



Full wwPDB EM Validation Report ⓘ

Jun 22, 2026 – 02:25 PM JST

PDB ID : 9UXW / pdb_00009uxw
EMDB ID : EMD-64603
Title : RNA polymerase II elongation complex stalled at SHL(-0.5) in the hexasome of the overlapping dinucleosome
Authors : Chen, Z.; Ho, C.; Tanaka, H.; Kujirai, T.; Ogasawara, M.; Ehara, H.; Sekine, S.; Takizawa, Y.; Kurumizaka, H.
Deposited on : 2025-05-14
Resolution : 3.74 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

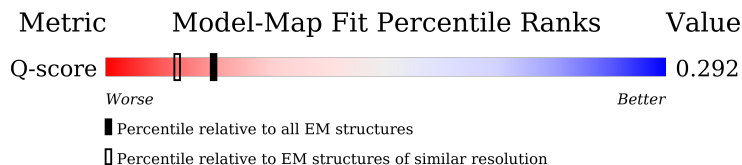
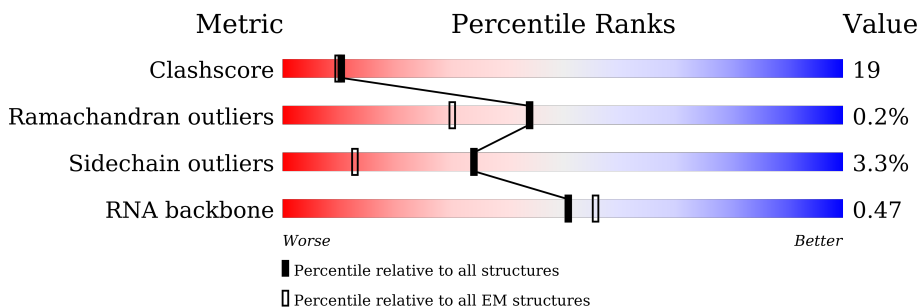
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.74 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	10346 (3.24 - 4.24)

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	A	1743	
2	B	1227	
3	C	304	

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Mol	Chain	Length	Quality of chain
4	D	186	
5	E	214	
6	F	155	
7	G	171	
8	H	145	
9	I	115	
10	J	72	
11	K	118	
12	L	72	
13	P	14	
14	T	254	
15	a	139	
15	e	139	
15	k	139	
15	m	139	
16	b	106	
16	f	106	
16	l	106	
16	n	106	
17	c	133	
17	g	133	
17	o	133	
18	d	129	
18	h	129	
18	p	129	

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Mol	Chain	Length	Quality of chain
19	N	254	<div><div></div><div>17%</div><div>39%</div><div>56%</div><div>5%</div></div>

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 51489 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 DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1402	Total	C	N	O	S	0	0
			11049	6966	1927	2086	70		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1164	Total	C	N	O	S	0	0
			9284	5848	1639	1739	58		

- Molecule 3 is a protein called RNA polymerase II third largest subunit B44, part of central core.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	263	Total	C	N	O	S	0	0
			2098	1319	354	413	12		

- Molecule 4 is a protein called RNA polymerase II subunit B32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	174	Total	C	N	O	S	0	0
			1349	828	244	274	3		

- Molecule 5 is a protein called RNA polymerase subunit ABC27, common to RNA polymerases I, II, and III.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	213	Total	C	N	O	S	0	0
			1741	1094	312	325	10		

- Molecule 6 is a protein called RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	84	Total	C	N	O	S	0	0
			677	429	114	131	3		

- Molecule 7 is a protein called RNA polymerase II subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1325	858	214	248	5		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	133	Total	C	N	O	S	0	0
			1053	671	169	209	4		

- Molecule 9 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	111	Total	C	N	O	S	0	0
			917	565	161	180	11		

- Molecule 10 is a protein called RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	67	Total	C	N	O	S	0	0
			554	355	97	96	6		

- Molecule 11 is a protein called RNA polymerase II subunit B12.5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	113	Total	C	N	O	S	0	0
			932	599	160	169	4		

- Molecule 12 is a protein called RNA polymerase subunit ABC10-alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	45	Total	C	N	O	S	0	0
			359	221	72	61	5		

- Molecule 13 is a RNA chain called RNA (5'-R(P*GP*UP*CP*GP*CP*UP*CP*UP*UP*C P*CP*UP*CP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	14	Total	C	N	O	P	0	0
			286	128	41	103	14		

- Molecule 14 is a DNA chain called DNA (254-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
14	T	254	Total	C	N	O	P	0	0
			5254	2480	1021	1499	254		

- Molecule 15 is a protein called Histone H3.3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	a	95	Total	C	N	O	S	0	0
			779	492	150	135	2		
15	e	95	Total	C	N	O	S	0	0
			779	492	150	135	2		
15	k	73	Total	C	N	O	S	0	0
			587	373	109	103	2		
15	m	95	Total	C	N	O	S	0	0
			779	492	150	135	2		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	-3	GLY	-	expression tag	UNP P84243
a	-2	SER	-	expression tag	UNP P84243
a	-1	HIS	-	expression tag	UNP P84243
e	-3	GLY	-	expression tag	UNP P84243
e	-2	SER	-	expression tag	UNP P84243
e	-1	HIS	-	expression tag	UNP P84243
k	-3	GLY	-	expression tag	UNP P84243
k	-2	SER	-	expression tag	UNP P84243
k	-1	HIS	-	expression tag	UNP P84243
m	-3	GLY	-	expression tag	UNP P84243
m	-2	SER	-	expression tag	UNP P84243
m	-1	HIS	-	expression tag	UNP P84243

- Molecule 16 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	b	78	Total	C	N	O	S	0	0
			619	391	120	107	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
16	f	78	Total	C	N	O	S	0	0
			619	391	120	107	1		
16	l	71	Total	C	N	O	S	0	0
			568	357	113	97	1		
16	n	78	Total	C	N	O	S	0	0
			619	391	120	107	1		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	-3	GLY	-	expression tag	UNP P62805
b	-2	SER	-	expression tag	UNP P62805
b	-1	HIS	-	expression tag	UNP P62805
f	-3	GLY	-	expression tag	UNP P62805
f	-2	SER	-	expression tag	UNP P62805
f	-1	HIS	-	expression tag	UNP P62805
l	-3	GLY	-	expression tag	UNP P62805
l	-2	SER	-	expression tag	UNP P62805
l	-1	HIS	-	expression tag	UNP P62805
n	-3	GLY	-	expression tag	UNP P62805
n	-2	SER	-	expression tag	UNP P62805
n	-1	HIS	-	expression tag	UNP P62805

- Molecule 17 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	c	98	Total	C	N	O	0	0
			757	475	149	133		
17	g	98	Total	C	N	O	0	0
			757	475	149	133		
17	o	97	Total	C	N	O	0	0
			752	472	148	132		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	-3	GLY	-	expression tag	UNP P04908
c	-2	SER	-	expression tag	UNP P04908
c	-1	HIS	-	expression tag	UNP P04908
g	-3	GLY	-	expression tag	UNP P04908
g	-2	SER	-	expression tag	UNP P04908
g	-1	HIS	-	expression tag	UNP P04908

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Chain	Residue	Modelled	Actual	Comment	Reference
o	-3	GLY	-	expression tag	UNP P04908
o	-2	SER	-	expression tag	UNP P04908
o	-1	HIS	-	expression tag	UNP P04908

- Molecule 18 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	d	90	Total	C	N	O	S	0	0
			698	440	123	133	2		
18	h	89	Total	C	N	O	S	0	0
			689	435	122	130	2		
18	p	87	Total	C	N	O	S	0	0
			679	430	120	127	2		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	-3	GLY	-	expression tag	UNP P06899
d	-2	SER	-	expression tag	UNP P06899
d	-1	HIS	-	expression tag	UNP P06899
h	-3	GLY	-	expression tag	UNP P06899
h	-2	SER	-	expression tag	UNP P06899
h	-1	HIS	-	expression tag	UNP P06899
p	-3	GLY	-	expression tag	UNP P06899
p	-2	SER	-	expression tag	UNP P06899
p	-1	HIS	-	expression tag	UNP P06899

- Molecule 19 is a DNA chain called DNA (254-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	242	Total	C	N	O	P	0	0
			4921	2342	865	1472	242		

- Molecule 20 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
20	A	2	Total	Zn	0
			2	2	
20	B	1	Total	Zn	0
			1	1	
20	C	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
20	I	2	Total 2	Zn 2	0
20	J	1	Total 1	Zn 1	0
20	L	1	Total 1	Zn 1	0

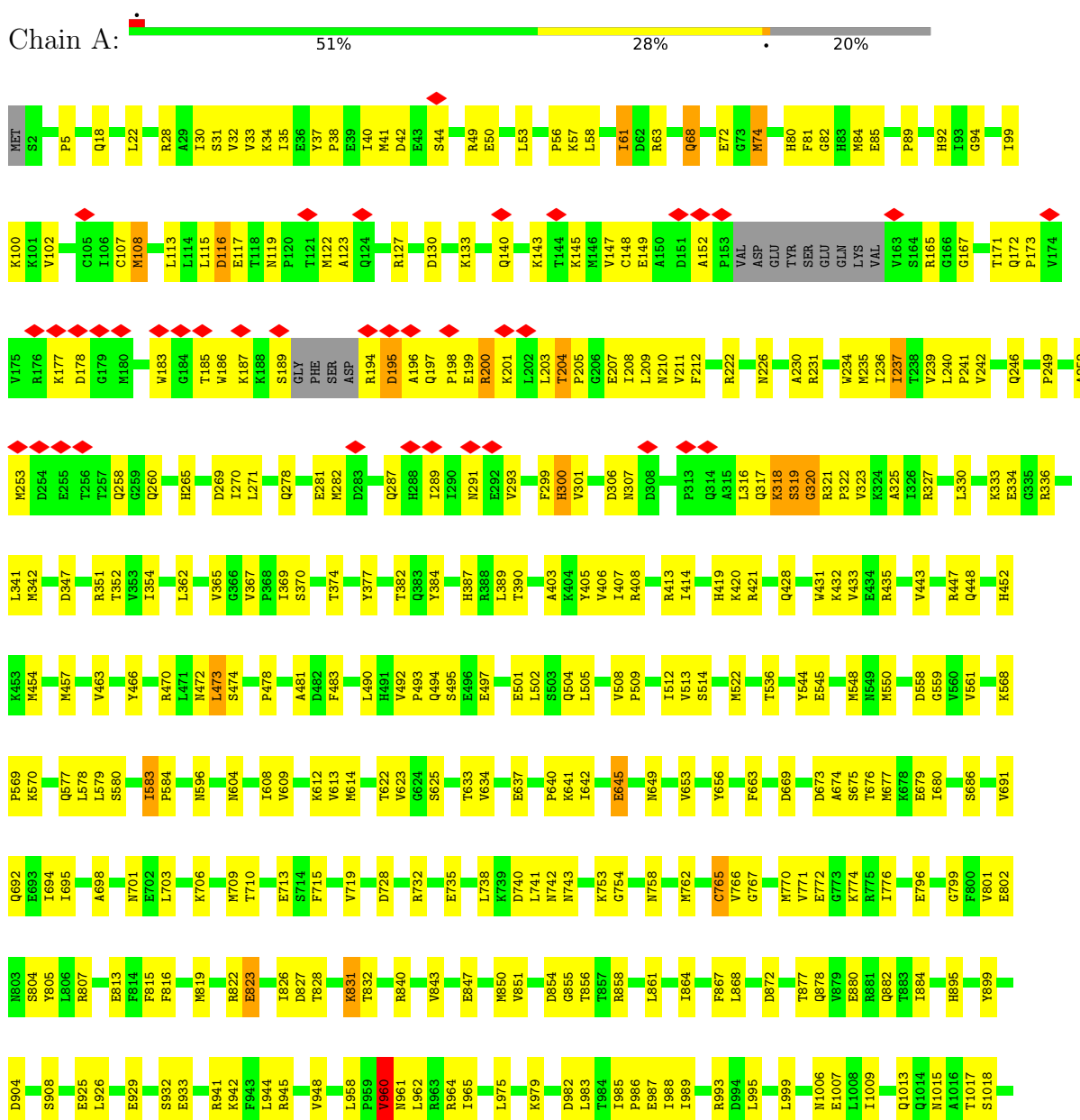
- Molecule 21 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
21	A	1	Total 1	Mg 1	0


3 Residue-property plots

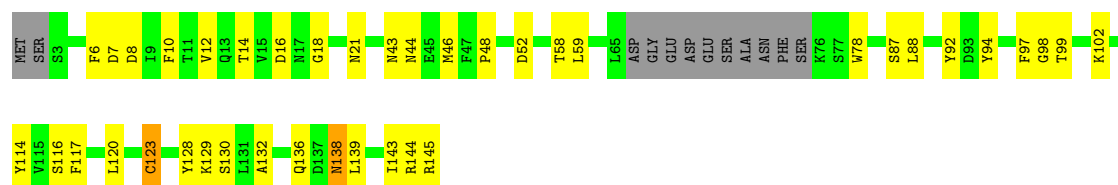
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: DNA-directed RNA polymerase subunit



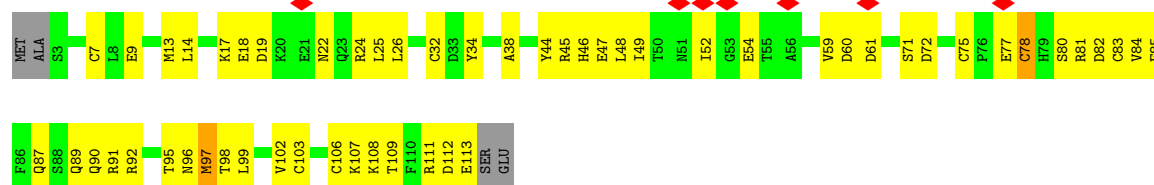


Chain H: 



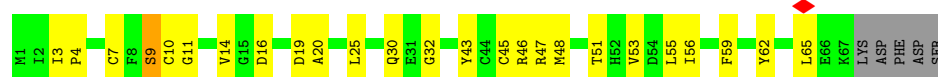
- Molecule 9: DNA-directed RNA polymerase subunit

Chain I: 



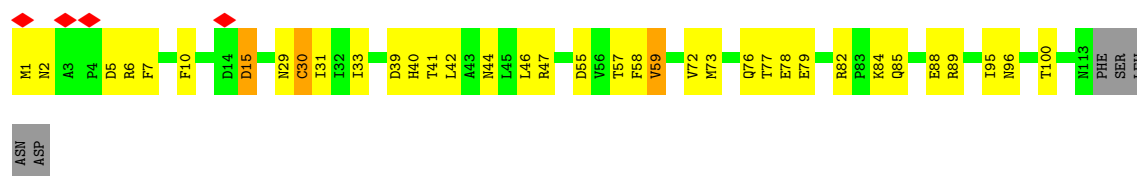
- Molecule 10: RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III

Chain J: 



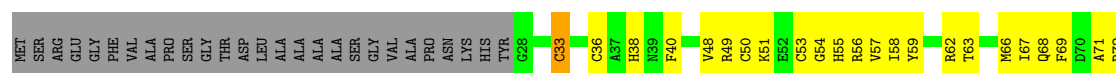
- Molecule 11: RNA polymerase II subunit B12.5

Chain K: 



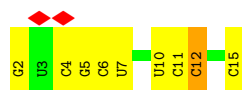
- Molecule 12: RNA polymerase subunit ABC10-alpha

Chain L: 

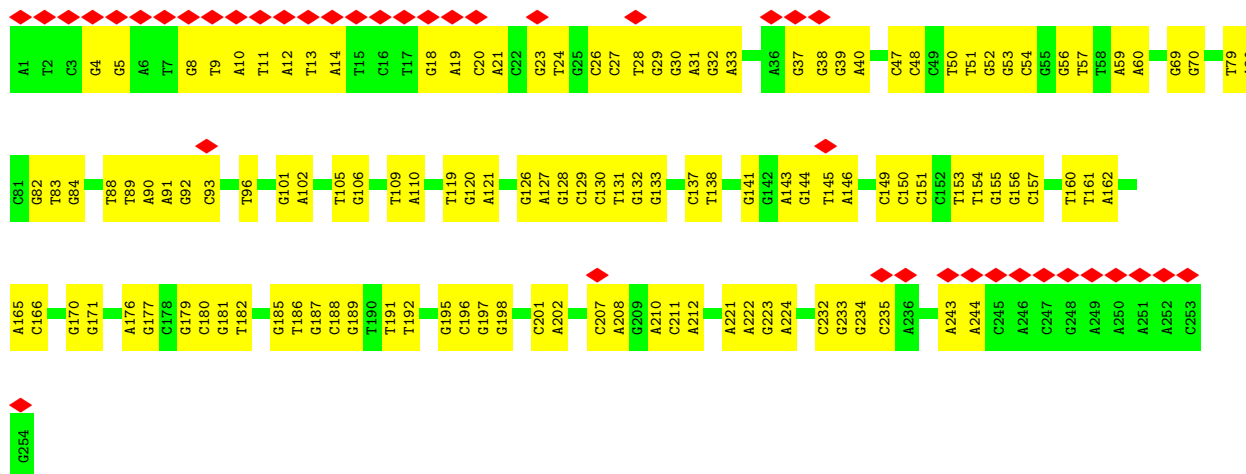


- Molecule 13: RNA (5'-R(P*GP*UP*CP*GP*CP*UP*CP*UP*UP*CP*CP*UP*CP*C)-3')

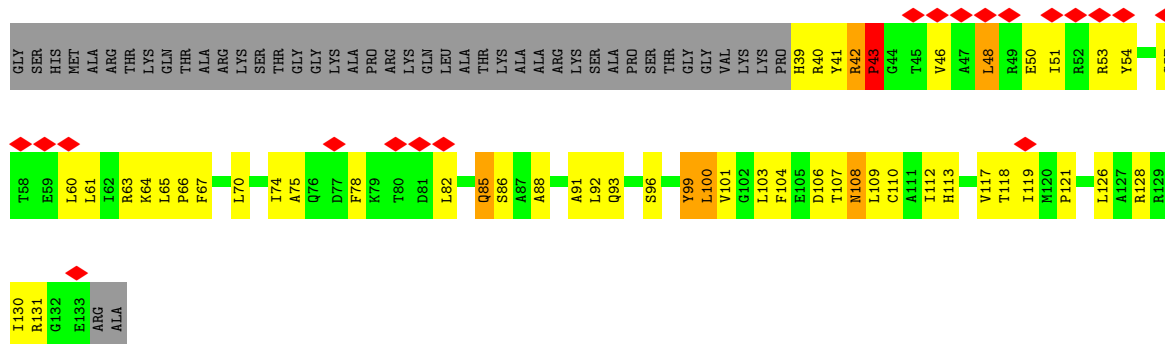
Chain P: 



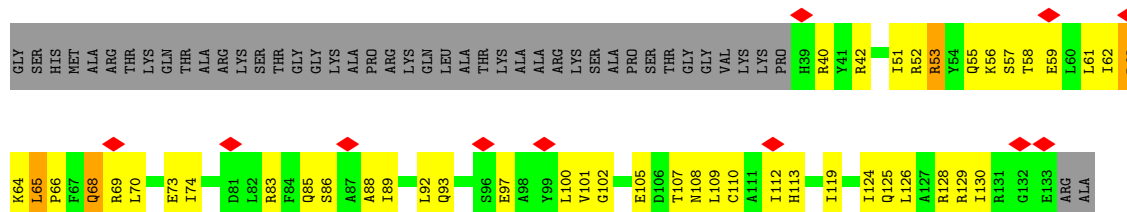
• Molecule 14: DNA (254-MER)



• Molecule 15: Histone H3.3

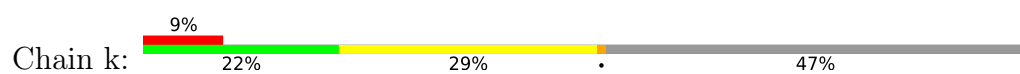


• Molecule 15: Histone H3.3



• Molecule 15: Histone H3.3



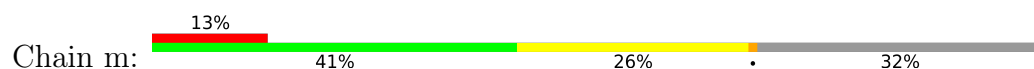


GLY SER THR GLU MET LEU ALA ARG THR LYS GLN THR ALA ARG LYS THR SER THR GLY LYS ALA PRO ARG LYS GLN LEU THR LYS ALA ARG LYS SER ALA PRO SER THR GLY VAL LYS LYS PRO HIS ARG THR ARG PRO GLY THR VAL ALA LEU ARG GLU ILE ARG TYR GLN LYS

SER THR GLU MET LEU L61 L62 L63 L64 L65 L66 L67 L68 L69 L70 L71 L72 D81 F84 A87 A88 I89 A91 L92 Q93 E94 A95 S96 E97 A98 A99 L100 L101 G102 L103 F104 E105 D106 T107 N108 L109 T112 H113 T118 T119 M120 P121 K122 D123 I124 Q125 L126 A127 R128 R129

I130 R131 G132 E133 ARG ALA

• Molecule 15: Histone H3.3



GLY SER HIS MET LEU ALA ARG THR LYS GLN THR ALA ARG LYS THR SER THR GLY LYS ALA PRO ARG LYS GLN LEU THR LYS ALA ARG LYS SER ALA PRO SER THR GLY VAL LYS LYS PRO H39 R40 Y41 T45 V46 A47 L48 E50 R53 Y54 Q55 K56 E59 L60

L61 L62 R63 F67 Q68 R69 L70 V71 R72 Q76 D77 F78 K79 T80 D81 L82 R83 L89 G90 A91 A92 L92 Q93 E94 A95 S96 E97 A98 Y99 L100 V101 E105 D106 T107 N108 H113 P121 I124 Q125 L126 A127 I130 R131 G132 E133 ARG ALA

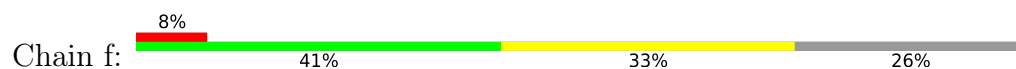
• Molecule 16: Histone H4



GLY SER HIS MET LEU ALA ARG THR LYS GLN THR ALA ARG LYS THR SER THR GLY LYS ALA PRO ARG LYS GLN LEU THR LYS ALA ARG LYS SER ALA PRO SER THR GLY VAL LYS LYS PRO H39 R40 Y41 T45 V46 A47 L48 E50 R53 Y54 Q55 K56 E59 L60

K59 V60 F61 L62 E63 R64 V65 I66 R67 Y72 H75 V81 M84 D85 V86 Y88 A89 L90 K91 R92 Q93 L97 Y98 G99 F100 G101 G102

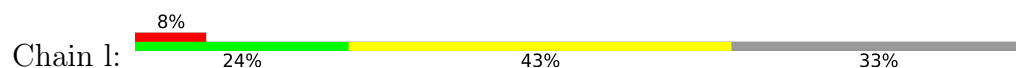
• Molecule 16: Histone H4

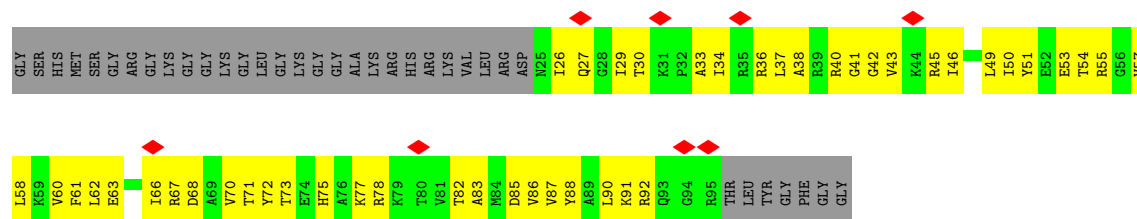


GLY SER HIS MET LEU ALA ARG THR LYS GLN THR ALA ARG LYS THR SER THR GLY LYS ALA PRO ARG LYS GLN LEU THR LYS ALA ARG LYS SER ALA PRO SER THR GLY VAL LYS LYS PRO H39 R40 Y41 T45 V46 A47 L48 E50 R53 Y54 Q55 K56 E59 L60

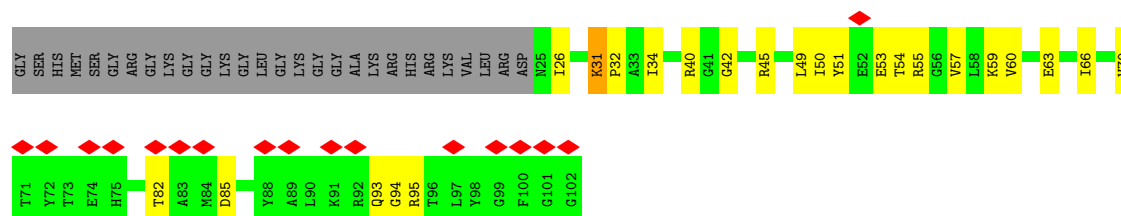
E63 D68 T71 Y72 H75 R78 T80 A83 V87 Y88 A89 L90 K91 R92 Q93 G94 R95 T96 L97 G101 G102

• Molecule 16: Histone H4

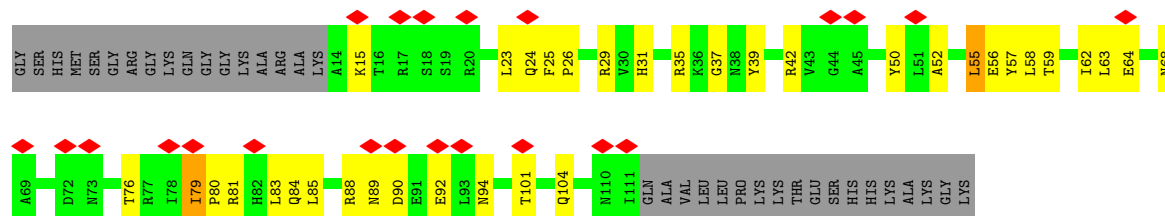




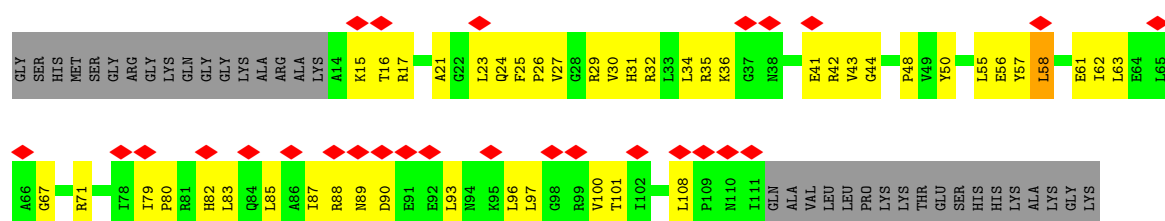
- Molecule 16: Histone H4



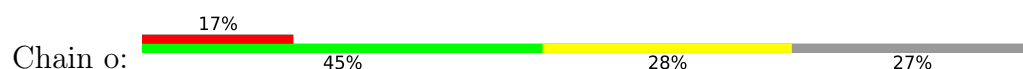
- Molecule 17: Histone H2A type 1-B/E



- Molecule 17: Histone H2A type 1-B/E

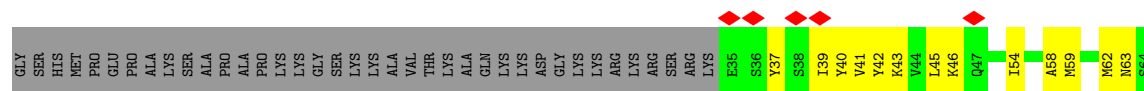


- Molecule 17: Histone H2A type 1-B/E

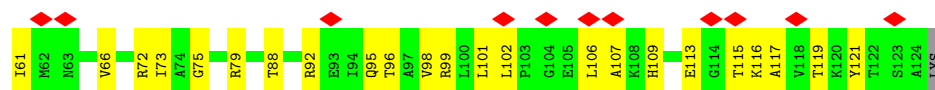




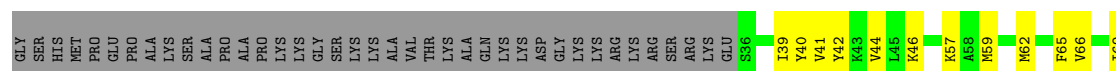
• Molecule 18: Histone H2B type 1-J



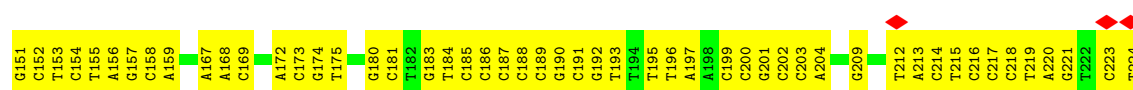
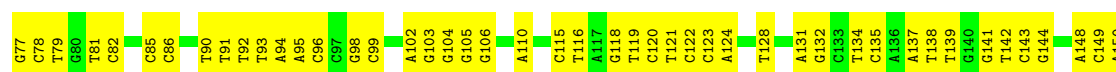
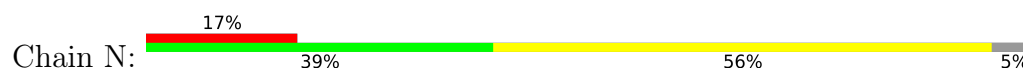
• Molecule 18: Histone H2B type 1-J



• Molecule 18: Histone H2B type 1-J



• Molecule 19: DNA (254-MER)



C225	C226	A227	G228	G229	C230	A231	C232	G233	T234	G235	T236	C237	A238	G239	A240	T241	A242	T243	A244	T245	A246	C247	A248	T249	C250	C251	G252	A253	T254
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	33000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	59.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.046	Depositor
Minimum map value	-0.022	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00777	Depositor
Map size (\AA)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.41	0/11252	0.56	0/15201
2	B	0.42	0/9464	0.57	0/12763
3	C	0.39	0/2139	0.49	0/2895
4	D	0.20	0/1361	0.50	0/1837
5	E	0.38	0/1773	0.62	0/2385
6	F	0.34	0/687	0.54	0/931
7	G	0.24	0/1354	0.55	0/1837
8	H	0.35	0/1070	0.45	0/1444
9	I	0.30	0/934	0.59	0/1257
10	J	0.49	0/563	0.59	0/753
11	K	0.40	0/953	0.50	0/1291
12	L	0.30	0/365	0.54	0/484
13	P	0.75	0/315	0.84	0/486
14	T	0.63	0/5912	0.88	0/9131
15	a	0.62	0/790	0.90	0/1060
15	e	0.65	0/790	0.91	0/1060
15	k	0.54	0/594	0.89	0/797
15	m	0.64	0/790	0.98	0/1060
16	b	0.62	0/626	0.86	0/837
16	f	0.49	0/626	0.82	0/837
16	l	0.55	0/573	0.88	0/767
16	n	0.62	0/626	0.87	0/837
17	c	0.60	0/766	0.97	0/1033
17	g	0.36	0/766	0.64	0/1033
17	o	0.26	0/761	0.59	0/1026
18	d	0.47	0/709	0.69	0/955
18	h	0.35	0/700	0.61	0/943
18	p	0.29	0/690	0.59	0/930
19	N	0.63	0/5504	0.91	0/8483
All	All	0.48	0/53453	0.70	0/74353

There are no bond length outliers.

