



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 08:58 PM UTC

PDB ID : 7XSX / pdb_00007xsx
EMDB ID : EMD-33436
Title : RNA polymerase II elongation complex transcribing a nucleosome (EC49)
Authors : Ehara, H.; Kujirai, T.; Shirouzu, M.; Kurumizaka, H.; Sekine, S.
Deposited on : 2022-05-15
Resolution : 3.80 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:

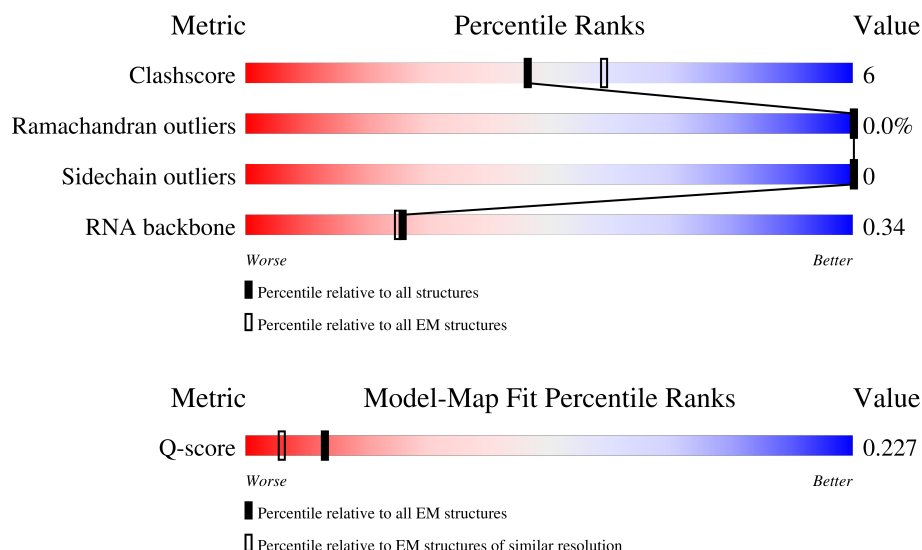
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.80 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	10198 (3.30 - 4.30)

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	M	113	
14	N	198	
15	P	19	
16	T	198	
17	V	108	
18	W	911	
19	m	1503	
20	n	417	
21	q	1084	
22	r	544	
23	u	459	
24	v	396	
25	x	395	
26	a	139	
26	e	139	
27	b	106	

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Mol	Chain	Length	Quality of chain
27	f	106	26% 56% 18% 26%
28	c	133	65% 65% 13% 23%
28	g	133	20% 44% 8% 47%
29	d	129	43% 62% 12% 26%
29	h	129	30% 61% 11% 28%
30	j	956	33% 47% 51%
31	k	531	65% 75% 5% 19%

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 81134 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	1404	Total	C	N	O	S	0	0
			11064	6975	1930	2089	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 DNA-directed RNA polymerases I, II, and III subunit RPABC1.

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 protein called Transcription elongation factor 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	64	Total	C	N	O	S	0	0
			505	318	82	99	6		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	GLY	-	expression tag	UNP C4QZ45
M	-1	PRO	-	expression tag	UNP C4QZ45
M	0	GLY	-	expression tag	UNP C4QZ45

- Molecule 14 is a DNA chain called DNA (198-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	97	Total	C	N	O	P	0	0
			2007	949	377	584	97		

- Molecule 15 is a RNA chain called RNA (5'-R(P*GP*AP*CP*CP*CP*GP*GP*GP*UP*GP*UP*CP*UP*UP*CP*CP*CP*CP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	19	Total	C	N	O	P	0	0
			399	178	66	136	19		

- Molecule 16 is a DNA chain called DNA (198-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	108	Total	C	N	O	P	0	0
			2202	1045	407	642	108		

- Molecule 17 is a protein called Transcription elongation factor SPT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	V	106	Total	C	N	O	S	0	0
			824	512	150	155	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	7	MET	-	initiating methionine	UNP C4R0E6

- Molecule 18 is a protein called Transcription elongation factor SPT5.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	W	533	Total	C	N	O	S	0	0
			4232	2666	752	812	2		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	-2	GLY	-	expression tag	UNP C4R370
W	-1	PRO	-	expression tag	UNP C4R370
W	0	GLY	-	expression tag	UNP C4R370

- Molecule 19 is a protein called Transcription elongation factor Spt6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	m	1187	Total	C	N	O	S	0	0
			9730	6162	1663	1877	28		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	-2	GLY	-	expression tag	UNP C4R7H2
m	-1	PRO	-	expression tag	UNP C4R7H2
m	0	GLY	-	expression tag	UNP C4R7H2

- Molecule 20 is a protein called Protein that interacts with Spt6p and copurifies with Spt5p and RNA polymerase II.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	n	139	Total	C	N	O	S	0	0
			1115	716	193	202	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	-2	GLY	-	expression tag	UNP C4R7L8
n	-1	PRO	-	expression tag	UNP C4R7L8
n	0	GLY	-	expression tag	UNP C4R7L8

- Molecule 21 is a protein called Component of the Paf1p complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	q	930	Total	C	N	O	S	0	0
			7552	4805	1283	1439	25		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
q	-39	MET	-	initiating methionine	UNP C4R6B2
q	-38	LYS	-	expression tag	UNP C4R6B2
q	-37	ASP	-	expression tag	UNP C4R6B2
q	-36	HIS	-	expression tag	UNP C4R6B2
q	-35	LEU	-	expression tag	UNP C4R6B2
q	-34	ILE	-	expression tag	UNP C4R6B2
q	-33	HIS	-	expression tag	UNP C4R6B2
q	-32	ASN	-	expression tag	UNP C4R6B2
q	-31	HIS	-	expression tag	UNP C4R6B2
q	-30	HIS	-	expression tag	UNP C4R6B2
q	-29	LYS	-	expression tag	UNP C4R6B2
q	-28	HIS	-	expression tag	UNP C4R6B2
q	-27	GLU	-	expression tag	UNP C4R6B2
q	-26	HIS	-	expression tag	UNP C4R6B2
q	-25	ALA	-	expression tag	UNP C4R6B2
q	-24	HIS	-	expression tag	UNP C4R6B2
q	-23	ALA	-	expression tag	UNP C4R6B2
q	-22	GLU	-	expression tag	UNP C4R6B2
q	-21	HIS	-	expression tag	UNP C4R6B2
q	-20	ASP	-	expression tag	UNP C4R6B2
q	-19	TYR	-	expression tag	UNP C4R6B2
q	-18	LYS	-	expression tag	UNP C4R6B2
q	-17	ASP	-	expression tag	UNP C4R6B2
q	-16	ASP	-	expression tag	UNP C4R6B2
q	-15	ASP	-	expression tag	UNP C4R6B2
q	-14	ASP	-	expression tag	UNP C4R6B2
q	-13	LYS	-	expression tag	UNP C4R6B2
q	-12	GLU	-	expression tag	UNP C4R6B2
q	-11	HIS	-	expression tag	UNP C4R6B2
q	-10	LEU	-	expression tag	UNP C4R6B2
q	-9	TYR	-	expression tag	UNP C4R6B2
q	-8	PHE	-	expression tag	UNP C4R6B2
q	-7	GLN	-	expression tag	UNP C4R6B2
q	-6	GLY	-	expression tag	UNP C4R6B2
q	-5	SER	-	expression tag	UNP C4R6B2
q	-4	SER	-	expression tag	UNP C4R6B2
q	-3	GLY	-	expression tag	UNP C4R6B2
q	-2	SER	-	expression tag	UNP C4R6B2
q	-1	SER	-	expression tag	UNP C4R6B2
q	0	GLY	-	expression tag	UNP C4R6B2

- Molecule 22 is a protein called RNAPII-associated chromatin remodeling Paf1 complex sub-

unit.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	r	266	Total	C	N	O	S	0	0
			2139	1342	374	412	11		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	-29	MET	-	initiating methionine	UNP F2QQ42
r	-28	LYS	-	expression tag	UNP F2QQ42
r	-27	ASP	-	expression tag	UNP F2QQ42
r	-26	HIS	-	expression tag	UNP F2QQ42
r	-25	LEU	-	expression tag	UNP F2QQ42
r	-24	ILE	-	expression tag	UNP F2QQ42
r	-23	HIS	-	expression tag	UNP F2QQ42
r	-22	ASN	-	expression tag	UNP F2QQ42
r	-21	HIS	-	expression tag	UNP F2QQ42
r	-20	HIS	-	expression tag	UNP F2QQ42
r	-19	LYS	-	expression tag	UNP F2QQ42
r	-18	HIS	-	expression tag	UNP F2QQ42
r	-17	GLU	-	expression tag	UNP F2QQ42
r	-16	HIS	-	expression tag	UNP F2QQ42
r	-15	ALA	-	expression tag	UNP F2QQ42
r	-14	HIS	-	expression tag	UNP F2QQ42
r	-13	ALA	-	expression tag	UNP F2QQ42
r	-12	GLU	-	expression tag	UNP F2QQ42
r	-11	HIS	-	expression tag	UNP F2QQ42
r	-10	LEU	-	expression tag	UNP F2QQ42
r	-9	TYR	-	expression tag	UNP F2QQ42
r	-8	PHE	-	expression tag	UNP F2QQ42
r	-7	GLN	-	expression tag	UNP F2QQ42
r	-6	GLY	-	expression tag	UNP F2QQ42
r	-5	SER	-	expression tag	UNP F2QQ42
r	-4	SER	-	expression tag	UNP F2QQ42
r	-3	GLY	-	expression tag	UNP F2QQ42
r	-2	SER	-	expression tag	UNP F2QQ42
r	-1	SER	-	expression tag	UNP F2QQ42
r	0	GLY	-	expression tag	UNP F2QQ42

