



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 12:50 PM UTC

PDB ID : 9R9X / pdb_00009r9x
EMDB ID : EMD-53863
Title : ssRNA-containing helical virus-like particle composed of PepMoV coat protein
Authors : Koritnik, N.; Kezar, A.; Podobnik, M.
Deposited on : 2025-05-20
Resolution : 3.64 Å (reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

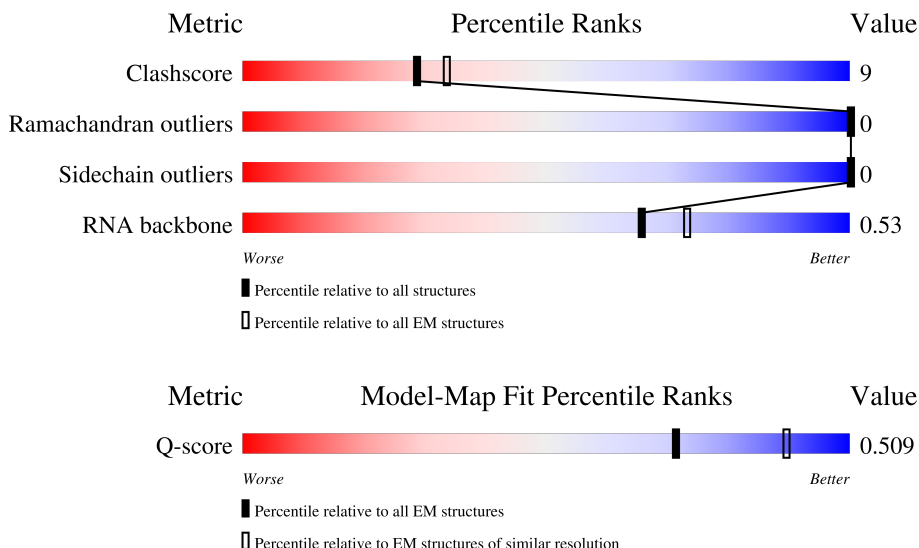
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.64 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11633 (3.14 - 4.14)

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	Aa	273	29% 67% 15% 18%
1	Ac	273	30% 66% 16% 18%
1	Ae	273	29% 65% 17% 18%

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Mol	Chain	Length	Quality of chain
1	Ag	273	29% 65% 17% 18%
1	Ai	273	29% 64% 18% 18%
1	Ak	273	29% 65% 17% 18%
1	Am	273	30% 66% 16% 18%
1	Ao	273	30% 66% 16% 18%
1	Aq	273	29% 65% 17% 18%
1	As	273	29% 64% 18% • 18%
1	Au	273	30% 64% 18% • 18%
1	Aw	273	29% 64% 18% • 18%
1	Ay	273	30% 63% 19% • 18%
1	Ba	273	29% 64% 18% • 18%
1	Bc	273	30% 65% 17% • 18%
1	Be	273	29% 63% 19% • 18%
1	Bg	273	31% 63% 19% • 18%
1	Bi	273	29% 63% 19% • 18%
1	Bk	273	30% 62% 19% • 18%
1	Bm	273	28% 63% 18% • 18%
1	Bo	273	28% 63% 19% • 18%
1	Bq	273	29% 63% 19% • 18%
1	Bs	273	29% 63% 19% • 18%
1	Bu	273	29% 64% 18% • 18%
1	Bw	273	28% 62% 20% • 18%
1	By	273	29% 62% 19% • 18%
1	Ca	273	29% 64% 17% • 18%
1	Cc	273	29% 64% 17% • 18%

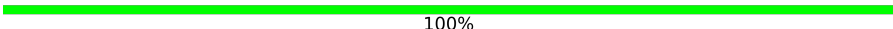
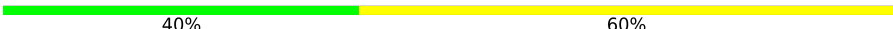
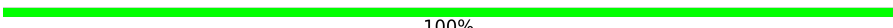
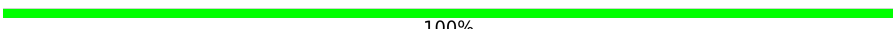
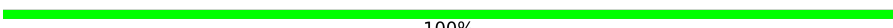
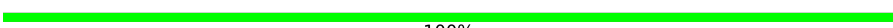
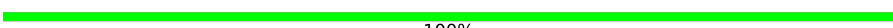
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Mol	Chain	Length	Quality of chain
1	Ce	273	
1	Cg	273	
1	Ci	273	
1	Ck	273	
1	Cm	273	
1	Co	273	
1	Cq	273	
1	Cs	273	
2	Ab	5	
2	Ad	5	
2	Af	5	
2	Ah	5	
2	Aj	5	
2	Al	5	
2	An	5	
2	Ap	5	
2	Ar	5	
2	At	5	
2	Av	5	
2	Ax	5	
2	Az	5	
2	Bb	5	
2	Bd	5	
2	Bf	5	
2	Bh	5	

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Mol	Chain	Length	Quality of chain
2	Bj	5	 40%60%
2	Bl	5	 80%20%
2	Bn	5	 100%
2	Bp	5	 40%60%
2	Br	5	 60%40%
2	Bt	5	 80%20%
2	Bv	5	 40%60%
2	Bx	5	 20%80%
2	Bz	5	 100%
2	Cb	5	 100%
2	Cd	5	 60%40%
2	Cf	5	 100%
2	Ch	5	 80%20%
2	Cj	5	 80%20%
2	Cl	5	 60%40%
2	Cn	5	 80%20%
2	Cp	5	 80%20%
2	Cr	5	 100%
2	Ct	5	 100%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 68508 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 Capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Ac	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Ae	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Ag	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Ai	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Ak	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Am	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Ao	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Aq	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	As	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Au	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Aw	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Ay	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Ba	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Bc	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Be	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Bg	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Bi	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Bk	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Bm	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Bo	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Bq	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Bs	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Bu	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Bw	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	By	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Ca	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Cc	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Ce	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Cg	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Ci	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Ck	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Cm	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Co	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Cq	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		
1	Cs	225	Total	C	N	O	S	0	0
			1803	1127	319	341	16		

- Molecule 2 is a RNA chain called RNA (5'-R(P*UP*UP*UP*UP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ab	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Ad	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Af	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Ah	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Aj	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Al	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	An	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Ap	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Ar	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	At	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Av	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Ax	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Az	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Bb	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Bd	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Bf	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Bh	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Bj	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Bl	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Bn	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Bp	5	Total	C	N	O	P	0	0
			100	45	10	40	5		
2	Br	5	Total	C	N	O	P	0	0
			100	45	10	40	5		

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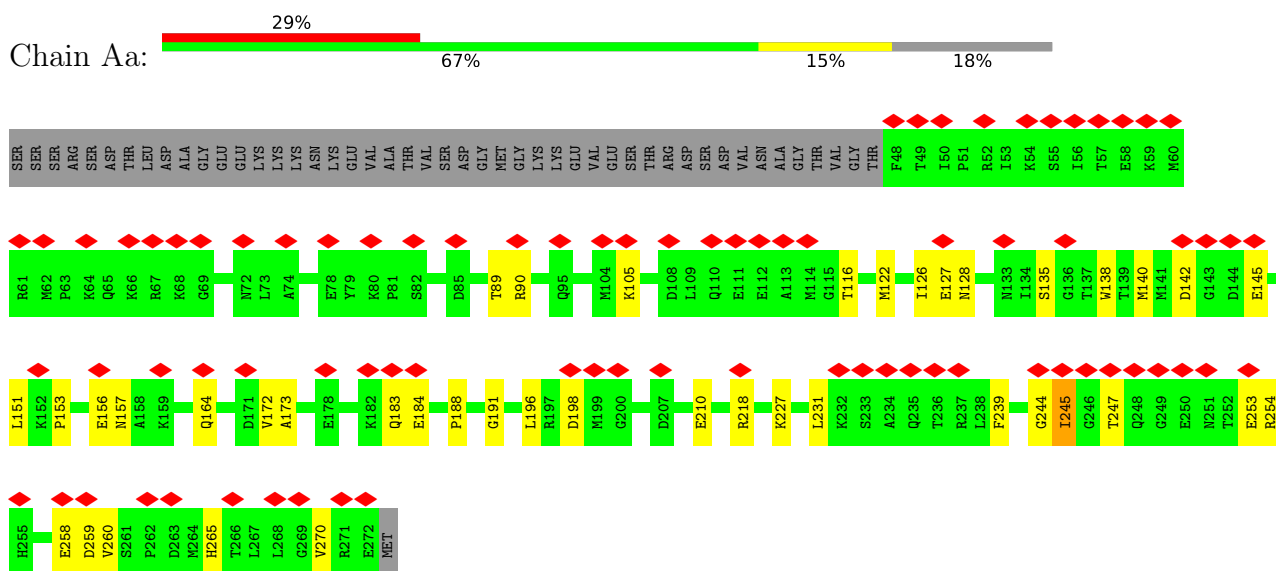
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Bt	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bv	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bx	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bz	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cb	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cd	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cf	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Ch	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cj	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cl	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cn	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cp	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cr	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Ct	5	Total 100	C 45	N 10	O 40	P 5	0	0

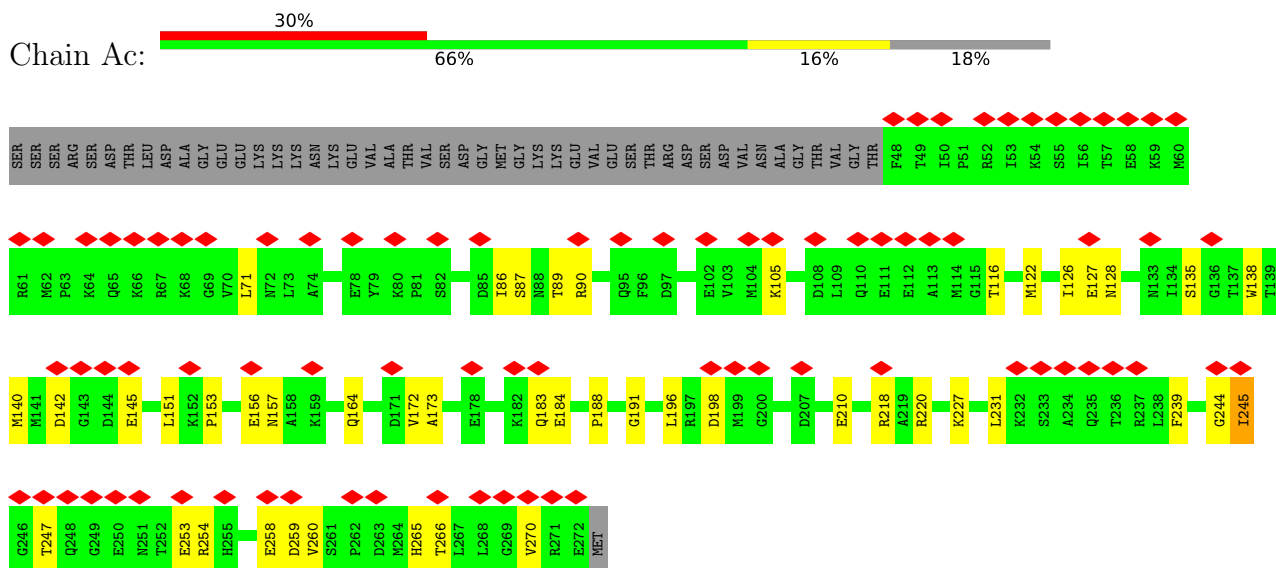
3 Residue-property plots [i](#)

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

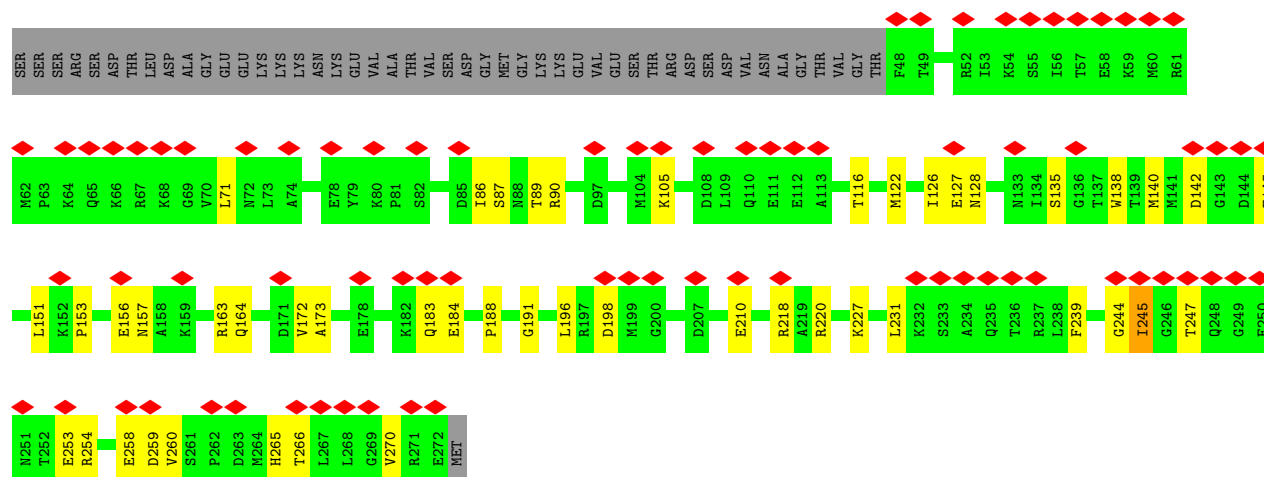
- Molecule 1: Capsid protein



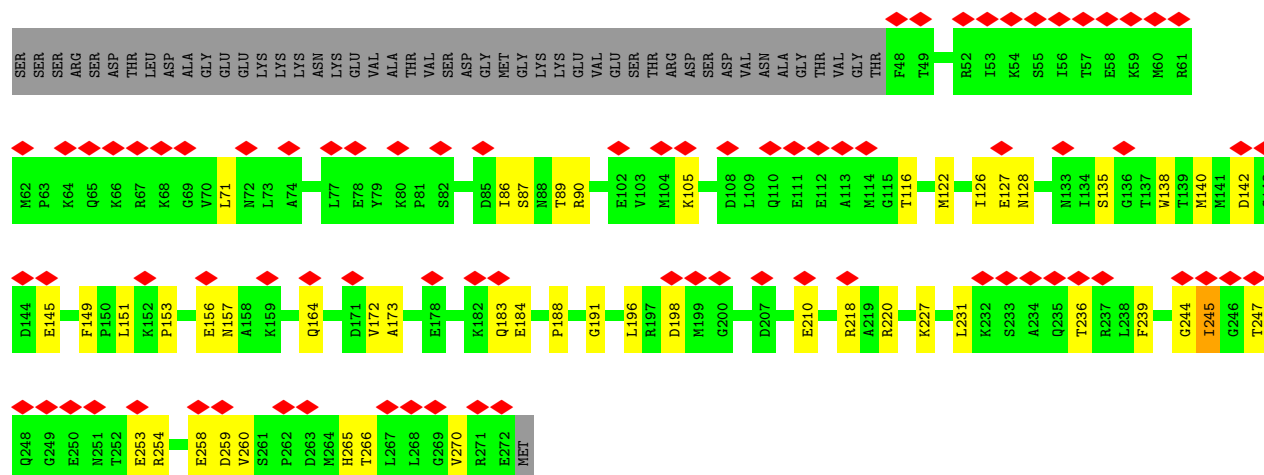
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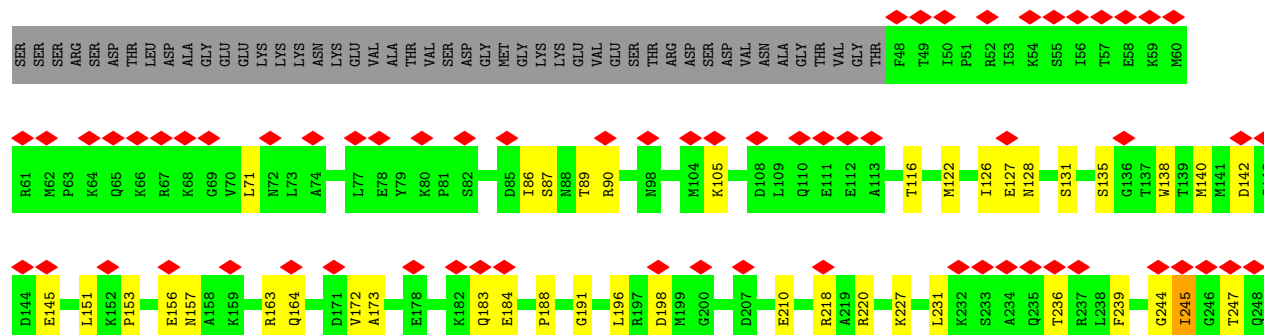
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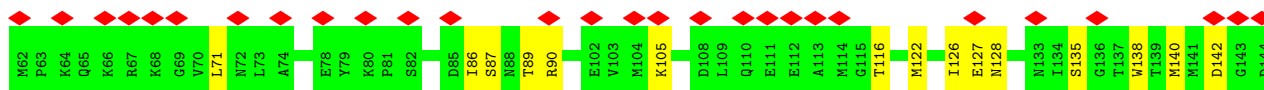


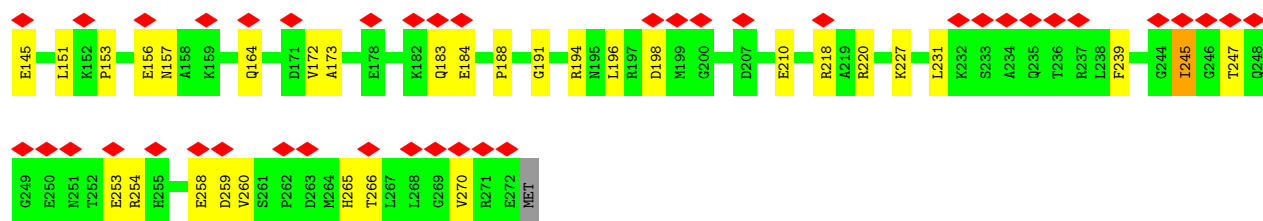
• Molecule 1: Capsid protein



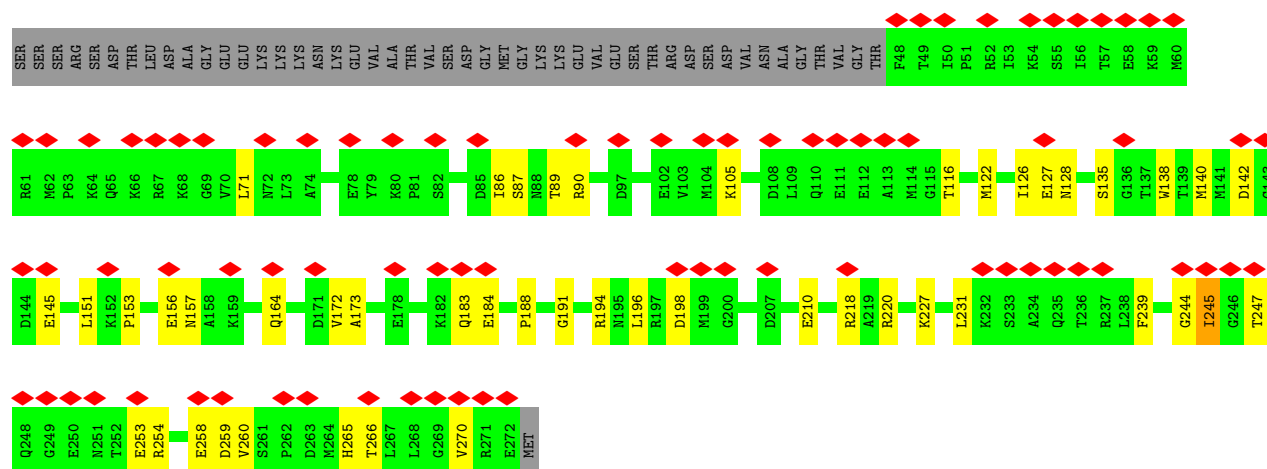
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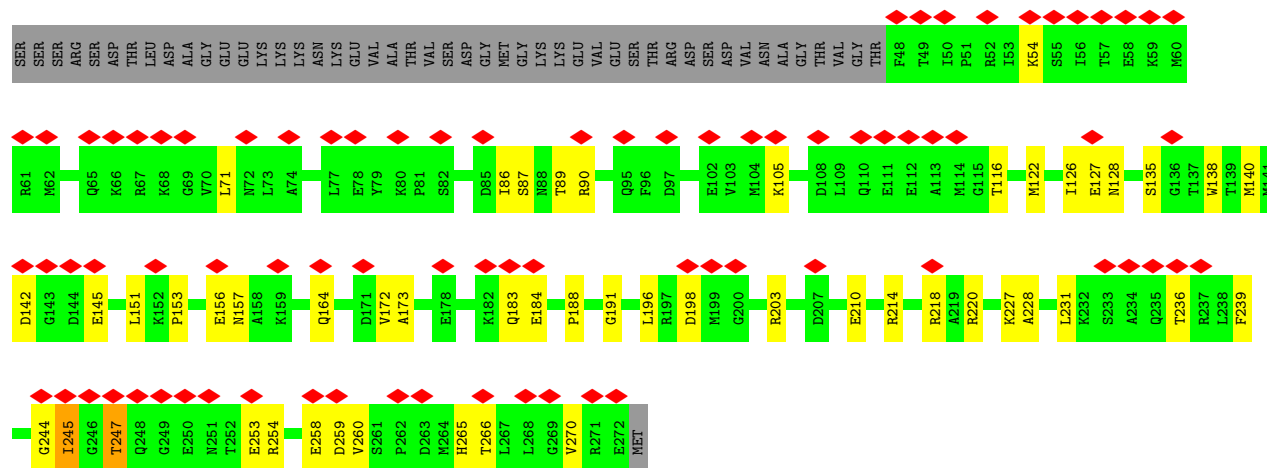




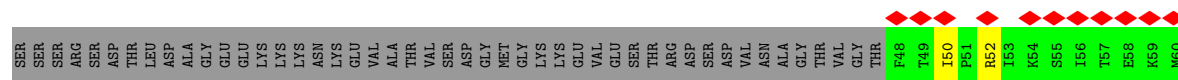
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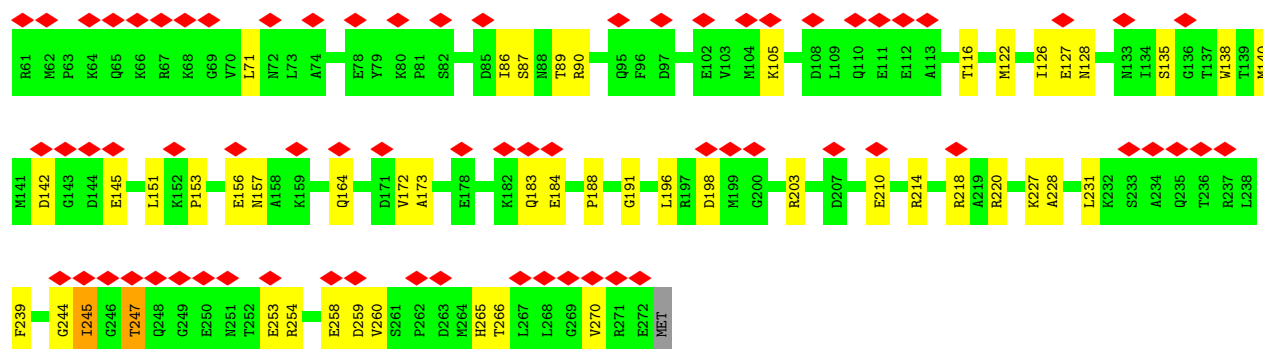


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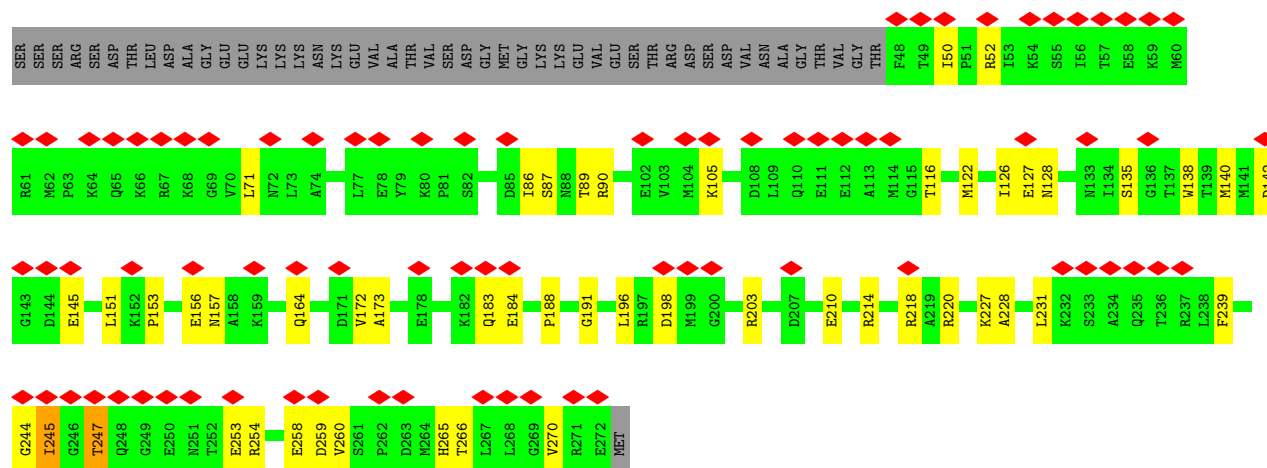


• Molecule 1: Capsid protein

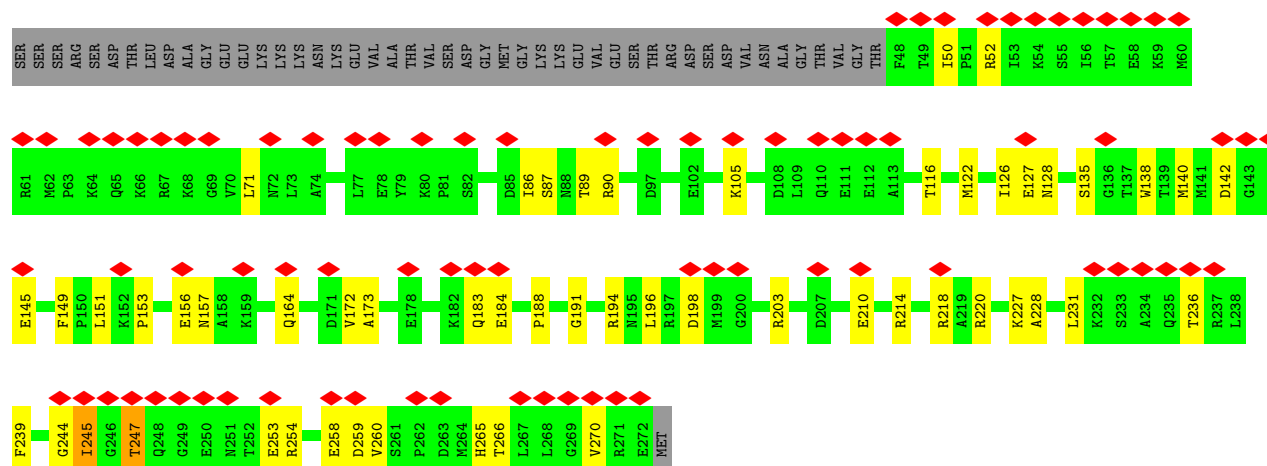




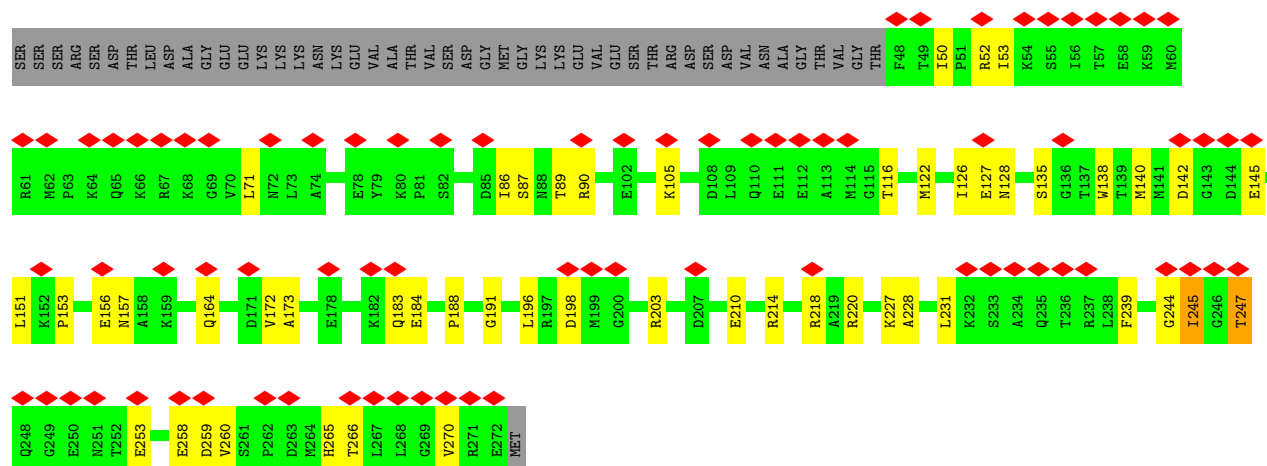
• Molecule 1: Capsid protein



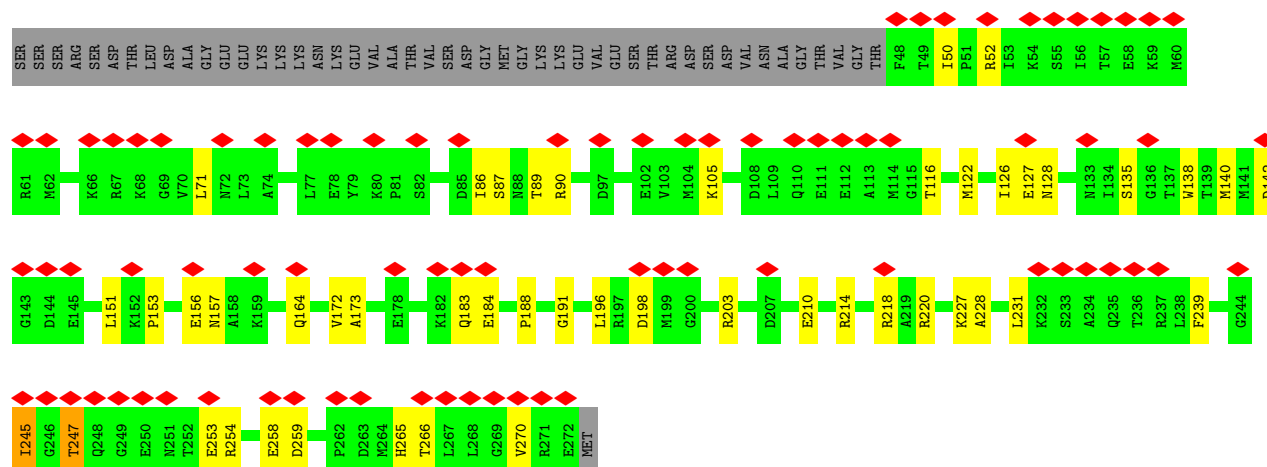
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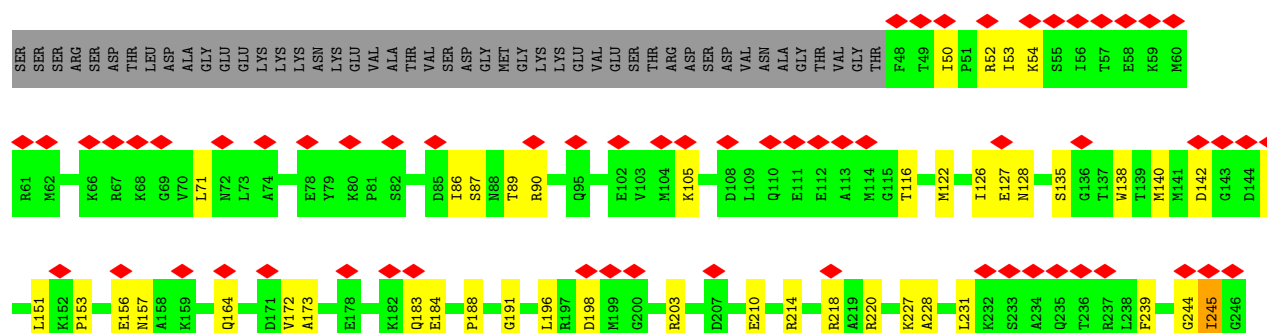
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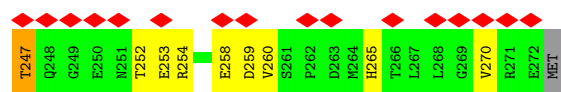