There are no bond angle outliers.

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	A	11049	0	11076	434	0
2	B	9284	0	9282	324	0
3	C	2098	0	2057	77	0
4	D	1349	0	1345	40	0
5	E	1741	0	1754	64	0
6	F	677	0	693	19	0
7	G	1325	0	1342	47	0
8	H	1053	0	1050	27	0
9	I	917	0	864	49	0
10	J	554	0	573	23	0
11	K	932	0	944	35	0
12	L	359	0	358	24	0
13	P	286	0	150	7	0
14	T	5254	0	2838	154	0
15	a	779	0	814	65	0
15	e	779	0	814	58	0
15	k	587	0	615	59	0
15	m	779	0	814	33	0
16	b	619	0	659	57	0
16	f	619	0	659	46	0
16	l	568	0	614	65	0
16	n	619	0	659	21	0
17	c	757	0	802	41	0
17	g	757	0	802	45	0
17	o	752	0	797	42	0
18	d	698	0	710	42	0
18	h	689	0	704	35	0
18	p	679	0	698	34	0
19	N	4921	0	2727	181	0
20	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	B	1	0	0	0	0
20	C	1	0	0	0	0
20	I	2	0	0	0	0
20	J	1	0	0	0	0
20	L	1	0	0	0	0
21	A	1	0	0	0	0
All	All	51489	0	47214	1837	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 19.