- Molecule 23 is a protein called Leo1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	u	208	Total	C	N	O	S	0	0
			1707	1063	304	337	3		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	-29	MET	-	initiating methionine	UNP C4R3K1
u	-28	LYS	-	expression tag	UNP C4R3K1
u	-27	ASP	-	expression tag	UNP C4R3K1
u	-26	HIS	-	expression tag	UNP C4R3K1
u	-25	LEU	-	expression tag	UNP C4R3K1
u	-24	ILE	-	expression tag	UNP C4R3K1
u	-23	HIS	-	expression tag	UNP C4R3K1
u	-22	ASN	-	expression tag	UNP C4R3K1
u	-21	HIS	-	expression tag	UNP C4R3K1
u	-20	HIS	-	expression tag	UNP C4R3K1
u	-19	LYS	-	expression tag	UNP C4R3K1
u	-18	HIS	-	expression tag	UNP C4R3K1
u	-17	GLU	-	expression tag	UNP C4R3K1
u	-16	HIS	-	expression tag	UNP C4R3K1
u	-15	ALA	-	expression tag	UNP C4R3K1
u	-14	HIS	-	expression tag	UNP C4R3K1
u	-13	ALA	-	expression tag	UNP C4R3K1
u	-12	GLU	-	expression tag	UNP C4R3K1
u	-11	HIS	-	expression tag	UNP C4R3K1
u	-10	LEU	-	expression tag	UNP C4R3K1
u	-9	TYR	-	expression tag	UNP C4R3K1
u	-8	PHE	-	expression tag	UNP C4R3K1
u	-7	GLN	-	expression tag	UNP C4R3K1
u	-6	GLY	-	expression tag	UNP C4R3K1
u	-5	SER	-	expression tag	UNP C4R3K1
u	-4	SER	-	expression tag	UNP C4R3K1
u	-3	GLY	-	expression tag	UNP C4R3K1
u	-2	SER	-	expression tag	UNP C4R3K1
u	-1	SER	-	expression tag	UNP C4R3K1
u	0	GLY	-	expression tag	UNP C4R3K1

- Molecule 24 is a protein called RNAP II-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	v	349	Total	C	N	O	S	0	0
			2878	1835	510	528	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	-2	GLY	-	expression tag	UNP C4R997

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Chain	Residue	Modelled	Actual	Comment	Reference
v	-1	SER	-	expression tag	UNP C4R997
v	0	ALA	-	expression tag	UNP C4R997

- Molecule 25 is a protein called Constituent of Paf1 complex with RNA polymerase II, Paf1p, Hpr1p, Ctr9, Leo1, Rtf1 and Ccr4p.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	x	205	Total	C	N	O	S	0	0
			1682	1086	287	307	2		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	-29	MET	-	initiating methionine	UNP C4R1E6
x	-28	LYS	-	expression tag	UNP C4R1E6
x	-27	ASP	-	expression tag	UNP C4R1E6
x	-26	HIS	-	expression tag	UNP C4R1E6
x	-25	LEU	-	expression tag	UNP C4R1E6
x	-24	ILE	-	expression tag	UNP C4R1E6
x	-23	HIS	-	expression tag	UNP C4R1E6
x	-22	ASN	-	expression tag	UNP C4R1E6
x	-21	HIS	-	expression tag	UNP C4R1E6
x	-20	HIS	-	expression tag	UNP C4R1E6
x	-19	LYS	-	expression tag	UNP C4R1E6
x	-18	HIS	-	expression tag	UNP C4R1E6
x	-17	GLU	-	expression tag	UNP C4R1E6
x	-16	HIS	-	expression tag	UNP C4R1E6
x	-15	ALA	-	expression tag	UNP C4R1E6
x	-14	HIS	-	expression tag	UNP C4R1E6
x	-13	ALA	-	expression tag	UNP C4R1E6
x	-12	GLU	-	expression tag	UNP C4R1E6
x	-11	HIS	-	expression tag	UNP C4R1E6
x	-10	LEU	-	expression tag	UNP C4R1E6
x	-9	TYR	-	expression tag	UNP C4R1E6
x	-8	PHE	-	expression tag	UNP C4R1E6
x	-7	GLN	-	expression tag	UNP C4R1E6
x	-6	GLY	-	expression tag	UNP C4R1E6
x	-5	SER	-	expression tag	UNP C4R1E6
x	-4	SER	-	expression tag	UNP C4R1E6
x	-3	GLY	-	expression tag	UNP C4R1E6
x	-2	SER	-	expression tag	UNP C4R1E6
x	-1	SER	-	expression tag	UNP C4R1E6

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Chain	Residue	Modelled	Actual	Comment	Reference
x	0	GLY	-	expression tag	UNP C4R1E6

- Molecule 26 is a protein called Histone H3.3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	76	Total	C	N	O	S	0	0
			615	390	115	108	2		
26	e	93	Total	C	N	O	S	0	0
			757	477	146	132	2		

There are 6 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

- Molecule 27 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	83	Total	C	N	O	S	0	0
			662	418	129	114	1		
27	f	78	Total	C	N	O	S	0	0
			619	391	120	107	1		

There are 6 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

- Molecule 28 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	c	103	Total	C	N	O	0	0
			796	502	155	139		
28	g	70	Total	C	N	O	0	0
			544	342	109	93		

There are 6 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

- Molecule 29 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	95	Total	C	N	O	S	0	0
			746	468	136	140	2		
29	h	93	Total	C	N	O	S	0	0
			725	456	130	137	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	-6	GLY	-	expression tag	UNP P06899
d	-5	SER	-	expression tag	UNP P06899
d	-4	HIS	-	expression tag	UNP P06899
h	-6	GLY	-	expression tag	UNP P06899
h	-5	SER	-	expression tag	UNP P06899
h	-4	HIS	-	expression tag	UNP P06899

- Molecule 30 is a protein called FACT complex subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	j	471	Total	C	N	O	S	0	0
			3832	2434	666	719	13		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	-2	GLY	-	expression tag	UNP C4QYQ8
j	-1	PRO	-	expression tag	UNP C4QYQ8
j	0	GLY	-	expression tag	UNP C4QYQ8

- Molecule 31 is a protein called FACT complex subunit POB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	k	429	Total	C	N	O	S	0	0
			3502	2215	613	664	10		

There are 3 discrepancies between the modelled and reference sequences:

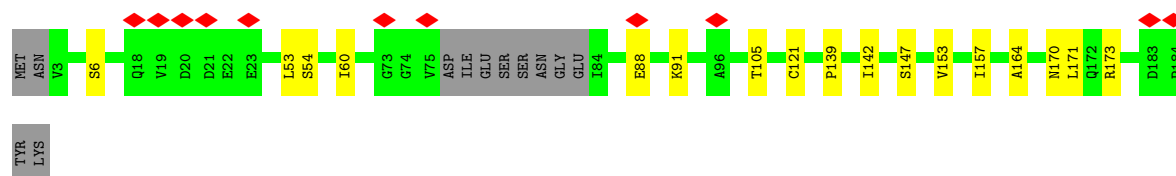
Chain	Residue	Modelled	Actual	Comment	Reference
k	-2	GLY	-	expression tag	UNP F2QNN8
k	-1	PRO	-	expression tag	UNP F2QNN8
k	0	GLY	-	expression tag	UNP F2QNN8

- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
32	A	2	Total	Zn	0
			2	2	
32	B	1	Total	Zn	0
			1	1	
32	C	1	Total	Zn	0
			1	1	
32	I	2	Total	Zn	0
			2	2	
32	J	1	Total	Zn	0
			1	1	
32	L	1	Total	Zn	0
			1	1	
32	M	1	Total	Zn	0
			1	1	
32	V	1	Total	Zn	0
			1	1	

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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



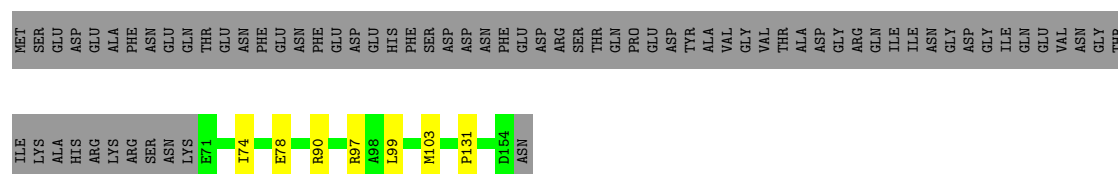
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E: 82% 17%



