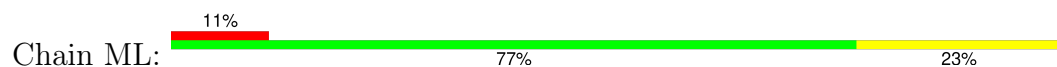
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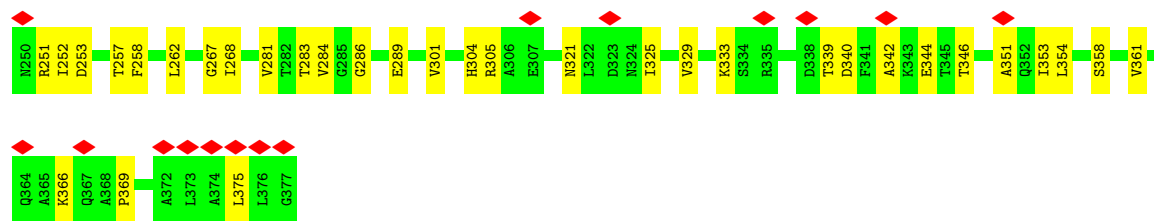


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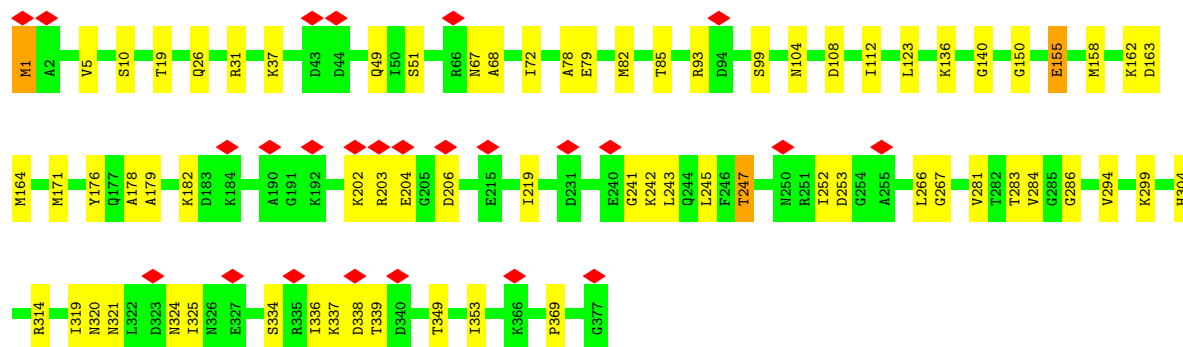
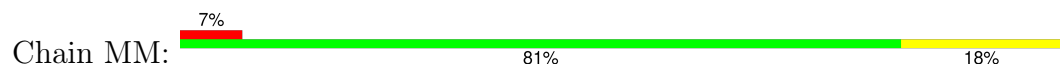


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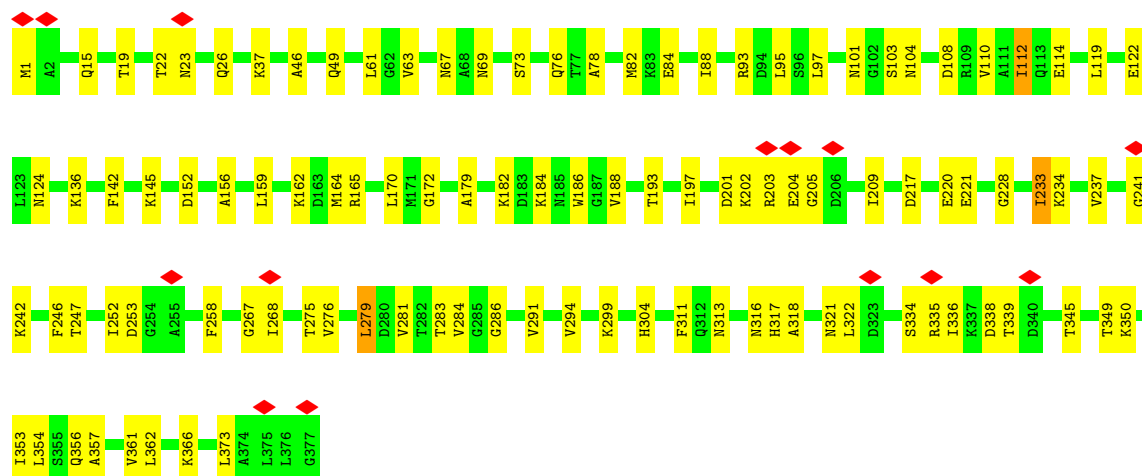
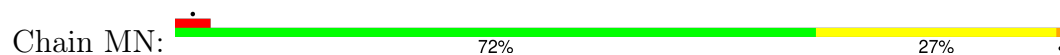




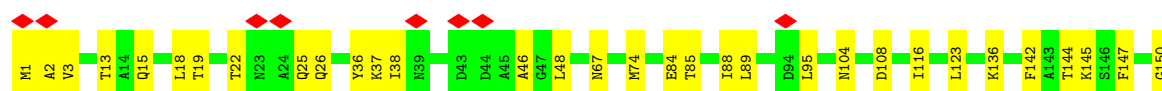
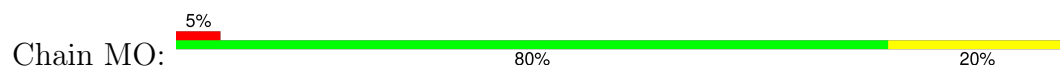
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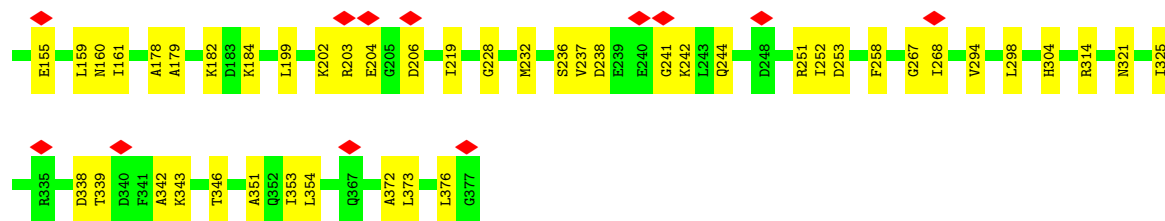


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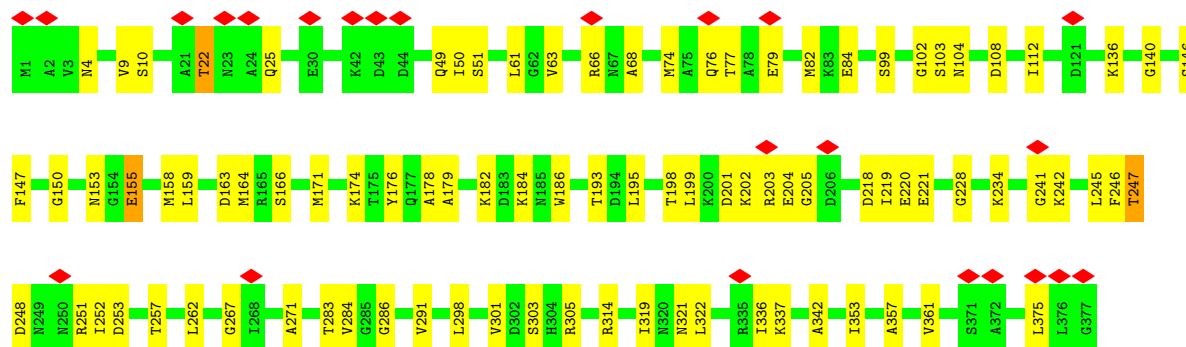
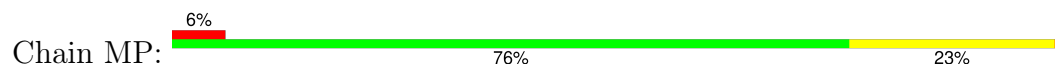


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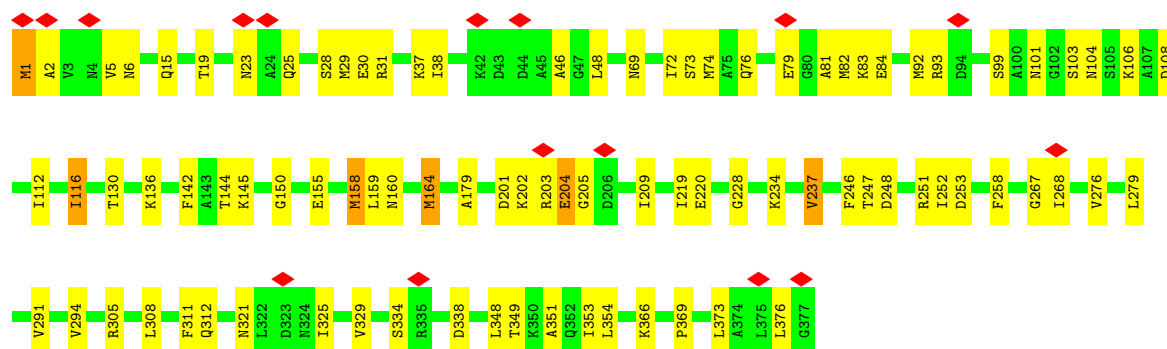
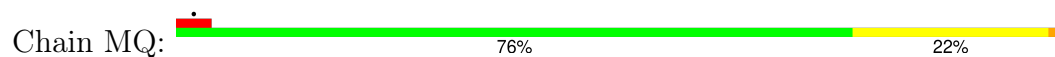




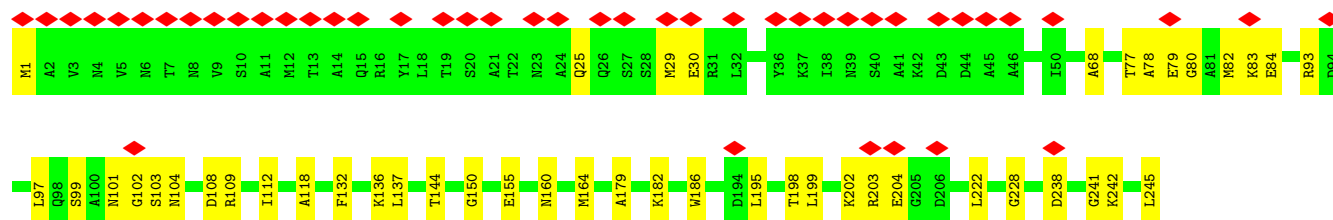
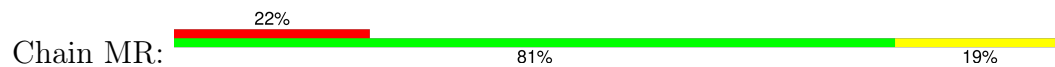
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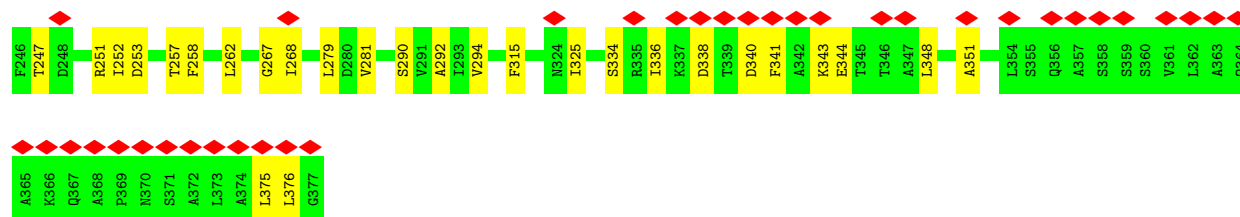


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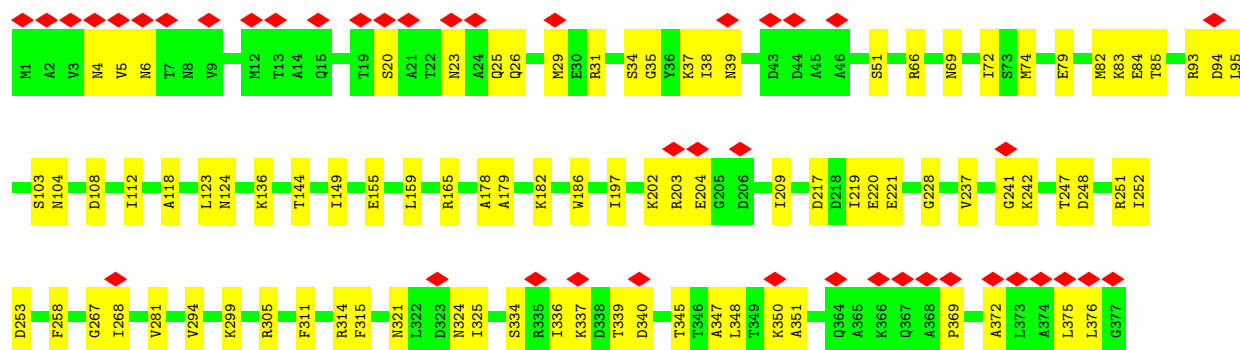
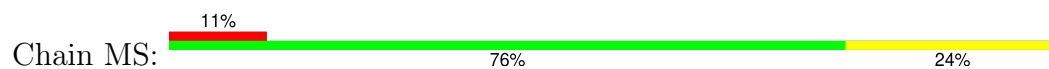


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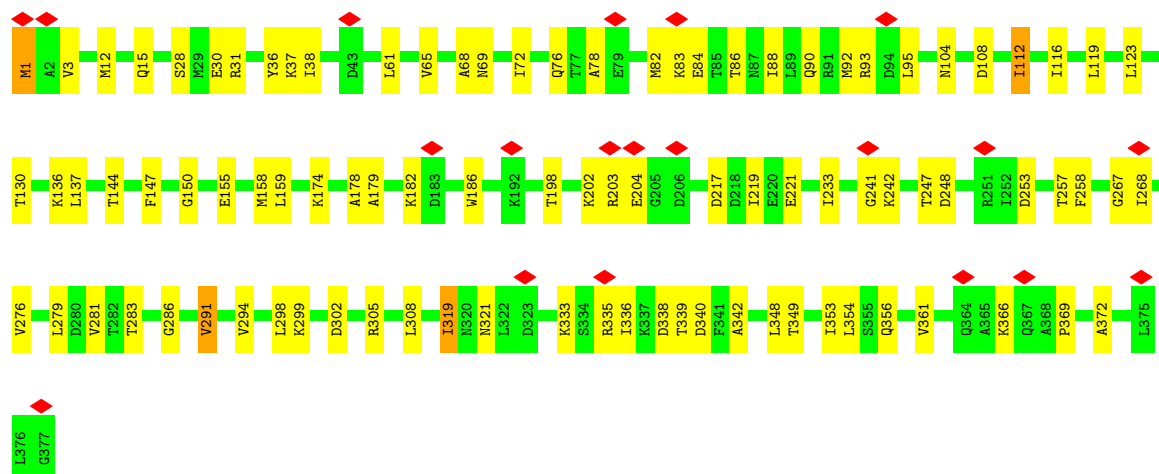
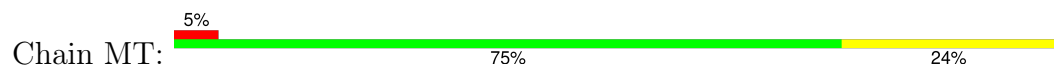




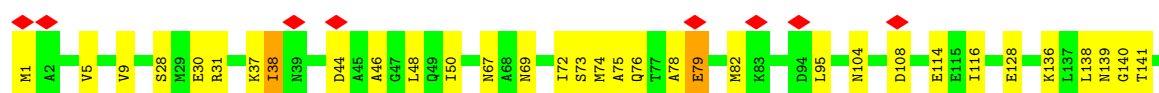
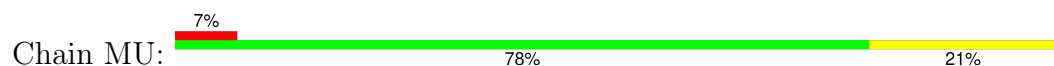
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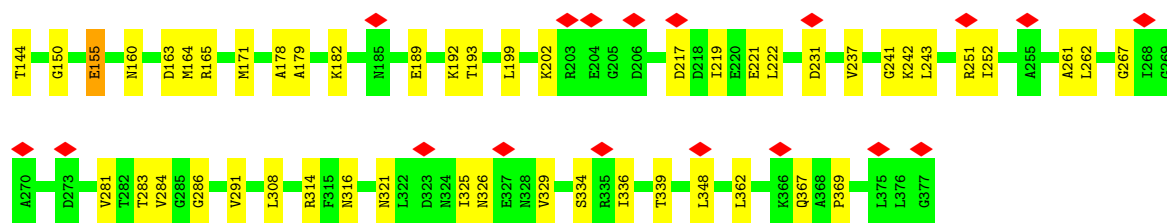


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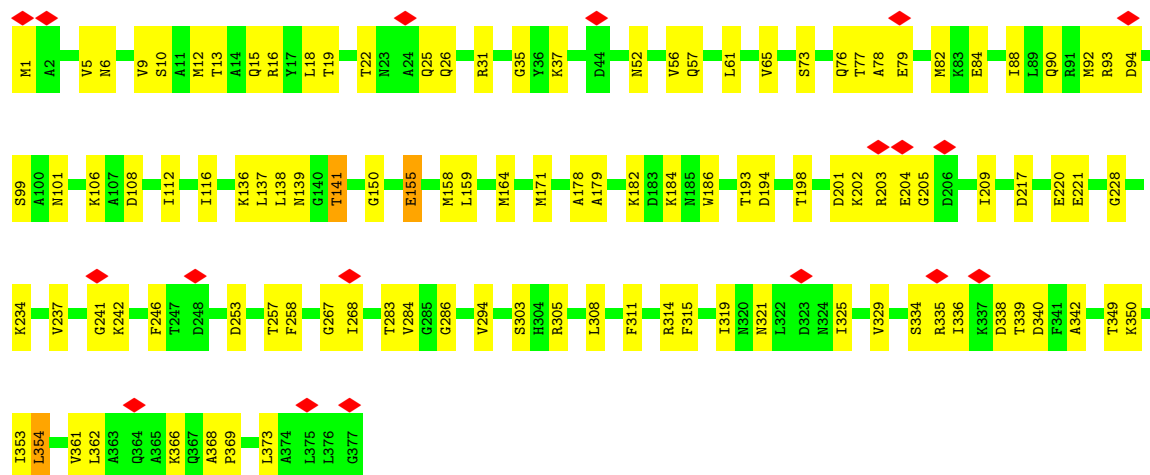
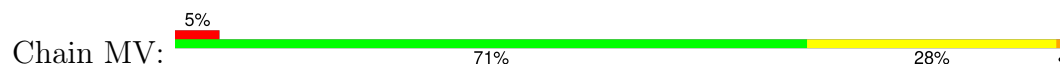


• Molecule 1: Flagellin C

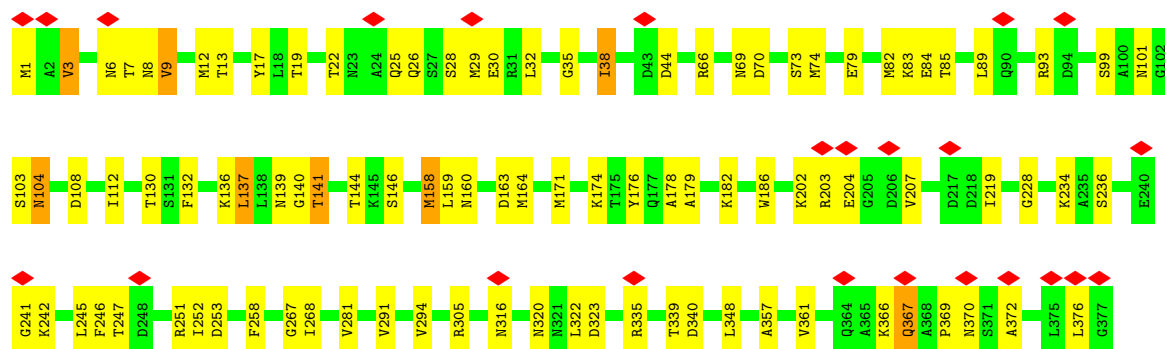
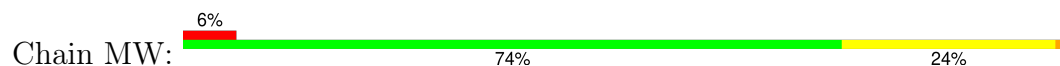




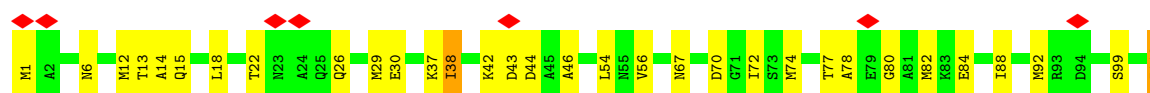
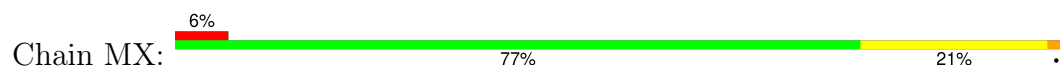
• Molecule 1: Flagellin C

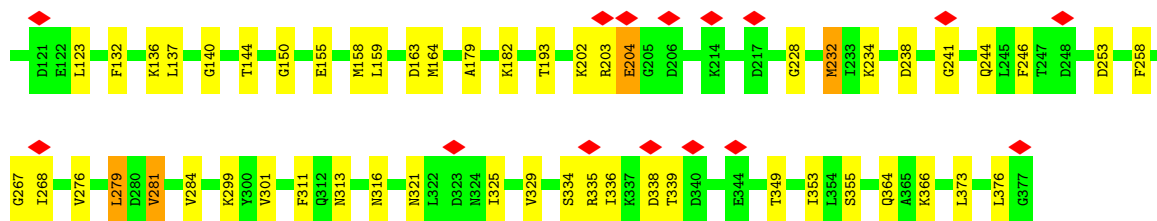


• Molecule 1: Flagellin C



• Molecule 1: Flagellin C





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	300613	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.480	Depositor
Minimum map value	-0.239	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.14	Depositor
Map size (Å)	478.464, 478.464, 478.464	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.068, 1.068, 1.068	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	M1	0.13	0/2811	0.33	0/3791
1	M2	0.12	0/2811	0.30	0/3791
1	M3	0.12	0/2811	0.31	1/3791 (0.0%)
1	M4	0.12	0/2811	0.34	0/3791
1	M5	0.13	0/2811	0.31	0/3791
1	M6	0.14	0/2811	0.33	0/3791
1	M7	0.13	0/2811	0.34	0/3791
1	M8	0.12	0/2811	0.30	0/3791
1	M9	0.14	0/2811	0.34	0/3791
1	MA	0.12	0/2811	0.34	0/3791
1	MB	0.13	0/2811	0.31	0/3791
1	MC	0.13	0/2811	0.33	0/3791
1	MD	0.13	0/2811	0.32	0/3791
1	ME	0.12	0/2811	0.31	0/3791
1	MF	0.12	0/2811	0.31	0/3791
1	MG	0.12	0/2811	0.30	0/3791
1	MH	0.14	0/2811	0.33	0/3791
1	MI	0.14	0/2811	0.33	0/3791
1	MJ	0.14	0/2811	0.32	0/3791
1	MK	0.13	0/2811	0.31	0/3791
1	ML	0.13	0/2811	0.36	0/3791
1	MM	0.12	0/2811	0.30	0/3791
1	MN	0.14	0/2811	0.32	0/3791
1	MO	0.13	0/2811	0.33	0/3791
1	MP	0.14	0/2811	0.33	0/3791
1	MQ	0.14	0/2811	0.32	0/3791
1	MR	0.12	0/2811	0.33	0/3791
1	MS	0.13	0/2811	0.33	0/3791
1	MT	0.13	0/2811	0.30	0/3791
1	MU	0.13	0/2811	0.32	0/3791
1	MV	0.14	0/2811	0.33	0/3791
1	MW	0.13	0/2811	0.33	0/3791
1	MX	0.13	0/2811	0.33	1/3791 (0.0%)
All	All	0.13	0/92763	0.32	2/125103 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	MX	204	GLU	CA-CB-CG	5.74	125.57	114.10
1	M3	30	GLU	N-CA-C	-5.15	108.02	114.56

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	M1	2794	0	2765	65	0
1	M2	2794	0	2765	59	0
1	M3	2794	0	2765	53	0
1	M4	2794	0	2765	52	0
1	M5	2794	0	2765	72	0
1	M6	2794	0	2765	69	0
1	M7	2794	0	2765	56	0
1	M8	2794	0	2765	52	0
1	M9	2794	0	2765	60	0
1	MA	2794	0	2765	54	0
1	MB	2794	0	2765	72	0
1	MC	2794	0	2765	68	0
1	MD	2794	0	2765	63	0
1	ME	2794	0	2765	61	0
1	MF	2794	0	2765	61	0
1	MG	2794	0	2765	47	0
1	MH	2794	0	2765	67	0
1	MI	2794	0	2765	58	0
1	MJ	2794	0	2765	58	0
1	MK	2794	0	2765	59	0
1	ML	2794	0	2765	63	0
1	MM	2794	0	2765	43	0
1	MN	2794	0	2765	69	0
1	MO	2794	0	2765	54	0
1	MP	2794	0	2765	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	MQ	2794	0	2765	73	0
1	MR	2794	0	2765	48	0
1	MS	2794	0	2765	62	0
1	MT	2794	0	2765	67	0
1	MU	2794	0	2765	50	0
1	MV	2794	0	2765	72	0
1	MW	2794	0	2765	79	0
1	MX	2794	0	2765	66	0
All	All	92202	0	91245	1744	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 10.