All (1837) 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)
14:T:12:DA:H2''	14:T:13:DT:C7	1.34	1.55
19:N:5:DT:C2'	19:N:6:DT:H71	1.36	1.54
19:N:5:DT:H2''	19:N:6:DT:C7	1.45	1.42
19:N:8:DG:H2''	19:N:9:DT:C7	1.48	1.42
19:N:8:DG:C2'	19:N:9:DT:H72	1.49	1.40
19:N:8:DG:C2'	19:N:9:DT:C7	2.00	1.39
14:T:12:DA:C2'	14:T:13:DT:H71	1.54	1.34
19:N:3:DT:C2'	19:N:4:DT:H71	1.58	1.30
19:N:5:DT:C2'	19:N:6:DT:C7	2.02	1.27
14:T:12:DA:C2'	14:T:13:DT:C7	2.10	1.21
14:T:23:DG:H2''	14:T:24:DT:H71	1.22	1.14
19:N:11:DT:H2''	19:N:12:DT:H71	1.24	1.12
19:N:8:DG:C1'	19:N:9:DT:H72	1.80	1.11
19:N:8:DG:H2''	19:N:9:DT:H73	1.06	1.05
19:N:233:DG:H2''	19:N:234:DT:H71	1.41	1.02
19:N:5:DT:H2'	19:N:6:DT:C7	1.86	1.02
14:T:23:DG:C2'	14:T:24:DT:H71	1.88	1.02
19:N:3:DT:H2''	19:N:4:DT:C7	1.90	1.01
15:m:63:ARG:HD3	19:N:98:DG:H4'	1.02	1.01
19:N:8:DG:N9	19:N:9:DT:H72	1.75	1.00
15:m:63:ARG:HD3	19:N:98:DG:C4'	1.94	0.98
19:N:2:DG:H2''	19:N:3:DT:H71	1.44	0.97
14:T:51:DT:H2''	14:T:52:DG:H5''	1.49	0.95
19:N:218:DC:C6	19:N:219:DT:H72	2.02	0.95
15:m:63:ARG:CD	19:N:98:DG:H4'	1.97	0.95
19:N:8:DG:H2'	19:N:9:DT:H72	1.46	0.95
19:N:3:DT:H2''	19:N:4:DT:H71	0.94	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:T:12:DA:C2'	14:T:13:DT:H73	1.99	0.91
19:N:3:DT:C2'	19:N:4:DT:C7	2.49	0.91
14:T:137:DC:H2'	14:T:138:DT:H71	1.53	0.91
15:e:63:ARG:HG3	15:e:66:PRO:HG2	1.53	0.90
19:N:5:DT:H2''	19:N:6:DT:C5	2.07	0.89
15:a:43:PRO:HB2	16:b:45:ARG:HH11	1.38	0.88
19:N:8:DG:C2'	19:N:9:DT:H73	1.83	0.88
2:B:793:ALA:HB3	2:B:856:PHE:HB2	1.55	0.87
19:N:183:DG:H2''	19:N:184:DT:H72	1.55	0.87
19:N:2:DG:H2''	19:N:3:DT:C7	2.03	0.87
2:B:394:PHE:H	2:B:510:THR:HG21	1.38	0.87
19:N:5:DT:H2'	19:N:6:DT:H73	1.55	0.87
19:N:5:DT:C2'	19:N:6:DT:H73	2.04	0.86
14:T:12:DA:H2''	14:T:13:DT:C5	2.09	0.86
19:N:11:DT:C2'	19:N:12:DT:H71	2.08	0.84
15:k:95:ALA:HB2	16:l:90:LEU:HD13	1.61	0.82
1:A:199:GLU:HG3	15:k:94:GLU:HA	1.61	0.81
15:a:70:LEU:HD22	16:b:29:ILE:HD11	1.62	0.81
19:N:236:DT:H2''	19:N:237:DC:C5	2.15	0.81
2:B:778:MET:HE2	2:B:1094:ARG:HD3	1.63	0.81
16:l:46:ILE:HG23	16:l:50:ILE:HD11	1.62	0.81
15:m:76:GLN:HE22	15:m:81:ASP:HB2	1.45	0.81
2:B:999:MET:HG3	2:B:1000:PRO:HD2	1.62	0.80
1:A:18:GLN:HB3	2:B:1215:ARG:HB2	1.64	0.80
2:B:269:LYS:HG3	2:B:331:SER:HB2	1.64	0.79
7:G:144:ARG:HH12	7:G:167:PHE:HD1	1.28	0.79
14:T:221:DA:H2	19:N:34:DT:H3	1.31	0.79
15:a:40:ARG:HB2	19:N:173:DC:H1'	1.64	0.79
1:A:776:ILE:HD13	1:A:799:GLY:HA3	1.63	0.79
19:N:2:DG:C2'	19:N:3:DT:H71	2.13	0.79
15:k:121:PRO:HA	15:k:124:ILE:HD12	1.66	0.78
9:I:78:CYS:H	9:I:108:LYS:HZ1	1.32	0.78
19:N:8:DG:C8	19:N:9:DT:H72	2.18	0.78
2:B:272:ILE:HG13	2:B:276:ILE:HD11	1.65	0.77
19:N:215:DT:H2''	19:N:216:DC:C5	2.20	0.77
3:C:175:ALA:HB2	10:J:10:CYS:HB2	1.67	0.76
14:T:91:DA:H1'	14:T:92:DG:H5'	1.68	0.76
1:A:197:GLN:HB2	15:k:96:SER:HB2	1.67	0.76
17:o:42:ARG:HE	19:N:35:DT:H4'	1.49	0.76
19:N:5:DT:H2'	19:N:6:DT:H71	1.50	0.76
1:A:199:GLU:HB2	15:k:97:GLU:HB2	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:LYS:HB2	14:T:208:DA:H61	1.51	0.76
16:b:26:ILE:HG13	16:b:59:LYS:HE3	1.68	0.76
1:A:1453:LEU:HD22	7:G:22:MET:HE2	1.68	0.76
15:a:121:PRO:HG2	16:b:49:LEU:HG	1.67	0.76
2:B:71:ILE:HA	2:B:127:ILE:HG22	1.68	0.76
15:k:100:LEU:HD21	16:l:37:LEU:HD13	1.67	0.75
2:B:220:ALA:O	2:B:252:ARG:NH1	2.20	0.75
1:A:933:GLU:HG3	1:A:989:ILE:HD12	1.66	0.75
10:J:19:ASP:OD1	10:J:20:ALA:N	2.19	0.75
14:T:12:DA:H2'	14:T:13:DT:C7	2.17	0.75
2:B:105:ARG:NH2	2:B:200:GLU:OE2	2.20	0.75
15:e:62:ILE:HB	15:e:93:GLN:HE21	1.51	0.75
1:A:932:SER:OG	1:A:933:GLU:OE2	2.03	0.75
14:T:188:DC:H2''	14:T:189:DG:H5'	1.67	0.75
18:d:78:SER:OG	18:d:82:HIS:NE2	2.20	0.74
15:a:119:ILE:HG21	16:b:43:VAL:HG22	1.66	0.74
7:G:92:SER:HA	7:G:139:LYS:HG3	1.68	0.74
19:N:235:DG:H2''	19:N:236:DT:C5	2.23	0.74
1:A:149:GLU:O	1:A:165:ARG:NH2	2.20	0.73
1:A:351:ARG:HD2	2:B:1128:LEU:HD11	1.69	0.73
1:A:466:TYR:HB2	1:A:470:ARG:HH12	1.52	0.73
1:A:1335:PHE:HA	1:A:1338:ILE:HG22	1.70	0.73
17:g:55:LEU:HD11	18:h:66:VAL:HG22	1.70	0.73
2:B:265:LEU:HD12	2:B:266:PRO:HD2	1.70	0.73
3:C:111:THR:O	3:C:147:LEU:N	2.20	0.73
14:T:191:DT:C6	14:T:192:DT:H72	2.24	0.72
19:N:2:DG:H2''	19:N:3:DT:C5	2.24	0.72
2:B:597:ARG:NH1	2:B:688:GLU:OE1	2.23	0.72
14:T:91:DA:H5'	15:a:63:ARG:HD3	1.71	0.72
2:B:101:PRO:HG2	2:B:172:LEU:HD11	1.70	0.72
19:N:214:DC:H1'	19:N:215:DT:H5'	1.70	0.72
17:c:64:GLU:O	17:c:68:ASN:ND2	2.22	0.72
18:p:102:LEU:HD12	18:p:106:LEU:HB3	1.71	0.72
1:A:197:GLN:HG3	16:l:58:LEU:HG	1.72	0.72
14:T:154:DT:H2''	14:T:155:DG:H5'	1.71	0.72
4:D:148:LEU:HD13	4:D:159:LEU:HD13	1.70	0.72
11:K:55:ASP:OD2	11:K:89:ARG:NH1	2.23	0.72
2:B:56:LEU:HD23	2:B:77:ILE:HD11	1.71	0.71
16:f:27:GLN:OE1	16:f:27:GLN:N	2.22	0.71
3:C:167:HIS:NE2	12:L:72:ARG:OXT	2.22	0.71
9:I:111:ARG:HE	9:I:113:GLU:HG2	1.56	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:N:8:DG:H2'	19:N:9:DT:C7	2.02	0.71
3:C:112:ASP:HA	3:C:146:LYS:HA	1.71	0.71
1:A:758:ASN:ND2	2:B:1021:MET:SD	2.64	0.71
3:C:266:ARG:HH22	11:K:82:ARG:HH11	1.39	0.71
1:A:895:HIS:O	1:A:899:TYR:HB2	1.91	0.71
15:a:40:ARG:HG3	19:N:172:DA:H1'	1.73	0.70
19:N:5:DT:H2''	19:N:6:DT:H71	0.72	0.70
17:g:31:HIS:CD2	17:g:35:ARG:HE	2.09	0.70
11:K:1:MET:HG3	11:K:2:ASN:HD22	1.56	0.70
1:A:691:VAL:HA	1:A:694:ILE:HD12	1.73	0.70
14:T:12:DA:H2''	14:T:13:DT:H71	0.72	0.70
18:d:62:MET:O	18:d:66:VAL:HG22	1.91	0.70
16:l:88:TYR:HA	16:l:91:LYS:HG3	1.72	0.70
14:T:4:DG:H2''	14:T:5:DG:H5'	1.73	0.70
16:b:65:VAL:HG12	16:b:93:GLN:HE22	1.56	0.70
9:I:107:LYS:O	9:I:107:LYS:HD3	1.91	0.70
14:T:119:DT:H2''	14:T:120:DG:C8	2.27	0.70
14:T:185:DG:C8	14:T:186:DT:H72	2.26	0.70
15:a:104:PHE:HB2	16:b:41:GLY:HA3	1.72	0.70
5:E:29:ILE:HG21	5:E:34:MET:HE3	1.74	0.70
12:L:50:CYS:HB3	12:L:55:HIS:H	1.56	0.70
1:A:382:THR:HG23	1:A:384:TYR:H	1.57	0.69
2:B:995:ARG:HH22	3:C:165:LYS:HG2	1.57	0.69
14:T:28:DT:H2''	14:T:29:DG:C8	2.27	0.69
2:B:686:VAL:HG13	2:B:687:ILE:HD12	1.75	0.69
2:B:910:ILE:HD13	2:B:940:PRO:HB3	1.73	0.69
2:B:285:PRO:HG2	2:B:288:GLU:HB2	1.75	0.69
14:T:130:DC:H2''	14:T:131:DT:C4	2.27	0.69
17:o:81:ARG:H	17:o:81:ARG:HD2	1.58	0.69
11:K:15:ASP:OD1	11:K:15:ASP:N	2.23	0.69
19:N:71:DG:H2'	19:N:72:DT:H72	1.76	0.68
14:T:137:DC:C2'	14:T:138:DT:H71	2.23	0.68
2:B:995:ARG:HH12	3:C:165:LYS:HA	1.59	0.68
7:G:1:MET:SD	7:G:2:PHE:N	2.66	0.68
2:B:351:LYS:HA	2:B:359:GLN:HE22	1.58	0.68
2:B:978:ASP:OD2	2:B:1094:ARG:NH1	2.27	0.68
19:N:192:DG:H2''	19:N:193:DT:H71	1.73	0.68
15:k:125:GLN:HB3	15:k:129:ARG:NH1	2.09	0.68
2:B:302:MET:HA	2:B:305:MET:HB2	1.76	0.68
9:I:111:ARG:CZ	9:I:112:ASP:H	2.06	0.68
2:B:366:ARG:NH2	2:B:560:GLU:OE2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:596:ASN:HB3	1:A:604:ASN:HD21	1.58	0.67
9:I:47:GLU:OE1	9:I:49:ILE:N	2.27	0.67
17:o:88:ARG:NH2	17:o:94:ASN:OD1	2.27	0.67
14:T:32:DG:C6	14:T:33:DA:C6	2.82	0.67
15:k:125:GLN:O	15:k:129:ARG:HG2	1.94	0.67
3:C:266:ARG:NH2	11:K:82:ARG:HH11	1.93	0.67
2:B:628:ARG:NH1	2:B:742:GLU:OE2	2.20	0.67
14:T:120:DG:C2	14:T:121:DA:C2	2.82	0.67
16:l:83:ALA:O	16:l:87:VAL:HG12	1.94	0.67
1:A:152:ALA:HB2	1:A:165:ARG:HB3	1.77	0.67
1:A:1148:VAL:HG22	1:A:1199:LEU:HB3	1.75	0.67
19:N:156:DA:H2''	19:N:157:DG:C8	2.30	0.67
19:N:118:DG:H2''	19:N:119:DT:H5'	1.76	0.67
15:e:107:THR:HG21	15:e:124:ILE:HG13	1.77	0.67
2:B:223:SER:OG	2:B:252:ARG:NH1	2.28	0.66
17:c:104:GLN:NE2	15:e:58:THR:OG1	2.28	0.66
1:A:1351:LEU:HD22	1:A:1375:VAL:HG12	1.76	0.66
7:G:1:MET:HA	7:G:79:TRP:HZ3	1.59	0.66
19:N:2:DG:C2'	19:N:3:DT:C7	2.73	0.66
12:L:38:HIS:HE1	12:L:51:LYS:HB2	1.60	0.66
7:G:39:THR:O	7:G:43:GLY:N	2.24	0.66
14:T:47:DC:H2''	14:T:48:DC:C6	2.30	0.66
15:k:123:ASP:HA	15:k:126:LEU:HD12	1.76	0.66
1:A:1163:THR:HG21	1:A:1168:ASP:HB3	1.77	0.66
2:B:267:TYR:HB2	2:B:348:ILE:HD11	1.75	0.66
2:B:337:ARG:HG2	2:B:340:LYS:HE2	1.76	0.66
17:c:92:GLU:HB2	18:d:103:PRO:HG2	1.77	0.66
15:e:63:ARG:CG	15:e:66:PRO:HG2	2.25	0.66
2:B:563:ASP:H	2:B:567:HIS:CE1	2.13	0.66
19:N:8:DG:H2''	19:N:9:DT:C5	2.29	0.66
1:A:1423:ASP:O	2:B:1220:ARG:NH1	2.29	0.66
16:b:87:VAL:HA	16:b:97:LEU:HD21	1.78	0.66
5:E:171:GLU:OE1	5:E:171:GLU:N	2.21	0.65
5:E:170:LYS:N	5:E:173:GLN:OE1	2.28	0.65
18:h:109:HIS:O	18:h:113:GLU:HG3	1.96	0.65
1:A:944:LEU:HA	1:A:948:VAL:HG22	1.79	0.65
2:B:283:VAL:HG22	2:B:289:ILE:HG13	1.79	0.65
14:T:234:DG:H2''	14:T:235:DC:H5'	1.78	0.65
2:B:159:GLY:HA2	2:B:443:SER:HB2	1.78	0.65
9:I:25:LEU:HD21	9:I:38:ALA:HB3	1.79	0.65
17:o:29:ARG:HD2	17:o:32:ARG:HH11	1.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:N:8:DG:C1'	19:N:9:DT:C7	2.60	0.65
19:N:71:DG:C2'	19:N:72:DT:H72	2.26	0.65
14:T:37:DG:H2''	14:T:38:DG:C8	2.31	0.65
4:D:33:GLU:O	7:G:5:LYS:NZ	2.29	0.65
11:K:29:ASN:ND2	11:K:78:GLU:O	2.30	0.65
1:A:199:GLU:HB2	15:k:97:GLU:CB	2.27	0.65
1:A:1207:LYS:HB3	1:A:1209:LEU:HD21	1.79	0.65
1:A:1126:ILE:HG23	1:A:1132:LYS:HB3	1.79	0.65
1:A:933:GLU:OE1	1:A:993:ARG:NH1	2.30	0.64
1:A:1194:LEU:HD11	1:A:1241:ARG:HB3	1.78	0.64
14:T:151:DC:OP1	15:m:83:ARG:HG2	1.97	0.64
1:A:1191:SER:O	1:A:1243:ARG:NH1	2.29	0.64
1:A:614:MET:HA	1:A:614:MET:HE3	1.80	0.64
2:B:489:ARG:NH1	2:B:532:LEU:O	2.31	0.64
2:B:1171:VAL:HG21	2:B:1191:ILE:HD11	1.78	0.64
14:T:165:DA:H61	19:N:90:DT:H3	1.43	0.64
5:E:91:THR:HA	5:E:94:ASN:ND2	2.12	0.64
14:T:19:DA:H2''	14:T:20:DC:C5	2.32	0.64
17:c:57:TYR:HE2	18:d:106:LEU:HD12	1.63	0.64
1:A:72:GLU:OE2	2:B:1176:LYS:NZ	2.31	0.64
12:L:38:HIS:CE1	12:L:51:LYS:HB2	2.33	0.64
15:m:40:ARG:HA	19:N:90:DT:H4'	1.78	0.64
17:o:51:LEU:O	17:o:55:LEU:HG	1.98	0.64
1:A:545:GLU:HA	1:A:548:MET:HG3	1.80	0.64
1:A:982:ASP:O	1:A:1041:ARG:NH1	2.31	0.63
15:k:128:ARG:HH22	16:l:57:VAL:HB	1.62	0.63
1:A:197:GLN:HB2	15:k:96:SER:CB	2.27	0.63
1:A:701:ASN:OD1	9:I:96:ASN:ND2	2.30	0.63
2:B:336:ILE:O	2:B:341:ARG:NH2	2.31	0.63
17:g:16:THR:HG23	19:N:228:DG:H4'	1.80	0.63
16:f:75:HIS:O	18:h:92:ARG:NH2	2.30	0.63
2:B:810:GLU:OE1	2:B:815:ARG:NH2	2.31	0.63
16:l:75:HIS:HE1	18:p:93:GLU:HG3	1.64	0.63
1:A:171:THR:HG1	1:A:186:TRP:CD1	2.17	0.63
1:A:178:ASP:HB3	1:A:183:TRP:HE1	1.64	0.63
1:A:544:TYR:CZ	1:A:548:MET:HE3	2.33	0.63
17:g:44:GLY:HA2	19:N:219:DT:H5''	1.81	0.63
18:p:41:VAL:HA	18:p:44:VAL:HG22	1.81	0.63
19:N:216:DC:H2''	19:N:217:DC:C4	2.33	0.63
1:A:72:GLU:OE2	2:B:1174:ASN:ND2	2.32	0.63
2:B:483:SER:HA	2:B:775:LYS:HG2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:21:ASN:O	8:H:44:ASN:ND2	2.32	0.63
15:a:109:LEU:HD21	15:e:129:ARG:HD2	1.80	0.63
14:T:88:DT:H1'	14:T:89:DT:H5'	1.81	0.62
17:g:35:ARG:NH2	17:g:36:LYS:HZ1	1.96	0.62
15:a:118:THR:HG23	16:b:45:ARG:HB3	1.81	0.62
15:e:126:LEU:O	15:e:130:ILE:HG12	1.99	0.62
1:A:102:VAL:HG11	1:A:212:PHE:HE1	1.64	0.62
14:T:23:DG:C2'	14:T:24:DT:C7	2.72	0.62
16:f:29:ILE:HG21	16:f:58:LEU:HD21	1.81	0.62
1:A:608:ILE:HD12	1:A:613:VAL:HG22	1.82	0.62
19:N:218:DC:N1	19:N:219:DT:H72	2.14	0.62
2:B:639:LYS:HG3	2:B:641:ASN:H	1.65	0.62
1:A:1207:LYS:O	1:A:1277:ARG:NH1	2.32	0.62
9:I:17:LYS:N	9:I:26:LEU:O	2.33	0.62
2:B:78:ARG:HB2	2:B:120:GLU:HB3	1.82	0.62
10:J:3:ILE:HD12	10:J:4:PRO:HD2	1.81	0.62
14:T:12:DA:H2'	14:T:13:DT:H73	1.76	0.62
3:C:54:THR:OG1	3:C:152:GLU:N	2.33	0.61
15:k:101:VAL:HA	15:k:104:PHE:HB2	1.81	0.61
14:T:132:DG:C2	19:N:124:DA:C2	2.88	0.61
16:b:54:THR:O	16:b:58:LEU:HG	2.00	0.61
18:d:95:GLN:HE21	18:d:99:ARG:HE	1.46	0.61
15:e:63:ARG:HH12	16:f:29:ILE:HG23	1.65	0.61
15:a:61:LEU:HD12	16:b:37:LEU:HD13	1.81	0.61
1:A:492:VAL:O	2:B:1150:ARG:NH1	2.34	0.61
3:C:53:ASN:ND2	3:C:59:ASP:OD1	2.33	0.61
6:F:122:MET:HA	6:F:122:MET:HE3	1.82	0.61
19:N:74:DC:H2''	19:N:75:DG:C8	2.36	0.61
4:D:68:SER:OG	4:D:71:ARG:NH1	2.33	0.61
15:a:96:SER:O	15:a:100:LEU:HG	2.00	0.61
18:h:73:ILE:HD13	18:h:101:LEU:HD12	1.81	0.61
19:N:149:DC:H2'	19:N:150:DA:C8	2.35	0.61
2:B:46:ILE:O	2:B:50:VAL:HG23	2.00	0.61
19:N:217:DC:H2''	19:N:218:DC:C5	2.35	0.61
1:A:447:ARG:HH12	13:P:15:C:H5'	1.65	0.61
1:A:569:PRO:HD2	8:H:46:MET:SD	2.40	0.61
2:B:184:LYS:HE3	10:J:65:LEU:HD21	1.82	0.61
9:I:78:CYS:CB	9:I:106:CYS:SG	2.88	0.61
18:p:42:TYR:HB2	18:p:59:MET:HE1	1.83	0.61
3:C:169:LYS:NZ	12:L:71:ALA:O	2.34	0.61
18:d:76:GLU:HG3	18:d:101:LEU:HD21	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:e:62:ILE:HB	15:e:93:GLN:NE2	2.14	0.61
18:h:98:VAL:HG13	18:h:102:LEU:HD12	1.82	0.61
4:D:69:ARG:HH21	4:D:69:ARG:HG3	1.66	0.61
2:B:628:ARG:HH12	2:B:742:GLU:CD	2.07	0.61
4:D:134:CYS:HA	4:D:137:LEU:HB3	1.83	0.61
6:F:133:VAL:HG22	6:F:147:GLY:HA2	1.81	0.61
15:a:113:HIS:CE1	15:e:126:LEU:HB2	2.36	0.61
4:D:57:ARG:HH22	4:D:61:ARG:HH11	1.48	0.60
5:E:27:TYR:CZ	5:E:77:LEU:HD13	2.36	0.60
14:T:233:DG:H2'	14:T:234:DG:H8	1.65	0.60
19:N:66:DC:H2''	19:N:67:DG:H5'	1.82	0.60
19:N:4:DT:H2'	19:N:5:DT:C6	2.36	0.60
19:N:202:DC:H2'	19:N:203:DC:C6	2.37	0.60
1:A:319:SER:HA	14:T:207:DC:O2	2.01	0.60
2:B:830:TYR:CZ	2:B:1000:PRO:HD3	2.35	0.60
5:E:54:ARG:NH2	5:E:112:GLN:OE1	2.34	0.60
1:A:1148:VAL:HG13	1:A:1199:LEU:HD22	1.83	0.60
2:B:226:SER:OG	2:B:227:HIS:N	2.35	0.60
2:B:982:SER:OG	2:B:983:ARG:N	2.33	0.60
15:e:63:ARG:NH1	16:f:29:ILE:HG23	2.17	0.60
19:N:143:DC:H2''	19:N:144:DG:C8	2.36	0.60
1:A:194:ARG:HG3	15:k:107:THR:HG21	1.84	0.60
14:T:39:DG:H1'	14:T:40:DA:C5	2.36	0.60
15:m:61:LEU:H	15:m:61:LEU:HD22	1.65	0.60
1:A:1202:ALA:HA	1:A:1205:LEU:HD12	1.84	0.60
1:A:1231:SER:HB3	1:A:1239:ILE:HG13	1.84	0.60
2:B:360:GLU:HB2	2:B:363:PHE:CE2	2.36	0.60
3:C:49:GLU:HB3	12:L:66:MET:SD	2.42	0.60
7:G:1:MET:HA	7:G:79:TRP:CZ3	2.36	0.60
1:A:196:ALA:HB3	15:k:100:LEU:HA	1.82	0.60
1:A:252:ALA:HA	1:A:258:GLN:HA	1.82	0.60
1:A:466:TYR:HB2	1:A:470:ARG:NH1	2.15	0.60
1:A:1015:ASN:OD1	5:E:206:ARG:NH2	2.35	0.60
14:T:10:DA:H61	19:N:245:DT:H3	1.49	0.60
17:c:59:THR:O	17:c:63:LEU:HG	2.00	0.60
18:h:54:ILE:HD13	18:h:59:MET:HE2	1.83	0.60
1:A:319:SER:C	1:A:321:ARG:H	2.09	0.60
19:N:8:DG:N9	19:N:9:DT:C7	2.61	0.60
1:A:35:ILE:HB	1:A:84:MET:SD	2.42	0.59
1:A:319:SER:HA	14:T:207:DC:C2	2.36	0.59
14:T:18:DG:H2''	14:T:19:DA:C8	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:k:125:GLN:HB3	15:k:129:ARG:CZ	2.31	0.59
19:N:218:DC:C2'	19:N:219:DT:C7	2.80	0.59
2:B:984:HIS:NE2	2:B:1028:GLU:OE1	2.35	0.59
18:p:76:GLU:O	18:p:80:LEU:HG	2.02	0.59
1:A:196:ALA:HB3	15:k:100:LEU:CA	2.32	0.59
1:A:802:GLU:OE1	1:A:802:GLU:N	2.35	0.59
1:A:1118:LEU:HD23	1:A:1332:SER:HB2	1.84	0.59
5:E:178:GLN:HA	5:E:214:LEU:HD12	1.83	0.59
1:A:1423:ASP:HB2	2:B:1220:ARG:HH12	1.67	0.59
2:B:316:ILE:HG23	2:B:321:VAL:HG23	1.84	0.59
2:B:481:TYR:O	2:B:484:THR:OG1	2.20	0.59
4:D:153:VAL:HG22	4:D:171:LEU:HG	1.83	0.59
15:e:88:ALA:O	15:e:92:LEU:HG	2.02	0.59
19:N:192:DG:C2'	19:N:193:DT:H71	2.32	0.59
1:A:196:ALA:HB3	15:k:100:LEU:HB2	1.84	0.59
1:A:826:ILE:HD11	2:B:505:ARG:HD3	1.85	0.59
2:B:15:GLU:OE1	2:B:15:GLU:N	2.35	0.59
2:B:825:VAL:HG22	2:B:1010:LEU:HB3	1.83	0.59
15:m:54:TYR:HB3	16:n:40:ARG:HG3	1.85	0.59
1:A:1129:ASP:OD2	1:A:1132:LYS:N	2.36	0.59
16:b:92:ARG:HB3	18:d:79:ARG:HH12	1.68	0.59
16:l:87:VAL:HA	16:l:90:LEU:HG	1.85	0.59
15:m:49:ARG:HB3	15:m:53:ARG:HH11	1.67	0.59
2:B:89:MET:HB2	2:B:99:MET:SD	2.43	0.59
1:A:307:ASN:HB2	1:A:325:ALA:HB2	1.84	0.59
2:B:320:GLU:HG3	2:B:342:ILE:HD11	1.84	0.59
4:D:101:VAL:HG22	7:G:105:PRO:HG3	1.85	0.59
8:H:102:LYS:HB3	8:H:114:TYR:HB2	1.85	0.59
1:A:334:GLU:OE1	1:A:334:GLU:N	2.33	0.59
1:A:609:VAL:O	1:A:612:LYS:N	2.36	0.59
9:I:59:VAL:HG13	9:I:61:ASP:H	1.66	0.59
15:k:118:THR:HG22	16:l:45:ARG:HD3	1.85	0.59
1:A:772:GLU:OE1	2:B:503:LYS:NZ	2.36	0.59
1:A:1230:TRP:HA	1:A:1240:ILE:HA	1.83	0.59
1:A:1263:LEU:HD12	1:A:1266:ILE:HD11	1.83	0.59
2:B:1174:ASN:HD21	2:B:1176:LYS:NZ	2.01	0.59
14:T:31:DA:OP1	17:g:17:ARG:N	2.34	0.59
17:c:79:ILE:HD11	17:c:81:ARG:HB3	1.84	0.59
14:T:221:DA:H2''	14:T:222:DA:C5	2.37	0.58
18:p:75:GLY:O	18:p:79:ARG:HG2	2.03	0.58
19:N:187:DC:H2''	19:N:188:DC:C5	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:GLY:HA3	1:A:1413:PHE:CE2	2.37	0.58
7:G:91:VAL:O	7:G:140:GLY:N	2.34	0.58
7:G:112:THR:HA	7:G:115:ILE:HD12	1.85	0.58
14:T:23:DG:H2''	14:T:24:DT:C7	2.15	0.58
1:A:92:HIS:HB2	1:A:237:ILE:HD11	1.85	0.58
5:E:45:ILE:O	5:E:53:GLN:NE2	2.37	0.58
15:a:103:LEU:O	15:a:107:THR:HG23	2.02	0.58
1:A:116:ASP:N	1:A:119:ASN:HD21	2.00	0.58
5:E:34:MET:HE2	5:E:34:MET:HA	1.86	0.58
16:b:72:TYR:HE2	18:d:83:TYR:CD2	2.22	0.58
2:B:1084:GLN:HE22	3:C:191:PHE:HA	1.69	0.58
4:D:115:PHE:CE2	4:D:124:VAL:HG11	2.38	0.58
9:I:60:ASP:OD1	9:I:107:LYS:HE3	2.03	0.58
1:A:116:ASP:O	1:A:119:ASN:ND2	2.36	0.58
1:A:1450:GLU:HB2	7:G:22:MET:HE3	1.85	0.58
4:D:57:ARG:HH11	4:D:110:ASN:HB2	1.68	0.58
16:b:90:LEU:HB2	16:b:97:LEU:HD22	1.84	0.58
3:C:69:ILE:HD11	3:C:115:SER:HB2	1.84	0.58
7:G:146:LYS:HB3	7:G:162:SER:HB3	1.85	0.58
17:g:31:HIS:HB3	17:g:35:ARG:HH11	1.68	0.58
19:N:2:DG:H2''	19:N:3:DT:C6	2.38	0.58
19:N:219:DT:H2'	19:N:220:DA:H8	1.68	0.58
6:F:127:GLN:HB3	6:F:129:LYS:HZ3	1.69	0.58
2:B:1161:HIS:HA	2:B:1193:GLN:HA	1.86	0.58
16:l:33:ALA:O	16:l:37:LEU:HG	2.04	0.58
15:m:79:LYS:HG2	15:m:80:THR:H	1.69	0.58
19:N:3:DT:H2'	19:N:4:DT:H71	1.72	0.58
19:N:203:DC:H2'	19:N:204:DA:C8	2.38	0.58
1:A:49:ARG:HE	1:A:50:GLU:N	2.02	0.58
1:A:1227:PHE:CZ	1:A:1229:MET:HB2	2.39	0.58
5:E:106:THR:HG22	5:E:130:ILE:HG22	1.86	0.58
14:T:56:DG:H1'	14:T:57:DT:H5'	1.84	0.58
18:d:105:GLU:H	18:d:105:GLU:CD	2.12	0.58
1:A:447:ARG:NH1	13:P:15:C:H5'	2.19	0.57
16:f:68:ASP:O	16:f:72:TYR:HD1	1.87	0.57
9:I:92:ARG:HB3	9:I:95:THR:HG23	1.84	0.57
15:a:43:PRO:HB2	16:b:45:ARG:NH1	2.14	0.57
19:N:85:DC:H2''	19:N:86:DC:C4	2.39	0.57
1:A:199:GLU:HG2	1:A:200:ARG:H	1.68	0.57
2:B:1156:ASP:OD2	2:B:1198:TYR:N	2.38	0.57
16:f:92:ARG:HD3	18:h:79:ARG:NH1	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:882:GLN:HE22	1:A:961:ASN:HA	1.70	0.57
2:B:658:GLY:O	2:B:676:TYR:N	2.37	0.57
15:k:100:LEU:HG	15:k:101:VAL:HG23	1.87	0.57
1:A:1341:VAL:HG12	1:A:1342:LEU:HD23	1.87	0.57
2:B:899:ILE:HD13	2:B:949:VAL:HG21	1.87	0.57
2:B:1038:ARG:HE	2:B:1058:LEU:HD12	1.70	0.57
1:A:1173:GLU:O	1:A:1177:SER:OG	2.21	0.57
4:D:104:LYS:HG3	7:G:104:GLY:HA2	1.86	0.57
13:P:10:U:H2'	13:P:11:C:C6	2.40	0.57
1:A:1168:ASP:OD2	1:A:1196:ARG:NH2	2.37	0.57
7:G:38:CYS:HB2	7:G:44:TYR:CZ	2.40	0.57
16:b:38:ALA:HB1	16:b:43:VAL:HG21	1.85	0.57
2:B:1196:ILE:HD11	2:B:1201:LYS:HB2	1.86	0.57
18:h:113:GLU:HA	18:h:116:LYS:HG2	1.87	0.57
1:A:706:LYS:HD2	1:A:709:MET:HE1	1.86	0.57
17:c:26:PRO:HD3	18:d:40:TYR:CG	2.40	0.57
1:A:347:ASP:OD1	2:B:1106:ARG:NE	2.38	0.56
1:A:1031:ARG:NH2	1:A:1035:GLU:OE2	2.38	0.56
3:C:103:ARG:NE	3:C:104:HIS:O	2.36	0.56
1:A:1447:MET:N	6:F:133:VAL:O	2.33	0.56
12:L:40:PHE:CZ	12:L:50:CYS:HA	2.39	0.56
5:E:25:ARG:HH11	5:E:186:TYR:C	2.12	0.56
9:I:97:MET:N	9:I:97:MET:SD	2.78	0.56
15:k:89:ILE:HG22	15:k:93:GLN:OE1	2.05	0.56
1:A:94:GLY:HA3	1:A:1413:PHE:HE2	1.70	0.56
1:A:850:MET:HE1	1:A:1438:PRO:O	2.06	0.56
1:A:999:LEU:O	1:A:1013:GLN:NE2	2.38	0.56
1:A:1143:THR:OG1	1:A:1277:ARG:N	2.35	0.56
2:B:588:MET:SD	2:B:592:THR:OG1	2.63	0.56
3:C:98:LEU:HB3	3:C:118:LEU:HD11	1.87	0.56
1:A:82:GLY:HA3	1:A:242:VAL:HB	1.86	0.56
1:A:454:MET:HE3	1:A:514:SER:HB2	1.87	0.56
1:A:776:ILE:H	1:A:776:ILE:HD12	1.71	0.56
16:f:88:TYR:O	16:f:92:ARG:HG2	2.05	0.56
17:g:58:LEU:O	17:g:62:ILE:HG22	2.06	0.56
2:B:1009:ASP:OD1	2:B:1009:ASP:N	2.38	0.56
17:c:25:PHE:HE1	18:d:41:VAL:HA	1.71	0.56
2:B:792:MET:HA	2:B:792:MET:HE3	1.87	0.56
1:A:457:MET:HE1	1:A:522:MET:HE1	1.88	0.56
8:H:12:VAL:HB	8:H:52:ASP:N	2.21	0.56
11:K:1:MET:HG3	11:K:2:ASN:ND2	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:33:CYS:HA	12:L:58:ILE:HG22	1.88	0.56
12:L:48:VAL:HG13	12:L:58:ILE:HD11	1.87	0.56
12:L:50:CYS:HB3	12:L:55:HIS:N	2.21	0.56
17:g:63:LEU:HD22	18:h:45:LEU:HD13	1.88	0.56
19:N:183:DG:H2''	19:N:184:DT:C7	2.32	0.56
1:A:40:ILE:HG12	1:A:53:LEU:HB2	1.88	0.56
1:A:231:ARG:HB2	1:A:234:TRP:CD2	2.40	0.56
1:A:321:ARG:HH22	1:A:323:VAL:HA	1.70	0.56
1:A:847:GLU:OE1	1:A:847:GLU:N	2.26	0.56
2:B:261:ILE:N	2:B:309:CYS:SG	2.74	0.56
2:B:360:GLU:HB2	2:B:363:PHE:HE2	1.71	0.56
3:C:87:CYS:SG	3:C:91:CYS:HB3	2.46	0.56
15:a:101:VAL:HA	15:a:104:PHE:CD2	2.40	0.56
16:l:29:ILE:HD13	16:l:58:LEU:HD22	1.87	0.56
18:p:69:ILE:O	18:p:73:ILE:HG12	2.06	0.56
1:A:318:LYS:C	1:A:320:GLY:H	2.14	0.56
2:B:855:PHE:HB3	2:B:970:THR:HG23	1.87	0.56
1:A:1102:ARG:NH1	1:A:1354:GLU:OE1	2.39	0.55
2:B:841:MET:SD	2:B:846:ILE:HD11	2.46	0.55
8:H:43:ASN:HB3	8:H:46:MET:HB3	1.87	0.55
18:h:115:THR:O	18:h:119:THR:HG22	2.05	0.55
16:l:75:HIS:CE1	18:p:93:GLU:HG3	2.40	0.55
16:f:91:LYS:NZ	18:h:79:ARG:HH12	2.05	0.55
17:g:96:LEU:O	18:h:72:ARG:NH2	2.33	0.55
19:N:30:DC:H2''	19:N:31:DT:H5'	1.89	0.55
1:A:1145:LEU:HD23	1:A:1271:LEU:HA	1.87	0.55
4:D:101:VAL:O	4:D:105:THR:HG23	2.06	0.55
8:H:129:LYS:HD2	8:H:130:SER:N	2.21	0.55
15:a:92:LEU:HD11	16:b:62:LEU:HD11	1.87	0.55
18:d:97:ALA:O	18:d:101:LEU:HG	2.06	0.55
16:n:49:LEU:O	16:n:53:GLU:HG3	2.06	0.55
1:A:377:TYR:HB3	1:A:435:ARG:HH22	1.72	0.55
2:B:636:ASP:HB3	2:B:639:LYS:HB3	1.89	0.55
16:f:71:THR:HG23	18:h:99:ARG:HD2	1.87	0.55
2:B:391:ARG:CZ	2:B:391:ARG:H	2.20	0.55
6:F:109:VAL:HG12	6:F:129:LYS:HE2	1.89	0.55
8:H:12:VAL:HB	8:H:52:ASP:H	1.70	0.55
14:T:155:DG:H2''	14:T:156:DG:C8	2.41	0.55
16:f:75:HIS:CG	18:h:96:THR:HG1	2.24	0.55
17:g:34:LEU:HD13	17:g:43:VAL:HG11	1.87	0.55
16:l:38:ALA:HB1	16:l:43:VAL:HB	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1017:THR:OG1	1:A:1021:GLN:OE1	2.21	0.55
1:A:1397:THR:O	1:A:1402:ARG:NH1	2.39	0.55
2:B:72:ASN:ND2	2:B:128:ASP:OD1	2.40	0.55
2:B:323:LEU:HD21	2:B:346:LYS:HG3	1.89	0.55
14:T:120:DG:N3	14:T:121:DA:C2	2.75	0.55
15:a:91:ALA:HB2	16:b:100:PHE:CE2	2.42	0.55
19:N:190:DG:C2	19:N:191:DC:C2	2.94	0.55
15:a:108:ASN:ND2	16:b:41:GLY:O	2.39	0.55
5:E:92:MET:HE2	5:E:92:MET:HA	1.88	0.55
7:G:22:MET:O	7:G:26:LEU:HG	2.06	0.55
9:I:90:GLN:OE1	9:I:92:ARG:N	2.40	0.55
14:T:109:DT:H1'	14:T:110:DA:H5'	1.88	0.55
19:N:218:DC:C2'	19:N:219:DT:H72	2.36	0.55
1:A:237:ILE:HD12	2:B:1211:ASN:ND2	2.21	0.55
1:A:577:GLN:O	1:A:580:SER:OG	2.23	0.55
1:A:1366:VAL:HG12	1:A:1371:MET:HE2	1.87	0.55
4:D:30:LEU:HB3	4:D:34:PHE:HB2	1.89	0.55
7:G:138:THR:HG22	7:G:139:LYS:H	1.71	0.55
14:T:47:DC:H2''	14:T:48:DC:C5	2.42	0.55
17:c:90:ASP:OD1	17:c:92:GLU:HG2	2.06	0.55
18:d:62:MET:N	18:d:62:MET:SD	2.79	0.55
16:l:71:THR:HG21	18:p:100:LEU:HG	1.89	0.55
16:n:66:ILE:O	16:n:70:VAL:HG23	2.06	0.55
19:N:64:DA:H1'	19:N:65:DA:H5'	1.87	0.55
1:A:407:ILE:HG13	1:A:413:ARG:HA	1.88	0.55
1:A:1006:ASN:OD1	1:A:1007:GLU:N	2.40	0.55
2:B:351:LYS:HA	2:B:359:GLN:NE2	2.22	0.55
2:B:492:ASN:OD1	2:B:493:THR:N	2.40	0.55
17:o:61:GLU:OE2	18:p:106:LEU:HD11	2.07	0.55
19:N:61:DT:H2''	19:N:62:DA:C8	2.42	0.55
1:A:113:LEU:HD13	1:A:222:ARG:HE	1.72	0.54
1:A:1428:SER:OG	1:A:1432:MET:SD	2.57	0.54
2:B:890:TYR:HA	2:B:893:LEU:HD23	1.88	0.54
14:T:84:DG:N3	15:a:40:ARG:NH1	2.54	0.54
17:g:87:ILE:HD12	17:g:93:LEU:HD13	1.90	0.54
16:l:33:ALA:O	16:l:36:ARG:HG2	2.07	0.54
16:l:50:ILE:O	16:l:54:THR:HG23	2.07	0.54
16:n:82:THR:HG23	16:n:85:ASP:H	1.73	0.54
19:N:203:DC:H2'	19:N:204:DA:H8	1.72	0.54
15:m:108:ASN:ND2	16:n:42:GLY:O	2.39	0.54
2:B:513:GLY:HA2	2:B:748:ILE:HG22	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:T:82:DG:P	16:b:46:ILE:H	2.29	0.54
14:T:145:DT:H2''	14:T:146:DA:H5'	1.89	0.54
17:c:90:ASP:O	17:c:94:ASN:HB2	2.07	0.54
15:k:89:ILE:HA	15:k:92:LEU:HB3	1.88	0.54
2:B:552:GLU:HA	2:B:556:MET:HB3	1.90	0.54
5:E:27:TYR:CD1	5:E:77:LEU:HD22	2.43	0.54
15:a:65:LEU:HB2	15:a:66:PRO:HD3	1.90	0.54
16:b:31:LYS:HE2	16:b:35:ARG:HH11	1.71	0.54
1:A:494:GLN:N	2:B:1149:GLU:OE2	2.41	0.54
1:A:1113:ILE:HD11	1:A:1116:PRO:HA	1.89	0.54
7:G:30:LEU:O	7:G:34:VAL:HG13	2.08	0.54
13:P:6:C:H2'	13:P:7:U:C6	2.43	0.54
14:T:27:DC:H2''	14:T:28:DT:C6	2.42	0.54
14:T:59:DA:H2''	14:T:60:DA:C8	2.43	0.54
15:e:125:GLN:HB3	15:e:129:ARG:HH11	1.72	0.54
1:A:32:VAL:HG22	2:B:1183:ARG:HH12	1.72	0.54
2:B:279:ARG:NE	2:B:284:VAL:O	2.39	0.54
3:C:76:VAL:HA	3:C:79:MET:HB2	1.89	0.54
4:D:139:PRO:HA	4:D:142:ILE:HD12	1.90	0.54
12:L:33:CYS:HB3	12:L:38:HIS:H	1.73	0.54
15:a:48:LEU:O	15:a:50:GLU:N	2.35	0.54
15:k:69:ARG:HH11	15:k:72:ARG:HG3	1.72	0.54
17:c:101:THR:HG23	16:f:95:ARG:NH1	2.23	0.54
16:l:66:ILE:O	16:l:70:VAL:HG12	2.07	0.54
16:n:54:THR:HA	16:n:57:VAL:HG12	1.89	0.54
1:A:406:VAL:O	1:A:414:ILE:N	2.41	0.54
1:A:640:PRO:HG2	1:A:641:LYS:HE2	1.87	0.54
1:A:926:LEU:HD11	1:A:986:PRO:HD3	1.89	0.54
1:A:1148:VAL:O	1:A:1200:ASP:N	2.40	0.54
5:E:184:ALA:HA	5:E:189:LEU:HD23	1.89	0.54
7:G:52:MET:HG3	7:G:53:ASN:OD1	2.07	0.54
15:a:130:ILE:HG21	15:e:130:ILE:HB	1.90	0.54
9:I:82:ASP:OD1	9:I:83:CYS:N	2.40	0.54
14:T:141:DG:N2	19:N:115:DC:O2	2.41	0.54
17:g:50:TYR:OH	18:h:95:GLN:HB3	2.08	0.54
17:g:80:PRO:HA	17:g:83:LEU:HD12	1.90	0.54
15:k:108:ASN:ND2	16:l:42:GLY:O	2.41	0.54
15:k:126:LEU:O	15:k:130:ILE:HG12	2.08	0.54
17:o:27:VAL:HG13	17:o:48:PRO:HB2	1.90	0.54
19:N:5:DT:OP2	19:N:5:DT:H73	2.07	0.54
19:N:153:DT:H2''	19:N:154:DC:C4	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:673:ASP:O	1:A:677:MET:HG3	2.08	0.54
2:B:236:GLU:OE2	2:B:544:SER:OG	2.24	0.54
1:A:199:GLU:HG2	1:A:200:ARG:N	2.23	0.53
17:g:41:GLU:OE1	17:g:41:GLU:N	2.40	0.53
19:N:15:DC:H2''	19:N:16:DC:C6	2.42	0.53
6:F:108:LEU:HD22	6:F:129:LYS:HB3	1.90	0.53
9:I:59:VAL:HG22	9:I:60:ASP:H	1.72	0.53
9:I:102:VAL:HG22	9:I:109:THR:HG22	1.91	0.53
14:T:82:DG:H2''	14:T:83:DT:H5'	1.90	0.53
19:N:215:DT:H2''	19:N:216:DC:C6	2.43	0.53
1:A:975:LEU:HD13	1:A:1039:LEU:HA	1.89	0.53
1:A:1118:LEU:HD13	1:A:1319:VAL:HG11	1.89	0.53
1:A:1190:GLN:HG3	1:A:1245:ILE:HG23	1.91	0.53
2:B:842:ASN:OD1	2:B:844:SER:N	2.42	0.53
7:G:116:PRO:HG3	7:G:164:LYS:HD2	1.91	0.53
14:T:51:DT:C2'	14:T:52:DG:H5''	2.30	0.53
18:d:37:TYR:O	18:d:41:VAL:HG23	2.08	0.53
15:e:62:ILE:HA	15:e:63:ARG:NH2	2.23	0.53
16:l:92:ARG:HD3	18:p:100:LEU:HD22	1.90	0.53
1:A:140:GLN:HG2	1:A:143:LYS:NZ	2.22	0.53
17:c:55:LEU:HD12	18:d:66:VAL:HG12	1.90	0.53
15:m:54:TYR:HD1	16:n:40:ARG:HH11	1.56	0.53
1:A:196:ALA:HB3	15:k:100:LEU:CB	2.38	0.53
2:B:220:ALA:O	2:B:223:SER:OG	2.26	0.53
2:B:394:PHE:H	2:B:510:THR:CG2	2.18	0.53
3:C:55:SER:OG	3:C:56:VAL:N	2.42	0.53
3:C:255:LEU:HD11	11:K:95:ILE:HD13	1.91	0.53
5:E:182:PRO:HA	5:E:185:ARG:HH21	1.73	0.53
16:b:61:PHE:O	16:b:65:VAL:HG13	2.09	0.53
15:e:100:LEU:HD11	16:f:37:LEU:HD22	1.91	0.53
17:o:97:LEU:HD12	17:o:100:VAL:HG21	1.91	0.53
1:A:306:ASP:CG	1:A:327:ARG:HD3	2.34	0.53
1:A:447:ARG:HE	1:A:481:ALA:HB2	1.74	0.53
1:A:765:CYS:SG	1:A:766:VAL:N	2.82	0.53
1:A:1129:ASP:HB3	1:A:1132:LYS:HD2	1.90	0.53
16:b:50:ILE:O	16:b:54:THR:HG23	2.08	0.53
18:p:46:LYS:HE2	18:p:46:LYS:HA	1.89	0.53
1:A:172:GLN:NE2	1:A:173:PRO:O	2.42	0.53
1:A:805:TYR:O	2:B:761:HIS:ND1	2.39	0.53
9:I:98:THR:HG22	9:I:111:ARG:HD3	1.91	0.53
14:T:129:DC:H2''	14:T:130:DC:C5	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:m:47:ALA:C	15:m:49:ARG:H	2.17	0.53
17:o:18:SER:O	17:o:23:LEU:N	2.42	0.53
17:o:81:ARG:HH22	18:p:57:LYS:NZ	2.05	0.53
1:A:197:GLN:HB3	1:A:198:PRO:HD2	1.90	0.53
1:A:240:LEU:HD12	1:A:241:PRO:HD2	1.91	0.53
1:A:1320:MET:SD	5:E:141:VAL:HG11	2.48	0.53
1:A:1447:MET:HA	1:A:1447:MET:HE3	1.91	0.53
11:K:82:ARG:NH1	11:K:85:GLN:HE22	2.07	0.53
16:l:88:TYR:HB3	16:l:91:LYS:HE3	1.91	0.53
1:A:41:MET:HE3	1:A:42:ASP:H	1.73	0.53
1:A:929:GLU:O	1:A:933:GLU:HG2	2.09	0.53
2:B:839:MET:HE3	2:B:988:GLY:O	2.09	0.53
10:J:10:CYS:SG	10:J:11:GLY:N	2.81	0.53
17:o:80:PRO:HD2	17:o:81:ARG:HH21	1.73	0.53
1:A:33:VAL:HG21	1:A:57:LYS:HD2	1.91	0.53
1:A:196:ALA:N	15:k:100:LEU:HD13	2.24	0.53
1:A:287:GLN:NE2	16:l:88:TYR:OH	2.41	0.53
1:A:1447:MET:HB2	6:F:133:VAL:HB	1.91	0.53
2:B:413:LEU:HD12	2:B:446:ILE:HA	1.91	0.53
14:T:82:DG:H5'	16:b:45:ARG:HG2	1.91	0.53