• Molecule 1: Capsid protein

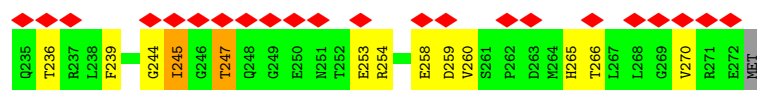
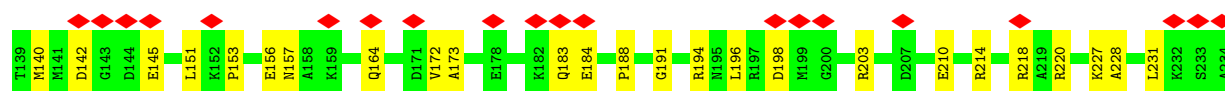
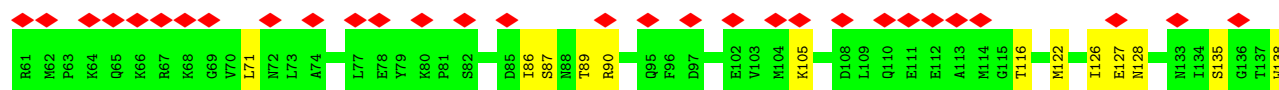
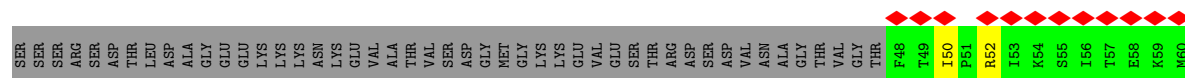


• Molecule 1: Capsid protein

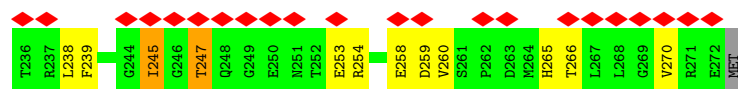
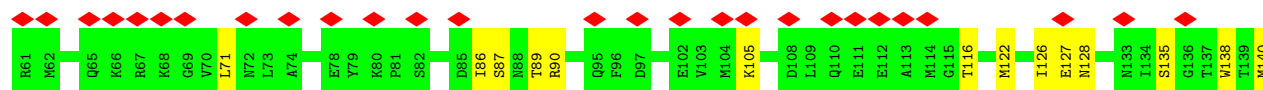
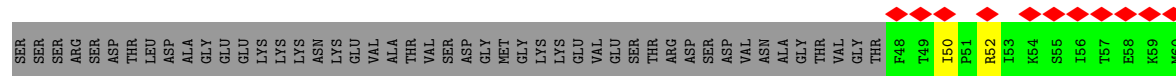




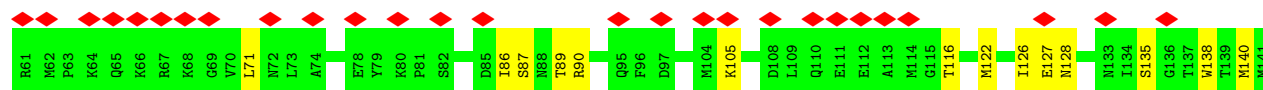
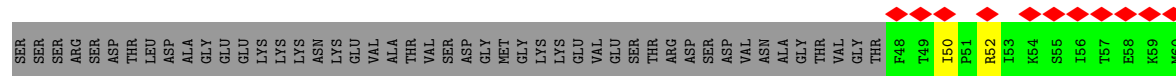
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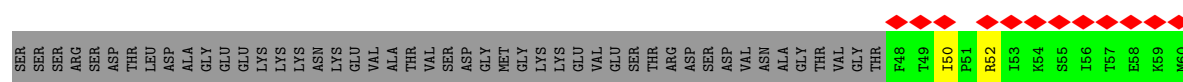


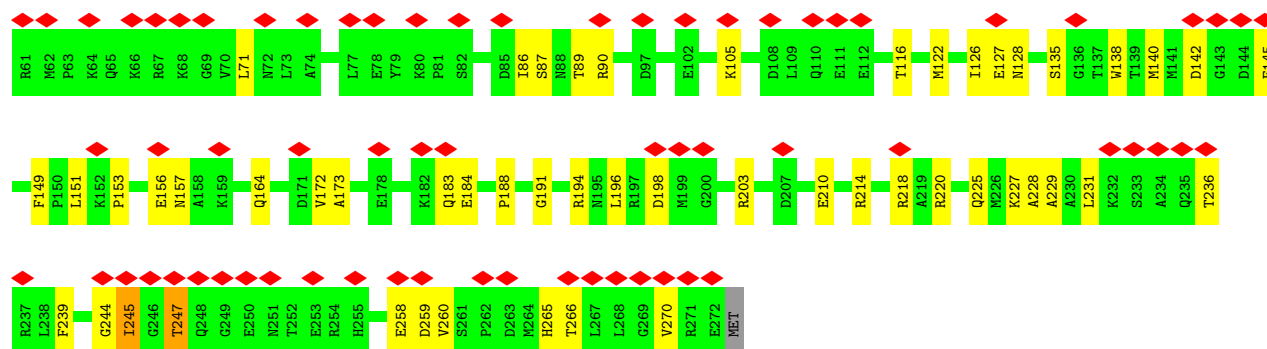
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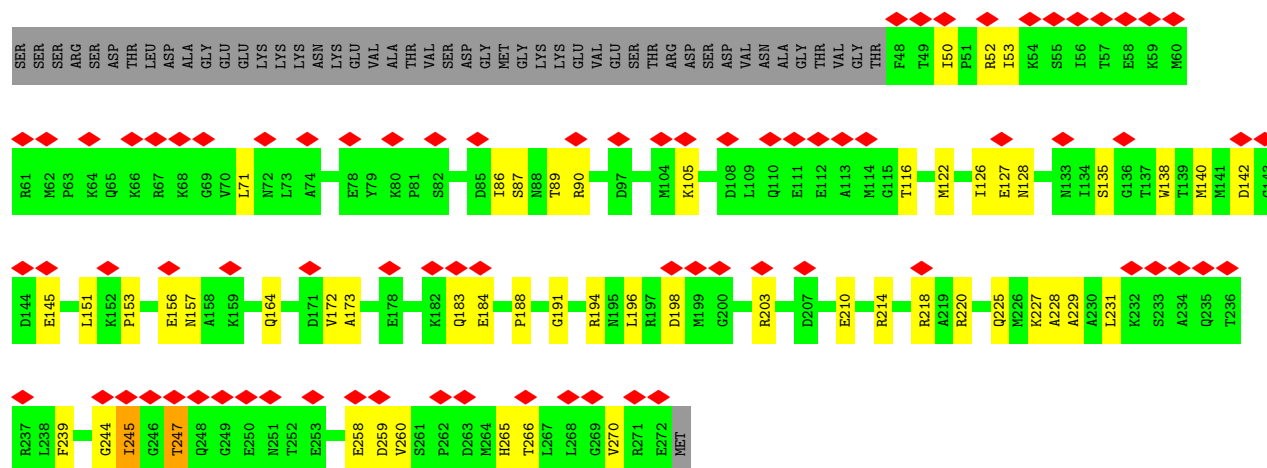
• Molecule 1: Capsid protein



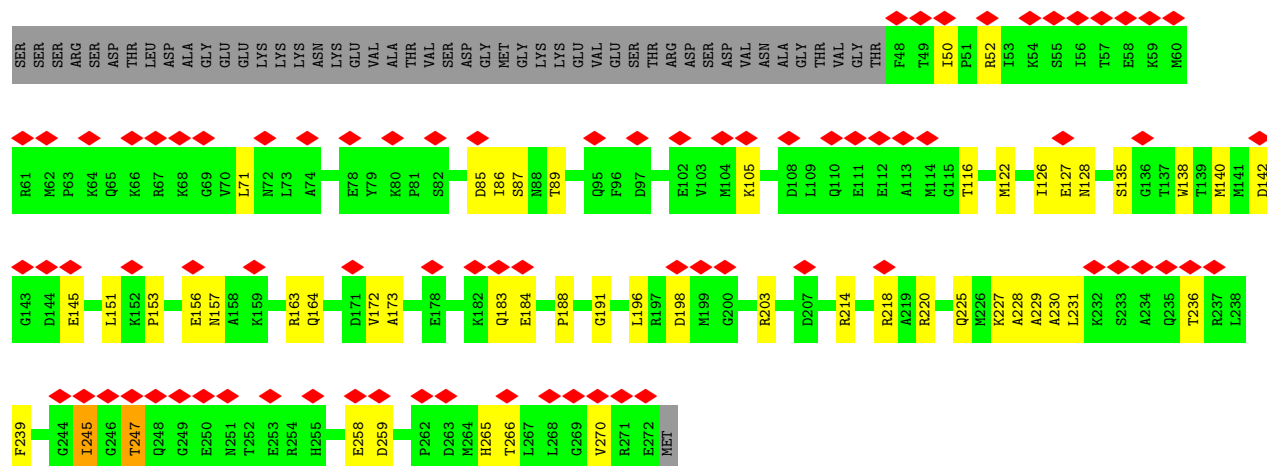




- Molecule 1: Capsid protein

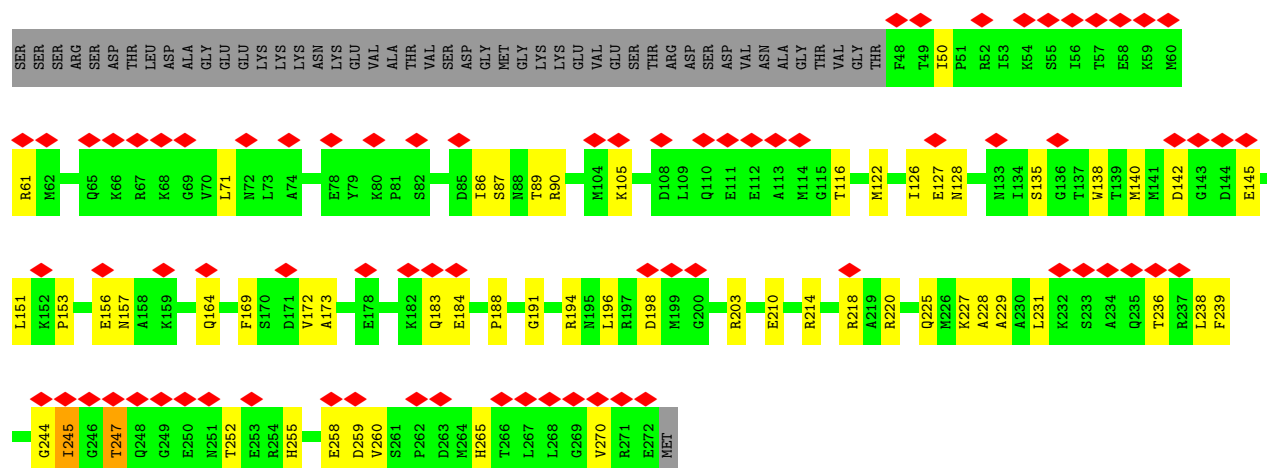


- Molecule 1: Capsid protein

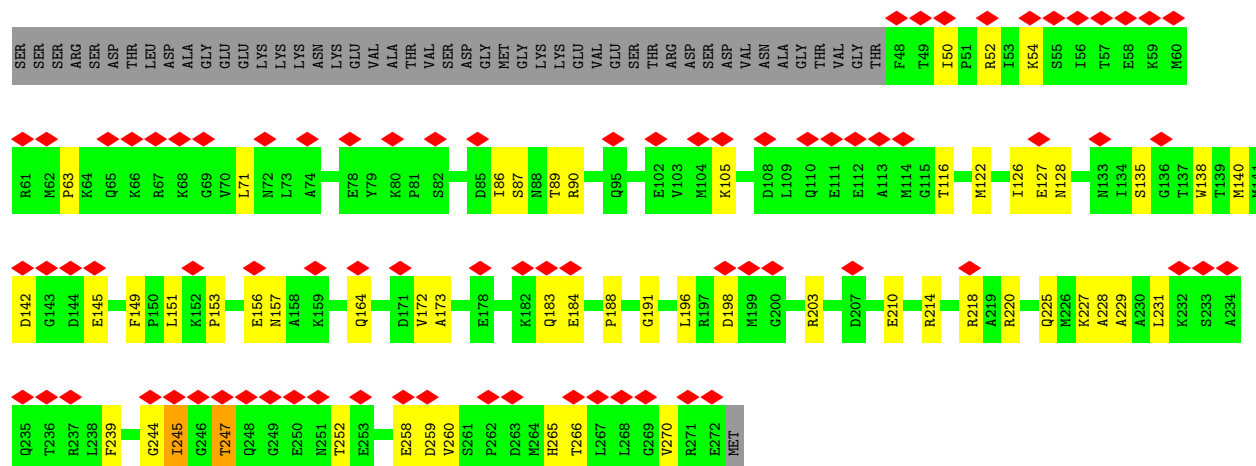


- Molecule 1: Capsid protein

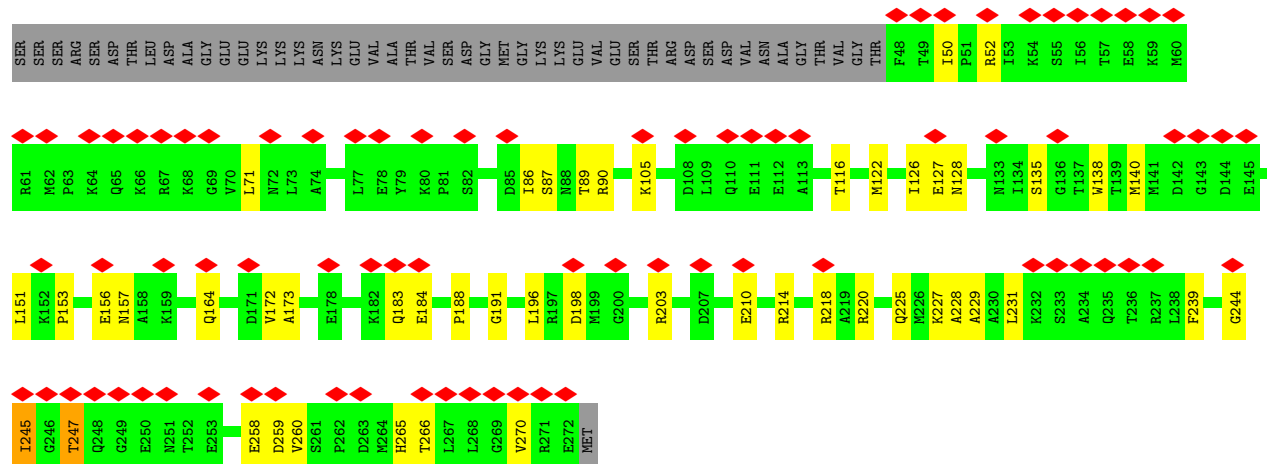


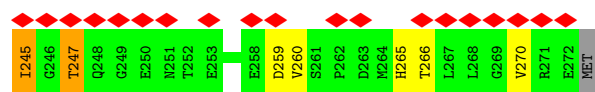


• Molecule 1: Capsid protein

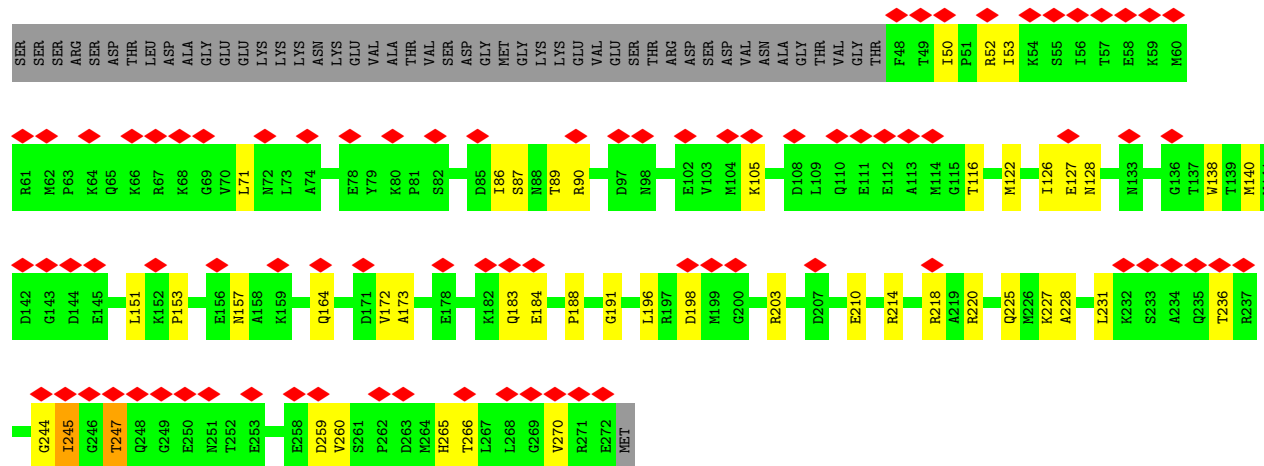


• Molecule 1: Capsid protein

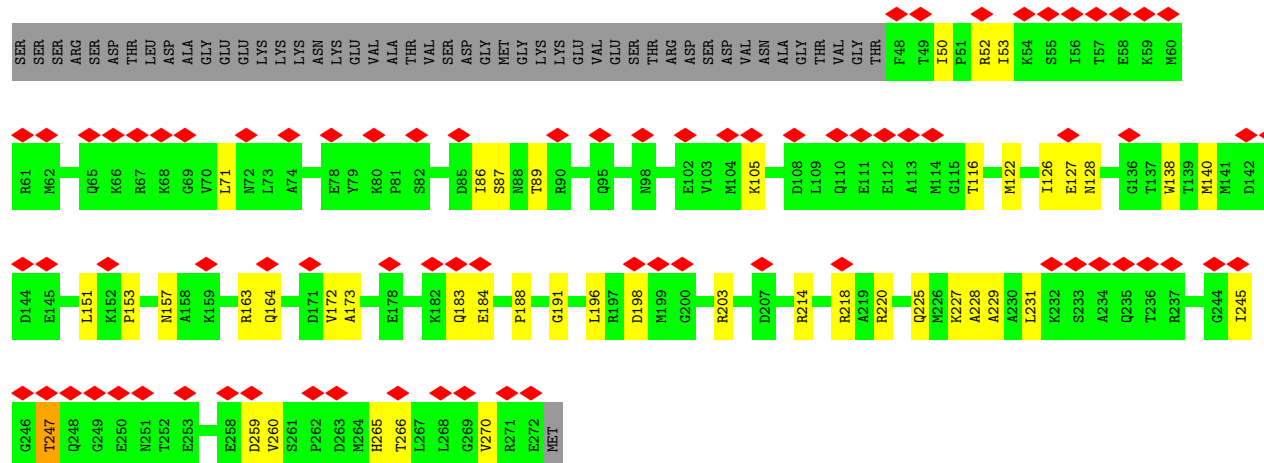




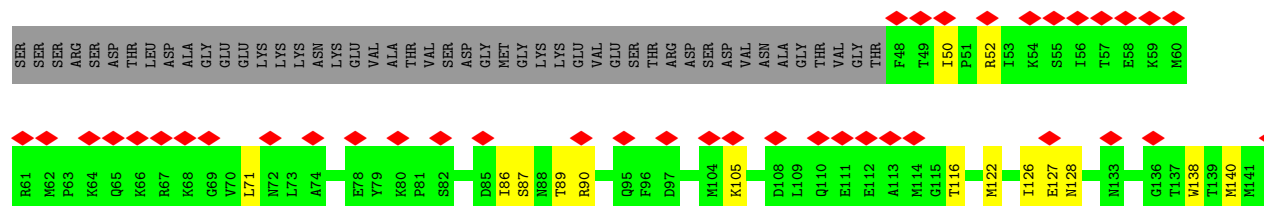
• Molecule 1: Capsid protein

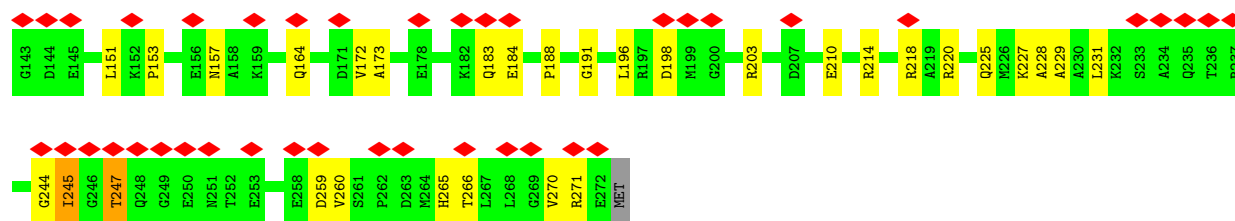


• Molecule 1: Capsid protein

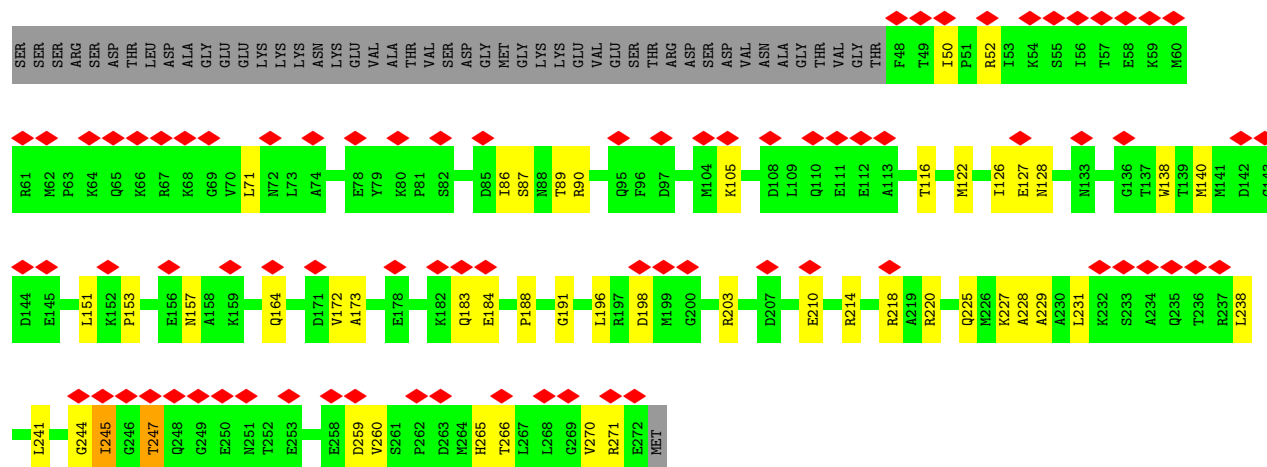


• Molecule 1: Capsid protein

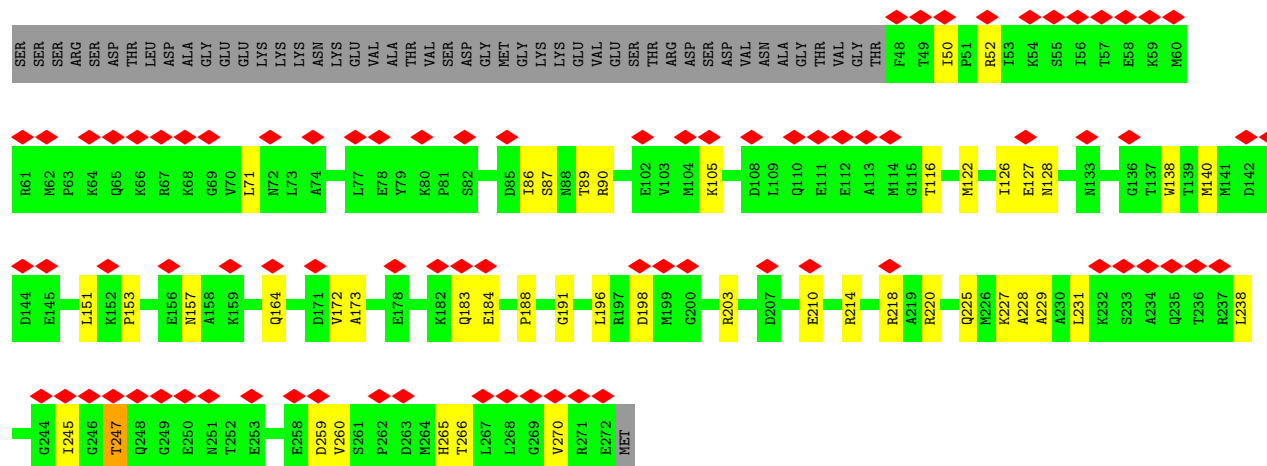




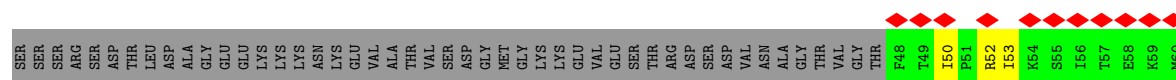
• Molecule 1: Capsid protein

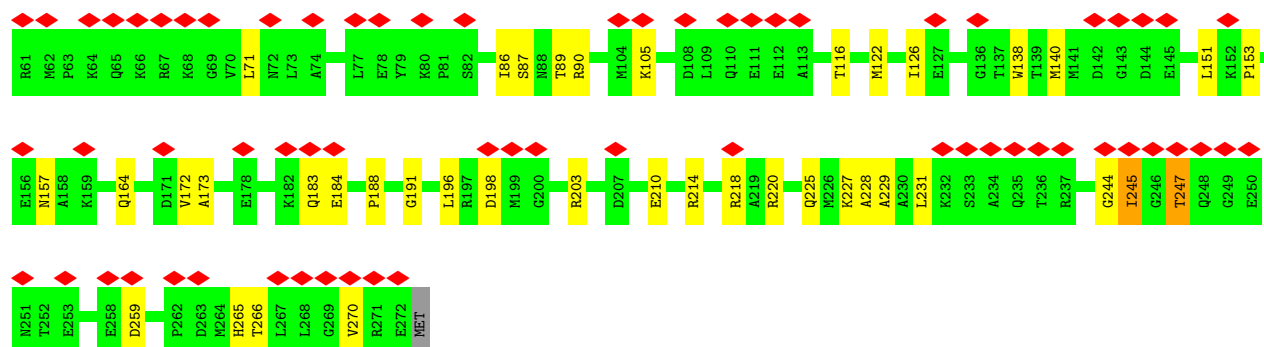


• Molecule 1: Capsid protein



• Molecule 1: Capsid protein





- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Ab: 80% 20%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Ad: 100%

There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Af: 60% 40%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Ah: 80% 20%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Aj: 60% 40%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

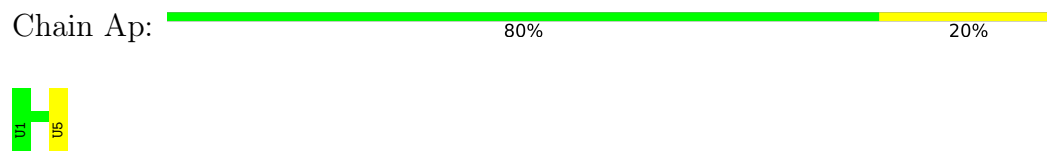
Chain Al: 80% 20%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



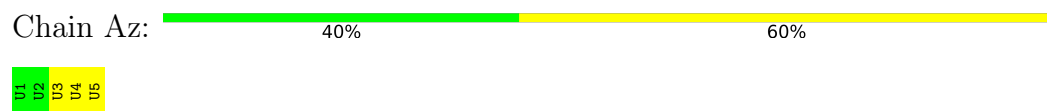
There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



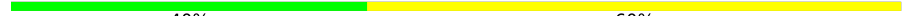
There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bf:  80% 20%

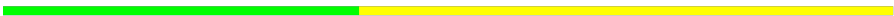


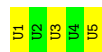
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bh:  40% 60%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bj:  40% 60%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bl:  80% 20%



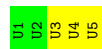
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bn:  100%

There are no outlier residues recorded for this chain.