All (1744) 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:M9:179:ALA:H	1:M9:267:GLY:HA3	1.42	0.84
1:MI:74:MET:HA	1:MI:77:THR:HG22	1.61	0.81
1:M6:99:SER:HB3	1:M6:112:ILE:HD12	1.63	0.81
1:MT:179:ALA:H	1:MT:267:GLY:HA3	1.45	0.80
1:M8:82:MET:HE1	1:M8:164:MET:HE1	1.61	0.80
1:MM:150:GLY:HA3	1:MM:155:GLU:HG3	1.63	0.80
1:MQ:179:ALA:H	1:MQ:267:GLY:HA3	1.46	0.80
1:MI:179:ALA:H	1:MI:267:GLY:HA3	1.47	0.80
1:MO:74:MET:HE1	1:MW:103:SER:HA	1.62	0.79
1:MD:150:GLY:HA3	1:MD:155:GLU:HG3	1.65	0.79
1:ML:82:MET:HA	1:ML:82:MET:HE3	1.63	0.79
1:MU:150:GLY:HA3	1:MU:155:GLU:HG3	1.65	0.78
1:MF:353:ILE:HG23	1:MV:373:LEU:HD23	1.66	0.78
1:MD:179:ALA:H	1:MD:267:GLY:HA3	1.47	0.78
1:MJ:179:ALA:H	1:MJ:267:GLY:HA3	1.45	0.78
1:MA:84:GLU:HG2	1:MF:321:ASN:HB2	1.66	0.78
1:MD:2:ALA:H	1:MV:19:THR:HG21	1.49	0.77
1:MF:179:ALA:H	1:MF:267:GLY:HA3	1.50	0.77
1:MM:179:ALA:H	1:MM:267:GLY:HA3	1.48	0.77
1:MN:179:ALA:H	1:MN:267:GLY:HA3	1.50	0.77
1:M1:82:MET:HA	1:M1:82:MET:HE3	1.66	0.76
1:MP:179:ALA:H	1:MP:267:GLY:HA3	1.50	0.76
1:MS:4:ASN:HD21	1:MS:6:ASN:HB3	1.50	0.76
1:M2:179:ALA:H	1:M2:267:GLY:HA3	1.51	0.75
1:MH:179:ALA:H	1:MH:267:GLY:HA3	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ME:179:ALA:H	1:ME:267:GLY:HA3	1.51	0.75
1:M1:179:ALA:H	1:M1:267:GLY:HA3	1.51	0.75
1:ML:179:ALA:H	1:ML:267:GLY:HA3	1.51	0.75
1:MT:36:TYR:HA	1:MT:338:ASP:HA	1.67	0.75
1:M8:179:ALA:H	1:M8:267:GLY:HA3	1.51	0.75
1:M5:95:LEU:HD11	1:M5:116:ILE:HD11	1.67	0.75
1:M4:82:MET:HA	1:M4:82:MET:HE3	1.68	0.74
1:M3:46:ALA:HB2	1:MW:112:ILE:HD11	1.70	0.74
1:MK:179:ALA:H	1:MK:267:GLY:HA3	1.50	0.74
1:MW:179:ALA:H	1:MW:267:GLY:HA3	1.51	0.74
1:MN:321:ASN:HB2	1:MQ:84:GLU:HG2	1.68	0.74
1:M7:251:ARG:HD2	1:M7:252:ILE:HG13	1.70	0.73
1:MA:179:ALA:H	1:MA:267:GLY:HA3	1.53	0.73
1:MD:182:LYS:H	1:MD:241:GLY:HA3	1.52	0.73
1:MW:3:VAL:HG23	1:MW:372:ALA:HB1	1.69	0.73
1:MV:182:LYS:H	1:MV:241:GLY:HA3	1.54	0.73
1:MR:82:MET:HA	1:MR:82:MET:HE3	1.70	0.73
1:M7:179:ALA:H	1:M7:267:GLY:HA3	1.54	0.73
1:M1:84:GLU:HG2	1:MV:321:ASN:HB2	1.70	0.73
1:MK:150:GLY:HA3	1:MK:155:GLU:HG3	1.70	0.72
1:MX:179:ALA:H	1:MX:267:GLY:HA3	1.53	0.72
1:M6:179:ALA:H	1:M6:267:GLY:HA3	1.53	0.72
1:M7:182:LYS:H	1:M7:241:GLY:HA3	1.55	0.72
1:M3:150:GLY:HA3	1:M3:155:GLU:HG3	1.70	0.72
1:MP:150:GLY:HA3	1:MP:155:GLU:HG3	1.70	0.72
1:M9:150:GLY:HA3	1:M9:155:GLU:HG3	1.72	0.72
1:MB:179:ALA:H	1:MB:267:GLY:HA3	1.53	0.72
1:M5:214:LYS:HG3	1:MC:165:ARG:HH22	1.55	0.72
1:M9:361:VAL:HA	1:M9:364:GLN:HB2	1.70	0.72
1:MQ:74:MET:HE1	1:MS:103:SER:HA	1.72	0.72
1:MV:179:ALA:H	1:MV:267:GLY:HA3	1.53	0.72
1:MO:179:ALA:H	1:MO:267:GLY:HA3	1.53	0.72
1:M8:150:GLY:HA3	1:M8:155:GLU:HG3	1.72	0.71
1:MX:150:GLY:HA3	1:MX:155:GLU:HG3	1.71	0.71
1:MR:84:GLU:HG2	1:MS:321:ASN:HB2	1.72	0.71
1:MN:182:LYS:H	1:MN:241:GLY:HA3	1.55	0.71
1:MR:179:ALA:H	1:MR:267:GLY:HA3	1.53	0.71
1:MI:82:MET:HA	1:MI:82:MET:HE3	1.72	0.71
1:ME:84:GLU:HG2	1:MH:321:ASN:HB2	1.72	0.70
1:MH:82:MET:HA	1:MH:82:MET:HE3	1.71	0.70
1:MF:99:SER:HB3	1:MF:112:ILE:HD12	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MG:179:ALA:H	1:MG:267:GLY:HA3	1.56	0.70
1:ML:69:ASN:HA	1:ML:72:ILE:HD12	1.72	0.70
1:MM:182:LYS:H	1:MM:241:GLY:HA3	1.57	0.70
1:MR:150:GLY:HA3	1:MR:155:GLU:HG3	1.74	0.70
1:MD:321:ASN:HB2	1:MV:84:GLU:HG2	1.74	0.70
1:MG:159:LEU:HB2	1:MG:311:PHE:HE1	1.57	0.70
1:M8:74:MET:HE1	1:MN:103:SER:HA	1.74	0.70
1:MV:150:GLY:HA3	1:MV:155:GLU:HG3	1.74	0.70
1:MX:82:MET:HE3	1:MX:82:MET:HA	1.74	0.69
1:M8:31:ARG:HH21	1:M8:37:LYS:HB2	1.57	0.69
1:M9:2:ALA:HB2	1:MX:22:THR:HG21	1.75	0.69
1:MA:149:ILE:HG21	1:MA:315:PHE:HE1	1.58	0.69
1:MC:74:MET:HE3	1:MI:103:SER:HA	1.74	0.69
1:MB:150:GLY:HA3	1:MB:155:GLU:HG3	1.74	0.69
1:M6:251:ARG:HG2	1:M6:252:ILE:HD12	1.75	0.69
1:M9:1:MET:HB2	1:MX:18:LEU:HD22	1.74	0.69
1:MU:179:ALA:H	1:MU:267:GLY:HA3	1.57	0.69
1:M3:82:MET:HA	1:M3:82:MET:HE3	1.74	0.69
1:MD:36:TYR:HA	1:MD:338:ASP:HA	1.75	0.69
1:MG:362:LEU:HD11	1:ML:375:LEU:HB2	1.74	0.69
1:MQ:99:SER:HA	1:MQ:104:ASN:HD21	1.58	0.69
1:MT:37:LYS:HB3	1:MT:339:THR:HB	1.73	0.69
1:M4:179:ALA:H	1:M4:267:GLY:HA3	1.58	0.68
1:M7:247:THR:HG23	1:M7:252:ILE:HB	1.76	0.68
1:M7:15:GLN:HA	1:M7:18:LEU:HG	1.74	0.68
1:MB:321:ASN:HB2	1:MK:84:GLU:HG2	1.76	0.68
1:MF:202:LYS:HE2	1:MF:253:ASP:HB3	1.75	0.68
1:MT:31:ARG:HD2	1:MT:37:LYS:HA	1.75	0.68
1:M2:182:LYS:H	1:M2:241:GLY:HA3	1.59	0.68
1:M4:149:ILE:HG21	1:M4:315:PHE:HE1	1.58	0.68
1:MO:36:TYR:HA	1:MO:338:ASP:HA	1.76	0.68
1:MT:182:LYS:H	1:MT:241:GLY:HA3	1.59	0.68
1:M4:150:GLY:HA3	1:M4:155:GLU:HG3	1.76	0.68
1:MV:106:LYS:H	1:MV:106:LYS:HE2	1.58	0.68
1:M6:321:ASN:HB2	1:MS:84:GLU:HG2	1.74	0.68
1:M9:321:ASN:HB2	1:MX:84:GLU:HG2	1.76	0.68
1:M1:321:ASN:HB2	1:M4:84:GLU:HG2	1.75	0.67
1:M3:179:ALA:H	1:M3:267:GLY:HA3	1.56	0.67
1:MO:150:GLY:HA3	1:MO:155:GLU:HG3	1.76	0.67
1:MT:68:ALA:HB3	1:MT:319:ILE:HD11	1.77	0.67
1:M3:1:MET:HE3	1:MO:19:THR:HA	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M6:38:ILE:HD11	1:M6:44:ASP:HB2	1.75	0.67
1:MV:31:ARG:HH21	1:MV:37:LYS:HB2	1.58	0.67
1:M9:81:ALA:HB2	1:M9:130:THR:HG21	1.77	0.67
1:M7:82:MET:HA	1:M7:82:MET:HE3	1.76	0.67
1:MT:150:GLY:HA3	1:MT:155:GLU:HG3	1.75	0.67
1:MS:69:ASN:HA	1:MS:72:ILE:HD12	1.76	0.67
1:MU:189:GLU:HG3	1:MU:192:LYS:HE2	1.77	0.67
1:M4:182:LYS:H	1:M4:241:GLY:HA3	1.60	0.66
1:MT:321:ASN:HB2	1:MW:84:GLU:HG2	1.76	0.66
1:MC:179:ALA:H	1:MC:267:GLY:HA3	1.60	0.66
1:MQ:82:MET:HE1	1:MQ:164:MET:HE1	1.77	0.66
1:MU:202:LYS:HG3	1:MU:251:ARG:HA	1.77	0.66
1:M8:138:LEU:HD22	1:M8:164:MET:HE3	1.78	0.66
1:MC:38:ILE:HD11	1:MC:44:ASP:HB3	1.76	0.66
1:M2:84:GLU:HG2	1:MU:321:ASN:HB2	1.76	0.66
1:MA:182:LYS:H	1:MA:241:GLY:HA3	1.61	0.66
1:ME:182:LYS:H	1:ME:241:GLY:HA3	1.59	0.66
1:MI:258:PHE:HB2	1:MI:268:ILE:HG23	1.77	0.66
1:MJ:36:TYR:HA	1:MJ:338:ASP:HA	1.77	0.66
1:M5:228:GLY:HA2	1:MC:136:LYS:HE2	1.76	0.66
1:MT:361:VAL:HG13	1:MW:29:MET:HB3	1.78	0.66
1:M5:15:GLN:HG2	1:MV:342:ALA:HB1	1.77	0.66
1:MQ:251:ARG:HG3	1:MQ:252:ILE:HD12	1.77	0.65
1:M6:182:LYS:H	1:M6:241:GLY:HA3	1.61	0.65
1:MI:228:GLY:HA2	1:MN:136:LYS:HE2	1.78	0.65
1:MB:2:ALA:H	1:MK:19:THR:HG21	1.61	0.65
1:M5:179:ALA:H	1:M5:267:GLY:HA3	1.59	0.65
1:MB:79:GLU:HA	1:MB:82:MET:HG2	1.78	0.65
1:MK:19:THR:HA	1:MK:22:THR:HB	1.79	0.65
1:M5:51:SER:HB2	1:M5:337:LYS:HG3	1.77	0.65
1:MQ:158:MET:HG3	1:MS:220:GLU:HG3	1.78	0.65
1:MV:52:ASN:O	1:MV:56:VAL:HG23	1.97	0.65
1:MM:37:LYS:HB3	1:MM:339:THR:HB	1.78	0.65
1:MS:258:PHE:HB2	1:MS:268:ILE:HG23	1.79	0.65
1:MV:99:SER:HB3	1:MV:112:ILE:HD13	1.79	0.64
1:MX:77:THR:HG21	1:MX:132:PHE:HD1	1.63	0.64
1:M4:37:LYS:HD2	1:M4:38:ILE:HG23	1.79	0.64
1:MJ:369:PRO:HB2	1:MP:353:ILE:HD13	1.79	0.64
1:MB:46:ALA:HB2	1:MP:112:ILE:HG13	1.80	0.64
1:MP:182:LYS:H	1:MP:241:GLY:HA3	1.63	0.64
1:M2:13:THR:HG21	1:MT:30:GLU:HB2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MC:82:MET:HE1	1:MC:164:MET:HE1	1.80	0.64
1:MF:95:LEU:HD11	1:MF:116:ILE:HD11	1.78	0.64
1:MG:37:LYS:HD2	1:MG:38:ILE:HG23	1.79	0.64
1:MD:247:THR:HG23	1:MD:252:ILE:HB	1.78	0.64
1:M4:69:ASN:HA	1:M4:72:ILE:HD12	1.80	0.64
1:M6:228:GLY:HA2	1:MQ:136:LYS:HE2	1.79	0.64
1:M9:38:ILE:HD12	1:M9:44:ASP:HB3	1.80	0.63
1:MU:182:LYS:H	1:MU:241:GLY:HA3	1.63	0.63
1:MS:95:LEU:HD21	1:MS:112:ILE:HG23	1.81	0.63
1:M7:84:GLU:HG2	1:ME:321:ASN:HB2	1.81	0.63
1:MF:69:ASN:HA	1:MF:72:ILE:HD12	1.80	0.63
1:MI:104:ASN:HB3	1:MI:108:ASP:HB2	1.79	0.63
1:M2:366:LYS:HZ3	1:MJ:345:THR:HG22	1.63	0.63
1:MP:22:THR:HA	1:MP:25:GLN:HB3	1.80	0.63
1:MG:136:LYS:HB3	1:MG:139:ASN:HB2	1.79	0.63
1:MI:31:ARG:HH21	1:MI:37:LYS:HB2	1.64	0.63
1:MN:46:ALA:HB2	1:MS:112:ILE:HD11	1.81	0.63
1:ME:122:GLU:HG2	1:MH:314:ARG:HE	1.63	0.63
1:MG:375:LEU:HG	1:MG:376:LEU:HD12	1.80	0.63
1:MS:179:ALA:H	1:MS:267:GLY:HA3	1.63	0.63
1:MG:182:LYS:H	1:MG:241:GLY:HA3	1.64	0.62
1:MX:234:LYS:HB2	1:MX:246:PHE:HB3	1.81	0.62
1:MD:136:LYS:HE2	1:MW:228:GLY:HA2	1.80	0.62
1:M7:228:GLY:HA2	1:MF:136:LYS:HE2	1.80	0.62
1:MB:42:LYS:HD2	1:MQ:312:GLN:HB2	1.81	0.62
1:M6:350:LYS:HE2	1:MQ:6:ASN:HA	1.81	0.62
1:ML:162:LYS:H	1:ML:304:HIS:CE1	2.18	0.62
1:M9:136:LYS:HE2	1:MO:228:GLY:HA2	1.82	0.62
1:MJ:15:GLN:HG2	1:MP:342:ALA:HB1	1.81	0.62
1:M2:144:THR:HG22	1:M2:160:ASN:HB3	1.82	0.62
1:ME:82:MET:HG3	1:ME:305:ARG:HG2	1.81	0.62
1:MF:346:THR:HG22	1:MV:366:LYS:HZ3	1.64	0.62
1:M1:112:ILE:HG13	1:MX:46:ALA:HB2	1.82	0.62
1:M5:10:SER:HB2	1:MI:26:GLN:HE22	1.63	0.62
1:M5:214:LYS:HE3	1:MC:165:ARG:HH12	1.64	0.62
1:ME:220:GLU:HB2	1:MT:158:MET:HE2	1.82	0.62
1:MX:74:MET:HA	1:MX:77:THR:HG22	1.81	0.61
1:MK:74:MET:HE1	1:MP:103:SER:HA	1.81	0.61
1:M1:373:LEU:HD22	1:MA:353:ILE:HG23	1.83	0.61
1:MR:334:SER:HA	1:MR:338:ASP:HB2	1.81	0.61
1:M9:258:PHE:HB2	1:M9:268:ILE:HG23	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MB:54:LEU:HD12	1:MB:329:VAL:HG13	1.82	0.61
1:MC:22:THR:HG23	1:MM:1:MET:HG3	1.81	0.61
1:MH:139:ASN:HB3	1:MH:141:THR:HG22	1.82	0.61
1:MR:182:LYS:H	1:MR:241:GLY:HA3	1.65	0.61
1:M8:136:LYS:HE2	1:MC:228:GLY:HA2	1.82	0.61
1:M9:182:LYS:H	1:M9:241:GLY:HA3	1.66	0.61
1:MA:93:ARG:HB2	1:MA:294:VAL:HG11	1.83	0.61
1:MG:202:LYS:HE3	1:MG:253:ASP:HB3	1.83	0.61
1:MP:136:LYS:HE2	1:MS:228:GLY:HA2	1.82	0.61
1:MO:251:ARG:HG3	1:MO:252:ILE:HD12	1.83	0.61
1:M1:99:SER:HB3	1:M1:112:ILE:HD13	1.83	0.61
1:M2:258:PHE:HB2	1:M2:268:ILE:HG23	1.82	0.61
1:MC:251:ARG:HG3	1:MC:252:ILE:HD12	1.83	0.61
1:MR:258:PHE:HB2	1:MR:268:ILE:HG23	1.82	0.61
1:M2:37:LYS:HB3	1:M2:339:THR:HB	1.83	0.60
1:MK:136:LYS:HE2	1:MQ:228:GLY:HA2	1.82	0.60
1:M4:251:ARG:HG3	1:M4:252:ILE:HG13	1.83	0.60
1:MH:15:GLN:HG2	1:ML:342:ALA:HB1	1.84	0.60
1:MV:325:ILE:O	1:MV:329:VAL:HG23	2.02	0.60
1:M2:150:GLY:HA3	1:M2:155:GLU:HG3	1.82	0.60
1:MB:49:GLN:HB3	1:MB:53:ARG:HH22	1.65	0.60
1:MP:174:LYS:HB2	1:MP:247:THR:HB	1.83	0.60
1:MW:144:THR:HG22	1:MW:160:ASN:HB2	1.83	0.60
1:MJ:3:VAL:H	1:ML:340:ASP:HB2	1.66	0.60
1:MM:85:THR:HG23	1:MM:123:LEU:HD11	1.83	0.60
1:M9:37:LYS:HB3	1:M9:339:THR:HB	1.83	0.60
1:MI:99:SER:HB2	1:MI:112:ILE:HD13	1.82	0.60
1:MS:51:SER:HB2	1:MS:337:LYS:HG3	1.82	0.60
1:MC:37:LYS:HB3	1:MC:339:THR:HB	1.84	0.60
1:MQ:258:PHE:HB2	1:MQ:268:ILE:HG23	1.82	0.60
1:M7:178:ALA:HB3	1:M7:242:LYS:HA	1.84	0.60
1:MN:95:LEU:HD21	1:MN:112:ILE:HG23	1.83	0.60
1:M7:31:ARG:HE	1:M7:37:LYS:HA	1.67	0.60
1:MD:22:THR:HA	1:MD:25:GLN:HB3	1.83	0.59
1:MO:353:ILE:HD12	1:MO:354:LEU:N	2.17	0.59
1:MA:190:ALA:HB2	1:MA:215:GLU:HG3	1.84	0.59
1:MB:136:LYS:HE2	1:MN:228:GLY:HA2	1.84	0.59
1:M1:334:SER:HA	1:M1:338:ASP:HB2	1.84	0.59
1:MA:247:THR:HG23	1:MA:252:ILE:HB	1.82	0.59
1:MA:251:ARG:HG3	1:MA:252:ILE:HD12	1.84	0.59
1:MQ:150:GLY:HA3	1:MQ:155:GLU:HG3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MU:37:LYS:HB3	1:MU:339:THR:HB	1.84	0.59
1:MB:85:THR:HG23	1:MB:123:LEU:HD21	1.83	0.59
1:MK:182:LYS:H	1:MK:241:GLY:HA3	1.66	0.59
1:MW:139:ASN:HB3	1:MW:141:THR:HG22	1.84	0.59
1:M8:51:SER:HB2	1:M8:337:LYS:HG3	1.85	0.59
1:MC:31:ARG:HH21	1:MC:37:LYS:HB2	1.67	0.59
1:MD:49:GLN:HE22	1:MF:306:ALA:HB2	1.66	0.59
1:MJ:37:LYS:HB3	1:MJ:339:THR:HB	1.84	0.59
1:M2:95:LEU:HD11	1:M2:116:ILE:HG12	1.85	0.59
1:M7:106:LYS:H	1:M7:106:LYS:HE2	1.66	0.59
1:MD:162:LYS:H	1:MD:304:HIS:CE1	2.21	0.59
1:M6:258:PHE:HB2	1:M6:268:ILE:HG23	1.85	0.59
1:M9:1:MET:HG3	1:MX:355:SER:HA	1.85	0.59
1:ML:247:THR:HG23	1:ML:252:ILE:HB	1.85	0.59
1:MJ:258:PHE:HB2	1:MJ:268:ILE:HG23	1.84	0.59
1:M1:202:LYS:HE3	1:M1:253:ASP:HB3	1.84	0.59
1:MO:202:LYS:HD3	1:MO:251:ARG:HA	1.85	0.59
1:MT:12:MET:HA	1:MT:15:GLN:HE21	1.67	0.59
1:M8:182:LYS:H	1:M8:241:GLY:HA3	1.66	0.58
1:MB:31:ARG:HH21	1:MB:37:LYS:HB2	1.68	0.58
1:MN:37:LYS:HB3	1:MN:339:THR:HB	1.84	0.58
1:MJ:84:GLU:HG3	1:MK:321:ASN:HB2	1.85	0.58
1:M4:26:GLN:HA	1:M4:29:MET:SD	2.42	0.58
1:MJ:18:LEU:O	1:MJ:22:THR:HG22	2.04	0.58
1:M3:1:MET:HE1	1:MO:18:LEU:HG	1.85	0.58
1:MB:364:GLN:HA	1:MB:364:GLN:HE21	1.69	0.58
1:MD:30:GLU:HB2	1:MO:13:THR:HG21	1.85	0.58
1:MK:202:LYS:HE3	1:MK:253:ASP:HB3	1.85	0.58
1:MW:258:PHE:HB2	1:MW:268:ILE:HG23	1.84	0.58
1:M1:159:LEU:HB2	1:M1:311:PHE:CE2	2.39	0.58
1:M8:136:LYS:HB3	1:M8:139:ASN:HB3	1.84	0.58
1:MA:144:THR:HG22	1:MA:160:ASN:HB3	1.84	0.58
1:MB:99:SER:HB3	1:MB:112:ILE:HG21	1.83	0.58
1:MF:82:MET:HA	1:MF:82:MET:HE3	1.84	0.58
1:MI:356:GLN:HB2	1:MN:373:LEU:HD11	1.85	0.58
1:MB:82:MET:HE1	1:MB:164:MET:SD	2.44	0.58
1:MM:162:LYS:H	1:MM:304:HIS:CE1	2.22	0.58
1:MX:78:ALA:HB2	1:MX:137:LEU:HD23	1.86	0.58
1:MH:112:ILE:HG13	1:MU:46:ALA:HB2	1.84	0.58
1:MW:251:ARG:HG3	1:MW:252:ILE:HD12	1.84	0.58
1:MD:228:GLY:HA2	1:MX:136:LYS:HE2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ME:19:THR:HA	1:MH:1:MET:SD	2.44	0.58
1:MF:93:ARG:HB2	1:MF:294:VAL:HG11	1.85	0.58
1:ML:136:LYS:HE2	1:MR:228:GLY:HA2	1.86	0.58
1:MN:61:LEU:HD12	1:MN:322:LEU:HB3	1.86	0.58
1:M4:228:GLY:HA2	1:M6:136:LYS:HE2	1.86	0.58
1:MA:77:THR:HG22	1:MF:328:ASN:HB3	1.86	0.58
1:MP:247:THR:HG23	1:MP:252:ILE:HB	1.86	0.58
1:MX:159:LEU:HB2	1:MX:311:PHE:CE1	2.39	0.58
1:M1:325:ILE:H	1:M1:325:ILE:HD12	1.70	0.57
1:M9:51:SER:HB2	1:M9:337:LYS:HG3	1.86	0.57
1:MA:258:PHE:HB2	1:MA:268:ILE:HG23	1.86	0.57
1:MO:182:LYS:H	1:MO:241:GLY:HA3	1.68	0.57
1:M5:84:GLU:HG2	1:MX:321:ASN:HB2	1.84	0.57
1:M7:92:MET:HE3	1:M7:116:ILE:HD12	1.85	0.57
1:MD:2:ALA:HA	1:MF:340:ASP:HB2	1.85	0.57
1:MD:29:MET:HE3	1:MD:348:LEU:HD21	1.86	0.57
1:MU:104:ASN:HB2	1:MU:108:ASP:HB2	1.87	0.57
1:M1:122:GLU:HG2	1:MV:314:ARG:HE	1.70	0.57
1:M1:182:LYS:H	1:M1:241:GLY:HA3	1.70	0.57
1:M4:325:ILE:H	1:M4:325:ILE:HD12	1.69	0.57
1:MI:68:ALA:HB3	1:MI:319:ILE:HD11	1.87	0.57
1:ME:198:THR:HB	1:ME:257:THR:HB	1.86	0.57
1:MJ:184:LYS:HB2	1:MU:144:THR:HG21	1.86	0.57
1:M2:228:GLY:HA2	1:M3:136:LYS:HE2	1.86	0.57
1:M5:37:LYS:HB3	1:M5:339:THR:HB	1.87	0.57
1:M9:313:ASN:HA	1:M9:316:ASN:HD21	1.68	0.57
1:MA:334:SER:HA	1:MA:338:ASP:HB2	1.86	0.57
1:MJ:251:ARG:HG3	1:MJ:252:ILE:HD12	1.86	0.57
1:MQ:93:ARG:HB2	1:MQ:294:VAL:HG11	1.85	0.57
1:M8:361:VAL:HG13	1:MB:29:MET:HB3	1.87	0.57
1:MD:349:THR:HG21	1:MX:366:LYS:HE3	1.87	0.57
1:M2:349:THR:O	1:M2:353:ILE:HD12	2.05	0.57
1:M2:364:GLN:HE22	1:MT:348:LEU:HD11	1.69	0.57
1:MD:174:LYS:HD2	1:MD:271:ALA:HB1	1.86	0.57
1:M7:258:PHE:HB2	1:M7:268:ILE:HG23	1.86	0.57
1:MS:159:LEU:HB2	1:MS:311:PHE:CE2	2.40	0.57
1:MG:251:ARG:HG3	1:MG:252:ILE:HG13	1.86	0.56
1:MH:84:GLU:HG3	1:MJ:321:ASN:HB2	1.87	0.56
1:MV:22:THR:HA	1:MV:25:GLN:HB3	1.86	0.56
1:MW:38:ILE:HD12	1:MW:44:ASP:HB3	1.86	0.56
1:MJ:5:VAL:HG23	1:MJ:369:PRO:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MQ:72:ILE:HD13	1:MQ:312:GLN:HE21	1.70	0.56
1:MH:69:ASN:HB3	1:MJ:335:ARG:HD2	1.86	0.56
1:MQ:92:MET:HG3	1:MQ:116:ILE:HD12	1.87	0.56
1:MW:93:ARG:HB2	1:MW:294:VAL:HG11	1.88	0.56
1:ML:5:VAL:HG23	1:ML:369:PRO:HB3	1.86	0.56
1:MO:1:MET:HE1	1:MO:3:VAL:HB	1.88	0.56
1:MX:258:PHE:HB2	1:MX:268:ILE:HG23	1.87	0.56
1:MN:247:THR:HG23	1:MN:252:ILE:HB	1.86	0.56
1:MW:104:ASN:HB2	1:MW:108:ASP:HB2	1.87	0.56
1:ME:353:ILE:HD11	1:MW:370:ASN:ND2	2.21	0.56
1:MJ:22:THR:HG23	1:MK:1:MET:HG3	1.88	0.56
1:M5:202:LYS:HE3	1:M5:253:ASP:HB3	1.88	0.56
1:MC:18:LEU:O	1:MC:22:THR:HG22	2.06	0.56
1:MG:357:ALA:O	1:MG:361:VAL:HG13	2.05	0.56
1:MI:247:THR:HG23	1:MI:252:ILE:HB	1.86	0.56
1:MO:161:ILE:HG23	1:MO:304:HIS:HE1	1.71	0.56
1:M6:336:ILE:HD13	1:MS:66:ARG:HH12	1.69	0.56
1:M7:104:ASN:HB2	1:M7:108:ASP:HB2	1.88	0.56
1:MF:161:ILE:HG23	1:MF:304:HIS:HE1	1.71	0.56
1:MH:162:LYS:H	1:MH:304:HIS:CE1	2.24	0.56
1:MQ:349:THR:O	1:MQ:353:ILE:HG12	2.06	0.56
1:MT:65:VAL:HG13	1:MT:319:ILE:HD12	1.88	0.56
1:MT:349:THR:O	1:MT:353:ILE:HD12	2.06	0.56
1:MV:184:LYS:HB2	1:MX:144:THR:HG21	1.88	0.56
1:M7:341:PHE:H	1:MW:3:VAL:HG13	1.70	0.56
1:M8:321:ASN:HB2	1:MB:84:GLU:HG2	1.86	0.56
1:MQ:325:ILE:O	1:MQ:329:VAL:HG22	2.06	0.56
1:MW:234:LYS:HB2	1:MW:246:PHE:HB3	1.87	0.55
1:M1:84:GLU:OE1	1:M1:84:GLU:HA	2.06	0.55
1:M3:202:LYS:HE3	1:M3:253:ASP:HB3	1.89	0.55
1:M4:375:LEU:HG	1:M4:376:LEU:HD23	1.88	0.55
1:M5:69:ASN:HB3	1:MX:335:ARG:HD2	1.89	0.55
1:M6:279:LEU:HG	1:M6:290:SER:HB2	1.88	0.55
1:MG:247:THR:HG23	1:MG:252:ILE:HB	1.88	0.55
1:M5:106:LYS:HZ2	1:MX:203:ARG:HH22	1.53	0.55
1:M6:10:SER:HB2	1:MS:26:GLN:HE22	1.71	0.55
1:MF:228:GLY:HA2	1:MV:136:LYS:HE2	1.88	0.55
1:ML:37:LYS:HB3	1:ML:339:THR:HB	1.87	0.55
1:MO:147:PHE:HE2	1:MO:159:LEU:HB3	1.71	0.55
1:MP:283:THR:HG23	1:MP:286:GLY:H	1.72	0.55
1:MV:258:PHE:HB2	1:MV:268:ILE:HG23	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M2:244:GLN:HE22	1:M2:289:GLU:HB2	1.71	0.55
1:MC:162:LYS:H	1:MC:304:HIS:CE1	2.25	0.55
1:MN:104:ASN:HB2	1:MN:108:ASP:HB2	1.88	0.55
1:MS:38:ILE:HD11	1:MS:337:LYS:HG2	1.88	0.55
1:MX:54:LEU:HD12	1:MX:329:VAL:HG13	1.88	0.55
1:M8:95:LEU:HD21	1:M8:112:ILE:HG23	1.87	0.55
1:ME:25:GLN:HB2	1:ME:351:ALA:HB1	1.89	0.55
1:MK:54:LEU:HD12	1:MK:329:VAL:HG23	1.88	0.55
1:ML:55:ASN:HB3	1:ML:333:LYS:HD2	1.89	0.55
1:MR:195:LEU:HD12	1:MR:262:LEU:HD23	1.88	0.55
1:M6:88:ILE:HD11	1:M6:119:LEU:HB3	1.88	0.55
1:M1:350:LYS:HE2	1:MI:6:ASN:HA	1.88	0.55
1:M7:325:ILE:HD12	1:M7:325:ILE:H	1.72	0.55
1:MB:367:GLN:CD	1:MB:367:GLN:H	2.15	0.55
1:MC:54:LEU:HD12	1:MC:329:VAL:HG13	1.87	0.55
1:MF:33:SER:HB2	1:MW:17:TYR:HB2	1.89	0.55
1:MT:202:LYS:HE3	1:MT:253:ASP:HB3	1.88	0.55
1:M2:366:LYS:NZ	1:MJ:345:THR:HG22	2.21	0.55
1:M4:195:LEU:HD12	1:M4:262:LEU:HD23	1.87	0.55
1:M5:36:TYR:HA	1:M5:338:ASP:HA	1.88	0.55
1:MF:37:LYS:HE2	1:MF:38:ILE:HG23	1.88	0.55
1:MO:321:ASN:O	1:MO:325:ILE:HD12	2.07	0.55
1:MT:336:ILE:HD13	1:MW:66:ARG:HH12	1.71	0.55
1:MU:5:VAL:HG23	1:MU:369:PRO:HB3	1.88	0.55
1:M9:95:LEU:HD11	1:M9:116:ILE:HD11	1.89	0.54
1:MT:82:MET:HG3	1:MT:305:ARG:HG2	1.89	0.54
1:MU:38:ILE:HD12	1:MU:44:ASP:HB3	1.89	0.54
1:M4:258:PHE:HB2	1:M4:268:ILE:HG23	1.87	0.54
1:MT:258:PHE:HB2	1:MT:268:ILE:HG23	1.89	0.54
1:ME:247:THR:HG23	1:ME:252:ILE:HB	1.89	0.54
1:MH:228:GLY:HA2	1:MT:136:LYS:HE2	1.89	0.54
1:M1:95:LEU:HD11	1:M1:116:ILE:HD11	1.89	0.54
1:M5:162:LYS:H	1:M5:304:HIS:CE1	2.25	0.54
1:M8:52:ASN:O	1:M8:56:VAL:HG23	2.07	0.54
1:MH:32:LEU:HA	1:MH:341:PHE:HE2	1.73	0.54
1:MH:82:MET:HE2	1:MH:301:VAL:HG13	1.89	0.54
1:MM:31:ARG:HH21	1:MM:37:LYS:HB2	1.71	0.54
1:MQ:219:ILE:HG13	1:MQ:237:VAL:HG11	1.89	0.54
1:MV:234:LYS:HB2	1:MV:246:PHE:HB3	1.89	0.54
1:MD:84:GLU:HG3	1:MO:321:ASN:HB2	1.89	0.54
1:M8:202:LYS:HE3	1:M8:253:ASP:HB3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MX:99:SER:HB3	1:MX:112:ILE:HG21	1.89	0.54
1:M8:162:LYS:H	1:M8:304:HIS:CE1	2.26	0.54
1:MC:49:GLN:HG3	1:MI:302:ASP:HB3	1.90	0.54
1:ME:258:PHE:HB2	1:ME:268:ILE:HG23	1.89	0.54
1:MH:375:LEU:HD23	1:MH:375:LEU:H	1.72	0.54
1:MS:104:ASN:HB2	1:MS:108:ASP:HB2	1.90	0.54
1:M1:228:GLY:HA2	1:MI:136:LYS:HE2	1.90	0.54
1:M6:252:ILE:O	1:M6:252:ILE:HG22	2.07	0.54
1:M7:99:SER:HA	1:M7:104:ASN:HD21	1.73	0.54
1:MM:219:ILE:HD11	1:MM:243:LEU:HD11	1.89	0.54
1:M1:346:THR:HG22	1:MI:366:LYS:HE2	1.90	0.54
1:MF:234:LYS:HB2	1:MF:246:PHE:HB3	1.89	0.54
1:MR:68:ALA:HA	1:MR:315:PHE:HE1	1.73	0.54
1:M5:5:VAL:HA	1:M5:369:PRO:HB3	1.89	0.54
1:M9:89:LEU:HD12	1:M9:294:VAL:HG13	1.88	0.54
1:MQ:247:THR:HG23	1:MQ:252:ILE:HB	1.89	0.54
1:M6:357:ALA:O	1:M6:361:VAL:HG23	2.08	0.53
1:MF:165:ARG:HB3	1:MF:165:ARG:HH11	1.73	0.53
1:MG:350:LYS:O	1:MG:354:LEU:HD12	2.08	0.53
1:ML:202:LYS:HE3	1:ML:253:ASP:HB3	1.91	0.53
1:M9:234:LYS:HB2	1:M9:246:PHE:HB3	1.91	0.53
1:MK:38:ILE:HD12	1:MK:44:ASP:HB3	1.89	0.53
1:M4:178:ALA:HB3	1:M4:242:LYS:HA	1.90	0.53
1:M5:369:PRO:HB2	1:MV:353:ILE:HD12	1.90	0.53
1:M7:159:LEU:HB2	1:M7:311:PHE:CE1	2.43	0.53
1:M4:149:ILE:HG21	1:M4:315:PHE:CE1	2.42	0.53
1:ME:202:LYS:HE3	1:ME:253:ASP:HB3	1.90	0.53
1:MK:325:ILE:O	1:MK:329:VAL:HG12	2.08	0.53
1:ME:162:LYS:H	1:ME:304:HIS:CE1	2.27	0.53
1:MI:342:ALA:HB1	1:MN:15:GLN:HG2	1.91	0.53
1:MM:99:SER:HB3	1:MM:112:ILE:HG21	1.89	0.53
1:MM:219:ILE:HG12	1:MM:241:GLY:HA2	1.91	0.53
1:MW:182:LYS:H	1:MW:241:GLY:HA3	1.72	0.53
1:MD:69:ASN:HA	1:MD:72:ILE:HD12	1.89	0.53
1:ME:82:MET:HA	1:ME:82:MET:HE3	1.90	0.53
1:MG:31:ARG:HB3	1:MG:37:LYS:HA	1.91	0.53
1:MX:78:ALA:O	1:MX:82:MET:HG2	2.09	0.53
1:MK:158:MET:HG2	1:MP:220:GLU:HG3	1.90	0.53
1:MO:294:VAL:O	1:MO:298:LEU:HD22	2.09	0.53
1:MP:195:LEU:HD12	1:MP:262:LEU:HD23	1.91	0.53
1:M6:364:GLN:CA	1:M6:364:GLN:HE21	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MC:321:ASN:HB2	1:MN:84:GLU:HG2	1.89	0.53
1:MJ:19:THR:HG23	1:MK:1:MET:HA	1.91	0.53
1:MP:147:PHE:HD2	1:MR:101:ASN:HD21	1.55	0.53
1:MB:313:ASN:HA	1:MB:316:ASN:HD21	1.73	0.53
1:MO:104:ASN:HB2	1:MO:108:ASP:HB2	1.91	0.53
1:MO:85:THR:HG23	1:MO:123:LEU:HD11	1.90	0.52
1:MP:202:LYS:HE3	1:MP:253:ASP:HB3	1.90	0.52
1:M1:375:LEU:HD23	1:M1:376:LEU:H	1.75	0.52
1:M3:172:GLY:HA3	1:M3:275:THR:HG22	1.91	0.52
1:M6:84:GLU:O	1:M6:88:ILE:HG22	2.09	0.52
1:M6:334:SER:HA	1:M6:338:ASP:HB2	1.91	0.52
1:M7:113:GLN:HE21	1:M7:117:THR:HG23	1.74	0.52
1:MD:50:ILE:HG23	1:MD:336:ILE:HD11	1.92	0.52
1:MG:303:SER:HA	1:MH:49:GLN:HE22	1.74	0.52
1:MQ:251:ARG:HG3	1:MQ:252:ILE:CD1	2.40	0.52
1:MR:144:THR:HG22	1:MR:160:ASN:HB3	1.91	0.52
1:MR:375:LEU:HD12	1:MR:376:LEU:HD23	1.90	0.52
1:M6:93:ARG:HB2	1:M6:294:VAL:HG11	1.90	0.52
1:MS:375:LEU:HG	1:MS:376:LEU:HD23	1.90	0.52
1:MW:367:GLN:HA	1:MW:370:ASN:OD1	2.09	0.52
1:M1:92:MET:HG2	1:M1:116:ILE:HD12	1.91	0.52
1:MA:202:LYS:HE3	1:MA:253:ASP:HB3	1.92	0.52
1:MC:93:ARG:HB2	1:MC:294:VAL:HG11	1.92	0.52
1:MI:252:ILE:O	1:MI:252:ILE:HG22	2.10	0.52
1:MQ:144:THR:HG22	1:MQ:160:ASN:HB3	1.91	0.52
1:MV:362:LEU:O	1:MV:366:LYS:HG2	2.08	0.52
1:M1:162:LYS:H	1:M1:304:HIS:CE1	2.27	0.52
1:M8:158:MET:HE1	1:MN:184:LYS:HA	1.90	0.52
1:MB:28:SER:HB3	1:MB:348:LEU:HD23	1.91	0.52
1:MB:93:ARG:HB2	1:MB:294:VAL:HG11	1.91	0.52
1:MJ:19:THR:HA	1:MK:1:MET:H1	1.73	0.52
1:MN:93:ARG:HB2	1:MN:294:VAL:HG11	1.91	0.52
1:MX:313:ASN:HA	1:MX:316:ASN:HD21	1.74	0.52
1:M8:197:ILE:HD12	1:M8:209:ILE:HD11	1.91	0.52
1:ML:84:GLU:HG2	1:MP:321:ASN:HB2	1.90	0.52
1:ML:283:THR:HG23	1:ML:286:GLY:H	1.74	0.52
1:MQ:202:LYS:HE3	1:MQ:253:ASP:HB3	1.91	0.52
1:MR:84:GLU:HA	1:MR:84:GLU:OE2	2.10	0.52
1:MS:93:ARG:HB2	1:MS:294:VAL:HG11	1.92	0.52
1:M5:3:VAL:HG22	1:M5:372:ALA:HB2	1.91	0.52
1:M5:302:ASP:HB3	1:MM:49:GLN:HE21	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MK:104:ASN:HB2	1:MK:108:ASP:HB2	1.92	0.52
1:M5:93:ARG:HB2	1:M5:294:VAL:HG11	1.91	0.52
1:M7:250:ASN:HD22	1:M7:300:TYR:HB2	1.75	0.52
1:MA:82:MET:HG3	1:MA:305:ARG:HG2	1.90	0.52
1:MB:61:LEU:HD12	1:MB:322:LEU:HB3	1.90	0.52
1:MC:182:LYS:H	1:MC:241:GLY:HA3	1.75	0.52
1:MK:14:ALA:HB1	1:MK:362:LEU:HD22	1.92	0.52
1:ML:31:ARG:HH21	1:ML:37:LYS:HB2	1.75	0.52
1:MR:104:ASN:HB2	1:MR:108:ASP:HB2	1.92	0.52
1:M9:251:ARG:HG3	1:M9:252:ILE:CD1	2.40	0.52
1:MI:203:ARG:O	1:MI:204:GLU:HG2	2.10	0.52
1:MK:68:ALA:HB3	1:MK:319:ILE:HD11	1.90	0.52
1:MP:82:MET:HG3	1:MP:305:ARG:HG2	1.91	0.52
1:MR:247:THR:HG23	1:MR:252:ILE:HB	1.92	0.52
1:M3:85:THR:HG23	1:M3:123:LEU:HD11	1.92	0.52
1:M4:104:ASN:HB2	1:M4:108:ASP:HB2	1.91	0.52
1:M9:252:ILE:O	1:M9:252:ILE:HG22	2.09	0.52
1:MC:144:THR:HG22	1:MC:160:ASN:HB3	1.91	0.52
1:MJ:104:ASN:HB2	1:MJ:108:ASP:HB2	1.91	0.52
1:MS:202:LYS:HE3	1:MS:253:ASP:HB3	1.91	0.52
1:M1:349:THR:HG21	1:MI:366:LYS:HG3	1.91	0.51
1:M5:325:ILE:O	1:M5:329:VAL:HG13	2.10	0.51
1:MD:283:THR:HG23	1:MD:286:GLY:H	1.75	0.51
1:MH:258:PHE:HB2	1:MH:268:ILE:HG23	1.92	0.51
1:MM:247:THR:HG23	1:MM:252:ILE:HB	1.92	0.51
1:MU:222:LEU:HD11	1:MU:262:LEU:HD21	1.92	0.51
1:M6:51:SER:HB2	1:M6:337:LYS:HD2	1.92	0.51
1:MH:65:VAL:HG13	1:MH:319:ILE:HD12	1.92	0.51
1:ML:25:GLN:HB2	1:ML:351:ALA:HB1	1.92	0.51
1:MR:222:LEU:HD11	1:MR:262:LEU:HD21	1.92	0.51
1:MR:325:ILE:H	1:MR:325:ILE:HD12	1.75	0.51
1:MV:90:GLN:HG3	1:MX:56:VAL:HG12	1.92	0.51
1:MW:130:THR:HG22	1:MW:137:LEU:HD23	1.91	0.51
1:MX:182:LYS:H	1:MX:241:GLY:HA3	1.76	0.51
1:M5:283:THR:HG23	1:M5:286:GLY:H	1.74	0.51
1:MC:148:GLN:HG2	1:MI:97:LEU:HD22	1.91	0.51
1:MF:182:LYS:H	1:MF:241:GLY:HA3	1.74	0.51
1:MH:233:ILE:HD12	1:MH:245:LEU:HD12	1.92	0.51
1:MJ:103:SER:HA	1:MU:74:MET:HE1	1.93	0.51
1:MK:220:GLU:HG2	1:MK:237:VAL:HG11	1.92	0.51
1:MQ:334:SER:HA	1:MQ:338:ASP:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MR:99:SER:HB3	1:MR:112:ILE:HD13	1.91	0.51
1:MS:247:THR:HG23	1:MS:252:ILE:HB	1.92	0.51
1:MW:320:ASN:HA	1:MW:323:ASP:HB2	1.92	0.51
1:M7:240:GLU:HB2	1:M7:242:LYS:HE2	1.93	0.51
1:MB:74:MET:HE1	1:MQ:103:SER:HA	1.92	0.51
1:MB:364:GLN:HA	1:MB:364:GLN:NE2	2.25	0.51
1:MG:349:THR:O	1:MG:353:ILE:HD13	2.11	0.51
1:MI:29:MET:H	1:MI:32:LEU:HD23	1.76	0.51
1:MR:202:LYS:HE3	1:MR:253:ASP:HB3	1.92	0.51
1:M1:222:LEU:HD11	1:M1:262:LEU:HD21	1.93	0.51
1:M3:99:SER:HB3	1:M3:112:ILE:HG21	1.93	0.51
1:MB:247:THR:HG23	1:MB:252:ILE:HB	1.93	0.51
1:MH:357:ALA:O	1:MH:361:VAL:HG23	2.11	0.51
1:MT:1:MET:H3	1:MW:19:THR:HG21	1.76	0.51
1:MI:93:ARG:HB2	1:MI:294:VAL:HG11	1.93	0.51
1:MR:251:ARG:HG3	1:MR:252:ILE:HG13	1.92	0.51
1:MT:95:LEU:HD11	1:MT:116:ILE:HD11	1.92	0.51
1:MU:219:ILE:HD11	1:MU:243:LEU:HD11	1.93	0.51
1:M2:93:ARG:HB2	1:M2:294:VAL:HG11	1.93	0.51
1:MJ:81:ALA:HB2	1:MJ:130:THR:HG21	1.92	0.51
1:MJ:202:LYS:HE3	1:MJ:253:ASP:HB3	1.92	0.51
1:MQ:82:MET:HG3	1:MQ:305:ARG:HG2	1.92	0.51
1:MV:178:ALA:HB3	1:MV:242:LYS:HA	1.92	0.51
1:M2:122:GLU:HG2	1:MU:314:ARG:HE	1.76	0.50
1:M6:202:LYS:HE3	1:M6:253:ASP:HB3	1.93	0.50
1:MH:1:MET:HE1	1:MH:3:VAL:HG13	1.93	0.50
1:MH:69:ASN:HA	1:MH:72:ILE:HG22	1.93	0.50
1:MN:159:LEU:HB2	1:MN:311:PHE:CE2	2.46	0.50
1:MR:93:ARG:HB2	1:MR:294:VAL:HG11	1.91	0.50
1:M2:366:LYS:HE2	1:MJ:346:THR:HG22	1.93	0.50
1:M6:19:THR:HA	1:MI:1:MET:SD	2.52	0.50
1:M8:366:LYS:HD3	1:MC:346:THR:HG22	1.93	0.50
1:M9:201:ASP:H	1:M9:205:GLY:HA2	1.77	0.50
1:MA:139:ASN:HB3	1:MA:141:THR:HG23	1.93	0.50
1:MC:202:LYS:HE3	1:MC:253:ASP:HB3	1.93	0.50
1:MD:356:GLN:HB3	1:MX:373:LEU:HD11	1.92	0.50
1:MF:18:LEU:HB3	1:MW:1:MET:N	2.27	0.50
1:ML:351:ALA:HA	1:ML:354:LEU:HD12	1.93	0.50
1:MR:78:ALA:HB2	1:MR:137:LEU:HD13	1.93	0.50
1:MS:182:LYS:H	1:MS:241:GLY:HA3	1.77	0.50
1:MU:31:ARG:HB3	1:MU:37:LYS:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MW:245:LEU:HG	1:MW:258:PHE:HZ	1.76	0.50
1:M3:37:LYS:HB3	1:M3:339:THR:HB	1.93	0.50
1:M3:144:THR:HG22	1:M3:160:ASN:HB3	1.94	0.50
1:M5:136:LYS:HE2	1:MV:228:GLY:HA2	1.93	0.50
1:M6:320:ASN:HA	1:M6:323:ASP:HB2	1.93	0.50
1:MN:162:LYS:H	1:MN:304:HIS:CE1	2.29	0.50
1:MV:101:ASN:HD21	1:MX:67:ASN:CG	2.20	0.50
1:MV:220:GLU:HA	1:MV:237:VAL:HG21	1.92	0.50
1:M2:247:THR:HG23	1:M2:252:ILE:HB	1.93	0.50
1:M7:182:LYS:HD2	1:M7:186:TRP:CE2	2.47	0.50
1:M8:104:ASN:HB2	1:M8:108:ASP:HB2	1.94	0.50
1:ME:217:ASP:OD1	1:ME:221:GLU:HB2	2.11	0.50
1:MH:95:LEU:HD13	1:MH:112:ILE:HG23	1.92	0.50
1:MN:234:LYS:HB2	1:MN:246:PHE:HB3	1.93	0.50
1:MU:139:ASN:HB3	1:MU:141:THR:HG22	1.94	0.50
1:MV:5:VAL:HA	1:MV:369:PRO:HB3	1.92	0.50
1:MG:258:PHE:HB2	1:MG:268:ILE:HG23	1.92	0.50
1:ML:29:MET:HB3	1:MP:361:VAL:HG13	1.93	0.50
1:M3:38:ILE:HD12	1:M3:44:ASP:HB3	1.92	0.50
1:M6:178:ALA:HB3	1:M6:242:LYS:HA	1.92	0.50
1:MH:93:ARG:HB2	1:MH:294:VAL:HG11	1.93	0.50
1:MK:49:GLN:HE22	1:MP:303:SER:HA	1.77	0.50
1:MX:334:SER:HA	1:MX:338:ASP:HB2	1.93	0.50
1:M1:321:ASN:O	1:M1:325:ILE:HD12	2.11	0.50
1:M5:251:ARG:HG3	1:M5:252:ILE:HD12	1.94	0.50
1:M6:201:ASP:HB3	1:M6:205:GLY:HA2	1.94	0.50
1:M9:120:ASN:HD21	1:M9:277:ASP:HA	1.76	0.50
1:MD:164:MET:HG2	1:MD:300:TYR:HE2	1.77	0.50
1:MG:69:ASN:HA	1:MG:72:ILE:HG22	1.94	0.50
1:MQ:252:ILE:HG22	1:MQ:252:ILE:O	2.12	0.50
1:MS:25:GLN:HB2	1:MS:351:ALA:HB1	1.93	0.50
1:MU:217:ASP:OD2	1:MU:221:GLU:HB2	2.12	0.50
1:MH:202:LYS:HE3	1:MH:253:ASP:HB3	1.93	0.50
1:MJ:88:ILE:HD12	1:MJ:119:LEU:HD22	1.93	0.50
1:MQ:203:ARG:O	1:MQ:204:GLU:HG3	2.11	0.50
1:MT:178:ALA:HB3	1:MT:242:LYS:HA	1.94	0.50
1:M5:38:ILE:HD11	1:M5:44:ASP:HB2	1.93	0.50
1:MC:78:ALA:HB2	1:MC:137:LEU:HD23	1.92	0.50
1:ME:22:THR:HA	1:ME:25:GLN:HB3	1.94	0.50
1:MH:144:THR:HG22	1:MH:160:ASN:HB2	1.93	0.50
1:MM:349:THR:O	1:MM:353:ILE:HG12	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MS:79:GLU:HA	1:MS:82:MET:HB2	1.94	0.50
1:MV:93:ARG:HB2	1:MV:294:VAL:HG11	1.94	0.50