17:c:50:TYR:CD1	18:d:114:GLY:HA3	2.43	0.53
7:G:116:PRO:HG3	7:G:164:LYS:HA	1.89	0.52
19:N:195:DT:H2''	19:N:196:DT:C6	2.44	0.52
3:C:39:GLU:OE2	11:K:41:THR:HG21	2.09	0.52
15:a:53:ARG:NH2	15:a:57:SER:OG	2.43	0.52
16:b:84:MET:HE3	16:b:84:MET:H	1.73	0.52
7:G:112:THR:HA	7:G:115:ILE:HB	1.92	0.52
14:T:185:DG:H2'	14:T:186:DT:H72	1.91	0.52
16:b:72:TYR:HH	18:d:83:TYR:HE2	1.57	0.52
1:A:728:ASP:HB3	1:A:732:ARG:HH12	1.73	0.52
3:C:266:ARG:HH22	11:K:82:ARG:NH1	2.06	0.52
12:L:49:ARG:HE	12:L:56:ARG:NH2	2.07	0.52
19:N:115:DC:C2'	19:N:116:DT:H71	2.40	0.52
2:B:337:ARG:H	2:B:340:LYS:HE2	1.75	0.52
2:B:630:LEU:HD12	2:B:690:VAL:HG11	1.90	0.52
4:D:3:VAL:HG23	7:G:39:THR:HB	1.92	0.52
12:L:36:CYS:SG	12:L:38:HIS:HB2	2.50	0.52
14:T:37:DG:H2''	14:T:38:DG:N7	2.24	0.52
16:l:73:THR:HG22	16:l:78:ARG:O	2.09	0.52
18:p:69:ILE:HD11	18:p:73:ILE:HD11	1.90	0.52
1:A:115:LEU:HB3	1:A:119:ASN:ND2	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:489:ARG:NH1	2:B:533:SER:O	2.38	0.52
3:C:62:ILE:O	3:C:66:LEU:HG	2.09	0.52
4:D:121:CYS:HA	4:D:124:VAL:HG22	1.91	0.52
1:A:645:GLU:OE1	1:A:649:ASN:ND2	2.42	0.52
3:C:5:PRO:HA	3:C:23:ASP:HB2	1.91	0.52
3:C:234:THR:OG1	3:C:235:THR:N	2.40	0.52
5:E:25:ARG:NH1	5:E:185:ARG:O	2.42	0.52
7:G:95:SER:OG	7:G:98:GLY:O	2.22	0.52
17:c:57:TYR:CE2	18:d:106:LEU:HD12	2.44	0.52
15:k:103:LEU:HB2	15:k:131:ARG:HH21	1.74	0.52
15:m:60:LEU:HB3	15:m:62:ILE:HG22	1.90	0.52
16:n:50:ILE:O	16:n:54:THR:HG22	2.09	0.52
1:A:108:MET:HG3	1:A:173:PRO:HG3	1.91	0.52
1:A:776:ILE:CD1	1:A:799:GLY:HA3	2.35	0.52
2:B:162:PRO:HG2	2:B:454:LEU:HD12	1.91	0.52
2:B:798:TYR:OH	3:C:65:ARG:NH2	2.39	0.52
2:B:847:ASP:HB3	3:C:167:HIS:CE1	2.45	0.52
14:T:146:DA:C2	19:N:110:DA:C2	2.98	0.52
17:g:25:PHE:CE2	17:g:56:GLU:HA	2.45	0.52
1:A:578:LEU:H	1:A:578:LEU:HD22	1.74	0.52
14:T:79:DT:H2"	14:T:80:DA:N7	2.25	0.52
15:m:101:VAL:HG22	15:m:105:GLU:OE2	2.09	0.52
1:A:74:MET:N	1:A:74:MET:SD	2.83	0.52
1:A:692:GLN:O	1:A:695:ILE:HG13	2.10	0.52
2:B:837:ASP:CG	2:B:1020:ARG:HH12	2.18	0.52
2:B:1163:CYS:HB3	2:B:1166:CYS:SG	2.49	0.52
9:I:32:CYS:SG	9:I:34:TYR:HB3	2.50	0.52
14:T:132:DG:C2	14:T:133:DG:C2	2.99	0.52
15:a:113:HIS:CG	15:e:126:LEU:HD13	2.45	0.52
1:A:1122:LEU:HD13	1:A:1126:ILE:HG22	1.91	0.51
2:B:394:PHE:HB2	2:B:510:THR:HG23	1.92	0.51
2:B:863:GLU:OE2	2:B:874:PHE:N	2.42	0.51
15:a:126:LEU:HD22	15:e:113:HIS:CG	2.45	0.51
18:p:66:VAL:HA	18:p:69:ILE:HG22	1.92	0.51
18:p:95:GLN:OE1	18:p:111:VAL:HG22	2.10	0.51
1:A:882:GLN:NE2	1:A:961:ASN:HA	2.25	0.51
2:B:227:HIS:NE2	2:B:382:ALA:HA	2.25	0.51
3:C:145:CYS:SG	3:C:146:LYS:N	2.83	0.51
17:c:88:ARG:HA	17:c:94:ASN:OD1	2.10	0.51
15:e:110:CYS:HB3	15:e:126:LEU:HD23	1.92	0.51
16:f:75:HIS:CE1	18:h:96:THR:HG1	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:o:59:THR:HA	17:o:62:ILE:HD11	1.91	0.51
19:N:11:DT:H2''	19:N:12:DT:C7	2.16	0.51
16:b:75:HIS:NE2	18:d:93:GLU:OE1	2.43	0.51
17:c:55:LEU:HD13	17:c:58:LEU:HD12	1.93	0.51
16:l:68:ASP:OD2	16:l:92:ARG:NH1	2.42	0.51
15:m:106:ASP:HB2	15:m:131:ARG:HH11	1.75	0.51
1:A:31:SER:O	2:B:1183:ARG:NH2	2.43	0.51
2:B:392:ASP:HB2	2:B:508:HIS:HD2	1.74	0.51
2:B:798:TYR:CD2	10:J:4:PRO:HG3	2.46	0.51
15:e:40:ARG:HG3	19:N:191:DC:H5''	1.92	0.51
18:p:73:ILE:HA	18:p:76:GLU:HG2	1.91	0.51
19:N:77:DG:C8	19:N:77:DG:H5'	2.45	0.51
1:A:204:THR:O	1:A:208:ILE:HG12	2.09	0.51
1:A:1113:ILE:HG12	1:A:1116:PRO:HG3	1.92	0.51
2:B:357:ILE:HG22	2:B:358:THR:HG22	1.92	0.51
14:T:210:DA:H2'	14:T:210:DA:N3	2.26	0.51
17:c:52:ALA:O	17:c:56:GLU:HG3	2.10	0.51
18:h:102:LEU:O	18:h:107:ALA:HB2	2.10	0.51
15:k:95:ALA:HB2	16:l:90:LEU:CD1	2.35	0.51
5:E:47:ASP:OD1	5:E:53:GLN:NE2	2.44	0.51
19:N:218:DC:H2'	19:N:219:DT:H72	1.91	0.51
1:A:130:ASP:HB3	1:A:133:LYS:HB2	1.93	0.51
1:A:622:THR:HG22	1:A:623:VAL:HG13	1.92	0.51
1:A:1122:LEU:HD21	1:A:1136:ILE:HG21	1.93	0.51
2:B:508:HIS:ND1	2:B:510:THR:HG22	2.26	0.51
4:D:65:LYS:NZ	4:D:84:ILE:O	2.43	0.51
2:B:102:GLN:HA	2:B:105:ARG:HG2	1.93	0.51
14:T:27:DC:H2''	14:T:28:DT:C5	2.46	0.51
14:T:154:DT:C2'	14:T:155:DG:H5'	2.40	0.51
16:b:31:LYS:HE3	16:b:51:TYR:CE2	2.46	0.51
2:B:89:MET:HE3	2:B:91:GLU:HG3	1.92	0.51
2:B:842:ASN:O	2:B:846:ILE:HG12	2.11	0.51
2:B:843:GLN:HB2	2:B:994:TYR:O	2.11	0.51
7:G:54:ILE:HD11	7:G:74:TYR:HB3	1.92	0.51
16:f:78:ARG:HE	19:N:209:DG:P	2.34	0.51
1:A:478:PRO:HG3	1:A:522:MET:HE2	1.92	0.51
1:A:1074:ILE:O	1:A:1077:PRO:HD2	2.11	0.51
2:B:259:ARG:HG2	2:B:305:MET:HE1	1.93	0.51
2:B:1082:MET:HA	2:B:1082:MET:HE2	1.92	0.51
4:D:98:ALA:O	4:D:102:VAL:HG22	2.10	0.51
9:I:7:CYS:SG	9:I:9:GLU:HG2	2.51	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:a:48:LEU:HD13	15:a:51:ILE:HB	1.93	0.51
1:A:861:LEU:HD11	1:A:1396:ASP:C	2.36	0.50
2:B:401:LEU:HG	2:B:402:ALA:H	1.76	0.50
10:J:48:MET:HE3	10:J:48:MET:O	2.11	0.50
17:c:31:HIS:CD2	17:c:35:ARG:HE	2.29	0.50
19:N:235:DG:H2''	19:N:236:DT:C4	2.45	0.50
2:B:102:GLN:HG2	2:B:103:GLU:N	2.26	0.50
14:T:69:DG:H5''	15:e:42:ARG:HH12	1.74	0.50
15:a:63:ARG:CZ	16:b:30:THR:HG21	2.40	0.50
2:B:562:TYR:CE1	2:B:567:HIS:HB2	2.46	0.50
8:H:16:ASP:OD1	8:H:18:GLY:N	2.44	0.50
9:I:75:CYS:HB3	9:I:108:LYS:HZ2	1.75	0.50
14:T:89:DT:H2''	14:T:90:DA:C8	2.47	0.50
14:T:233:DG:H2'	14:T:234:DG:C8	2.45	0.50
15:a:108:ASN:HD21	16:b:42:GLY:C	2.20	0.50
17:c:85:LEU:O	17:c:89:ASN:ND2	2.44	0.50
17:g:90:ASP:OD1	17:g:93:LEU:N	2.30	0.50
16:n:59:LYS:HG3	16:n:63:GLU:OE2	2.11	0.50
1:A:34:LYS:HZ1	1:A:85:GLU:HB3	1.76	0.50
1:A:89:PRO:HG2	1:A:205:PRO:HB2	1.93	0.50
9:I:13:MET:HE3	9:I:14:LEU:O	2.11	0.50
15:e:63:ARG:HH11	16:f:29:ILE:HA	1.76	0.50
15:e:119:ILE:HD12	16:f:43:VAL:HG22	1.93	0.50
17:g:71:ARG:NH1	18:h:52:THR:OG1	2.44	0.50
15:k:68:GLN:HG2	15:k:89:ILE:HD12	1.93	0.50
15:k:128:ARG:NH2	16:l:57:VAL:HB	2.26	0.50
19:N:239:DG:C6	19:N:240:DA:C6	3.00	0.50
1:A:352:THR:HB	2:B:1103:ILE:HG13	1.93	0.50
2:B:1182:CYS:O	2:B:1186:LYS:N	2.44	0.50
18:d:95:GLN:HE21	18:d:99:ARG:NE	2.10	0.50
17:g:21:ALA:O	17:g:23:LEU:HG	2.10	0.50
15:k:103:LEU:HD13	15:k:131:ARG:HD3	1.94	0.50
1:A:1195:LEU:HB2	1:A:1242:CYS:HB3	1.94	0.50
1:A:1401:MET:HE1	1:A:1428:SER:HB3	1.94	0.50
2:B:230:GLU:HB3	2:B:246:GLN:HG3	1.93	0.50
3:C:239:LYS:O	3:C:243:VAL:HG23	2.11	0.50
5:E:98:ARG:O	5:E:101:GLU:HG3	2.12	0.50
1:A:570:LYS:HD3	3:C:221:TYR:HB2	1.94	0.50
1:A:1330:THR:O	5:E:146:HIS:NE2	2.43	0.50
1:A:1338:ILE:HD11	1:A:1342:LEU:HD12	1.94	0.50
10:J:47:ARG:HG3	10:J:48:MET:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:HIS:O	1:A:390:THR:OG1	2.27	0.50
8:H:117:PHE:HB2	8:H:120:LEU:HB2	1.94	0.50
11:K:77:THR:OG1	11:K:78:GLU:N	2.44	0.50
12:L:67:ILE:HD12	12:L:68:GLN:H	1.77	0.50
15:a:100:LEU:HD22	16:b:58:LEU:HD22	1.93	0.50
17:c:23:LEU:HB3	17:c:56:GLU:OE2	2.11	0.50
1:A:35:ILE:O	1:A:84:MET:HE1	2.11	0.50
1:A:149:GLU:O	1:A:167:GLY:HA3	2.12	0.50
2:B:13:THR:N	2:B:16:ASP:OD2	2.37	0.50
2:B:855:PHE:CE2	2:B:972:LYS:HE3	2.46	0.50
5:E:60:LEU:HD12	5:E:61:ALA:N	2.26	0.50
14:T:32:DG:C6	14:T:33:DA:C5	3.00	0.50
14:T:130:DC:H2''	14:T:131:DT:C5	2.47	0.50
16:f:60:VAL:HA	16:f:63:GLU:OE1	2.11	0.50
15:k:71:VAL:HG21	15:k:89:ILE:HD13	1.93	0.50
19:N:103:DG:H2''	19:N:104:DG:C8	2.47	0.50
1:A:497:GLU:O	1:A:501:GLU:HG2	2.12	0.49
3:C:38:ALA:HA	3:C:164:ALA:HB3	1.93	0.49
17:g:67:GLY:O	17:g:71:ARG:HG2	2.11	0.49
18:p:107:ALA:O	18:p:111:VAL:HG23	2.11	0.49
19:N:6:DT:H2''	19:N:7:DC:C6	2.47	0.49
2:B:534:LEU:HD23	2:B:747:MET:HE1	1.95	0.49
2:B:1021:MET:O	2:B:1023:VAL:HG23	2.11	0.49
7:G:25:TYR:O	7:G:28:GLU:HG2	2.11	0.49
19:N:151:DG:C2	19:N:152:DC:C2	2.99	0.49
19:N:219:DT:H2'	19:N:220:DA:C8	2.46	0.49
1:A:81:PHE:CE2	1:A:241:PRO:HB2	2.47	0.49
1:A:691:VAL:O	1:A:695:ILE:HG12	2.12	0.49
5:E:47:ASP:HB2	5:E:49:MET:SD	2.53	0.49
10:J:47:ARG:NH2	10:J:48:MET:SD	2.85	0.49
15:a:39:HIS:HA	19:N:174:DG:OP1	2.11	0.49
15:a:113:HIS:HE1	15:e:129:ARG:NH1	2.10	0.49
16:b:97:LEU:HD23	16:b:97:LEU:H	1.78	0.49
19:N:5:DT:H2''	19:N:6:DT:C6	2.46	0.49
19:N:212:DT:H2''	19:N:213:DA:H8	1.78	0.49
1:A:278:GLN:O	1:A:281:GLU:HG2	2.13	0.49
1:A:1192:PRO:HA	1:A:1243:ARG:HH12	1.78	0.49
2:B:634:GLU:OE1	2:B:646:ARG:NE	2.45	0.49
6:F:93:ILE:HD11	6:F:134:ILE:HD11	1.94	0.49
15:m:97:GLU:HA	15:m:100:LEU:HG	1.94	0.49
17:o:26:PRO:HG2	17:o:29:ARG:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:o:55:LEU:HD13	18:p:66:VAL:HG23	1.94	0.49
17:o:58:LEU:HA	17:o:61:GLU:OE1	2.12	0.49
1:A:147:VAL:HG23	16:l:40:ARG:HH21	1.76	0.49
1:A:185:THR:HG23	1:A:199:GLU:HB3	1.94	0.49
1:A:509:PRO:O	1:A:512:ILE:HD12	2.12	0.49
1:A:1165:ILE:O	1:A:1169:PHE:N	2.39	0.49
2:B:206:GLN:HE21	2:B:472:VAL:HG13	1.77	0.49
2:B:904:ARG:NH2	12:L:67:ILE:HD11	2.28	0.49
3:C:248:ILE:O	3:C:252:GLN:HG3	2.12	0.49
15:a:48:LEU:HD22	15:a:51:ILE:HD12	1.93	0.49
15:a:119:ILE:HD11	16:b:46:ILE:HG23	1.94	0.49
17:g:31:HIS:HD2	17:g:35:ARG:HE	1.56	0.49
15:k:70:LEU:HD22	16:l:26:ILE:HA	1.93	0.49
19:N:8:DG:C4	19:N:9:DT:C4	3.00	0.49
19:N:151:DG:C2	19:N:152:DC:O2	2.65	0.49
1:A:327:ARG:HE	1:A:1409:VAL:HG11	1.77	0.49
1:A:354:ILE:HG13	1:A:483:PHE:HD1	1.78	0.49
1:A:443:VAL:HG21	1:A:490:LEU:HD11	1.94	0.49
2:B:826:ALA:HB2	2:B:1087:PHE:CE1	2.48	0.49
2:B:886:LYS:HG2	2:B:936:ASP:OD2	2.12	0.49
14:T:156:DG:H2''	14:T:157:DC:C6	2.47	0.49
16:b:67:ARG:NH1	18:d:99:ARG:O	2.46	0.49
16:f:25:ASN:N	16:f:27:GLN:OE1	2.46	0.49
1:A:536:THR:HG21	1:A:579:LEU:HD22	1.95	0.49
1:A:1400:LEU:HB3	1:A:1429:GLU:HG3	1.95	0.49
5:E:138:ASP:OD1	5:E:138:ASP:N	2.32	0.49
15:e:59:GLU:H	15:e:59:GLU:CD	2.20	0.49
15:e:65:LEU:HB2	19:N:199:DC:OP2	2.12	0.49
1:A:58:LEU:O	1:A:80:HIS:N	2.45	0.49
1:A:200:ARG:HD3	15:k:64:LYS:NZ	2.28	0.49
2:B:119:MET:O	2:B:153:GLY:N	2.46	0.49
2:B:832:GLY:CA	2:B:835:GLN:HE21	2.26	0.49
5:E:66:GLU:CD	5:E:66:GLU:H	2.18	0.49
6:F:110:ASP:OD1	6:F:110:ASP:N	2.42	0.49
7:G:15:PRO:HA	7:G:18:PHE:CE1	2.47	0.49
9:I:102:VAL:HG12	9:I:103:CYS:O	2.13	0.49
14:T:105:DT:H2''	14:T:106:DG:H5'	1.95	0.49
15:e:101:VAL:O	15:e:105:GLU:HG3	2.12	0.49
15:e:102:GLY:HA2	15:e:105:GLU:CD	2.37	0.49
16:f:49:LEU:HD12	16:f:49:LEU:H	1.77	0.49
16:f:56:GLY:O	16:f:60:VAL:HG13	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:f:88:TYR:HA	16:f:91:LYS:HZ2	1.77	0.49
16:l:34:ILE:HA	16:l:37:LEU:HG	1.95	0.49
19:N:91:DT:H2'	19:N:92:DT:C6	2.48	0.49
1:A:674:ALA:HA	1:A:677:MET:SD	2.53	0.49
1:A:1316:LEU:O	1:A:1317:ALA:C	2.55	0.49
2:B:60:GLN:HE22	2:B:62:ALA:HB2	1.77	0.49
18:h:116:LYS:HG3	18:h:117:ALA:N	2.26	0.49
1:A:762:MET:HE3	2:B:1023:VAL:HG22	1.95	0.49
1:A:1143:THR:HG1	1:A:1277:ARG:H	1.59	0.49
2:B:547:ILE:HG12	2:B:619:ILE:HG21	1.95	0.49
2:B:1060:ARG:HB2	2:B:1066:SER:HB3	1.95	0.49
7:G:27:ARG:NH2	7:G:54:ILE:O	2.46	0.49
8:H:87:SER:OG	8:H:88:LEU:N	2.46	0.49
14:T:32:DG:O6	14:T:33:DA:N6	2.45	0.49
14:T:120:DG:C2	14:T:121:DA:H2	2.26	0.49
1:A:5:PRO:HG2	2:B:1159:ARG:HH12	1.78	0.48
2:B:419:ARG:O	2:B:423:ARG:HG2	2.12	0.48
2:B:884:ARG:HD2	13:P:2:G:C8	2.48	0.48
3:C:92:ASP:OD1	3:C:93:GLU:N	2.46	0.48
4:D:107:ASP:O	4:D:111:THR:OG1	2.22	0.48
15:a:42:ARG:HB3	19:N:175:DT:H5'	1.94	0.48
17:g:29:ARG:HA	17:g:32:ARG:HG3	1.94	0.48
16:l:54:THR:O	16:l:58:LEU:HD13	2.12	0.48
1:A:321:ARG:NH2	1:A:323:VAL:HA	2.29	0.48
1:A:872:ASP:OD2	1:A:1369:ARG:NH1	2.46	0.48
3:C:4:GLU:HB3	3:C:5:PRO:HD3	1.96	0.48
3:C:196:ASP:OD2	3:C:199:LYS:HG2	2.12	0.48
5:E:27:TYR:CE1	5:E:77:LEU:HD13	2.48	0.48
7:G:33:ASP:OD1	7:G:33:ASP:N	2.45	0.48
14:T:20:DC:C4	14:T:21:DA:N6	2.81	0.48
16:b:84:MET:H	16:b:84:MET:CE	2.25	0.48
16:f:83:ALA:O	16:f:87:VAL:HG13	2.13	0.48
16:l:30:THR:O	16:l:34:ILE:HD12	2.13	0.48
19:N:167:DA:H2''	19:N:168:DA:N7	2.29	0.48
2:B:1166:CYS:HB3	2:B:1185:CYS:SG	2.52	0.48
17:c:24:GLN:N	17:c:56:GLU:OE2	2.46	0.48
17:g:42:ARG:HE	18:h:88:THR:HG22	1.77	0.48
15:k:72:ARG:HD3	15:k:84:PHE:CD1	2.48	0.48
1:A:123:ALA:O	1:A:127:ARG:HG2	2.13	0.48
2:B:293:ILE:HG13	2:B:294:CYS:N	2.27	0.48
9:I:24:ARG:HA	9:I:24:ARG:NH2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:30:GLN:OE1	10:J:32:GLY:N	2.46	0.48
15:a:85:GLN:HB2	16:b:81:VAL:O	2.13	0.48
15:e:83:ARG:O	16:f:80:THR:HA	2.12	0.48
17:g:79:ILE:HG12	17:g:82:HIS:ND1	2.28	0.48
18:p:96:THR:HA	18:p:99:ARG:HE	1.78	0.48
19:N:218:DC:C2	19:N:219:DT:C5	3.00	0.48
19:N:233:DG:H2''	19:N:234:DT:C7	2.29	0.48
2:B:349:LEU:O	2:B:353:LEU:HB3	2.13	0.48
2:B:480:THR:HG23	2:B:483:SER:H	1.77	0.48
2:B:1161:HIS:CD2	2:B:1193:GLN:HB3	2.48	0.48
14:T:50:DT:H2''	14:T:51:DT:C5	2.49	0.48
18:d:54:ILE:HG12	18:d:58:ALA:HB3	1.96	0.48
17:o:26:PRO:HD3	18:p:40:TYR:CG	2.49	0.48
1:A:1448:ILE:HG22	7:G:59:GLY:O	2.12	0.48
2:B:855:PHE:HE1	2:B:857:ARG:HE	1.62	0.48
4:D:122:THR:HA	4:D:125:ASP:OD2	2.14	0.48
10:J:53:VAL:HG13	10:J:55:LEU:HD21	1.96	0.48
15:e:128:ARG:HH11	16:f:61:PHE:HE1	1.62	0.48
19:N:158:DC:H2''	19:N:159:DA:H5'	1.95	0.48
19:N:189:DC:H2''	19:N:190:DG:H5'	1.96	0.48
1:A:822:ARG:HH12	2:B:507:LEU:HD13	1.79	0.48
2:B:12:ILE:HG13	2:B:16:ASP:HB2	1.96	0.48
2:B:572:ARG:NH1	2:B:616:GLU:OE2	2.46	0.48
2:B:864:LYS:N	2:B:872:GLU:OE1	2.47	0.48
2:B:953:LEU:HD12	2:B:953:LEU:HA	1.67	0.48
9:I:75:CYS:HB3	9:I:108:LYS:NZ	2.29	0.48
16:f:75:HIS:ND1	18:h:96:THR:OG1	2.33	0.48
17:o:17:ARG:HH21	19:N:28:DC:P	2.37	0.48
19:N:202:DC:H2'	19:N:203:DC:H6	1.74	0.48
2:B:201:LYS:NZ	2:B:455:ALA:O	2.47	0.48
2:B:218:LYS:N	2:B:388:GLN:OE1	2.47	0.48
2:B:268:VAL:HG13	2:B:329:ARG:O	2.14	0.48
14:T:84:DG:H1'	15:a:40:ARG:HH12	1.79	0.48
14:T:153:DT:H3	19:N:102:DA:H61	1.62	0.48
15:a:110:CYS:SG	15:a:126:LEU:HD23	2.54	0.48
16:f:31:LYS:HE3	16:f:51:TYR:CE2	2.49	0.48
17:g:62:ILE:HD11	17:g:83:LEU:HD22	1.95	0.48
19:N:105:DG:H2''	19:N:106:DG:C8	2.48	0.48
1:A:899:TYR:O	1:A:1031:ARG:NE	2.46	0.48
1:A:1078:ALA:HA	1:A:1081:MET:SD	2.54	0.48
3:C:165:LYS:O	11:K:6:ARG:NH1	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:T:56:DG:C2'	14:T:57:DT:H72	2.43	0.48
3:C:85:CYS:HB2	3:C:94:CYS:SG	2.54	0.48
3:C:166:GLU:HA	11:K:6:ARG:HB3	1.95	0.48
15:a:67:PHE:CZ	15:a:93:GLN:HA	2.49	0.48
16:n:34:ILE:HG21	16:n:54:THR:HG21	1.96	0.48
1:A:513:VAL:HG12	1:A:877:THR:HB	1.96	0.47
1:A:987:GLU:OE1	1:A:1041:ARG:NH2	2.47	0.47
1:A:1136:ILE:O	1:A:1140:ILE:HG22	2.14	0.47
16:b:57:VAL:O	16:b:61:PHE:HD1	1.97	0.47
18:d:39:ILE:HG13	18:d:40:TYR:CD2	2.49	0.47
16:f:58:LEU:O	16:f:62:LEU:HG	2.13	0.47
16:f:91:LYS:HZ1	18:h:79:ARG:HH12	1.61	0.47
19:N:196:DT:H2'	19:N:197:DA:C8	2.49	0.47
1:A:37:TYR:CD2	1:A:49:ARG:HD3	2.49	0.47
1:A:203:LEU:HD22	1:A:208:ILE:HD11	1.95	0.47
2:B:597:ARG:HA	2:B:602:ILE:HG22	1.96	0.47
1:A:84:MET:HB2	1:A:240:LEU:HB3	1.95	0.47
1:A:864:ILE:HG23	5:E:175:PRO:HD3	1.96	0.47
3:C:248:ILE:HG22	3:C:252:GLN:OE1	2.15	0.47
8:H:7:ASP:OD1	8:H:8:ASP:N	2.47	0.47
14:T:82:DG:N2	19:N:173:DC:O2	2.40	0.47
14:T:185:DG:H2''	14:T:186:DT:H6	1.78	0.47
19:N:93:DT:C4	19:N:94:DA:N6	2.82	0.47
1:A:872:ASP:OD1	1:A:872:ASP:N	2.46	0.47
1:A:1150:SER:O	9:I:49:ILE:HG12	2.15	0.47
1:A:1229:MET:HE3	1:A:1230:TRP:H	1.80	0.47
2:B:117:LEU:O	2:B:156:VAL:HG22	2.14	0.47
2:B:1123:SER:HB3	14:T:202:DA:OP2	2.14	0.47
3:C:65:ARG:HH22	10:J:4:PRO:HA	1.78	0.47
14:T:31:DA:H3'	17:g:17:ARG:HG3	1.96	0.47
14:T:165:DA:H2''	14:T:166:DC:H5'	1.96	0.47
17:g:42:ARG:HE	18:h:88:THR:CG2	2.27	0.47
15:k:108:ASN:O	15:k:112:ILE:HG12	2.14	0.47
1:A:140:GLN:HA	1:A:143:LYS:HE3	1.97	0.47
1:A:985:ILE:N	1:A:986:PRO:HD2	2.29	0.47
2:B:369:PHE:HB3	2:B:559:LEU:HD21	1.97	0.47
2:B:563:ASP:H	2:B:567:HIS:HE1	1.61	0.47
12:L:40:PHE:HZ	12:L:50:CYS:HA	1.78	0.47
16:f:37:LEU:O	16:f:40:ARG:HB2	2.14	0.47
16:l:75:HIS:HB2	18:p:96:THR:HG21	1.96	0.47
15:m:50:GLU:O	15:m:53:ARG:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:N:143:DC:H2''	19:N:144:DG:N7	2.29	0.47
1:A:199:GLU:HB2	15:k:97:GLU:HG3	1.95	0.47
1:A:405:TYR:HE2	1:A:413:ARG:HD3	1.80	0.47
1:A:854:ASP:OD2	1:A:858:ARG:NH1	2.47	0.47
1:A:1040:ASN:OD1	1:A:1042:ASP:N	2.48	0.47
1:A:1296:ASP:N	1:A:1300:GLU:O	2.46	0.47
2:B:479:TYR:CE2	2:B:1096:ARG:HB3	2.49	0.47
2:B:593:MET:HE2	2:B:593:MET:HA	1.95	0.47
5:E:76:THR:H	5:E:105:SER:HB2	1.78	0.47
8:H:138:ASN:OD1	8:H:138:ASN:N	2.47	0.47
16:l:72:TYR:HB3	16:l:85:ASP:HB3	1.95	0.47
18:p:62:MET:O	18:p:66:VAL:HG12	2.15	0.47
1:A:186:TRP:CZ3	1:A:201:LYS:HB3	2.50	0.47
1:A:231:ARG:HB2	1:A:234:TRP:CG	2.50	0.47
1:A:1032:ARG:HB2	1:A:1032:ARG:CZ	2.43	0.47
1:A:1143:THR:OG1	1:A:1277:ARG:HG2	2.15	0.47
1:A:1191:SER:HG	1:A:1193:TRP:CD1	2.33	0.47
1:A:1229:MET:HB3	1:A:1241:ARG:HH21	1.80	0.47
1:A:1270:MET:O	1:A:1274:ILE:HG12	2.15	0.47
2:B:323:LEU:HB3	2:B:342:ILE:HG13	1.97	0.47
2:B:539:SER:HB3	2:B:625:ARG:HB2	1.96	0.47
2:B:559:LEU:HB2	2:B:581:GLY:HA2	1.97	0.47
2:B:760:ASP:N	2:B:760:ASP:OD1	2.44	0.47
2:B:857:ARG:O	2:B:968:MET:N	2.45	0.47
7:G:145:LEU:HD23	7:G:161:GLY:HA3	1.96	0.47
14:T:185:DG:H2''	14:T:186:DT:C6	2.49	0.47
19:N:121:DT:H2''	19:N:122:DC:C5	2.50	0.47
19:N:131:DA:H2''	19:N:132:DG:O5'	2.14	0.47
19:N:233:DG:C2'	19:N:234:DT:H71	2.28	0.47
1:A:561:VAL:HG13	8:H:78:TRP:HB3	1.96	0.47
1:A:1204:MET:HE1	1:A:1209:LEU:O	2.15	0.47
1:A:1227:PHE:O	1:A:1242:CYS:HA	2.15	0.47
4:D:64:LEU:HD13	4:D:89:LEU:HB3	1.97	0.47
14:T:59:DA:H2''	14:T:60:DA:N7	2.30	0.47
18:d:73:ILE:HD13	18:d:101:LEU:HD12	1.97	0.47
1:A:209:LEU:HD22	1:A:236:ILE:HG21	1.95	0.47
2:B:1023:VAL:HG12	2:B:1027:ILE:CD1	2.45	0.47
3:C:6:LYS:O	3:C:22:SER:OG	2.30	0.47
8:H:6:PHE:HD2	8:H:59:LEU:HD23	1.79	0.47
8:H:92:TYR:HD1	8:H:144:ARG:HB2	1.79	0.47
10:J:56:ILE:HD12	10:J:59:PHE:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:T:8:DG:H2'	14:T:9:DT:C6	2.50	0.47
15:e:63:ARG:HG3	15:e:66:PRO:CG	2.35	0.47
19:N:252:DG:H2''	19:N:253:DA:O5'	2.15	0.47
1:A:208:ILE:HG22	1:A:212:PHE:CE2	2.50	0.47
1:A:884:ILE:HG12	1:A:1023:LEU:HD13	1.97	0.47
2:B:27:GLU:OE2	2:B:679:SER:OG	2.22	0.47
2:B:706:ASP:N	2:B:706:ASP:OD1	2.48	0.47
2:B:832:GLY:HA2	2:B:835:GLN:HE21	1.80	0.47
4:D:117:ASP:O	4:D:121:CYS:SG	2.64	0.47
8:H:7:ASP:HB2	8:H:58:THR:HG23	1.96	0.47
10:J:43:TYR:HA	10:J:46:ARG:HB2	1.97	0.47
16:b:46:ILE:HG22	16:b:50:ILE:HG21	1.96	0.47
18:d:98:VAL:HG13	18:d:102:LEU:HD12	1.97	0.47
19:N:115:DC:H2''	19:N:116:DT:H71	1.97	0.47
1:A:958:LEU:HD12	1:A:1023:LEU:HD22	1.97	0.46
2:B:22:SER:HG	2:B:811:TYR:HH	1.60	0.46
2:B:549:ASN:O	2:B:552:GLU:HG3	2.15	0.46
15:a:119:ILE:HD13	16:b:43:VAL:HG21	1.97	0.46
16:f:91:LYS:HE2	18:h:79:ARG:HH22	1.80	0.46
1:A:171:THR:HG21	1:A:187:LYS:H	1.80	0.46
1:A:194:ARG:HD3	15:k:124:ILE:HG12	1.95	0.46
1:A:319:SER:C	1:A:321:ARG:N	2.73	0.46
1:A:864:ILE:HG21	5:E:174:LEU:HD23	1.97	0.46
1:A:1453:LEU:HD22	7:G:22:MET:CE	2.43	0.46
2:B:1021:MET:SD	2:B:1021:MET:N	2.88	0.46
3:C:69:ILE:HD11	3:C:115:SER:CB	2.46	0.46
3:C:191:PHE:HB3	3:C:201:TRP:NE1	2.30	0.46
4:D:90:ALA:HB2	4:D:106:LEU:HD12	1.98	0.46
4:D:117:ASP:O	4:D:120:THR:OG1	2.31	0.46
16:l:71:THR:HG23	18:p:99:ARG:HG3	1.97	0.46
19:N:199:DC:H2''	19:N:200:DC:H5'	1.96	0.46
1:A:56:PRO:HB2	1:A:68:GLN:OE1	2.15	0.46
1:A:189:SER:C	15:k:102:GLY:H	2.23	0.46
6:F:79:ARG:HA	6:F:144:GLU:OE2	2.16	0.46
14:T:128:DG:N2	19:N:128:DT:C2	2.83	0.46
1:A:342:MET:HB3	2:B:1135:ARG:HH22	1.80	0.46
1:A:895:HIS:O	1:A:899:TYR:CB	2.62	0.46
14:T:143:DA:H2''	14:T:144:DG:C8	2.50	0.46
17:c:104:GLN:HA	15:e:58:THR:HB	1.97	0.46
17:g:83:LEU:HD13	18:h:61:ILE:HG21	1.98	0.46
18:h:75:GLY:O	18:h:79:ARG:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:k:84:PHE:CD2	15:k:89:ILE:HG13	2.51	0.46
15:k:113:HIS:CG	15:m:126:LEU:HD12	2.51	0.46
16:l:34:ILE:HD12	16:l:34:ILE:H	1.80	0.46
18:p:79:ARG:HB3	18:p:83:TYR:CZ	2.51	0.46
1:A:1338:ILE:HD11	1:A:1342:LEU:CD1	2.45	0.46
2:B:279:ARG:NH1	2:B:284:VAL:O	2.48	0.46
2:B:863:GLU:HG3	2:B:874:PHE:CZ	2.50	0.46
3:C:214:LYS:N	3:C:217:GLU:OE1	2.47	0.46
14:T:160:DT:H4'	15:m:63:ARG:NH1	2.31	0.46
15:e:57:SER:HB2	15:e:59:GLU:OE1	2.16	0.46
15:e:126:LEU:O	15:e:129:ARG:HG2	2.15	0.46
15:k:67:PHE:O	15:k:71:VAL:HG23	2.15	0.46
15:m:69:ARG:NH1	19:N:98:DG:OP1	2.49	0.46
19:N:118:DG:H2'	19:N:119:DT:H72	1.96	0.46
1:A:102:VAL:HG11	1:A:212:PHE:CE1	2.46	0.46
1:A:149:GLU:HG3	1:A:165:ARG:HD3	1.97	0.46
1:A:207:GLU:HA	1:A:210:ASN:HD21	1.80	0.46
1:A:740:ASP:OD1	1:A:741:LEU:N	2.49	0.46
1:A:1039:LEU:HD23	1:A:1043:ALA:HB1	1.96	0.46
1:A:1217:LYS:O	1:A:1220:GLU:HG2	2.16	0.46
2:B:773:MET:O	2:B:776:GLN:N	2.48	0.46
2:B:992:VAL:HG13	2:B:994:TYR:HE1	1.80	0.46
3:C:50:ILE:HD12	12:L:69:PHE:HE2	1.81	0.46
3:C:108:GLU:OE1	3:C:108:GLU:N	2.48	0.46
5:E:120:ASN:HA	5:E:123:ILE:HD12	1.96	0.46
15:e:40:ARG:NH1	19:N:190:DG:N3	2.64	0.46
16:f:68:ASP:O	16:f:72:TYR:CD1	2.68	0.46
15:k:68:GLN:O	15:k:72:ARG:HG2	2.16	0.46
16:l:83:ALA:HA	16:l:86:VAL:HG22	1.98	0.46
3:C:91:CYS:SG	3:C:94:CYS:N	2.87	0.46
7:G:4:LEU:HD23	7:G:4:LEU:HA	1.80	0.46
8:H:8:ASP:HB3	8:H:10:PHE:CE1	2.51	0.46
11:K:55:ASP:O	11:K:77:THR:OG1	2.23	0.46
15:a:75:ALA:HB1	15:a:82:LEU:HD23	1.97	0.46
17:c:59:THR:HG22	18:d:65:PHE:HE2	1.81	0.46
18:d:110:ALA:O	18:d:113:GLU:HG2	2.16	0.46
17:o:25:PHE:HZ	17:o:59:THR:HG21	1.81	0.46
18:p:102:LEU:HD12	18:p:106:LEU:HD12	1.96	0.46
1:A:198:PRO:O	15:k:93:GLN:HB2	2.15	0.46
1:A:370:SER:O	1:A:374:THR:HG23	2.16	0.46
1:A:1149:THR:HA	1:A:1199:LEU:HD23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1345:GLU:HG3	5:E:197:ILE:HG21	1.98	0.46
2:B:31:VAL:HG11	2:B:488:LEU:HD13	1.98	0.46
2:B:508:HIS:CG	2:B:510:THR:HG22	2.50	0.46
5:E:42:ARG:O	5:E:46:CYS:HB2	2.15	0.46
14:T:181:DG:H2''	14:T:182:DT:O5'	2.15	0.46
15:a:113:HIS:NE2	15:e:126:LEU:HB2	2.31	0.46
17:o:80:PRO:HD2	17:o:81:ARG:NH2	2.31	0.46
17:o:96:LEU:HB3	17:o:97:LEU:HD22	1.97	0.46
1:A:1064:GLU:HG2	1:A:1066:VAL:HG13	1.98	0.46
3:C:35:THR:C	3:C:37:LEU:H	2.23	0.46
3:C:162:GLY:HA3	3:C:170:TRP:CE2	2.51	0.46
4:D:65:LYS:NZ	4:D:89:LEU:HD11	2.31	0.46
5:E:3:ASP:OD1	5:E:3:ASP:N	2.47	0.46
14:T:185:DG:H2'	14:T:186:DT:C7	2.46	0.46
16:f:57:VAL:O	16:f:60:VAL:HG22	2.15	0.46
17:g:24:GLN:HG2	17:g:56:GLU:OE2	2.16	0.46
15:k:120:MET:HE3	15:k:121:PRO:HD2	1.98	0.46
19:N:180:DG:C2	19:N:181:DC:N3	2.84	0.46
1:A:200:ARG:HD3	15:k:64:LYS:HZ3	1.81	0.46
1:A:770:MET:HE2	1:A:770:MET:HB2	1.76	0.46
4:D:118:GLU:O	4:D:122:THR:OG1	2.33	0.46
5:E:161:SER:OG	5:E:165:GLN:OE1	2.27	0.46
14:T:32:DG:C5	14:T:33:DA:N7	2.84	0.46
16:b:59:LYS:HD3	16:b:59:LYS:HA	1.71	0.46
1:A:100:LYS:NZ	1:A:177:LYS:HB2	2.30	0.45
1:A:735:GLU:HA	1:A:738:LEU:HG	1.97	0.45
2:B:452:TYR:CZ	2:B:456:THR:HG21	2.50	0.45
11:K:29:ASN:HD22	11:K:79:GLU:HA	1.80	0.45
15:a:104:PHE:CE2	16:b:37:LEU:HB3	2.52	0.45
17:g:21:ALA:HB2	18:h:121:TYR:CE2	2.51	0.45
1:A:941:ARG:HH22	1:A:945:ARG:NH2	2.14	0.45
2:B:746:SER:HB2	2:B:1046:PRO:HG2	1.98	0.45
4:D:103:LYS:HD3	4:D:107:ASP:OD2	2.15	0.45
15:e:66:PRO:HA	15:e:69:ARG:HD2	1.99	0.45
17:o:97:LEU:HB3	17:o:100:VAL:HB	1.97	0.45
19:N:141:DG:H2'	19:N:142:DT:H72	1.98	0.45
1:A:32:VAL:HG22	2:B:1183:ARG:HH22	1.81	0.45
1:A:226:ASN:HB3	1:A:230:ALA:H	1.81	0.45
1:A:419:HIS:NE2	1:A:421:ARG:HB2	2.30	0.45
2:B:478:ARG:HA	2:B:484:THR:CG2	2.46	0.45
2:B:1076:HIS:CE1	11:K:40:HIS:CE1	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:78:CYS:HB2	9:I:106:CYS:SG	2.53	0.45
16:l:46:ILE:HG23	16:l:50:ILE:CD1	2.39	0.45
3:C:34:ARG:CZ	11:K:40:HIS:HB2	2.46	0.45
7:G:115:ILE:HG23	7:G:119:LEU:HD23	1.98	0.45
15:a:106:ASP:OD2	15:a:131:ARG:NE	2.47	0.45
17:g:27:VAL:HG13	17:g:48:PRO:HB2	1.97	0.45
1:A:1316:LEU:O	1:A:1319:VAL:HG12	2.16	0.45
2:B:551:LEU:HD23	2:B:551:LEU:HA	1.80	0.45
15:a:74:ILE:HD12	16:b:62:LEU:HD23	1.99	0.45
16:b:29:ILE:HD12	16:b:29:ILE:N	2.31	0.45
17:g:108:LEU:H	17:g:108:LEU:HD12	1.82	0.45
15:k:105:GLU:OE2	16:l:41:GLY:HA2	2.16	0.45
17:o:31:HIS:CE1	17:o:35:ARG:HE	2.35	0.45
2:B:567:HIS:HB3	2:B:584:ARG:HH12	1.80	0.45
2:B:1148:LYS:O	2:B:1152:MET:HB2	2.17	0.45
4:D:28:LEU:HD21	4:D:138:HIS:ND1	2.31	0.45
6:F:127:GLN:HB3	6:F:129:LYS:NZ	2.32	0.45
8:H:92:TYR:CD1	8:H:144:ARG:HB2	2.52	0.45
14:T:92:DG:H2''	14:T:93:DC:C5	2.52	0.45
17:c:26:PRO:HG2	17:c:29:ARG:HB3	1.99	0.45
17:g:42:ARG:HD2	19:N:220:DA:H5'	1.98	0.45
17:o:81:ARG:HH22	18:p:57:LYS:HZ2	1.64	0.45
17:o:90:ASP:OD1	17:o:93:LEU:N	2.43	0.45
2:B:85:SER:OG	2:B:114:PRO:HD2	2.16	0.45
5:E:157:ASP:OD1	5:E:157:ASP:C	2.59	0.45
17:g:31:HIS:CE1	17:g:48:PRO:HD3	2.52	0.45
1:A:342:MET:HB3	2:B:1135:ARG:NH2	2.31	0.45
1:A:377:TYR:HB3	1:A:435:ARG:NH2	2.31	0.45
1:A:715:PHE:O	1:A:719:VAL:HG23	2.16	0.45
1:A:738:LEU:HB3	1:A:742:ASN:HD22	1.82	0.45
1:A:854:ASP:OD1	1:A:855:GLY:N	2.50	0.45
2:B:337:ARG:HG2	2:B:340:LYS:HG3	1.97	0.45
4:D:120:THR:O	4:D:124:VAL:HG22	2.17	0.45
8:H:48:PRO:O	8:H:145:ARG:NH1	2.50	0.45
17:o:73:ASN:O	17:o:74:LYS:HG2	2.16	0.45
19:N:185:DC:H2''	19:N:186:DC:C5	2.52	0.45
19:N:218:DC:H2'	19:N:219:DT:C7	2.47	0.45
1:A:35:ILE:HG13	1:A:242:VAL:HG21	1.98	0.45
1:A:1237:LYS:HB3	1:A:1239:ILE:HG23	1.97	0.45
2:B:35:LEU:HA	2:B:35:LEU:HD23	1.78	0.45
2:B:35:LEU:HD22	2:B:167:SER:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:808:ALA:O	2:B:812:LEU:HG	2.17	0.45
2:B:844:SER:OG	2:B:996:HIS:HB2	2.17	0.45
7:G:108:VAL:HG22	7:G:159:ALA:HB3	1.97	0.45
18:d:63:ASN:O	18:d:67:ASN:ND2	2.50	0.45
15:m:76:GLN:HE22	15:m:81:ASP:CB	2.20	0.45
17:o:102:ILE:HD13	17:o:102:ILE:HA	1.81	0.45
19:N:98:DG:H2''	19:N:99:DC:C6	2.51	0.45
1:A:197:GLN:HE22	16:l:61:PHE:HD1	1.63	0.45
1:A:316:LEU:HD12	1:A:320:GLY:HA2	1.99	0.45
1:A:698:ALA:HA	1:A:703:LEU:HD11	1.98	0.45
1:A:1153:GLU:HG2	9:I:45:ARG:HD3	1.99	0.45
1:A:1289:LYS:HD3	1:A:1305:GLU:HB3	1.98	0.45
2:B:84:LEU:HD13	2:B:84:LEU:HA	1.84	0.45
2:B:206:GLN:NE2	2:B:472:VAL:HG22	2.32	0.45
4:D:137:LEU:HG	4:D:142:ILE:HG13	1.98	0.45
14:T:186:DT:H2''	14:T:187:DG:H5'	1.98	0.45
16:b:72:TYR:HB3	16:b:85:ASP:CG	2.41	0.45
16:l:51:TYR:HB3	16:l:55:ARG:NH1	2.32	0.45
15:m:98:ALA:O	15:m:101:VAL:HG12	2.17	0.45
17:o:90:ASP:OD1	17:o:92:GLU:HB3	2.16	0.45
1:A:319:SER:O	1:A:321:ARG:N	2.48	0.44
1:A:1204:MET:SD	1:A:1209:LEU:HB2	2.58	0.44
2:B:164:MET:HG3	2:B:192:GLY:HA2	1.99	0.44
6:F:138:LEU:HD23	6:F:143:TYR:HA	2.00	0.44
10:J:19:ASP:OD1	10:J:19:ASP:C	2.60	0.44
11:K:57:THR:OG1	11:K:76:GLN:HG2	2.17	0.44
14:T:131:DT:H3'	17:c:76:THR:HG21	1.99	0.44
1:A:321:ARG:NH2	1:A:322:PRO:O	2.51	0.44
1:A:796:GLU:H	1:A:796:GLU:CD	2.25	0.44
3:C:196:ASP:OD2	3:C:198:LYS:HB3	2.17	0.44
5:E:170:LYS:O	5:E:173:GLN:HB2	2.17	0.44
7:G:42:PHE:HB3	7:G:78:VAL:HG21	1.99	0.44
8:H:94:TYR:HB3	8:H:143:ILE:HB	1.99	0.44
10:J:7:CYS:HA	10:J:48:MET:HG3	1.99	0.44
14:T:101:DG:N2	19:N:155:DT:O2	2.50	0.44
14:T:106:DG:O6	19:N:148:DA:N6	2.50	0.44
15:a:43:PRO:HB3	19:N:174:DG:N2	2.32	0.44
18:d:54:ILE:HG21	18:d:59:MET:SD	2.56	0.44
17:g:88:ARG:NH2	17:g:97:LEU:O	2.47	0.44
19:N:19:DT:H2''	19:N:20:DG:H8	1.83	0.44
3:C:100:LEU:HD12	3:C:101:SER:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:a:40:ARG:HD2	15:a:40:ARG:HA	1.78	0.44
15:e:64:LYS:O	15:e:65:LEU:C	2.60	0.44
16:f:38:ALA:O	16:f:43:VAL:HG23	2.17	0.44
16:l:49:LEU:H	16:l:49:LEU:HD12	1.83	0.44
16:l:62:LEU:HG	16:l:66:ILE:HD11	1.99	0.44
16:l:63:GLU:OE2	16:l:67:ARG:NH1	2.50	0.44
16:n:54:THR:HA	16:n:57:VAL:CG1	2.47	0.44
1:A:260:GLN:NE2	1:A:265:HIS:HB2	2.32	0.44
1:A:1344:ILE:O	1:A:1347:THR:HG22	2.17	0.44
2:B:538:ILE:HD13	2:B:538:ILE:HA	1.88	0.44
5:E:115:ILE:HG12	5:E:120:ASN:OD1	2.17	0.44
14:T:70:DG:H4'	16:f:45:ARG:HD2	1.99	0.44
17:o:75:LYS:HE3	17:o:79:ILE:HG21	1.99	0.44
1:A:289:ILE:O	1:A:293:VAL:HG23	2.17	0.44
1:A:550:MET:HG3	1:A:656:TYR:CE2	2.53	0.44
1:A:558:ASP:OD1	1:A:559:GLY:N	2.50	0.44
2:B:323:LEU:HA	2:B:323:LEU:HD12	1.70	0.44
2:B:636:ASP:CG	2:B:639:LYS:H	2.25	0.44
2:B:645:LEU:HD23	2:B:645:LEU:HA	1.87	0.44
2:B:751:VAL:HG13	2:B:752:ALA:N	2.32	0.44
2:B:955:THR:HB	12:L:57:VAL:HG22	1.98	0.44
9:I:54:GLU:HA	9:I:90:GLN:HB2	1.98	0.44
18:d:72:ARG:O	18:d:76:GLU:HG2	2.17	0.44
18:d:110:ALA:HA	18:d:113:GLU:OE2	2.18	0.44
15:e:70:LEU:CD1	16:f:26:ILE:HG13	2.47	0.44
15:e:125:GLN:CB	15:e:129:ARG:HH11	2.30	0.44
15:m:59:GLU:O	16:n:40:ARG:NH2	2.50	0.44