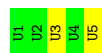
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bp:  40% 60%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Br:  60% 40%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bt:  80% 20%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



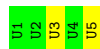
There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

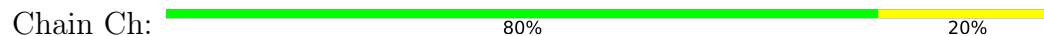


- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

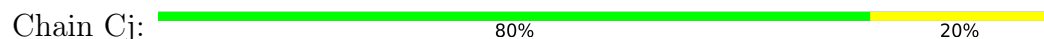


There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



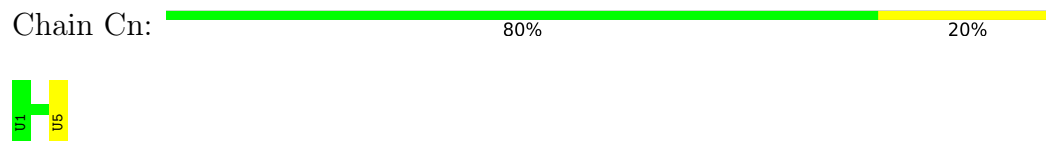
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



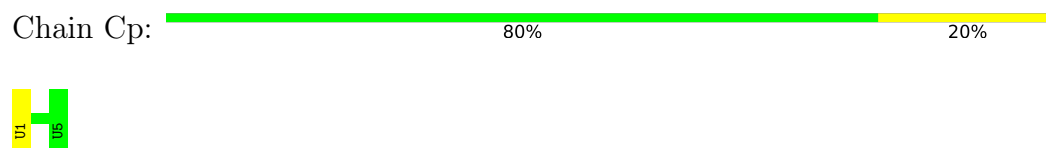
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



There are no outlier residues recorded for this chain.

- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-40.99°, rise=3.93 Å, axial sym=C1	Depositor
Number of segments used	36808	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{Å}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	150000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	6.359	Depositor
Minimum map value	-4.592	Depositor
Average map value	0.019	Depositor
Map value standard deviation	0.377	Depositor
Recommended contour level	1.82	Depositor
Map size (Å)	332.5, 332.5, 332.5	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	Aa	0.47	0/1839	0.63	2/2480 (0.1%)
1	Ac	0.47	0/1839	0.63	2/2480 (0.1%)
1	Ae	0.47	0/1839	0.63	2/2480 (0.1%)
1	Ag	0.47	0/1839	0.63	2/2480 (0.1%)
1	Ai	0.47	0/1839	0.63	2/2480 (0.1%)
1	Ak	0.47	0/1839	0.63	2/2480 (0.1%)
1	Am	0.46	0/1839	0.63	2/2480 (0.1%)
1	Ao	0.47	0/1839	0.63	2/2480 (0.1%)
1	Aq	0.47	0/1839	0.63	2/2480 (0.1%)
1	As	0.47	0/1839	0.63	2/2480 (0.1%)
1	Au	0.47	0/1839	0.63	2/2480 (0.1%)
1	Aw	0.47	0/1839	0.63	2/2480 (0.1%)
1	Ay	0.47	0/1839	0.63	2/2480 (0.1%)
1	Ba	0.47	0/1839	0.63	2/2480 (0.1%)
1	Bc	0.47	0/1839	0.63	2/2480 (0.1%)
1	Be	0.47	0/1839	0.63	2/2480 (0.1%)
1	Bg	0.47	0/1839	0.63	2/2480 (0.1%)
1	Bi	0.47	0/1839	0.63	2/2480 (0.1%)
1	Bk	0.47	0/1839	0.63	2/2480 (0.1%)
1	Bm	0.47	0/1839	0.63	2/2480 (0.1%)
1	Bo	0.47	0/1839	0.63	2/2480 (0.1%)
1	Bq	0.47	0/1839	0.63	2/2480 (0.1%)
1	Bs	0.47	0/1839	0.63	2/2480 (0.1%)
1	Bu	0.46	0/1839	0.63	2/2480 (0.1%)
1	Bw	0.47	0/1839	0.63	2/2480 (0.1%)
1	By	0.47	0/1839	0.63	2/2480 (0.1%)
1	Ca	0.47	0/1839	0.63	2/2480 (0.1%)
1	Cc	0.47	0/1839	0.63	2/2480 (0.1%)
1	Ce	0.47	0/1839	0.63	2/2480 (0.1%)
1	Cg	0.47	0/1839	0.63	2/2480 (0.1%)
1	Ci	0.47	0/1839	0.63	2/2480 (0.1%)
1	Ck	0.47	0/1839	0.63	2/2480 (0.1%)
1	Cm	0.47	0/1839	0.63	2/2480 (0.1%)
1	Co	0.47	0/1839	0.63	2/2480 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Cq	0.47	0/1839	0.63	2/2480 (0.1%)
1	Cs	0.47	0/1839	0.63	2/2480 (0.1%)
2	Ab	0.22	0/109	0.19	0/166
2	Ad	0.22	0/109	0.19	0/166
2	Af	0.22	0/109	0.19	0/166
2	Ah	0.22	0/109	0.19	0/166
2	Aj	0.22	0/109	0.19	0/166
2	Al	0.21	0/109	0.20	0/166
2	An	0.22	0/109	0.19	0/166
2	Ap	0.21	0/109	0.19	0/166
2	Ar	0.22	0/109	0.19	0/166
2	At	0.22	0/109	0.19	0/166
2	Av	0.22	0/109	0.19	0/166
2	Ax	0.22	0/109	0.19	0/166
2	Az	0.22	0/109	0.19	0/166
2	Bb	0.22	0/109	0.19	0/166
2	Bd	0.21	0/109	0.20	0/166
2	Bf	0.21	0/109	0.19	0/166
2	Bh	0.22	0/109	0.19	0/166
2	Bj	0.22	0/109	0.20	0/166
2	Bl	0.22	0/109	0.19	0/166
2	Bn	0.22	0/109	0.19	0/166
2	Bp	0.21	0/109	0.20	0/166
2	Br	0.22	0/109	0.19	0/166
2	Bt	0.22	0/109	0.19	0/166
2	Bv	0.22	0/109	0.20	0/166
2	Bx	0.22	0/109	0.19	0/166
2	Bz	0.22	0/109	0.19	0/166
2	Cb	0.22	0/109	0.19	0/166
2	Cd	0.22	0/109	0.19	0/166
2	Cf	0.22	0/109	0.19	0/166
2	Ch	0.21	0/109	0.20	0/166
2	Cj	0.22	0/109	0.19	0/166
2	Cl	0.22	0/109	0.19	0/166
2	Cn	0.22	0/109	0.19	0/166
2	Cp	0.21	0/109	0.19	0/166
2	Cr	0.21	0/109	0.19	0/166
2	Ct	0.22	0/109	0.20	0/166
All	All	0.46	0/70128	0.61	72/95256 (0.1%)

There are no bond length outliers.

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ce	245	ILE	N-CA-C	-6.14	107.27	113.47
1	Am	245	ILE	N-CA-C	-6.13	107.28	113.47
1	Be	245	ILE	N-CA-C	-6.13	107.28	113.47
1	Cc	245	ILE	N-CA-C	-6.11	107.30	113.47
1	Cg	245	ILE	N-CA-C	-6.11	107.30	113.47
1	Bk	245	ILE	N-CA-C	-6.10	107.31	113.47
1	Ao	245	ILE	N-CA-C	-6.10	107.31	113.47
1	Ca	245	ILE	N-CA-C	-6.10	107.31	113.47
1	Ai	245	ILE	N-CA-C	-6.10	107.31	113.47
1	Aq	245	ILE	N-CA-C	-6.10	107.31	113.47
1	Ay	245	ILE	N-CA-C	-6.09	107.31	113.47
1	Ba	245	ILE	N-CA-C	-6.09	107.31	113.47
1	Aw	245	ILE	N-CA-C	-6.08	107.33	113.47
1	Bg	245	ILE	N-CA-C	-6.08	107.33	113.47
1	Bw	245	ILE	N-CA-C	-6.08	107.33	113.47
1	Co	245	ILE	N-CA-C	-6.08	107.33	113.47
1	Cs	245	ILE	N-CA-C	-6.08	107.33	113.47
1	Bi	245	ILE	N-CA-C	-6.08	107.33	113.47
1	As	245	ILE	N-CA-C	-6.08	107.33	113.47
1	Ck	245	ILE	N-CA-C	-6.07	107.34	113.47
1	Bo	245	ILE	N-CA-C	-6.07	107.34	113.47
1	Cm	245	ILE	N-CA-C	-6.07	107.34	113.47
1	Ae	245	ILE	N-CA-C	-6.06	107.35	113.47
1	Aa	245	ILE	N-CA-C	-6.06	107.35	113.47
1	Bm	245	ILE	N-CA-C	-6.06	107.35	113.47
1	Bq	245	ILE	N-CA-C	-6.06	107.35	113.47
1	Bs	245	ILE	N-CA-C	-6.06	107.35	113.47
1	Ci	245	ILE	N-CA-C	-6.05	107.36	113.47
1	Ak	245	ILE	N-CA-C	-6.05	107.36	113.47
1	Au	245	ILE	N-CA-C	-6.04	107.37	113.47
1	Cq	245	ILE	N-CA-C	-6.04	107.37	113.47
1	Ac	245	ILE	N-CA-C	-6.04	107.37	113.47
1	By	245	ILE	N-CA-C	-6.04	107.37	113.47
1	Ag	245	ILE	N-CA-C	-6.03	107.38	113.47
1	Bu	245	ILE	N-CA-C	-6.03	107.38	113.47
1	Bc	245	ILE	N-CA-C	-6.02	107.39	113.47
1	Cc	247	THR	N-CA-C	-5.97	106.04	113.38
1	Ai	247	THR	N-CA-C	-5.96	106.06	113.38
1	Ck	247	THR	N-CA-C	-5.94	106.08	113.38
1	Bk	247	THR	N-CA-C	-5.94	106.08	113.38
1	Ac	247	THR	N-CA-C	-5.93	106.09	113.38
1	Aa	247	THR	N-CA-C	-5.92	106.09	113.38
1	Be	247	THR	N-CA-C	-5.92	106.09	113.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Bi	247	THR	N-CA-C	-5.92	106.10	113.38
1	Bw	247	THR	N-CA-C	-5.92	106.10	113.38
1	Cg	247	THR	N-CA-C	-5.91	106.11	113.38
1	Cq	247	THR	N-CA-C	-5.91	106.11	113.38
1	Bs	247	THR	N-CA-C	-5.91	106.11	113.38
1	Au	247	THR	N-CA-C	-5.91	106.11	113.38
1	Am	247	THR	N-CA-C	-5.91	106.11	113.38
1	Aq	247	THR	N-CA-C	-5.91	106.12	113.38
1	Ba	247	THR	N-CA-C	-5.91	106.12	113.38
1	Cm	247	THR	N-CA-C	-5.91	106.12	113.38
1	Cs	247	THR	N-CA-C	-5.91	106.12	113.38
1	Ca	247	THR	N-CA-C	-5.90	106.12	113.38
1	Ae	247	THR	N-CA-C	-5.90	106.12	113.38
1	Bo	247	THR	N-CA-C	-5.90	106.12	113.38
1	Ak	247	THR	N-CA-C	-5.89	106.13	113.38
1	Aw	247	THR	N-CA-C	-5.89	106.13	113.38
1	By	247	THR	N-CA-C	-5.89	106.13	113.38
1	Co	247	THR	N-CA-C	-5.89	106.13	113.38
1	Bc	247	THR	N-CA-C	-5.89	106.14	113.38
1	Bm	247	THR	N-CA-C	-5.89	106.14	113.38
1	Bu	247	THR	N-CA-C	-5.89	106.14	113.38
1	Ce	247	THR	N-CA-C	-5.89	106.14	113.38
1	As	247	THR	N-CA-C	-5.88	106.14	113.38
1	Ao	247	THR	N-CA-C	-5.88	106.15	113.38
1	Bg	247	THR	N-CA-C	-5.84	106.19	113.38
1	Ay	247	THR	N-CA-C	-5.84	106.19	113.38
1	Bq	247	THR	N-CA-C	-5.84	106.19	113.38
1	Ag	247	THR	N-CA-C	-5.84	106.20	113.38
1	Ci	247	THR	N-CA-C	-5.83	106.21	113.38