1:MW:25:GLN:O	1:MW:29:MET:HE2	2.11	0.50
1:M4:202:LYS:HE3	1:M4:253:ASP:HB3	1.94	0.49
1:M7:88:ILE:O	1:M7:92:MET:HG3	2.12	0.49
1:M8:201:ASP:HB3	1:M8:205:GLY:HA2	1.94	0.49
1:MC:334:SER:HA	1:MC:338:ASP:HB2	1.94	0.49
1:MD:362:LEU:O	1:MD:366:LYS:HG3	2.12	0.49
1:MK:258:PHE:HB2	1:MK:268:ILE:HG23	1.93	0.49
1:ML:4:ASN:HD21	1:ML:6:ASN:HB2	1.77	0.49
1:M2:22:THR:HA	1:M2:25:GLN:HB3	1.94	0.49
1:MC:10:SER:HB3	1:MN:26:GLN:HG3	1.94	0.49
1:ME:203:ARG:O	1:ME:204:GLU:HG3	2.11	0.49
1:MJ:325:ILE:O	1:MJ:329:VAL:HG13	2.12	0.49
1:MP:74:MET:HA	1:MP:77:THR:OG1	2.11	0.49
1:M3:82:MET:HG3	1:M3:305:ARG:HG2	1.93	0.49
1:MA:85:THR:HG23	1:MA:123:LEU:HD22	1.95	0.49
1:MA:95:LEU:HD11	1:MA:116:ILE:HD11	1.93	0.49
1:ME:3:VAL:HG11	1:ME:375:LEU:HD13	1.93	0.49
1:MM:164:MET:HB3	1:MM:171:MET:HE1	1.95	0.49
1:MM:202:LYS:HE3	1:MM:253:ASP:HB3	1.93	0.49
1:MO:202:LYS:HE2	1:MO:253:ASP:HB3	1.94	0.49
1:MO:251:ARG:HG3	1:MO:252:ILE:CD1	2.42	0.49
1:MQ:72:ILE:HG23	1:MQ:312:GLN:NE2	2.28	0.49
1:M5:203:ARG:O	1:M5:204:GLU:HG2	2.12	0.49
1:M6:101:ASN:HD22	1:MN:67:ASN:HD21	1.59	0.49
1:ME:184:LYS:HE3	1:MT:144:THR:HG22	1.93	0.49
1:M8:37:LYS:HB3	1:M8:339:THR:HB	1.94	0.49
1:MH:15:GLN:HE22	1:ML:346:THR:HG21	1.78	0.49
1:MH:29:MET:HB3	1:MJ:361:VAL:HG13	1.95	0.49
1:ML:234:LYS:HB2	1:ML:246:PHE:HB3	1.94	0.49
1:MX:334:SER:C	1:MX:336:ILE:H	2.20	0.49
1:M5:104:ASN:HB2	1:M5:108:ASP:HB2	1.94	0.49
1:M7:32:LEU:HD11	1:MW:376:LEU:HD21	1.93	0.49
1:M7:321:ASN:O	1:M7:325:ILE:HD12	2.13	0.49
1:M8:28:SER:HB3	1:M8:348:LEU:HD23	1.95	0.49
1:M8:334:SER:C	1:M8:336:ILE:H	2.21	0.49
1:MB:72:ILE:HD12	1:MB:75:ALA:HB3	1.95	0.49
1:MB:203:ARG:O	1:MB:204:GLU:HG3	2.13	0.49
1:MD:99:SER:HB2	1:MD:112:ILE:HD12	1.94	0.49
1:M1:37:LYS:HB3	1:M1:339:THR:HB	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MI:178:ALA:HB3	1:MI:242:LYS:HA	1.94	0.49
1:ML:195:LEU:HD12	1:ML:262:LEU:HD23	1.95	0.49
1:ML:325:ILE:O	1:ML:329:VAL:HG13	2.13	0.49
1:MP:164:MET:SD	1:MP:301:VAL:HG22	2.52	0.49
1:MV:18:LEU:HD12	1:MV:362:LEU:HD11	1.95	0.49
1:M6:25:GLN:HB2	1:M6:351:ALA:HB1	1.95	0.49
1:M6:362:LEU:O	1:M6:366:LYS:HG2	2.13	0.49
1:MD:178:ALA:HB3	1:MD:242:LYS:HA	1.94	0.49
1:ME:95:LEU:HD11	1:ME:116:ILE:HD11	1.94	0.49
1:MO:258:PHE:HB2	1:MO:268:ILE:HG23	1.93	0.49
1:MC:161:ILE:HA	1:MC:304:HIS:HE1	1.77	0.49
1:MC:174:LYS:HB2	1:MC:247:THR:HB	1.95	0.49
1:MD:93:ARG:HB2	1:MD:294:VAL:HG11	1.94	0.49
1:MD:122:GLU:HG2	1:MO:314:ARG:HE	1.76	0.49
1:MF:79:GLU:HA	1:MF:82:MET:HB2	1.94	0.49
1:MN:78:ALA:O	1:MN:82:MET:HG2	2.13	0.49
1:MO:2:ALA:HB1	1:MW:340:ASP:HB3	1.94	0.49
1:MR:279:LEU:HD21	1:MR:290:SER:HB2	1.95	0.49
1:M3:55:ASN:HD22	1:MT:90:GLN:HE22	1.61	0.48
1:M4:218:ASP:OD1	1:M4:221:GLU:HG3	2.13	0.48
1:MC:26:GLN:HE22	1:MM:10:SER:HB2	1.78	0.48
1:MC:29:MET:H	1:MC:32:LEU:HD23	1.78	0.48
1:MF:203:ARG:O	1:MF:204:GLU:HG3	2.13	0.48
1:MH:82:MET:SD	1:MH:164:MET:HE1	2.52	0.48
1:MK:162:LYS:H	1:MK:304:HIS:CE1	2.31	0.48
1:MK:217:ASP:OD2	1:MK:221:GLU:HB2	2.13	0.48
1:ML:203:ARG:O	1:ML:204:GLU:HG2	2.13	0.48
1:MW:251:ARG:HG3	1:MW:252:ILE:CD1	2.43	0.48
1:M2:174:LYS:HG2	1:M2:271:ALA:HB1	1.95	0.48
1:M5:182:LYS:HD2	1:M5:186:TRP:CE2	2.47	0.48
1:MA:108:ASP:O	1:MA:112:ILE:HG13	2.12	0.48
1:MG:79:GLU:HA	1:MG:82:MET:HG2	1.95	0.48
1:MI:8:ASN:HB3	1:MI:11:ALA:HB3	1.95	0.48
1:MI:202:LYS:HE3	1:MI:253:ASP:HB3	1.95	0.48
1:MK:80:GLY:HA2	1:MK:83:LYS:HD3	1.95	0.48
1:MT:182:LYS:HD2	1:MT:186:TRP:CE2	2.48	0.48
1:MT:203:ARG:O	1:MT:204:GLU:HG2	2.13	0.48
1:MW:252:ILE:O	1:MW:252:ILE:HG22	2.13	0.48
1:M5:77:THR:HG21	1:M5:132:PHE:HD1	1.79	0.48
1:M5:81:ALA:HB2	1:M5:130:THR:HG21	1.94	0.48
1:M6:79:GLU:HA	1:M6:82:MET:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M8:328:ASN:HB3	1:MB:77:THR:HG22	1.95	0.48
1:ME:93:ARG:HB2	1:ME:294:VAL:HG11	1.94	0.48
1:MH:78:ALA:HB2	1:MH:137:LEU:HD23	1.94	0.48
1:MH:82:MET:HG3	1:MH:305:ARG:HG2	1.94	0.48
1:MK:334:SER:C	1:MK:336:ILE:H	2.22	0.48
1:MN:349:THR:O	1:MN:353:ILE:HD13	2.13	0.48
1:MX:159:LEU:HB2	1:MX:311:PHE:HE1	1.78	0.48
1:M2:148:GLN:HG2	1:MH:97:LEU:HD22	1.95	0.48
1:M5:136:LYS:HA	1:M5:136:LYS:HD3	1.65	0.48
1:M8:3:VAL:HG23	1:M8:3:VAL:O	2.13	0.48
1:M9:92:MET:HG2	1:M9:116:ILE:HD12	1.94	0.48
1:MB:52:ASN:O	1:MB:56:VAL:HG12	2.13	0.48
1:MG:203:ARG:O	1:MG:204:GLU:HG2	2.13	0.48
1:MI:345:THR:HG22	1:MN:366:LYS:HE3	1.95	0.48
1:MJ:173:GLY:HA2	1:MJ:249:ASN:HB2	1.94	0.48
1:MR:118:ALA:HB1	1:MS:314:ARG:HD2	1.95	0.48
1:MR:136:LYS:HD3	1:MR:136:LYS:HA	1.59	0.48
1:MS:182:LYS:HD2	1:MS:186:TRP:CE2	2.48	0.48
1:MT:335:ARG:HD2	1:MW:69:ASN:HB3	1.95	0.48
1:MU:28:SER:HB3	1:MU:348:LEU:HD23	1.95	0.48
1:M3:10:SER:HB3	1:MO:26:GLN:OE1	2.13	0.48
1:MA:72:ILE:O	1:MA:76:GLN:HG2	2.13	0.48
1:MC:104:ASN:HB2	1:MC:108:ASP:HB2	1.94	0.48
1:MK:140:GLY:HA3	1:MK:163:ASP:HB2	1.95	0.48
1:MO:95:LEU:HD11	1:MO:116:ILE:HG12	1.95	0.48
1:MV:349:THR:O	1:MV:353:ILE:HG13	2.14	0.48
1:M5:217:ASP:OD1	1:M5:221:GLU:HB2	2.14	0.48
1:M6:220:GLU:OE1	1:MN:156:ALA:HB3	2.13	0.48
1:ME:373:LEU:HD23	1:MG:353:ILE:HG13	1.95	0.48
1:MH:334:SER:C	1:MH:336:ILE:H	2.22	0.48
1:MP:251:ARG:HG3	1:MP:252:ILE:HD12	1.96	0.48
1:MQ:136:LYS:HD3	1:MQ:136:LYS:HA	1.61	0.48
1:M1:82:MET:HE2	1:M1:301:VAL:HG13	1.95	0.48
1:M4:162:LYS:H	1:M4:304:HIS:CE1	2.31	0.48
1:M5:84:GLU:O	1:M5:88:ILE:HD12	2.14	0.48
1:MA:149:ILE:HG21	1:MA:315:PHE:CE1	2.44	0.48
1:MB:67:ASN:CG	1:MQ:101:ASN:HD21	2.21	0.48
1:MC:313:ASN:HA	1:MC:316:ASN:HD21	1.77	0.48
1:MF:69:ASN:HB3	1:MW:335:ARG:HD2	1.94	0.48
1:MG:26:GLN:HA	1:MG:29:MET:HE1	1.94	0.48
1:MH:54:LEU:HD12	1:MH:329:VAL:HG13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MI:75:ALA:HB1	1:MI:312:GLN:HG2	1.95	0.48
1:MJ:203:ARG:O	1:MJ:204:GLU:HG3	2.13	0.48
1:MS:321:ASN:O	1:MS:325:ILE:HG12	2.13	0.48
1:MT:92:MET:HE1	1:MT:123:LEU:HD23	1.94	0.48
1:MX:37:LYS:HB3	1:MX:339:THR:HB	1.94	0.48
1:M1:136:LYS:HD3	1:M1:136:LYS:HA	1.64	0.48
1:M6:129:THR:HG22	1:MI:155:GLU:HG3	1.96	0.48
1:M7:113:GLN:NE2	1:M7:117:THR:HG23	2.28	0.48
1:MK:9:VAL:O	1:MK:13:THR:HG23	2.13	0.48
1:MS:149:ILE:HG21	1:MS:315:PHE:CE1	2.49	0.48
1:MW:366:LYS:O	1:MW:369:PRO:HD2	2.13	0.48
1:MA:31:ARG:HE	1:MA:37:LYS:HA	1.79	0.48
1:MD:82:MET:HG3	1:MD:305:ARG:HG2	1.95	0.48
1:MG:93:ARG:HB2	1:MG:294:VAL:HG11	1.95	0.48
1:MW:93:ARG:HG3	1:MW:291:VAL:HG23	1.96	0.48
1:M5:140:GLY:HA3	1:M5:163:ASP:HB2	1.95	0.48
1:M8:315:PHE:O	1:M8:319:ILE:HG12	2.14	0.48
1:MH:99:SER:HB3	1:MH:112:ILE:HD13	1.95	0.48
1:MP:176:TYR:HB2	1:MP:245:LEU:HB2	1.95	0.48
1:MQ:321:ASN:O	1:MQ:325:ILE:HD12	2.14	0.48
1:MS:334:SER:C	1:MS:336:ILE:H	2.22	0.48
1:M2:19:THR:O	1:M2:23:ASN:HB2	2.14	0.47
1:M3:9:VAL:O	1:M3:13:THR:HG22	2.14	0.47
1:MC:79:GLU:O	1:MC:82:MET:HB2	2.14	0.47
1:MD:136:LYS:HD3	1:MD:136:LYS:HA	1.64	0.47
1:MN:318:ALA:O	1:MN:322:LEU:HG	2.14	0.47
1:MP:104:ASN:HB2	1:MP:108:ASP:HB2	1.96	0.47
1:MQ:31:ARG:HE	1:MQ:37:LYS:HA	1.79	0.47
1:MT:78:ALA:HB2	1:MT:137:LEU:HD23	1.96	0.47
1:MU:136:LYS:HD3	1:MU:136:LYS:HA	1.72	0.47
1:MU:334:SER:C	1:MU:336:ILE:H	2.22	0.47
1:MX:349:THR:O	1:MX:353:ILE:HG12	2.14	0.47
1:M9:251:ARG:C	1:M9:252:ILE:HD12	2.39	0.47
1:M9:362:LEU:O	1:M9:366:LYS:HG2	2.14	0.47
1:MG:82:MET:HG3	1:MG:305:ARG:HG2	1.96	0.47
1:MI:334:SER:HA	1:MI:338:ASP:HB2	1.96	0.47
1:MK:78:ALA:O	1:MK:82:MET:HE2	2.14	0.47
1:MN:82:MET:SD	1:MN:164:MET:HE1	2.54	0.47
1:MW:89:LEU:HD12	1:MW:294:VAL:HG13	1.95	0.47
1:M5:201:ASP:HB3	1:M5:205:GLY:HA2	1.96	0.47
1:M7:334:SER:C	1:M7:336:ILE:H	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MG:95:LEU:HD11	1:MG:116:ILE:HD11	1.97	0.47
1:MJ:144:THR:HG21	1:ML:184:LYS:HB3	1.95	0.47
1:MN:276:VAL:O	1:MN:279:LEU:HB3	2.15	0.47
1:MQ:104:ASN:HB2	1:MQ:108:ASP:HB2	1.95	0.47
1:M3:234:LYS:HB2	1:M3:246:PHE:HB3	1.97	0.47
1:M4:99:SER:HB2	1:M4:112:ILE:HD12	1.95	0.47
1:M4:103:SER:HA	1:MI:74:MET:CE	2.45	0.47
1:M8:189:GLU:HG3	1:M8:192:LYS:HD3	1.97	0.47
1:ME:82:MET:SD	1:ME:164:MET:HE1	2.54	0.47
1:MN:350:LYS:O	1:MN:354:LEU:HD22	2.14	0.47
1:M3:203:ARG:O	1:M3:204:GLU:HG2	2.15	0.47
1:M8:203:ARG:O	1:M8:204:GLU:HG2	2.14	0.47
1:MP:22:THR:OG1	1:MQ:1:MET:HE1	2.14	0.47
1:MW:82:MET:HE1	1:MW:164:MET:SD	2.54	0.47
1:M4:144:THR:HG22	1:M4:160:ASN:HB3	1.97	0.47
1:M6:95:LEU:HD21	1:M6:116:ILE:HD11	1.95	0.47
1:MB:144:THR:HG22	1:MB:160:ASN:HB3	1.96	0.47
1:ME:346:THR:HG22	1:MW:366:LYS:HD3	1.97	0.47
1:MF:136:LYS:HD3	1:MF:136:LYS:HA	1.60	0.47
1:MM:334:SER:C	1:MM:336:ILE:H	2.22	0.47
1:M4:93:ARG:HB2	1:M4:294:VAL:HG11	1.95	0.47
1:M9:201:ASP:HB3	1:M9:204:GLU:O	2.15	0.47
1:MB:73:SER:O	1:MB:77:THR:HG23	2.15	0.47
1:MB:140:GLY:HA3	1:MB:163:ASP:HB2	1.97	0.47
1:MC:130:THR:HG22	1:MM:325:ILE:HD11	1.97	0.47
1:MD:89:LEU:HD12	1:MD:294:VAL:HG13	1.95	0.47
1:MJ:136:LYS:HE2	1:MP:228:GLY:HA2	1.96	0.47
1:MJ:252:ILE:O	1:MJ:252:ILE:HG22	2.15	0.47
1:MJ:313:ASN:HA	1:MJ:316:ASN:HD21	1.78	0.47
1:ML:258:PHE:HB2	1:ML:268:ILE:HG23	1.95	0.47
1:MO:85:THR:O	1:MO:89:LEU:HD12	2.15	0.47
1:MU:192:LYS:HG3	1:MU:261:ALA:HB1	1.96	0.47
1:MV:136:LYS:HD3	1:MV:136:LYS:HA	1.65	0.47
1:MW:29:MET:H	1:MW:32:LEU:HD12	1.80	0.47
1:MW:85:THR:HG21	1:MW:164:MET:HE1	1.96	0.47
1:MW:146:SER:HA	1:MW:158:MET:HA	1.95	0.47
1:M1:372:ALA:O	1:M1:375:LEU:HD22	2.14	0.47
1:M5:6:ASN:HA	1:MV:350:LYS:HE2	1.96	0.47
1:MC:247:THR:HG23	1:MC:252:ILE:HB	1.97	0.47
1:MD:130:THR:HG22	1:MD:137:LEU:HD23	1.97	0.47
1:MF:140:GLY:HA3	1:MF:163:ASP:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MF:162:LYS:HD3	1:MF:304:HIS:CD2	2.49	0.47
1:MN:334:SER:C	1:MN:336:ILE:H	2.23	0.47
1:MQ:81:ALA:HB2	1:MQ:130:THR:HG21	1.97	0.47
1:MV:159:LEU:HB2	1:MV:311:PHE:CE2	2.50	0.47
1:M5:78:ALA:O	1:M5:82:MET:HG2	2.15	0.47
1:MD:54:LEU:HD12	1:MD:329:VAL:HB	1.97	0.47
1:MK:298:LEU:HD23	1:MK:298:LEU:HA	1.80	0.47
1:ML:232:MET:HE3	1:ML:232:MET:HB2	1.77	0.47
1:MT:61:LEU:O	1:MT:65:VAL:HG23	2.14	0.47
1:MV:9:VAL:O	1:MV:13:THR:HG23	2.15	0.47
1:MV:202:LYS:HE3	1:MV:253:ASP:HB3	1.95	0.47
1:M5:364:GLN:HA	1:M5:367:GLN:OE1	2.15	0.47
1:MA:79:GLU:O	1:MA:82:MET:HB2	2.15	0.47
1:ML:358:SER:O	1:ML:361:VAL:HG12	2.15	0.47
1:MP:68:ALA:HB3	1:MP:319:ILE:HD11	1.97	0.47
1:MW:176:TYR:HB2	1:MW:245:LEU:HB2	1.97	0.47
1:M6:302:ASP:HB3	1:MN:49:GLN:HE21	1.80	0.46
1:M6:334:SER:C	1:M6:336:ILE:H	2.22	0.46
1:ME:66:ARG:HH12	1:MH:336:ILE:HD13	1.79	0.46
1:MG:112:ILE:HG12	1:MJ:46:ALA:HB2	1.97	0.46
1:ML:198:THR:HB	1:ML:257:THR:HB	1.97	0.46
1:M1:29:MET:HE2	1:M1:29:MET:HB3	1.80	0.46
1:M3:93:ARG:HB2	1:M3:294:VAL:HG11	1.97	0.46
1:M3:258:PHE:HB2	1:M3:268:ILE:HG23	1.98	0.46
1:M6:3:VAL:HG13	1:M6:3:VAL:O	2.15	0.46
1:M9:28:SER:C	1:M9:30:GLU:H	2.23	0.46
1:M9:217:ASP:OD1	1:M9:221:GLU:HB2	2.15	0.46
1:MA:203:ARG:O	1:MA:204:GLU:HG2	2.14	0.46
1:MD:61:LEU:O	1:MD:65:VAL:HG23	2.15	0.46
1:MH:1:MET:HE2	1:MH:2:ALA:N	2.30	0.46
1:MK:48:LEU:HD21	1:MP:305:ARG:CZ	2.46	0.46
1:MN:142:PHE:CZ	1:MN:145:LYS:HG3	2.50	0.46
1:MP:74:MET:HE1	1:MR:103:SER:HA	1.97	0.46
1:MV:57:GLN:HG2	1:MV:329:VAL:HG11	1.96	0.46
1:M3:79:GLU:HA	1:M3:82:MET:HG2	1.98	0.46
1:M6:234:LYS:HB2	1:M6:246:PHE:HB3	1.96	0.46
1:MD:366:LYS:O	1:MD:369:PRO:HD2	2.16	0.46
1:MI:251:ARG:HG3	1:MI:252:ILE:HD12	1.96	0.46
1:MK:364:GLN:H	1:MK:364:GLN:CD	2.23	0.46
1:MN:172:GLY:HA3	1:MN:275:THR:HA	1.97	0.46
1:MR:340:ASP:OD1	1:MR:343:LYS:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MU:283:THR:HG23	1:MU:286:GLY:H	1.80	0.46
1:M2:29:MET:HG3	1:M2:348:LEU:HD21	1.97	0.46
1:M2:104:ASN:HB2	1:M2:108:ASP:HB2	1.97	0.46
1:M5:95:LEU:HD13	1:M5:112:ILE:HG23	1.96	0.46
1:M6:198:THR:HB	1:M6:257:THR:HB	1.97	0.46
1:M9:84:GLU:O	1:M9:88:ILE:HG13	2.15	0.46
1:MA:234:LYS:HB2	1:MA:246:PHE:HB3	1.96	0.46
1:MC:209:ILE:HD12	1:MC:209:ILE:O	2.15	0.46
1:MD:161:ILE:HA	1:MD:304:HIS:CE1	2.51	0.46
1:MM:136:LYS:HD3	1:MM:136:LYS:HA	1.69	0.46
1:MM:136:LYS:HE2	1:MX:228:GLY:HA2	1.98	0.46
1:MN:188:VAL:HG12	1:MN:193:THR:HG22	1.97	0.46
1:MX:12:MET:HA	1:MX:15:GLN:HB2	1.96	0.46
1:M1:247:THR:HG23	1:M1:252:ILE:HB	1.97	0.46
1:M2:373:LEU:HD11	1:MJ:356:GLN:HB3	1.97	0.46
1:M4:82:MET:HE2	1:M4:301:VAL:HG13	1.97	0.46
1:MA:321:ASN:O	1:MA:325:ILE:HG12	2.15	0.46
1:MB:53:ARG:HB2	1:MB:53:ARG:CZ	2.45	0.46
1:MB:334:SER:C	1:MB:336:ILE:H	2.23	0.46
1:MC:203:ARG:O	1:MC:204:GLU:HG2	2.15	0.46
1:ME:124:ASN:HB3	1:ME:165:ARG:HH12	1.81	0.46
1:MH:333:LYS:HE3	1:MH:333:LYS:HB3	1.59	0.46
1:MK:136:LYS:HD3	1:MK:136:LYS:HA	1.60	0.46
1:MN:220:GLU:HA	1:MN:237:VAL:HG21	1.96	0.46
1:MO:48:LEU:HD21	1:MW:305:ARG:CZ	2.46	0.46
1:MT:219:ILE:HG12	1:MT:241:GLY:HA2	1.97	0.46
1:M2:203:ARG:O	1:M2:204:GLU:HG2	2.16	0.46
1:M4:113:GLN:NE2	1:M4:117:THR:HG23	2.30	0.46
1:M5:197:ILE:HD12	1:M5:209:ILE:HD11	1.98	0.46
1:M6:203:ARG:O	1:M6:204:GLU:HG2	2.15	0.46
1:MA:198:THR:HB	1:MA:257:THR:HB	1.97	0.46
1:MB:61:LEU:HD22	1:MB:151:ALA:HB2	1.98	0.46
1:MK:65:VAL:HG13	1:MK:319:ILE:HD12	1.98	0.46
1:ML:14:ALA:O	1:ML:18:LEU:HD12	2.16	0.46
1:ML:122:GLU:HG2	1:MP:314:ARG:HE	1.81	0.46
1:MO:67:ASN:HB3	1:MW:101:ASN:HD22	1.81	0.46
1:MT:174:LYS:HB2	1:MT:247:THR:HB	1.98	0.46
1:MU:138:LEU:HD13	1:MU:164:MET:HE2	1.98	0.46
1:MW:9:VAL:O	1:MW:13:THR:HG23	2.16	0.46
1:MC:234:LYS:HB2	1:MC:246:PHE:HB3	1.97	0.46
1:MR:83:LYS:HB3	1:MR:83:LYS:HE2	1.61	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MW:79:GLU:HA	1:MW:82:MET:HB2	1.96	0.46
1:M3:51:SER:HB2	1:M3:337:LYS:HG3	1.98	0.46
1:M5:82:MET:HA	1:M5:82:MET:HE3	1.97	0.46
1:M6:364:GLN:HE21	1:M6:364:GLN:C	2.23	0.46
1:M8:243:LEU:HD13	1:M8:266:LEU:HD13	1.98	0.46
1:MB:75:ALA:HB1	1:MB:312:GLN:HG2	1.96	0.46
1:MB:161:ILE:HG23	1:MB:304:HIS:HE1	1.81	0.46
1:MB:195:LEU:HD12	1:MB:262:LEU:HD23	1.97	0.46
1:ML:84:GLU:O	1:ML:88:ILE:HG13	2.16	0.46
1:MP:147:PHE:HE1	1:MP:159:LEU:HB3	1.81	0.46
1:M5:10:SER:HB2	1:MI:26:GLN:NE2	2.29	0.46
1:M5:15:GLN:HG3	1:M5:362:LEU:HD21	1.97	0.46
1:M5:361:VAL:HA	1:M5:364:GLN:NE2	2.31	0.46
1:M7:99:SER:HA	1:M7:104:ASN:ND2	2.31	0.46
1:M8:67:ASN:CG	1:MN:101:ASN:HD21	2.23	0.46
1:MD:28:SER:O	1:MD:29:MET:HG2	2.15	0.46
1:MD:364:GLN:HA	1:MD:367:GLN:HG2	1.98	0.46
1:ME:228:GLY:HA2	1:MW:136:LYS:HE2	1.97	0.46
1:MF:178:ALA:HB3	1:MF:242:LYS:HA	1.97	0.46
1:MI:81:ALA:HB2	1:MI:130:THR:HG21	1.98	0.46
1:MI:251:ARG:HG3	1:MI:252:ILE:CD1	2.46	0.46
1:MO:142:PHE:CZ	1:MO:145:LYS:HG3	2.50	0.46
1:MO:219:ILE:HG23	1:MO:237:VAL:HG21	1.97	0.46
1:MQ:48:LEU:HD21	1:MS:305:ARG:CZ	2.46	0.46
1:MR:29:MET:HG3	1:MR:348:LEU:HD11	1.98	0.46
1:MS:203:ARG:O	1:MS:204:GLU:HG2	2.15	0.46
1:MV:340:ASP:C	1:MV:340:ASP:OD1	2.59	0.46
1:M5:308:LEU:HD12	1:M5:308:LEU:HA	1.81	0.46
1:M6:68:ALA:HA	1:M6:315:PHE:HE1	1.80	0.46
1:M7:106:LYS:H	1:M7:106:LYS:CE	2.28	0.46
1:M7:202:LYS:HE3	1:M7:253:ASP:HB3	1.98	0.46
1:M7:203:ARG:O	1:M7:204:GLU:HG2	2.17	0.46
1:M9:178:ALA:HB3	1:M9:242:LYS:HA	1.98	0.46
1:MD:10:SER:HB3	1:MV:26:GLN:HG3	1.98	0.46
1:MF:247:THR:HG23	1:MF:252:ILE:HB	1.97	0.46
1:MG:306:ALA:HB2	1:MH:49:GLN:HE21	1.80	0.46
1:MO:136:LYS:HD3	1:MO:136:LYS:HA	1.62	0.46
1:MP:178:ALA:HB3	1:MP:242:LYS:HA	1.98	0.46
1:M2:42:LYS:HG2	1:MH:312:GLN:HB3	1.97	0.45
1:M2:46:ALA:HB2	1:ME:112:ILE:HD11	1.97	0.45
1:M4:82:MET:HG3	1:M4:305:ARG:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M7:78:ALA:O	1:M7:82:MET:HG2	2.16	0.45
1:M8:1:MET:N	1:MB:19:THR:HA	2.31	0.45
1:M9:3:VAL:HG13	1:M9:3:VAL:O	2.16	0.45
1:M9:238:ASP:HB3	1:M9:244:GLN:CD	2.41	0.45
1:MA:245:LEU:HG	1:MA:258:PHE:HZ	1.80	0.45
1:MB:114:GLU:HA	1:MB:114:GLU:OE2	2.15	0.45
1:MD:350:LYS:HE2	1:MX:6:ASN:HD22	1.80	0.45
1:MI:182:LYS:HD2	1:MI:186:TRP:CE2	2.51	0.45
1:ML:136:LYS:HD3	1:ML:136:LYS:HA	1.62	0.45
1:MM:93:ARG:HB2	1:MM:294:VAL:HG11	1.98	0.45
1:MO:182:LYS:HZ3	1:MO:182:LYS:HG2	1.67	0.45
1:MS:35:GLY:C	1:MS:339:THR:HG22	2.41	0.45
1:MS:82:MET:HG3	1:MS:305:ARG:HG2	1.98	0.45
1:MU:72:ILE:HD12	1:MU:75:ALA:HB3	1.98	0.45
1:MU:78:ALA:O	1:MU:82:MET:HG2	2.16	0.45
1:MV:61:LEU:O	1:MV:65:VAL:HG23	2.16	0.45
1:MX:158:MET:HB2	1:MX:158:MET:HE3	1.80	0.45
1:MX:202:LYS:HE3	1:MX:253:ASP:HB3	1.98	0.45
1:M2:195:LEU:HD12	1:M2:262:LEU:HD23	1.98	0.45
1:M5:19:THR:HG21	1:MX:1:MET:HB2	1.97	0.45
1:MB:258:PHE:HB2	1:MB:268:ILE:HG23	1.99	0.45
1:MG:104:ASN:HB2	1:MG:108:ASP:HB2	1.99	0.45
1:MJ:93:ARG:HB2	1:MJ:294:VAL:HG11	1.98	0.45
1:MJ:142:PHE:CZ	1:MJ:145:LYS:HG3	2.52	0.45
1:MN:19:THR:O	1:MN:23:ASN:HB2	2.16	0.45
1:MP:203:ARG:O	1:MP:204:GLU:HG2	2.16	0.45
1:MV:106:LYS:H	1:MV:106:LYS:CE	2.27	0.45
1:MW:357:ALA:O	1:MW:361:VAL:HG23	2.16	0.45
1:M5:77:THR:HG21	1:M5:132:PHE:CD1	2.51	0.45
1:M5:113:GLN:HB2	1:M5:281:VAL:O	2.17	0.45
1:M5:247:THR:HG23	1:M5:252:ILE:HB	1.98	0.45
1:M7:83:LYS:HD2	1:ME:324:ASN:ND2	2.31	0.45
1:MC:283:THR:HG23	1:MC:286:GLY:H	1.82	0.45
1:ME:358:SER:O	1:ME:361:VAL:HG12	2.17	0.45
1:ME:366:LYS:O	1:ME:369:PRO:HD2	2.17	0.45
1:MF:18:LEU:HB3	1:MW:1:MET:H3	1.80	0.45
1:MH:201:ASP:HB3	1:MH:205:GLY:HA2	1.98	0.45
1:MH:313:ASN:HA	1:MH:316:ASN:HD21	1.79	0.45
1:MP:51:SER:HB2	1:MP:337:LYS:HE3	1.98	0.45
1:MP:76:GLN:HA	1:MP:79:GLU:HB2	1.98	0.45
1:MP:198:THR:HB	1:MP:257:THR:HB	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MU:367:GLN:N	1:MU:367:GLN:OE1	2.50	0.45
1:M1:340:ASP:OD1	1:M1:343:LYS:HG2	2.16	0.45
1:M5:101:ASN:HD21	1:MM:67:ASN:CG	2.25	0.45
1:M5:281:VAL:O	1:M5:281:VAL:HG13	2.16	0.45
1:M6:99:SER:OG	1:M6:281:VAL:HG21	2.16	0.45
1:M6:238:ASP:HB3	1:M6:244:GLN:CD	2.42	0.45
1:M7:93:ARG:HB2	1:M7:294:VAL:HG11	1.98	0.45
1:M8:182:LYS:HD2	1:M8:186:TRP:CE2	2.52	0.45
1:MB:366:LYS:HE3	1:MN:345:THR:HG22	1.98	0.45
1:MG:159:LEU:HD13	1:MG:311:PHE:CD1	2.51	0.45
1:ML:353:ILE:C	1:ML:353:ILE:HD12	2.41	0.45
1:MM:243:LEU:HD13	1:MM:266:LEU:HD13	1.99	0.45
1:MU:231:ASP:OD2	1:MU:231:ASP:C	2.60	0.45
1:M3:195:LEU:HD12	1:M3:262:LEU:HD23	1.99	0.45
1:MA:150:GLY:HA3	1:MA:155:GLU:HG3	1.98	0.45
1:MT:93:ARG:HB2	1:MT:294:VAL:HG11	1.98	0.45
1:M2:335:ARG:HD2	1:MT:69:ASN:HB3	1.99	0.45
1:M6:353:ILE:HD12	1:M6:353:ILE:H	1.81	0.45
1:MA:37:LYS:HB3	1:MA:339:THR:HB	1.97	0.45
1:MD:202:LYS:HE3	1:MD:253:ASP:HB3	1.98	0.45
1:ME:136:LYS:HD3	1:ME:136:LYS:HA	1.64	0.45
1:MF:22:THR:HA	1:MF:25:GLN:HB3	1.99	0.45
1:MK:82:MET:HE1	1:MK:138:LEU:HD11	1.97	0.45
1:MN:283:THR:HG23	1:MN:286:GLY:H	1.81	0.45
1:MN:313:ASN:HA	1:MN:316:ASN:HD21	1.81	0.45
1:MS:83:LYS:HB3	1:MS:83:LYS:HE2	1.76	0.45
1:MU:140:GLY:HA3	1:MU:163:ASP:HB2	1.99	0.45
1:MV:203:ARG:O	1:MV:204:GLU:HG2	2.16	0.45
1:MW:158:MET:HE3	1:MW:158:MET:HB3	1.84	0.45
1:M2:3:VAL:HG22	1:M2:372:ALA:HB2	1.99	0.45
1:M4:120:ASN:HD21	1:M4:277:ASP:HA	1.82	0.45
1:MB:136:LYS:HD3	1:MB:136:LYS:HA	1.66	0.45
1:MC:147:PHE:HE2	1:MC:159:LEU:HB3	1.82	0.45
1:MC:349:THR:O	1:MC:353:ILE:HD12	2.17	0.45
1:MG:84:GLU:HG3	1:ML:321:ASN:HB2	1.99	0.45
1:MJ:138:LEU:HD13	1:MJ:164:MET:HE2	1.99	0.45
1:MK:161:ILE:HA	1:MK:304:HIS:CE1	2.51	0.45
1:MQ:234:LYS:HB2	1:MQ:246:PHE:HB3	1.99	0.45
1:MT:298:LEU:HD23	1:MT:298:LEU:HA	1.76	0.45
1:M2:77:THR:HG21	1:M2:132:PHE:HD1	1.82	0.45
1:M4:61:LEU:HD13	1:M4:326:ASN:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M8:110:VAL:O	1:M8:114:GLU:HG2	2.17	0.45
1:M8:350:LYS:HG3	1:M8:354:LEU:HD12	1.98	0.45
1:M9:182:LYS:HD2	1:M9:186:TRP:CE2	2.51	0.45
1:M9:202:LYS:HG2	1:M9:251:ARG:HA	1.99	0.45
1:MD:231:ASP:OD2	1:MD:231:ASP:C	2.60	0.45
1:MH:5:VAL:HB	1:ML:353:ILE:HD11	1.99	0.45
1:MH:366:LYS:O	1:MH:369:PRO:HD2	2.16	0.45
1:MN:299:LYS:HE3	1:MN:299:LYS:HB2	1.82	0.45
1:MP:4:ASN:C	1:MP:4:ASN:OD1	2.59	0.45
1:MU:73:SER:O	1:MU:76:GLN:HG3	2.17	0.45
1:MV:201:ASP:HB3	1:MV:205:GLY:HA2	1.98	0.45
1:M2:49:GLN:HE22	1:MH:303:SER:HA	1.81	0.45
1:M9:55:ASN:C	1:M9:55:ASN:HD22	2.25	0.45
1:M9:82:MET:HG3	1:M9:305:ARG:HG2	1.98	0.45
1:M9:219:ILE:HG12	1:M9:241:GLY:HA2	1.99	0.45
1:MD:161:ILE:HA	1:MD:304:HIS:HE1	1.82	0.45
1:MH:77:THR:HG21	1:MH:132:PHE:HD1	1.81	0.45
1:MJ:101:ASN:HD21	1:MU:67:ASN:CG	2.25	0.45
1:MK:35:GLY:C	1:MK:339:THR:HG22	2.42	0.45
1:MN:202:LYS:HE3	1:MN:253:ASP:HB3	1.98	0.45
1:MR:182:LYS:HD2	1:MR:186:TRP:CD1	2.52	0.45
1:MV:283:THR:HG23	1:MV:286:GLY:H	1.82	0.45
1:MW:1:MET:HG2	1:MW:3:VAL:HB	1.99	0.45
1:MW:219:ILE:HG12	1:MW:241:GLY:HA2	1.98	0.45
1:M3:79:GLU:O	1:M3:82:MET:HB2	2.17	0.45
1:M7:346:THR:HG21	1:MF:15:GLN:HE22	1.82	0.45
1:MD:74:MET:HB2	1:MD:74:MET:HE3	1.66	0.45
1:ML:82:MET:HE2	1:ML:301:VAL:HG13	1.98	0.45
1:MM:79:GLU:HA	1:MM:82:MET:HG2	1.99	0.45
1:MM:283:THR:HG23	1:MM:286:GLY:H	1.82	0.45
1:MP:218:ASP:OD1	1:MP:221:GLU:HG3	2.17	0.45
1:MR:80:GLY:HA2	1:MS:324:ASN:ND2	2.31	0.45
1:MS:159:LEU:HB2	1:MS:311:PHE:HE2	1.80	0.45
1:MW:182:LYS:HD2	1:MW:186:TRP:CE2	2.52	0.45
1:M1:366:LYS:O	1:M1:369:PRO:HD2	2.17	0.44
1:M5:321:ASN:O	1:M5:325:ILE:HD12	2.16	0.44
1:MB:88:ILE:HG22	1:MB:92:MET:HE2	1.99	0.44
1:MB:318:ALA:O	1:MB:322:LEU:HG	2.17	0.44
1:MC:321:ASN:O	1:MC:325:ILE:HG12	2.17	0.44
1:MD:95:LEU:HD21	1:MD:115:GLU:HG2	1.99	0.44
1:ML:82:MET:HG3	1:ML:305:ARG:HG2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MQ:25:GLN:HB2	1:MQ:351:ALA:HB1	1.99	0.44
1:M1:66:ARG:HH12	1:MV:336:ILE:HD13	1.82	0.44
1:M1:182:LYS:HD2	1:M1:186:TRP:CE2	2.51	0.44
1:M2:362:LEU:O	1:M2:366:LYS:HG2	2.17	0.44
1:M3:2:ALA:HA	1:MT:340:ASP:HB3	1.99	0.44
1:ME:92:MET:HG2	1:ME:116:ILE:HD12	1.99	0.44
1:MF:31:ARG:H	1:MF:31:ARG:HG3	1.56	0.44
1:MG:159:LEU:HB2	1:MG:311:PHE:CE1	2.46	0.44
1:MJ:251:ARG:HG3	1:MJ:252:ILE:CD1	2.47	0.44
1:MK:182:LYS:HD2	1:MK:186:TRP:CE2	2.52	0.44
1:MM:203:ARG:O	1:MM:204:GLU:HG2	2.17	0.44
1:MO:373:LEU:HD11	1:MT:356:GLN:HB3	1.98	0.44
1:MR:198:THR:HB	1:MR:257:THR:HB	1.99	0.44
1:MX:14:ALA:O	1:MX:18:LEU:HB2	2.17	0.44
1:MX:276:VAL:O	1:MX:279:LEU:HB3	2.17	0.44
1:M1:77:THR:HG21	1:M1:132:PHE:CD1	2.52	0.44
1:M6:372:ALA:O	1:M6:375:LEU:HD22	2.18	0.44
1:M8:219:ILE:HG12	1:M8:241:GLY:HA2	2.00	0.44
1:MD:201:ASP:HB3	1:MD:205:GLY:HA2	1.99	0.44
1:MF:238:ASP:HB3	1:MF:244:GLN:OE1	2.18	0.44
1:MG:136:LYS:HD3	1:MG:136:LYS:HA	1.61	0.44
1:ML:217:ASP:OD1	1:ML:221:GLU:HB2	2.16	0.44
1:MN:311:PHE:CD1	1:MN:311:PHE:C	2.94	0.44
1:MO:238:ASP:HB3	1:MO:244:GLN:CD	2.42	0.44
1:MR:199:LEU:HD12	1:MR:199:LEU:HA	1.84	0.44
1:M3:49:GLN:HE21	1:MT:302:ASP:HB3	1.83	0.44
1:M5:149:ILE:HG21	1:M5:315:PHE:CE1	2.53	0.44
1:M6:199:LEU:HG	1:M6:252:ILE:HG23	1.98	0.44
1:M6:353:ILE:HG23	1:MQ:373:LEU:HD22	1.98	0.44
1:M9:136:LYS:HD3	1:M9:136:LYS:HA	1.58	0.44
1:M9:328:ASN:HD22	1:MX:77:THR:HA	1.83	0.44
1:MB:202:LYS:HE3	1:MB:253:ASP:HB3	1.98	0.44
1:MC:118:ALA:HB1	1:MM:314:ARG:HD2	1.99	0.44
1:MC:219:ILE:HG12	1:MC:241:GLY:HA2	2.00	0.44
1:ME:340:ASP:HB2	1:MT:3:VAL:H	1.82	0.44
1:MI:1:MET:HE2	1:MI:3:VAL:HB	1.99	0.44
1:MI:201:ASP:HB3	1:MI:205:GLY:HA2	1.99	0.44
1:MP:63:VAL:HG11	1:MR:97:LEU:HB3	1.98	0.44
1:MS:51:SER:HB3	1:MS:336:ILE:HG22	1.98	0.44
1:MV:139:ASN:HB3	1:MV:141:THR:HG23	1.99	0.44
1:MV:198:THR:HB	1:MV:257:THR:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MW:82:MET:HG3	1:MW:305:ARG:HG2	1.99	0.44
1:M3:320:ASN:HA	1:M3:323:ASP:HB2	1.99	0.44
1:M4:103:SER:HA	1:MI:74:MET:HE3	2.00	0.44
1:M4:203:ARG:O	1:M4:204:GLU:HG2	2.18	0.44
1:M7:136:LYS:HA	1:M7:136:LYS:HD3	1.60	0.44
1:MA:112:ILE:HG12	1:MD:46:ALA:HB2	2.00	0.44
1:MB:74:MET:HA	1:MB:77:THR:HG1	1.82	0.44
1:MB:83:LYS:HB2	1:MB:83:LYS:HE2	1.83	0.44
1:ME:276:VAL:O	1:ME:279:LEU:HB3	2.17	0.44
1:MG:88:ILE:HG23	1:MG:119:LEU:HD22	1.99	0.44
1:MI:357:ALA:O	1:MI:361:VAL:HG23	2.17	0.44
1:MK:88:ILE:HD12	1:MK:119:LEU:HD22	2.00	0.44
1:MK:203:ARG:O	1:MK:204:GLU:HG2	2.16	0.44
1:MQ:201:ASP:HB3	1:MQ:205:GLY:HA2	1.99	0.44
1:MU:171:MET:HE2	1:MU:171:MET:HB2	1.83	0.44
1:M1:359:SER:HA	1:M1:362:LEU:HD12	2.00	0.44
1:M4:200:LYS:HD2	1:M4:201:ASP:H	1.83	0.44
1:M7:340:ASP:C	1:M7:340:ASP:OD1	2.61	0.44
1:M9:1:MET:CG	1:MX:355:SER:HA	2.48	0.44
1:MC:80:GLY:HA3	1:MM:324:ASN:OD1	2.18	0.44
1:MH:203:ARG:O	1:MH:204:GLU:HG2	2.18	0.44
1:MI:147:PHE:HE2	1:MI:159:LEU:HB3	1.83	0.44
1:MK:234:LYS:HB2	1:MK:246:PHE:HB3	1.99	0.44
1:MO:203:ARG:O	1:MO:204:GLU:HG2	2.17	0.44
1:MQ:5:VAL:HG12	1:MQ:369:PRO:HB3	1.99	0.44
1:MQ:164:MET:HE2	1:MQ:164:MET:HB3	1.82	0.44
1:MW:140:GLY:HA3	1:MW:163:ASP:HB2	2.00	0.44
1:M2:22:THR:OG1	1:MU:1:MET:HE2	2.18	0.44
1:M2:202:LYS:HE3	1:M2:253:ASP:HB3	2.00	0.44
1:MA:159:LEU:HB2	1:MA:311:PHE:CE1	2.52	0.44
1:MG:93:ARG:HG2	1:MG:291:VAL:HG23	1.98	0.44
1:MI:52:ASN:O	1:MI:56:VAL:HG13	2.17	0.44
1:MV:78:ALA:HB2	1:MV:137:LEU:HD13	1.99	0.44
1:M2:130:THR:HG22	1:MU:325:ILE:HD11	2.00	0.44
1:M2:244:GLN:NE2	1:M2:289:GLU:HB2	2.32	0.44
1:M4:366:LYS:O	1:M4:369:PRO:HD2	2.17	0.44
1:M7:103:SER:HA	1:MW:74:MET:CE	2.48	0.44
1:MA:116:ILE:HD13	1:MA:116:ILE:HA	1.77	0.44
1:MJ:342:ALA:O	1:MJ:346:THR:HG23	2.17	0.44
1:MN:357:ALA:O	1:MN:361:VAL:HG23	2.17	0.44
1:MS:20:SER:HA	1:MS:23:ASN:ND2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MT:28:SER:C	1:MT:30:GLU:H	2.26	0.44
1:MW:203:ARG:O	1:MW:204:GLU:HG2	2.18	0.44
1:M3:220:GLU:HG2	1:M3:237:VAL:HG21	2.00	0.44
1:M7:116:ILE:HD13	1:M7:116:ILE:HA	1.85	0.44
1:MC:313:ASN:HA	1:MC:316:ASN:ND2	2.33	0.44
1:MD:74:MET:HE1	1:MF:103:SER:HA	2.00	0.44
1:MF:14:ALA:O	1:MF:18:LEU:HG	2.18	0.44
1:MH:15:GLN:HG3	1:MH:362:LEU:HD21	1.99	0.44
1:MJ:82:MET:O	1:MJ:86:THR:HG22	2.18	0.44
1:MK:50:ILE:O	1:MK:54:LEU:HD22	2.17	0.44
1:MK:61:LEU:O	1:MK:65:VAL:HG23	2.18	0.44
1:MK:209:ILE:HD12	1:MK:209:ILE:O	2.18	0.44
1:MN:124:ASN:HB3	1:MN:165:ARG:HH12	1.83	0.44
1:MP:84:GLU:HG2	1:MQ:321:ASN:HB2	2.00	0.44
1:M4:165:ARG:NH1	1:M4:165:ARG:HB3	2.33	0.43
1:M5:184:LYS:HD3	1:MM:158:MET:SD	2.58	0.43
1:M6:112:ILE:HG12	1:MC:46:ALA:HB2	2.00	0.43
1:MB:25:GLN:HB2	1:MB:351:ALA:HB1	2.00	0.43
1:MF:112:ILE:HG12	1:MO:46:ALA:HB2	1.98	0.43
1:MI:164:MET:HB3	1:MI:164:MET:HE2	1.71	0.43
1:MJ:140:GLY:HA3	1:MJ:163:ASP:HB2	1.98	0.43
1:MK:144:THR:HG21	1:MP:184:LYS:HB2	2.00	0.43
1:MN:335:ARG:HD2	1:MQ:69:ASN:HB3	2.00	0.43
1:MP:252:ILE:O	1:MP:252:ILE:HG22	2.18	0.43
1:MX:140:GLY:HA3	1:MX:163:ASP:HB2	2.00	0.43
1:M1:26:GLN:HE22	1:MV:10:SER:HB3	1.83	0.43
1:M4:37:LYS:HB3	1:M4:339:THR:HB	1.99	0.43
1:M5:178:ALA:HB3	1:M5:242:LYS:HA	1.99	0.43
1:M7:50:ILE:HD12	1:M7:51:SER:N	2.33	0.43
1:M8:28:SER:C	1:M8:30:GLU:H	2.25	0.43
1:M9:31:ARG:H	1:M9:31:ARG:HG2	1.52	0.43
1:M9:74:MET:HE3	1:M9:74:MET:HB3	1.89	0.43
1:MA:31:ARG:H	1:MA:31:ARG:HG2	1.55	0.43
1:MA:68:ALA:O	1:MA:72:ILE:HG13	2.18	0.43
1:MB:335:ARG:HD2	1:MK:69:ASN:HB3	2.00	0.43
1:MC:201:ASP:HB3	1:MC:205:GLY:HA2	2.00	0.43
1:MH:136:LYS:O	1:MH:142:PHE:HB2	2.18	0.43
1:MJ:162:LYS:HD2	1:MJ:304:HIS:CG	2.53	0.43
1:MM:104:ASN:HB2	1:MM:108:ASP:HB2	2.00	0.43
1:MN:73:SER:HA	1:MN:76:GLN:HE21	1.83	0.43
1:MU:95:LEU:HD11	1:MU:116:ILE:HG12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MW:83:LYS:HE2	1:MW:83:LYS:HB3	1.76	0.43
1:MW:178:ALA:HB3	1:MW:242:LYS:HA	1.99	0.43
1:M1:33:SER:HB3	1:MV:361:VAL:HG11	2.00	0.43
1:M2:136:LYS:HE2	1:MJ:228:GLY:HA2	1.99	0.43
1:M8:220:GLU:HG2	1:M8:237:VAL:HG11	1.99	0.43
1:M9:200:LYS:HA	1:M9:200:LYS:HD2	1.79	0.43
1:M9:366:LYS:O	1:M9:369:PRO:HD2	2.18	0.43
1:MB:42:LYS:HD2	1:MQ:312:GLN:CB	2.47	0.43
1:ME:5:VAL:HG23	1:ME:369:PRO:HB3	2.00	0.43
1:MF:199:LEU:HD12	1:MF:199:LEU:HA	1.81	0.43
1:MG:292:ALA:HB2	1:MH:153:ASN:ND2	2.34	0.43
1:MJ:343:LYS:HB3	1:MJ:343:LYS:HE3	1.70	0.43
1:MK:342:ALA:O	1:MK:346:THR:HG23	2.18	0.43
1:MP:219:ILE:HD12	1:MP:219:ILE:HA	1.83	0.43
1:MP:375:LEU:HD21	1:MR:341:PHE:HB3	2.00	0.43
1:MQ:159:LEU:HB2	1:MQ:311:PHE:CE2	2.53	0.43
1:MS:248:ASP:OD2	1:MS:248:ASP:C	2.62	0.43
1:MT:104:ASN:HB2	1:MT:108:ASP:HB2	2.00	0.43
1:MT:276:VAL:O	1:MT:279:LEU:HB3	2.19	0.43
1:M1:28:SER:C	1:M1:30:GLU:H	2.26	0.43
1:MB:82:MET:HG3	1:MB:305:ARG:HG2	1.99	0.43
1:MD:8:ASN:O	1:MD:12:MET:HG3	2.18	0.43
1:ME:342:ALA:O	1:ME:346:THR:HG23	2.17	0.43
1:MI:38:ILE:HD13	1:MI:38:ILE:HA	1.78	0.43
1:MI:243:LEU:HD13	1:MI:266:LEU:HD13	1.99	0.43
1:MJ:72:ILE:HD12	1:MJ:72:ILE:HA	1.80	0.43
1:MK:161:ILE:HA	1:MK:304:HIS:HE1	1.83	0.43
1:MM:176:TYR:HB2	1:MM:245:LEU:HB2	1.99	0.43
1:MT:72:ILE:O	1:MT:76:GLN:HG2	2.18	0.43
1:MX:22:THR:HG22	1:MX:26:GLN:HB2	2.00	0.43
1:M1:93:ARG:HB2	1:M1:294:VAL:HG11	1.99	0.43
1:M4:101:ASN:HB3	1:M4:103:SER:H	1.83	0.43
1:MB:349:THR:O	1:MB:353:ILE:HG12	2.18	0.43
1:MC:25:GLN:HB2	1:MC:351:ALA:HB1	2.00	0.43
1:MF:84:GLU:O	1:MF:88:ILE:HG12	2.19	0.43
1:MF:334:SER:C	1:MF:336:ILE:H	2.25	0.43
1:MG:234:LYS:HB2	1:MG:246:PHE:HB3	2.00	0.43