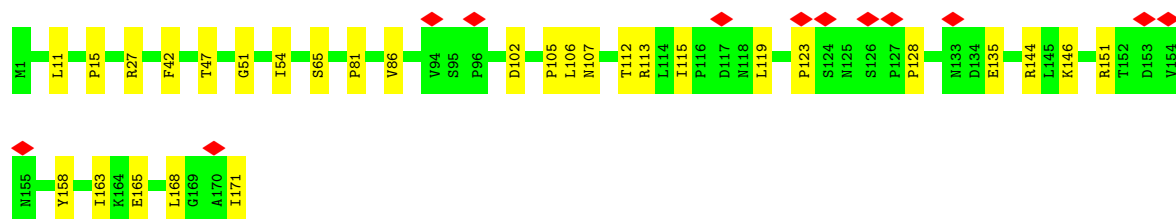
- Molecule 6: RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III

Chain F: 50% 5% 46%



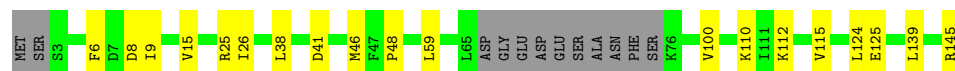
- Molecule 7: RNA polymerase II subunit

Chain G: 7% 83% 17%



- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

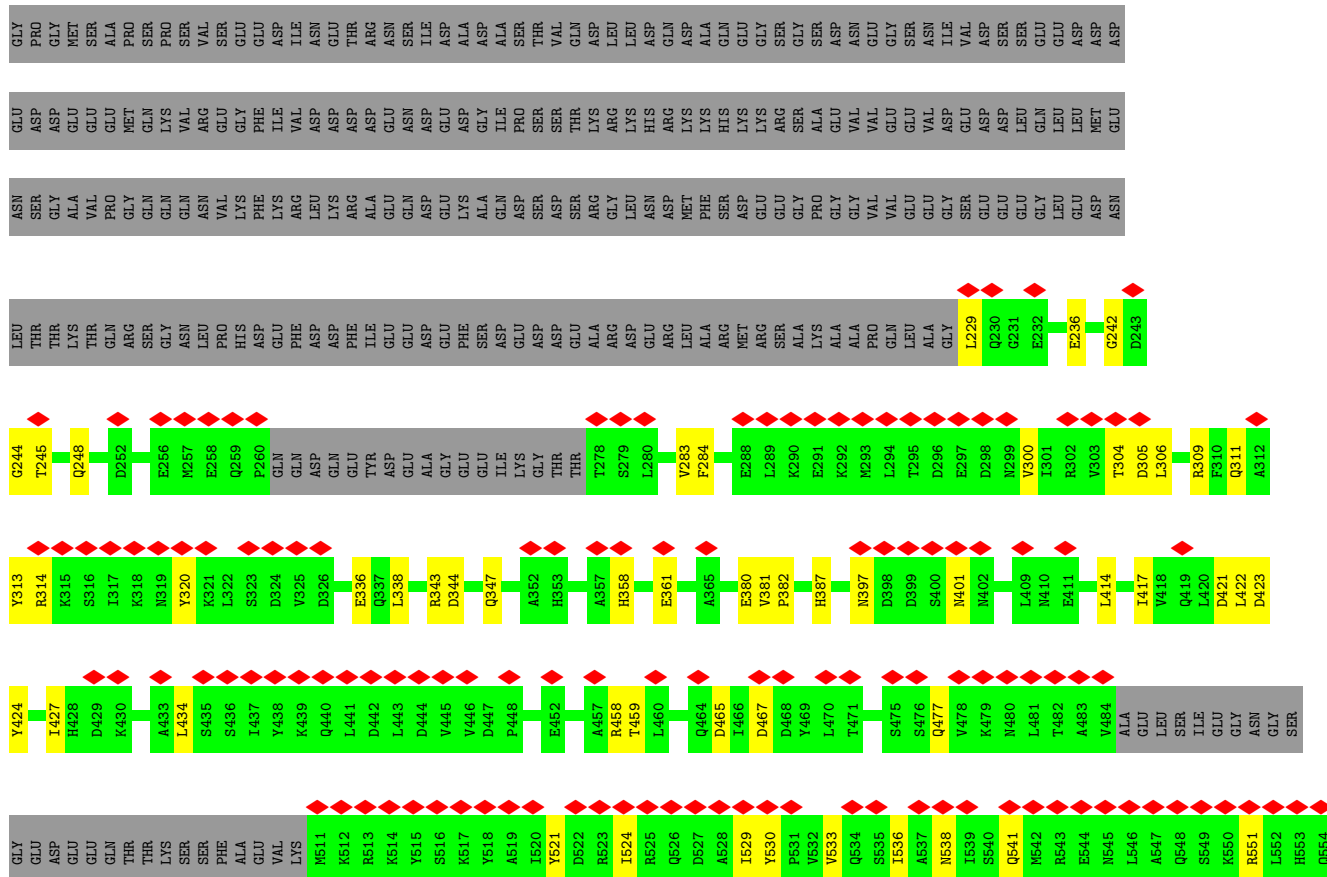
Chain H: 79% 13% 8%



- Molecule 9: DNA-directed RNA polymerase subunit

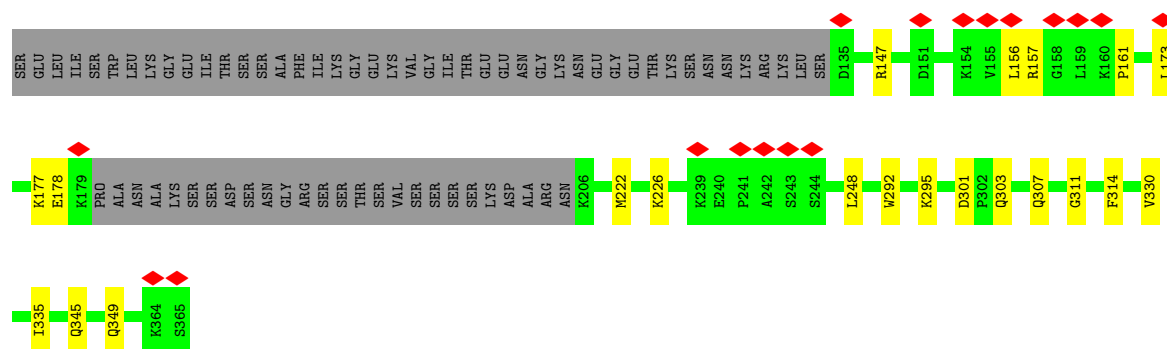
Chain I: 80% 17% 3%

- Molecule 19: Transcription elongation factor Spt6

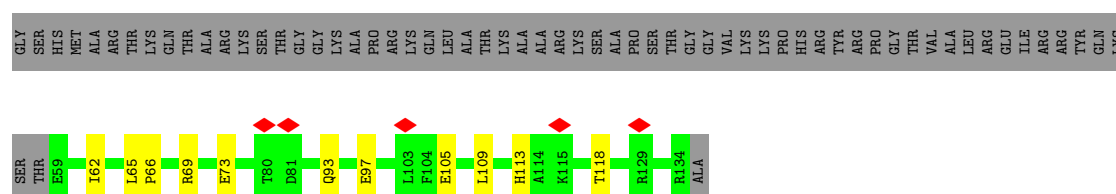




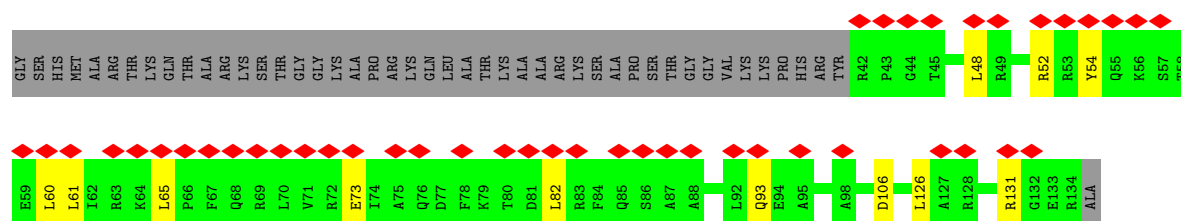




• Molecule 26: Histone H3.3



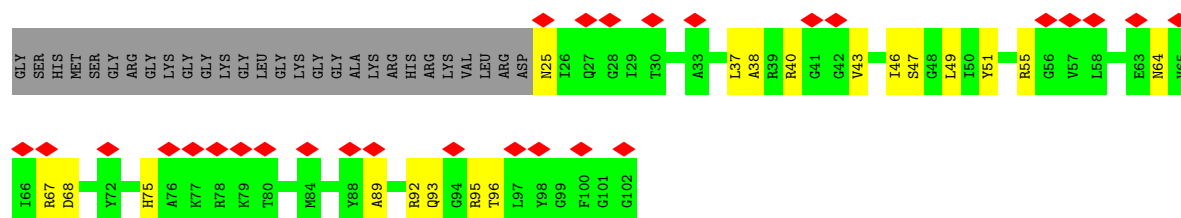
• Molecule 26: Histone H3.3



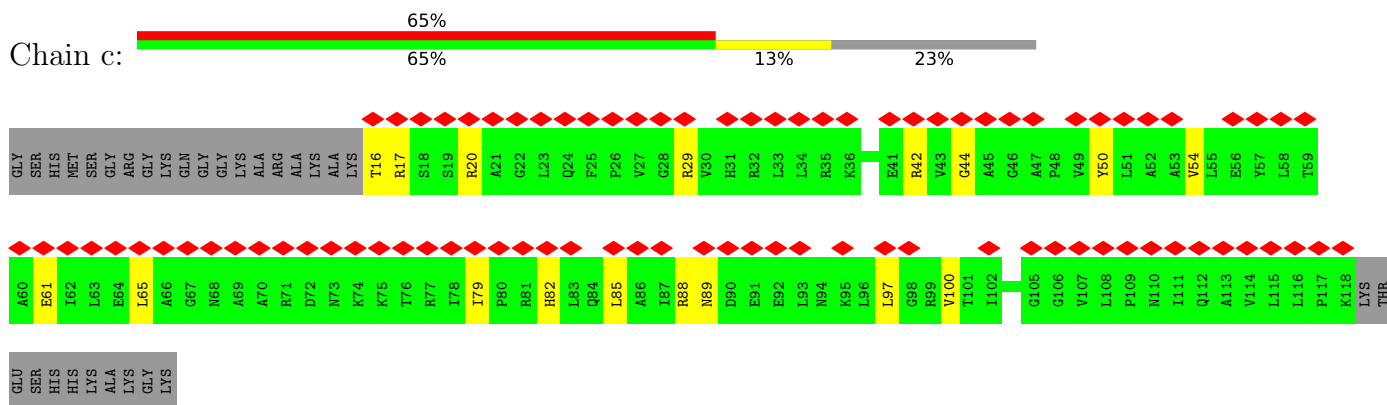
• Molecule 27: Histone H4



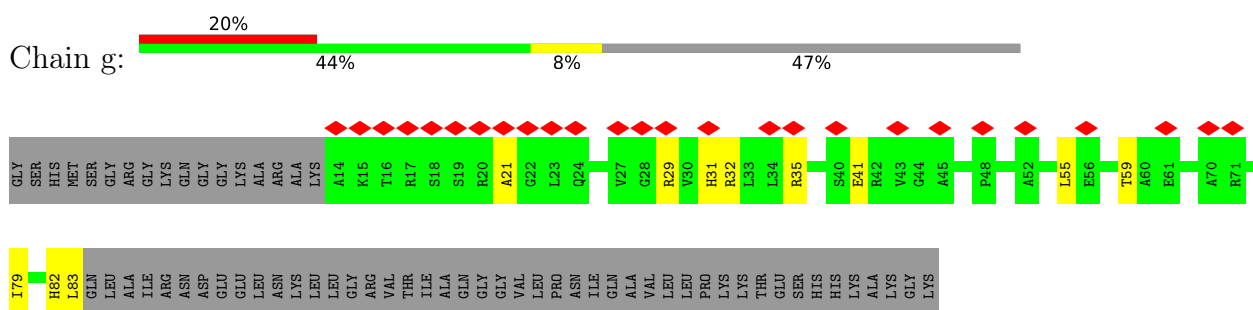
• Molecule 27: Histone H4



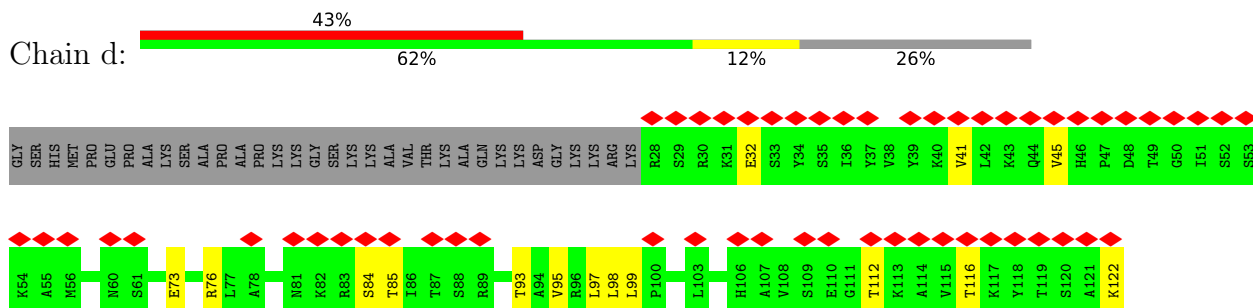
- Molecule 28: Histone H2A type 1-B/E



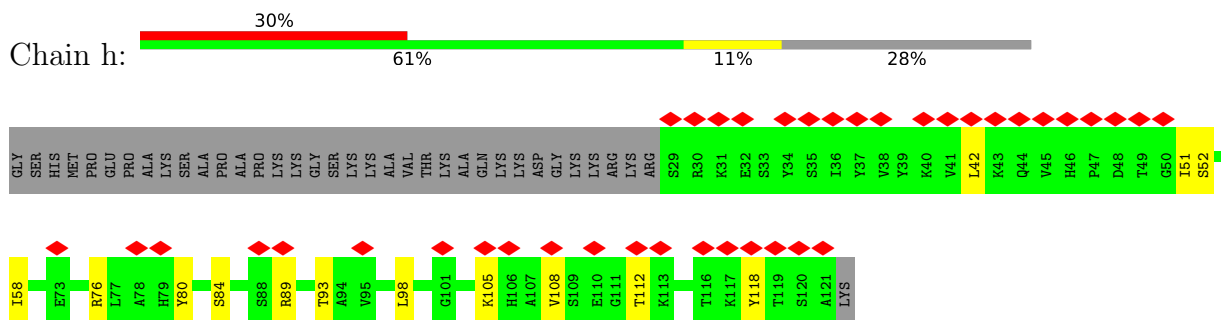
- Molecule 28: Histone H2A type 1-B/E



- Molecule 29: Histone H2B type 1-J



- Molecule 29: Histone H2B type 1-J



- Molecule 30: FACT complex subunit







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53755	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 ($e^-/\text{\AA}^2$)	51	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	0.123	Depositor
Minimum map value	-0.040	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.013	Depositor
Map size ($\text{\AA}$)	356.16, 356.16, 356.16	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.484, 1.484, 1.484	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.23	0/11267	0.31	1/15222 (0.0%)
2	B	0.23	0/9464	0.30	0/12763
3	C	0.25	0/2139	0.30	0/2895
4	D	0.10	0/1361	0.24	0/1837
5	E	0.22	0/1773	0.34	0/2385
6	F	0.24	0/687	0.26	0/931
7	G	0.15	0/1354	0.28	0/1837
8	H	0.23	0/1070	0.28	0/1444
9	I	0.10	0/934	0.25	0/1257
10	J	0.25	0/563	0.28	0/753
11	K	0.24	0/953	0.29	0/1291
12	L	0.20	0/365	0.27	0/484
13	M	0.10	0/513	0.25	0/693
14	N	0.51	0/2253	0.79	0/3478
15	P	0.34	0/443	0.51	0/687
16	T	0.50	0/2469	0.77	0/3804
17	V	0.10	0/840	0.21	0/1140
18	W	0.11	0/4300	0.26	0/5812
19	m	0.11	0/9925	0.25	0/13424
20	n	0.10	0/1132	0.23	0/1526
21	q	0.10	0/7689	0.21	0/10368
22	r	0.11	0/2169	0.24	0/2901