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Aa	1803	0	1775	39	0
1	Ac	1803	0	1775	46	0
1	Ae	1803	0	1775	47	0
1	Ag	1803	0	1775	48	0
1	Ai	1803	0	1775	53	0
1	Ak	1803	0	1775	48	0
1	Am	1803	0	1775	48	0
1	Ao	1803	0	1775	44	0
1	Aq	1803	0	1775	49	0
1	As	1803	0	1775	61	0
1	Au	1803	0	1775	57	0
1	Aw	1803	0	1775	60	0
1	Ay	1803	0	1775	66	0
1	Ba	1803	0	1775	59	0
1	Bc	1803	0	1775	53	0
1	Be	1803	0	1775	59	0
1	Bg	1803	0	1775	59	0
1	Bi	1803	0	1775	63	0
1	Bk	1803	0	1775	66	0
1	Bm	1803	0	1775	60	0
1	Bo	1803	0	1775	65	0
1	Bq	1803	0	1775	62	0
1	Bs	1803	0	1775	63	0
1	Bu	1803	0	1775	65	0
1	Bw	1803	0	1775	71	0
1	By	1803	0	1775	63	0
1	Ca	1803	0	1775	54	0
1	Cc	1803	0	1775	52	0
1	Ce	1803	0	1775	46	0
1	Cg	1803	0	1775	47	0
1	Ci	1803	0	1775	46	0
1	Ck	1803	0	1775	47	0
1	Cm	1803	0	1775	49	0
1	Co	1803	0	1775	54	0
1	Cq	1803	0	1775	48	0
1	Cs	1803	0	1775	37	0
2	Ab	100	0	51	1	0
2	Ad	100	0	51	0	0
2	Af	100	0	51	2	0
2	Ah	100	0	51	1	0
2	Aj	100	0	51	7	0
2	Al	100	0	51	1	0
2	An	100	0	51	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Ap	100	0	51	1	0
2	Ar	100	0	51	3	0
2	At	100	0	51	3	0
2	Av	100	0	51	0	0
2	Ax	100	0	51	0	0
2	Az	100	0	51	7	0
2	Bb	100	0	51	0	0
2	Bd	100	0	51	0	0
2	Bf	100	0	51	1	0
2	Bh	100	0	51	4	0
2	Bj	100	0	51	5	0
2	Bl	100	0	51	2	0
2	Bn	100	0	51	0	0
2	Bp	100	0	51	4	0
2	Br	100	0	51	2	0
2	Bt	100	0	51	1	0
2	Bv	100	0	51	8	0
2	Bx	100	0	51	6	0
2	Bz	100	0	51	0	0
2	Cb	100	0	51	0	0
2	Cd	100	0	51	2	0
2	Cf	100	0	51	0	0
2	Ch	100	0	51	1	0
2	Cj	100	0	51	1	0
2	Cl	100	0	51	3	0
2	Cn	100	0	51	1	0
2	Cp	100	0	51	1	0
2	Cr	100	0	51	0	0
2	Ct	100	0	51	0	0
All	All	68508	0	65736	1267	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (1267) 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:Co:172:VAL:HG11	1:Cq:71:LEU:HD13	1.68	0.76
1:Ag:172:VAL:HG11	1:Ai:71:LEU:HD13	1.69	0.74
1:Au:172:VAL:HG11	1:Aw:71:LEU:HD13	1.70	0.74
1:Ay:172:VAL:HG11	1:Ba:71:LEU:HD13	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bw:245:ILE:HG21	1:Co:231:LEU:CB	2.17	0.74
1:Ci:172:VAL:HG11	1:Ck:71:LEU:HD13	1.69	0.74
1:Ac:172:VAL:HG11	1:Ae:71:LEU:HD13	1.70	0.74
1:Bm:172:VAL:HG11	1:Bo:71:LEU:HD13	1.70	0.74
1:Bw:172:VAL:HG11	1:By:71:LEU:HD13	1.70	0.74
1:Bq:172:VAL:HG11	1:Bs:71:LEU:HD13	1.69	0.73
1:By:172:VAL:HG11	1:Ca:71:LEU:HD13	1.71	0.73
1:Bg:172:VAL:HG11	1:Bi:71:LEU:HD13	1.71	0.73
1:Cm:172:VAL:HG11	1:Co:71:LEU:HD13	1.71	0.73
1:Ak:172:VAL:HG11	1:Am:71:LEU:HD13	1.70	0.73
1:Ca:172:VAL:HG11	1:Cc:71:LEU:HD13	1.71	0.73
1:Ce:172:VAL:HG11	1:Cg:71:LEU:HD13	1.70	0.73
1:Cq:172:VAL:HG11	1:Cs:71:LEU:HD13	1.70	0.73
1:Ao:172:VAL:HG11	1:Aq:71:LEU:HD13	1.70	0.73
1:Bc:172:VAL:HG11	1:Be:71:LEU:HD13	1.70	0.73
1:Be:172:VAL:HG11	1:Bg:71:LEU:HD13	1.72	0.72
1:Am:172:VAL:HG11	1:Ao:71:LEU:HD13	1.72	0.72
1:Aa:172:VAL:HG11	1:Ac:71:LEU:HD13	1.73	0.71
1:Cc:172:VAL:HG11	1:Ce:71:LEU:HD13	1.73	0.71
1:Aw:172:VAL:HG11	1:Ay:71:LEU:HD13	1.72	0.71
1:As:172:VAL:HG11	1:Au:71:LEU:HD13	1.73	0.71
1:Bo:172:VAL:HG11	1:Bq:71:LEU:HD13	1.72	0.71
1:Bu:172:VAL:HG11	1:Bw:71:LEU:HD13	1.73	0.71
1:Cg:172:VAL:HG11	1:Ci:71:LEU:HD13	1.72	0.71
1:Bi:172:VAL:HG11	1:Bk:71:LEU:HD13	1.73	0.71
1:Bk:172:VAL:HG11	1:Bm:71:LEU:HD13	1.73	0.71
1:Ae:172:VAL:HG11	1:Ag:71:LEU:HD13	1.72	0.71
1:Aq:172:VAL:HG11	1:As:71:LEU:HD13	1.73	0.70
1:Ba:172:VAL:HG11	1:Bc:71:LEU:HD13	1.73	0.70
1:Bs:172:VAL:HG11	1:Bu:71:LEU:HD13	1.73	0.70
1:Ck:172:VAL:HG11	1:Cm:71:LEU:HD13	1.73	0.70
1:Ai:172:VAL:HG11	1:Ak:71:LEU:HD13	1.73	0.70
1:Aa:245:ILE:HG21	1:As:231:LEU:CB	2.22	0.70
1:By:245:ILE:HG21	1:Cq:231:LEU:CB	2.22	0.69
1:As:245:ILE:HG21	1:Bk:231:LEU:CB	2.22	0.69
1:Ae:245:ILE:HG21	1:Aw:231:LEU:CB	2.22	0.69
1:Ao:245:ILE:HG21	1:Bg:231:LEU:CB	2.23	0.69
1:Bu:245:ILE:HG21	1:Cm:231:LEU:CB	2.23	0.69
1:Ca:245:ILE:HG21	1:Cs:231:LEU:CB	2.23	0.69
1:Bc:245:ILE:HG21	1:Bu:231:LEU:CB	2.23	0.68
1:Bg:245:ILE:HG21	1:By:231:LEU:CB	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ag:245:ILE:HG21	1:Ay:231:LEU:CB	2.23	0.68
1:Cm:270:VAL:HB	1:Co:270:VAL:HG22	1.74	0.68
1:Au:245:ILE:HG21	1:Bm:231:LEU:CB	2.23	0.68
1:Ak:245:ILE:HG21	1:Bc:231:LEU:CB	2.24	0.68
1:Ba:245:ILE:HG21	1:Bs:231:LEU:CB	2.23	0.68
1:Aq:245:ILE:HG21	1:Bi:231:LEU:CB	2.23	0.68
1:Ay:245:ILE:HG21	1:Bq:231:LEU:CB	2.23	0.68
1:Ai:245:ILE:HG21	1:Ba:231:LEU:CB	2.24	0.68
1:Bi:245:ILE:HG21	1:Ca:231:LEU:CB	2.23	0.68
1:Ac:245:ILE:HG21	1:Au:231:LEU:CB	2.23	0.68
1:Bk:245:ILE:HG21	1:Cc:231:LEU:CB	2.24	0.68
1:Bs:245:ILE:HG21	1:Ck:231:LEU:CB	2.24	0.68
1:Aw:245:ILE:HG21	1:Bo:231:LEU:CB	2.23	0.67
1:Ai:227:LYS:HG3	2:Aj:4:U:C4	2.30	0.67
1:Am:245:ILE:HG21	1:Be:231:LEU:CB	2.23	0.67
1:Bm:245:ILE:HG21	1:Ce:231:LEU:CB	2.25	0.67
1:Bo:245:ILE:HG21	1:Cg:231:LEU:CB	2.25	0.66
1:Bq:245:ILE:HG21	1:Ci:231:LEU:CB	2.25	0.66
1:Be:245:ILE:HG21	1:Bw:231:LEU:CB	2.25	0.66
1:Bw:270:VAL:HB	1:By:270:VAL:HG22	1.77	0.66
1:Bk:194:ARG:NH2	2:Bl:5:U:OP1	2.29	0.65
1:Bu:227:LYS:HG3	2:Bv:4:U:C4	2.32	0.64
1:Aa:183:GLN:HG3	1:Aa:184:GLU:H	1.64	0.63
1:Cc:183:GLN:HG3	1:Cc:184:GLU:H	1.64	0.63
1:Ay:270:VAL:HB	1:Ba:270:VAL:HG22	1.81	0.63
1:Ci:270:VAL:HB	1:Ck:270:VAL:HG22	1.81	0.63
1:Bg:183:GLN:HG3	1:Bg:184:GLU:H	1.64	0.62
1:Bi:183:GLN:HG3	1:Bi:184:GLU:H	1.64	0.62
1:Co:183:GLN:HG3	1:Co:184:GLU:H	1.64	0.62
1:Ca:183:GLN:HG3	1:Ca:184:GLU:H	1.64	0.62
1:Ai:227:LYS:HG3	2:Aj:4:U:N3	2.13	0.62
1:Ac:183:GLN:HG3	1:Ac:184:GLU:H	1.64	0.62
1:Am:183:GLN:HG3	1:Am:184:GLU:H	1.64	0.62
1:Ao:183:GLN:HG3	1:Ao:184:GLU:H	1.64	0.62
1:Bi:194:ARG:NH1	2:Bj:5:U:OP1	2.33	0.62
1:By:183:GLN:HG3	1:By:184:GLU:H	1.64	0.62
1:Au:183:GLN:HG3	1:Au:184:GLU:H	1.64	0.62
1:Ba:183:GLN:HG3	1:Ba:184:GLU:H	1.64	0.62
1:Bk:183:GLN:HG3	1:Bk:184:GLU:H	1.64	0.62
1:Bw:245:ILE:HG21	1:Co:231:LEU:HB3	1.80	0.62
1:Cq:183:GLN:HG3	1:Cq:184:GLU:H	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bo:183:GLN:HG3	1:Bo:184:GLU:H	1.64	0.61
1:Bq:183:GLN:HG3	1:Bq:184:GLU:H	1.64	0.61
1:Cm:183:GLN:HG3	1:Cm:184:GLU:H	1.64	0.61
1:As:183:GLN:HG3	1:As:184:GLU:H	1.64	0.61
1:Aw:183:GLN:HG3	1:Aw:184:GLU:H	1.64	0.61
1:Ay:183:GLN:HG3	1:Ay:184:GLU:H	1.64	0.61
1:Ag:270:VAL:HB	1:Ai:270:VAL:HG22	1.81	0.61
1:Ck:183:GLN:HG3	1:Ck:184:GLU:H	1.64	0.61
1:Ak:183:GLN:HG3	1:Ak:184:GLU:H	1.64	0.61
1:Bc:183:GLN:HG3	1:Bc:184:GLU:H	1.64	0.61
1:Be:183:GLN:HG3	1:Be:184:GLU:H	1.64	0.61
1:Cs:183:GLN:HG3	1:Cs:184:GLU:H	1.64	0.61
1:Bw:183:GLN:HG3	1:Bw:184:GLU:H	1.64	0.61
1:Ce:183:GLN:HG3	1:Ce:184:GLU:H	1.64	0.61
1:Aq:183:GLN:HG3	1:Aq:184:GLU:H	1.64	0.61
1:Bu:183:GLN:HG3	1:Bu:184:GLU:H	1.64	0.61
1:Bq:270:VAL:HB	1:Bs:270:VAL:HG22	1.81	0.61
1:Ai:183:GLN:HG3	1:Ai:184:GLU:H	1.64	0.61
1:Bs:183:GLN:HG3	1:Bs:184:GLU:H	1.64	0.61
1:Au:270:VAL:HB	1:Aw:270:VAL:HG22	1.83	0.60
1:Ce:270:VAL:HB	1:Cg:270:VAL:HG22	1.83	0.60
1:Ci:183:GLN:HG3	1:Ci:184:GLU:H	1.64	0.60
1:Ae:183:GLN:HG3	1:Ae:184:GLU:H	1.64	0.60
1:Bm:183:GLN:HG3	1:Bm:184:GLU:H	1.64	0.60
1:Ck:188:PRO:O	1:Ck:191:GLY:N	2.29	0.60
1:Bu:188:PRO:O	1:Bu:191:GLY:N	2.29	0.60
1:Ag:183:GLN:HG3	1:Ag:184:GLU:H	1.64	0.60
1:Cg:183:GLN:HG3	1:Cg:184:GLU:H	1.64	0.60
1:Be:188:PRO:O	1:Be:191:GLY:N	2.29	0.60
1:Ao:188:PRO:O	1:Ao:191:GLY:N	2.29	0.60
1:Bm:270:VAL:HB	1:Bo:270:VAL:HG22	1.83	0.60
1:Bg:270:VAL:HB	1:Bi:270:VAL:HG22	1.84	0.60
1:By:270:VAL:HB	1:Ca:270:VAL:HG22	1.83	0.60
1:Ac:270:VAL:HB	1:Ae:270:VAL:HG22	1.83	0.59
1:Cq:270:VAL:HB	1:Cs:270:VAL:HG22	1.84	0.59
1:Ca:270:VAL:HB	1:Cc:270:VAL:HG22	1.84	0.59
1:Am:270:VAL:HB	1:Ao:270:VAL:HG22	1.84	0.59
1:Ao:270:VAL:HB	1:Aq:270:VAL:HG22	1.84	0.59
1:Ci:188:PRO:O	1:Ci:191:GLY:N	2.29	0.59
1:Bo:194:ARG:NH2	2:Bp:5:U:OP1	2.34	0.58
1:Bs:188:PRO:O	1:Bs:191:GLY:N	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cg:188:PRO:O	1:Cg:191:GLY:N	2.29	0.58
1:Bq:188:PRO:O	1:Bq:191:GLY:N	2.30	0.58
1:Bw:245:ILE:HD12	1:Co:228:ALA:HA	1.84	0.58
1:Aa:270:VAL:HB	1:Ac:270:VAL:HG22	1.86	0.58
1:Bc:188:PRO:O	1:Bc:191:GLY:N	2.29	0.58
1:Bk:270:VAL:HB	1:Bm:270:VAL:HG22	1.86	0.58
1:Ae:245:ILE:HG21	1:Aw:231:LEU:HB3	1.86	0.58
1:Aq:270:VAL:HB	1:As:270:VAL:HG22	1.86	0.58
1:Am:188:PRO:O	1:Am:191:GLY:N	2.29	0.58
1:Ba:188:PRO:O	1:Ba:191:GLY:N	2.29	0.58
1:As:245:ILE:HG21	1:Bk:231:LEU:HB3	1.86	0.58
1:Bw:245:ILE:HG21	1:Co:231:LEU:HB2	1.84	0.58
1:Ac:245:ILE:HG21	1:Au:231:LEU:HB3	1.86	0.58
1:Ca:245:ILE:HG21	1:Cs:231:LEU:HB3	1.86	0.58
1:Bc:270:VAL:HB	1:Be:270:VAL:HG22	1.86	0.58
1:Aw:245:ILE:HG21	1:Bo:231:LEU:HB3	1.86	0.57
1:By:245:ILE:HG21	1:Cq:231:LEU:HB3	1.85	0.57
1:Aq:245:ILE:HG21	1:Bi:231:LEU:HB3	1.86	0.57
1:Be:270:VAL:HB	1:Bg:270:VAL:HG22	1.84	0.57
1:Bi:245:ILE:HG21	1:Ca:231:LEU:HB3	1.86	0.57
1:Bi:270:VAL:HB	1:Bk:270:VAL:HG22	1.86	0.57
1:Cc:270:VAL:HB	1:Ce:270:VAL:HG22	1.86	0.57
1:Au:245:ILE:HG21	1:Bm:231:LEU:HB3	1.86	0.57
1:As:270:VAL:HB	1:Au:270:VAL:HG22	1.86	0.57
1:Aa:245:ILE:HG21	1:As:231:LEU:HB3	1.85	0.57
1:Ay:188:PRO:O	1:Ay:191:GLY:N	2.29	0.57
1:Ay:245:ILE:HG21	1:Bq:231:LEU:HB3	1.86	0.57
1:Bk:245:ILE:HG21	1:Cc:231:LEU:HB3	1.87	0.57
2:Bv:5:U:H3'	2:Bx:1:U:P	2.45	0.57
1:Ai:188:PRO:O	1:Ai:191:GLY:N	2.29	0.57
1:Bo:270:VAL:HB	1:Bq:270:VAL:HG22	1.87	0.57
1:Bw:236:THR:CG2	2:Bx:3:U:H1'	2.35	0.57
1:Ae:270:VAL:HB	1:Ag:270:VAL:HG22	1.87	0.57
1:Ag:245:ILE:HG21	1:Ay:231:LEU:HB3	1.86	0.57
1:Ao:245:ILE:HG21	1:Bg:231:LEU:HB3	1.86	0.57
1:Bo:188:PRO:O	1:Bo:191:GLY:N	2.29	0.57
1:Bu:245:ILE:HG21	1:Cm:231:LEU:HB3	1.86	0.57
1:Ai:163:ARG:NH1	2:Aj:3:U:P	2.78	0.56
1:Ak:270:VAL:HB	1:Am:270:VAL:HG22	1.86	0.56
1:Bg:245:ILE:HG21	1:By:231:LEU:HB3	1.87	0.56
1:Ak:188:PRO:O	1:Ak:191:GLY:N	2.29	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Aa:188:PRO:O	1:Aa:191:GLY:N	2.29	0.56
1:Ay:227:LYS:HG3	2:Az:4:U:C4	2.40	0.56
1:Bo:245:ILE:HG21	1:Cg:231:LEU:HB3	1.87	0.56
1:Ba:245:ILE:HG21	1:Bs:231:LEU:HB3	1.86	0.56
1:Bs:270:VAL:HB	1:Bu:270:VAL:HG22	1.88	0.56
1:Bu:270:VAL:HB	1:Bw:270:VAL:HG22	1.88	0.56
1:Ak:245:ILE:HG21	1:Bc:231:LEU:HB3	1.87	0.56
1:Ce:188:PRO:O	1:Ce:191:GLY:N	2.30	0.56
1:Aa:245:ILE:HG21	1:As:231:LEU:HB2	1.88	0.56
1:Ai:270:VAL:HB	1:Ak:270:VAL:HG22	1.88	0.56
1:Am:245:ILE:HG21	1:Be:231:LEU:HB3	1.86	0.56
1:Bq:245:ILE:HG21	1:Ci:231:LEU:HB3	1.87	0.56
1:Bs:245:ILE:HG21	1:Ck:231:LEU:HB3	1.86	0.56
1:Ai:245:ILE:HG21	1:Ba:231:LEU:HB3	1.87	0.55
1:Au:253:GLU:HA	1:Cc:225:GLN:NE2	2.21	0.55
1:Aw:270:VAL:HB	1:Ay:270:VAL:HG22	1.87	0.55
1:Bw:258:GLU:HG2	1:Co:247:THR:CG2	2.36	0.55
1:Ay:227:LYS:HG3	2:Az:4:U:N3	2.21	0.55
1:Ba:270:VAL:HB	1:Bc:270:VAL:HG22	1.88	0.55
1:Co:198:ASP:OD2	1:Co:218:ARG:NH2	2.36	0.55
1:Cg:270:VAL:HB	1:Ci:270:VAL:HG22	1.87	0.55
1:Ag:188:PRO:O	1:Ag:191:GLY:N	2.29	0.55
1:Be:245:ILE:HG21	1:Bw:231:LEU:HB3	1.87	0.55
1:Ca:198:ASP:OD2	1:Ca:218:ARG:NH2	2.36	0.55
1:Aa:245:ILE:HD12	1:As:228:ALA:HA	1.89	0.55
1:Bc:245:ILE:HG21	1:Bu:231:LEU:HB3	1.86	0.55
1:By:198:ASP:OD2	1:By:218:ARG:NH2	2.36	0.55
1:Ag:236:THR:CG2	2:Ah:3:U:H1'	2.37	0.55
1:Cc:198:ASP:OD2	1:Cc:218:ARG:NH2	2.36	0.55
1:Ck:270:VAL:HB	1:Cm:270:VAL:HG22	1.88	0.55
1:Cs:188:PRO:O	1:Cs:191:GLY:N	2.30	0.55
1:Ac:245:ILE:HG21	1:Au:231:LEU:HB2	1.89	0.55
1:Aw:245:ILE:HG21	1:Bo:231:LEU:HB2	1.89	0.55
1:As:245:ILE:HD12	1:Bk:228:ALA:HA	1.89	0.55
1:Ag:198:ASP:OD2	1:Ag:218:ARG:NH2	2.36	0.54
1:Aw:188:PRO:O	1:Aw:191:GLY:N	2.29	0.54
1:Bm:245:ILE:HG21	1:Ce:231:LEU:HB3	1.88	0.54
1:Bu:227:LYS:HG3	2:Bv:4:U:N3	2.22	0.54
1:Cc:188:PRO:O	1:Cc:191:GLY:N	2.29	0.54
1:Ay:253:GLU:HA	1:Cg:225:GLN:NE2	2.22	0.54
1:Bi:245:ILE:HG21	1:Ca:231:LEU:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:By:188:PRO:O	1:By:191:GLY:N	2.29	0.54
1:Ae:245:ILE:HD12	1:Aw:228:ALA:HA	1.89	0.54
1:Ak:253:GLU:HA	1:Bs:225:GLN:NE2	2.22	0.54
1:Bm:198:ASP:OD2	1:Bm:218:ARG:NH2	2.36	0.54
1:Ae:245:ILE:HG21	1:Aw:231:LEU:HB2	1.89	0.54
1:Bi:231:LEU:CD2	2:Bj:3:U:H2'	2.37	0.54
1:Ac:245:ILE:HD12	1:Au:228:ALA:HA	1.90	0.54
1:Aw:198:ASP:OD2	1:Aw:218:ARG:NH2	2.36	0.54
1:Bw:128:ASN:ND2	1:By:86:ILE:O	2.40	0.54
1:Aq:188:PRO:O	1:Aq:191:GLY:N	2.29	0.54
1:As:245:ILE:HG21	1:Bk:231:LEU:HB2	1.89	0.54
1:Au:245:ILE:HG21	1:Bm:231:LEU:HB2	1.90	0.54
1:Bi:198:ASP:OD2	1:Bi:218:ARG:NH2	2.36	0.54
1:Bu:128:ASN:ND2	1:Bw:86:ILE:O	2.41	0.54
1:Bw:198:ASP:OD2	1:Bw:218:ARG:NH2	2.36	0.54
1:Ai:236:THR:CG2	2:Aj:3:U:O2	2.55	0.54
1:Aq:245:ILE:HD12	1:Bi:228:ALA:HA	1.90	0.54
1:Aw:245:ILE:HD12	1:Bo:228:ALA:HA	1.90	0.54
1:Ay:236:THR:CG2	2:Az:3:U:H1'	2.37	0.54
1:Bk:198:ASP:OD2	1:Bk:218:ARG:NH2	2.36	0.54
1:Ca:245:ILE:HG21	1:Cs:231:LEU:HB2	1.90	0.54
1:Cm:198:ASP:OD2	1:Cm:218:ARG:NH2	2.36	0.54
1:Bk:253:GLU:HA	1:Cs:225:GLN:NE2	2.23	0.54
1:Bm:188:PRO:O	1:Bm:191:GLY:N	2.29	0.54
1:Ck:227:LYS:HG3	2:Cl:4:U:C4	2.43	0.54
1:Bg:245:ILE:HG21	1:By:231:LEU:HB2	1.90	0.54
1:Bg:198:ASP:OD2	1:Bg:218:ARG:NH2	2.36	0.53
1:Co:188:PRO:O	1:Co:191:GLY:N	2.29	0.53
1:Aq:245:ILE:HG21	1:Bi:231:LEU:HB2	1.89	0.53
1:Ay:245:ILE:HG21	1:Bq:231:LEU:HB2	1.90	0.53
1:Ao:245:ILE:HG21	1:Bg:231:LEU:HB2	1.90	0.53
1:Au:198:ASP:OD2	1:Au:218:ARG:NH2	2.36	0.53
1:By:245:ILE:HG21	1:Cq:231:LEU:HB2	1.89	0.53
1:By:245:ILE:HD12	1:Cq:228:ALA:HA	1.90	0.53
1:Ag:253:GLU:HA	1:Bo:225:GLN:NE2	2.24	0.53
1:Au:245:ILE:HD12	1:Bm:228:ALA:HA	1.90	0.53
1:Bc:253:GLU:HA	1:Ck:225:GLN:NE2	2.23	0.53
1:As:198:ASP:OD2	1:As:218:ARG:NH2	2.36	0.53
1:Bk:245:ILE:HG21	1:Cc:231:LEU:HB2	1.90	0.53
1:Bk:245:ILE:HD12	1:Cc:228:ALA:HA	1.91	0.53
1:Bs:194:ARG:NH2	2:Bt:5:U:OP1	2.37	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Co:127:GLU:HG3	1:Cq:86:ILE:CD1	2.38	0.53
1:Ae:198:ASP:OD2	1:Ae:218:ARG:NH2	2.36	0.53
1:Bi:245:ILE:HD12	1:Ca:228:ALA:HA	1.90	0.53
1:Ac:253:GLU:HA	1:Bk:225:GLN:NE2	2.24	0.53
1:Ag:245:ILE:HD12	1:Ay:228:ALA:HA	1.90	0.53
1:Aq:198:ASP:OD2	1:Aq:218:ARG:NH2	2.36	0.53
1:Ca:245:ILE:HD12	1:Cs:228:ALA:HA	1.91	0.53
1:Co:128:ASN:ND2	1:Cq:86:ILE:O	2.41	0.53
1:Ag:128:ASN:ND2	1:Ai:86:ILE:O	2.42	0.53
1:Ag:245:ILE:HG21	1:Ay:231:LEU:HB2	1.89	0.53
1:Bu:245:ILE:HD12	1:Cm:228:ALA:HA	1.90	0.53
1:Am:245:ILE:HG21	1:Be:231:LEU:HB2	1.90	0.53
1:As:227:LYS:HG3	2:At:4:U:C4	2.44	0.53
1:Ay:245:ILE:HD12	1:Bq:228:ALA:HA	1.90	0.53
1:Cq:188:PRO:O	1:Cq:191:GLY:N	2.29	0.53
1:Ao:245:ILE:HD12	1:Bg:228:ALA:HA	1.90	0.52
1:As:128:ASN:HD21	1:Au:87:SER:HA	1.75	0.52
1:Be:128:ASN:ND2	1:Bg:86:ILE:O	2.42	0.52
1:Bg:188:PRO:O	1:Bg:191:GLY:N	2.29	0.52
1:Bg:245:ILE:HD12	1:By:228:ALA:HA	1.90	0.52
1:Bu:245:ILE:HG21	1:Cm:231:LEU:HB2	1.90	0.52
1:Ca:188:PRO:O	1:Ca:191:GLY:N	2.29	0.52
1:Ao:128:ASN:ND2	1:Aq:86:ILE:O	2.42	0.52
1:As:253:GLU:HA	1:Ca:225:GLN:NE2	2.24	0.52
1:Bk:128:ASN:HD21	1:Bm:87:SER:HA	1.75	0.52
1:Aa:128:ASN:HD21	1:Ac:87:SER:HA	1.75	0.52
1:Ai:245:ILE:HG21	1:Ba:231:LEU:HB2	1.90	0.52
1:Aw:253:GLU:HA	1:Ce:225:GLN:NE2	2.25	0.52
1:Ay:128:ASN:ND2	1:Ba:86:ILE:O	2.42	0.52
1:Bi:194:ARG:NH2	2:Bj:5:U:OP1	2.39	0.52
1:Cg:128:ASN:HD21	1:Ci:87:SER:HA	1.75	0.52
1:Bu:198:ASP:OD2	1:Bu:218:ARG:NH2	2.36	0.52
1:Ac:198:ASP:OD2	1:Ac:218:ARG:NH2	2.36	0.52
1:Ba:245:ILE:HG21	1:Bs:231:LEU:HB2	1.90	0.52
1:Ba:245:ILE:HD12	1:Bs:228:ALA:HA	1.90	0.52
1:Bc:245:ILE:HD12	1:Bu:228:ALA:HA	1.91	0.52
1:Be:198:ASP:OD2	1:Be:218:ARG:NH2	2.36	0.52
1:Bk:188:PRO:O	1:Bk:191:GLY:N	2.29	0.52
1:Bq:127:GLU:HG3	1:Bs:86:ILE:CD1	2.39	0.52
1:Bs:245:ILE:HG21	1:Ck:231:LEU:HB2	1.90	0.52
1:Ci:127:GLU:HG3	1:Ck:86:ILE:CD1	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ck:198:ASP:OD2	1:Ck:218:ARG:NH2	2.36	0.52
1:Ae:128:ASN:HD21	1:Ag:87:SER:HA	1.75	0.52
1:Ag:127:GLU:HG3	1:Ai:86:ILE:CD1	2.39	0.52
1:Ak:245:ILE:HG21	1:Bc:231:LEU:HB2	1.90	0.52
1:Am:245:ILE:HD12	1:Be:228:ALA:HA	1.90	0.52
1:Bm:135:SER:HB2	1:Ce:203:ARG:HH22	1.75	0.52
1:Aa:253:GLU:HA	1:Bi:225:GLN:NE2	2.25	0.52
1:Ae:188:PRO:O	1:Ae:191:GLY:N	2.29	0.52
1:Ai:198:ASP:OD2	1:Ai:218:ARG:NH2	2.36	0.52
1:Ao:198:ASP:OD2	1:Ao:218:ARG:NH2	2.36	0.52
1:Ay:127:GLU:HG3	1:Ba:86:ILE:CD1	2.40	0.52
1:Ay:198:ASP:OD2	1:Ay:218:ARG:NH2	2.36	0.52
1:Bo:128:ASN:HD21	1:Bq:87:SER:HA	1.75	0.52
1:Bo:198:ASP:OD2	1:Bo:218:ARG:NH2	2.36	0.52
1:Bq:245:ILE:HG21	1:Ci:231:LEU:HB2	1.91	0.52
1:Bw:188:PRO:O	1:Bw:191:GLY:N	2.29	0.52
1:Cc:128:ASN:HD21	1:Ce:87:SER:HA	1.75	0.52
1:Aa:198:ASP:OD2	1:Aa:218:ARG:NH2	2.36	0.52
1:Ao:253:GLU:HA	1:Bw:225:GLN:NE2	2.24	0.52
1:Aw:128:ASN:HD21	1:Ay:87:SER:HA	1.75	0.52
1:Bg:128:ASN:ND2	1:Bi:86:ILE:O	2.42	0.52
1:Bm:128:ASN:ND2	1:Bo:86:ILE:O	2.43	0.52
1:Bw:260:VAL:HG22	1:By:266:THR:O	2.09	0.52
1:Ai:245:ILE:HD12	1:Ba:228:ALA:HA	1.91	0.52
1:Bc:245:ILE:HG21	1:Bu:231:LEU:HB2	1.90	0.52
1:Bq:128:ASN:ND2	1:Bs:86:ILE:O	2.42	0.52
1:Am:128:ASN:HD21	1:Ao:87:SER:HA	1.75	0.52
1:Aq:128:ASN:HD21	1:As:87:SER:HA	1.74	0.52
1:Bk:135:SER:HB2	1:Cc:203:ARG:HH22	1.75	0.52
1:Ca:135:SER:HB2	1:Cs:203:ARG:HH22	1.75	0.52
1:Ce:198:ASP:OD2	1:Ce:218:ARG:NH2	2.36	0.52
1:Cm:188:PRO:O	1:Cm:191:GLY:N	2.29	0.52
1:Ac:127:GLU:HG3	1:Ae:86:ILE:CD1	2.40	0.51
1:Am:196:LEU:O	1:Ao:220:ARG:NH1	2.43	0.51
1:Bm:245:ILE:HD12	1:Ce:228:ALA:HA	1.92	0.51
1:Bo:245:ILE:HG21	1:Cg:231:LEU:HB2	1.92	0.51
1:Bw:127:GLU:HG3	1:By:86:ILE:CD1	2.40	0.51
1:Ck:128:ASN:HD21	1:Cm:87:SER:HA	1.75	0.51
1:Cm:128:ASN:ND2	1:Co:86:ILE:O	2.43	0.51
1:Ak:245:ILE:HD12	1:Bc:228:ALA:HA	1.91	0.51
1:Au:127:GLU:HG3	1:Aw:86:ILE:CD1	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Au:188:PRO:O	1:Au:191:GLY:N	2.29	0.51
1:Ba:128:ASN:HD21	1:Bc:87:SER:HA	1.75	0.51
1:Be:128:ASN:HD21	1:Bg:87:SER:HA	1.75	0.51
1:Be:196:LEU:O	1:Bg:220:ARG:NH1	2.43	0.51
1:Bm:127:GLU:HG3	1:Bo:86:ILE:CD1	2.40	0.51
1:Bs:128:ASN:HD21	1:Bu:87:SER:HA	1.75	0.51
1:By:128:ASN:HD21	1:Ca:87:SER:HA	1.76	0.51
1:By:135:SER:HB2	1:Cq:203:ARG:HH22	1.75	0.51
1:Bi:128:ASN:HD21	1:Bk:87:SER:HA	1.75	0.51
1:Bs:245:ILE:HD12	1:Ck:228:ALA:HA	1.91	0.51
1:Bu:127:GLU:HG3	1:Bw:86:ILE:CD1	2.41	0.51
1:Bw:142:ASP:HB2	1:Cq:50:ILE:HD12	1.92	0.51
1:Ce:128:ASN:ND2	1:Cg:86:ILE:O	2.43	0.51
1:Ci:236:THR:CG2	2:Cj:3:U:H1'	2.40	0.51
1:Ai:128:ASN:HD21	1:Ak:87:SER:HA	1.75	0.51
1:Bg:127:GLU:HG3	1:Bi:86:ILE:CD1	2.41	0.51
1:Bg:128:ASN:HD21	1:Bi:87:SER:HA	1.76	0.51
1:Ce:127:GLU:HG3	1:Cg:86:ILE:CD1	2.41	0.51
1:Ao:128:ASN:HD21	1:Aq:87:SER:HA	1.76	0.51
1:Bk:194:ARG:NH1	2:Bl:5:U:OP1	2.42	0.51
1:Bo:245:ILE:HD12	1:Cg:228:ALA:HA	1.92	0.51
1:By:127:GLU:HG3	1:Ca:86:ILE:CD1	2.41	0.51
1:Co:270:VAL:HB	1:Cq:270:VAL:HG22	1.91	0.51
1:Ak:127:GLU:HG3	1:Am:86:ILE:CD1	2.41	0.51
1:Bq:245:ILE:HD12	1:Ci:228:ALA:HA	1.92	0.51
1:Ao:127:GLU:HG3	1:Aq:86:ILE:CD1	2.41	0.51
1:Bc:127:GLU:HG3	1:Be:86:ILE:CD1	2.41	0.51
1:Bu:196:LEU:O	1:Bw:220:ARG:NH1	2.44	0.51
1:Cq:127:GLU:HG3	1:Cs:86:ILE:CD1	2.41	0.51
1:Ac:135:SER:HB2	1:Au:203:ARG:HH22	1.76	0.51
1:Bi:253:GLU:HA	1:Cq:225:GLN:NE2	2.25	0.51
1:Cc:128:ASN:ND2	1:Ce:86:ILE:O	2.44	0.51
1:Cq:128:ASN:HD21	1:Cs:87:SER:HA	1.76	0.51
1:Aq:253:GLU:HA	1:By:225:GLN:NE2	2.26	0.51
1:Be:245:ILE:HG21	1:Bw:231:LEU:HB2	1.91	0.51
1:Bg:253:GLU:HA	1:Co:225:GLN:NE2	2.25	0.51
1:Bm:128:ASN:HD21	1:Bo:87:SER:HA	1.76	0.51
1:Co:172:VAL:HG21	1:Cq:71:LEU:CD1	2.41	0.51
1:Bc:135:SER:HB2	1:Bu:203:ARG:HH22	1.76	0.51
1:By:128:ASN:ND2	1:Ca:86:ILE:O	2.42	0.51
1:Am:231:LEU:CD2	2:An:3:U:H2'	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Be:245:ILE:HD12	1:Bw:228:ALA:HA	1.92	0.50
1:Ae:128:ASN:ND2	1:Ag:86:ILE:O	2.44	0.50
1:Bm:142:ASP:HB2	1:Cg:50:ILE:HD12	1.93	0.50
1:Bm:245:ILE:HG21	1:Ce:231:LEU:HB2	1.92	0.50
1:Ca:127:GLU:HG3	1:Cc:86:ILE:CD1	2.41	0.50
1:Ca:128:ASN:HD21	1:Cc:87:SER:HA	1.77	0.50
1:Ci:128:ASN:ND2	1:Ck:86:ILE:O	2.42	0.50
1:Ck:196:LEU:O	1:Cm:220:ARG:NH1	2.44	0.50
1:Ac:128:ASN:HD21	1:Ae:87:SER:HA	1.76	0.50
1:Ay:135:SER:HB2	1:Bq:203:ARG:HH22	1.76	0.50
1:Bc:198:ASP:OD2	1:Bc:218:ARG:NH2	2.36	0.50
1:Be:127:GLU:HG3	1:Bg:86:ILE:CD1	2.41	0.50
1:Ai:196:LEU:O	1:Ak:220:ARG:NH1	2.44	0.50
1:Am:198:ASP:OD2	1:Am:218:ARG:NH2	2.36	0.50
1:Au:196:LEU:O	1:Aw:220:ARG:NH1	2.44	0.50
1:Aw:128:ASN:ND2	1:Ay:86:ILE:O	2.44	0.50
1:Bk:142:ASP:HB2	1:Ce:50:ILE:HD12	1.94	0.50
1:Ce:128:ASN:HD21	1:Cg:87:SER:HA	1.76	0.50
1:Ay:128:ASN:HD21	1:Ba:87:SER:HA	1.77	0.50
1:Bo:135:SER:HB2	1:Cg:203:ARG:HH22	1.76	0.50
1:Bs:198:ASP:OD2	1:Bs:218:ARG:NH2	2.36	0.50
1:Cm:127:GLU:HG3	1:Co:86:ILE:CD1	2.42	0.50
1:Co:128:ASN:HD21	1:Cq:87:SER:HA	1.77	0.50
1:Aa:135:SER:HB2	1:As:203:ARG:HH22	1.77	0.50
1:Ag:135:SER:HB2	1:Ay:203:ARG:HH22	1.76	0.50
1:Ai:135:SER:HB2	1:Ba:203:ARG:HH22	1.77	0.50
1:Am:127:GLU:HG3	1:Ao:86:ILE:CD1	2.41	0.50
1:Am:253:GLU:HA	1:Bu:225:GLN:NE2	2.25	0.50
1:Bg:135:SER:HB2	1:By:203:ARG:HH22	1.77	0.50
1:Bm:156:GLU:HB3	1:Ce:214:ARG:HB3	1.94	0.50
1:Bu:128:ASN:HD21	1:Bw:87:SER:HA	1.75	0.50
1:Bu:142:ASP:HB2	1:Co:50:ILE:HD12	1.93	0.50
1:Ae:135:SER:HB2	1:Aw:203:ARG:HH22	1.77	0.50
1:Aq:196:LEU:O	1:As:220:ARG:NH1	2.43	0.50
1:Ba:135:SER:HB2	1:Bs:203:ARG:HH22	1.77	0.50
1:Bi:135:SER:HB2	1:Ca:203:ARG:HH22	1.77	0.50
1:Bi:188:PRO:O	1:Bi:191:GLY:N	2.29	0.50
1:Bs:135:SER:HB2	1:Ck:203:ARG:HH22	1.77	0.50
1:Co:196:LEU:O	1:Cq:220:ARG:NH1	2.44	0.50
1:Ae:253:GLU:HA	1:Bm:225:GLN:NE2	2.27	0.50
1:Ag:128:ASN:HD21	1:Ai:87:SER:HA	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ai:253:GLU:HA	1:Bq:225:GLN:NE2	2.26	0.50
1:Bu:135:SER:HB2	1:Cm:203:ARG:HH22	1.76	0.50
1:Ci:198:ASP:OD2	1:Ci:218:ARG:NH2	2.36	0.50
1:Au:128:ASN:HD21	1:Aw:87:SER:HA	1.76	0.50
1:Au:135:SER:HB2	1:Bm:203:ARG:HH22	1.76	0.50
1:Ba:196:LEU:O	1:Bc:220:ARG:NH1	2.44	0.50
1:Bq:135:SER:HB2	1:Ci:203:ARG:HH22	1.76	0.50
1:Bq:196:LEU:O	1:Bs:220:ARG:NH1	2.44	0.50
1:Cq:196:LEU:O	1:Cs:220:ARG:NH1	2.44	0.50
1:Ao:135:SER:HB2	1:Bg:203:ARG:HH22	1.77	0.49
1:Ao:196:LEU:O	1:Aq:220:ARG:NH1	2.44	0.49
1:Ay:172:VAL:HG21	1:Ba:71:LEU:CD1	2.42	0.49
1:Bo:128:ASN:ND2	1:Bq:86:ILE:O	2.44	0.49
1:Bo:156:GLU:HB3	1:Cg:214:ARG:HB3	1.94	0.49
1:By:196:LEU:O	1:Ca:220:ARG:NH1	2.44	0.49
1:Am:135:SER:HB2	1:Be:203:ARG:HH22	1.76	0.49
1:As:188:PRO:O	1:As:191:GLY:N	2.29	0.49
1:Bq:142:ASP:HB2	1:Ck:50:ILE:HD12	1.94	0.49
1:By:172:VAL:HG21	1:Ca:71:LEU:CD1	2.43	0.49
1:Ci:196:LEU:O	1:Ck:220:ARG:NH1	2.44	0.49
1:Cm:128:ASN:HD21	1:Co:87:SER:HA	1.77	0.49