1:MK:145:LYS:HB3	1:MP:102:GLY:HA3	2.00	0.43
1:MS:217:ASP:OD1	1:MS:221:GLU:HB2	2.19	0.43
1:MU:50:ILE:HD12	1:MU:50:ILE:HA	1.91	0.43
1:MV:334:SER:HA	1:MV:338:ASP:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MW:164:MET:HE2	1:MW:164:MET:HB3	1.65	0.43
1:M6:366:LYS:O	1:M6:369:PRO:HD2	2.19	0.43
1:M7:198:THR:HB	1:M7:257:THR:HB	2.00	0.43
1:MA:276:VAL:O	1:MA:279:LEU:HB3	2.19	0.43
1:MC:231:ASP:OD2	1:MC:231:ASP:C	2.61	0.43
1:MD:72:ILE:O	1:MD:76:GLN:HG2	2.18	0.43
1:MM:78:ALA:O	1:MM:82:MET:HG2	2.19	0.43
1:MN:217:ASP:OD1	1:MN:221:GLU:HB2	2.18	0.43
1:MS:136:LYS:HA	1:MS:136:LYS:HD3	1.63	0.43
1:MS:347:ALA:HA	1:MS:350:LYS:HG2	2.01	0.43
1:M1:172:GLY:HA3	1:M1:275:THR:HA	2.01	0.43
1:M3:333:LYS:HE3	1:M3:337:LYS:HD3	2.00	0.43
1:M8:158:MET:HE2	1:MN:184:LYS:HE3	1.99	0.43
1:MA:217:ASP:OD1	1:MA:221:GLU:HB2	2.19	0.43
1:MD:217:ASP:OD1	1:MD:221:GLU:HB2	2.17	0.43
1:MF:182:LYS:HD2	1:MF:186:TRP:CE2	2.54	0.43
1:MO:15:GLN:HG2	1:MT:342:ALA:HB1	1.99	0.43
1:MR:203:ARG:O	1:MR:204:GLU:HG2	2.18	0.43
1:MS:31:ARG:HD2	1:MS:37:LYS:HA	1.99	0.43
1:M2:182:LYS:HD2	1:M2:186:TRP:CE2	2.53	0.43
1:M4:358:SER:O	1:M4:361:VAL:HG12	2.19	0.43
1:M9:344:GLU:HA	1:M9:344:GLU:OE2	2.18	0.43
1:MA:99:SER:HB3	1:MA:112:ILE:HG21	2.00	0.43
1:MA:326:ASN:HA	1:MA:329:VAL:HG22	2.01	0.43
1:MK:93:ARG:HB2	1:MK:294:VAL:HG11	2.00	0.43
1:ML:366:LYS:O	1:ML:369:PRO:HD2	2.18	0.43
1:MP:153:ASN:ND2	1:MR:292:ALA:HB2	2.33	0.43
1:MQ:79:GLU:HA	1:MQ:82:MET:HB2	2.01	0.43
1:MR:79:GLU:HA	1:MR:82:MET:HG2	2.00	0.43
1:MV:171:MET:HE2	1:MV:171:MET:HB2	1.86	0.43
1:M3:83:LYS:HB3	1:M3:83:LYS:HE2	1.78	0.43
1:M3:95:LEU:HD11	1:M3:116:ILE:HG12	2.00	0.43
1:M6:201:ASP:OD2	1:M6:232:MET:HE1	2.17	0.43
1:M8:79:GLU:O	1:M8:82:MET:HB2	2.19	0.43
1:ME:176:TYR:HB2	1:ME:245:LEU:HB2	2.01	0.43
1:MK:69:ASN:HA	1:MK:72:ILE:HG22	2.01	0.43
1:MQ:219:ILE:HD12	1:MQ:219:ILE:HA	1.85	0.43
1:MQ:248:ASP:C	1:MQ:248:ASP:OD2	2.62	0.43
1:M1:203:ARG:O	1:M1:204:GLU:HG2	2.19	0.43
1:M3:366:LYS:NZ	1:M3:366:LYS:HB3	2.33	0.43
1:M5:28:SER:C	1:M5:30:GLU:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M8:97:LEU:HD23	1:M8:97:LEU:HA	1.87	0.43
1:M8:276:VAL:O	1:M8:279:LEU:HB3	2.19	0.43
1:M9:366:LYS:HE2	1:MO:346:THR:HG22	2.00	0.43
1:MA:29:MET:HB3	1:MF:361:VAL:HG13	2.00	0.43
1:MA:138:LEU:HD22	1:MA:164:MET:HE2	2.01	0.43
1:MC:161:ILE:HA	1:MC:304:HIS:CE1	2.54	0.43
1:ME:29:MET:HE3	1:ME:29:MET:HB2	1.78	0.43
1:MG:31:ARG:H	1:MG:31:ARG:HG3	1.48	0.43
1:MG:299:LYS:HE2	1:MG:299:LYS:HB3	1.64	0.43
1:MH:370:ASN:HA	1:MH:373:LEU:HD23	1.99	0.43
1:MJ:31:ARG:HD3	1:MJ:37:LYS:HA	1.99	0.43
1:MM:334:SER:HA	1:MM:338:ASP:HB2	2.01	0.43
1:MO:89:LEU:HB3	1:MO:294:VAL:HG13	2.01	0.43
1:MQ:83:LYS:HB3	1:MQ:83:LYS:HE2	1.80	0.43
1:MV:217:ASP:OD1	1:MV:221:GLU:HB2	2.18	0.43
1:MV:321:ASN:O	1:MV:325:ILE:HD12	2.19	0.43
1:MW:99:SER:HB2	1:MW:112:ILE:HG13	2.01	0.43
1:M1:31:ARG:H	1:M1:31:ARG:HG3	1.69	0.42
1:M1:311:PHE:CD1	1:M1:311:PHE:C	2.96	0.42
1:M2:88:ILE:HD12	1:M2:119:LEU:HD22	2.01	0.42
1:M3:334:SER:HA	1:M3:338:ASP:HB2	1.99	0.42
1:M5:242:LYS:H	1:M5:242:LYS:HG3	1.66	0.42
1:M6:140:GLY:HA3	1:M6:163:ASP:HB2	2.01	0.42
1:MD:88:ILE:O	1:MD:92:MET:HG3	2.19	0.42
1:MD:345:THR:O	1:MD:349:THR:HG23	2.19	0.42
1:ME:136:LYS:O	1:ME:142:PHE:HB2	2.18	0.42
1:MH:124:ASN:HB3	1:MH:165:ARG:HH12	1.84	0.42
1:MI:251:ARG:C	1:MI:252:ILE:HD12	2.44	0.42
1:MJ:48:LEU:HD21	1:ML:305:ARG:CZ	2.49	0.42
1:MM:51:SER:HB2	1:MM:337:LYS:HG3	2.01	0.42
1:MO:144:THR:HG22	1:MO:160:ASN:HB3	2.00	0.42
1:MV:368:ALA:HB3	1:MV:369:PRO:HD3	2.01	0.42
1:MX:364:GLN:OE1	1:MX:364:GLN:HA	2.19	0.42
1:M2:342:ALA:C	1:M3:15:GLN:HE22	2.26	0.42
1:M8:5:VAL:HA	1:M8:369:PRO:HB3	2.01	0.42
1:MA:38:ILE:HD13	1:MA:38:ILE:HA	1.84	0.42
1:MA:73:SER:HA	1:MA:76:GLN:HE21	1.84	0.42
1:MA:159:LEU:HD22	1:MA:311:PHE:CZ	2.55	0.42
1:MC:74:MET:CE	1:MI:103:SER:HA	2.45	0.42
1:MC:243:LEU:HD13	1:MC:266:LEU:HD13	2.00	0.42
1:ME:199:LEU:HD12	1:ME:199:LEU:HA	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MI:219:ILE:HD11	1:MI:243:LEU:HD11	2.02	0.42
1:ML:353:ILE:HD12	1:ML:354:LEU:N	2.34	0.42
1:MN:1:MET:HB3	1:MQ:23:ASN:OD1	2.19	0.42
1:MO:178:ALA:HB3	1:MO:242:LYS:HA	2.00	0.42
1:MR:336:ILE:HD13	1:MR:336:ILE:HA	1.88	0.42
1:MS:311:PHE:CD1	1:MS:311:PHE:C	2.97	0.42
1:MT:136:LYS:HD3	1:MT:136:LYS:HA	1.65	0.42
1:MV:354:LEU:HD13	1:MV:354:LEU:HA	1.88	0.42
1:M3:153:ASN:HB3	1:MT:291:VAL:HG11	2.02	0.42
1:M4:77:THR:HG21	1:M4:132:PHE:CD1	2.53	0.42
1:M6:138:LEU:HD13	1:M6:164:MET:HE2	2.01	0.42
1:M7:20:SER:HA	1:M7:23:ASN:ND2	2.35	0.42
1:MA:251:ARG:HG3	1:MA:252:ILE:CD1	2.48	0.42
1:MB:158:MET:HG2	1:MQ:220:GLU:HG3	2.00	0.42
1:MC:72:ILE:O	1:MC:76:GLN:HG2	2.19	0.42
1:MF:20:SER:HA	1:MF:23:ASN:ND2	2.34	0.42
1:MH:3:VAL:O	1:MH:3:VAL:HG23	2.20	0.42
1:MJ:305:ARG:CZ	1:MU:48:LEU:HD21	2.48	0.42
1:ML:140:GLY:HA3	1:ML:163:ASP:HB2	2.01	0.42
1:ML:236:SER:O	1:ML:243:LEU:HA	2.18	0.42
1:MR:77:THR:HG21	1:MR:132:PHE:CD1	2.53	0.42
1:MS:85:THR:HG23	1:MS:123:LEU:HD12	2.02	0.42
1:MS:219:ILE:HG13	1:MS:237:VAL:HG11	2.01	0.42
1:MT:158:MET:HB2	1:MT:158:MET:HE3	1.79	0.42
1:M4:116:ILE:HD13	1:M4:116:ILE:HA	1.88	0.42
1:M9:324:ASN:C	1:M9:324:ASN:OD1	2.62	0.42
1:MB:313:ASN:HA	1:MB:316:ASN:ND2	2.34	0.42
1:MC:74:MET:HA	1:MC:77:THR:OG1	2.19	0.42
1:MF:159:LEU:HB2	1:MF:311:PHE:CE1	2.54	0.42
1:MJ:97:LEU:HD13	1:MJ:291:VAL:HG21	2.02	0.42
1:MP:248:ASP:OD2	1:MP:248:ASP:C	2.63	0.42
1:MQ:354:LEU:HD23	1:MQ:354:LEU:HA	1.77	0.42
1:MR:78:ALA:O	1:MR:82:MET:HG2	2.19	0.42
1:MT:3:VAL:HG22	1:MT:372:ALA:HB2	2.01	0.42
1:MT:92:MET:HE3	1:MT:119:LEU:HB3	2.02	0.42
1:MT:283:THR:HG23	1:MT:286:GLY:H	1.84	0.42
1:MU:326:ASN:HA	1:MU:329:VAL:HG22	2.01	0.42
1:MW:35:GLY:C	1:MW:339:THR:HG22	2.44	0.42
1:MX:232:MET:HB2	1:MX:232:MET:HE3	1.73	0.42
1:M1:258:PHE:HB2	1:M1:268:ILE:HG23	2.01	0.42
1:M2:276:VAL:O	1:M2:279:LEU:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M4:233:ILE:HD12	1:M4:245:LEU:HD12	2.02	0.42
1:M5:184:LYS:NZ	1:MM:158:MET:HG3	2.34	0.42
1:M6:81:ALA:O	1:M6:85:THR:HG22	2.20	0.42
1:MC:74:MET:HE2	1:MC:132:PHE:CE2	2.54	0.42
1:MD:203:ARG:O	1:MD:204:GLU:HG2	2.20	0.42
1:MF:198:THR:HB	1:MF:257:THR:HB	2.00	0.42
1:MG:311:PHE:HD2	1:MG:311:PHE:O	2.03	0.42
1:MJ:88:ILE:HD11	1:MK:317:HIS:CG	2.54	0.42
1:ML:248:ASP:OD2	1:ML:248:ASP:C	2.62	0.42
1:MM:72:ILE:HD12	1:MM:72:ILE:HA	1.80	0.42
1:MN:338:ASP:OD2	1:MN:338:ASP:C	2.62	0.42
1:MQ:2:ALA:HA	1:MS:340:ASP:HB3	2.02	0.42
1:MT:333:LYS:HB3	1:MT:333:LYS:HE3	1.80	0.42
1:MU:199:LEU:HD23	1:MU:199:LEU:HA	1.81	0.42
1:MX:299:LYS:HB2	1:MX:299:LYS:HE3	1.73	0.42
1:M1:251:ARG:HG3	1:M1:252:ILE:HG13	2.02	0.42
1:M2:248:ASP:OD2	1:M2:248:ASP:C	2.63	0.42
1:M3:46:ALA:O	1:M3:50:ILE:HG22	2.20	0.42
1:M3:219:ILE:HD12	1:M3:219:ILE:HA	1.83	0.42
1:M5:95:LEU:HD12	1:M5:96:SER:N	2.34	0.42
1:M7:31:ARG:H	1:M7:31:ARG:HG2	1.51	0.42
1:M7:170:LEU:H	1:M7:170:LEU:HD12	1.84	0.42
1:MC:162:LYS:HE2	1:MC:300:TYR:HE1	1.83	0.42
1:MF:88:ILE:HG23	1:MF:119:LEU:HD22	2.01	0.42
1:MH:136:LYS:HD3	1:MH:136:LYS:HA	1.67	0.42
1:ML:52:ASN:HA	1:ML:55:ASN:ND2	2.35	0.42
1:MO:342:ALA:O	1:MO:346:THR:HG23	2.19	0.42
1:MT:95:LEU:HD13	1:MT:112:ILE:HG23	2.01	0.42
1:MU:69:ASN:HA	1:MU:72:ILE:HG22	2.01	0.42
1:MU:178:ALA:HB3	1:MU:242:LYS:HA	2.02	0.42
1:MW:70:ASP:HA	1:MW:73:SER:HB3	2.02	0.42
1:MX:70:ASP:C	1:MX:70:ASP:OD1	2.62	0.42
1:MX:92:MET:HE1	1:MX:123:LEU:HD12	2.01	0.42
1:MB:104:ASN:HB2	1:MB:108:ASP:HB2	2.01	0.42
1:MC:219:ILE:HD11	1:MC:243:LEU:HD11	1.99	0.42
1:MI:342:ALA:O	1:MI:346:THR:HG23	2.19	0.42
1:MN:97:LEU:HD23	1:MN:97:LEU:HA	1.85	0.42
1:MN:110:VAL:O	1:MN:114:GLU:HG2	2.20	0.42
1:MN:136:LYS:HA	1:MN:136:LYS:HD3	1.65	0.42
1:MS:299:LYS:HE3	1:MS:299:LYS:HB2	1.85	0.42
1:MV:315:PHE:O	1:MV:319:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M1:22:THR:OG1	1:MV:1:MET:HE3	2.20	0.42
1:M2:219:ILE:HD12	1:M2:219:ILE:HA	1.89	0.42
1:M2:366:LYS:O	1:M2:369:PRO:HD2	2.20	0.42
1:M6:314:ARG:HD2	1:MS:118:ALA:HB1	2.02	0.42
1:M9:48:LEU:HD21	1:MD:305:ARG:CZ	2.50	0.42
1:MA:375:LEU:HG	1:MA:376:LEU:HD12	2.01	0.42
1:MB:182:LYS:HD2	1:MB:186:TRP:CE2	2.54	0.42
1:MC:232:MET:HE2	1:MC:232:MET:HB2	1.98	0.42
1:MF:165:ARG:HB3	1:MF:165:ARG:NH1	2.34	0.42
1:MF:343:LYS:HE2	1:MF:343:LYS:HB3	1.85	0.42
1:MN:182:LYS:HD2	1:MN:186:TRP:CE2	2.55	0.42
1:MU:128:GLU:OE2	1:MU:165:ARG:HD2	2.20	0.42
1:MV:12:MET:HA	1:MV:15:GLN:HE21	1.85	0.42
1:MX:77:THR:HG21	1:MX:132:PHE:CD1	2.50	0.42
1:M1:342:ALA:O	1:M1:346:THR:HG23	2.19	0.42
1:M3:251:ARG:HG3	1:M3:252:ILE:HG12	2.02	0.42
1:M6:286:GLY:O	1:M6:290:SER:HB3	2.20	0.42
1:M7:82:MET:SD	1:M7:164:MET:HE1	2.60	0.42
1:MA:171:MET:O	1:MA:171:MET:HE3	2.20	0.42
1:MB:69:ASN:O	1:MB:72:ILE:HG22	2.20	0.42
1:MB:250:ASN:HD22	1:MB:300:TYR:HB2	1.84	0.42
1:ME:366:LYS:NZ	1:MG:345:THR:HG22	2.35	0.42
1:MF:283:THR:HG23	1:MF:286:GLY:H	1.84	0.42
1:MF:375:LEU:HG	1:MF:376:LEU:HG	2.02	0.42
1:MH:29:MET:HB3	1:MJ:361:VAL:CG1	2.50	0.42
1:MK:201:ASP:HB3	1:MK:205:GLY:HA2	2.02	0.42
1:ML:110:VAL:O	1:ML:114:GLU:HG2	2.19	0.42
1:MN:197:ILE:HD12	1:MN:209:ILE:HD11	2.00	0.42
1:MN:201:ASP:HB3	1:MN:205:GLY:HA2	2.02	0.42
1:MO:37:LYS:HB3	1:MO:339:THR:HB	2.01	0.42
1:MO:184:LYS:HD3	1:MO:184:LYS:HA	1.84	0.42
1:MP:63:VAL:O	1:MP:66:ARG:HG2	2.19	0.42
1:MR:82:MET:SD	1:MR:164:MET:HE1	2.60	0.42
1:MS:178:ALA:HB3	1:MS:242:LYS:HA	2.02	0.42
1:MS:251:ARG:HG3	1:MS:252:ILE:HG12	2.02	0.42
1:MT:86:THR:O	1:MT:90:GLN:HG3	2.20	0.42
1:M1:49:GLN:H	1:M1:49:GLN:HG2	1.69	0.42
1:M8:116:ILE:HD13	1:M8:116:ILE:HA	1.92	0.42
1:MA:182:LYS:HD2	1:MA:186:TRP:NE1	2.35	0.42
1:MA:201:ASP:HB3	1:MA:205:GLY:HA2	2.02	0.42
1:MB:178:ALA:HB3	1:MB:242:LYS:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MC:252:ILE:HG22	1:MC:252:ILE:O	2.19	0.42
1:MD:299:LYS:HE3	1:MD:299:LYS:HB2	1.89	0.42
1:MG:360:SER:O	1:MG:364:GLN:HG2	2.19	0.42
1:MH:338:ASP:OD2	1:MH:338:ASP:C	2.62	0.42
1:MM:68:ALA:HB3	1:MM:319:ILE:HD11	2.01	0.42
1:MP:174:LYS:HD2	1:MP:271:ALA:HB1	2.01	0.42
1:MQ:38:ILE:HD13	1:MQ:38:ILE:HA	1.79	0.42
1:MU:316:ASN:OD1	1:MU:316:ASN:N	2.53	0.42
1:M3:321:ASN:O	1:M3:325:ILE:HD12	2.20	0.41
1:M5:69:ASN:HA	1:M5:72:ILE:HG22	2.02	0.41
1:M6:232:MET:HE2	1:M6:232:MET:HB3	1.83	0.41
1:M8:84:GLU:O	1:M8:88:ILE:HG12	2.20	0.41
1:MB:162:LYS:H	1:MB:304:HIS:CE1	2.38	0.41
1:ME:112:ILE:HD13	1:ME:112:ILE:HA	1.88	0.41
1:MJ:136:LYS:HD3	1:MJ:136:LYS:HA	1.68	0.41
1:MK:92:MET:HG2	1:MK:116:ILE:HD12	2.02	0.41
1:ML:182:LYS:HD2	1:ML:186:TRP:CE2	2.55	0.41
1:MM:5:VAL:HG23	1:MM:369:PRO:HB3	2.01	0.41
1:MP:201:ASP:HB3	1:MP:205:GLY:HA2	2.01	0.41
1:MQ:29:MET:HE2	1:MQ:29:MET:HB3	1.87	0.41
1:MQ:46:ALA:HB2	1:MR:112:ILE:HG13	2.02	0.41
1:MR:25:GLN:HB2	1:MR:351:ALA:HB1	2.01	0.41
1:MT:84:GLU:O	1:MT:88:ILE:HG12	2.19	0.41
1:MT:366:LYS:O	1:MT:369:PRO:HD2	2.19	0.41
1:MU:252:ILE:O	1:MU:252:ILE:HG22	2.20	0.41
1:MW:174:LYS:HB2	1:MW:247:THR:HB	2.01	0.41
1:M2:5:VAL:HG23	1:M2:369:PRO:HB3	2.00	0.41
1:M2:86:THR:HG22	1:M2:90:GLN:OE1	2.20	0.41
1:M5:72:ILE:O	1:M5:76:GLN:HG2	2.20	0.41
1:M5:219:ILE:HD12	1:M5:222:LEU:HD23	2.01	0.41
1:M8:82:MET:HE1	1:M8:164:MET:CE	2.42	0.41
1:ME:22:THR:HG23	1:MH:1:MET:SD	2.60	0.41
1:ME:35:GLY:C	1:ME:339:THR:HG22	2.45	0.41
1:ME:172:GLY:HA3	1:ME:275:THR:HA	2.02	0.41
1:MF:251:ARG:HG3	1:MF:252:ILE:HG12	2.02	0.41
1:MH:334:SER:HA	1:MH:338:ASP:HB3	2.02	0.41
1:MJ:276:VAL:O	1:MJ:279:LEU:HB3	2.20	0.41
1:MP:99:SER:HB3	1:MP:112:ILE:HD13	2.02	0.41
1:MS:155:GLU:O	1:MS:155:GLU:HG2	2.19	0.41
1:MV:19:THR:HA	1:MV:22:THR:HB	2.01	0.41
1:MX:38:ILE:HD12	1:MX:44:ASP:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MX:82:MET:HE1	1:MX:164:MET:SD	2.59	0.41
1:M1:54:LEU:HD12	1:M1:329:VAL:HB	2.03	0.41
1:M1:242:LYS:H	1:M1:242:LYS:HG3	1.66	0.41
1:M1:305:ARG:CZ	1:M5:48:LEU:HD21	2.50	0.41
1:M1:361:VAL:HG11	1:M4:33:SER:HB3	2.01	0.41
1:M3:82:MET:SD	1:M3:164:MET:HE1	2.60	0.41
1:M4:283:THR:HG23	1:M4:286:GLY:H	1.85	0.41
1:M5:159:LEU:HB2	1:M5:311:PHE:CE2	2.55	0.41
1:M7:311:PHE:CD2	1:M7:311:PHE:C	2.98	0.41
1:M9:79:GLU:O	1:M9:82:MET:HB2	2.20	0.41
1:MG:28:SER:OG	1:MG:348:LEU:HD23	2.20	0.41
1:MI:97:LEU:HD23	1:MI:97:LEU:HA	1.88	0.41
1:ML:52:ASN:HA	1:ML:55:ASN:HD21	1.85	0.41
1:ML:77:THR:HG21	1:ML:132:PHE:CD1	2.55	0.41
1:ML:77:THR:HG21	1:ML:132:PHE:HD1	1.85	0.41
1:ML:251:ARG:C	1:ML:252:ILE:HD13	2.45	0.41
1:MN:203:ARG:C	1:MN:204:GLU:HG3	2.45	0.41
1:MO:84:GLU:O	1:MO:88:ILE:HG12	2.20	0.41
1:MQ:142:PHE:CE2	1:MQ:145:LYS:HD2	2.55	0.41
1:MS:29:MET:HG3	1:MS:348:LEU:HD11	2.01	0.41
1:MS:112:ILE:HD13	1:MS:112:ILE:HA	1.83	0.41
1:MU:242:LYS:H	1:MU:242:LYS:HG3	1.69	0.41
1:M2:325:ILE:HD11	1:MT:130:THR:HG22	2.03	0.41
1:M5:299:LYS:HE3	1:M5:299:LYS:HB2	1.86	0.41
1:M6:17:TYR:CD2	1:MS:34:SER:HB3	2.55	0.41
1:M6:124:ASN:HB3	1:M6:165:ARG:HH12	1.85	0.41
1:M8:360:SER:O	1:M8:364:GLN:HG2	2.20	0.41
1:MB:8:ASN:O	1:MB:12:MET:HG3	2.20	0.41
1:MB:325:ILE:HD11	1:MK:130:THR:HG22	2.02	0.41
1:MC:136:LYS:HA	1:MC:136:LYS:HD3	1.64	0.41
1:MC:197:ILE:HD12	1:MC:209:ILE:HD11	2.01	0.41
1:ML:251:ARG:HG3	1:ML:252:ILE:CD1	2.50	0.41
1:MP:50:ILE:HG23	1:MP:336:ILE:HD11	2.03	0.41
1:MP:136:LYS:HD3	1:MP:136:LYS:HA	1.67	0.41
1:MU:155:GLU:H	1:MU:155:GLU:HG2	1.69	0.41
1:MX:321:ASN:O	1:MX:325:ILE:HD12	2.21	0.41
1:M1:248:ASP:OD2	1:M1:248:ASP:C	2.63	0.41
1:M2:25:GLN:HB2	1:M2:351:ALA:HB1	2.02	0.41
1:M3:199:LEU:HD12	1:M3:199:LEU:HA	1.85	0.41
1:M5:352:GLN:HE22	1:MX:364:GLN:NE2	2.18	0.41
1:MA:95:LEU:HD11	1:MA:116:ILE:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MB:69:ASN:HA	1:MB:72:ILE:HG22	2.02	0.41
1:MC:195:LEU:HD12	1:MC:262:LEU:HD23	2.03	0.41
1:MC:251:ARG:HG3	1:MC:252:ILE:CD1	2.48	0.41
1:MC:299:LYS:HE3	1:MC:299:LYS:HB2	1.88	0.41
1:MJ:321:ASN:O	1:MJ:325:ILE:HG12	2.20	0.41
1:ML:18:LEU:HG	1:ML:358:SER:HB2	2.03	0.41
1:ML:31:ARG:H	1:ML:31:ARG:HG3	1.62	0.41
1:MM:321:ASN:O	1:MM:325:ILE:HG13	2.21	0.41
1:MP:234:LYS:HB2	1:MP:246:PHE:HB3	2.02	0.41
1:MT:248:ASP:OD1	1:MT:248:ASP:C	2.63	0.41
1:MU:144:THR:HG22	1:MU:160:ASN:HB2	2.03	0.41
1:MV:182:LYS:HD2	1:MV:186:TRP:CE2	2.55	0.41
1:MV:366:LYS:O	1:MV:369:PRO:HD2	2.21	0.41
1:M3:55:ASN:ND2	1:MT:90:GLN:HE22	2.18	0.41
1:M3:182:LYS:HD2	1:M3:186:TRP:CE2	2.55	0.41
1:M4:82:MET:HE1	1:M4:164:MET:SD	2.60	0.41
1:M5:182:LYS:H	1:M5:241:GLY:HA3	1.85	0.41
1:M6:375:LEU:HD23	1:M6:376:LEU:H	1.85	0.41
1:M7:68:ALA:O	1:M7:72:ILE:HG13	2.21	0.41
1:M7:150:GLY:HA3	1:M7:155:GLU:HG3	2.02	0.41
1:M8:124:ASN:O	1:M8:128:GLU:HG2	2.21	0.41
1:ME:68:ALA:HA	1:ME:315:PHE:HE2	1.85	0.41
1:ME:178:ALA:HB3	1:ME:242:LYS:HA	2.01	0.41
1:MF:343:LYS:HA	1:MV:15:GLN:OE1	2.21	0.41
1:MG:136:LYS:HG3	1:MG:139:ASN:HD22	1.85	0.41
1:MG:364:GLN:HA	1:MG:367:GLN:HE22	1.86	0.41
1:MK:250:ASN:HD22	1:MK:300:TYR:HB2	1.86	0.41
1:MN:19:THR:HA	1:MN:22:THR:OG1	2.21	0.41
1:MP:140:GLY:HA3	1:MP:163:ASP:HB2	2.01	0.41
1:MQ:83:LYS:HG2	1:MQ:305:ARG:NH2	2.35	0.41
1:MT:28:SER:HB3	1:MT:348:LEU:HD23	2.02	0.41
1:MT:299:LYS:HE3	1:MT:299:LYS:HB2	1.86	0.41
1:MV:35:GLY:C	1:MV:339:THR:HG22	2.46	0.41
1:MV:138:LEU:HD13	1:MV:164:MET:HE2	2.02	0.41
1:MW:8:ASN:O	1:MW:12:MET:HG3	2.21	0.41
1:MW:245:LEU:HD13	1:MW:245:LEU:HA	1.92	0.41
1:M2:82:MET:HG3	1:M2:305:ARG:HG2	2.01	0.41
1:M2:189:GLU:HG3	1:M2:192:LYS:HD3	2.03	0.41
1:M2:238:ASP:CG	1:M2:239:GLU:H	2.29	0.41
1:M3:174:LYS:HB2	1:M3:247:THR:HB	2.01	0.41
1:M4:136:LYS:HD3	1:M4:136:LYS:HA	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M5:136:LYS:O	1:M5:142:PHE:HB2	2.21	0.41
1:M6:86:THR:O	1:M6:90:GLN:HG3	2.21	0.41
1:M6:174:LYS:HB2	1:M6:247:THR:HB	2.03	0.41
1:M6:364:GLN:O	1:M6:364:GLN:NE2	2.50	0.41
1:M7:35:GLY:HA3	1:MW:6:ASN:ND2	2.36	0.41
1:M9:116:ILE:HD13	1:M9:116:ILE:HA	1.82	0.41
1:MA:80:GLY:HA3	1:MF:324:ASN:OD1	2.21	0.41
1:MF:219:ILE:HG12	1:MF:241:GLY:HA2	2.02	0.41
1:MH:247:THR:HG23	1:MH:252:ILE:HB	2.02	0.41
1:MI:37:LYS:N	1:MI:339:THR:HB	2.36	0.41
1:ML:344:GLU:OE2	1:ML:344:GLU:HA	2.21	0.41
1:MS:372:ALA:O	1:MS:375:LEU:HD22	2.21	0.41
1:MT:38:ILE:HD13	1:MT:38:ILE:HA	1.86	0.41
1:M1:140:GLY:HA3	1:M1:163:ASP:HB3	2.03	0.41
1:M2:324:ASN:ND2	1:MT:83:LYS:HD2	2.35	0.41
1:M3:153:ASN:HB3	1:MT:291:VAL:CG1	2.50	0.41
1:M6:136:LYS:HA	1:M6:136:LYS:HD3	1.68	0.41
1:M7:199:LEU:HD23	1:M7:199:LEU:HA	1.80	0.41
1:M9:32:LEU:CD1	1:M9:344:GLU:HG3	2.51	0.41
1:MA:336:ILE:HD13	1:MA:336:ILE:HA	1.88	0.41
1:MB:48:LEU:HD21	1:MQ:305:ARG:CZ	2.50	0.41
1:MC:335:ARG:HD2	1:MN:69:ASN:HB3	2.01	0.41
1:MD:31:ARG:HD3	1:MD:344:GLU:CD	2.46	0.41
1:MD:275:THR:H	1:MD:278:THR:CG2	2.34	0.41
1:ME:28:SER:C	1:ME:30:GLU:H	2.29	0.41
1:MF:171:MET:HE2	1:MF:171:MET:HB2	1.88	0.41
1:MF:176:TYR:HB2	1:MF:245:LEU:HB2	2.03	0.41
1:MJ:366:LYS:O	1:MJ:369:PRO:HD2	2.21	0.41
1:MN:88:ILE:HD12	1:MN:119:LEU:HD22	2.03	0.41
1:MQ:366:LYS:O	1:MQ:369:PRO:HD2	2.21	0.41
1:MT:147:PHE:HE2	1:MT:159:LEU:HB3	1.85	0.41
1:MW:132:PHE:HB2	1:MW:137:LEU:HD21	2.01	0.41
1:MX:99:SER:OG	1:MX:281:VAL:HG21	2.19	0.41
1:M1:38:ILE:HD13	1:M1:38:ILE:HA	1.81	0.41
1:M1:95:LEU:HD11	1:M1:116:ILE:CD1	2.50	0.41
1:M1:276:VAL:O	1:M1:279:LEU:HB3	2.21	0.41
1:M1:368:ALA:HB3	1:M1:369:PRO:HD3	2.02	0.41
1:M3:82:MET:HE1	1:M3:164:MET:SD	2.61	0.41
1:M3:116:ILE:HD13	1:M3:116:ILE:HA	1.86	0.41
1:M5:106:LYS:NZ	1:MX:203:ARG:HH22	2.18	0.41
1:M5:195:LEU:HB2	1:M5:262:LEU:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M5:364:GLN:H	1:M5:364:GLN:CD	2.29	0.41
1:M7:177:GLN:OE1	1:M7:177:GLN:HA	2.20	0.41
1:M7:341:PHE:HB2	1:MW:3:VAL:HG21	2.01	0.41
1:M8:74:MET:HE2	1:M8:74:MET:HB2	1.75	0.41
1:M8:200:LYS:HD2	1:M8:201:ASP:H	1.86	0.41
1:M9:104:ASN:HB2	1:M9:108:ASP:HB2	2.03	0.41
1:MB:219:ILE:HD12	1:MB:219:ILE:HA	1.86	0.41
1:MC:252:ILE:HD12	1:MC:252:ILE:N	2.36	0.41
1:MC:314:ARG:HE	1:MN:122:GLU:HG2	1.86	0.41
1:ME:76:GLN:HA	1:ME:79:GLU:HB2	2.03	0.41
1:ME:353:ILE:HD11	1:MW:370:ASN:HD22	1.83	0.41
1:MF:248:ASP:OD2	1:MF:248:ASP:C	2.63	0.41
1:MH:74:MET:HE3	1:MH:74:MET:HB3	1.86	0.41
1:MI:219:ILE:HG13	1:MI:237:VAL:HG11	2.03	0.41
1:ML:82:MET:HE1	1:ML:164:MET:SD	2.61	0.41
1:ML:101:ASN:HB3	1:ML:103:SER:H	1.86	0.41
1:MM:140:GLY:HA3	1:MM:163:ASP:HB2	2.03	0.41
1:MN:15:GLN:HG3	1:MN:362:LEU:HD11	2.02	0.41
1:MN:170:LEU:HD12	1:MN:170:LEU:HA	1.93	0.41
1:MP:319:ILE:HD13	1:MP:319:ILE:HA	1.85	0.41
1:MQ:28:SER:C	1:MQ:30:GLU:H	2.29	0.41
1:MQ:209:ILE:HD12	1:MQ:209:ILE:O	2.21	0.41
1:MR:30:GLU:N	1:MR:30:GLU:OE2	2.54	0.41
1:MR:102:GLY:HA2	1:MR:109:ARG:NH2	2.36	0.41
1:MR:238:ASP:OD2	1:MR:242:LYS:HB2	2.21	0.41
1:MS:124:ASN:HB3	1:MS:165:ARG:HH12	1.86	0.41
1:MU:1:MET:HE3	1:MU:1:MET:HB3	1.95	0.41
1:MV:308:LEU:HD23	1:MV:308:LEU:HA	1.81	0.41
1:MW:242:LYS:H	1:MW:242:LYS:HG3	1.65	0.41
1:MW:316:ASN:HD22	1:MW:316:ASN:HA	1.74	0.41
1:MX:42:LYS:HG3	1:MX:43:ASP:N	2.35	0.41
1:MX:136:LYS:HD3	1:MX:136:LYS:HA	1.65	0.41
1:MX:311:PHE:C	1:MX:311:PHE:CD2	2.99	0.41
1:M4:55:ASN:HB2	1:M4:333:LYS:HZ1	1.86	0.41
1:M4:97:LEU:HD23	1:M4:97:LEU:HA	1.93	0.41
1:M6:251:ARG:CG	1:M6:252:ILE:HD12	2.49	0.41
1:M7:50:ILE:H	1:M7:50:ILE:HG13	1.68	0.41
1:M8:161:ILE:HA	1:M8:304:HIS:CE1	2.55	0.41
1:M9:72:ILE:HD12	1:M9:72:ILE:HA	1.88	0.41
1:M9:324:ASN:HD21	1:MX:80:GLY:HA2	1.86	0.41
1:MB:373:LEU:HD11	1:MN:356:GLN:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MD:1:MET:HE2	1:MV:16:ARG:HG2	2.03	0.41
1:MD:328:ASN:HD22	1:MV:77:THR:HA	1.85	0.41
1:MG:78:ALA:HB2	1:MG:137:LEU:HD13	2.02	0.41
1:MH:92:MET:HE2	1:MH:119:LEU:HB2	2.03	0.41
1:MI:18:LEU:O	1:MI:22:THR:HG22	2.21	0.41
1:MK:362:LEU:O	1:MK:366:LYS:HG2	2.21	0.41
1:ML:178:ALA:HB3	1:ML:242:LYS:HA	2.03	0.41
1:MO:3:VAL:HG22	1:MO:372:ALA:HB2	2.03	0.41
1:MO:22:THR:O	1:MO:26:GLN:HB2	2.21	0.41
1:MO:199:LEU:HD13	1:MO:252:ILE:HG21	2.03	0.41
1:MQ:155:GLU:H	1:MQ:155:GLU:HG2	1.69	0.41
1:MS:5:VAL:HG12	1:MS:369:PRO:HB3	2.03	0.41
1:MW:22:THR:O	1:MW:26:GLN:HB2	2.21	0.41
1:MW:83:LYS:HG2	1:MW:305:ARG:NH2	2.36	0.41
1:MW:136:LYS:HD3	1:MW:136:LYS:HA	1.77	0.41
1:M1:69:ASN:HB3	1:MV:335:ARG:HD2	2.02	0.40
1:M1:367:GLN:OE1	1:M1:367:GLN:N	2.54	0.40
1:M4:79:GLU:HA	1:M4:82:MET:HG2	2.02	0.40
1:M6:368:ALA:HB3	1:M6:369:PRO:HD3	2.03	0.40
1:M7:30:GLU:N	1:M7:30:GLU:OE1	2.55	0.40
1:M8:85:THR:HG23	1:M8:123:LEU:HD11	2.01	0.40
1:MB:248:ASP:OD2	1:MB:248:ASP:C	2.64	0.40
1:ME:69:ASN:HB3	1:MH:335:ARG:HD2	2.03	0.40
1:MG:37:LYS:H	1:MG:37:LYS:HG3	1.63	0.40
1:MH:61:LEU:O	1:MH:65:VAL:HG23	2.21	0.40
1:MH:276:VAL:O	1:MH:279:LEU:HB3	2.21	0.40
1:MK:366:LYS:O	1:MK:369:PRO:HD2	2.21	0.40
1:ML:76:GLN:HA	1:ML:79:GLU:HB2	2.02	0.40
1:MN:313:ASN:O	1:MN:317:HIS:HD2	2.04	0.40
1:MO:25:GLN:HB2	1:MO:351:ALA:HB1	2.03	0.40
1:MP:99:SER:HA	1:MP:104:ASN:HD21	1.86	0.40
1:MP:146:SER:HA	1:MP:158:MET:HA	2.02	0.40
1:MQ:106:LYS:HB2	1:MQ:106:LYS:HE2	1.92	0.40
1:MV:82:MET:HG3	1:MV:305:ARG:HG2	2.03	0.40
1:MW:28:SER:HB3	1:MW:348:LEU:HD23	2.02	0.40
1:MW:251:ARG:C	1:MW:252:ILE:HD12	2.46	0.40
1:M1:150:GLY:HA3	1:M1:155:GLU:HG3	2.03	0.40
1:M1:375:LEU:HD23	1:M1:376:LEU:N	2.35	0.40
1:M2:136:LYS:HA	1:M2:136:LYS:HD3	1.70	0.40
1:M3:159:LEU:HD22	1:M3:311:PHE:CE2	2.57	0.40
1:M3:201:ASP:HB3	1:M3:205:GLY:HA2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M4:299:LYS:HE3	1:M4:299:LYS:HB2	1.86	0.40
1:M6:342:ALA:HB1	1:MQ:15:GLN:OE1	2.22	0.40
1:M9:334:SER:HA	1:M9:338:ASP:HB2	2.03	0.40
1:M9:368:ALA:HB3	1:M9:369:PRO:HD3	2.02	0.40
1:M9:375:LEU:HD11	1:MD:345:THR:HG21	2.02	0.40
1:MF:20:SER:HA	1:MF:23:ASN:HD21	1.87	0.40
1:MF:28:SER:C	1:MF:30:GLU:H	2.29	0.40
1:MH:77:THR:HG21	1:MH:132:PHE:CD1	2.57	0.40
1:MH:283:THR:HG23	1:MH:286:GLY:H	1.86	0.40
1:MJ:358:SER:O	1:MJ:361:VAL:HB	2.21	0.40
1:MN:233:ILE:HD13	1:MN:246:PHE:O	2.21	0.40
1:MN:258:PHE:HB2	1:MN:268:ILE:HG23	2.03	0.40
1:MP:66:ARG:HH21	1:MQ:37:LYS:NZ	2.19	0.40
1:MP:357:ALA:O	1:MP:361:VAL:HG23	2.21	0.40
1:MQ:31:ARG:H	1:MQ:31:ARG:HG2	1.53	0.40
1:MQ:276:VAL:O	1:MQ:279:LEU:HB3	2.20	0.40
1:MS:39:ASN:N	1:MS:39:ASN:OD1	2.53	0.40
1:MV:88:ILE:HG22	1:MV:92:MET:HE3	2.03	0.40
1:MW:202:LYS:HE3	1:MW:253:ASP:HB3	2.04	0.40
1:M2:319:ILE:HD13	1:M2:319:ILE:HA	1.93	0.40
1:M6:28:SER:C	1:M6:30:GLU:H	2.29	0.40
1:M7:30:GLU:HB2	1:ME:17:TYR:HE2	1.86	0.40
1:M9:328:ASN:ND2	1:MX:77:THR:HA	2.36	0.40
1:MA:364:GLN:HA	1:MA:367:GLN:HE22	1.87	0.40
1:MB:5:VAL:HA	1:MB:369:PRO:HB3	2.04	0.40
1:ME:248:ASP:OD2	1:ME:248:ASP:C	2.64	0.40
1:MF:74:MET:HE3	1:MF:147:PHE:HE1	1.87	0.40
1:MG:50:ILE:HD13	1:MG:50:ILE:HA	1.89	0.40
1:MI:82:MET:HE2	1:MI:301:VAL:HG13	2.03	0.40
1:MM:299:LYS:HE3	1:MM:299:LYS:HB2	1.91	0.40
1:MO:199:LEU:HD23	1:MO:199:LEU:HA	1.90	0.40
1:MO:353:ILE:HD12	1:MO:353:ILE:C	2.46	0.40
1:MP:182:LYS:HD2	1:MP:186:TRP:CE2	2.56	0.40
1:MQ:73:SER:O	1:MQ:76:GLN:HG2	2.21	0.40
1:MS:144:THR:HA	1:MS:159:LEU:O	2.22	0.40
1:MS:197:ILE:HD12	1:MS:209:ILE:HD11	2.03	0.40
1:MW:245:LEU:HG	1:MW:258:PHE:CZ	2.55	0.40
1:MX:88:ILE:HG21	1:MX:123:LEU:HG	2.03	0.40
1:MX:238:ASP:HB3	1:MX:244:GLN:OE1	2.20	0.40
1:M1:136:LYS:O	1:M1:142:PHE:HB2	2.22	0.40
1:M4:61:LEU:HD23	1:M4:322:LEU:HD12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M4:88:ILE:HD12	1:M4:119:LEU:HD22	2.02	0.40
1:M5:86:THR:O	1:M5:90:GLN:HG3	2.21	0.40
1:M6:81:ALA:HB2	1:M6:130:THR:HG21	2.04	0.40
1:M6:84:GLU:HG3	1:MI:321:ASN:HB2	2.02	0.40
1:M9:1:MET:SD	1:MX:18:LEU:HA	2.61	0.40
1:MA:182:LYS:HD2	1:MA:186:TRP:CE2	2.56	0.40
1:MB:54:LEU:HD13	1:MB:54:LEU:HA	1.95	0.40
1:MD:182:LYS:HD2	1:MD:186:TRP:CE2	2.56	0.40
1:MD:219:ILE:HD12	1:MD:219:ILE:HA	1.86	0.40
1:ME:77:THR:HG21	1:ME:132:PHE:HD1	1.87	0.40
1:ME:83:LYS:NZ	1:ME:83:LYS:HB3	2.37	0.40
1:MG:311:PHE:CD2	1:MG:311:PHE:C	3.00	0.40
1:MH:178:ALA:HB3	1:MH:242:LYS:HA	2.02	0.40
1:ML:95:LEU:HD23	1:ML:95:LEU:H	1.87	0.40
1:MM:178:ALA:HB3	1:MM:242:LYS:HA	2.02	0.40
1:MQ:1:MET:HB2	1:MQ:2:ALA:H	1.57	0.40
1:MQ:376:LEU:HB2	1:MS:345:THR:HG21	2.03	0.40
1:MT:217:ASP:OD1	1:MT:221:GLU:HB2	2.21	0.40
1:MV:73:SER:O	1:MV:76:GLN:HG2	2.21	0.40
1:M1:149:ILE:HG21	1:M1:315:PHE:CE2	2.57	0.40
1:M2:35:GLY:C	1:M2:339:THR:HG22	2.46	0.40
1:M2:155:GLU:H	1:M2:155:GLU:HG2	1.72	0.40
1:M3:74:MET:HE2	1:M3:132:PHE:CE2	2.56	0.40
1:M3:349:THR:O	1:M3:353:ILE:HG22	2.22	0.40
1:M4:372:ALA:O	1:M4:375:LEU:HD22	2.22	0.40
1:M7:119:LEU:O	1:M7:122:GLU:HB2	2.21	0.40
1:M9:209:ILE:HD13	1:M9:209:ILE:HA	1.88	0.40
1:MB:366:LYS:HB3	1:MB:366:LYS:HE2	1.81	0.40
1:ME:38:ILE:HD13	1:ME:38:ILE:HA	1.81	0.40
1:ME:182:LYS:HD2	1:ME:186:TRP:CE2	2.57	0.40
1:ME:361:VAL:HA	1:ME:364:GLN:HG2	2.03	0.40
1:MI:349:THR:O	1:MI:353:ILE:HD13	2.21	0.40
1:ML:26:GLN:OE1	1:MP:10:SER:HB3	2.22	0.40
1:MO:343:LYS:NZ	1:MO:343:LYS:HB2	2.36	0.40
1:MP:61:LEU:HD12	1:MP:322:LEU:HB3	2.03	0.40
1:MT:198:THR:HB	1:MT:257:THR:HB	2.02	0.40
1:MU:79:GLU:O	1:MU:82:MET:HB2	2.22	0.40
1:MX:203:ARG:C	1:MX:204:GLU:OE1	2.64	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	M1	375/377 (100%)	356 (95%)	19 (5%)	0	100	100
1	M2	375/377 (100%)	362 (96%)	13 (4%)	0	100	100
1	M3	375/377 (100%)	359 (96%)	16 (4%)	0	100	100
1	M4	375/377 (100%)	356 (95%)	19 (5%)	0	100	100
1	M5	375/377 (100%)	358 (96%)	17 (4%)	0	100	100
1	M6	375/377 (100%)	361 (96%)	14 (4%)	0	100	100
1	M7	375/377 (100%)	361 (96%)	14 (4%)	0	100	100
1	M8	375/377 (100%)	359 (96%)	16 (4%)	0	100	100
1	M9	375/377 (100%)	362 (96%)	13 (4%)	0	100	100
1	MA	375/377 (100%)	362 (96%)	13 (4%)	0	100	100
1	MB	375/377 (100%)	362 (96%)	13 (4%)	0	100	100
1	MC	375/377 (100%)	365 (97%)	10 (3%)	0	100	100
1	MD	375/377 (100%)	361 (96%)	14 (4%)	0	100	100
1	ME	375/377 (100%)	357 (95%)	18 (5%)	0	100	100
1	MF	375/377 (100%)	359 (96%)	16 (4%)	0	100	100
1	MG	375/377 (100%)	359 (96%)	16 (4%)	0	100	100
1	MH	375/377 (100%)	362 (96%)	13 (4%)	0	100	100
1	MI	375/377 (100%)	358 (96%)	17 (4%)	0	100	100
1	MJ	375/377 (100%)	358 (96%)	17 (4%)	0	100	100
1	MK	375/377 (100%)	360 (96%)	15 (4%)	0	100	100
1	ML	375/377 (100%)	359 (96%)	16 (4%)	0	100	100
1	MM	375/377 (100%)	361 (96%)	14 (4%)	0	100	100
1	MN	375/377 (100%)	362 (96%)	13 (4%)	0	100	100
1	MO	375/377 (100%)	361 (96%)	14 (4%)	0	100	100
1	MP	375/377 (100%)	356 (95%)	19 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	MQ	375/377 (100%)	359 (96%)	16 (4%)	0	100	100
1	MR	375/377 (100%)	364 (97%)	11 (3%)	0	100	100
1	MS	375/377 (100%)	359 (96%)	16 (4%)	0	100	100
1	MT	375/377 (100%)	361 (96%)	14 (4%)	0	100	100
1	MU	375/377 (100%)	360 (96%)	15 (4%)	0	100	100
1	MV	375/377 (100%)	355 (95%)	20 (5%)	0	100	100
1	MW	375/377 (100%)	361 (96%)	14 (4%)	0	100	100
1	MX	375/377 (100%)	359 (96%)	16 (4%)	0	100	100
All	All	12375/12441 (100%)	11874 (96%)	501 (4%)	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	M1	295/295 (100%)	282 (96%)	13 (4%)	24	52
1	M2	295/295 (100%)	286 (97%)	9 (3%)	35	62
1	M3	295/295 (100%)	285 (97%)	10 (3%)	32	60
1	M4	295/295 (100%)	282 (96%)	13 (4%)	24	52
1	M5	295/295 (100%)	288 (98%)	7 (2%)	44	68
1	M6	295/295 (100%)	285 (97%)	10 (3%)	32	60
1	M7	295/295 (100%)	286 (97%)	9 (3%)	35	62
1	M8	295/295 (100%)	283 (96%)	12 (4%)	26	54
1	M9	295/295 (100%)	285 (97%)	10 (3%)	32	60
1	MA	295/295 (100%)	285 (97%)	10 (3%)	32	60
1	MB	295/295 (100%)	283 (96%)	12 (4%)	26	54
1	MC	295/295 (100%)	278 (94%)	17 (6%)	17	44
1	MD	295/295 (100%)	285 (97%)	10 (3%)	32	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	ME	295/295 (100%)	285 (97%)	10 (3%)	32	60
1	MF	295/295 (100%)	292 (99%)	3 (1%)	73	85
1	MG	295/295 (100%)	285 (97%)	10 (3%)	32	60
1	MH	295/295 (100%)	284 (96%)	11 (4%)	29	57
1	MI	295/295 (100%)	281 (95%)	14 (5%)	22	51
1	MJ	295/295 (100%)	281 (95%)	14 (5%)	22	51
1	MK	295/295 (100%)	284 (96%)	11 (4%)	29	57
1	ML	295/295 (100%)	286 (97%)	9 (3%)	35	62
1	MM	295/295 (100%)	286 (97%)	9 (3%)	35	62
1	MN	295/295 (100%)	286 (97%)	9 (3%)	35	62
1	MO	295/295 (100%)	290 (98%)	5 (2%)	56	75
1	MP	295/295 (100%)	283 (96%)	12 (4%)	26	54
1	MQ	295/295 (100%)	284 (96%)	11 (4%)	29	57
1	MR	295/295 (100%)	291 (99%)	4 (1%)	62	80
1	MS	295/295 (100%)	292 (99%)	3 (1%)	73	85
1	MT	295/295 (100%)	287 (97%)	8 (3%)	40	65
1	MU	295/295 (100%)	282 (96%)	13 (4%)	24	52
1	MV	295/295 (100%)	281 (95%)	14 (5%)	22	51
1	MW	295/295 (100%)	279 (95%)	16 (5%)	18	46
1	MX	295/295 (100%)	282 (96%)	13 (4%)	24	52
All	All	9735/9735 (100%)	9394 (96%)	341 (4%)	33	59