23	u	0.10	0/1740	0.23	0/2347
24	v	0.11	0/2944	0.24	0/3973
25	x	0.13	0/1716	0.25	0/2310
26	a	0.20	0/622	0.35	0/834
26	e	0.26	0/766	0.42	0/1027
27	b	0.22	0/669	0.46	0/894
27	f	0.25	0/626	0.42	0/837
28	c	0.23	0/806	0.40	0/1089
28	g	0.34	0/552	0.46	0/743
29	d	0.22	0/757	0.35	0/1015

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
29	h	0.20	0/736	0.35	0/990
30	j	0.80	0/3909	1.15	0/5264
31	k	0.77	0/3579	1.12	0/4833
All	All	0.31	0/83085	0.47	1/113088 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
14	N	0	6
16	T	0	10
30	j	0	1
31	k	0	2
All	All	0	19

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1001	VAL	N-CA-C	-5.79	107.17	112.96

There are no chirality outliers.

All (19) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	N	-10	DG	Sidechain
14	N	-12	DA	Sidechain
14	N	-5	DG	Sidechain
14	N	-6	DG	Sidechain
14	N	44	DT	Sidechain
14	N	46	DG	Sidechain
16	T	-46	DC	Sidechain
16	T	-47	DT	Sidechain
16	T	-49	DG	Sidechain
16	T	-52	DG	Sidechain
16	T	-53	DG	Sidechain
16	T	-54	DA	Sidechain
16	T	1	DT	Sidechain
16	T	13	DT	Sidechain

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Mol	Chain	Res	Type	Group
16	T	4	DC	Sidechain
16	T	7	DC	Sidechain
30	j	616	ARG	Sidechain
31	k	292	ARG	Sidechain
31	k	58	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11064	0	11090	118	0
2	B	9284	0	9282	135	0
3	C	2098	0	2057	24	0
4	D	1349	0	1345	10	0
5	E	1741	0	1754	25	0
6	F	677	0	693	7	0
7	G	1325	0	1342	19	0
8	H	1053	0	1050	11	0
9	I	917	0	867	16	0
10	J	554	0	573	6	0
11	K	932	0	944	14	0
12	L	359	0	358	6	0
13	M	505	0	495	5	0
14	N	2007	0	1091	45	0
15	P	399	0	205	10	0
16	T	2202	0	1210	40	0
17	V	824	0	795	17	0
18	W	4232	0	4278	67	0
19	m	9730	0	9588	144	0
20	n	1115	0	1186	25	0
21	q	7552	0	7545	107	0
22	r	2139	0	2155	39	0
23	u	1707	0	1676	27	0
24	v	2878	0	2873	58	0
25	x	1682	0	1731	16	0
26	a	615	0	645	12	0
26	e	757	0	798	10	0
27	b	662	0	709	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	f	619	0	659	21	0
28	c	796	0	848	14	0
28	g	544	0	574	11	0
29	d	746	0	771	11	0
29	h	725	0	745	12	0
30	j	3832	0	3792	28	0
31	k	3502	0	3436	26	0
32	A	2	0	0	0	0
32	B	1	0	0	0	0
32	C	1	0	0	0	0
32	I	2	0	0	0	0
32	J	1	0	0	0	0
32	L	1	0	0	0	0
32	M	1	0	0	0	0
32	V	1	0	0	0	0
33	A	1	0	0	0	0
All	All	81134	0	79160	971	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 6.