1:Aq:128:ASN:ND2	1:As:86:ILE:O	2.44	0.49
1:Au:128:ASN:ND2	1:Aw:86:ILE:O	2.43	0.49
1:Ba:253:GLU:HA	1:Ci:225:GLN:NE2	2.26	0.49
1:Bm:196:LEU:O	1:Bo:220:ARG:NH1	2.44	0.49
1:Bo:142:ASP:HB2	1:Ci:50:ILE:HD12	1.94	0.49
1:Bq:128:ASN:HD21	1:Bs:87:SER:HA	1.77	0.49
1:Bs:196:LEU:O	1:Bu:220:ARG:NH1	2.44	0.49
1:Ci:172:VAL:HG21	1:Ck:71:LEU:CD1	2.42	0.49
1:Ae:163:ARG:NH1	2:Af:3:U:P	2.85	0.49
1:Ao:172:VAL:HG21	1:Aq:71:LEU:CD1	2.43	0.49
1:Aq:135:SER:HB2	1:Bi:203:ARG:HH22	1.77	0.49
1:Be:253:GLU:HA	1:Cm:225:GLN:NE2	2.27	0.49
1:Bg:172:VAL:HG21	1:Bi:71:LEU:CD1	2.42	0.49
1:Ca:156:GLU:HB3	1:Cs:214:ARG:HB3	1.94	0.49
1:Ae:196:LEU:O	1:Ag:220:ARG:NH1	2.44	0.49
1:Ak:236:THR:CG2	2:Al:3:U:H1'	2.43	0.49
1:Ay:196:LEU:O	1:Ba:220:ARG:NH1	2.44	0.49
1:Ak:128:ASN:ND2	1:Am:86:ILE:O	2.44	0.49
1:Ak:135:SER:HB2	1:Bc:203:ARG:HH22	1.76	0.49
1:Aw:135:SER:HB2	1:Bo:203:ARG:HH22	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bc:196:LEU:O	1:Be:220:ARG:NH1	2.45	0.49
1:Bi:196:LEU:O	1:Bk:220:ARG:NH1	2.44	0.49
1:Cq:128:ASN:ND2	1:Cs:86:ILE:O	2.42	0.49
1:Cq:172:VAL:HG21	1:Cs:71:LEU:CD1	2.43	0.49
1:Bg:196:LEU:O	1:Bi:220:ARG:NH1	2.44	0.49
1:Bk:156:GLU:HB3	1:Cc:214:ARG:HB3	1.94	0.49
1:Bq:172:VAL:HG21	1:Bs:71:LEU:CD1	2.42	0.49
1:Ac:188:PRO:O	1:Ac:191:GLY:N	2.29	0.49
1:Ai:128:ASN:ND2	1:Ak:86:ILE:O	2.45	0.49
1:Ak:198:ASP:OD2	1:Ak:218:ARG:NH2	2.36	0.49
1:As:135:SER:HB2	1:Bk:203:ARG:HH22	1.77	0.49
1:Bi:142:ASP:HB2	1:Cc:50:ILE:HD12	1.95	0.49
1:Bw:128:ASN:HD21	1:By:87:SER:HA	1.77	0.49
1:Cc:196:LEU:O	1:Ce:220:ARG:NH1	2.45	0.49
1:Aa:128:ASN:ND2	1:Ac:86:ILE:O	2.44	0.49
1:Ac:172:VAL:HG21	1:Ae:71:LEU:CD1	2.43	0.49
1:Ag:172:VAL:HG21	1:Ai:71:LEU:CD1	2.42	0.49
1:Ak:128:ASN:HD21	1:Am:87:SER:HA	1.77	0.49
1:Bu:156:GLU:HB3	1:Cm:214:ARG:HB3	1.94	0.49
1:Ce:172:VAL:HG21	1:Cg:71:LEU:CD1	2.43	0.49
1:Cg:128:ASN:ND2	1:Ci:86:ILE:O	2.44	0.49
1:Cg:196:LEU:O	1:Ci:220:ARG:NH1	2.44	0.49
1:Ci:128:ASN:HD21	1:Ck:87:SER:HA	1.77	0.49
1:Ac:156:GLU:HB3	1:Au:214:ARG:HB3	1.95	0.48
1:Aw:122:MET:SD	1:Aw:172:VAL:HG12	2.53	0.48
1:Bc:128:ASN:HD21	1:Be:87:SER:HA	1.77	0.48
1:Bg:194:ARG:NH2	2:Bh:5:U:OP1	2.43	0.48
2:Bh:5:U:O3'	2:Bj:1:U:P	2.71	0.48
1:Bi:127:GLU:HG3	1:Bk:86:ILE:CD1	2.43	0.48
1:Bs:156:GLU:HB3	1:Ck:214:ARG:HB3	1.94	0.48
1:Bw:196:LEU:O	1:By:220:ARG:NH1	2.46	0.48
1:Ac:128:ASN:ND2	1:Ae:86:ILE:O	2.43	0.48
1:Au:172:VAL:HG21	1:Aw:71:LEU:CD1	2.43	0.48
1:Bw:245:ILE:CG2	1:Co:231:LEU:HB2	2.43	0.48
1:Aa:122:MET:SD	1:Aa:172:VAL:HG12	2.54	0.48
1:Bm:122:MET:SD	1:Bm:172:VAL:HG12	2.54	0.48
1:Bw:122:MET:SD	1:Bw:172:VAL:HG12	2.54	0.48
1:Cc:122:MET:SD	1:Cc:172:VAL:HG12	2.54	0.48
1:Ag:196:LEU:O	1:Ai:220:ARG:NH1	2.44	0.48
1:Ak:196:LEU:O	1:Am:220:ARG:NH1	2.45	0.48
1:Am:172:VAL:HG21	1:Ao:71:LEU:CD1	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Aq:127:GLU:HG3	1:As:86:ILE:CD1	2.43	0.48
1:Bg:122:MET:SD	1:Bg:172:VAL:HG12	2.54	0.48
1:As:142:ASP:HB2	1:Bm:50:ILE:HD12	1.96	0.48
1:Au:122:MET:SD	1:Au:172:VAL:HG12	2.54	0.48
1:Aw:127:GLU:HG3	1:Ay:86:ILE:CD1	2.43	0.48
1:Aw:156:GLU:HB3	1:Bo:214:ARG:HB3	1.95	0.48
1:Bc:172:VAL:HG21	1:Be:71:LEU:CD1	2.44	0.48
1:Be:135:SER:HB2	1:Bw:203:ARG:HH22	1.78	0.48
1:Bi:122:MET:SD	1:Bi:172:VAL:HG12	2.54	0.48
1:Bm:145:GLU:CD	1:Cg:52:ARG:HH12	2.21	0.48
1:Ac:122:MET:SD	1:Ac:172:VAL:HG12	2.54	0.48
1:Ae:127:GLU:HG3	1:Ag:86:ILE:CD1	2.43	0.48
1:Am:122:MET:SD	1:Am:172:VAL:HG12	2.54	0.48
1:Am:128:ASN:ND2	1:Ao:86:ILE:O	2.42	0.48
1:As:122:MET:SD	1:As:172:VAL:HG12	2.54	0.48
1:Bc:156:GLU:HB3	1:Bu:214:ARG:HB3	1.95	0.48
1:Bi:128:ASN:ND2	1:Bk:86:ILE:O	2.44	0.48
1:Bm:172:VAL:HG21	1:Bo:71:LEU:CD1	2.43	0.48
1:By:122:MET:SD	1:By:172:VAL:HG12	2.54	0.48
1:Ce:122:MET:SD	1:Ce:172:VAL:HG12	2.54	0.48
1:Co:122:MET:SD	1:Co:172:VAL:HG12	2.53	0.48
1:Cq:122:MET:SD	1:Cq:172:VAL:HG12	2.54	0.48
1:Cs:122:MET:SD	1:Cs:172:VAL:HG12	2.54	0.48
1:Aa:127:GLU:HG3	1:Ac:86:ILE:CD1	2.43	0.48
1:Aq:122:MET:SD	1:Aq:172:VAL:HG12	2.54	0.48
1:As:127:GLU:HG3	1:Au:86:ILE:CD1	2.43	0.48
1:As:156:GLU:HB3	1:Bk:214:ARG:HB3	1.96	0.48
1:Au:142:ASP:HB2	1:Bo:50:ILE:HD12	1.96	0.48
1:Bi:156:GLU:HB3	1:Ca:214:ARG:HB3	1.95	0.48
1:Ca:122:MET:SD	1:Ca:172:VAL:HG12	2.54	0.48
1:Ca:196:LEU:O	1:Cc:220:ARG:NH1	2.44	0.48
1:Cc:127:GLU:HG3	1:Ce:86:ILE:CD1	2.43	0.48
1:Ce:196:LEU:O	1:Cg:220:ARG:NH1	2.44	0.48
1:Cg:122:MET:SD	1:Cg:172:VAL:HG12	2.54	0.48
1:Cm:172:VAL:HG21	1:Co:71:LEU:CD1	2.44	0.48
1:Ag:142:ASP:HB2	1:Ba:50:ILE:HD12	1.96	0.48
1:Ak:142:ASP:HB2	1:Be:50:ILE:HD12	1.95	0.48
1:Ak:156:GLU:HB3	1:Bc:214:ARG:HB3	1.95	0.48
1:Ak:239:PHE:CE1	1:Ba:196:LEU:HD13	2.49	0.48
1:Aw:196:LEU:O	1:Ay:220:ARG:NH1	2.44	0.48
1:Ba:198:ASP:OD2	1:Ba:218:ARG:NH2	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Be:172:VAL:HG21	1:Bg:71:LEU:CD1	2.44	0.48
1:Bk:122:MET:SD	1:Bk:172:VAL:HG12	2.54	0.48
1:Bk:127:GLU:HG3	1:Bm:86:ILE:CD1	2.43	0.48
1:Bq:156:GLU:HB3	1:Ci:214:ARG:HB3	1.94	0.48
1:Cm:122:MET:SD	1:Cm:172:VAL:HG12	2.54	0.48
1:Ac:142:ASP:HB2	1:Aw:50:ILE:HD12	1.96	0.48
1:Ag:122:MET:SD	1:Ag:172:VAL:HG12	2.54	0.48
1:Am:156:GLU:HB3	1:Be:214:ARG:HB3	1.95	0.48
1:Aw:172:VAL:HG21	1:Ay:71:LEU:CD1	2.44	0.48
1:Ba:128:ASN:ND2	1:Bc:86:ILE:O	2.45	0.48
1:Bo:196:LEU:O	1:Bq:220:ARG:NH1	2.44	0.48
1:Cg:127:GLU:HG3	1:Ci:86:ILE:CD1	2.43	0.48
1:Cs:198:ASP:OD2	1:Cs:218:ARG:NH2	2.36	0.48
1:Ag:156:GLU:HB3	1:Ay:214:ARG:HB3	1.95	0.48
1:Ay:122:MET:SD	1:Ay:172:VAL:HG12	2.54	0.48
1:Ay:142:ASP:HB2	1:Bs:50:ILE:HD12	1.96	0.48
1:Be:122:MET:SD	1:Be:172:VAL:HG12	2.54	0.48
1:Bk:254:ARG:HD2	1:Cs:229:ALA:HB2	1.96	0.48
1:Ck:163:ARG:NH1	2:Cl:3:U:P	2.87	0.48
1:Aa:196:LEU:O	1:Ac:220:ARG:NH1	2.45	0.47
1:Ae:122:MET:SD	1:Ae:172:VAL:HG12	2.53	0.47
1:Ag:239:PHE:CE1	1:Aw:196:LEU:HD13	2.49	0.47
1:Ai:236:THR:HG23	2:Aj:3:U:O2	2.14	0.47
1:Bm:239:PHE:CE1	1:Cc:196:LEU:HD13	2.49	0.47
1:Bo:122:MET:SD	1:Bo:172:VAL:HG12	2.53	0.47
1:Bq:198:ASP:OD2	1:Bq:218:ARG:NH2	2.36	0.47
1:By:156:GLU:HB3	1:Cq:214:ARG:HB3	1.95	0.47
1:Cg:172:VAL:HG21	1:Ci:71:LEU:CD1	2.44	0.47
1:Ci:122:MET:SD	1:Ci:172:VAL:HG12	2.54	0.47
1:Ai:156:GLU:HB3	1:Ba:214:ARG:HB3	1.95	0.47
1:Ak:122:MET:SD	1:Ak:172:VAL:HG12	2.54	0.47
1:Ao:122:MET:SD	1:Ao:172:VAL:HG12	2.54	0.47
1:Ay:239:PHE:CE1	1:Bo:196:LEU:HD13	2.49	0.47
1:Ba:156:GLU:HB3	1:Bs:214:ARG:HB3	1.95	0.47
1:Bc:128:ASN:ND2	1:Be:86:ILE:O	2.44	0.47
1:Bc:239:PHE:CE1	1:Bs:196:LEU:HD13	2.49	0.47
1:Bo:227:LYS:HG3	2:Bp:4:U:C4	2.48	0.47
1:Bs:172:VAL:HG21	1:Bu:71:LEU:CD1	2.44	0.47
1:Ck:122:MET:SD	1:Ck:172:VAL:HG12	2.54	0.47
1:Aa:172:VAL:HG21	1:Ac:71:LEU:CD1	2.45	0.47
1:Ai:122:MET:SD	1:Ai:172:VAL:HG12	2.54	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ak:172:VAL:HG21	1:Am:71:LEU:CD1	2.44	0.47
1:Ak:254:ARG:HD2	1:Bs:229:ALA:HB2	1.97	0.47
1:As:128:ASN:ND2	1:Au:86:ILE:O	2.44	0.47
1:Ba:122:MET:SD	1:Ba:172:VAL:HG12	2.54	0.47
1:Bo:127:GLU:HG3	1:Bq:86:ILE:CD1	2.43	0.47
1:By:142:ASP:HB2	1:Cs:50:ILE:HD12	1.97	0.47
1:Ca:128:ASN:ND2	1:Cc:86:ILE:O	2.43	0.47
1:Aa:142:ASP:HB2	1:Au:50:ILE:HD12	1.97	0.47
1:Aq:142:ASP:HB2	1:Bk:50:ILE:HD12	1.97	0.47
1:Ba:172:VAL:HG21	1:Bc:71:LEU:CD1	2.45	0.47
1:Bs:122:MET:SD	1:Bs:172:VAL:HG12	2.53	0.47
1:Bu:122:MET:SD	1:Bu:172:VAL:HG12	2.54	0.47
1:Cc:172:VAL:HG21	1:Ce:71:LEU:CD1	2.45	0.47
1:Cg:198:ASP:OD2	1:Cg:218:ARG:NH2	2.36	0.47
1:Cm:196:LEU:O	1:Co:220:ARG:NH1	2.47	0.47
1:Au:156:GLU:HB3	1:Bm:214:ARG:HB3	1.95	0.47
1:Aw:142:ASP:HB2	1:Bq:50:ILE:HD12	1.97	0.47
1:Bg:142:ASP:HB2	1:Ca:50:ILE:HD12	1.97	0.47
1:Bk:128:ASN:ND2	1:Bm:86:ILE:O	2.44	0.47
1:Bk:172:VAL:HG21	1:Bm:71:LEU:CD1	2.45	0.47
1:Bq:145:GLU:CD	1:Ck:52:ARG:HH12	2.22	0.47
1:Bs:127:GLU:HG3	1:Bu:86:ILE:CD1	2.44	0.47
1:Ca:172:VAL:HG21	1:Cc:71:LEU:CD1	2.44	0.47
1:Ae:172:VAL:HG21	1:Ag:71:LEU:CD1	2.44	0.47
1:Ag:254:ARG:HD2	1:Bo:229:ALA:HB2	1.96	0.47
1:Ay:156:GLU:HB3	1:Bq:214:ARG:HB3	1.95	0.47
1:Bk:259:ASP:OD2	1:Bk:265:HIS:ND1	2.48	0.47
1:Bs:142:ASP:HB2	1:Cm:50:ILE:HD12	1.96	0.47
1:Ck:127:GLU:HG3	1:Cm:86:ILE:CD1	2.44	0.47
1:Aa:156:GLU:HB3	1:As:214:ARG:HB3	1.96	0.47
1:Ac:259:ASP:OD2	1:Ac:265:HIS:ND1	2.48	0.47
1:Ae:142:ASP:HB2	1:Ay:50:ILE:HD12	1.97	0.47
1:Ae:156:GLU:HB3	1:Aw:214:ARG:HB3	1.95	0.47
1:Ae:259:ASP:OD2	1:Ae:265:HIS:ND1	2.48	0.47
1:Ai:127:GLU:HG3	1:Ak:86:ILE:CD1	2.44	0.47
1:Ai:142:ASP:HB2	1:Bc:50:ILE:HD12	1.96	0.47
1:Ai:172:VAL:HG21	1:Ak:71:LEU:CD1	2.44	0.47
1:Ai:259:ASP:OD2	1:Ai:265:HIS:ND1	2.48	0.47
1:Ao:156:GLU:HB3	1:Bg:214:ARG:HB3	1.95	0.47
1:As:172:VAL:HG21	1:Au:71:LEU:CD1	2.45	0.47
1:Au:259:ASP:OD2	1:Au:265:HIS:ND1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ba:127:GLU:HG3	1:Bc:86:ILE:CD1	2.44	0.47
1:Ba:259:ASP:OD2	1:Ba:265:HIS:ND1	2.48	0.47
1:Bc:122:MET:SD	1:Bc:172:VAL:HG12	2.54	0.47
1:Be:142:ASP:HB2	1:By:50:ILE:HD12	1.97	0.47
1:Be:259:ASP:OD2	1:Be:265:HIS:ND1	2.48	0.47
1:Bw:236:THR:HG21	2:Bx:3:U:H1'	1.97	0.47
1:Ca:259:ASP:OD2	1:Ca:265:HIS:ND1	2.48	0.47
1:Ck:172:VAL:HG21	1:Cm:71:LEU:CD1	2.44	0.47
1:Cm:259:ASP:OD2	1:Cm:265:HIS:ND1	2.48	0.47
1:Ac:196:LEU:O	1:Ae:220:ARG:NH1	2.44	0.47
1:Ai:138:TRP:CD1	1:Ai:151:LEU:HD13	2.50	0.47
1:Ao:259:ASP:OD2	1:Ao:265:HIS:ND1	2.48	0.47
1:As:196:LEU:O	1:Au:220:ARG:NH1	2.45	0.47
1:As:259:ASP:OD2	1:As:265:HIS:ND1	2.48	0.47
1:Bi:172:VAL:HG21	1:Bk:71:LEU:CD1	2.45	0.47
1:Bi:259:ASP:OD2	1:Bi:265:HIS:ND1	2.48	0.47
1:Bq:122:MET:SD	1:Bq:172:VAL:HG12	2.54	0.47
1:Cc:259:ASP:OD2	1:Cc:265:HIS:ND1	2.48	0.47
1:Ci:259:ASP:OD2	1:Ci:265:HIS:ND1	2.48	0.47
1:Cq:138:TRP:CD1	1:Cq:151:LEU:HD13	2.50	0.47
1:Cq:259:ASP:OD2	1:Cq:265:HIS:ND1	2.48	0.47
1:Aa:259:ASP:OD2	1:Aa:265:HIS:ND1	2.48	0.47
1:Au:254:ARG:HD2	1:Cc:229:ALA:HB2	1.97	0.47
1:Aw:259:ASP:OD2	1:Aw:265:HIS:ND1	2.48	0.47
1:Bg:138:TRP:CD1	1:Bg:151:LEU:HD13	2.50	0.47
1:Bi:138:TRP:CD1	1:Bi:151:LEU:HD13	2.50	0.47
1:Bm:259:ASP:OD2	1:Bm:265:HIS:ND1	2.48	0.47
1:Bu:259:ASP:OD2	1:Bu:265:HIS:ND1	2.48	0.47
1:Bw:259:ASP:OD2	1:Bw:265:HIS:ND1	2.48	0.47
1:Cc:138:TRP:CD1	1:Cc:151:LEU:HD13	2.50	0.47
1:Cs:259:ASP:OD2	1:Cs:265:HIS:ND1	2.48	0.47
1:Aa:254:ARG:HD2	1:Bi:229:ALA:HB2	1.97	0.47
1:Ao:138:TRP:CD1	1:Ao:151:LEU:HD13	2.50	0.47
1:Au:239:PHE:CE1	1:Bk:196:LEU:HD13	2.50	0.47
1:Bc:138:TRP:CD1	1:Bc:151:LEU:HD13	2.50	0.47
1:Bo:172:VAL:HG21	1:Bq:71:LEU:CD1	2.44	0.47
1:Bq:259:ASP:OD2	1:Bq:265:HIS:ND1	2.48	0.47
1:By:138:TRP:CD1	1:By:151:LEU:HD13	2.50	0.47
1:Ci:138:TRP:CD1	1:Ci:151:LEU:HD13	2.50	0.47
1:Ck:259:ASP:OD2	1:Ck:265:HIS:ND1	2.48	0.47
1:Aa:138:TRP:CD1	1:Aa:151:LEU:HD13	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ac:138:TRP:CD1	1:Ac:151:LEU:HD13	2.50	0.46
1:Ac:254:ARG:HD2	1:Bk:229:ALA:HB2	1.97	0.46
1:Ag:259:ASP:OD2	1:Ag:265:HIS:ND1	2.48	0.46
1:Ak:259:ASP:OD2	1:Ak:265:HIS:ND1	2.48	0.46
1:Am:142:ASP:HB2	1:Bg:50:ILE:HD12	1.97	0.46
1:Am:259:ASP:OD2	1:Am:265:HIS:ND1	2.48	0.46
1:Aq:172:VAL:HG21	1:As:71:LEU:CD1	2.45	0.46
1:Bu:172:VAL:HG21	1:Bw:71:LEU:CD1	2.45	0.46
1:Ck:138:TRP:CD1	1:Ck:151:LEU:HD13	2.50	0.46
1:Ak:253:GLU:HA	1:Bs:225:GLN:HE22	1.80	0.46
1:Am:138:TRP:CD1	1:Am:151:LEU:HD13	2.50	0.46
1:As:254:ARG:HD2	1:Ca:229:ALA:HB2	1.98	0.46
1:Au:138:TRP:CD1	1:Au:151:LEU:HD13	2.50	0.46
1:Ay:253:GLU:HA	1:Cg:225:GLN:HE22	1.80	0.46
1:Ba:138:TRP:CD1	1:Ba:151:LEU:HD13	2.50	0.46
1:Be:138:TRP:CD1	1:Be:151:LEU:HD13	2.50	0.46
1:Bg:156:GLU:HB3	1:By:214:ARG:HB3	1.95	0.46
1:Bg:259:ASP:OD2	1:Bg:265:HIS:ND1	2.48	0.46
1:Bk:138:TRP:CD1	1:Bk:151:LEU:HD13	2.50	0.46
1:Bk:196:LEU:O	1:Bm:220:ARG:NH1	2.45	0.46
1:Bo:138:TRP:CD1	1:Bo:151:LEU:HD13	2.50	0.46
1:Bs:259:ASP:OD2	1:Bs:265:HIS:ND1	2.48	0.46
1:Ce:259:ASP:OD2	1:Ce:265:HIS:ND1	2.48	0.46
1:Co:260:VAL:HG22	1:Cq:266:THR:O	2.15	0.46
1:Ag:138:TRP:CD1	1:Ag:151:LEU:HD13	2.50	0.46
1:Aq:138:TRP:CD1	1:Aq:151:LEU:HD13	2.50	0.46
1:Aq:156:GLU:HB3	1:Bi:214:ARG:HB3	1.95	0.46
1:As:239:PHE:CE1	1:Bi:196:LEU:HD13	2.50	0.46
1:Au:253:GLU:HA	1:Cc:225:GLN:HE22	1.79	0.46
1:Aw:138:TRP:CD1	1:Aw:151:LEU:HD13	2.50	0.46
1:Ba:142:ASP:HB2	1:Bu:50:ILE:HD12	1.96	0.46
1:Bq:138:TRP:CD1	1:Bq:151:LEU:HD13	2.50	0.46
1:Bs:128:ASN:ND2	1:Bu:86:ILE:O	2.45	0.46
1:Bu:138:TRP:CD1	1:Bu:151:LEU:HD13	2.50	0.46
1:Bw:138:TRP:CD1	1:Bw:151:LEU:HD13	2.50	0.46
1:Bw:227:LYS:HG3	2:Bx:4:U:N3	2.31	0.46
1:By:259:ASP:OD2	1:By:265:HIS:ND1	2.48	0.46
1:Ca:138:TRP:CD1	1:Ca:151:LEU:HD13	2.50	0.46
1:Cc:239:PHE:CE1	1:Cs:196:LEU:HD13	2.50	0.46
1:Cs:138:TRP:CD1	1:Cs:151:LEU:HD13	2.50	0.46
1:Ao:142:ASP:HB2	1:Bi:50:ILE:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Aq:259:ASP:OD2	1:Aq:265:HIS:ND1	2.48	0.46
1:Bw:135:SER:HB2	1:Co:203:ARG:HH22	1.80	0.46
1:Ce:138:TRP:CD1	1:Ce:151:LEU:HD13	2.50	0.46
1:Co:138:TRP:CD1	1:Co:151:LEU:HD13	2.50	0.46
1:Am:254:ARG:HD2	1:Bu:229:ALA:HB2	1.98	0.46
1:Be:254:ARG:HD2	1:Cm:229:ALA:HB2	1.98	0.46
1:Bq:239:PHE:CE1	1:Cg:196:LEU:HD13	2.51	0.46
1:Bu:236:THR:CG2	2:Bv:3:U:H1'	2.46	0.46
1:Bw:172:VAL:HG21	1:By:71:LEU:CD1	2.45	0.46
1:Co:259:ASP:OD2	1:Co:265:HIS:ND1	2.48	0.46
1:Aa:239:PHE:CE1	1:Aq:196:LEU:HD13	2.50	0.46
1:Ay:194:ARG:NH2	2:Az:5:U:OP1	2.48	0.46
1:Ay:259:ASP:OD2	1:Ay:265:HIS:ND1	2.48	0.46
1:Bo:259:ASP:OD2	1:Bo:265:HIS:ND1	2.48	0.46
1:Bs:138:TRP:CD1	1:Bs:151:LEU:HD13	2.50	0.46
1:Bw:156:GLU:HB3	1:Co:214:ARG:HB3	1.97	0.46
1:Cg:259:ASP:OD2	1:Cg:265:HIS:ND1	2.48	0.46
1:Cq:198:ASP:OD2	1:Cq:218:ARG:NH2	2.36	0.46
1:Ak:138:TRP:CD1	1:Ak:151:LEU:HD13	2.50	0.46
1:Ak:145:GLU:CD	1:Be:52:ARG:HH12	2.23	0.46
1:Aq:194:ARG:NH1	2:Ar:5:U:OP1	2.47	0.46
1:Bc:259:ASP:OD2	1:Bc:265:HIS:ND1	2.48	0.46
1:Bk:239:PHE:CE1	1:Ca:196:LEU:HD13	2.50	0.46
1:Bk:253:GLU:HA	1:Cs:225:GLN:HE22	1.81	0.46
1:Bw:145:GLU:CD	1:Cq:52:ARG:HH12	2.23	0.46
1:Ao:194:ARG:NH2	2:Ap:5:U:OP1	2.45	0.46
1:Bc:253:GLU:HA	1:Ck:225:GLN:HE22	1.81	0.46
1:Cg:138:TRP:CD1	1:Cg:151:LEU:HD13	2.50	0.46
1:Ac:239:PHE:CE1	1:As:196:LEU:HD13	2.50	0.46
1:Am:194:ARG:NH1	2:An:5:U:OP1	2.44	0.46
1:Aw:239:PHE:CE1	1:Bm:196:LEU:HD13	2.51	0.46
1:Ay:138:TRP:CD1	1:Ay:151:LEU:HD13	2.50	0.46
1:Ba:105:LYS:O	1:Ba:105:LYS:HG2	2.16	0.46
1:Bi:145:GLU:CD	1:Cc:52:ARG:HH12	2.24	0.46
1:Bw:194:ARG:NH2	2:Bx:5:U:OP1	2.48	0.46
1:Ae:239:PHE:CE1	1:Au:196:LEU:HD13	2.51	0.46
1:Ai:105:LYS:O	1:Ai:105:LYS:HG2	2.16	0.46
1:As:138:TRP:CD1	1:As:151:LEU:HD13	2.50	0.46
1:Bi:239:PHE:CE1	1:By:196:LEU:HD13	2.51	0.46
1:Bq:105:LYS:O	1:Bq:105:LYS:HG2	2.16	0.46
1:Cm:105:LYS:O	1:Cm:105:LYS:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bc:254:ARG:HD2	1:Ck:229:ALA:HB2	1.98	0.45
1:Bi:254:ARG:HD2	1:Cq:229:ALA:HB2	1.99	0.45
1:Bw:105:LYS:HG2	1:Bw:105:LYS:O	2.16	0.45
1:Ck:227:LYS:HG3	2:Cl:4:U:N3	2.31	0.45
1:Ae:138:TRP:CD1	1:Ae:151:LEU:HD13	2.50	0.45
1:Ai:239:PHE:CE1	1:Ay:196:LEU:HD13	2.52	0.45
1:Ak:105:LYS:O	1:Ak:105:LYS:HG2	2.16	0.45
1:Am:239:PHE:CE1	1:Bc:196:LEU:HD13	2.50	0.45
1:Aw:105:LYS:O	1:Aw:105:LYS:HG2	2.16	0.45
1:Be:156:GLU:HB3	1:Bw:214:ARG:HB3	1.98	0.45
1:Bm:138:TRP:CD1	1:Bm:151:LEU:HD13	2.50	0.45
1:Bo:239:PHE:CE1	1:Ce:196:LEU:HD13	2.52	0.45
1:Ag:145:GLU:CD	1:Ba:52:ARG:HH12	2.24	0.45
1:Ai:163:ARG:HH11	2:Aj:3:U:P	2.40	0.45
1:Ao:105:LYS:O	1:Ao:105:LYS:HG2	2.16	0.45
1:Ay:105:LYS:HG2	1:Ay:105:LYS:O	2.16	0.45
1:Be:239:PHE:CE1	1:Bu:196:LEU:HD13	2.50	0.45
1:Bk:145:GLU:CD	1:Ce:52:ARG:HH12	2.23	0.45
1:Ca:105:LYS:O	1:Ca:105:LYS:HG2	2.16	0.45
1:Ca:258:GLU:HG2	1:Cs:247:THR:CG2	2.46	0.45
1:Ci:105:LYS:HG2	1:Ci:105:LYS:O	2.16	0.45
1:Cm:138:TRP:CD1	1:Cm:151:LEU:HD13	2.50	0.45
1:Co:105:LYS:O	1:Co:105:LYS:HG2	2.16	0.45
1:Aa:105:LYS:HG2	1:Aa:105:LYS:O	2.16	0.45
1:Au:105:LYS:HG2	1:Au:105:LYS:O	2.16	0.45
1:Be:105:LYS:O	1:Be:105:LYS:HG2	2.16	0.45
1:Bu:239:PHE:CE1	1:Ck:196:LEU:HD13	2.51	0.45
1:By:145:GLU:CD	1:Cs:52:ARG:HH12	2.24	0.45
1:Aw:89:THR:O	1:Aw:164:GLN:HG3	2.17	0.45
1:Bg:105:LYS:O	1:Bg:105:LYS:HG2	2.16	0.45
1:Bi:105:LYS:O	1:Bi:105:LYS:HG2	2.16	0.45
1:Cc:105:LYS:O	1:Cc:105:LYS:HG2	2.16	0.45
1:Cm:126:ILE:HD11	1:Cm:173:ALA:HB1	1.99	0.45
1:Ag:253:GLU:HA	1:Bo:225:GLN:HE22	1.81	0.45
1:Ai:89:THR:O	1:Ai:164:GLN:HG3	2.17	0.45
1:Ba:239:PHE:CE1	1:Bq:196:LEU:HD13	2.52	0.45
1:Bo:227:LYS:HG3	2:Bp:4:U:N3	2.32	0.45
1:Bs:105:LYS:O	1:Bs:105:LYS:HG2	2.16	0.45
1:Bu:105:LYS:O	1:Bu:105:LYS:HG2	2.16	0.45
1:Cc:89:THR:O	1:Cc:164:GLN:HG3	2.17	0.45
1:Cm:89:THR:O	1:Cm:164:GLN:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ac:105:LYS:O	1:Ac:105:LYS:HG2	2.16	0.45
1:Ae:89:THR:O	1:Ae:164:GLN:HG3	2.17	0.45
1:Ba:89:THR:O	1:Ba:164:GLN:HG3	2.17	0.45
1:Bc:126:ILE:HD11	1:Bc:173:ALA:HB1	1.99	0.45
1:Bk:89:THR:O	1:Bk:164:GLN:HG3	2.17	0.45
1:Bk:105:LYS:HG2	1:Bk:105:LYS:O	2.16	0.45
1:Bo:89:THR:O	1:Bo:164:GLN:HG3	2.17	0.45
1:Cc:194:ARG:NH2	2:Cd:5:U:OP1	2.46	0.45
1:Aa:258:GLU:HG2	1:As:247:THR:CG2	2.47	0.45
1:Ac:258:GLU:HG2	1:Au:247:THR:CG2	2.47	0.45
1:Ae:258:GLU:HG2	1:Aw:247:THR:CG2	2.47	0.45
1:Ag:258:GLU:HG2	1:Ay:247:THR:CG2	2.47	0.45
1:Au:145:GLU:CD	1:Bo:52:ARG:HH12	2.24	0.45
1:Ay:145:GLU:CD	1:Bs:52:ARG:HH12	2.24	0.45
1:Bs:145:GLU:CD	1:Cm:52:ARG:HH12	2.24	0.45
1:Bu:89:THR:O	1:Bu:164:GLN:HG3	2.17	0.45
1:Ca:239:PHE:CE1	1:Cq:196:LEU:HD13	2.50	0.45
1:Ci:89:THR:O	1:Ci:164:GLN:HG3	2.17	0.45
1:Cs:105:LYS:O	1:Cs:105:LYS:HG2	2.16	0.45
1:Am:126:ILE:HD11	1:Am:173:ALA:HB1	1.99	0.45
1:As:105:LYS:O	1:As:105:LYS:HG2	2.16	0.45
1:As:253:GLU:HA	1:Ca:225:GLN:HE22	1.82	0.45
1:Ay:153:PRO:O	1:Ay:157:ASN:ND2	2.50	0.45
1:Ay:254:ARG:HD2	1:Cg:229:ALA:HB2	1.99	0.45
1:Bm:142:ASP:CB	1:Cg:50:ILE:HD12	2.47	0.45
1:Bo:145:GLU:CD	1:Ci:52:ARG:HH12	2.24	0.45
1:Bs:89:THR:O	1:Bs:164:GLN:HG3	2.17	0.45
1:Bw:126:ILE:HD11	1:Bw:173:ALA:HB1	1.99	0.45
1:Bw:245:ILE:CG2	1:Co:231:LEU:CB	2.91	0.45
1:Cg:105:LYS:O	1:Cg:105:LYS:HG2	2.16	0.45
1:Ci:153:PRO:O	1:Ci:157:ASN:ND2	2.50	0.45
1:Cq:105:LYS:O	1:Cq:105:LYS:HG2	2.16	0.45
1:Ac:89:THR:O	1:Ac:164:GLN:HG3	2.17	0.45
1:Ag:105:LYS:O	1:Ag:105:LYS:HG2	2.16	0.45
1:Ak:126:ILE:HD11	1:Ak:173:ALA:HB1	1.99	0.45
1:Am:89:THR:O	1:Am:164:GLN:HG3	2.17	0.45
1:Ao:89:THR:O	1:Ao:164:GLN:HG3	2.17	0.45
1:Ao:126:ILE:HD11	1:Ao:173:ALA:HB1	1.99	0.45
1:Aq:89:THR:O	1:Aq:164:GLN:HG3	2.17	0.45
1:Aq:153:PRO:O	1:Aq:157:ASN:ND2	2.50	0.45
1:Aq:239:PHE:CE1	1:Bg:196:LEU:HD13	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Be:126:ILE:HD11	1:Be:173:ALA:HB1	1.99	0.45
1:Bg:153:PRO:O	1:Bg:157:ASN:ND2	2.50	0.45
1:Bi:89:THR:O	1:Bi:164:GLN:HG3	2.17	0.45
1:Bk:258:GLU:HG2	1:Cc:247:THR:CG2	2.47	0.45
1:Bm:105:LYS:O	1:Bm:105:LYS:HG2	2.16	0.45
1:Bu:126:ILE:HD11	1:Bu:173:ALA:HB1	1.99	0.45
1:By:105:LYS:O	1:By:105:LYS:HG2	2.16	0.45
1:Cg:89:THR:O	1:Cg:164:GLN:HG3	2.17	0.45
1:Ck:126:ILE:HD11	1:Ck:173:ALA:HB1	1.99	0.45
1:Ck:128:ASN:ND2	1:Cm:86:ILE:O	2.45	0.45
1:Cq:153:PRO:O	1:Cq:157:ASN:ND2	2.50	0.45
1:Ac:145:GLU:CD	1:Aw:52:ARG:HH12	2.25	0.44
1:Ai:153:PRO:O	1:Ai:157:ASN:ND2	2.50	0.44
1:Am:153:PRO:O	1:Am:157:ASN:ND2	2.50	0.44
1:Ao:253:GLU:HA	1:Bw:225:GLN:HE22	1.82	0.44
1:Aw:253:GLU:HA	1:Ce:225:GLN:HE22	1.82	0.44
1:Bc:89:THR:O	1:Bc:164:GLN:HG3	2.17	0.44
1:Bc:105:LYS:HG2	1:Bc:105:LYS:O	2.16	0.44
1:Bg:126:ILE:HD11	1:Bg:173:ALA:HB1	1.99	0.44
1:Bo:153:PRO:O	1:Bo:157:ASN:ND2	2.50	0.44
1:Bs:126:ILE:HD11	1:Bs:173:ALA:HB1	1.99	0.44
1:Bu:142:ASP:CB	1:Co:50:ILE:HD12	2.47	0.44
1:Bw:153:PRO:O	1:Bw:157:ASN:ND2	2.50	0.44
1:By:258:GLU:HG2	1:Cq:247:THR:CG2	2.46	0.44
1:Ce:105:LYS:HG2	1:Ce:105:LYS:O	2.16	0.44
1:Aa:153:PRO:O	1:Aa:157:ASN:ND2	2.50	0.44
1:Ac:126:ILE:HD11	1:Ac:173:ALA:HB1	1.99	0.44
1:Ac:153:PRO:O	1:Ac:157:ASN:ND2	2.50	0.44
1:Ai:145:GLU:CD	1:Bc:52:ARG:HH12	2.25	0.44
1:Am:105:LYS:O	1:Am:105:LYS:HG2	2.16	0.44
1:As:89:THR:O	1:As:164:GLN:HG3	2.17	0.44
1:Ba:145:GLU:CD	1:Bu:52:ARG:HH12	2.25	0.44
1:Bm:153:PRO:O	1:Bm:157:ASN:ND2	2.50	0.44
1:Bs:153:PRO:O	1:Bs:157:ASN:ND2	2.50	0.44
1:Cc:153:PRO:O	1:Cc:157:ASN:ND2	2.50	0.44
1:Ce:89:THR:O	1:Ce:164:GLN:HG3	2.17	0.44
1:Ck:105:LYS:O	1:Ck:105:LYS:HG2	2.16	0.44
1:Cm:153:PRO:O	1:Cm:157:ASN:ND2	2.50	0.44
1:Bc:153:PRO:O	1:Bc:157:ASN:ND2	2.50	0.44
1:Bg:89:THR:O	1:Bg:164:GLN:HG3	2.17	0.44
1:Bg:258:GLU:HG2	1:By:247:THR:CG2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bm:126:ILE:HD11	1:Bm:173:ALA:HB1	1.99	0.44
1:Bo:105:LYS:HG2	1:Bo:105:LYS:O	2.16	0.44
1:Bq:89:THR:O	1:Bq:164:GLN:HG3	2.17	0.44
1:Bw:245:ILE:HG13	1:Co:231:LEU:HD12	2.00	0.44
1:By:126:ILE:HD11	1:By:173:ALA:HB1	1.99	0.44
1:Ca:89:THR:O	1:Ca:164:GLN:HG3	2.17	0.44
1:Ca:153:PRO:O	1:Ca:157:ASN:ND2	2.50	0.44
1:Cq:126:ILE:HD11	1:Cq:173:ALA:HB1	1.99	0.44
1:Cs:153:PRO:O	1:Cs:157:ASN:ND2	2.50	0.44
1:Aa:245:ILE:CG2	1:As:231:LEU:HB2	2.47	0.44
1:Ag:153:PRO:O	1:Ag:157:ASN:ND2	2.50	0.44
1:Ai:126:ILE:HD11	1:Ai:173:ALA:HB1	1.99	0.44
1:Ao:239:PHE:CE1	1:Be:196:LEU:HD13	2.51	0.44
1:Aq:105:LYS:HG2	1:Aq:105:LYS:O	2.16	0.44
1:As:153:PRO:O	1:As:157:ASN:ND2	2.50	0.44
1:Aw:153:PRO:O	1:Aw:157:ASN:ND2	2.50	0.44
1:Ay:258:GLU:HG2	1:Bq:247:THR:CG2	2.48	0.44
1:Cc:126:ILE:HD11	1:Cc:173:ALA:HB1	1.99	0.44
1:Ce:153:PRO:O	1:Ce:157:ASN:ND2	2.50	0.44
1:Cg:126:ILE:HD11	1:Cg:173:ALA:HB1	1.99	0.44
1:Ck:89:THR:O	1:Ck:164:GLN:HG3	2.17	0.44
2:Cn:5:U:O3'	2:Cp:1:U:P	2.76	0.44
1:Co:126:ILE:HD11	1:Co:173:ALA:HB1	1.99	0.44
1:Ac:253:GLU:HA	1:Bk:225:GLN:HE22	1.82	0.44
1:Ae:105:LYS:O	1:Ae:105:LYS:HG2	2.16	0.44
1:Ae:126:ILE:HD11	1:Ae:173:ALA:HB1	1.99	0.44
1:Ae:227:LYS:HG3	2:Af:4:U:C4	2.53	0.44
1:Aw:126:ILE:HD11	1:Aw:173:ALA:HB1	1.99	0.44
1:Co:89:THR:O	1:Co:164:GLN:HG3	2.17	0.44
1:Ak:89:THR:O	1:Ak:164:GLN:HG3	2.17	0.44
1:Ak:153:PRO:O	1:Ak:157:ASN:ND2	2.50	0.44
1:Am:145:GLU:CD	1:Bg:52:ARG:HH12	2.26	0.44
1:Aq:126:ILE:HD11	1:Aq:173:ALA:HB1	1.99	0.44
1:Aw:258:GLU:HG2	1:Bo:247:THR:CG2	2.48	0.44
1:Ba:126:ILE:HD11	1:Ba:173:ALA:HB1	1.99	0.44
1:Bc:258:GLU:HG2	1:Bu:247:THR:CG2	2.48	0.44
1:Be:89:THR:O	1:Be:164:GLN:HG3	2.17	0.44
1:Bi:153:PRO:O	1:Bi:157:ASN:ND2	2.50	0.44
1:Ac:245:ILE:CG2	1:Au:231:LEU:HB2	2.48	0.44
1:Ae:153:PRO:O	1:Ae:157:ASN:ND2	2.50	0.44
1:Ao:145:GLU:CD	1:Bi:52:ARG:HH12	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:As:126:ILE:HD11	1:As:173:ALA:HB1	1.99	0.44