All (341) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M1	1	MET
1	M1	9	VAL
1	M1	22	THR
1	M1	33	SER
1	M1	39	ASN
1	M1	63	VAL
1	M1	112	ILE
1	M1	193	THR
1	M1	232	MET
1	M1	233	ILE

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Mol	Chain	Res	Type
1	M1	245	LEU
1	M1	350	LYS
1	M1	354	LEU
1	M2	22	THR
1	M2	38	ILE
1	M2	83	LYS
1	M2	112	ILE
1	M2	158	MET
1	M2	174	LYS
1	M2	193	THR
1	M2	281	VAL
1	M2	362	LEU
1	M3	1	MET
1	M3	10	SER
1	M3	13	THR
1	M3	30	GLU
1	M3	38	ILE
1	M3	199	LEU
1	M3	237	VAL
1	M3	281	VAL
1	M3	291	VAL
1	M3	333	LYS
1	M4	94	ASP
1	M4	112	ILE
1	M4	117	THR
1	M4	128	GLU
1	M4	141	THR
1	M4	171	MET
1	M4	233	ILE
1	M4	242	LYS
1	M4	252	ILE
1	M4	281	VAL
1	M4	284	VAL
1	M4	291	VAL
1	M4	322	LEU
1	M5	26	GLN
1	M5	30	GLU
1	M5	171	MET
1	M5	193	THR
1	M5	236	SER
1	M5	284	VAL
1	M5	301	VAL