All (971) 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)
16:T:-43:DT:H5''	28:c:16:THR:HA	1.50	0.92
30:j:587:ARG:HH12	31:k:287:ARG:CD	1.85	0.89
31:k:286:LEU:HD12	31:k:296:LEU:HD21	1.54	0.89
16:T:-2:DC:H2''	16:T:-1:DG:C8	2.11	0.86
14:N:-51:DG:H2''	14:N:-50:DT:H71	1.57	0.86
31:k:116:GLN:NE2	31:k:125:ASN:HD22	1.75	0.85
14:N:-22:DA:N6	14:N:-21:DA:C6	2.48	0.81
27:f:49:LEU:HD21	30:j:727:LEU:HG	1.60	0.80
31:k:116:GLN:CD	31:k:125:ASN:ND2	2.40	0.79
14:N:-51:DG:C2'	14:N:-50:DT:H71	2.14	0.78
21:q:793:VAL:HG11	21:q:830:LEU:HG	1.64	0.78
14:N:-48:DC:H2''	14:N:-47:DC:C6	2.20	0.77
14:N:-37:DG:N2	16:T:37:DC:O2	2.16	0.76
27:f:49:LEU:HD21	30:j:727:LEU:CG	2.14	0.75
2:B:1166:CYS:HB3	2:B:1185:CYS:SG	2.26	0.75
31:k:116:GLN:CD	31:k:125:ASN:HD22	1.95	0.74
30:j:587:ARG:HH12	31:k:287:ARG:HD3	1.52	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:73:LYS:HG2	2:B:125:THR:HG22	1.70	0.74
21:q:390:LEU:HB3	21:q:409:LEU:HD21	1.70	0.73
26:a:105:GLU:OE2	30:j:867:LEU:HD22	1.90	0.71
30:j:587:ARG:HH12	31:k:287:ARG:HD2	1.55	0.71
18:W:524:GLU:O	20:n:232:GLN:NE2	2.23	0.71
14:N:-22:DA:C6	14:N:-21:DA:C6	2.78	0.71
2:B:792:MET:HE2	2:B:857:ARG:HH22	1.54	0.71
1:A:807:ARG:NH1	2:B:724:LYS:O	2.23	0.70
1:A:1207:LYS:O	1:A:1277:ARG:NH2	2.24	0.69
8:H:112:LYS:HG2	8:H:125:GLU:HG3	1.73	0.69
1:A:1262:MET:SD	1:A:1265:ARG:NH2	2.66	0.69
19:m:1160:ASP:O	19:m:1163:ARG:NH1	2.26	0.69
1:A:831:LYS:NZ	1:A:1079:THR:O	2.25	0.69
5:E:60:LEU:O	21:q:915:ARG:NH1	2.23	0.69
2:B:550:PHE:HB3	2:B:593:MET:HE1	1.75	0.69
21:q:531:GLU:O	21:q:535:ASN:N	2.25	0.69
18:W:487:ILE:HD11	18:W:531:ARG:HB2	1.76	0.68
21:q:922:ALA:O	21:q:926:ASN:ND2	2.26	0.68
18:W:303:ILE:HB	20:n:286:ARG:HH22	1.58	0.68
1:A:107:CYS:SG	1:A:172:GLN:NE2	2.66	0.68
21:q:578:GLN:NE2	21:q:582:ASP:OD1	2.26	0.68
21:q:59:ALA:HB1	21:q:63:LEU:HD12	1.77	0.67
22:r:490:VAL:HG22	22:r:495:ARG:HE	1.60	0.67
10:J:47:ARG:NH1	10:J:48:MET:SD	2.67	0.67
2:B:223:SER:O	2:B:252:ARG:NH2	2.27	0.66
9:I:45:ARG:NH2	9:I:47:GLU:OE2	2.29	0.66
22:r:230:ARG:NH1	22:r:292:SER:OG	2.28	0.66
21:q:169:ASP:OD1	21:q:185:LYS:NZ	2.28	0.66
19:m:617:ILE:HG13	19:m:649:LEU:HD11	1.78	0.66
19:m:382:PRO:HG2	19:m:955:ASN:HD22	1.58	0.66
16:T:25:DG:H2'	16:T:26:DG:C8	2.31	0.66
19:m:380:GLU:HG3	19:m:382:PRO:HD2	1.77	0.65
1:A:673:ASP:OD1	1:A:737:ASN:ND2	2.29	0.65
19:m:682:ASP:O	19:m:686:ASN:ND2	2.28	0.65
1:A:887:ILE:O	1:A:945:ARG:NH2	2.30	0.65
2:B:267:TYR:HB2	2:B:348:ILE:HD11	1.77	0.65
2:B:613:ARG:HH21	9:I:62:ILE:HD11	1.61	0.65
18:W:342:GLU:HB3	18:W:351:ARG:HB3	1.79	0.65
3:C:266:ARG:HD2	11:K:84:LYS:HZ1	1.61	0.65
16:T:25:DG:H2'	16:T:26:DG:H8	1.62	0.65
21:q:31:LYS:HB2	21:q:57:GLU:HA	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:x:292:TRP:HA	25:x:295:LYS:HE2	1.79	0.65
1:A:127:ARG:O	1:A:129:ARG:NH1	2.30	0.64
27:b:26:ILE:HG13	27:b:55:ARG:HD3	1.79	0.64
1:A:447:ARG:HB2	1:A:488:MET:HE3	1.77	0.64
20:n:260:MET:HG3	20:n:284:TRP:HZ3	1.63	0.64
17:V:89:ARG:NH1	17:V:109:ASP:OD2	2.31	0.64
18:W:327:ARG:NH2	18:W:441:ASN:O	2.30	0.64
30:j:587:ARG:NH1	31:k:287:ARG:CD	2.60	0.64
19:m:343:ARG:NH1	19:m:347:GLN:OE1	2.31	0.64
25:x:157:ARG:HB3	25:x:161:PRO:HB3	1.78	0.64
27:f:68:ASP:OD2	27:f:93:GLN:NE2	2.30	0.64
2:B:285:PRO:HG2	2:B:288:GLU:HB2	1.80	0.64
19:m:551:ARG:NH2	19:m:689:LYS:O	2.31	0.64
22:r:269:ASP:HB3	22:r:349:LEU:HD21	1.80	0.64
26:a:109:LEU:HD21	30:j:888:THR:HG21	1.80	0.63
2:B:254:ASP:H	2:B:259:ARG:HH21	1.44	0.63
4:D:153:VAL:HG13	4:D:171:LEU:HD23	1.78	0.63
21:q:793:VAL:HG13	21:q:826:ALA:HB1	1.79	0.63
1:A:466:TYR:HB2	1:A:470:ARG:HH22	1.63	0.63
1:A:881:ARG:HH21	1:A:955:ASN:HB3	1.64	0.63
21:q:590:ARG:NH1	21:q:618:THR:OG1	2.31	0.62
16:T:42:DC:OP1	18:W:433:GLN:NE2	2.33	0.62
19:m:434:LEU:HD11	19:m:467:ASP:HB2	1.81	0.62
19:m:1101:ASP:OD1	19:m:1132:GLN:NE2	2.32	0.62
21:q:780:TYR:O	21:q:784:LYS:N	2.31	0.62
21:q:155:TYR:HA	21:q:160:ARG:HD3	1.80	0.62
14:N:-22:DA:N6	14:N:-21:DA:N6	2.47	0.62
23:u:199:LEU:HD11	24:v:211:PHE:HB3	1.81	0.62
27:f:49:LEU:CD2	30:j:727:LEU:HD11	2.29	0.62
1:A:1158:PRO:HA	1:A:1192:PRO:HB3	1.80	0.62
18:W:351:ARG:HA	18:W:429:THR:HA	1.81	0.62
21:q:65:LEU:HD13	24:v:81:ILE:HG12	1.81	0.62
26:a:69:ARG:HB3	27:b:25:ASN:HD22	1.65	0.62
19:m:358:HIS:HB3	19:m:361:GLU:HB2	1.82	0.61
19:m:1221:LEU:HD11	19:m:1233:SER:HB2	1.82	0.61
1:A:1130:ILE:HG12	1:A:1134:LYS:HE2	1.81	0.61
11:K:57:THR:OG1	11:K:76:GLN:OE1	2.17	0.61
23:u:80:TYR:CZ	24:v:356:ASN:HB2	2.36	0.61
19:m:730:ASP:OD1	19:m:733:ARG:NH2	2.34	0.61
21:q:210:PRO:O	21:q:217:ARG:NH2	2.25	0.61
1:A:361:GLU:OE1	1:A:460:ARG:NH2	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1201:ARG:NH2	1:A:1235:ALA:O	2.33	0.61
16:T:-26:DT:H2''	16:T:-25:DA:C8	2.36	0.61
27:f:49:LEU:HD21	30:j:727:LEU:CD1	2.30	0.61
19:m:672:VAL:O	19:m:720:GLN:NE2	2.34	0.60