1:A:195:ASP:CG	16:l:54:THR:HG22	2.43	0.44
1:A:270:ILE:HD13	1:A:300:HIS:HB3	1.99	0.44
1:A:341:LEU:HB3	1:A:1432:MET:CG	2.48	0.44
1:A:408:ARG:HG3	1:A:431:TRP:CZ2	2.52	0.44
1:A:1143:THR:OG1	1:A:1276:LEU:HB2	2.17	0.44
2:B:848:ARG:NH2	10:J:9:SER:O	2.51	0.44
2:B:993:THR:C	2:B:994:TYR:HD1	2.25	0.44
4:D:58:LEU:HD11	4:D:121:CYS:SG	2.58	0.44
5:E:23:ALA:HB2	5:E:29:ILE:HG13	1.99	0.44
7:G:82:PHE:HB2	7:G:85:GLU:HG3	1.98	0.44
7:G:146:LYS:H	7:G:162:SER:H	1.64	0.44
14:T:32:DG:OP2	17:g:17:ARG:HD3	2.17	0.44
14:T:179:DG:H2''	14:T:180:DC:C5	2.53	0.44
14:T:188:DC:C2'	14:T:189:DG:H5'	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:a:85:GLN:O	15:a:88:ALA:N	2.50	0.44
17:c:29:ARG:NH1	18:d:40:TYR:OH	2.50	0.44
15:e:62:ILE:HA	15:e:63:ARG:HH21	1.82	0.44
15:e:73:GLU:OE1	15:e:74:ILE:HG13	2.18	0.44
16:f:26:ILE:H	16:f:26:ILE:HD12	1.82	0.44
15:k:72:ARG:HA	15:k:72:ARG:NE	2.33	0.44
15:k:103:LEU:HB2	15:k:131:ARG:NH2	2.32	0.44
15:m:76:GLN:NE2	15:m:81:ASP:HB2	2.23	0.44
17:o:84:GLN:HE21	17:o:88:ARG:HE	1.66	0.44
19:N:8:DG:C1'	19:N:9:DT:C5	3.01	0.44
19:N:218:DC:H2''	19:N:219:DT:C7	2.47	0.44
1:A:307:ASN:CB	1:A:325:ALA:HB2	2.47	0.44
1:A:327:ARG:HG3	1:A:1409:VAL:HG21	2.00	0.44
1:A:389:LEU:HD13	1:A:433:VAL:HG11	2.00	0.44
1:A:473:LEU:H	1:A:473:LEU:HG	1.53	0.44
1:A:868:LEU:HA	1:A:868:LEU:HD12	1.73	0.44
1:A:985:ILE:HA	1:A:988:ILE:HD12	1.99	0.44
1:A:1210:THR:O	1:A:1214:VAL:HG23	2.17	0.44
3:C:20:MET:HG3	3:C:227:ARG:NH1	2.33	0.44
4:D:128:LEU:HD11	4:D:178:LEU:HD11	1.99	0.44
7:G:6:ASP:N	7:G:6:ASP:OD1	2.40	0.44
17:c:25:PHE:HD1	18:d:40:TYR:HB2	1.83	0.44
17:c:64:GLU:HG3	17:c:68:ASN:HD21	1.81	0.44
18:d:95:GLN:NE2	18:d:99:ARG:HE	2.14	0.44
18:h:92:ARG:O	18:h:95:GLN:HG2	2.17	0.44
17:o:25:PHE:CZ	17:o:59:THR:HG21	2.53	0.44
19:N:225:DC:H2''	19:N:226:DC:C6	2.52	0.44
1:A:18:GLN:O	2:B:1215:ARG:HG3	2.17	0.44
1:A:428:GLN:OE1	1:A:428:GLN:N	2.51	0.44
1:A:483:PHE:O	2:B:989:THR:HG22	2.17	0.44
1:A:942:LYS:HD2	1:A:942:LYS:C	2.43	0.44
1:A:1378:MET:HE2	1:A:1378:MET:HB2	1.93	0.44
1:A:1428:SER:O	1:A:1431:VAL:N	2.51	0.44
2:B:56:LEU:HB3	2:B:77:ILE:HG13	1.99	0.44
3:C:14:ASP:OD1	3:C:14:ASP:N	2.51	0.44
5:E:164:LEU:HD23	5:E:164:LEU:HA	1.74	0.44
14:T:162:DA:N6	19:N:92:DT:O4	2.51	0.44
16:l:83:ALA:HA	16:l:86:VAL:CG2	2.48	0.44
1:A:187:LYS:HE2	15:k:61:LEU:HD21	1.99	0.44
1:A:240:LEU:HD12	1:A:240:LEU:HA	1.83	0.44
1:A:807:ARG:NH2	2:B:724:LYS:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1168:ASP:OD1	1:A:1241:ARG:HD2	2.17	0.44
2:B:436:ASN:ND2	2:B:438:ASN:HB2	2.33	0.44
4:D:141:GLU:OE2	4:D:162:SER:OG	2.30	0.44
9:I:87:GLN:O	9:I:89:GLN:NE2	2.51	0.44
12:L:53:CYS:SG	12:L:55:HIS:HB2	2.58	0.44
14:T:23:DG:H2'	14:T:24:DT:H71	1.91	0.44
17:c:24:GLN:H	17:c:56:GLU:CD	2.26	0.44
15:m:93:GLN:O	15:m:97:GLU:HG2	2.18	0.44
1:A:807:ARG:HH11	2:B:722:THR:C	2.26	0.43
2:B:535:LEU:HA	2:B:535:LEU:HD23	1.80	0.43
2:B:751:VAL:HG13	2:B:752:ALA:H	1.83	0.43
2:B:784:ASN:HB3	10:J:62:TYR:OH	2.18	0.43
2:B:1111:VAL:HB	2:B:1116:ARG:C	2.43	0.43
2:B:1152:MET:O	2:B:1157:ALA:HB2	2.18	0.43
2:B:1201:LYS:HD3	2:B:1205:GLN:NE2	2.32	0.43
10:J:45:CYS:O	10:J:48:MET:HB2	2.17	0.43
11:K:96:ASN:O	11:K:100:THR:HG22	2.18	0.43
14:T:14:DA:N1	19:N:242:DA:C6	2.86	0.43
18:d:43:LYS:HA	18:d:46:LYS:HE3	2.00	0.43
15:m:121:PRO:O	15:m:124:ILE:HG13	2.17	0.43
16:n:93:GLN:OE1	16:n:95:ARG:HG2	2.18	0.43
19:N:167:DA:H2''	19:N:168:DA:C8	2.53	0.43
1:A:99:ILE:HD11	1:A:235:MET:HG3	2.00	0.43
1:A:804:SER:O	1:A:807:ARG:N	2.45	0.43
2:B:568:THR:HG23	2:B:569:LYS:HG2	2.00	0.43
5:E:45:ILE:HD12	5:E:56:LEU:HB3	2.01	0.43
14:T:32:DG:C4	14:T:33:DA:C8	3.06	0.43
17:o:58:LEU:O	17:o:62:ILE:HG13	2.18	0.43
19:N:220:DA:H2''	19:N:221:DG:C8	2.53	0.43
1:A:269:ASP:HB3	1:A:300:HIS:CD2	2.53	0.43
1:A:840:ARG:NH1	2:B:1136:ASP:OD2	2.51	0.43
2:B:302:MET:HB3	2:B:379:LEU:HD13	2.00	0.43
2:B:540:ILE:C	2:B:623:VAL:HG23	2.43	0.43
5:E:27:TYR:HA	5:E:63:PRO:HA	2.00	0.43
14:T:13:DT:O5'	14:T:13:DT:H6	2.01	0.43
14:T:165:DA:H2''	14:T:166:DC:C5'	2.48	0.43
16:b:87:VAL:HG22	16:b:97:LEU:HD11	2.00	0.43
18:d:42:TYR:CE1	18:d:45:LEU:HD23	2.53	0.43
17:g:88:ARG:NH1	17:g:100:VAL:O	2.50	0.43
16:l:92:ARG:O	16:l:92:ARG:HG2	2.18	0.43
19:N:168:DA:H2'	19:N:169:DC:C4	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:PRO:HB2	1:A:68:GLN:CD	2.43	0.43
1:A:63:ARG:HA	1:A:74:MET:HE2	2.01	0.43
1:A:198:PRO:O	15:k:96:SER:OG	2.37	0.43
1:A:199:GLU:HB2	15:k:97:GLU:CG	2.48	0.43
1:A:278:GLN:HA	1:A:281:GLU:OE2	2.18	0.43
1:A:843:VAL:O	1:A:847:GLU:HB3	2.18	0.43
2:B:579:TRP:CD1	2:B:581:GLY:H	2.35	0.43
2:B:766:ARG:HD3	2:B:766:ARG:HA	1.70	0.43
2:B:866:PHE:HB2	2:B:870:ILE:HB	2.00	0.43
2:B:1169:MET:HE3	2:B:1169:MET:HB3	1.93	0.43
4:D:33:GLU:O	4:D:38:GLN:NE2	2.52	0.43
17:c:84:GLN:O	17:c:88:ARG:HG2	2.18	0.43
16:f:90:LEU:HB3	16:f:95:ARG:O	2.18	0.43
18:p:91:SER:HA	18:p:94:ILE:HD12	2.00	0.43
1:A:22:LEU:HG	2:B:1213:ALA:HB2	2.00	0.43
1:A:140:GLN:HG2	1:A:143:LYS:HZ2	1.83	0.43
1:A:403:ALA:HA	1:A:435:ARG:HA	1.98	0.43
1:A:504:GLN:O	1:A:505:LEU:HD23	2.18	0.43
1:A:633:THR:O	1:A:637:GLU:HG2	2.18	0.43
1:A:1106:ILE:HG22	1:A:1107:LEU:HD23	2.00	0.43
2:B:338:ARG:HG2	2:B:341:ARG:HH11	1.84	0.43
5:E:152:HIS:CE1	5:E:183:VAL:HG11	2.54	0.43
14:T:126:DG:C6	14:T:127:DA:C6	3.06	0.43
17:c:37:GLY:HA3	17:c:39:TYR:CE2	2.53	0.43
16:l:75:HIS:HB2	18:p:96:THR:CG2	2.48	0.43
19:N:137:DA:OP2	19:N:137:DA:H2'	2.18	0.43
1:A:1408:THR:O	1:A:1412:LEU:HD23	2.19	0.43
2:B:376:ASN:O	2:B:379:LEU:HG	2.19	0.43
2:B:1065:GLN:HG2	2:B:1069:PHE:HB2	1.99	0.43
4:D:61:ARG:HH21	4:D:65:LYS:HE2	1.84	0.43
6:F:116:ASP:O	6:F:120:ILE:HG12	2.18	0.43
7:G:5:LYS:HB2	7:G:7:LEU:HD21	2.00	0.43
14:T:39:DG:H1'	14:T:40:DA:C4	2.54	0.43
14:T:50:DT:H5'	15:e:86:SER:H	1.84	0.43
14:T:133:DG:N2	19:N:123:DC:O2	2.52	0.43
15:a:99:TYR:OH	16:b:57:VAL:HG12	2.19	0.43
17:c:80:PRO:HA	17:c:83:LEU:HD12	2.00	0.43
16:l:78:ARG:NH2	16:l:82:THR:OG1	2.50	0.43
15:m:69:ARG:O	15:m:72:ARG:HG2	2.19	0.43
19:N:81:DT:C4	19:N:82:DC:N4	2.87	0.43
19:N:223:DC:H2''	19:N:224:DT:C7	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:365:VAL:O	1:A:367:VAL:HG23	2.18	0.43
1:A:856:THR:HG22	1:A:867:PHE:HA	2.01	0.43
1:A:878:GLN:HB3	1:A:1058:SER:HB2	2.01	0.43
1:A:1226:LEU:HD22	1:A:1244:VAL:HG22	2.00	0.43
2:B:207:GLU:OE1	2:B:493:THR:OG1	2.36	0.43
2:B:1160:VAL:O	2:B:1194:LEU:N	2.29	0.43
7:G:4:LEU:HD13	7:G:75:ARG:NH1	2.34	0.43
10:J:14:VAL:C	10:J:16:ASP:H	2.27	0.43
14:T:29:DG:H2''	14:T:30:DG:N7	2.34	0.43
14:T:180:DC:H2''	14:T:181:DG:C8	2.53	0.43
15:a:51:ILE:HG12	16:b:39:ARG:O	2.18	0.43
17:g:55:LEU:HD21	18:h:66:VAL:HG13	2.01	0.43
18:p:65:PHE:C	18:p:65:PHE:CD1	2.95	0.43
19:N:95:DA:H2''	19:N:96:DC:C6	2.54	0.43
1:A:649:ASN:O	1:A:653:VAL:HG12	2.18	0.43
2:B:35:LEU:HD23	2:B:164:MET:SD	2.59	0.43
2:B:479:TYR:HD1	2:B:479:TYR:HA	1.71	0.43
2:B:816:GLU:O	2:B:817:LEU:HD23	2.19	0.43
2:B:958:GLN:NE2	2:B:958:GLN:O	2.51	0.43
2:B:1174:ASN:HD21	2:B:1176:LYS:HZ3	1.63	0.43
5:E:94:ASN:OD1	5:E:95:PHE:N	2.51	0.43
8:H:136:GLN:HB2	8:H:139:LEU:HD21	2.01	0.43
9:I:44:TYR:CZ	9:I:46:HIS:HB2	2.54	0.43
15:e:52:ARG:HE	15:e:52:ARG:C	2.26	0.43
16:f:72:TYR:OH	16:f:92:ARG:HG3	2.19	0.43
17:g:79:ILE:HG12	17:g:82:HIS:CE1	2.53	0.43
15:k:65:LEU:HB3	15:k:66:PRO:HD3	2.01	0.43
19:N:19:DT:H2''	19:N:20:DG:C8	2.54	0.43
19:N:174:DG:H2''	19:N:175:DT:C5	2.53	0.43
1:A:115:LEU:HD11	1:A:145:LYS:HB3	2.01	0.43
1:A:583:ILE:HG23	1:A:584:PRO:HD2	2.01	0.43
2:B:262:LYS:HA	2:B:273:PRO:HA	2.01	0.43
2:B:300:TRP:CD1	2:B:300:TRP:H	2.37	0.43
2:B:575:VAL:O	2:B:578:VAL:HG22	2.19	0.43
2:B:782:LEU:HD23	2:B:782:LEU:HA	1.79	0.43
5:E:37:SER:H	5:E:40:GLU:CD	2.27	0.43
8:H:114:TYR:CE1	8:H:123:CYS:HB2	2.54	0.43
9:I:19:ASP:CG	9:I:22:ASN:HB2	2.44	0.43
11:K:30:CYS:HB2	11:K:76:GLN:HB2	2.01	0.43
16:f:50:ILE:HA	16:f:50:ILE:HD13	1.79	0.43
16:l:27:GLN:HE22	16:l:55:ARG:NH2	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:l:57:VAL:HA	16:l:60:VAL:HG22	2.00	0.43
15:m:127:ALA:O	15:m:130:ILE:HG22	2.19	0.43
17:o:93:LEU:HD23	17:o:93:LEU:HA	1.89	0.43
1:A:230:ALA:HB2	1:A:1419:ALA:HB2	1.99	0.43
1:A:801:VAL:HG13	1:A:813:GLU:CD	2.44	0.43
1:A:995:LEU:HD22	1:A:1048:LEU:HD13	2.00	0.43
1:A:1157:ASP:N	1:A:1192:PRO:O	2.46	0.43
1:A:1295:PRO:HD3	1:A:1301:TYR:CE1	2.54	0.43
2:B:462:GLN:OE1	2:B:463:LYS:HD2	2.19	0.43
3:C:36:MET:HE2	3:C:36:MET:HB3	1.91	0.43
3:C:54:THR:OG1	3:C:152:GLU:O	2.29	0.43
5:E:8:ILE:HD13	5:E:52:PRO:HG3	2.00	0.43
14:T:92:DG:OP2	15:a:64:LYS:HB3	2.19	0.43
14:T:149:DC:H2''	14:T:150:DC:C6	2.53	0.43
14:T:243:DA:H1'	14:T:244:DA:H5'	2.01	0.43
15:a:40:ARG:CB	19:N:173:DC:H1'	2.42	0.43
16:f:68:ASP:O	16:f:71:THR:HB	2.18	0.43
16:l:82:THR:N	16:l:85:ASP:OD2	2.50	0.43
19:N:138:DT:H2''	19:N:139:DT:H5'	2.01	0.43
1:A:1436:LEU:HA	1:A:1436:LEU:HD12	1.74	0.42
2:B:90:THR:O	2:B:958:GLN:NE2	2.48	0.42
2:B:905:VAL:HG12	2:B:947:GLY:O	2.19	0.42
2:B:997:GLU:HG2	2:B:998:ASP:N	2.34	0.42
2:B:1084:GLN:NE2	3:C:191:PHE:HA	2.34	0.42
3:C:52:MET:HE1	3:C:152:GLU:HB3	2.01	0.42
7:G:5:LYS:HB3	7:G:5:LYS:HE3	1.77	0.42
7:G:23:ASN:HA	7:G:26:LEU:HD12	2.00	0.42
7:G:144:ARG:NH1	7:G:167:PHE:HD1	2.05	0.42
9:I:18:GLU:HA	9:I:25:LEU:HA	1.99	0.42
9:I:19:ASP:CG	9:I:22:ASN:H	2.27	0.42
10:J:14:VAL:O	10:J:16:ASP:N	2.52	0.42
1:A:99:ILE:HG13	1:A:235:MET:HE2	2.01	0.42
1:A:235:MET:C	1:A:235:MET:SD	3.02	0.42
1:A:828:THR:HA	1:A:831:LYS:HG2	2.02	0.42
1:A:1033:ILE:HD13	1:A:1044:PHE:HE1	1.85	0.42
1:A:1267:GLU:OE1	1:A:1268:ALA:N	2.52	0.42
2:B:330:GLY:O	2:B:344:TYR:OH	2.31	0.42
11:K:5:ASP:OD1	11:K:5:ASP:N	2.52	0.42
11:K:85:GLN:HA	11:K:88:GLU:HG2	2.01	0.42
14:T:9:DT:OP1	15:a:53:ARG:HD3	2.18	0.42
14:T:82:DG:H1'	15:a:42:ARG:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:T:170:DG:C2	14:T:171:DG:C2	3.07	0.42
14:T:191:DT:C2'	14:T:192:DT:H72	2.50	0.42
15:a:78:PHE:CD1	15:a:78:PHE:C	2.97	0.42
15:m:79:LYS:HG2	15:m:80:THR:N	2.35	0.42
19:N:75:DG:H2''	19:N:76:DC:C5	2.55	0.42
19:N:172:DA:H2''	19:N:173:DC:C6	2.54	0.42
1:A:38:PRO:HG3	1:A:271:LEU:HG	2.00	0.42
1:A:209:LEU:HD12	1:A:209:LEU:HA	1.70	0.42
1:A:669:ASP:CG	1:A:743:ASN:HD22	2.25	0.42
1:A:765:CYS:SG	1:A:767:GLY:N	2.92	0.42
1:A:925:GLU:HG2	1:A:926:LEU:N	2.35	0.42
2:B:904:ARG:HH22	12:L:67:ILE:HD11	1.83	0.42
6:F:137:TYR:C	6:F:138:LEU:HD22	2.44	0.42
9:I:52:ILE:HD12	9:I:52:ILE:H	1.83	0.42
14:T:131:DT:H1'	14:T:132:DG:H5'	2.00	0.42
16:l:91:LYS:HD2	16:l:92:ARG:N	2.34	0.42
19:N:225:DC:H2''	19:N:226:DC:C5	2.54	0.42
1:A:330:LEU:HD22	1:A:336:ARG:CB	2.49	0.42
1:A:369:ILE:HD13	1:A:463:VAL:HG12	2.00	0.42
1:A:1339:LEU:HD22	1:A:1384:LEU:HD23	2.01	0.42
1:A:1344:ILE:CD1	1:A:1382:GLY:HA2	2.49	0.42
2:B:533:SER:OG	2:B:748:ILE:O	2.31	0.42
2:B:540:ILE:N	2:B:605:GLU:OE2	2.52	0.42
2:B:556:MET:HE1	2:B:581:GLY:C	2.45	0.42
3:C:113:VAL:HG23	3:C:144:LEU:HB2	2.01	0.42
3:C:118:LEU:HD12	3:C:119:ILE:H	1.85	0.42
5:E:155:LEU:HB2	5:E:194:VAL:O	2.19	0.42
14:T:176:DA:H2''	14:T:177:DG:C8	2.54	0.42
14:T:212:DA:H5'	14:T:212:DA:C8	2.54	0.42
16:b:89:ALA:HA	16:b:92:ARG:HG2	2.02	0.42
17:c:31:HIS:CG	17:c:35:ARG:HH11	2.37	0.42
17:c:59:THR:HA	17:c:62:ILE:HG22	2.02	0.42
16:l:51:TYR:O	16:l:54:THR:OG1	2.32	0.42
19:N:218:DC:H2''	19:N:219:DT:H73	2.02	0.42
1:A:470:ARG:HG3	1:A:470:ARG:HH21	1.85	0.42
1:A:880:GLU:OE1	1:A:964:ARG:NH1	2.51	0.42
1:A:1345:GLU:OE1	5:E:199:ARG:NH2	2.52	0.42
2:B:390:ASP:HA	2:B:391:ARG:NH1	2.34	0.42
2:B:878:THR:O	2:B:882:THR:OG1	2.28	0.42
3:C:24:VAL:CG2	3:C:28:LEU:HD23	2.50	0.42
6:F:98:ALA:HB1	6:F:117:PRO:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:116:ASP:OD2	6:F:118:LEU:HB3	2.20	0.42
14:T:26:DC:H2''	14:T:27:DC:C6	2.54	0.42
14:T:29:DG:H2''	14:T:30:DG:C8	2.53	0.42
14:T:90:DA:H4'	14:T:91:DA:O5'	2.20	0.42
16:b:26:ILE:HD11	16:b:55:ARG:HB3	2.01	0.42
17:c:25:PHE:HD1	18:d:40:TYR:CB	2.32	0.42
15:e:70:LEU:HD13	16:f:26:ILE:HA	2.01	0.42
15:k:97:GLU:HA	15:k:100:LEU:HB3	2.01	0.42
17:o:58:LEU:O	17:o:61:GLU:HG2	2.19	0.42
1:A:84:MET:N	1:A:240:LEU:O	2.53	0.42
1:A:282:MET:HE3	1:A:282:MET:HB3	1.86	0.42
1:A:545:GLU:CA	1:A:548:MET:HG3	2.49	0.42
1:A:840:ARG:HA	1:A:840:ARG:CZ	2.49	0.42
1:A:880:GLU:OE1	1:A:961:ASN:HB2	2.20	0.42
1:A:1033:ILE:HG23	1:A:1039:LEU:HD13	2.02	0.42
1:A:1156:TYR:HD2	1:A:1193:TRP:CZ3	2.38	0.42
2:B:394:PHE:N	2:B:510:THR:HG21	2.18	0.42
2:B:632:ILE:HD12	2:B:686:VAL:C	2.45	0.42
2:B:797:TYR:HB3	2:B:798:TYR:CD1	2.54	0.42
14:T:31:DA:H2''	14:T:32:DG:H5''	2.02	0.42
14:T:210:DA:H2''	14:T:211:DC:C6	2.54	0.42
16:b:72:TYR:HE2	18:d:83:TYR:HD2	1.68	0.42
19:N:8:DG:H2''	19:N:9:DT:C6	2.54	0.42
19:N:120:DC:C2'	19:N:121:DT:H71	2.49	0.42
1:A:333:LYS:NZ	14:T:198:DG:OP1	2.47	0.42
1:A:419:HIS:CE1	1:A:421:ARG:HB2	2.54	0.42
2:B:83:TYR:N	2:B:116:TYR:O	2.32	0.42
2:B:273:PRO:O	2:B:276:ILE:HG12	2.19	0.42
2:B:462:GLN:OE1	14:T:207:DC:H4'	2.20	0.42
2:B:858:SER:HA	2:B:966:VAL:O	2.19	0.42
3:C:266:ARG:HH21	11:K:84:LYS:HE2	1.83	0.42
4:D:57:ARG:HD3	4:D:116:LYS:HZ3	1.84	0.42
5:E:142:ASN:HB3	5:E:145:HIS:CD2	2.55	0.42
7:G:119:LEU:HD11	7:G:130:TYR:HB3	2.02	0.42
8:H:128:TYR:O	8:H:132:ALA:HB2	2.19	0.42
9:I:72:ASP:HA	9:I:81:ARG:O	2.19	0.42
9:I:78:CYS:HB3	9:I:108:LYS:HZ1	1.84	0.42
9:I:91:ARG:O	9:I:91:ARG:NH2	2.52	0.42
18:h:73:ILE:HD13	18:h:73:ILE:HA	1.86	0.42
17:o:15:LYS:O	19:N:28:DC:H5''	2.19	0.42
17:o:17:ARG:HA	17:o:20:ARG:HG3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:o:81:ARG:H	17:o:81:ARG:CD	2.29	0.42
19:N:118:DG:C8	19:N:119:DT:H72	2.53	0.42
1:A:187:LYS:NZ	16:l:37:LEU:HA	2.35	0.42
1:A:246:GLN:O	1:A:249:PRO:HD3	2.19	0.42
1:A:815:PHE:CD2	2:B:512:TRP:HE3	2.38	0.42
2:B:563:ASP:HB2	2:B:566:GLN:HB3	2.02	0.42
2:B:708:GLN:OE1	2:B:708:GLN:N	2.52	0.42
2:B:905:VAL:HG22	2:B:906:SER:H	1.83	0.42
5:E:4:ASN:O	5:E:7:ILE:HG13	2.20	0.42
5:E:200:ARG:O	5:E:200:ARG:HG3	2.19	0.42
8:H:138:ASN:C	8:H:139:LEU:HD22	2.44	0.42
11:K:46:LEU:HD12	11:K:46:LEU:HA	1.75	0.42
14:T:153:DT:H2''	14:T:154:DT:O5'	2.20	0.42
17:c:25:PHE:HE1	18:d:41:VAL:CA	2.31	0.42
15:e:62:ILE:HD12	15:e:93:GLN:HG3	2.01	0.42
15:e:68:GLN:NE2	15:e:89:ILE:HD13	2.35	0.42
19:N:216:DC:H2''	19:N:217:DC:N4	2.35	0.42
1:A:270:ILE:HD12	1:A:301:VAL:HG22	2.02	0.42
1:A:1122:LEU:HD11	1:A:1309:LEU:HD11	2.02	0.42
2:B:174:THR:O	2:B:175:LEU:HB2	2.20	0.42
2:B:227:HIS:HD2	2:B:381:CYS:SG	2.43	0.42
2:B:227:HIS:CE1	2:B:382:ALA:HA	2.55	0.42
2:B:322:ALA:O	2:B:325:PHE:HB3	2.20	0.42
2:B:364:GLU:O	2:B:368:THR:HG23	2.19	0.42
2:B:613:ARG:HB3	2:B:614:GLU:OE1	2.20	0.42
2:B:691:ASP:O	2:B:695:GLU:HG3	2.20	0.42
3:C:97:VAL:C	3:C:98:LEU:HD12	2.45	0.42
10:J:65:LEU:HD12	12:L:59:TYR:HE2	1.85	0.42
11:K:82:ARG:HG3	11:K:82:ARG:HH21	1.85	0.42
16:n:31:LYS:HG3	16:n:51:TYR:CE2	2.55	0.42
1:A:119:ASN:HB2	1:A:122:MET:HG3	2.02	0.42
1:A:710:THR:N	1:A:713:GLU:OE1	2.52	0.42
1:A:753:LYS:HG3	1:A:754:GLY:N	2.35	0.42
1:A:983:LEU:HD12	1:A:983:LEU:HA	1.84	0.42
1:A:1400:LEU:HB3	1:A:1429:GLU:CG	2.50	0.42
2:B:755:ILE:O	2:B:983:ARG:NH2	2.53	0.42
2:B:859:TYR:OH	2:B:941:LEU:HD12	2.19	0.42
9:I:47:GLU:OE1	9:I:48:LEU:N	2.53	0.42
14:T:14:DA:N6	19:N:242:DA:H61	2.17	0.42
14:T:28:DT:H2''	14:T:29:DG:N7	2.34	0.42
15:a:99:TYR:CD2	15:a:100:LEU:HD23	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:c:55:LEU:HD13	17:c:55:LEU:HA	1.83	0.42
15:e:101:VAL:HG12	15:e:105:GLU:OE2	2.20	0.42
16:l:50:ILE:HA	16:l:53:GLU:OE2	2.19	0.42
19:N:172:DA:H2''	19:N:173:DC:O4'	2.20	0.42
19:N:183:DG:H2''	19:N:184:DT:C5	2.55	0.42
1:A:152:ALA:HA	1:A:165:ARG:HD2	2.01	0.41
1:A:470:ARG:HG3	1:A:470:ARG:NH2	2.35	0.41
2:B:855:PHE:CD2	2:B:972:LYS:HE3	2.55	0.41
2:B:952:VAL:HG22	2:B:966:VAL:HG23	2.02	0.41
2:B:1001:PHE:CE2	2:B:1073:TYR:HB2	2.55	0.41
3:C:73:SER:HB2	3:C:238:LEU:HD21	2.01	0.41
4:D:121:CYS:HA	4:D:124:VAL:CG2	2.50	0.41
12:L:62:ARG:HG3	12:L:63:THR:O	2.20	0.41
14:T:32:DG:C6	14:T:33:DA:N6	2.88	0.41
14:T:37:DG:H2''	14:T:38:DG:C5	2.55	0.41
17:g:26:PRO:O	17:g:30:VAL:HG23	2.20	0.41
16:n:31:LYS:HE3	16:n:31:LYS:HB3	1.84	0.41
17:o:25:PHE:CD2	17:o:55:LEU:HB2	2.55	0.41
1:A:82:GLY:CA	1:A:242:VAL:HB	2.49	0.41
1:A:420:LYS:O	1:A:420:LYS:NZ	2.40	0.41
1:A:579:LEU:HA	1:A:579:LEU:HD12	1.85	0.41
1:A:985:ILE:O	1:A:989:ILE:HG12	2.20	0.41
3:C:111:THR:N	3:C:147:LEU:O	2.39	0.41
5:E:74:LEU:HD12	5:E:74:LEU:HA	1.76	0.41
9:I:77:GLU:HG2	9:I:108:LYS:HE2	2.02	0.41
1:A:508:VAL:HB	1:A:509:PRO:HD3	2.02	0.41
1:A:771:VAL:O	1:A:774:LYS:N	2.52	0.41
2:B:15:GLU:O	2:B:19:THR:OG1	2.34	0.41
2:B:579:TRP:NE1	2:B:581:GLY:O	2.41	0.41
2:B:1122:ARG:HB3	14:T:201:DC:H3'	2.01	0.41
3:C:99:GLU:OE2	3:C:101:SER:HB2	2.19	0.41
4:D:65:LYS:HZ3	4:D:89:LEU:HD11	1.85	0.41
11:K:39:ASP:OD1	11:K:39:ASP:C	2.63	0.41
14:T:53:DG:H2''	14:T:54:DC:O5'	2.20	0.41
14:T:170:DG:N2	14:T:171:DG:C2	2.88	0.41
17:c:15:LYS:HB2	19:N:139:DT:OP1	2.21	0.41
15:e:65:LEU:HB3	15:e:66:PRO:CD	2.50	0.41
17:g:57:TYR:HB2	18:h:113:GLU:OE1	2.20	0.41
15:k:105:GLU:O	15:k:109:LEU:HG	2.20	0.41
16:l:51:TYR:O	16:l:55:ARG:HG2	2.20	0.41
1:A:117:GLU:HA	1:A:122:MET:CE	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:562:TYR:HD1	2:B:567:HIS:ND1	2.18	0.41
3:C:214:LYS:HB2	3:C:217:GLU:HG3	2.01	0.41
11:K:31:ILE:HD12	11:K:31:ILE:O	2.19	0.41
14:T:101:DG:H2''	14:T:102:DA:N7	2.35	0.41
14:T:161:DT:H3'	16:n:32:PRO:HG2	2.01	0.41
15:a:50:GLU:OE1	16:b:39:ARG:HB3	2.20	0.41
19:N:134:DT:H2''	19:N:135:DC:C5	2.56	0.41
1:A:208:ILE:O	1:A:211:VAL:HB	2.21	0.41
1:A:452:HIS:ND1	1:A:452:HIS:N	2.69	0.41
1:A:548:MET:CE	11:K:58:PHE:HA	2.51	0.41
1:A:568:LYS:NZ	8:H:92:TYR:O	2.51	0.41
1:A:1118:LEU:CD2	1:A:1332:SER:HB2	2.50	0.41
1:A:1335:PHE:CA	1:A:1338:ILE:HG22	2.47	0.41
2:B:44:THR:OG1	2:B:45:SER:N	2.53	0.41
2:B:113:SER:HB3	2:B:163:ILE:HD11	2.03	0.41
2:B:428:CYS:SG	2:B:433:ARG:NH2	2.93	0.41
2:B:1084:GLN:H	2:B:1084:GLN:CD	2.28	0.41
3:C:107:GLU:HA	3:C:149:ASN:HB3	2.02	0.41
3:C:262:LEU:HD11	11:K:84:LYS:HG3	2.02	0.41
11:K:44:ASN:OD1	11:K:47:ARG:NH1	2.53	0.41
15:a:60:LEU:HD13	15:a:93:GLN:CD	2.45	0.41
15:a:128:ARG:NH2	16:b:57:VAL:HG22	2.36	0.41
15:e:53:ARG:HA	15:e:56:LYS:HE3	2.02	0.41
16:f:75:HIS:HB2	18:h:99:ARG:HH22	1.86	0.41
17:g:85:LEU:O	17:g:89:ASN:ND2	2.53	0.41
1:A:32:VAL:HG12	1:A:33:VAL:HG23	2.01	0.41
1:A:84:MET:O	1:A:239:VAL:HA	2.21	0.41
1:A:107:CYS:HB2	1:A:148:CYS:HB2	2.03	0.41
1:A:334:GLU:H	1:A:334:GLU:CD	2.22	0.41
1:A:362:LEU:HD11	1:A:474:SER:HB2	2.01	0.41
1:A:709:MET:SD	1:A:709:MET:N	2.94	0.41
1:A:823:GLU:O	1:A:827:ASP:HB2	2.20	0.41
1:A:1195:LEU:HD12	1:A:1242:CYS:SG	2.61	0.41
2:B:207:GLU:HA	2:B:399:LEU:HD23	2.01	0.41
2:B:247:ILE:HD11	2:B:261:ILE:HG22	2.01	0.41
2:B:290:LEU:HA	2:B:293:ILE:HG12	2.03	0.41
2:B:431:THR:O	2:B:432:ASP:C	2.64	0.41
2:B:803:LEU:HD12	2:B:803:LEU:HA	1.77	0.41
3:C:21:LEU:O	3:C:227:ARG:HA	2.20	0.41
3:C:172:PRO:O	3:C:235:THR:HG23	2.20	0.41
16:f:58:LEU:HD12	16:f:59:LYS:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:k:123:ASP:HA	15:k:126:LEU:CD1	2.48	0.41
16:n:26:ILE:HD11	16:n:55:ARG:HB3	2.03	0.41
16:n:93:GLN:OE1	16:n:95:ARG:NH2	2.54	0.41
19:N:78:DC:H2''	19:N:79:DT:C5	2.55	0.41
19:N:189:DC:H2''	19:N:190:DG:C5'	2.51	0.41
19:N:201:DG:H2''	19:N:202:DC:C5'	2.51	0.41
1:A:195:ASP:HB2	16:l:57:VAL:HG11	2.02	0.41
1:A:472:ASN:OD1	1:A:473:LEU:N	2.53	0.41
1:A:493:PRO:O	1:A:494:GLN:NE2	2.54	0.41
1:A:676:THR:O	1:A:680:ILE:HG12	2.21	0.41
1:A:816:PHE:HA	1:A:819:MET:HE3	2.03	0.41
1:A:1401:MET:SD	1:A:1426:GLY:HA3	2.61	0.41
2:B:221:ALA:O	2:B:223:SER:N	2.52	0.41
2:B:866:PHE:N	2:B:870:ILE:O	2.53	0.41
2:B:879:ARG:HG2	2:B:885:LEU:HD11	2.02	0.41
6:F:94:LEU:HA	6:F:94:LEU:HD23	1.86	0.41
14:T:10:DA:H2''	14:T:11:DT:C5'	2.50	0.41
15:a:85:GLN:O	15:a:86:SER:C	2.64	0.41
15:e:70:LEU:HD11	16:f:59:LYS:HD3	2.02	0.41
16:l:86:VAL:O	16:l:90:LEU:HG	2.21	0.41
17:o:31:HIS:CD2	17:o:35:ARG:HE	2.38	0.41
1:A:851:VAL:HG12	1:A:1064:GLU:O	2.21	0.41
1:A:979:LYS:O	1:A:1038:ARG:NH1	2.53	0.41
2:B:50:VAL:HA	2:B:414:PHE:CE2	2.56	0.41
2:B:58:LEU:HD22	2:B:426:GLN:HG2	2.03	0.41
2:B:639:LYS:HZ2	2:B:640:ASP:N	2.19	0.41
2:B:1202:LEU:HD23	2:B:1202:LEU:C	2.46	0.41
3:C:22:SER:HA	3:C:226:ASN:O	2.20	0.41
5:E:2:GLU:HG2	5:E:4:ASN:H	1.86	0.41
11:K:31:ILE:HD13	11:K:33:ILE:CG2	2.50	0.41
15:m:76:GLN:HA	15:m:79:LYS:O	2.21	0.41
1:A:61:ILE:C	1:A:74:MET:HE1	2.46	0.41
1:A:299:PHE:HD2	1:A:300:HIS:HD1	1.68	0.41
1:A:354:ILE:HG13	1:A:483:PHE:CD1	2.56	0.41
1:A:457:MET:HE1	1:A:522:MET:CE	2.50	0.41
1:A:502:LEU:HD11	2:B:1146:PHE:HE2	1.86	0.41
1:A:960:VAL:HG22	1:A:962:LEU:HD12	2.03	0.41
1:A:1168:ASP:OD2	1:A:1196:ARG:HD2	2.20	0.41
1:A:1400:LEU:HD12	1:A:1400:LEU:HA	1.96	0.41
1:A:1444:PHE:CZ	6:F:89:GLU:HA	2.56	0.41
2:B:46:ILE:HG23	2:B:47:GLN:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:186:CYS:SG	2:B:188:TYR:HB2	2.60	0.41
2:B:409:LEU:HD12	2:B:409:LEU:HA	1.80	0.41
2:B:887:HIS:HB2	13:P:2:G:H1	1.86	0.41
2:B:941:LEU:HD12	2:B:942:ARG:N	2.35	0.41
2:B:1152:MET:HB3	2:B:1153:GLU:OE1	2.21	0.41
4:D:173:ARG:HD2	4:D:173:ARG:C	2.46	0.41
5:E:99:ILE:HD12	5:E:104:PHE:HD2	1.86	0.41
8:H:97:PHE:HD1	8:H:98:GLY:N	2.19	0.41
9:I:78:CYS:HB2	9:I:106:CYS:HB3	2.03	0.41
10:J:48:MET:HE3	10:J:48:MET:CA	2.51	0.41
11:K:47:ARG:HG3	11:K:59:VAL:HG22	2.02	0.41
14:T:165:DA:C5	14:T:166:DC:C4	3.09	0.41
14:T:222:DA:C2	14:T:223:DG:O6	2.73	0.41
14:T:232:DC:H4'	17:o:29:ARG:NH1	2.36	0.41
15:a:126:LEU:HD11	15:e:109:LEU:HG	2.03	0.41
17:c:29:ARG:NH1	18:d:40:TYR:CE2	2.89	0.41
15:e:51:ILE:O	15:e:55:GLN:HG3	2.20	0.41
15:e:70:LEU:HD13	16:f:26:ILE:HG13	2.03	0.41
17:g:61:GLU:HG2	18:h:106:LEU:HD21	2.03	0.41
16:l:75:HIS:C	16:l:77:LYS:H	2.29	0.41
16:l:87:VAL:HG13	16:l:88:TYR:HD1	1.86	0.41
16:l:88:TYR:HA	16:l:91:LYS:CG	2.45	0.41
2:B:301:GLN:O	2:B:304:GLU:HG3	2.21	0.41
2:B:509:ASN:OD1	2:B:509:ASN:N	2.54	0.41
2:B:796:LEU:HD12	2:B:796:LEU:HA	1.89	0.41
5:E:27:TYR:CE2	5:E:77:LEU:HB2	2.56	0.41
5:E:146:HIS:CE1	5:E:148:LEU:HG	2.56	0.41
5:E:177:ILE:HG23	5:E:213:CYS:HA	2.02	0.41
9:I:19:ASP:OD2	9:I:22:ASN:HB2	2.21	0.41
9:I:75:CYS:SG	9:I:80:SER:HB2	2.61	0.41
14:T:96:DT:H3	19:N:159:DA:H61	1.69	0.41
15:a:104:PHE:CZ	16:b:37:LEU:HB3	2.56	0.41
15:k:62:ILE:HG12	16:l:29:ILE:HA	2.03	0.41
15:m:70:LEU:HD13	16:n:26:ILE:N	2.36	0.41
17:o:84:GLN:NE2	17:o:88:ARG:HE	2.19	0.41
19:N:118:DG:H2''	19:N:119:DT:C5'	2.48	0.41
1:A:41:MET:HG3	1:A:44:SER:H	1.86	0.40
1:A:904:ASP:O	1:A:908:SER:HB2	2.21	0.40
1:A:1344:ILE:HD11	1:A:1382:GLY:O	2.21	0.40
2:B:177:GLU:O	2:B:180:LEU:HB2	2.21	0.40
4:D:57:ARG:HH11	4:D:110:ASN:CB	2.33	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:77:LEU:HD12	5:E:77:LEU:HA	1.86	0.40
5:E:93:ARG:HG2	5:E:94:ASN:N	2.36	0.40
9:I:71:SER:HB2	9:I:85:PHE:CE1	2.56	0.40
9:I:84:VAL:O	9:I:102:VAL:N	2.54	0.40
12:L:66:MET:SD	12:L:67:ILE:N	2.95	0.40
16:b:98:TYR:CZ	17:g:100:VAL:HG11	2.56	0.40
17:g:57:TYR:OH	18:h:106:LEU:HA	2.21	0.40
16:n:34:ILE:CG2	16:n:54:THR:HG21	2.50	0.40
1:A:318:LYS:C	1:A:320:GLY:N	2.76	0.40
1:A:692:GLN:OE1	1:A:695:ILE:HD11	2.21	0.40
1:A:840:ARG:NH1	1:A:843:VAL:HB	2.37	0.40
1:A:1015:ASN:O	1:A:1018:SER:OG	2.38	0.40
1:A:1126:ILE:HG21	1:A:1136:ILE:HG13	2.03	0.40
1:A:1198:GLU:OE2	1:A:1238:LEU:N	2.49	0.40
1:A:1359:ILE:HD12	1:A:1359:ILE:HA	1.91	0.40
1:A:1428:SER:O	1:A:1432:MET:SD	2.79	0.40
2:B:698:ILE:HG22	2:B:699:MET:H	1.86	0.40
2:B:1152:MET:CE	2:B:1157:ALA:HA	2.51	0.40
3:C:52:MET:CE	3:C:152:GLU:HB3	2.51	0.40
5:E:19:LYS:HD2	5:E:33:GLU:HG3	2.03	0.40
5:E:54:ARG:HA	5:E:57:MET:HE1	2.02	0.40
7:G:60:ARG:HB3	7:G:60:ARG:CZ	2.52	0.40
8:H:129:LYS:HD2	8:H:129:LYS:C	2.46	0.40
11:K:7:PHE:HA	11:K:10:PHE:CZ	2.55	0.40
13:P:12:C:H4'	13:P:12:C:OP1	2.21	0.40
14:T:19:DA:H2''	14:T:20:DC:C4	2.57	0.40
14:T:137:DC:H2''	14:T:138:DT:H6	1.86	0.40
14:T:197:DG:OP1	14:T:197:DG:H4'	2.20	0.40
14:T:223:DG:H2''	14:T:224:DA:O5'	2.22	0.40
15:a:53:ARG:NH2	15:a:54:TYR:CD1	2.89	0.40
15:e:61:LEU:HD12	15:e:61:LEU:H	1.85	0.40
15:e:85:GLN:O	15:e:88:ALA:N	2.54	0.40
16:l:71:THR:CG2	18:p:99:ARG:HG3	2.52	0.40
16:l:87:VAL:HG13	16:l:88:TYR:CD1	2.55	0.40
17:o:15:LYS:HG2	17:o:16:THR:N	2.36	0.40
18:p:76:GLU:CD	18:p:97:ALA:HB1	2.46	0.40
19:N:41:DG:C8	19:N:41:DG:H5'	2.55	0.40
1:A:28:ARG:HH21	1:A:239:VAL:HB	1.86	0.40
1:A:663:PHE:HB3	2:B:829:CYS:SG	2.61	0.40
1:A:675:SER:O	1:A:679:GLU:HG2	2.21	0.40
1:A:1153:GLU:CG	9:I:45:ARG:HD3	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:237:LYS:HD3	2:B:237:LYS:HA	1.88	0.40
2:B:245:MET:HE1	2:B:374:MET:SD	2.62	0.40
2:B:690:VAL:HG23	2:B:694:GLU:HB3	2.02	0.40
2:B:755:ILE:HD13	2:B:755:ILE:HA	1.85	0.40
2:B:841:MET:HE3	2:B:1010:LEU:HD13	2.03	0.40
3:C:166:GLU:HG3	11:K:6:ARG:HB2	2.02	0.40
5:E:77:LEU:HD12	5:E:106:THR:OG1	2.21	0.40
6:F:103:MET:HE2	6:F:103:MET:HB2	1.96	0.40
16:b:49:LEU:O	16:b:52:GLU:HG2	2.21	0.40
15:m:47:ALA:C	15:m:49:ARG:N	2.80	0.40
16:n:94:GLY:C	16:n:95:ARG:HD3	2.46	0.40
1:A:85:GLU:HA	1:A:239:VAL:HG23	2.02	0.40
1:A:1400:LEU:O	1:A:1404:SER:OG	2.39	0.40
2:B:74:ARG:HB2	2:B:124:PHE:O	2.22	0.40
2:B:272:ILE:HD11	2:B:277:VAL:HB	2.04	0.40
2:B:302:MET:O	2:B:306:LEU:HG	2.21	0.40
2:B:1079:LYS:HE3	3:C:188:HIS:CE1	2.57	0.40
5:E:31:GLN:O	5:E:34:MET:HB2	2.22	0.40
5:E:63:PRO:HB2	5:E:68:LEU:HB2	2.02	0.40
9:I:19:ASP:OD1	9:I:19:ASP:C	2.63	0.40
9:I:99:LEU:O	9:I:111:ARG:HD2	2.22	0.40
12:L:49:ARG:NH1	12:L:54:GLY:O	2.54	0.40
15:a:108:ASN:ND2	16:b:42:GLY:C	2.79	0.40
16:b:62:LEU:O	16:b:65:VAL:HG22	2.22	0.40
17:c:29:ARG:NH2	18:d:40:TYR:HE2	2.19	0.40
17:c:42:ARG:O	18:d:89:ILE:HD11	2.22	0.40
15:e:93:GLN:O	15:e:97:GLU:HG3	2.22	0.40
15:k:97:GLU:C	15:k:99:TYR:N	2.78	0.40
19:N:8:DG:C8	19:N:9:DT:C7	3.00	0.40
19:N:14:DC:H2'	19:N:15:DC:C4	2.56	0.40
1:A:195:ASP:HB2	16:l:57:VAL:CG1	2.51	0.40
1:A:642:ILE:O	1:A:645:GLU:HG3	2.22	0.40
1:A:1154:ILE:HB	9:I:44:TYR:HB3	2.03	0.40
1:A:1288:VAL:HB	1:A:1310:GLU:OE1	2.22	0.40
2:B:280:ALA:HB1	2:B:323:LEU:HD13	2.04	0.40
2:B:476:LEU:HA	2:B:476:LEU:HD12	1.75	0.40
2:B:562:TYR:CE1	2:B:564:PRO:HA	2.57	0.40
3:C:139:ASP:OD1	3:C:141:GLY:N	2.53	0.40
3:C:143:LEU:HD12	3:C:144:LEU:H	1.87	0.40
5:E:59:PHE:H	5:E:79:VAL:HG22	1.86	0.40
7:G:103:VAL:O	7:G:106:LEU:HB3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:T:195:DG:H2''	14:T:196:DC:C5	2.57	0.40
15:a:112:ILE:HD12	15:a:112:ILE:HA	1.91	0.40
15:e:108:ASN:O	15:e:112:ILE:HG12	2.22	0.40
18:h:40:TYR:O	18:h:44:VAL:HG23	2.21	0.40
17:o:96:LEU:HD13	18:p:103:PRO:HD3	2.03	0.40
18:p:39:ILE:H	18:p:39:ILE:HG12	1.61	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1390/1743 (80%)	1289 (93%)	96 (7%)	5 (0%)	30	60
2	B	1154/1227 (94%)	1063 (92%)	91 (8%)	0	100	100
3	C	261/304 (86%)	249 (95%)	12 (5%)	0	100	100
4	D	170/186 (91%)	164 (96%)	6 (4%)	0	100	100
5	E	211/214 (99%)	206 (98%)	5 (2%)	0	100	100
6	F	82/155 (53%)	76 (93%)	6 (7%)	0	100	100
7	G	169/171 (99%)	161 (95%)	8 (5%)	0	100	100
8	H	129/145 (89%)	118 (92%)	11 (8%)	0	100	100
9	I	109/115 (95%)	99 (91%)	10 (9%)	0	100	100
10	J	65/72 (90%)	63 (97%)	1 (2%)	1 (2%)	8	36
11	K	111/118 (94%)	104 (94%)	7 (6%)	0	100	100
12	L	43/72 (60%)	41 (95%)	2 (5%)	0	100	100
15	a	93/139 (67%)	85 (91%)	6 (6%)	2 (2%)	5	31
15	e	93/139 (67%)	88 (95%)	5 (5%)	0	100	100
15	k	71/139 (51%)	67 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	m	93/139 (67%)	87 (94%)	5 (5%)	1 (1%)	11	41
16	b	76/106 (72%)	73 (96%)	3 (4%)	0	100	100
16	f	76/106 (72%)	73 (96%)	3 (4%)	0	100	100
16	l	69/106 (65%)	65 (94%)	4 (6%)	0	100	100
16	n	76/106 (72%)	70 (92%)	6 (8%)	0	100	100
17	c	96/133 (72%)	92 (96%)	4 (4%)	0	100	100
17	g	96/133 (72%)	94 (98%)	1 (1%)	1 (1%)	12	43
17	o	95/133 (71%)	92 (97%)	3 (3%)	0	100	100
18	d	88/129 (68%)	85 (97%)	3 (3%)	0	100	100
18	h	87/129 (67%)	85 (98%)	2 (2%)	0	100	100
18	p	85/129 (66%)	83 (98%)	2 (2%)	0	100	100
All	All	5088/6288 (81%)	4772 (94%)	306 (6%)	10 (0%)	44	71