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Mol	Chain	Res	Type
1	M6	22	THR
1	M6	30	GLU
1	M6	33	SER
1	M6	76	GLN
1	M6	97	LEU
1	M6	128	GLU
1	M6	158	MET
1	M6	233	ILE
1	M6	281	VAL
1	M6	364	GLN
1	M7	74	MET
1	M7	94	ASP
1	M7	97	LEU
1	M7	116	ILE
1	M7	157	VAL
1	M7	236	SER
1	M7	281	VAL
1	M7	284	VAL
1	M7	291	VAL
1	M8	38	ILE
1	M8	112	ILE
1	M8	122	GLU
1	M8	155	GLU
1	M8	177	GLN
1	M8	193	THR
1	M8	220	GLU
1	M8	236	SER
1	M8	268	ILE
1	M8	281	VAL
1	M8	308	LEU
1	M8	376	LEU
1	M9	1	MET
1	M9	5	VAL
1	M9	89	LEU
1	M9	114	GLU
1	M9	128	GLU
1	M9	189	GLU
1	M9	253	ASP
1	M9	281	VAL
1	M9	362	LEU
1	M9	364	GLN
1	MA	12	MET

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Mol	Chain	Res	Type
1	MA	33	SER
1	MA	39	ASN
1	MA	79	GLU
1	MA	94	ASP
1	MA	116	ILE
1	MA	247	THR
1	MA	281	VAL
1	MA	284	VAL
1	MA	291	VAL
1	MB	9	VAL
1	MB	10	SER
1	MB	112	ILE
1	MB	137	LEU
1	MB	155	GLU
1	MB	158	MET
1	MB	193	THR
1	MB	204	GLU
1	MB	281	VAL
1	MB	284	VAL
1	MB	319	ILE
1	MB	364	GLN
1	MC	1	MET
1	MC	10	SER
1	MC	30	GLU
1	MC	33	SER
1	MC	39	ASN
1	MC	79	GLU
1	MC	106	LYS
1	MC	116	ILE
1	MC	155	GLU
1	MC	196	THR
1	MC	236	SER
1	MC	237	VAL
1	MC	281	VAL
1	MC	308	LEU
1	MC	329	VAL
1	MC	348	LEU
1	MC	353	ILE
1	MD	15	GLN
1	MD	22	THR
1	MD	29	MET
1	MD	33	SER