1:A:39:GLU:OE2	1:A:49:ARG:NH1	2.34	0.60
18:W:784:ASN:HB2	18:W:785:PRO:HD3	1.81	0.60
21:q:348:ASP:HB3	21:q:351:GLN:HB3	1.82	0.60
21:q:708:GLN:OE1	21:q:739:LYS:NZ	2.34	0.60
23:u:108:VAL:HG22	23:u:219:VAL:HB	1.83	0.60
14:N:21:DG:H2''	14:N:22:DT:H5'	1.83	0.60
19:m:421:ASP:OD1	19:m:422:LEU:N	2.34	0.60
1:A:466:TYR:HB2	1:A:470:ARG:NH2	2.16	0.60
19:m:458:ARG:HG3	19:m:459:THR:HG23	1.83	0.60
18:W:527:THR:HA	18:W:530:LEU:HD12	1.84	0.60
19:m:424:TYR:HA	19:m:427:ILE:HG12	1.83	0.60
19:m:607:ILE:HG22	19:m:719:VAL:HG11	1.83	0.60
21:q:253:ILE:HG12	21:q:297:LEU:HD21	1.84	0.60
1:A:149:GLU:HB2	1:A:165:ARG:HD3	1.83	0.60
2:B:235:LEU:HD23	2:B:242:ILE:HG13	1.83	0.60
22:r:408:ASP:OD1	24:v:133:TYR:N	2.32	0.60
2:B:489:ARG:NH2	2:B:533:SER:O	2.35	0.60
14:N:-40:DC:H2''	14:N:-39:DT:H71	1.84	0.59
1:A:22:LEU:HG	2:B:1213:ALA:HB2	1.83	0.59
2:B:10:ASP:HB3	2:B:649:LYS:HG3	1.84	0.59
17:V:57:LEU:HD11	17:V:81:LEU:HD22	1.84	0.59
24:v:312:LYS:HB3	24:v:315:GLU:HG2	1.85	0.59
14:N:-22:DA:N1	14:N:-21:DA:C2	2.71	0.59
18:W:327:ARG:NH1	18:W:335:GLY:O	2.36	0.59
20:n:217:ARG:HG3	20:n:259:VAL:HG21	1.84	0.59
2:B:353:LEU:O	2:B:367:LYS:NZ	2.34	0.59
1:A:85:GLU:O	1:A:274:ASN:ND2	2.33	0.59
3:C:53:ASN:ND2	3:C:59:ASP:OD1	2.24	0.59
19:m:785:ASP:O	19:m:912:GLN:NE2	2.35	0.59
21:q:72:VAL:HG21	24:v:75:LEU:HD13	1.85	0.59
24:v:29:LEU:N	25:x:147:ARG:O	2.35	0.59
1:A:1157:ASP:O	1:A:1243:ARG:NH2	2.29	0.59
31:k:116:GLN:NE2	31:k:125:ASN:ND2	2.47	0.59
2:B:409:LEU:HD23	2:B:450:LEU:HD23	1.85	0.58
2:B:63:GLN:NE2	2:B:70:ASN:OD1	2.35	0.58
7:G:27:ARG:NH1	7:G:54:ILE:O	2.36	0.58
2:B:50:VAL:HG21	2:B:82:ILE:HD11	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:294:CYS:SG	2:B:295:TYR:N	2.76	0.58
17:V:9:GLU:HA	17:V:20:PRO:HA	1.84	0.58
21:q:806:LEU:O	21:q:811:ARG:NH1	2.36	0.58
26:e:54:TYR:O	27:f:40:ARG:NE	2.37	0.58
19:m:570:MET:HA	19:m:577:THR:HG21	1.84	0.58
21:q:690:LYS:NZ	25:x:178:GLU:OE1	2.36	0.58
23:u:191:THR:HG22	23:u:219:VAL:HG22	1.85	0.58
16:T:-6:DT:H2"	16:T:-5:DA:N7	2.18	0.58
21:q:766:MET:HG3	21:q:770:LYS:HE3	1.86	0.58
1:A:677:MET:HG3	2:B:722:THR:HB	1.84	0.58
22:r:194:LYS:HB2	22:r:316:LEU:HD12	1.84	0.58
3:C:38:ALA:HA	3:C:164:ALA:HB3	1.85	0.58
24:v:267:TYR:HB3	24:v:297:TYR:HB3	1.85	0.58
1:A:227:GLU:OE1	1:A:231:ARG:NH1	2.36	0.57
5:E:101:GLU:HG3	5:E:102:LYS:HG2	1.86	0.57
23:u:145:ILE:O	23:u:149:THR:OG1	2.17	0.57
30:j:587:ARG:NH1	31:k:287:ARG:HD3	2.18	0.57
18:W:665:ARG:HB2	18:W:708:ILE:HD11	1.86	0.57
2:B:91:GLU:OE2	2:B:97:HIS:NE2	2.29	0.57
7:G:86:VAL:HG22	7:G:146:LYS:HB2	1.86	0.57
26:a:69:ARG:HB3	27:b:25:ASN:ND2	2.18	0.57
23:u:121:PHE:HB3	23:u:153:ARG:HB3	1.85	0.57
1:A:63:ARG:NH2	15:P:0:G:OP1	2.37	0.57
2:B:928:ARG:NH2	19:m:777:ASP:O	2.36	0.57
18:W:392:ARG:NH1	18:W:398:GLU:OE1	2.36	0.57
24:v:56:LYS:O	24:v:60:ARG:NH2	2.37	0.57
17:V:13:MET:N	17:V:49:CYS:O	2.26	0.57
19:m:245:THR:HA	19:m:248:GLN:HB2	1.86	0.57
1:A:568:LYS:HG2	1:A:569:PRO:HA	1.87	0.57
14:N:5:DT:H2"	14:N:6:DA:N7	2.19	0.57
14:N:7:DC:H2"	14:N:8:DG:C8	2.40	0.57
2:B:290:LEU:HD21	2:B:310:ILE:HD11	1.87	0.56
19:m:300:VAL:O	19:m:304:THR:OG1	2.20	0.56
30:j:609:GLY:HA3	30:j:612:LYS:HD2	1.86	0.56
31:k:141:ASN:ND2	31:k:256:LYS:HD3	2.20	0.56
1:A:999:LEU:O	1:A:1013:GLN:NE2	2.37	0.56
2:B:336:ILE:O	2:B:341:ARG:NH1	2.38	0.56
6:F:103:MET:HE3	7:G:15:PRO:HG2	1.87	0.56
18:W:232:ARG:HH12	18:W:235:LYS:HE3	1.71	0.56
22:r:200:ASP:HB3	22:r:319:VAL:HG11	1.87	0.56
17:V:58:VAL:N	17:V:82:TYR:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:48:PRO:O	8:H:145:ARG:NH1	2.36	0.56
18:W:352:LEU:HD11	18:W:435:LEU:HD11	1.87	0.56
3:C:175:ALA:HB2	10:J:10:CYS:HB2	1.88	0.56
19:m:309:ARG:HH21	19:m:978:CYS:HA	1.69	0.56
19:m:1177:SER:O	19:m:1194:ARG:NH1	2.37	0.56
24:v:316:ASP:HB2	24:v:333:ILE:HB	1.88	0.56
31:k:103:LYS:HE2	31:k:130:PRO:HG3	1.86	0.56
5:E:28:PHE:HB2	5:E:64:THR:HG22	1.88	0.56
29:d:112:THR:O	29:d:116:THR:HG23	2.05	0.56
16:T:-21:DC:H2''	16:T:-20:DC:H5'	1.88	0.56
1:A:1331:TYR:OH	1:A:1354:GLU:OE2	2.21	0.56
5:E:19:LYS:NZ	5:E:33:GLU:O	2.34	0.56
14:N:-22:DA:N6	14:N:-21:DA:N1	2.54	0.56
20:n:163:LEU:HD11	20:n:194:VAL:HG22	1.88	0.56
23:u:209:LEU:HB2	24:v:252:PHE:HB2	1.87	0.55
1:A:149:GLU:O	1:A:165:ARG:NH1	2.38	0.55
19:m:956:LEU:O	19:m:1046:ARG:NH2	2.39	0.55
1:A:916:TYR:OH	1:A:983:LEU:O	2.19	0.55
24:v:54:PHE:O	24:v:58:ASN:N	2.34	0.55
27:b:92:ARG:NH2	29:d:97:LEU:O	2.40	0.55
7:G:151:ARG:HB3	7:G:158:TYR:HB2	1.89	0.55
19:m:529:ILE:HD11	19:m:566:ILE:HG12	1.87	0.55
19:m:956:LEU:HD11	19:m:1138:ILE:HG21	1.88	0.55
21:q:569:ASN:O	21:q:603:LYS:NZ	2.40	0.55
31:k:108:ARG:CZ	31:k:127:ASN:HD22	2.19	0.55
1:A:1452:LEU:HD23	6:F:131:PRO:HA	1.89	0.55
2:B:904:ARG:HH12	2:B:946:ASN:HB2	1.72	0.55
21:q:239:ASN:HA	21:q:242:LYS:HD2	1.89	0.55