1:Au:89:THR:O	1:Au:164:GLN:HG3	2.17	0.44
1:Au:126:ILE:HD11	1:Au:173:ALA:HB1	1.99	0.44
1:Ba:258:GLU:HG2	1:Bs:247:THR:CG2	2.48	0.44
1:Bg:145:GLU:CD	1:Ca:52:ARG:HH12	2.25	0.44
1:Bi:126:ILE:HD11	1:Bi:173:ALA:HB1	1.99	0.44
1:Bo:126:ILE:HD11	1:Bo:173:ALA:HB1	1.99	0.44
1:Bu:85:ASP:OD2	1:Bw:61:ARG:NH2	2.51	0.44
1:By:153:PRO:O	1:By:157:ASN:ND2	2.50	0.44
1:Ce:126:ILE:HD11	1:Ce:173:ALA:HB1	1.99	0.44
1:Ck:153:PRO:O	1:Ck:157:ASN:ND2	2.50	0.44
1:Aa:89:THR:O	1:Aa:164:GLN:HG3	2.17	0.44
1:Au:258:GLU:HG2	1:Bm:247:THR:CG2	2.48	0.44
1:Bk:126:ILE:HD11	1:Bk:173:ALA:HB1	1.99	0.44
1:Bk:153:PRO:O	1:Bk:157:ASN:ND2	2.50	0.44
1:Bm:89:THR:O	1:Bm:164:GLN:HG3	2.17	0.44
1:Cg:153:PRO:O	1:Cg:157:ASN:ND2	2.50	0.44
1:Ae:254:ARG:HD2	1:Bm:229:ALA:HB2	2.00	0.44
1:Ag:89:THR:O	1:Ag:164:GLN:HG3	2.17	0.44
1:Ag:126:ILE:HD11	1:Ag:173:ALA:HB1	1.99	0.44
1:Am:253:GLU:HA	1:Bu:225:GLN:HE22	1.83	0.44
1:Aq:253:GLU:HA	1:By:225:GLN:HE22	1.83	0.44
1:As:258:GLU:HG2	1:Bk:247:THR:CG2	2.47	0.44
1:Aw:245:ILE:CG2	1:Bo:231:LEU:HB2	2.48	0.44
1:Ay:89:THR:O	1:Ay:164:GLN:HG3	2.17	0.44
1:Bi:258:GLU:HG2	1:Ca:247:THR:CG2	2.48	0.44
1:Bq:260:VAL:HG22	1:Bs:266:THR:O	2.18	0.44
1:Bw:89:THR:O	1:Bw:164:GLN:HG3	2.17	0.44
1:By:89:THR:O	1:By:164:GLN:HG3	2.17	0.44
1:Bi:126:ILE:HD11	1:Bi:173:ALA:HB1	1.99	0.44
1:Cq:89:THR:O	1:Cq:164:GLN:HG3	2.17	0.44
1:Ae:245:ILE:CG2	1:Aw:231:LEU:HB2	2.48	0.43
1:Bi:258:GLU:HG2	1:Ba:247:THR:CG2	2.48	0.43
1:Ay:126:ILE:HD11	1:Ay:173:ALA:HB1	1.99	0.43
1:Bc:142:ASP:HB2	1:Bw:50:ILE:HD12	2.00	0.43
1:Bq:126:ILE:HD11	1:Bq:173:ALA:HB1	1.99	0.43
1:Bq:142:ASP:CB	1:Ck:50:ILE:HD12	2.48	0.43
1:Bq:153:PRO:O	1:Bq:157:ASN:ND2	2.50	0.43
1:By:245:ILE:CG2	1:Cq:231:LEU:HB2	2.48	0.43
1:Co:153:PRO:O	1:Co:157:ASN:ND2	2.50	0.43
1:Cs:89:THR:O	1:Cs:164:GLN:HG3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cs:126:ILE:HD11	1:Cs:173:ALA:HB1	1.99	0.43
1:Aa:126:ILE:HD11	1:Aa:173:ALA:HB1	1.99	0.43
1:Aq:245:ILE:CG2	1:Bi:231:LEU:HB2	2.48	0.43
1:Aq:254:ARG:HD2	1:By:229:ALA:HB2	2.00	0.43
1:Bc:116:THR:HG22	1:Bc:140:MET:HE1	2.00	0.43
1:Bi:231:LEU:HD22	2:Bj:3:U:H2'	1.99	0.43
1:Bm:116:THR:HG22	1:Bm:140:MET:HE1	2.01	0.43
1:Bu:258:GLU:HG2	1:Cm:247:THR:CG2	2.48	0.43
1:Bw:116:THR:HG22	1:Bw:140:MET:HE1	2.00	0.43
1:Ca:126:ILE:HD11	1:Ca:173:ALA:HB1	1.99	0.43
1:Ca:245:ILE:CG2	1:Cs:231:LEU:HB2	2.48	0.43
1:Cg:116:THR:HG22	1:Cg:140:MET:HE1	2.00	0.43
1:Cs:116:THR:HG22	1:Cs:140:MET:HE1	2.00	0.43
1:Ao:153:PRO:O	1:Ao:157:ASN:ND2	2.50	0.43
1:Aq:116:THR:HG22	1:Aq:140:MET:HE1	2.01	0.43
1:As:245:ILE:CG2	1:Bk:231:LEU:HB2	2.48	0.43
1:Ay:260:VAL:HG22	1:Ba:266:THR:O	2.18	0.43
1:Be:145:GLU:CD	1:By:52:ARG:HH12	2.26	0.43
1:Bk:116:THR:HG22	1:Bk:140:MET:HE1	2.01	0.43
1:Bu:231:LEU:HD11	2:Bv:4:U:C5	2.53	0.43
1:Bw:142:ASP:CB	1:Cq:50:ILE:HD12	2.48	0.43
1:By:116:THR:HG22	1:By:140:MET:HE1	2.01	0.43
1:Ae:116:THR:HG22	1:Ae:140:MET:HE1	2.01	0.43
1:As:236:THR:CG2	2:At:3:U:H1'	2.48	0.43
1:Ba:153:PRO:O	1:Ba:157:ASN:ND2	2.50	0.43
1:Bk:245:ILE:CG2	1:Cc:231:LEU:HB2	2.49	0.43
1:Bo:142:ASP:CB	1:Ci:50:ILE:HD12	2.48	0.43
1:Cm:271:ARG:HA	1:Co:271:ARG:O	2.17	0.43
1:Am:260:VAL:HG22	1:Ao:266:THR:O	2.19	0.43
1:As:116:THR:HG22	1:As:140:MET:HE1	2.01	0.43
1:As:145:GLU:CD	1:Bm:52:ARG:HH12	2.26	0.43
1:Bg:239:PHE:CE1	1:Bw:196:LEU:HD13	2.53	0.43
1:Bi:245:ILE:CG2	1:Ca:231:LEU:HB2	2.48	0.43
1:Bq:236:THR:CG2	2:Br:3:U:H1'	2.48	0.43
1:Ce:116:THR:HG22	1:Ce:140:MET:HE1	2.00	0.43
1:Cq:116:THR:HG22	1:Cq:140:MET:HE1	2.01	0.43
1:Ag:116:THR:HG22	1:Ag:140:MET:HE1	2.01	0.43
1:Ai:131:SER:OG	2:Aj:4:U:OP1	2.28	0.43
1:Au:153:PRO:O	1:Au:157:ASN:ND2	2.50	0.43
1:Be:116:THR:HG22	1:Be:140:MET:HE1	2.01	0.43
1:Be:153:PRO:O	1:Be:157:ASN:ND2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bg:245:ILE:CG2	1:By:231:LEU:HB2	2.48	0.43
1:Bi:253:GLU:HA	1:Cq:225:GLN:HE22	1.82	0.43
1:Bo:116:THR:HG22	1:Bo:140:MET:HE1	2.00	0.43
1:Bu:153:PRO:O	1:Bu:157:ASN:ND2	2.50	0.43
1:Aa:253:GLU:HA	1:Bi:225:GLN:HE22	1.83	0.43
1:Ag:172:VAL:HG11	1:Ai:71:LEU:CD1	2.46	0.43
1:Ai:116:THR:HG22	1:Ai:140:MET:HE1	2.01	0.43
1:Ao:254:ARG:HD2	1:Bw:229:ALA:HB2	2.01	0.43
1:Bm:258:GLU:HG2	1:Ce:247:THR:CG2	2.48	0.43
1:Bu:145:GLU:CD	1:Co:52:ARG:HH12	2.26	0.43
1:Ca:116:THR:HG22	1:Ca:140:MET:HE1	2.00	0.43
1:Ci:116:THR:HG22	1:Ci:140:MET:HE1	2.01	0.43
1:Ck:116:THR:HG22	1:Ck:140:MET:HE1	2.01	0.43
1:Ac:116:THR:HG22	1:Ac:140:MET:HE1	2.00	0.43
1:Am:258:GLU:HG2	1:Be:247:THR:CG2	2.48	0.43
1:Ao:116:THR:HG22	1:Ao:140:MET:HE1	2.00	0.43
1:Ao:245:ILE:CG2	1:Bg:231:LEU:HB2	2.48	0.43
1:Ao:258:GLU:HG2	1:Bg:247:THR:CG2	2.48	0.43
1:As:260:VAL:HG22	1:Au:266:THR:O	2.19	0.43
1:Au:245:ILE:CG2	1:Bm:231:LEU:HB2	2.49	0.43
1:Ay:245:ILE:CG2	1:Bq:231:LEU:HB2	2.48	0.43
1:Ba:116:THR:HG22	1:Ba:140:MET:HE1	2.01	0.43
1:Ba:253:GLU:HA	1:Bi:225:GLN:HE22	1.83	0.43
1:Bi:142:ASP:CB	1:Cc:50:ILE:HD12	2.49	0.43
1:Bs:142:ASP:CB	1:Cm:50:ILE:HD12	2.49	0.43
1:Aq:145:GLU:CD	1:Bk:52:ARG:HH12	2.26	0.43
1:Aq:258:GLU:HG2	1:Bi:247:THR:CG2	2.48	0.43
1:Bk:142:ASP:CB	1:Ce:50:ILE:HD12	2.48	0.43
1:Bs:260:VAL:HG22	1:Bu:266:THR:O	2.19	0.43
1:Bu:116:THR:HG22	1:Bu:140:MET:HE1	2.00	0.43
1:Ak:116:THR:HG22	1:Ak:140:MET:HE1	2.01	0.43
1:Au:116:THR:HG22	1:Au:140:MET:HE1	2.01	0.43
1:Ay:236:THR:HG21	2:Az:3:U:H1'	2.01	0.43
1:Ba:260:VAL:HG22	1:Bc:266:THR:O	2.19	0.43
1:Bg:236:THR:CG2	2:Bh:3:U:H1'	2.49	0.43
1:Bg:253:GLU:HA	1:Co:225:GLN:HE22	1.84	0.43
1:Bs:239:PHE:CE1	1:Ci:196:LEU:HD13	2.54	0.43
1:Bw:239:PHE:CE1	1:Cm:196:LEU:HD13	2.53	0.43
1:Ae:253:GLU:HA	1:Bm:225:GLN:HE22	1.84	0.42
1:Ai:245:ILE:CG2	1:Ba:231:LEU:HB2	2.49	0.42
1:Ai:253:GLU:HA	1:Bq:225:GLN:HE22	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ao:260:VAL:HG22	1:Aq:266:THR:O	2.19	0.42
1:Bg:116:THR:HG22	1:Bg:140:MET:HE1	2.00	0.42
1:Bi:116:THR:HG22	1:Bi:140:MET:HE1	2.00	0.42
1:Bm:227:LYS:HG2	1:Bm:231:LEU:HD12	2.01	0.42
1:Bw:255:HIS:O	1:Co:241:LEU:HA	2.18	0.42
1:Cc:260:VAL:HG22	1:Cc:266:THR:O	2.19	0.42
1:Cm:116:THR:HG22	1:Cm:140:MET:HE1	2.01	0.42
1:Cm:227:LYS:HG2	1:Cm:231:LEU:HD12	2.01	0.42
1:Aw:227:LYS:HG2	1:Aw:231:LEU:HD12	2.02	0.42
1:Ay:116:THR:HG22	1:Ay:140:MET:HE1	2.00	0.42
1:Ba:227:LYS:HG2	1:Ba:231:LEU:HD12	2.02	0.42
1:Bm:172:VAL:HG11	1:Bo:71:LEU:CD1	2.47	0.42
1:Bq:258:GLU:HG2	1:Ci:247:THR:CG2	2.49	0.42
1:Bs:258:GLU:HG2	1:Ck:247:THR:CG2	2.48	0.42
1:Aa:231:LEU:CD2	2:Ab:3:U:H2'	2.49	0.42
1:Ag:260:VAL:HG22	1:Ai:266:THR:O	2.18	0.42
1:Ak:227:LYS:HG2	1:Ak:231:LEU:HD12	2.02	0.42
1:Be:253:GLU:HA	1:Cm:225:GLN:HE22	1.84	0.42
1:Be:260:VAL:HG22	1:Bg:266:THR:O	2.19	0.42
1:Bq:172:VAL:HG11	1:Bs:71:LEU:CD1	2.46	0.42
1:Bq:227:LYS:HG2	1:Bq:231:LEU:HD12	2.01	0.42
1:Ci:227:LYS:HG2	1:Ci:231:LEU:HD12	2.01	0.42
1:Ci:260:VAL:HG22	1:Ck:266:THR:O	2.18	0.42
1:Aa:145:GLU:CD	1:Au:52:ARG:HH12	2.27	0.42
1:Aa:245:ILE:CG2	1:As:231:LEU:CB	2.96	0.42
1:Ag:227:LYS:HG2	1:Ag:231:LEU:HD12	2.02	0.42
1:Ai:254:ARG:HD2	1:Bq:229:ALA:HB2	2.01	0.42
1:Ak:142:ASP:CB	1:Be:50:ILE:HD12	2.50	0.42
1:Ak:258:GLU:HG2	1:Bc:247:THR:CG2	2.48	0.42
1:Aq:260:VAL:HG22	1:As:266:THR:O	2.19	0.42
1:Au:260:VAL:HG22	1:Aw:266:THR:O	2.19	0.42
2:Bf:5:U:O3'	2:Bh:1:U:P	2.78	0.42
1:Bm:149:PHE:CD1	1:Cg:53:ILE:HD12	2.54	0.42
1:Bu:231:LEU:HD21	2:Bv:4:U:C6	2.54	0.42
1:Bw:252:THR:HG22	1:Co:238:LEU:HD22	2.01	0.42
1:By:245:ILE:CG2	1:Cq:231:LEU:CB	2.96	0.42
1:Cc:227:LYS:HG2	1:Cc:231:LEU:HD12	2.02	0.42
1:Ck:260:VAL:HG22	1:Cm:266:THR:O	2.19	0.42
1:Cm:260:VAL:HG22	1:Co:266:THR:O	2.19	0.42
1:Co:116:THR:HG22	1:Co:140:MET:HE1	2.01	0.42
1:Co:127:GLU:HG3	1:Cq:86:ILE:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ae:145:GLU:CD	1:Ay:52:ARG:HH12	2.27	0.42
1:Aw:145:GLU:CD	1:Bq:52:ARG:HH12	2.26	0.42
1:Aw:260:VAL:HG22	1:Ay:266:THR:O	2.20	0.42
1:Ay:231:LEU:HD21	2:Az:4:U:C6	2.55	0.42
1:Bc:245:ILE:CG2	1:Bu:231:LEU:HB2	2.49	0.42
1:Bg:227:LYS:HG2	1:Bg:231:LEU:HD12	2.01	0.42
1:Bo:258:GLU:HG2	1:Cg:247:THR:CG2	2.49	0.42
1:Bq:116:THR:HG22	1:Bq:140:MET:HE1	2.01	0.42
1:Bq:194:ARG:NH2	2:Br:5:U:OP1	2.46	0.42
1:Bu:227:LYS:HG2	1:Bu:231:LEU:HD12	2.02	0.42
1:Bw:227:LYS:HG3	2:Bx:4:U:C4	2.54	0.42
1:Bw:227:LYS:HG2	1:Bw:231:LEU:HD12	2.02	0.42
1:Ce:227:LYS:HG2	1:Ce:231:LEU:HD12	2.02	0.42
1:Ce:260:VAL:HG22	1:Cg:266:THR:O	2.19	0.42
1:Cq:260:VAL:HG22	1:Cs:266:THR:O	2.19	0.42
1:Aa:116:THR:HG22	1:Aa:140:MET:HE1	2.01	0.42
1:Aa:227:LYS:HG2	1:Aa:231:LEU:HD12	2.02	0.42
1:Be:227:LYS:HG2	1:Be:231:LEU:HD12	2.02	0.42
1:Bg:254:ARG:HD2	1:Co:229:ALA:HB2	2.02	0.42
1:Bk:260:VAL:HG22	1:Bm:266:THR:O	2.19	0.42
1:Bq:149:PHE:CD1	1:Ck:53:ILE:HD12	2.55	0.42
1:Cc:116:THR:HG22	1:Cc:140:MET:HE1	2.01	0.42
1:Ae:227:LYS:HG2	1:Ae:231:LEU:HD12	2.02	0.42
1:Ai:227:LYS:HG2	1:Ai:231:LEU:HD12	2.01	0.42
1:Bg:260:VAL:HG22	1:Bi:266:THR:O	2.19	0.42
1:Cs:227:LYS:HG2	1:Cs:231:LEU:HD12	2.02	0.42
1:Ac:260:VAL:HG22	1:Ae:266:THR:O	2.19	0.42
1:Am:116:THR:HG22	1:Am:140:MET:HE1	2.01	0.42
1:Ao:227:LYS:HG2	1:Ao:231:LEU:HD12	2.02	0.42
1:Aq:227:LYS:HG2	1:Aq:231:LEU:HD12	2.02	0.42
1:Aw:116:THR:HG22	1:Aw:140:MET:HE1	2.00	0.42
1:Bi:260:VAL:HG22	1:Bk:266:THR:O	2.20	0.42
1:Bo:227:LYS:HG2	1:Bo:231:LEU:HD12	2.02	0.42
1:Bs:227:LYS:HG2	1:Bs:231:LEU:HD12	2.02	0.42
1:Bw:127:GLU:HG3	1:By:86:ILE:HD11	2.02	0.42
1:Bw:245:ILE:HD12	1:Co:228:ALA:CA	2.47	0.42
1:Ae:260:VAL:HG22	1:Ag:266:THR:O	2.20	0.42
1:Ag:245:ILE:CG2	1:Ay:231:LEU:HB2	2.48	0.42
1:Ai:260:VAL:HG22	1:Ak:266:THR:O	2.19	0.42
1:As:245:ILE:CG2	1:Bk:231:LEU:CB	2.96	0.42
1:By:260:VAL:HG22	1:Ca:266:THR:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cg:227:LYS:HG2	1:Cg:231:LEU:HD12	2.02	0.42
1:Cg:260:VAL:HG22	1:Ci:266:THR:O	2.19	0.42
1:Ck:227:LYS:HG2	1:Ck:231:LEU:HD12	2.02	0.42
1:Aa:260:VAL:HG22	1:Ac:266:THR:O	2.19	0.42
1:Ak:245:ILE:CG2	1:Bc:231:LEU:HB2	2.49	0.42
1:Aw:254:ARG:HD2	1:Ce:229:ALA:HB2	2.01	0.42
1:Ac:227:LYS:HG2	1:Ac:231:LEU:HD12	2.02	0.41
1:Au:227:LYS:HG2	1:Au:231:LEU:HD12	2.02	0.41
1:Bs:116:THR:HG22	1:Bs:140:MET:HE1	2.01	0.41
1:Ae:245:ILE:CG2	1:Aw:231:LEU:CB	2.97	0.41
1:Au:142:ASP:CB	1:Bo:50:ILE:HD12	2.50	0.41
1:Be:258:GLU:HG2	1:Bw:247:THR:CG2	2.50	0.41
1:Bo:260:VAL:HG22	1:Bq:266:THR:O	2.19	0.41
1:Ae:244:GLY:O	1:Ae:245:ILE:HD13	2.21	0.41
1:As:227:LYS:HG2	1:As:231:LEU:HD12	2.02	0.41
1:Ay:142:ASP:CB	1:Bs:50:ILE:HD12	2.50	0.41
1:Bq:245:ILE:CG2	1:Ci:231:LEU:HB2	2.50	0.41
1:Bu:245:ILE:CG2	1:Cm:231:LEU:HB2	2.49	0.41
1:Cg:244:GLY:O	1:Cg:245:ILE:HD13	2.21	0.41
1:Bm:244:GLY:O	1:Bm:245:ILE:HD13	2.21	0.41
1:Cg:236:THR:CG2	2:Ch:3:U:H1'	2.50	0.41
1:Cs:90:ARG:NH2	1:Cs:210:GLU:OE2	2.54	0.41
1:Am:231:LEU:HD22	2:An:3:U:C2	2.55	0.41
1:Aw:245:ILE:CG2	1:Bo:231:LEU:CB	2.97	0.41
1:Ay:244:GLY:O	1:Ay:245:ILE:HD13	2.21	0.41
1:Bc:227:LYS:HG2	1:Bc:231:LEU:HD12	2.02	0.41
1:Bk:227:LYS:HG2	1:Bk:231:LEU:HD12	2.02	0.41
1:Bo:244:GLY:O	1:Bo:245:ILE:HD13	2.21	0.41
1:Co:90:ARG:NH2	1:Co:210:GLU:OE2	2.54	0.41
1:Co:227:LYS:HG2	1:Co:231:LEU:HD12	2.02	0.41
1:Cq:90:ARG:NH2	1:Cq:210:GLU:OE2	2.54	0.41
1:Ag:149:PHE:CD1	1:Ba:53:ILE:HD12	2.56	0.41
1:Aw:244:GLY:O	1:Aw:245:ILE:HD13	2.21	0.41
1:Ay:231:LEU:HD11	2:Az:4:U:C5	2.56	0.41
1:Bi:227:LYS:HG2	1:Bi:231:LEU:HD12	2.02	0.41
1:Bk:244:GLY:O	1:Bk:245:ILE:HD13	2.21	0.41
1:Bq:90:ARG:NH2	1:Bq:210:GLU:OE2	2.54	0.41
1:Bs:122:MET:HE2	1:Bs:122:MET:HB3	1.99	0.41
1:Bw:90:ARG:NH2	1:Bw:210:GLU:OE2	2.54	0.41
1:Ca:90:ARG:NH2	1:Ca:210:GLU:OE2	2.54	0.41
1:Cq:227:LYS:HG2	1:Cq:231:LEU:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ac:142:ASP:CB	1:Aw:50:ILE:HD12	2.51	0.41
1:Ai:90:ARG:NH2	1:Ai:210:GLU:OE2	2.54	0.41
1:Ai:142:ASP:CB	1:Bc:50:ILE:HD12	2.50	0.41
1:Am:90:ARG:NH2	1:Am:210:GLU:OE2	2.53	0.41
1:Ao:90:ARG:NH2	1:Ao:210:GLU:OE2	2.54	0.41
1:Aq:142:ASP:CB	1:Bk:50:ILE:HD12	2.51	0.41
1:As:244:GLY:O	1:As:245:ILE:HD13	2.21	0.41
1:Ba:142:ASP:CB	1:Bu:50:ILE:HD12	2.50	0.41
1:Bk:245:ILE:CG2	1:Cc:231:LEU:CB	2.97	0.41
1:Bm:260:VAL:HG22	1:Bo:266:THR:O	2.20	0.41
1:By:227:LYS:HG2	1:By:231:LEU:HD12	2.02	0.41
1:Ca:260:VAL:HG22	1:Cc:266:THR:O	2.19	0.41
1:Cc:90:ARG:NH2	1:Cc:210:GLU:OE2	2.54	0.41
1:Ce:244:GLY:O	1:Ce:245:ILE:HD13	2.21	0.41
1:Cg:90:ARG:NH2	1:Cg:210:GLU:OE2	2.54	0.41
1:Cm:122:MET:HE2	1:Cm:122:MET:HB3	1.99	0.41
1:Am:245:ILE:CG2	1:Be:231:LEU:HB2	2.49	0.41
1:As:142:ASP:CB	1:Bm:50:ILE:HD12	2.50	0.41
1:Ay:90:ARG:NH2	1:Ay:210:GLU:OE2	2.54	0.41
1:Ay:227:LYS:HG2	1:Ay:231:LEU:HD12	2.02	0.41
1:Ba:90:ARG:NH2	1:Ba:210:GLU:OE2	2.54	0.41
1:Bg:90:ARG:NH2	1:Bg:210:GLU:OE2	2.54	0.41
1:Bo:245:ILE:CG2	1:Cg:231:LEU:HB2	2.51	0.41
1:Ca:227:LYS:HG2	1:Ca:231:LEU:HD12	2.02	0.41
1:Ci:90:ARG:NH2	1:Ci:210:GLU:OE2	2.54	0.41
1:Cs:244:GLY:O	1:Cs:245:ILE:HD13	2.21	0.41
1:Ag:244:GLY:O	1:Ag:245:ILE:HD13	2.21	0.41
1:Ak:90:ARG:NH2	1:Ak:210:GLU:OE2	2.54	0.41
1:Am:227:LYS:HG2	1:Am:231:LEU:HD12	2.02	0.41
1:Aq:194:ARG:NH2	2:Ar:5:U:OP1	2.53	0.41
1:As:227:LYS:HG3	2:At:4:U:N3	2.36	0.41
1:Be:90:ARG:NH2	1:Be:210:GLU:OE2	2.54	0.41
1:Be:245:ILE:CG2	1:Bw:231:LEU:HB2	2.50	0.41
1:Bk:90:ARG:NH2	1:Bk:210:GLU:OE2	2.54	0.41
1:Bq:244:GLY:O	1:Bq:245:ILE:HD13	2.21	0.41
1:Bs:245:ILE:CG2	1:Ck:231:LEU:HB2	2.50	0.41
1:Bu:163:ARG:NH1	2:Bv:3:U:P	2.94	0.41
1:By:90:ARG:NH2	1:By:210:GLU:OE2	2.54	0.41
1:Cc:238:LEU:HD12	1:Cc:238:LEU:HA	1.94	0.41
1:Cc:244:GLY:O	1:Cc:245:ILE:HD13	2.21	0.41
1:Ce:90:ARG:NH2	1:Ce:210:GLU:OE2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Co:244:GLY:O	1:Co:245:ILE:HD13	2.21	0.41
1:Ac:122:MET:HE2	1:Ac:122:MET:HB3	1.99	0.41
1:Am:142:ASP:CB	1:Bg:50:ILE:HD12	2.51	0.41
1:Au:244:GLY:O	1:Au:245:ILE:HD13	2.21	0.41
1:Bk:105:LYS:HB2	1:Bk:105:LYS:HE3	2.00	0.41
1:Bm:90:ARG:NH2	1:Bm:210:GLU:OE2	2.54	0.41
1:Bs:244:GLY:O	1:Bs:245:ILE:HD13	2.21	0.41
1:Bu:230:ALA:CB	2:Bv:4:U:H1'	2.51	0.41
1:Bw:169:PHE:CD1	1:By:63:PRO:HG2	2.56	0.41
1:Bw:258:GLU:HG2	1:Co:247:THR:HG22	2.02	0.41
1:Aa:90:ARG:NH2	1:Aa:210:GLU:OE2	2.54	0.40
1:As:90:ARG:NH2	1:As:210:GLU:OE2	2.54	0.40
1:Ba:245:ILE:CG2	1:Bs:231:LEU:HB2	2.49	0.40
1:Be:142:ASP:CB	1:By:50:ILE:HD12	2.51	0.40
1:Be:252:THR:HG22	1:Bw:238:LEU:HD22	2.03	0.40
1:Bi:90:ARG:NH2	1:Bi:210:GLU:OE2	2.54	0.40
1:Bi:238:LEU:HD12	1:Bi:238:LEU:HA	1.94	0.40
1:By:245:ILE:HG13	1:Cq:231:LEU:HD12	2.03	0.40
1:Ca:244:GLY:O	1:Ca:245:ILE:HD13	2.21	0.40
1:Cc:172:VAL:HG11	1:Ce:71:LEU:CD1	2.49	0.40
1:Cm:90:ARG:NH2	1:Cm:210:GLU:OE2	2.54	0.40
1:Ac:244:GLY:O	1:Ac:245:ILE:HD13	2.21	0.40
1:Ae:90:ARG:NH2	1:Ae:210:GLU:OE2	2.54	0.40
1:Ak:172:VAL:HG11	1:Am:71:LEU:CD1	2.46	0.40
1:Aq:244:GLY:O	1:Aq:245:ILE:HD13	2.21	0.40
1:Ay:149:PHE:CD1	1:Bs:53:ILE:HD12	2.56	0.40
1:Ay:172:VAL:HG11	1:Ba:71:LEU:CD1	2.46	0.40
1:Ba:244:GLY:O	1:Ba:245:ILE:HD13	2.21	0.40
1:Bc:90:ARG:NH2	1:Bc:210:GLU:OE2	2.54	0.40
1:Bg:142:ASP:CB	1:Ca:50:ILE:HD12	2.51	0.40
1:Bo:90:ARG:NH2	1:Bo:210:GLU:OE2	2.54	0.40
1:Bo:105:LYS:HB2	1:Bo:105:LYS:HE3	2.00	0.40
1:Bs:90:ARG:NH2	1:Bs:210:GLU:OE2	2.54	0.40
1:Bu:245:ILE:HD12	1:Cm:228:ALA:CA	2.52	0.40
1:Cc:236:THR:CG2	2:Cd:3:U:H1'	2.52	0.40
1:Aa:142:ASP:CB	1:Au:50:ILE:HD12	2.51	0.40
1:Ag:90:ARG:NH2	1:Ag:210:GLU:OE2	2.54	0.40
1:Ak:149:PHE:CD1	1:Be:53:ILE:HD12	2.56	0.40
1:Ak:260:VAL:HG22	1:Am:266:THR:O	2.21	0.40
1:Aq:90:ARG:NH2	1:Aq:210:GLU:OE2	2.54	0.40
1:Aq:231:LEU:CD2	2:Ar:3:U:H2'	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Aw:142:ASP:CB	1:Bq:50:ILE:HD12	2.51	0.40
1:Ba:245:ILE:HD12	1:Bs:228:ALA:CA	2.52	0.40
1:Bk:252:THR:HG22	1:Cc:238:LEU:HD22	2.04	0.40
1:Bm:105:LYS:HB2	1:Bm:105:LYS:HE3	2.00	0.40
1:Bm:245:ILE:CG2	1:Ce:231:LEU:HB2	2.51	0.40
1:Bo:149:PHE:CD1	1:Ci:53:ILE:HD12	2.57	0.40
1:Bu:127:GLU:HG3	1:Bw:86:ILE:HD11	2.03	0.40
1:Bu:245:ILE:CG2	1:Cm:231:LEU:CB	2.97	0.40
1:By:54:LYS:HE2	1:By:54:LYS:HB3	1.90	0.40
1:Ac:90:ARG:NH2	1:Ac:210:GLU:OE2	2.54	0.40
1:Ai:244:GLY:O	1:Ai:245:ILE:HD13	2.21	0.40
1:As:54:LYS:HE2	1:As:54:LYS:HB3	1.90	0.40
1:Au:90:ARG:NH2	1:Au:210:GLU:OE2	2.54	0.40
1:Aw:172:VAL:HG11	1:Ay:71:LEU:CD1	2.48	0.40
1:Bo:163:ARG:NH1	2:Bp:3:U:P	2.95	0.40
1:Bq:127:GLU:HG3	1:Bs:86:ILE:HD11	2.03	0.40
1:Bw:244:GLY:O	1:Bw:245:ILE:HD13	2.21	0.40
1:By:239:PHE:CE1	1:Co:196:LEU:HD13	2.56	0.40
1:By:244:GLY:O	1:By:245:ILE:HD13	2.21	0.40
1:By:252:THR:HG22	1:Cq:238:LEU:HD22	2.04	0.40
1:Ci:244:GLY:O	1:Ci:245:ILE:HD13	2.21	0.40
1:Cm:244:GLY:O	1:Cm:245:ILE:HD13	2.21	0.40
1:Aa:244:GLY:O	1:Aa:245:ILE:HD13	2.21	0.40
1:Ag:142:ASP:CB	1:Ba:50:ILE:HD12	2.50	0.40
1:Ak:244:GLY:O	1:Ak:245:ILE:HD13	2.21	0.40
1:As:122:MET:HE2	1:As:122:MET:HB3	1.99	0.40
1:Aw:90:ARG:NH2	1:Aw:210:GLU:OE2	2.54	0.40
1:Be:54:LYS:HE2	1:Be:54:LYS:HB3	1.90	0.40
1:Be:244:GLY:O	1:Be:245:ILE:HD13	2.21	0.40
1:Bg:244:GLY:O	1:Bg:245:ILE:HD13	2.21	0.40
1:Bw:122:MET:HE2	1:Bw:122:MET:HB3	1.99	0.40
1:By:149:PHE:CD1	1:Cs:53:ILE:HD12	2.57	0.40
1:Co:238:LEU:HD12	1:Co:238:LEU:HA	1.94	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Aa	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Ac	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Ae	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Ag	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Ai	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Ak	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Am	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Ao	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Aq	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	As	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Au	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Aw	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Ay	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Ba	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Bc	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Be	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Bg	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Bi	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Bk	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Bm	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Bo	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Bq	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Bs	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Bu	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Bw	223/273 (82%)	215 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	By	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Ca	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Cc	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Ce	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Cg	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Ci	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Ck	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Cm	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Co	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Cq	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
1	Cs	223/273 (82%)	215 (96%)	8 (4%)	0	100	100
All	All	8028/9828 (82%)	7740 (96%)	288 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Aa	195/235 (83%)	195 (100%)	0	100	100
1	Ac	195/235 (83%)	195 (100%)	0	100	100
1	Ae	195/235 (83%)	195 (100%)	0	100	100
1	Ag	195/235 (83%)	195 (100%)	0	100	100
1	Ai	195/235 (83%)	195 (100%)	0	100	100
1	Ak	195/235 (83%)	195 (100%)	0	100	100
1	Am	195/235 (83%)	195 (100%)	0	100	100
1	Ao	195/235 (83%)	195 (100%)	0	100	100
1	Aq	195/235 (83%)	195 (100%)	0	100	100
1	As	195/235 (83%)	195 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Au	195/235 (83%)	195 (100%)	0	100	100
1	Aw	195/235 (83%)	195 (100%)	0	100	100
1	Ay	195/235 (83%)	195 (100%)	0	100	100
1	Ba	195/235 (83%)	195 (100%)	0	100	100
1	Bc	195/235 (83%)	195 (100%)	0	100	100
1	Be	195/235 (83%)	195 (100%)	0	100	100
1	Bg	195/235 (83%)	195 (100%)	0	100	100
1	Bi	195/235 (83%)	195 (100%)	0	100	100
1	Bk	195/235 (83%)	195 (100%)	0	100	100
1	Bm	195/235 (83%)	195 (100%)	0	100	100
1	Bo	195/235 (83%)	195 (100%)	0	100	100
1	Bq	195/235 (83%)	195 (100%)	0	100	100
1	Bs	195/235 (83%)	195 (100%)	0	100	100
1	Bu	195/235 (83%)	195 (100%)	0	100	100
1	Bw	195/235 (83%)	195 (100%)	0	100	100
1	By	195/235 (83%)	195 (100%)	0	100	100
1	Ca	195/235 (83%)	195 (100%)	0	100	100
1	Cc	195/235 (83%)	195 (100%)	0	100	100
1	Ce	195/235 (83%)	195 (100%)	0	100	100
1	Cg	195/235 (83%)	195 (100%)	0	100	100
1	Ci	195/235 (83%)	195 (100%)	0	100	100
1	Ck	195/235 (83%)	195 (100%)	0	100	100
1	Cm	195/235 (83%)	195 (100%)	0	100	100
1	Co	195/235 (83%)	195 (100%)	0	100	100
1	Cq	195/235 (83%)	195 (100%)	0	100	100
1	Cs	195/235 (83%)	195 (100%)	0	100	100
All	All	7020/8460 (83%)	7020 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	Aa	98	ASN
1	Ac	98	ASN
1	Ae	98	ASN
1	Ag	98	ASN
1	Ai	98	ASN
1	Ak	98	ASN
1	Am	98	ASN
1	Ao	98	ASN
1	Aq	98	ASN
1	As	98	ASN
1	Au	98	ASN
1	Aw	98	ASN
1	Ay	98	ASN
1	Ba	98	ASN
1	Bc	98	ASN
1	Be	98	ASN
1	Bg	98	ASN
1	Bi	98	ASN
1	Bk	98	ASN
1	Bm	98	ASN
1	Bo	98	ASN
1	Bq	98	ASN
1	Bs	98	ASN
1	Bu	98	ASN
1	Bw	98	ASN
1	Bw	119	ASN
1	By	98	ASN
1	Ca	98	ASN
1	Ca	119	ASN
1	Cc	98	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	Ab	4/5 (80%)	0	0
2	Ad	4/5 (80%)	0	0
2	Af	4/5 (80%)	0	0
2	Ah	4/5 (80%)	0	0
2	Aj	4/5 (80%)	0	0
2	Al	4/5 (80%)	0	0
2	An	4/5 (80%)	0	0
2	Ap	4/5 (80%)	0	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	Ar	4/5 (80%)	0	0
2	At	4/5 (80%)	0	0
2	Av	4/5 (80%)	0	0
2	Ax	4/5 (80%)	0	0
2	Az	4/5 (80%)	0	0
2	Bb	4/5 (80%)	0	0
2	Bd	4/5 (80%)	0	0
2	Bf	4/5 (80%)	0	0
2	Bh	4/5 (80%)	0	0
2	Bj	4/5 (80%)	0	0
2	Bl	4/5 (80%)	0	0
2	Bn	4/5 (80%)	0	0
2	Bp	4/5 (80%)	0	0
2	Br	4/5 (80%)	0	0
2	Bt	4/5 (80%)	0	0
2	Bv	4/5 (80%)	0	0
2	Bx	4/5 (80%)	0	0
2	Bz	4/5 (80%)	0	0
2	Cb	4/5 (80%)	0	0
2	Cd	4/5 (80%)	0	0
2	Cf	4/5 (80%)	0	0
2	Ch	4/5 (80%)	0	0
2	Cj	4/5 (80%)	0	0
2	Cl	4/5 (80%)	0	0
2	Cn	4/5 (80%)	0	0
2	Cp	4/5 (80%)	0	0
2	Cr	4/5 (80%)	0	0
2	Ct	4/5 (80%)	0	0
All	All	144/180 (80%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