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Mol	Chain	Res	Type
1	MD	101	ASN
1	MD	145	LYS
1	MD	180	ASN
1	MD	182	LYS
1	MD	247	THR
1	MD	281	VAL
1	ME	22	THR
1	ME	31	ARG
1	ME	33	SER
1	ME	63	VAL
1	ME	101	ASN
1	ME	115	GLU
1	ME	281	VAL
1	ME	308	LEU
1	ME	375	LEU
1	ME	376	LEU
1	MF	1	MET
1	MF	245	LEU
1	MF	350	LYS
1	MG	1	MET
1	MG	17	TYR
1	MG	31	ARG
1	MG	33	SER
1	MG	63	VAL
1	MG	94	ASP
1	MG	257	THR
1	MG	281	VAL
1	MG	290	SER
1	MG	353	ILE
1	MH	123	LEU
1	MH	128	GLU
1	MH	141	THR
1	MH	180	ASN
1	MH	206	ASP
1	MH	236	SER
1	MH	239	GLU
1	MH	281	VAL
1	MH	320	ASN
1	MH	350	LYS
1	MH	373	LEU
1	MI	1	MET
1	MI	19	THR

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Mol	Chain	Res	Type
1	MI	30	GLU
1	MI	101	ASN
1	MI	193	THR
1	MI	209	ILE
1	MI	233	ILE
1	MI	237	VAL
1	MI	281	VAL
1	MI	301	VAL
1	MI	319	ILE
1	MI	324	ASN
1	MI	366	LYS
1	MI	373	LEU
1	MJ	3	VAL
1	MJ	26	GLN
1	MJ	33	SER
1	MJ	49	GLN
1	MJ	94	ASP
1	MJ	97	LEU
1	MJ	182	LYS
1	MJ	193	THR
1	MJ	281	VAL
1	MJ	284	VAL
1	MJ	303	SER
1	MJ	308	LEU
1	MJ	330	ASN
1	MJ	354	LEU
1	MK	1	MET
1	MK	30	GLU
1	MK	38	ILE
1	MK	72	ILE
1	MK	141	THR
1	MK	155	GLU
1	MK	193	THR
1	MK	281	VAL
1	MK	308	LEU
1	MK	337	LYS
1	MK	362	LEU
1	ML	18	LEU
1	ML	37	LYS
1	ML	79	GLU
1	ML	116	ILE
1	ML	128	GLU

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Mol	Chain	Res	Type
1	ML	193	THR
1	ML	281	VAL
1	ML	284	VAL
1	ML	289	GLU
1	MM	1	MET
1	MM	19	THR
1	MM	26	GLN
1	MM	155	GLU
1	MM	206	ASP
1	MM	247	THR
1	MM	281	VAL
1	MM	284	VAL
1	MM	320	ASN
1	MN	63	VAL
1	MN	112	ILE
1	MN	152	ASP
1	MN	233	ILE
1	MN	242	LYS
1	MN	279	LEU
1	MN	281	VAL
1	MN	284	VAL
1	MN	291	VAL
1	MO	38	ILE
1	MO	206	ASP
1	MO	232	MET
1	MO	236	SER
1	MO	376	LEU
1	MP	9	VAL
1	MP	22	THR
1	MP	49	GLN
1	MP	155	GLU
1	MP	166	SER
1	MP	171	MET
1	MP	193	THR
1	MP	199	LEU
1	MP	247	THR
1	MP	284	VAL
1	MP	291	VAL
1	MP	298	LEU
1	MQ	1	MET
1	MQ	19	THR
1	MQ	112	ILE

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Mol	Chain	Res	Type
1	MQ	116	ILE
1	MQ	158	MET
1	MQ	164	MET
1	MQ	204	GLU
1	MQ	237	VAL
1	MQ	291	VAL
1	MQ	308	LEU
1	MQ	348	LEU
1	MR	1	MET
1	MR	245	LEU
1	MR	281	VAL
1	MR	344	GLU
1	MS	74	MET
1	MS	94	ASP
1	MS	281	VAL
1	MT	1	MET
1	MT	112	ILE
1	MT	233	ILE
1	MT	281	VAL
1	MT	291	VAL
1	MT	308	LEU
1	MT	319	ILE
1	MT	354	LEU
1	MU	9	VAL
1	MU	30	GLU
1	MU	38	ILE
1	MU	79	GLU
1	MU	114	GLU
1	MU	155	GLU
1	MU	193	THR
1	MU	237	VAL
1	MU	281	VAL
1	MU	284	VAL
1	MU	291	VAL
1	MU	308	LEU
1	MU	362	LEU
1	MV	6	ASN
1	MV	79	GLU
1	MV	94	ASP
1	MV	108	ASP
1	MV	116	ILE
1	MV	141	THR

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Mol	Chain	Res	Type
1	MV	155	GLU
1	MV	158	MET
1	MV	193	THR
1	MV	194	ASP
1	MV	209	ILE
1	MV	284	VAL
1	MV	303	SER
1	MV	354	LEU
1	MW	3	VAL
1	MW	7	THR
1	MW	9	VAL
1	MW	30	GLU
1	MW	38	ILE
1	MW	104	ASN
1	MW	137	LEU
1	MW	141	THR
1	MW	158	MET
1	MW	159	LEU
1	MW	171	MET
1	MW	207	VAL
1	MW	236	SER
1	MW	281	VAL
1	MW	322	LEU
1	MW	367	GLN
1	MX	13	THR
1	MX	29	MET
1	MX	30	GLU
1	MX	38	ILE
1	MX	72	ILE
1	MX	112	ILE
1	MX	193	THR
1	MX	232	MET
1	MX	279	LEU
1	MX	281	VAL
1	MX	284	VAL
1	MX	301	VAL
1	MX	376	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (144) such sidechains are listed below:

Mol	Chain	Res	Type
1	M1	4	ASN

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Mol	Chain	Res	Type
1	M1	67	ASN
1	M1	120	ASN
1	M1	326	ASN
1	M1	328	ASN
1	M1	356	GLN
1	M2	120	ASN
1	M2	185	ASN
1	M2	244	GLN
1	M2	352	GLN
1	M3	23	ASN
1	M3	52	ASN
1	M3	120	ASN
1	M3	148	GLN
1	M3	160	ASN
1	M3	330	ASN
1	M4	120	ASN
1	M4	313	ASN
1	M4	321	ASN
1	M5	120	ASN
1	M5	304	HIS
1	M5	324	ASN
1	M5	352	GLN
1	M5	364	GLN
1	M6	49	GLN
1	M6	52	ASN
1	M6	67	ASN
1	M6	120	ASN
1	M7	49	GLN
1	M7	67	ASN
1	M7	321	ASN
1	M7	326	ASN
1	M8	25	GLN
1	M8	55	ASN
1	M8	120	ASN
1	M8	313	ASN
1	M9	52	ASN
1	M9	160	ASN
1	M9	212	ASN
1	MA	15	GLN
1	MA	67	ASN
1	MA	120	ASN
1	MA	313	ASN

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Mol	Chain	Res	Type
1	MB	15	GLN
1	MB	23	ASN
1	MB	113	GLN
1	MB	120	ASN
1	MB	304	HIS
1	MB	330	ASN
1	MB	364	GLN
1	MC	120	ASN
1	MC	244	GLN
1	MC	304	HIS
1	MC	326	ASN
1	MC	352	GLN
1	MD	313	ASN
1	ME	49	GLN
1	ME	90	GLN
1	ME	120	ASN
1	ME	321	ASN
1	MF	67	ASN
1	MF	160	ASN
1	MF	364	GLN
1	MG	49	GLN
1	MG	67	ASN
1	MG	120	ASN
1	MG	312	GLN
1	MG	321	ASN
1	MH	49	GLN
1	MH	120	ASN
1	MI	26	GLN
1	MI	104	ASN
1	MI	160	ASN
1	MI	244	GLN
1	MI	313	ASN
1	MJ	49	GLN
1	MJ	180	ASN
1	MJ	324	ASN
1	MJ	330	ASN
1	MK	49	GLN
1	MK	160	ASN
1	MK	185	ASN
1	MK	304	HIS
1	MK	313	ASN
1	MK	352	GLN

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Mol	Chain	Res	Type
1	ML	49	GLN
1	ML	52	ASN
1	ML	55	ASN
1	ML	67	ASN
1	ML	76	GLN
1	ML	120	ASN
1	ML	185	ASN
1	MM	23	ASN
1	MM	25	GLN
1	MM	90	GLN
1	MM	120	ASN
1	MM	330	ASN
1	MM	364	GLN
1	MN	90	GLN
1	MO	15	GLN
1	MO	55	ASN
1	MO	304	HIS
1	MO	324	ASN
1	MP	15	GLN
1	MP	120	ASN
1	MP	160	ASN
1	MP	313	ASN
1	MQ	90	GLN
1	MQ	104	ASN
1	MQ	120	ASN
1	MQ	180	ASN
1	MQ	313	ASN
1	MQ	326	ASN
1	MQ	328	ASN
1	MR	55	ASN
1	MR	90	GLN
1	MR	120	ASN
1	MR	160	ASN
1	MR	321	ASN
1	MR	326	ASN
1	MS	26	GLN
1	MS	67	ASN
1	MS	120	ASN
1	MS	124	ASN
1	MS	244	GLN
1	MS	312	GLN
1	MS	326	ASN

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Mol	Chain	Res	Type
1	MT	55	ASN
1	MT	90	GLN
1	MT	288	GLN
1	MU	15	GLN
1	MU	244	GLN
1	MU	326	ASN
1	MU	364	GLN
1	MV	49	GLN
1	MV	120	ASN
1	MW	67	ASN
1	MW	120	ASN
1	MW	244	GLN
1	MW	324	ASN
1	MX	6	ASN
1	MX	26	GLN
1	MX	101	ASN
1	MX	120	ASN

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 ⓘ

There are no chain breaks in this entry.

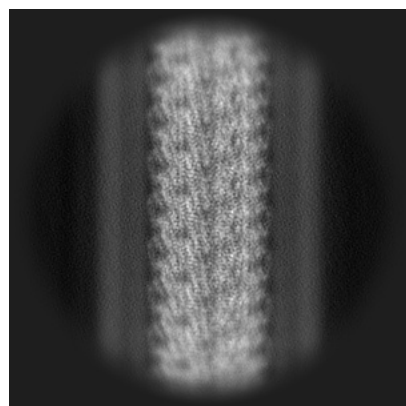
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49131. These allow visual inspection of the internal detail of the map and identification of artifacts.

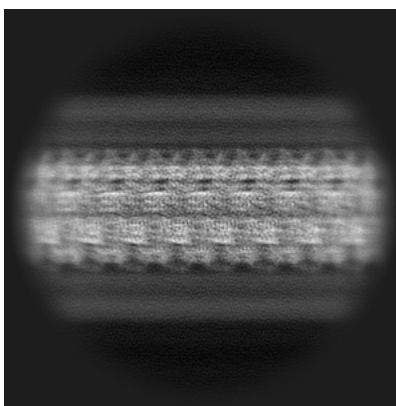
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

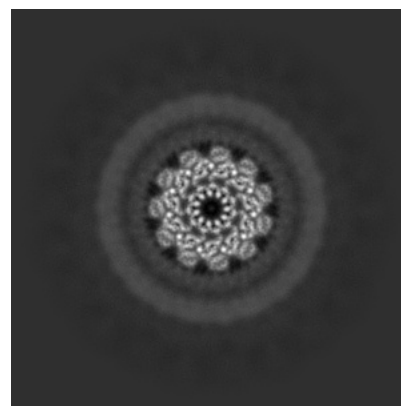
6.1.1 Primary map



X

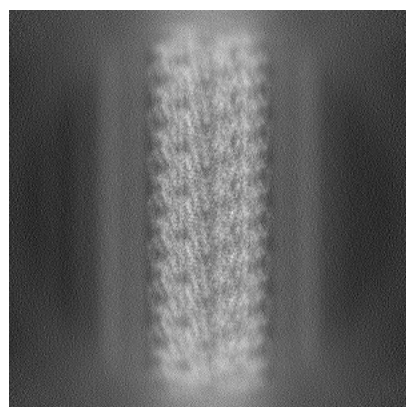


Y

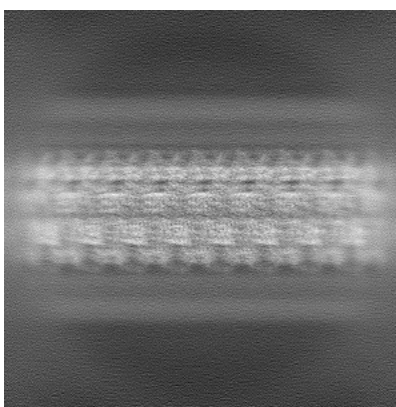


Z

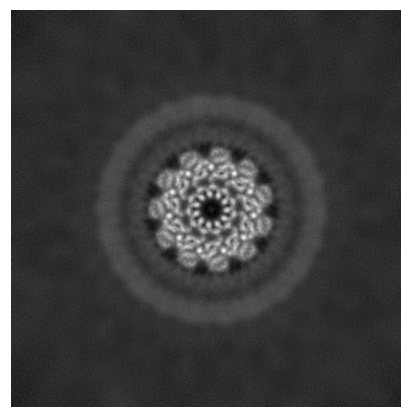
6.1.2 Raw map



X



Y

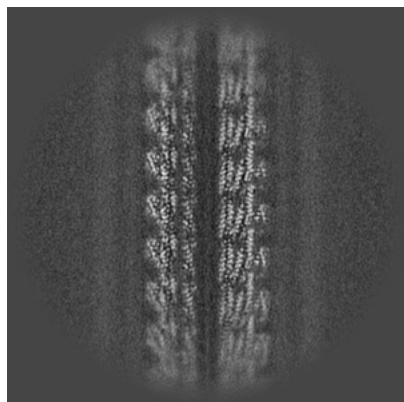


Z

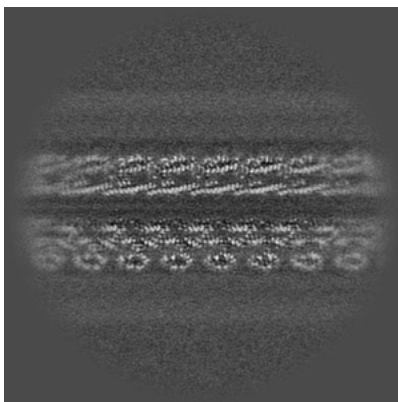
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

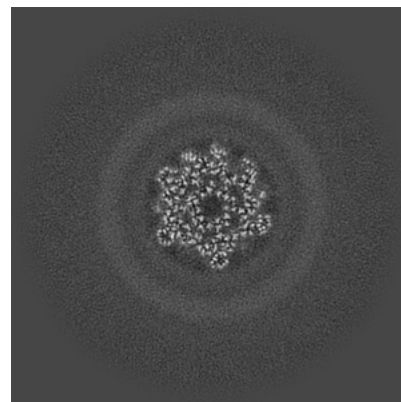
6.2.1 Primary map



X Index: 224

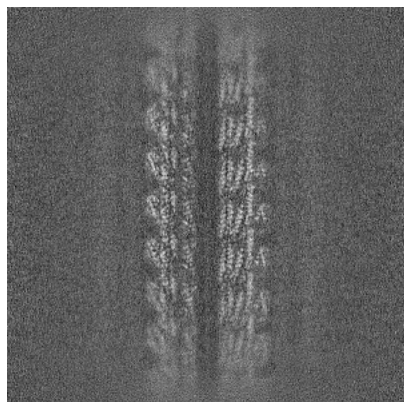


Y Index: 224

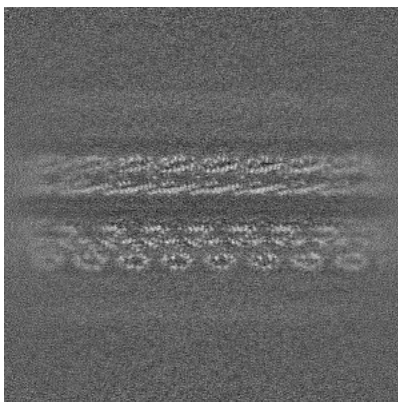


Z Index: 224

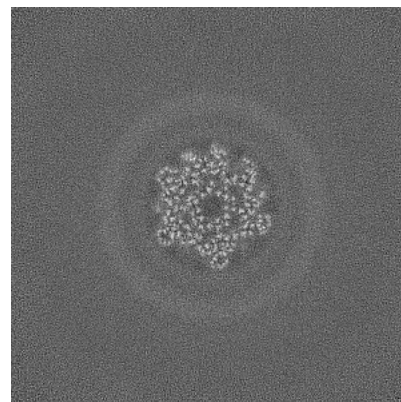
6.2.2 Raw map



X Index: 224



Y Index: 224

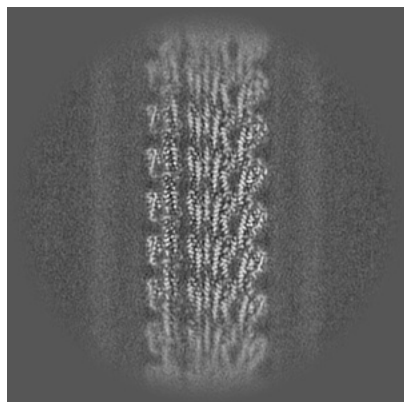


Z Index: 224

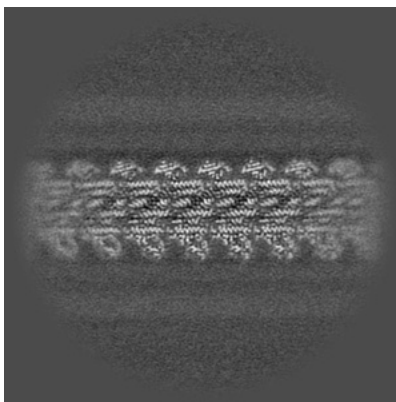
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

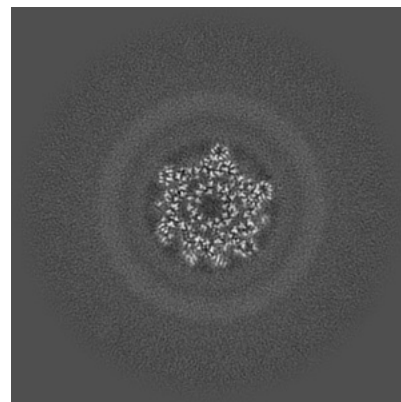
6.3.1 Primary map



X Index: 240

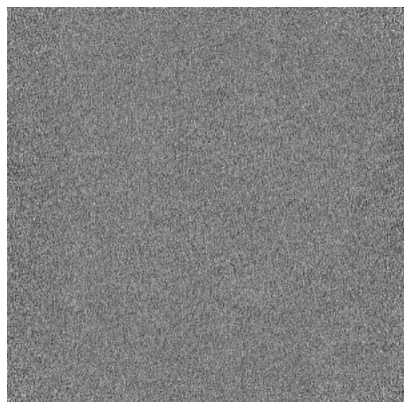


Y Index: 264

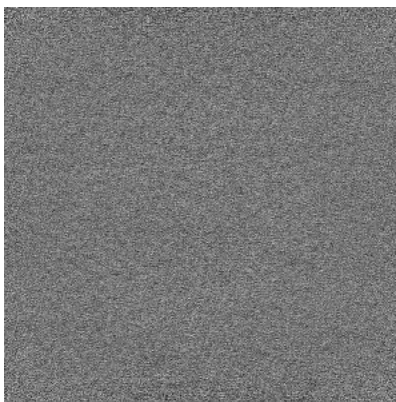


Z Index: 212

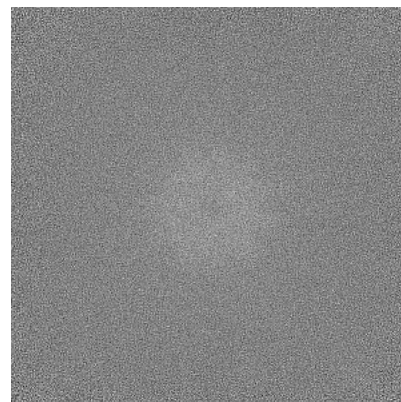
6.3.2 Raw map



X Index: 0



Y Index: 0

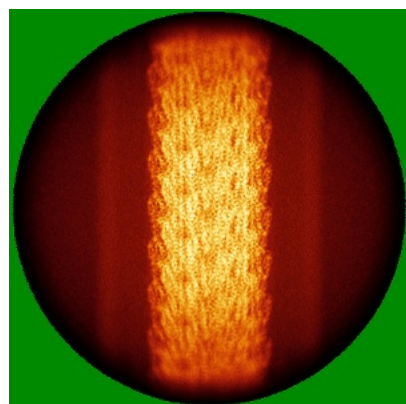


Z Index: 0

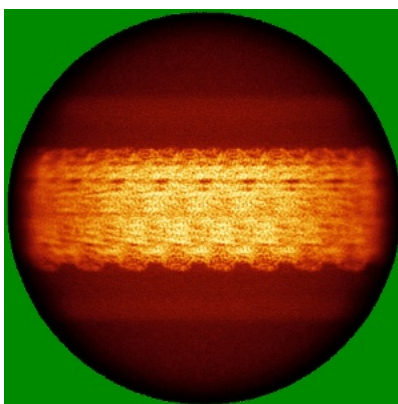
The images above show the largest variance slices of the map in three orthogonal directions.