19:m:1205:ASP:OD2	19:m:1207:ARG:NH2	2.40	0.55
20:n:229:PRO:O	20:n:234:GLN:NE2	2.37	0.55
1:A:327:ARG:HG3	1:A:1409:VAL:HG21	1.89	0.54
8:H:15:VAL:HG22	8:H:26:ILE:HG22	1.89	0.54
21:q:641:ALA:HB1	21:q:655:LYS:HG3	1.89	0.54
22:r:223:VAL:HG22	22:r:325:GLN:HG2	1.88	0.54
23:u:89:SER:HB3	24:v:365:ARG:HE	1.72	0.54
1:A:1210:THR:HB	1:A:1213:GLN:HG3	1.90	0.54
1:A:807:ARG:HD3	2:B:725:ARG:HA	1.89	0.54
7:G:102:ASP:OD1	7:G:107:ASN:ND2	2.32	0.54
17:V:10:ARG:HA	17:V:52:SER:HA	1.90	0.54
19:m:465:ASP:OD1	19:m:604:ARG:NH1	2.40	0.54
2:B:72:ASN:ND2	2:B:128:ASP:OD1	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:V:15:CYS:HB3	17:V:32:CYS:SG	2.46	0.54
1:A:569:PRO:HD2	8:H:46:MET:HE2	1.89	0.54
2:B:926:GLY:O	19:m:778:ALA:N	2.31	0.54
2:B:1084:GLN:HG2	3:C:201:TRP:CH2	2.41	0.54
19:m:533:VAL:HG22	19:m:589:VAL:HG13	1.90	0.54
8:H:100:VAL:HG22	8:H:115:VAL:HG22	1.89	0.54
11:K:29:ASN:ND2	11:K:78:GLU:O	2.41	0.54
11:K:103:HIS:NE2	11:K:107:GLU:OE2	2.40	0.54
23:u:80:TYR:OH	24:v:352:VAL:O	2.22	0.54
24:v:74:TYR:HE1	24:v:87:LEU:HD12	1.73	0.54
1:A:218:GLU:OE1	1:A:222:ARG:NH1	2.40	0.54
21:q:41:PHE:CG	21:q:70:VAL:HG11	2.42	0.54
18:W:332:LYS:O	18:W:388:ARG:NH1	2.41	0.54
19:m:1024:TYR:CG	19:m:1135:TYR:HE2	2.26	0.54
18:W:451:GLN:NE2	18:W:454:GLU:OE1	2.41	0.53
2:B:301:GLN:O	2:B:304:GLU:HG3	2.08	0.53
8:H:59:LEU:HD23	8:H:139:LEU:HD13	1.91	0.53
21:q:766:MET:HE1	21:q:799:ILE:HG23	1.89	0.53
1:A:533:ARG:HD3	1:A:750:ALA:HB2	1.91	0.53
2:B:59:ASP:HB3	2:B:74:ARG:HG3	1.91	0.53
18:W:325:TYR:OH	18:W:451:GLN:OE1	2.23	0.53
30:j:728:MET:HE3	30:j:752:TYR:CD2	2.44	0.53
1:A:351:ARG:HB2	2:B:1128:LEU:HD21	1.91	0.53
2:B:592:THR:HG23	23:u:226:PHE:CE1	2.44	0.53
2:B:245:MET:HE1	2:B:371:LEU:HD11	1.91	0.53
18:W:220:THR:N	18:W:223:ASP:OD2	2.33	0.53
21:q:170:ASN:HA	21:q:173:LYS:HD2	1.91	0.53
28:c:79:ILE:HG12	28:c:82:HIS:CE1	2.44	0.53
14:N:37:DC:H2''	14:N:38:DG:C8	2.44	0.53
21:q:155:TYR:HB3	21:q:160:ARG:HB2	1.90	0.53
2:B:248:LYS:NZ	2:B:264:THR:OG1	2.42	0.53
5:E:81:PHE:HE1	5:E:110:ILE:HD13	1.74	0.53
19:m:1425:LYS:NZ	19:m:1430:SER:O	2.30	0.53
19:m:236:GLU:OE2	20:n:252:ARG:NH2	2.41	0.53
9:I:17:LYS:N	9:I:26:LEU:O	2.39	0.53
21:q:317:LEU:HD23	22:r:514:LEU:HD12	1.91	0.53
21:q:451:ARG:NH1	24:v:35:GLU:OE1	2.42	0.53
1:A:977:ARG:HD2	1:A:979:LYS:HZ1	1.74	0.52
21:q:218:LEU:HA	21:q:237:TRP:HE1	1.73	0.52
2:B:797:TYR:HE1	2:B:854:LEU:HD13	1.74	0.52
7:G:144:ARG:HB2	7:G:171:ILE:HD13	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:6:U:H2'	15:P:7:C:C6	2.44	0.52
21:q:408:LEU:HD13	24:v:44:LEU:HD22	1.92	0.52
4:D:60:ILE:HG13	7:G:47:THR:HG21	1.90	0.52
19:m:1170:VAL:O	19:m:1215:THR:OG1	2.19	0.52
2:B:906:SER:OG	18:W:781:GLU:OE1	2.24	0.52
4:D:6:SER:HB3	7:G:42:PHE:HZ	1.73	0.52
9:I:104:LEU:O	9:I:107:LYS:NZ	2.39	0.52
17:V:10:ARG:HG2	17:V:52:SER:HB3	1.92	0.52
28:g:83:LEU:O	30:j:865:PHE:CE1	2.63	0.52
2:B:1163:CYS:HB3	2:B:1166:CYS:SG	2.49	0.52
13:M:46:LEU:HD11	13:M:55:SER:HB3	1.90	0.52
26:e:48:LEU:O	26:e:52:ARG:HG3	2.09	0.52
19:m:1056:ARG:HB3	19:m:1076:MET:HB3	1.92	0.52
24:v:262:LYS:HD3	24:v:305:GLN:HE21	1.74	0.52
2:B:904:ARG:NH1	2:B:905:VAL:O	2.43	0.52
14:N:-42:DG:C8	14:N:-41:DT:H71	2.45	0.52
19:m:1047:ILE:HG12	19:m:1127:ILE:HG12	1.91	0.52
27:b:92:ARG:HH12	29:d:98:LEU:HD23	1.74	0.52
5:E:47:ASP:OD2	5:E:53:GLN:NE2	2.19	0.52
22:r:276:PHE:HB2	22:r:279:GLN:HB2	1.91	0.52
24:v:258:ASN:OD1	24:v:261:ASN:N	2.40	0.52
16:T:-14:DA:H2''	16:T:-13:DA:C8	2.45	0.52
24:v:104:PRO:HA	24:v:107:ARG:HD3	1.92	0.52
1:A:801:VAL:HG22	1:A:813:GLU:HB3	1.92	0.51
2:B:936:ASP:OD1	2:B:938:SER:OG	2.26	0.51
10:J:23:ARG:NH2	22:r:399:LYS:HZ1	2.07	0.51
18:W:513:SER:N	18:W:519:ASN:OD1	2.41	0.51
19:m:465:ASP:OD2	19:m:608:ARG:NH2	2.43	0.51
19:m:1121:ARG:HA	19:m:1124:LEU:HD12	1.91	0.51
2:B:83:TYR:HB2	2:B:116:TYR:HB2	1.92	0.51
14:N:-49:DG:H2''	14:N:-48:DC:C5	2.45	0.51
16:T:-12:DC:H2''	16:T:-11:DG:C8	2.45	0.51
18:W:260:TYR:HD1	18:W:276:ALA:HA	1.75	0.51
28:c:88:ARG:NH1	28:c:97:LEU:O	2.31	0.51
27:f:89:ALA:O	27:f:93:GLN:HG2	2.10	0.51
1:A:10:PRO:HG2	2:B:1192:TYR:HD1	1.74	0.51
18:W:563:GLU:HG2	18:W:574:ILE:HG12	1.93	0.51
21:q:308:LYS:NZ	22:r:504:SER:O	2.38	0.51
1:A:771:VAL:HG13	1:A:823:GLU:HG3	1.92	0.51
2:B:74:ARG:HB2	2:B:124:PHE:HB2	1.92	0.51
18:W:334:LYS:N	18:W:388:ARG:HH12	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:q:250:ASN:HA	21:q:253:ILE:HD12	1.91	0.51
24:v:263:TRP:HE1	24:v:356:ASN:HD21	1.59	0.51
28:c:85:LEU:O	28:c:89:ASN:HB2	2.11	0.51
21:q:871:TYR:CZ	21:q:875:ILE:HD11	2.45	0.51
29:d:41:VAL:O	29:d:45:VAL:HG22	2.10	0.51
2:B:547:ILE:HG21	2:B:619:ILE:HG21	1.93	0.51
14:N:-40:DC:H2''	14:N:-39:DT:C7	2.40	0.51
19:m:1046:ARG:HG3	19:m:1135:TYR:HE1	1.76	0.51
21:q:274:THR:HG23	22:r:506:ILE:HG12	1.93	0.51
16:T:-36:DT:H2''	16:T:-35:DA:N7	2.25	0.51