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1316	LEU
15	a	46	VAL
1	A	320	GLY
1	A	960	VAL
1	A	200	ARG
10	J	9	SER
17	g	15	LYS
15	m	48	LEU
15	a	43	PRO
1	A	319	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1217/1528 (80%)	1177 (97%)	40 (3%)	33	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	1018/1077 (94%)	989 (97%)	29 (3%)	38	58
3	C	236/264 (89%)	228 (97%)	8 (3%)	32	55
4	D	149/160 (93%)	148 (99%)	1 (1%)	76	77
5	E	196/197 (100%)	187 (95%)	9 (5%)	24	49
6	F	75/137 (55%)	71 (95%)	4 (5%)	20	46
7	G	148/148 (100%)	144 (97%)	4 (3%)	39	59
8	H	120/130 (92%)	115 (96%)	5 (4%)	26	51
9	I	106/109 (97%)	104 (98%)	2 (2%)	50	65
10	J	61/66 (92%)	59 (97%)	2 (3%)	33	55
11	K	104/109 (95%)	98 (94%)	6 (6%)	18	45
12	L	38/56 (68%)	37 (97%)	1 (3%)	40	60
15	a	81/112 (72%)	72 (89%)	9 (11%)	6	25
15	e	81/112 (72%)	77 (95%)	4 (5%)	22	48
15	k	61/112 (54%)	59 (97%)	2 (3%)	33	55
15	m	81/112 (72%)	75 (93%)	6 (7%)	13	39
16	b	63/81 (78%)	60 (95%)	3 (5%)	23	48
16	f	63/81 (78%)	62 (98%)	1 (2%)	55	68
16	l	59/81 (73%)	59 (100%)	0	100	100
16	n	63/81 (78%)	60 (95%)	3 (5%)	23	48
17	c	77/102 (76%)	75 (97%)	2 (3%)	40	60
17	g	77/102 (76%)	75 (97%)	2 (3%)	40	60
17	o	77/102 (76%)	77 (100%)	0	100	100
18	d	76/107 (71%)	74 (97%)	2 (3%)	40	60
18	h	75/107 (70%)	75 (100%)	0	100	100
18	p	74/107 (69%)	73 (99%)	1 (1%)	59	70
All	All	4476/5380 (83%)	4330 (97%)	146 (3%)	34	55