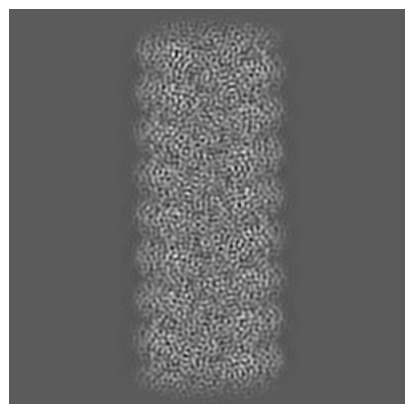
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53863. These allow visual inspection of the internal detail of the map and identification of artifacts.

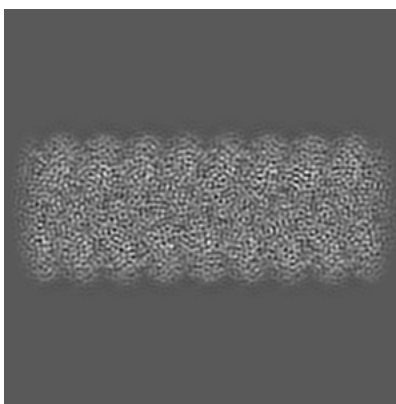
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

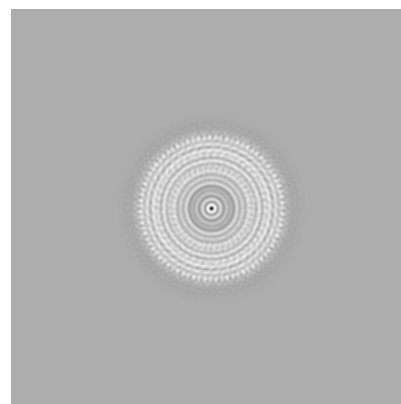
6.1.1 Primary map



X

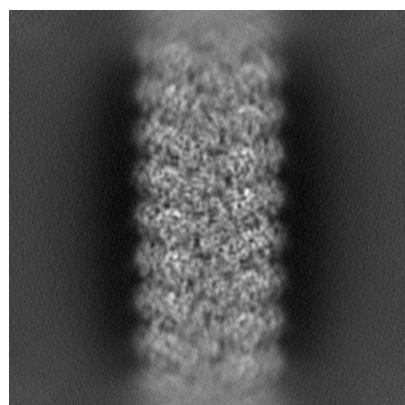


Y

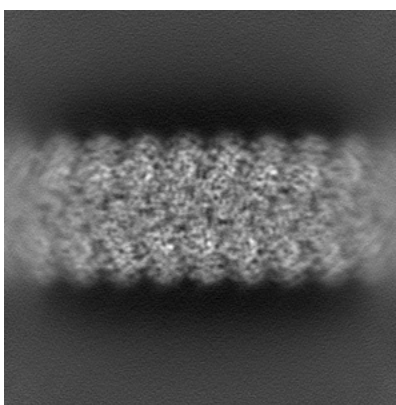


Z

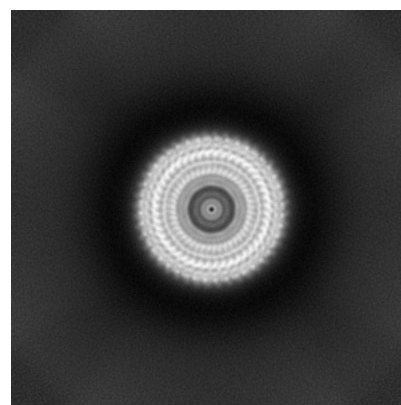
6.1.2 Raw map



X



Y

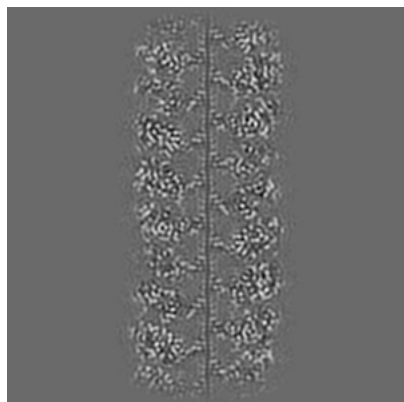


Z

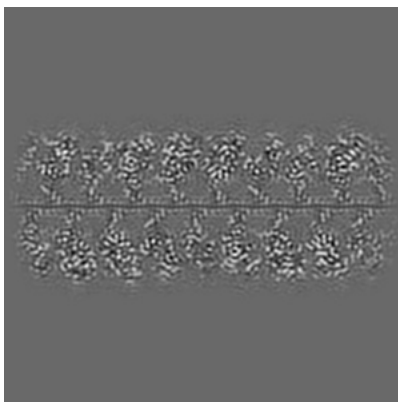
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

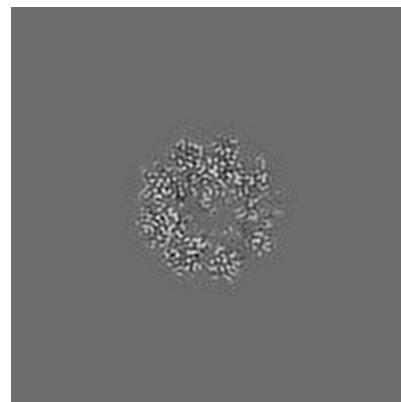
6.2.1 Primary map



X Index: 175

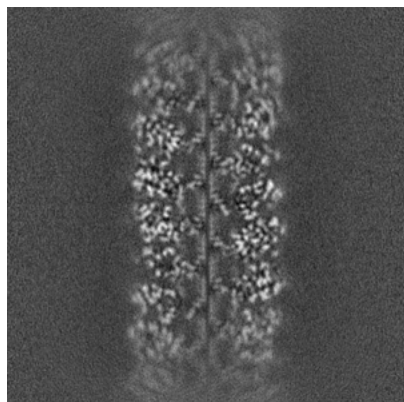


Y Index: 175

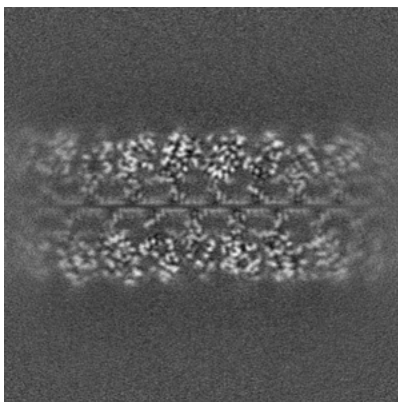


Z Index: 175

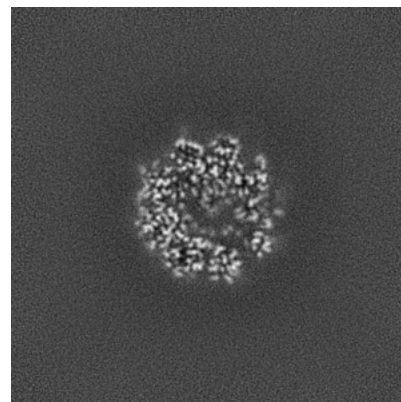
6.2.2 Raw map



X Index: 175



Y Index: 175

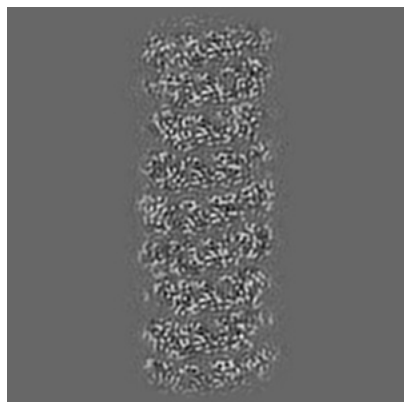


Z Index: 175

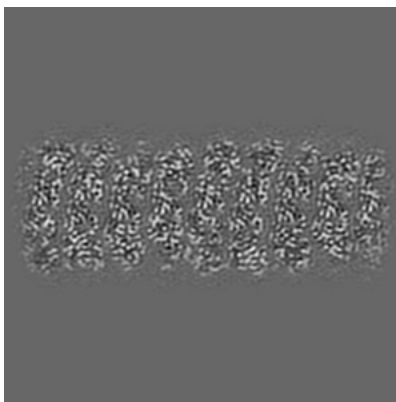
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