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

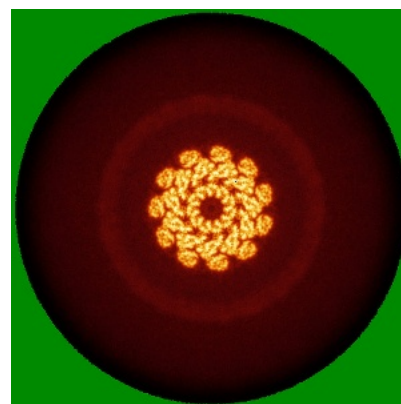
6.4.1 Primary map



X

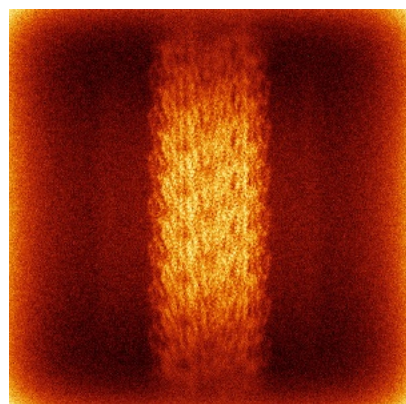


Y

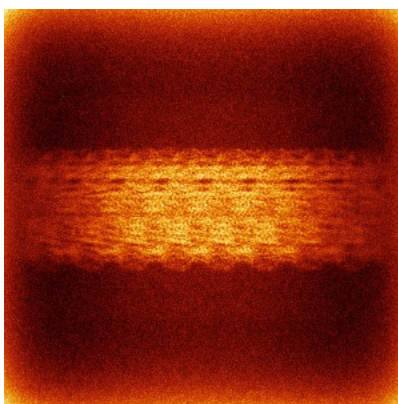


Z

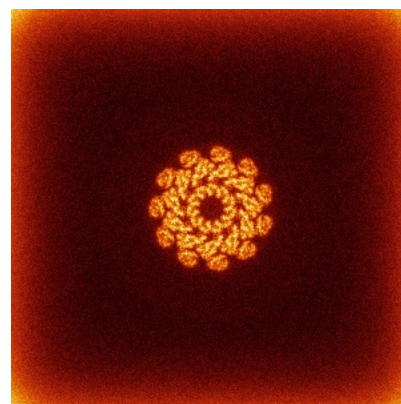
6.4.2 Raw map



X



Y

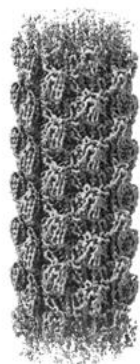


Z

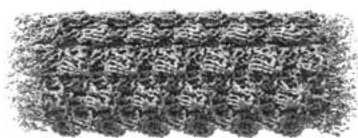
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

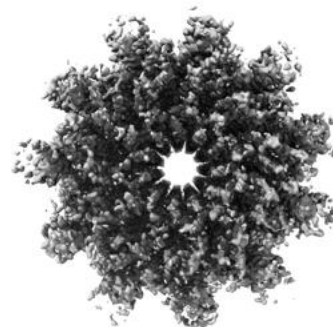
6.5.1 Primary map



X



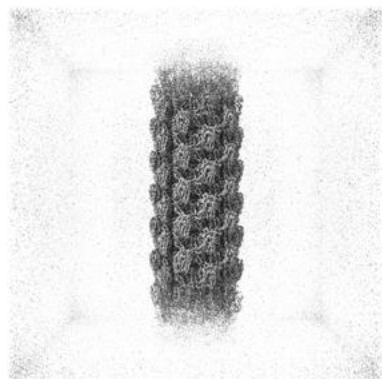
Y



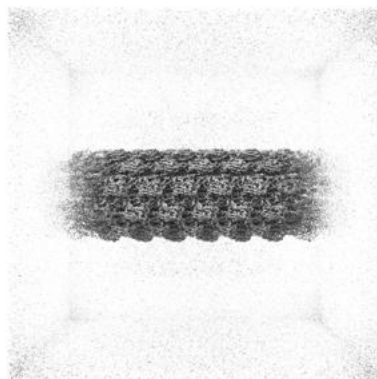
Z

The images above show the 3D surface view of the map at the recommended contour level 0.14. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

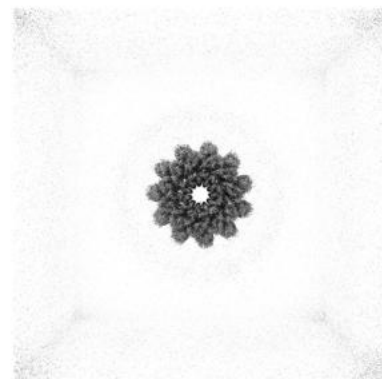
6.5.2 Raw map



X



Y



Z

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.

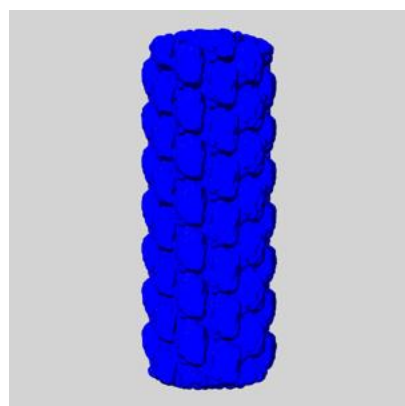
6.6 Mask visualisation [i](#)

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

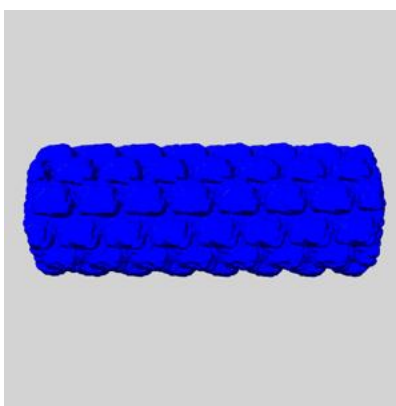
A mask typically either:

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

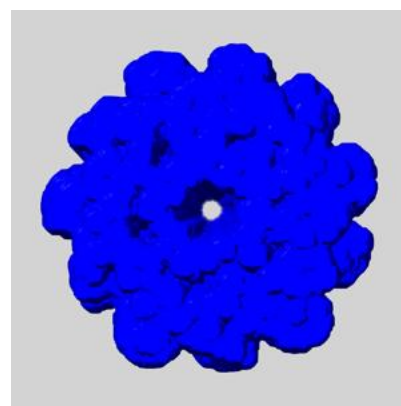
6.6.1 emd_49131_msk_1.map [i](#)



X



Y

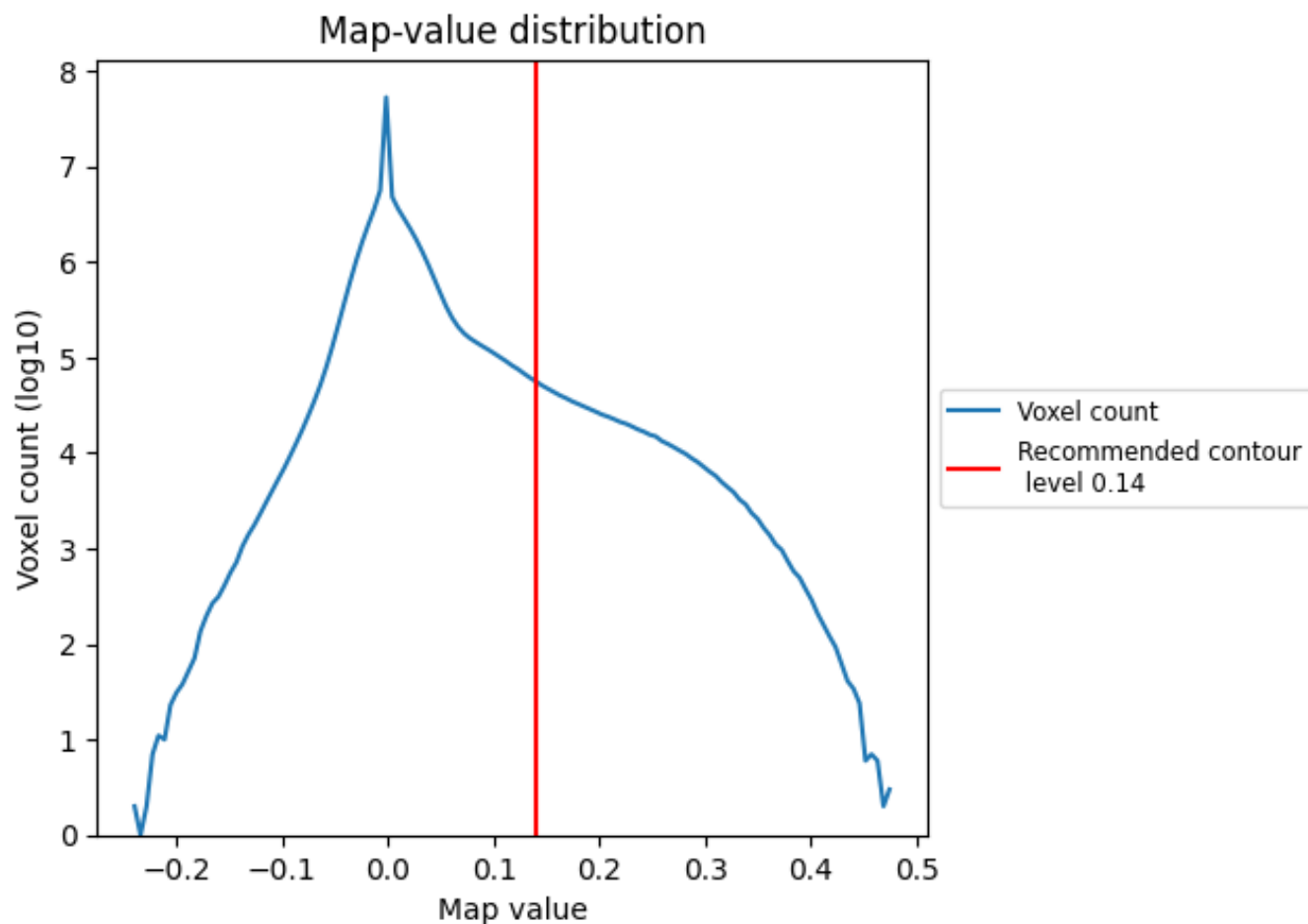


Z

7 Map analysis [i](#)

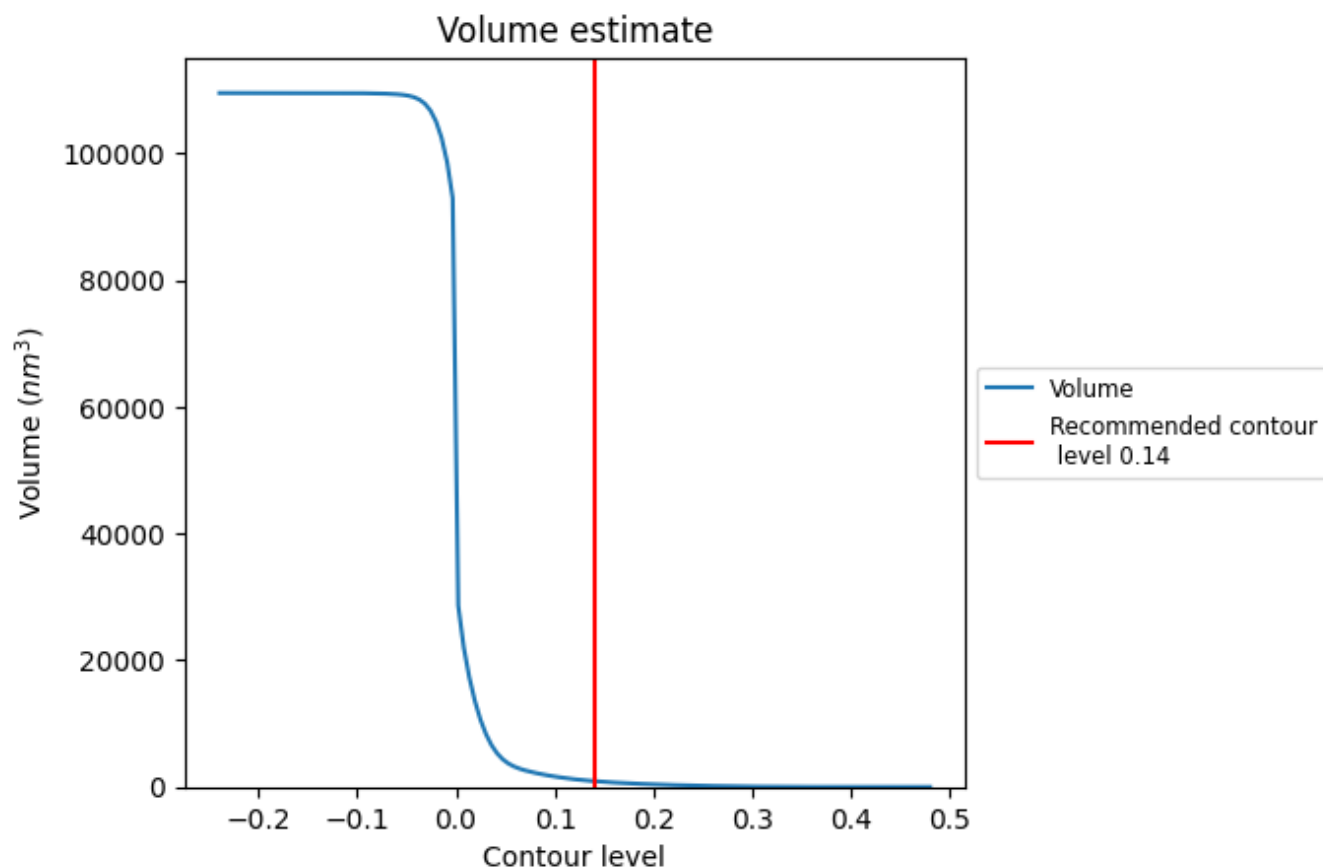
This section contains the results of statistical analysis of the map.

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.

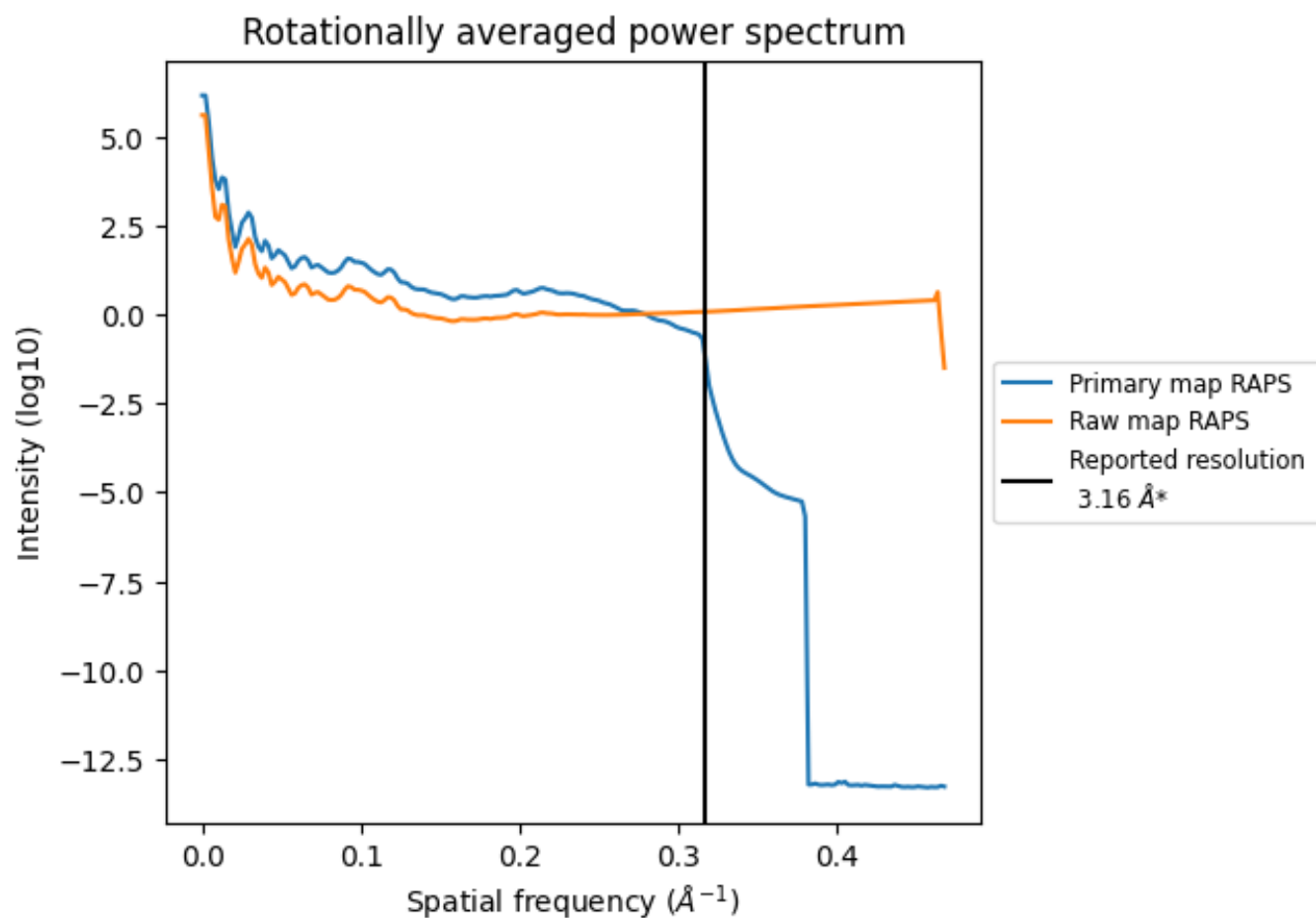
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 916 nm³; this corresponds to an approximate mass of 827 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 ⓘ

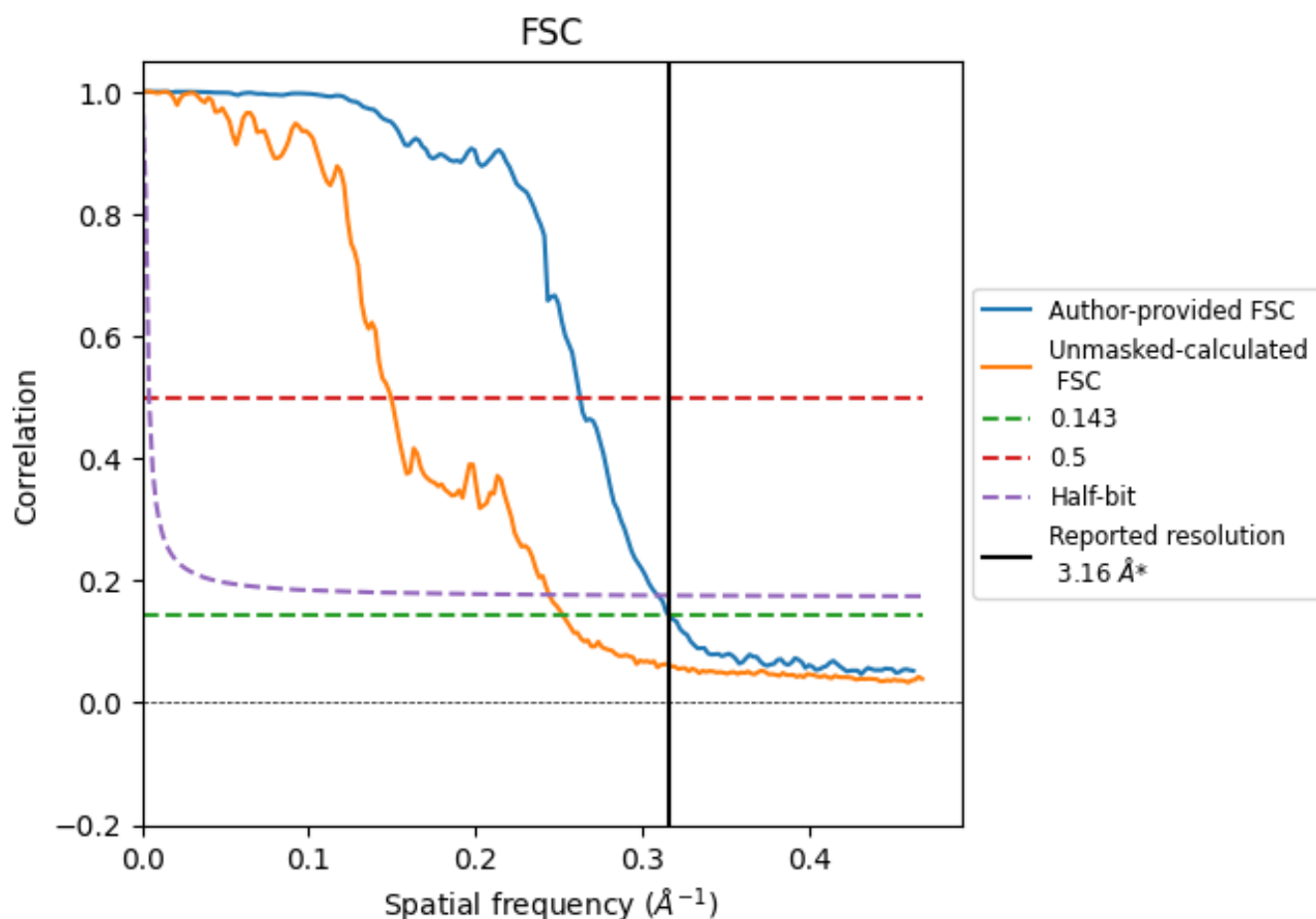


*Reported resolution corresponds to spatial frequency of 0.316 Å⁻¹

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 0.316 \AA^{-1}

8.2 Resolution estimates [i](#)

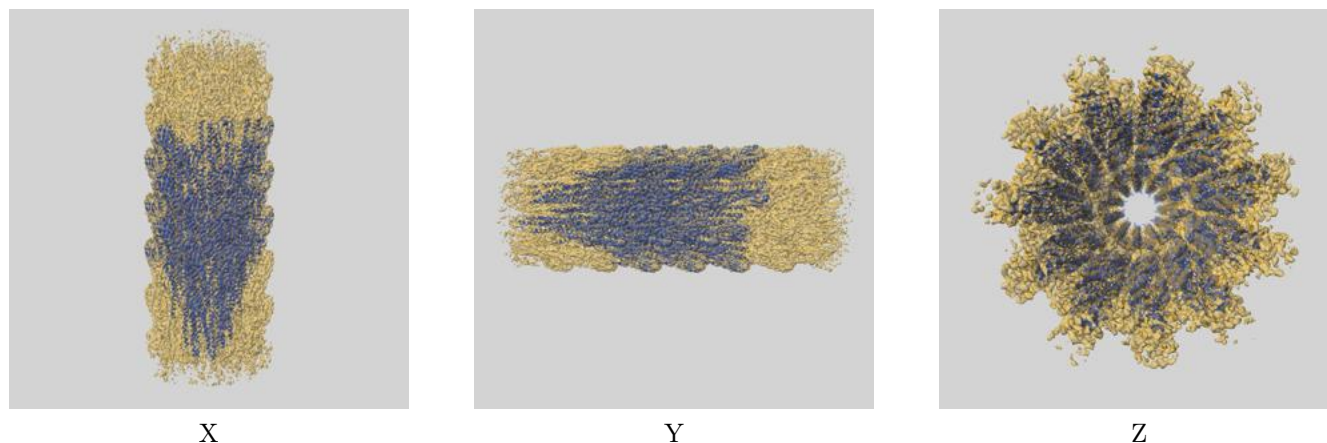
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.16	-	-
Author-provided FSC curve	3.16	3.81	3.23
Unmasked-calculated*	3.96	6.70	4.09

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.96 differs from the reported value 3.16 by more than 10 %

9 Map-model fit [i](#)

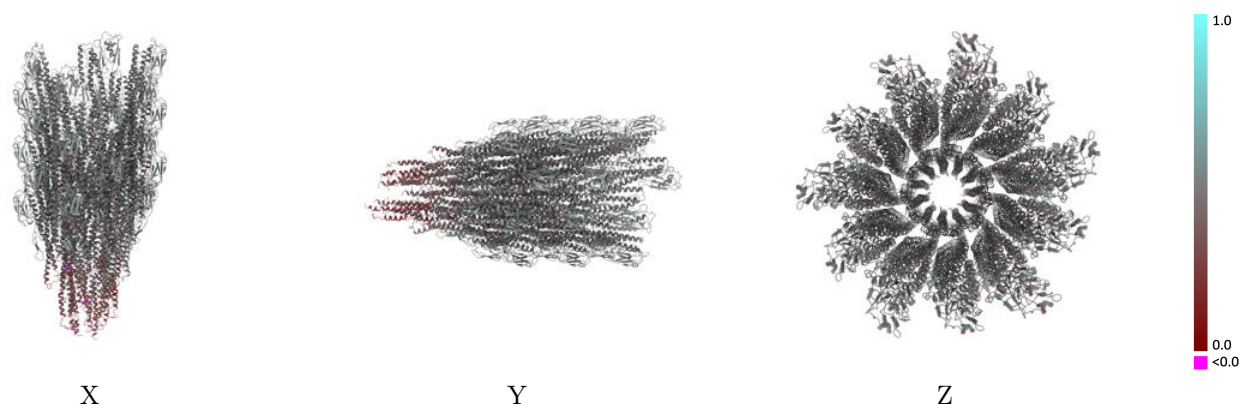
This section contains information regarding the fit between EMDB map EMD-49131 and PDB model 9N8M. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



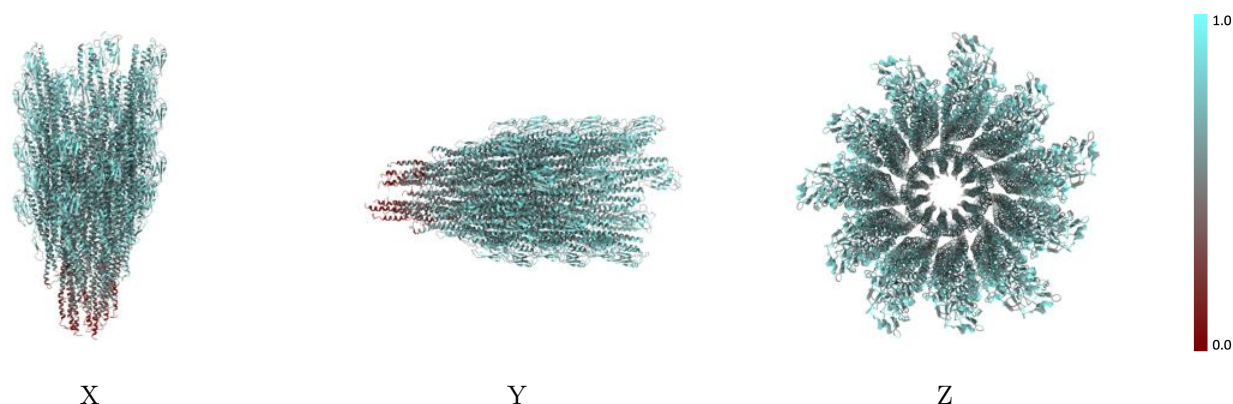
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



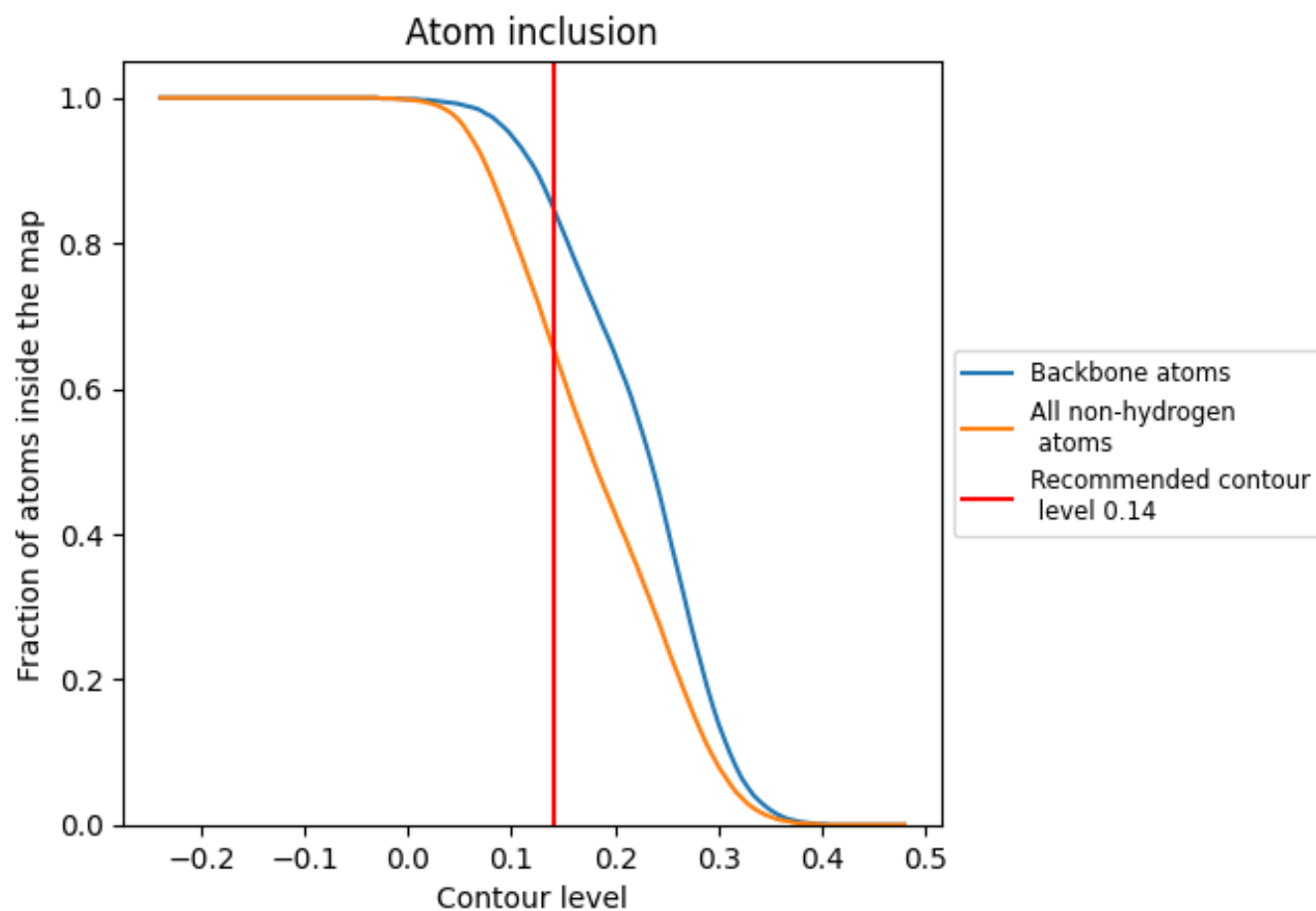
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.14).





































































9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 66% 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 (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6570	 0.4610
M1	 0.6630	 0.4590
M2	 0.6780	 0.4750
M3	 0.6710	 0.4690
M4	 0.6150	 0.4390
M5	 0.6800	 0.4750
M6	 0.6650	 0.4600
M7	 0.5850	 0.4200
M8	 0.6540	 0.4570
M9	 0.6670	 0.4580
MA	 0.6100	 0.4330
MB	 0.6720	 0.4700
MC	 0.6750	 0.4760
MD	 0.6830	 0.4750
ME	 0.6400	 0.4510
MF	 0.6500	 0.4500
MG	 0.5750	 0.4240
MH	 0.6730	 0.4730
MI	 0.6840	 0.4760
MJ	 0.6860	 0.4730
MK	 0.6870	 0.4770
ML	 0.6330	 0.4440
MM	 0.6600	 0.4620
MN	 0.6730	 0.4770
MO	 0.6710	 0.4720
MP	 0.6650	 0.4710
MQ	 0.6820	 0.4760
MR	 0.5700	 0.4190
MS	 0.6400	 0.4450
MT	 0.6740	 0.4720
MU	 0.6770	 0.4700
MV	 0.6800	 0.4720
MW	 0.6710	 0.4690
MX	 0.6760	 0.4690