All (146) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ILE
1	A	61	ILE
1	A	68	GLN

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Mol	Chain	Res	Type
1	A	74	MET
1	A	108	MET
1	A	116	ASP
1	A	195	ASP
1	A	204	THR
1	A	237	ILE
1	A	253	MET
1	A	291	ASN
1	A	300	HIS
1	A	317	GLN
1	A	318	LYS
1	A	432	LYS
1	A	448	GLN
1	A	473	LEU
1	A	495	SER
1	A	583	ILE
1	A	625	SER
1	A	634	VAL
1	A	645	GLU
1	A	686	SER
1	A	765	CYS
1	A	823	GLU
1	A	831	LYS
1	A	832	THR
1	A	960	VAL
1	A	965	ILE
1	A	1009	ILE
1	A	1112	ASN
1	A	1113	ILE
1	A	1204	MET
1	A	1270	MET
1	A	1287	MET
1	A	1290	HIS
1	A	1302	LYS
1	A	1335	PHE
1	A	1357	ASN
1	A	1366	VAL
2	B	76	GLU
2	B	96	THR
2	B	128	ASP
2	B	167	SER
2	B	213	ILE

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Mol	Chain	Res	Type
2	B	230	GLU
2	B	233	SER
2	B	305	MET
2	B	389	ASP
2	B	435	PHE
2	B	463	LYS
2	B	542	SER
2	B	561	ASP
2	B	609	ILE
2	B	618	LYS
2	B	682	VAL
2	B	690	VAL
2	B	780	VAL
2	B	831	SER
2	B	931	TYR
2	B	944	THR
2	B	970	THR
2	B	1007	VAL
2	B	1009	ASP
2	B	1026	LEU
2	B	1115	THR
2	B	1169	MET
2	B	1205	GLN
2	B	1218	THR
3	C	26	LEU
3	C	37	LEU
3	C	55	SER
3	C	129	VAL
3	C	188	HIS
3	C	204	SER
3	C	234	THR
3	C	258	VAL
4	D	122	THR
5	E	47	ASP
5	E	53	GLN
5	E	79	VAL
5	E	87	VAL
5	E	121	LYS
5	E	163	LEU
5	E	177	ILE
5	E	189	LEU
5	E	212	ILE

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Mol	Chain	Res	Type
6	F	75	LEU
6	F	93	ILE
6	F	103	MET
6	F	111	ILE
7	G	12	THR
7	G	26	LEU
7	G	39	THR
7	G	130	TYR
8	H	14	THR
8	H	99	THR
8	H	116	SER
8	H	123	CYS
8	H	138	ASN
9	I	78	CYS
9	I	97	MET
10	J	25	LEU
10	J	51	THR
11	K	15	ASP
11	K	30	CYS
11	K	42	LEU
11	K	59	VAL
11	K	72	VAL
11	K	73	MET
12	L	33	CYS
15	a	41	TYR
15	a	42	ARG
15	a	43	PRO
15	a	48	LEU
15	a	85	GLN
15	a	99	TYR
15	a	100	LEU
15	a	108	ASN
15	a	117	VAL
16	b	46	ILE
16	b	52	GLU
16	b	84	MET
17	c	55	LEU
17	c	79	ILE
18	d	65	PHE
18	d	93	GLU
15	e	53	ARG
15	e	63	ARG

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Mol	Chain	Res	Type
15	e	65	LEU
15	e	68	GLN
16	f	96	THR
17	g	58	LEU
17	g	101	THR
15	k	62	ILE
15	k	108	ASN
15	m	45	THR
15	m	46	VAL
15	m	48	LEU
15	m	61	LEU
15	m	67	PHE
15	m	113	HIS
16	n	31	LYS
16	n	45	ARG
16	n	60	VAL
18	p	106	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	ASN
1	A	197	GLN
1	A	312	GLN
1	A	364	GLN
1	A	742	ASN
1	A	758	ASN
1	A	1108	ASN
1	A	1137	GLN
2	B	794	ASN
2	B	835	GLN
2	B	927	GLN
2	B	1062	ASN
2	B	1141	HIS
2	B	1174	ASN
3	C	30	ASN
3	C	242	GLN
4	D	44	ASN
4	D	130	ASN
5	E	62	ASN
8	H	136	GLN
11	K	40	HIS

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Mol	Chain	Res	Type
15	a	85	GLN
15	a	108	ASN
16	b	93	GLN
17	c	38	ASN
17	c	68	ASN
17	c	104	GLN
18	d	84	ASN
18	d	95	GLN
15	e	68	GLN
15	e	93	GLN
17	g	31	HIS
17	g	89	ASN
18	h	95	GLN
15	m	76	GLN
15	m	93	GLN
17	o	31	HIS
17	o	110	ASN
18	p	67	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	P	13/14 (92%)	3 (23%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
13	P	4	C
13	P	5	G
13	P	12	C

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

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

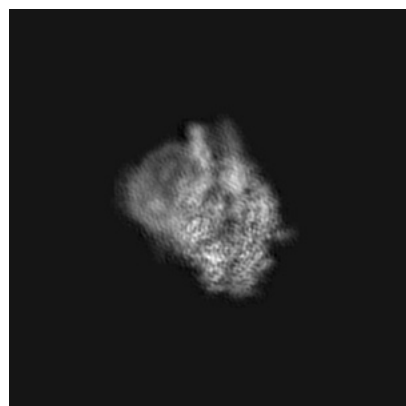
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64603. These allow visual inspection of the internal detail of the map and identification of artifacts.

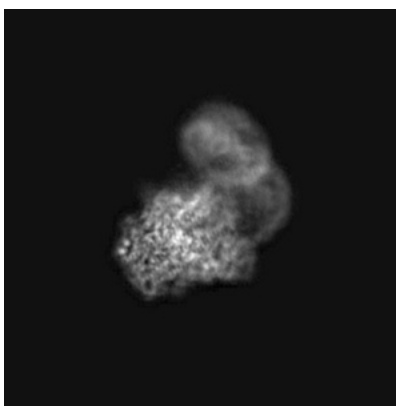
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

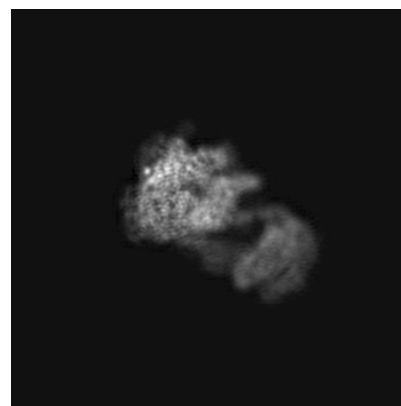
6.1.1 Primary map



X

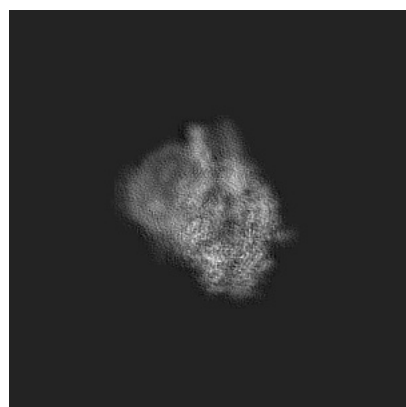


Y

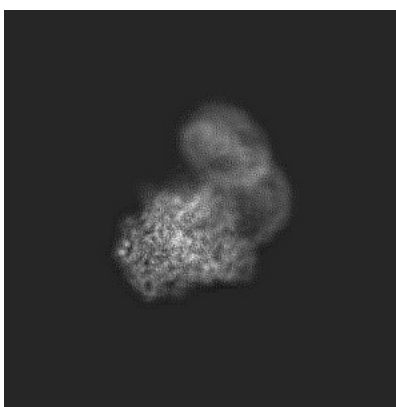


Z

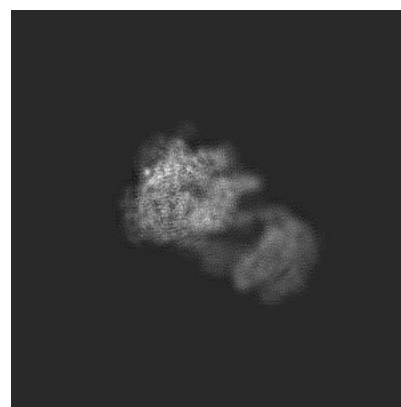
6.1.2 Raw map



X



Y

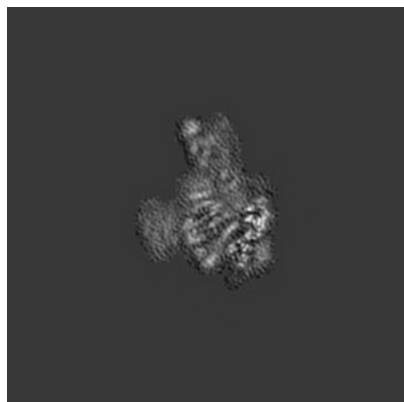


Z

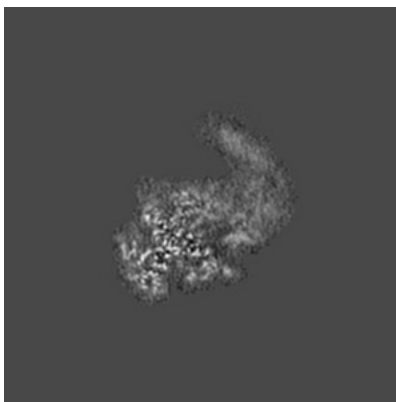
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

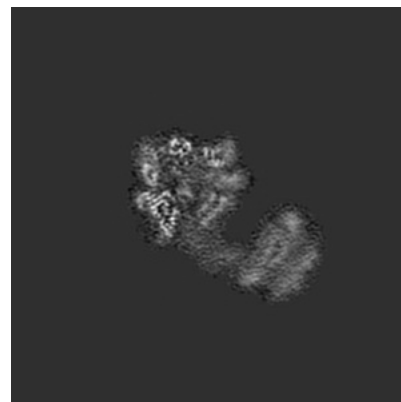
6.2.1 Primary map



X Index: 200

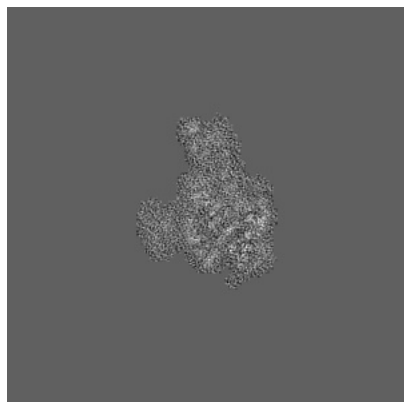


Y Index: 200

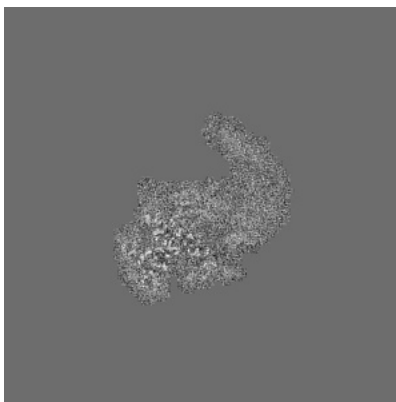


Z Index: 200

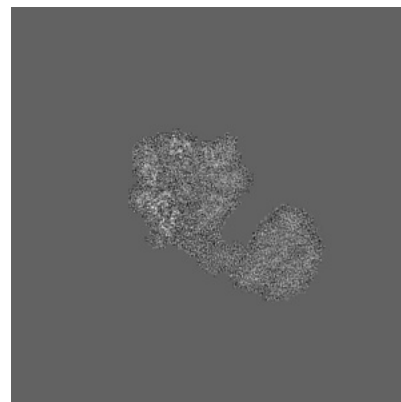
6.2.2 Raw map



X Index: 200



Y Index: 200

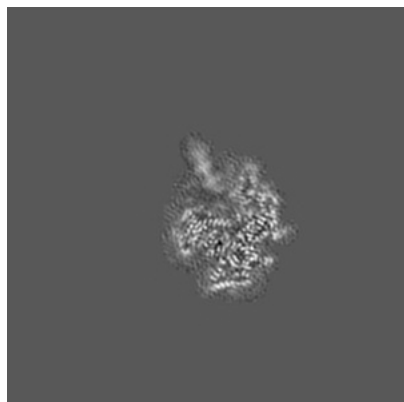


Z Index: 200

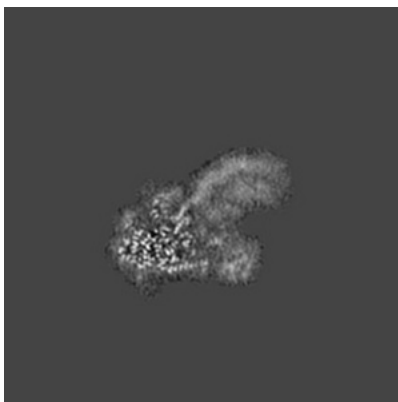
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

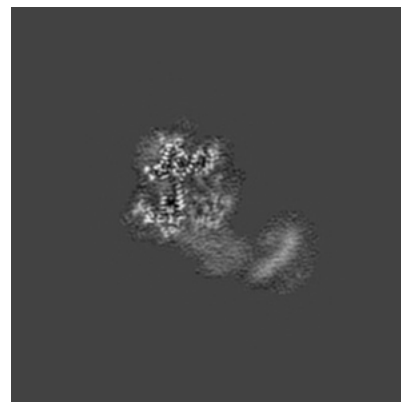
6.3.1 Primary map



X Index: 167

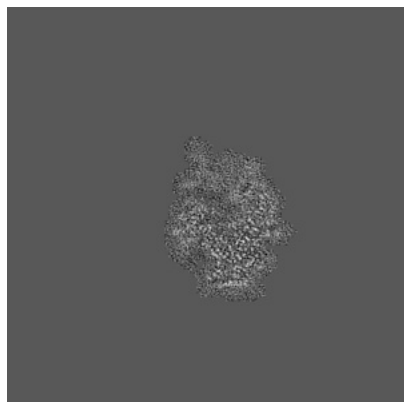


Y Index: 227

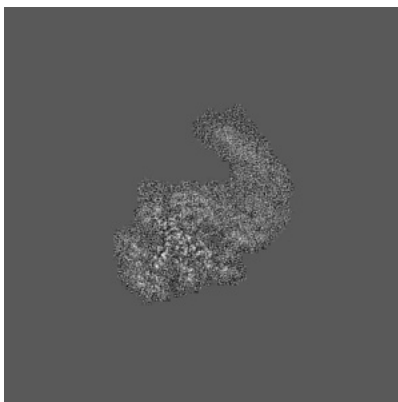


Z Index: 186

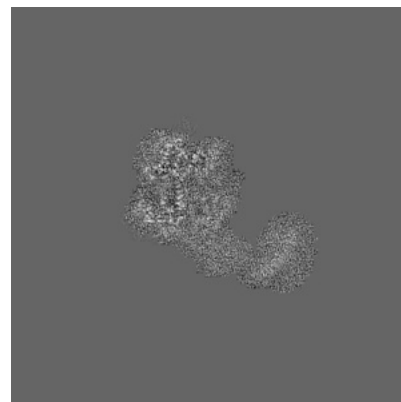
6.3.2 Raw map



X Index: 164



Y Index: 197

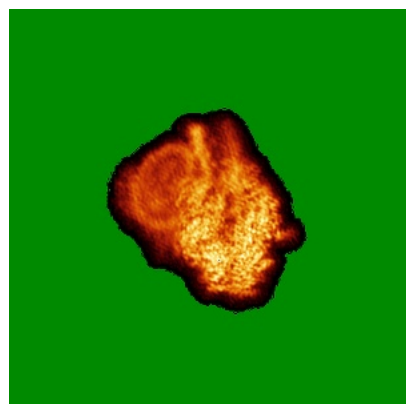


Z Index: 186

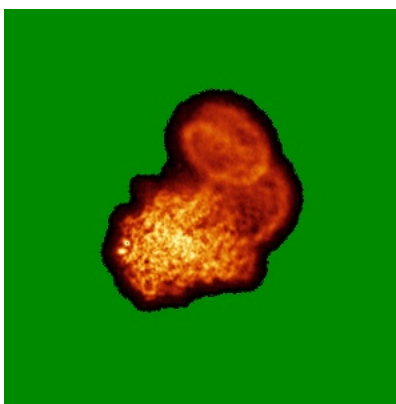
The images above show the largest variance slices of the map in three orthogonal directions.