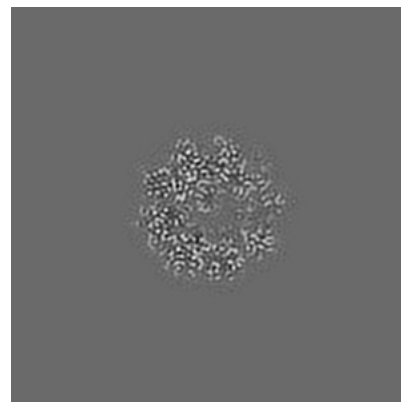
6.3.1 Primary map



X Index: 145

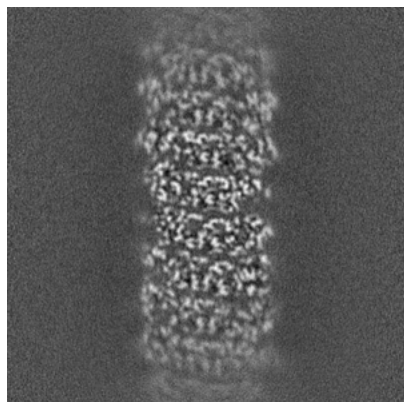


Y Index: 205

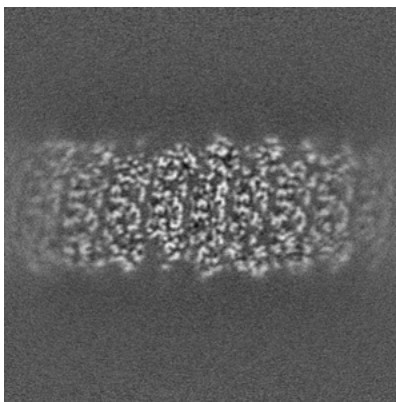


Z Index: 172

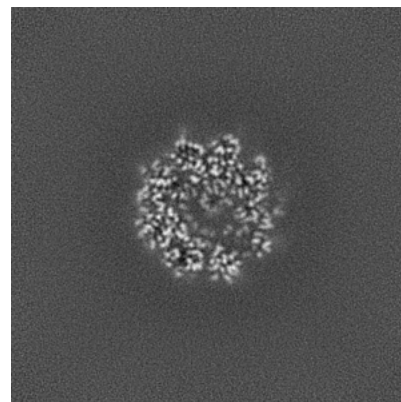
6.3.2 Raw map



X Index: 207



Y Index: 207

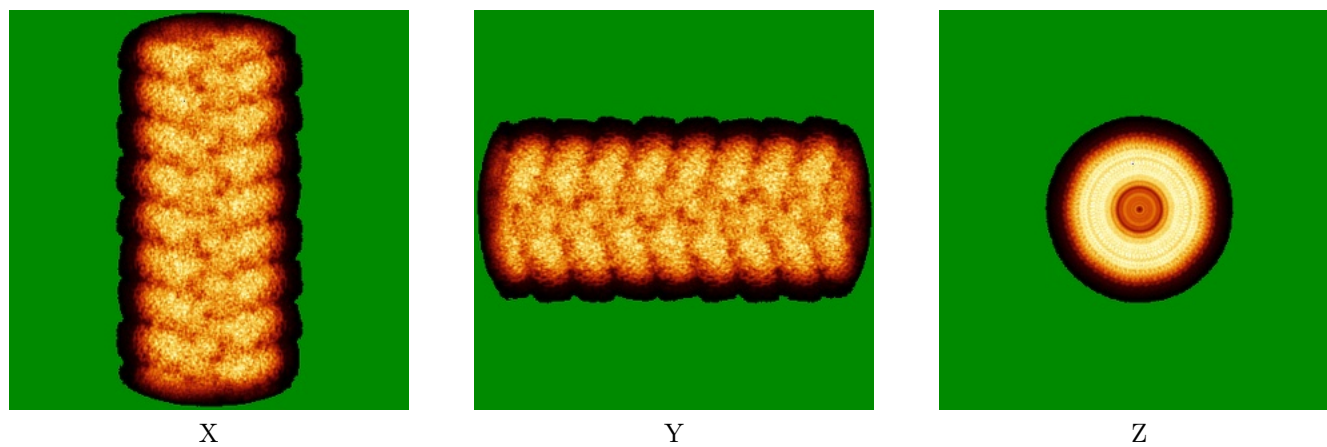


Z Index: 176

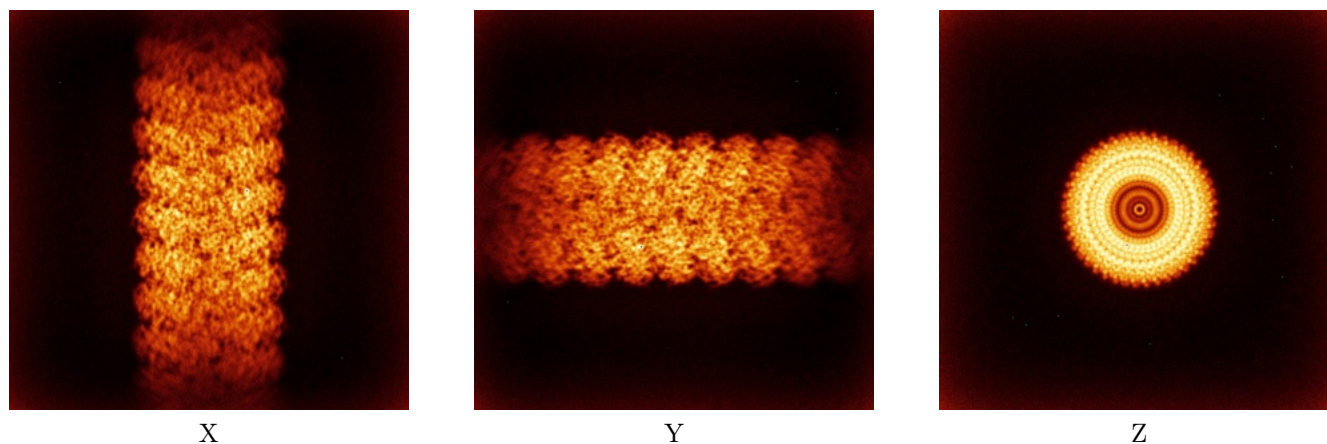
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

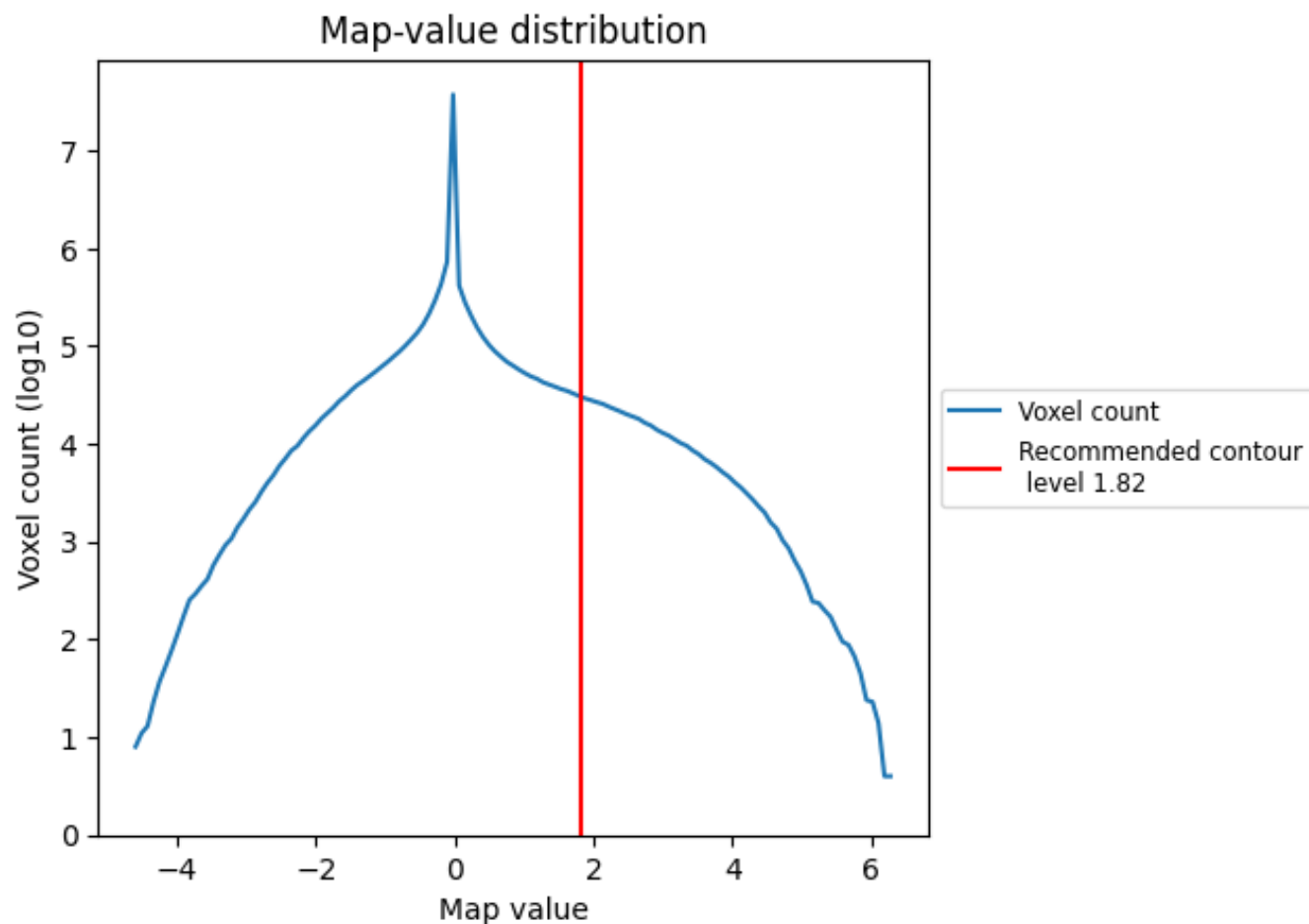
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

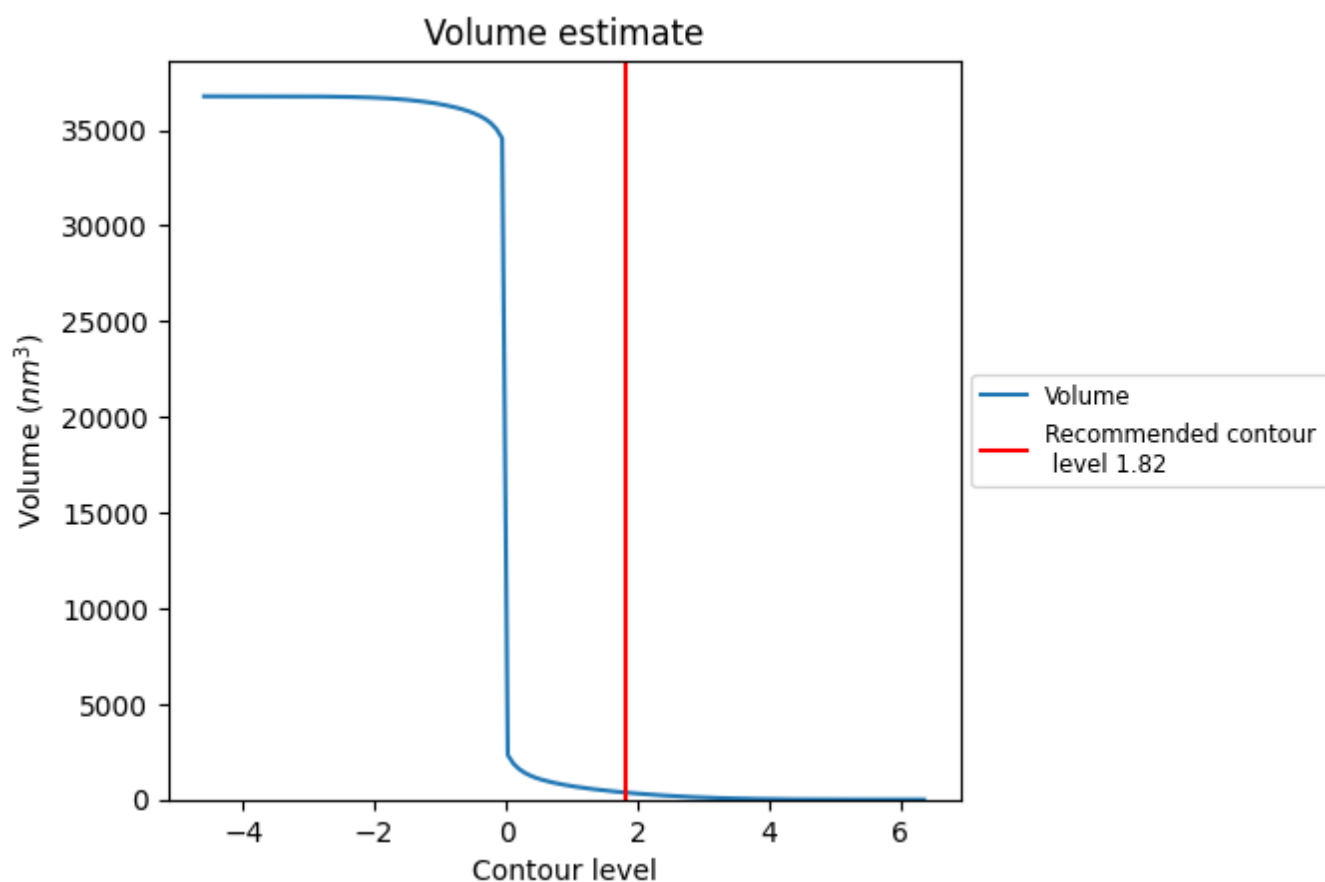
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

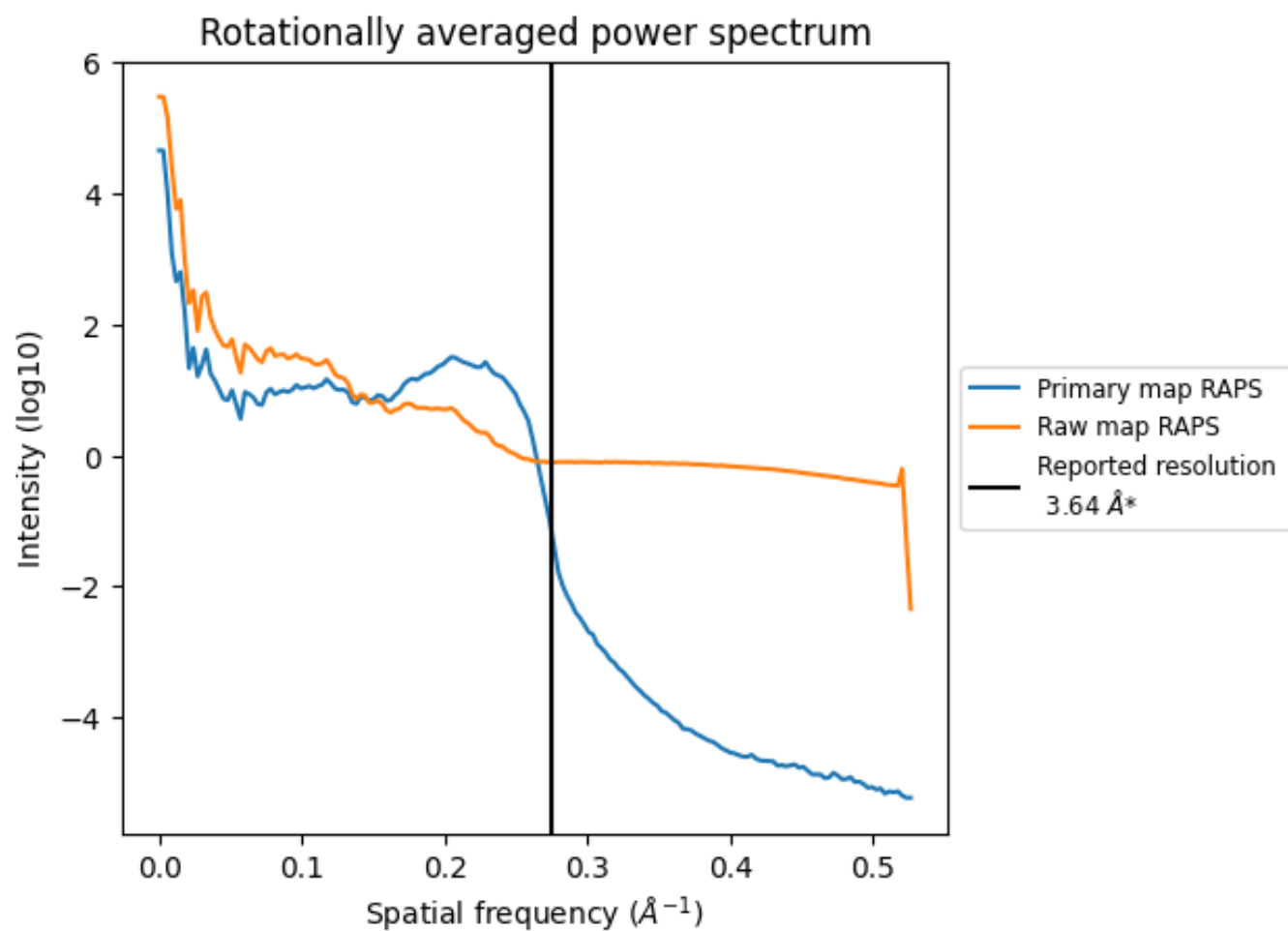
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 366 nm³; this corresponds to an approximate mass of 331 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 ⓘ

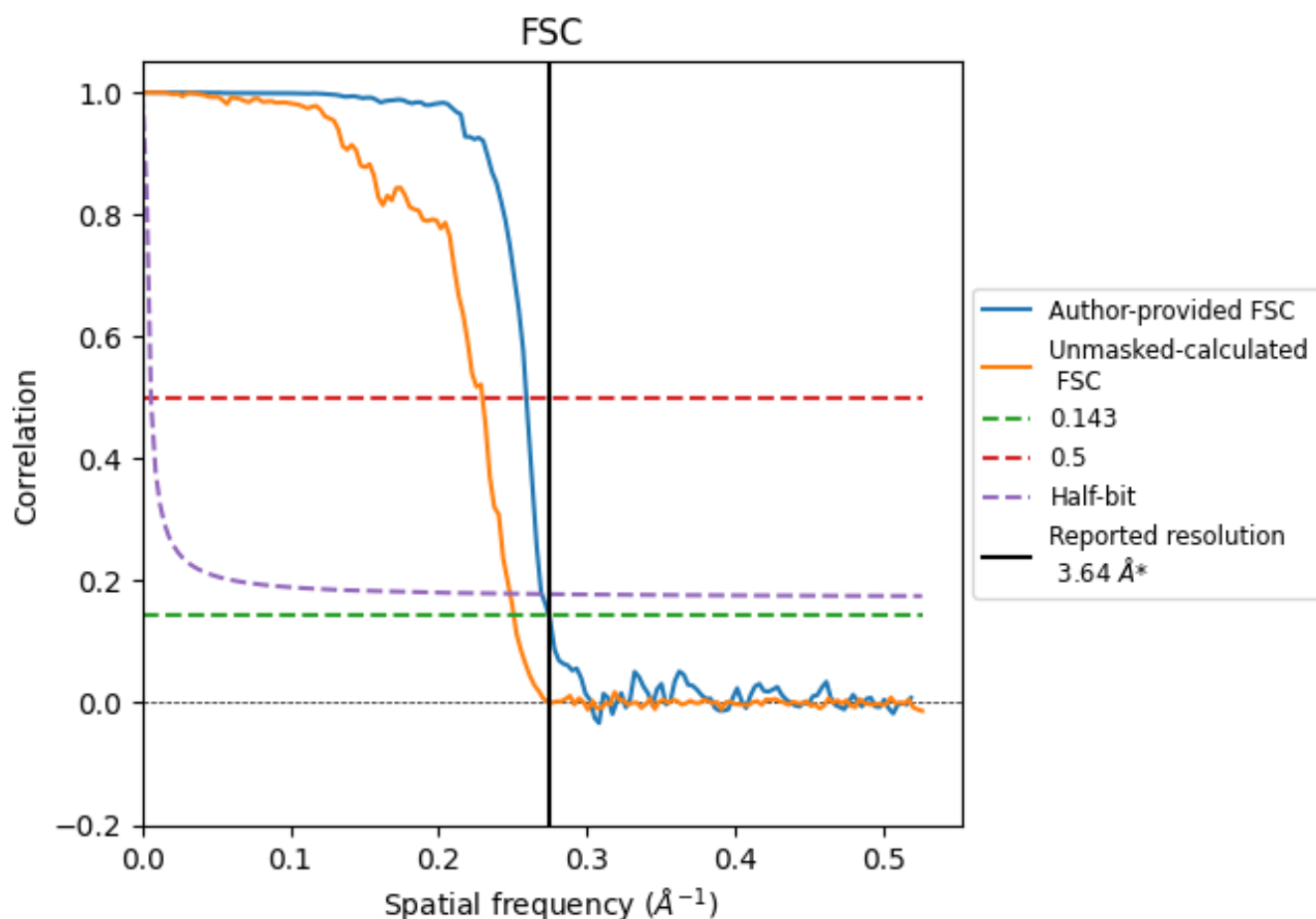


*Reported resolution corresponds to spatial frequency of 0.275 Å⁻¹

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 0.275 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.64	-	-
Author-provided FSC curve	3.64	3.86	3.71
Unmasked-calculated*	3.99	4.36	4.03

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

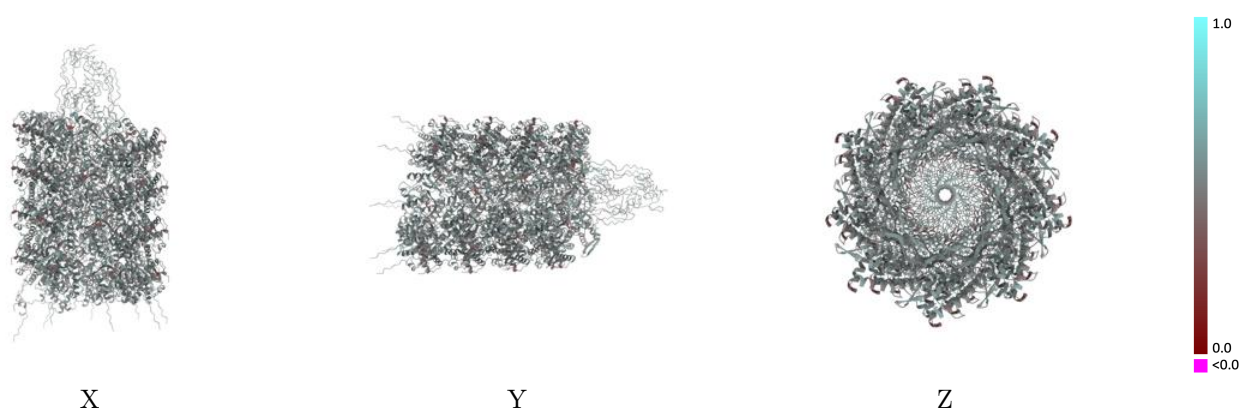
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53863 and PDB model 9R9X. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)

This section was not generated.

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

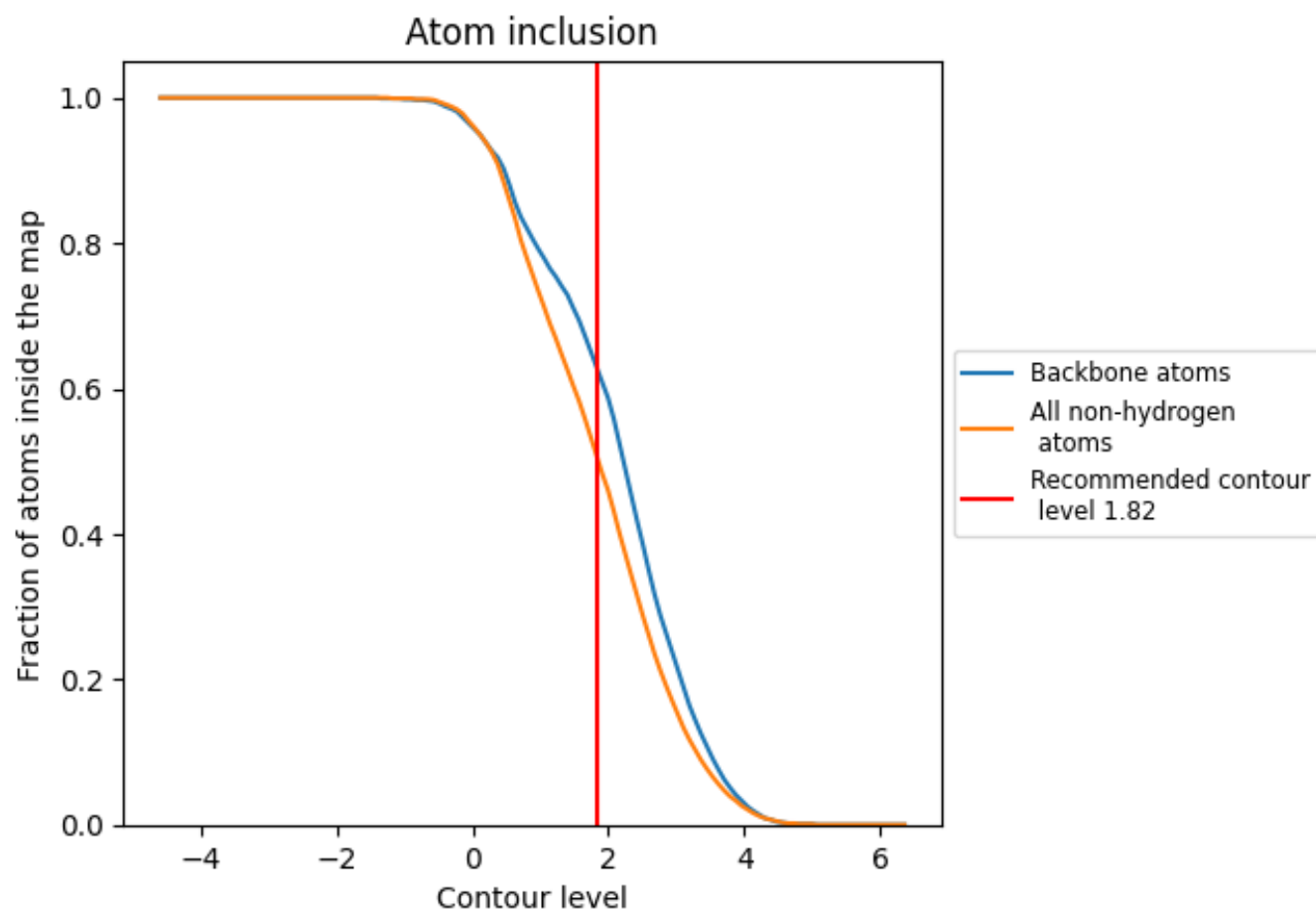


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 51% 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 (1.82) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5090	 0.5090
Aa	 0.4950	 0.5090
Ab	 0.7200	 0.5160
Ac	 0.4980	 0.5080
Ad	 0.7300	 0.5150
Ae	 0.4980	 0.5090
Af	 0.6600	 0.4950
Ag	 0.4940	 0.5080
Ah	 0.7000	 0.5020
Ai	 0.4990	 0.5090
Aj	 0.6600	 0.4620
Ak	 0.5000	 0.5100
Al	 0.7000	 0.5050
Am	 0.4950	 0.5080
An	 0.7600	 0.5100
Ao	 0.4970	 0.5100
Ap	 0.7300	 0.5150
Aq	 0.4990	 0.5100
Ar	 0.7300	 0.5150
As	 0.4960	 0.5090
At	 0.7000	 0.4930
Au	 0.5010	 0.5090
Av	 0.7200	 0.5160
Aw	 0.4970	 0.5090
Ax	 0.7300	 0.5070
Ay	 0.4960	 0.5080
Az	 0.6700	 0.4830
Ba	 0.4980	 0.5100
Bb	 0.7400	 0.5190
Bc	 0.4970	 0.5100
Bd	 0.7400	 0.5130
Be	 0.4940	 0.5090
Bf	 0.6800	 0.5110
Bg	 0.4910	 0.5090
Bh	 0.7500	 0.5120



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Chain	Atom inclusion	Q-score
Bi	 0.4960	 0.5090
Bj	 0.7100	 0.5020
Bk	 0.4940	 0.5090
Bl	 0.7300	 0.5030
Bm	 0.5020	 0.5100
Bn	 0.7400	 0.5150
Bo	 0.4990	 0.5090
Bp	 0.6900	 0.4880
Bq	 0.4980	 0.5090
Br	 0.6900	 0.5080
Bs	 0.4990	 0.5090
Bt	 0.7300	 0.5000
Bu	 0.4950	 0.5100
Bv	 0.6900	 0.4860
Bw	 0.4950	 0.5090
Bx	 0.6700	 0.4900
By	 0.4980	 0.5090
Bz	 0.7100	 0.5160
Ca	 0.4940	 0.5100
Cb	 0.7400	 0.5180
Cc	 0.4990	 0.5090
Cd	 0.7000	 0.5040
Ce	 0.4990	 0.5090
Cf	 0.7100	 0.5130
Cg	 0.4920	 0.5070
Ch	 0.7800	 0.5120
Ci	 0.4980	 0.5080
Cj	 0.7100	 0.5070
Ck	 0.4950	 0.5090
Cl	 0.6500	 0.4900
Cm	 0.4980	 0.5090
Cn	 0.7200	 0.5200
Co	 0.4960	 0.5090
Cp	 0.7600	 0.5150
Cq	 0.4980	 0.5090
Cr	 0.7100	 0.5150
Cs	 0.4990	 0.5100
Ct	 0.7300	 0.5170