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

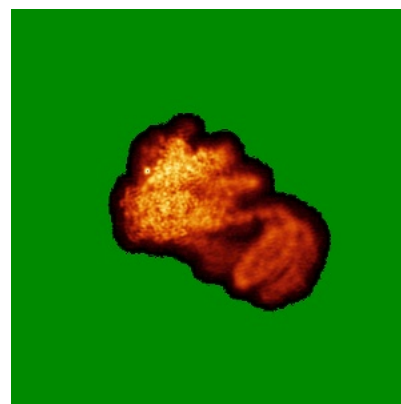
6.4.1 Primary map



X

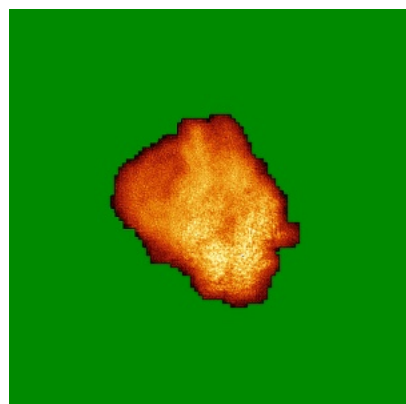


Y

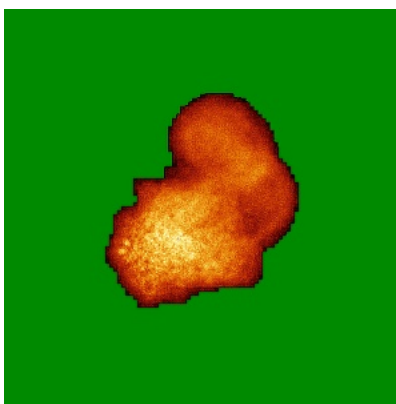


Z

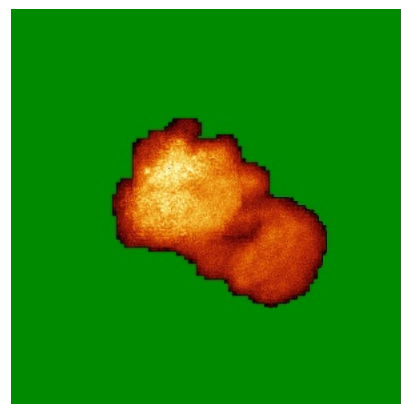
6.4.2 Raw map



X



Y

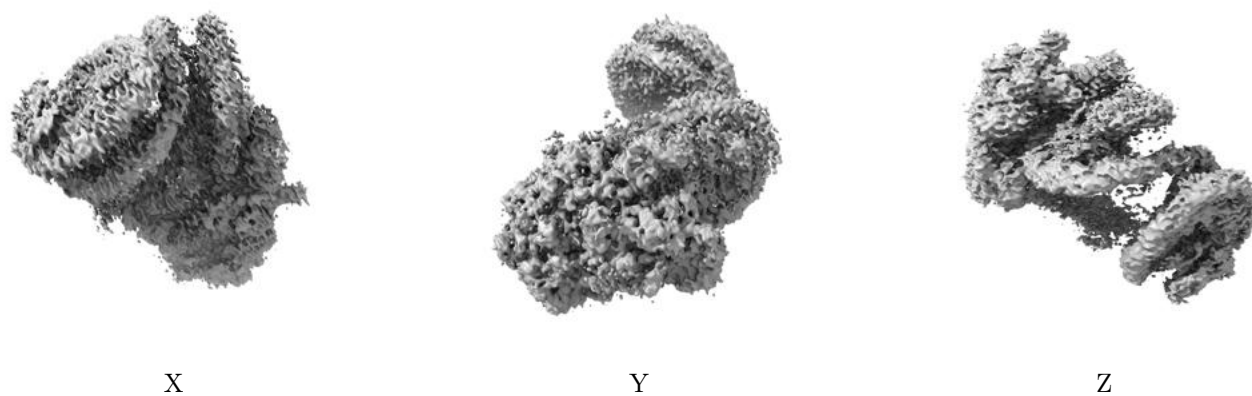


Z

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

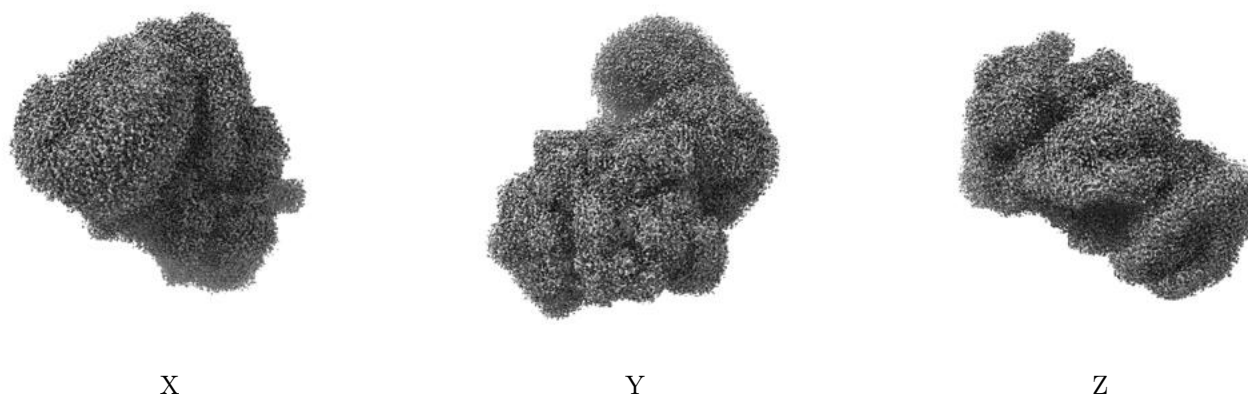
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00777. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

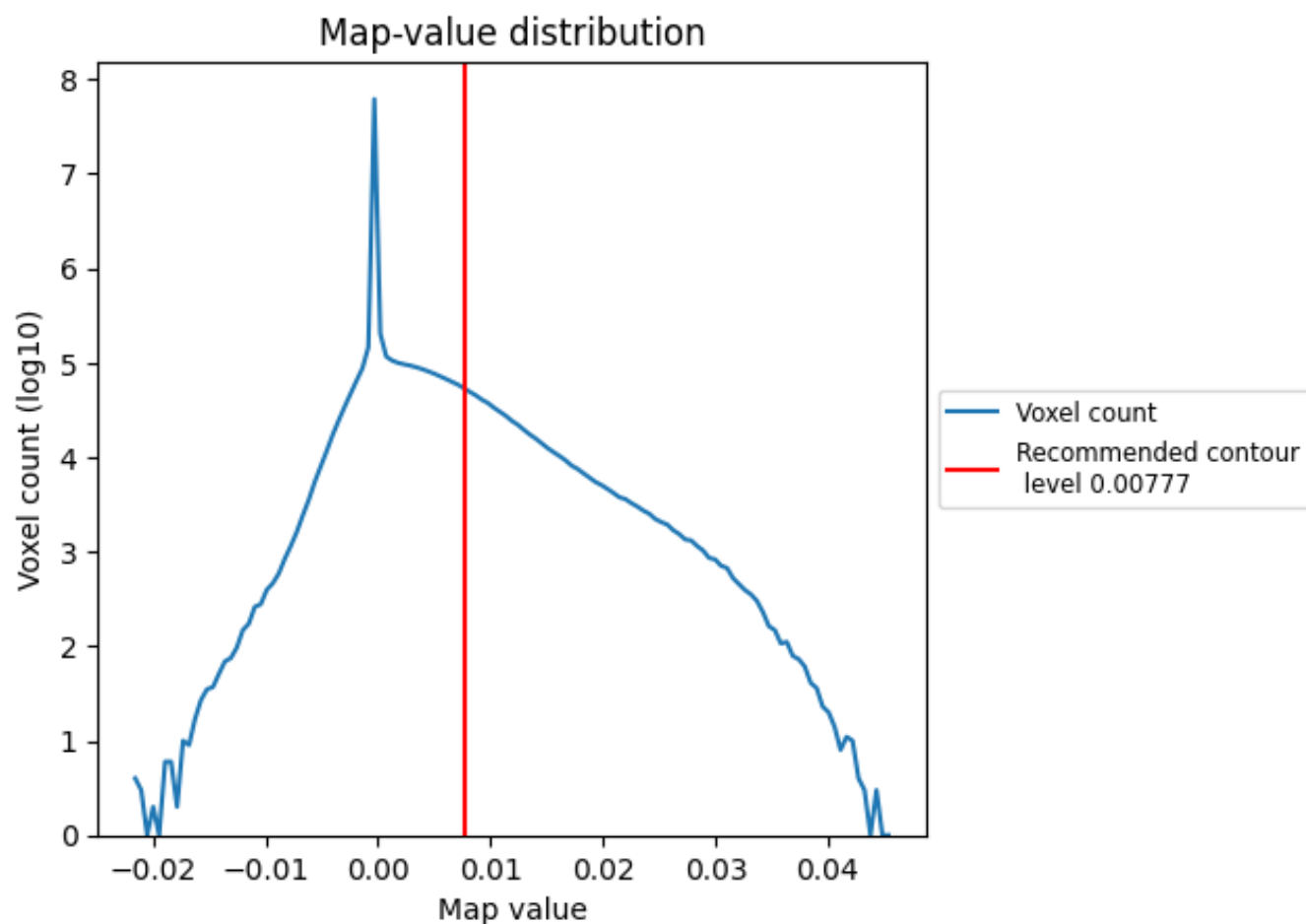
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

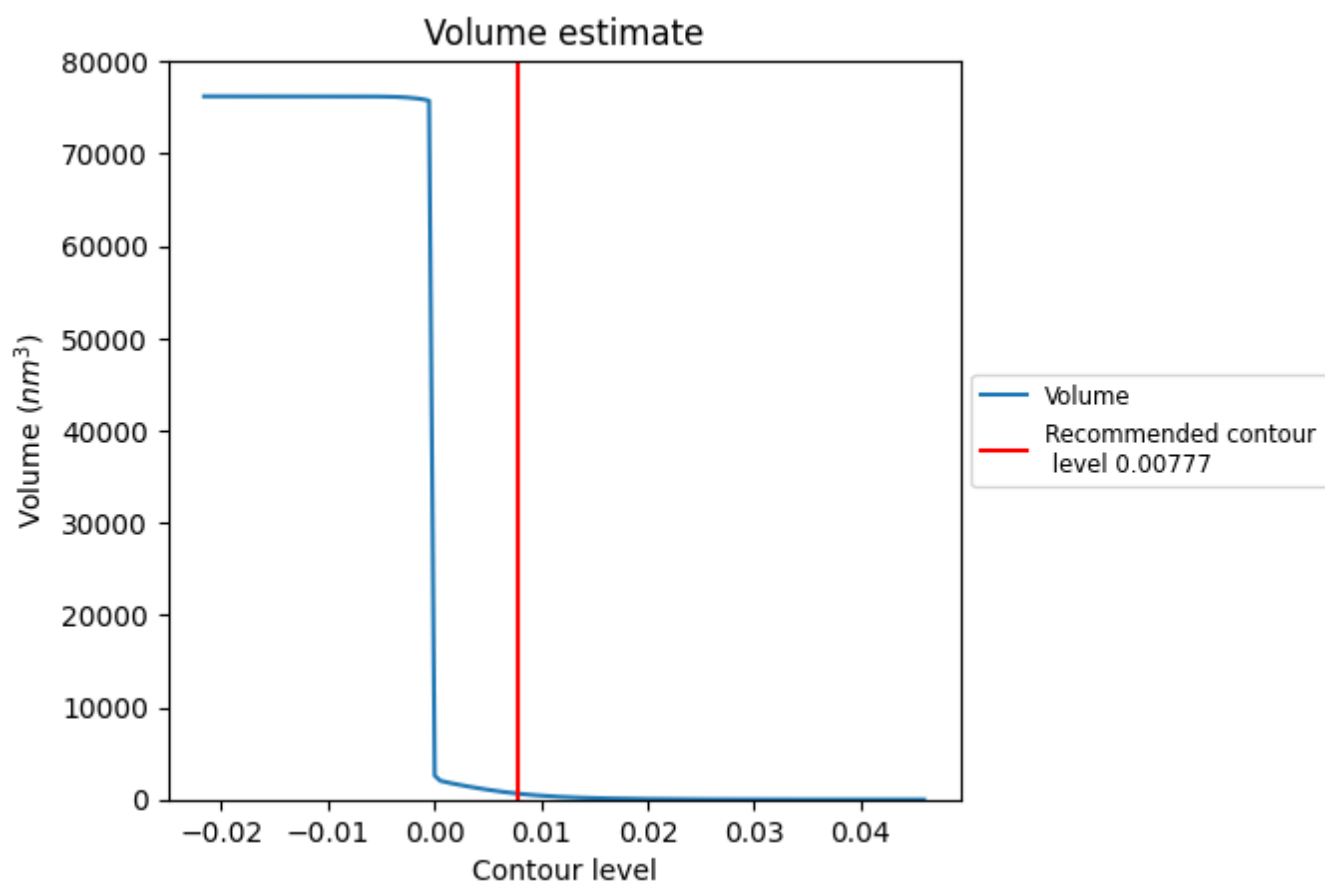
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

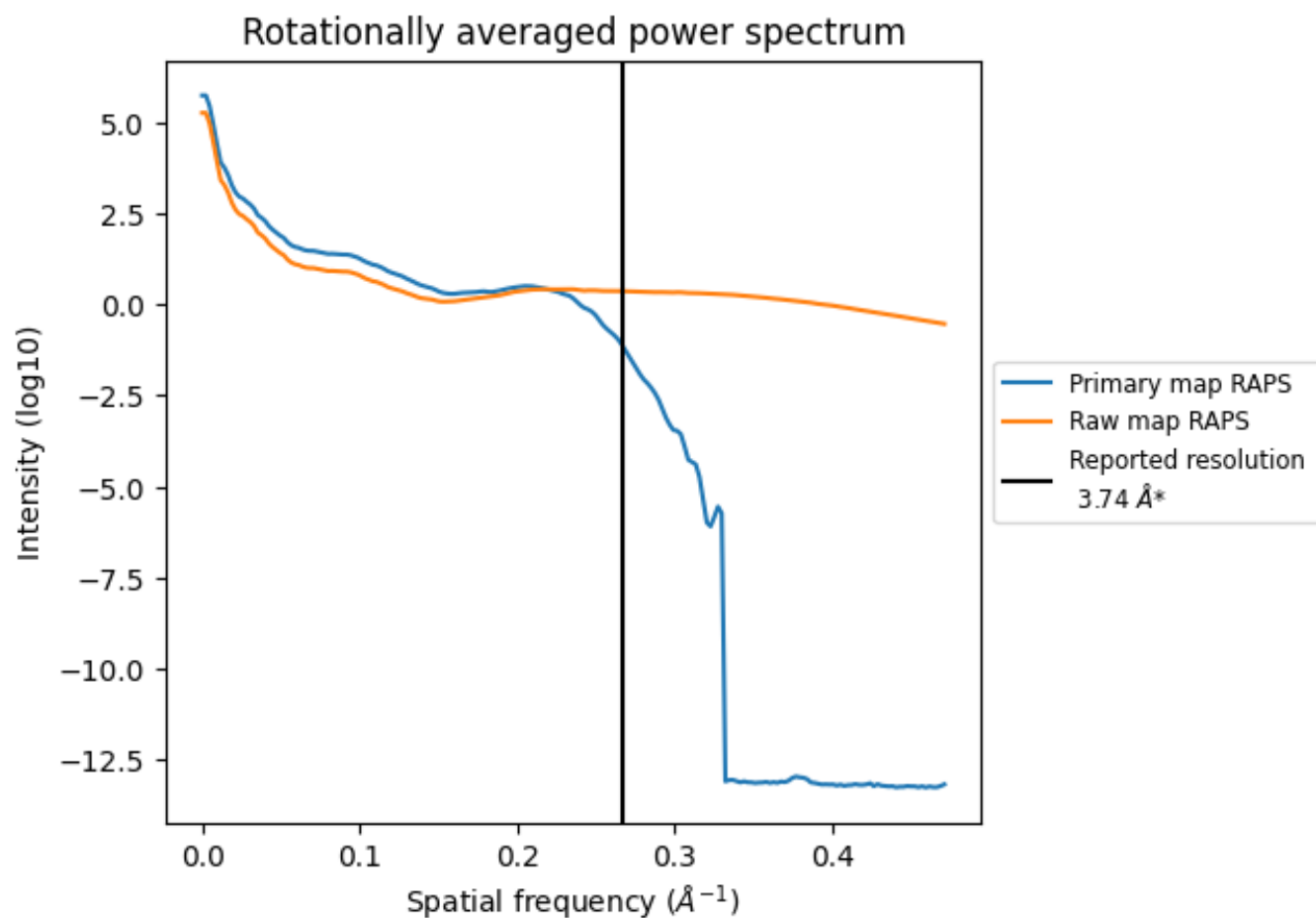
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 654 nm³; this corresponds to an approximate mass of 591 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 ⓘ

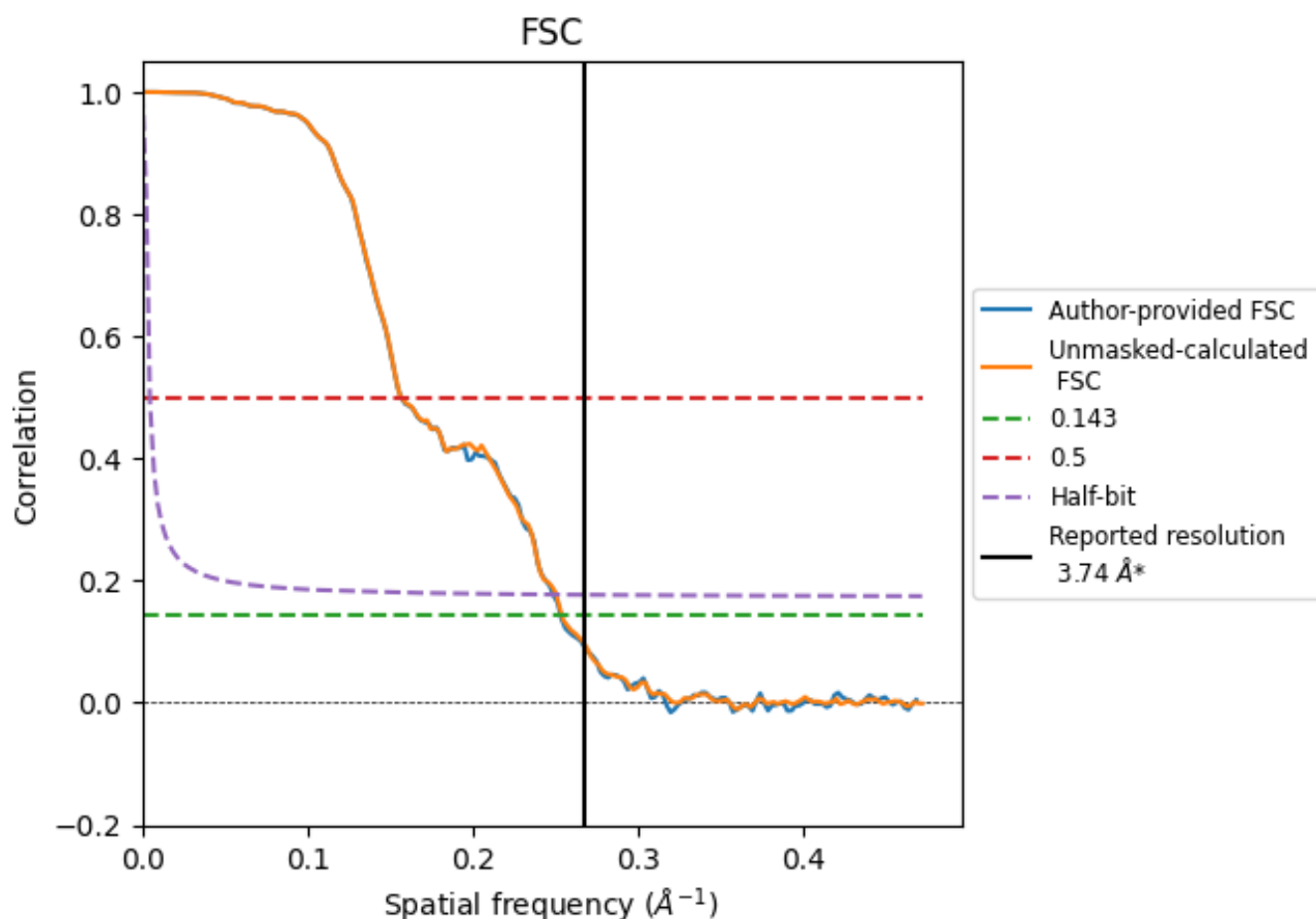


*Reported resolution corresponds to spatial frequency of 0.267 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.267 \AA^{-1}

8.2 Resolution estimates [i](#)

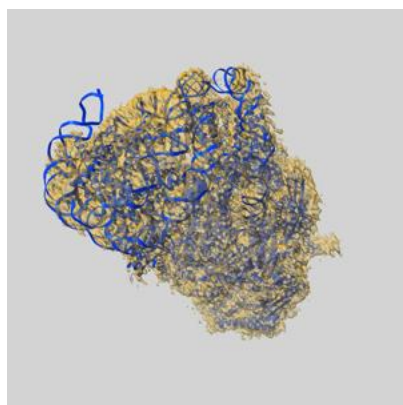
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.74	-	-
Author-provided FSC curve	3.95	6.38	4.02
Unmasked-calculated*	3.94	6.37	4.00

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

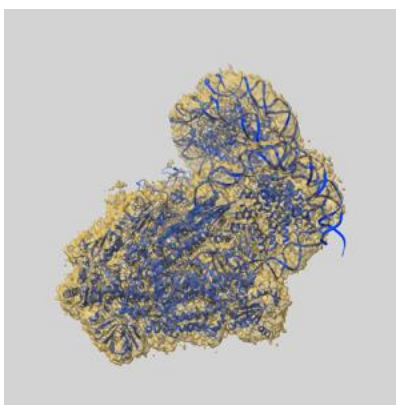
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64603 and PDB model 9UXW. Per-residue inclusion information can be found in section [3](#) on page [11](#).

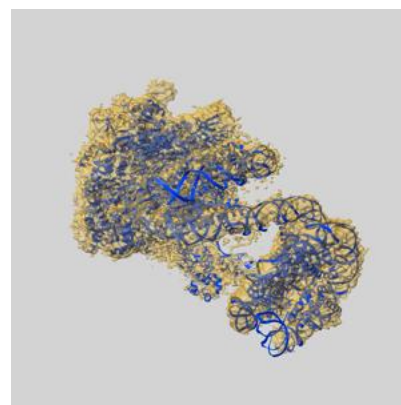
9.1 Map-model overlay [i](#)



X



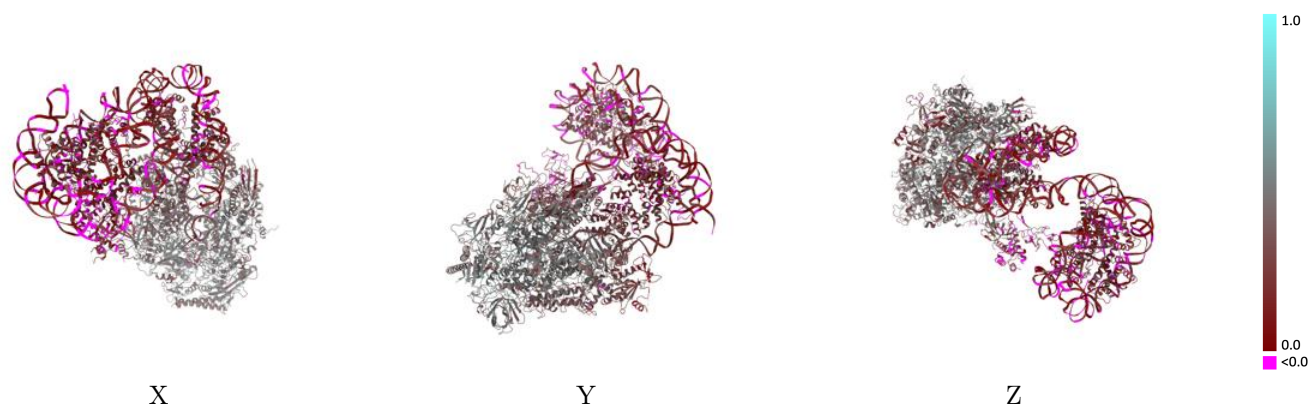
Y



Z

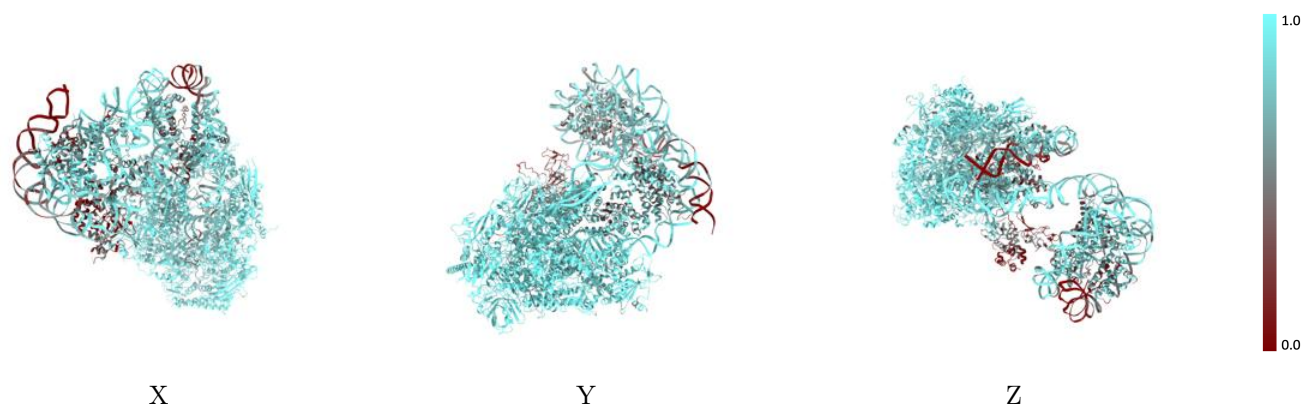
The images above show the 3D surface view of the map at the recommended contour level 0.00777 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



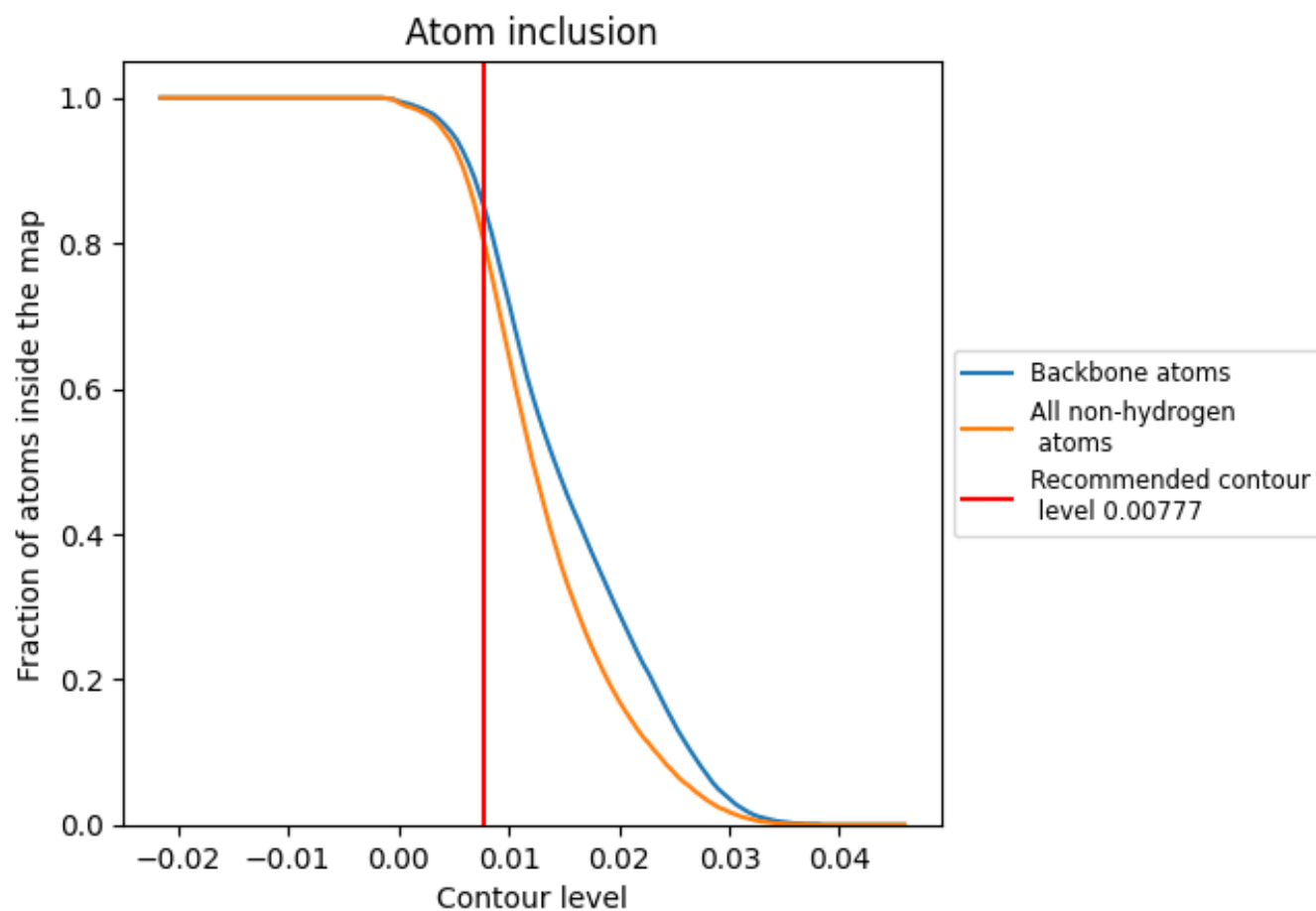
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00777).





























































9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.00777) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8020	 0.2920
A	 0.9050	 0.3960
B	 0.9150	 0.4240
C	 0.9580	 0.4490
D	 0.2640	 0.1120
E	 0.9470	 0.4070
F	 0.9680	 0.4320
G	 0.4770	 0.1940
H	 0.9830	 0.4450
I	 0.8770	 0.2630
J	 0.9670	 0.4430
K	 0.9390	 0.4310
L	 0.9400	 0.3880
N	 0.6890	 0.1100
P	 0.7940	 0.2530
T	 0.6980	 0.1160
a	 0.6370	 0.1420
b	 0.7330	 0.1620
c	 0.6460	 0.1520
d	 0.6660	 0.1500
e	 0.7550	 0.1650
f	 0.7330	 0.1490
g	 0.6310	 0.1540
h	 0.6840	 0.1450
k	 0.6910	 0.2480
l	 0.6830	 0.2160
m	 0.6410	 0.2010
n	 0.6170	 0.2150
o	 0.6710	 0.1480
p	 0.7820	 0.1750