16:T:-10:DC:H2''	16:T:-9:DA:H8	1.75	0.51
24:v:233:GLY:O	24:v:244:ASN:ND2	2.44	0.51
2:B:86:ARG:NH1	22:r:369:GLU:OE2	2.44	0.51
2:B:316:ILE:HG23	2:B:321:VAL:HG23	1.92	0.51
16:T:-44:DA:H2''	16:T:-43:DT:O5'	2.10	0.51
21:q:676:ASN:HA	25:x:156:LEU:HD12	1.93	0.51
24:v:210:VAL:HG13	24:v:334:VAL:HG21	1.92	0.51
2:B:622:ASP:OD1	2:B:623:VAL:N	2.40	0.51
13:M:38:LEU:HA	13:M:45:GLY:HA2	1.91	0.51
16:T:-2:DC:H2''	16:T:-1:DG:H8	1.71	0.51
18:W:494:LEU:HD21	20:n:183:PRO:HG3	1.92	0.51
19:m:995:ILE:HD12	19:m:1010:LEU:HD21	1.92	0.51
20:n:206:SER:O	20:n:210:ASN:ND2	2.44	0.51
23:u:170:ILE:HD11	24:v:200:PHE:HD1	1.76	0.51
1:A:1223:SER:OG	1:A:1224:ASP:N	2.44	0.51
5:E:87:VAL:HG23	5:E:91:THR:HB	1.91	0.51
19:m:1261:ASN:OD1	19:m:1264:ARG:NH2	2.39	0.51
21:q:286:SER:HA	21:q:289:LYS:HD2	1.92	0.51
7:G:119:LEU:HD21	7:G:135:GLU:HB2	1.93	0.50
18:W:644:ASN:ND2	18:W:647:GLN:OE1	2.44	0.50
19:m:1172:VAL:HA	19:m:1182:VAL:HG12	1.93	0.50
28:g:55:LEU:O	28:g:59:THR:HG23	2.11	0.50
5:E:28:PHE:HE2	21:q:915:ARG:HB2	1.75	0.50
18:W:222:ASP:O	18:W:277:ARG:NH2	2.30	0.50
11:K:65:HIS:HB3	11:K:68:PHE:HD2	1.75	0.50
19:m:766:LEU:HD13	19:m:783:PHE:HB2	1.93	0.50
1:A:1153:GLU:OE2	9:I:45:ARG:NH1	2.40	0.50
19:m:338:LEU:HD11	19:m:417:ILE:HD11	1.91	0.50
1:A:669:ASP:OD2	1:A:743:ASN:ND2	2.29	0.50
13:M:33:SER:HA	13:M:50:LYS:HE2	1.93	0.50
18:W:326:VAL:HA	18:W:440:ILE:HD13	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:m:1062:ALA:HB3	19:m:1083:MET:HE1	1.92	0.50
21:q:568:SER:O	21:q:571:ASN:ND2	2.45	0.50
18:W:464:ILE:O	18:W:468:LEU:HG	2.12	0.50
19:m:1027:PHE:HB3	19:m:1134:ARG:HH12	1.76	0.50
27:f:49:LEU:HD21	30:j:727:LEU:HD11	1.93	0.50
1:A:168:CYS:SG	1:A:170:ASN:ND2	2.85	0.50
1:A:543:GLU:OE2	1:A:570:LYS:NZ	2.43	0.50
4:D:105:THR:HG22	7:G:105:PRO:HD3	1.94	0.50
18:W:634:PRO:HA	18:W:637:ILE:HD12	1.94	0.50
21:q:160:ARG:NH2	21:q:163:GLU:OE1	2.44	0.50
21:q:404:GLU:OE1	21:q:404:GLU:N	2.42	0.50
1:A:89:PRO:HB3	1:A:238:THR:HG22	1.92	0.50
21:q:109:PHE:CD1	21:q:130:ALA:HB1	2.46	0.50
21:q:189:LEU:HD22	21:q:194:LYS:HD2	1.94	0.50
2:B:607:SER:HB3	2:B:620:PHE:HB2	1.94	0.50
14:N:38:DG:H4'	28:c:42:ARG:HD3	1.94	0.50
2:B:498:ASP:HB3	14:N:-23:DA:C4	2.47	0.49
17:V:63:ASN:HB3	17:V:75:ASP:HA	1.94	0.49
19:m:840:ASN:O	19:m:844:ASN:ND2	2.44	0.49
22:r:261:LEU:HB3	22:r:266:ASN:HB3	1.94	0.49
27:b:98:TYR:HB3	29:h:58:ILE:HG23	1.94	0.49
26:e:61:LEU:HD12	27:f:37:LEU:HD23	1.94	0.49
1:A:1190:GLN:HA	1:A:1245:ILE:HA	1.94	0.49
2:B:514:LEU:HD22	2:B:626:VAL:HG12	1.94	0.49
27:f:75:HIS:O	29:h:89:ARG:NH1	2.45	0.49
19:m:562:PRO:HG3	19:m:700:TRP:CE3	2.47	0.49
26:a:105:GLU:OE2	30:j:867:LEU:CD2	2.59	0.49
1:A:738:LEU:HD13	1:A:742:ASN:HD22	1.77	0.49
2:B:928:ARG:NH1	19:m:776:GLY:H	2.11	0.49
9:I:29:CYS:CB	9:I:32:CYS:SG	2.99	0.49
19:m:977:VAL:HB	19:m:980:LEU:HD12	1.94	0.49
2:B:58:LEU:O	2:B:75:TYR:N	2.36	0.49
2:B:74:ARG:HH22	2:B:126:SER:HB3	1.77	0.49
2:B:436:ASN:C	2:B:438:ASN:H	2.20	0.49
18:W:590:ILE:O	18:W:593:SER:OG	2.26	0.49
19:m:244:GLY:O	19:m:248:GLN:N	2.44	0.49
21:q:718:HIS:ND1	21:q:733:TYR:OH	2.38	0.49
28:g:79:ILE:HG12	28:g:82:HIS:CE1	2.48	0.49
1:A:119:ASN:OD1	1:A:121:THR:OG1	2.23	0.49
14:N:5:DT:H2''	14:N:6:DA:C8	2.47	0.49
1:A:122:MET:O	1:A:126:ILE:HG12	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:556:MET:HE3	2:B:581:GLY:HA3	1.93	0.49
2:B:610:ARG:NH2	9:I:61:ASP:OD2	2.46	0.49
18:W:704:ARG:NH1	19:m:632:GLU:OE2	2.43	0.49
1:A:321:ARG:NH1	2:B:466:MET:SD	2.86	0.49
9:I:103:CYS:SG	9:I:104:LEU:N	2.86	0.49
19:m:655:LEU:HG	19:m:659:MET:HE3	1.95	0.49
2:B:318:ASP:HB3	2:B:321:VAL:HG22	1.94	0.49
14:N:-45:DG:H2''	14:N:-44:DG:H5'	1.95	0.49
19:m:242:GLY:HA3	20:n:258:LYS:HG2	1.94	0.49
19:m:343:ARG:NH2	19:m:344:ASP:OD1	2.46	0.49
19:m:917:GLU:OE2	19:m:969:TYR:OH	2.24	0.49
19:m:1257:ILE:HG22	19:m:1261:ASN:HD21	1.77	0.49
19:m:1337:GLU:HB2	19:m:1348:VAL:HB	1.95	0.49
31:k:239:ILE:CG2	31:k:246:LEU:HD11	2.43	0.49
2:B:479:TYR:CZ	2:B:1096:ARG:HB3	2.48	0.49
5:E:81:PHE:CE1	5:E:110:ILE:HD13	2.48	0.49
14:N:39:DA:H2''	14:N:40:DC:H5'	1.95	0.49
2:B:766:ARG:HH21	2:B:1020:ARG:HD3	1.78	0.48
16:T:-10:DC:H2''	16:T:-9:DA:C8	2.48	0.48
19:m:770:PHE:HB3	19:m:779:VAL:HG22	1.95	0.48
24:v:36:LYS:HB2	24:v:39:PRO:HD2	1.95	0.48
1:A:1150:SER:OG	1:A:1198:GLU:O	2.32	0.48
3:C:66:LEU:HD11	3:C:155:ILE:HD12	1.95	0.48
18:W:666:GLU:HB2	18:W:671:ARG:HA	1.95	0.48
19:m:1062:ALA:HA	19:m:1103:LEU:HD21	1.95	0.48
20:n:207:ILE:HG23	20:n:212:LEU:HB3	1.94	0.48
22:r:208:ARG:N	22:r:291:ASP:OD1	2.44	0.48
2:B:300:TRP:HA	2:B:303:LEU:HD12	1.94	0.48
21:q:305:TYR:CZ	22:r:512:LEU:HD11	2.48	0.48
27:f:93:GLN:HB2	27:f:95:ARG:HG2	1.95	0.48
1:A:343:GLY:O	2:B:1129:ARG:NH1	2.45	0.48
3:C:88:GLU:HG2	18:W:759:ARG:HD2	1.95	0.48
7:G:112:THR:HA	7:G:115:ILE:HD12	1.95	0.48
9:I:96:ASN:OD1	9:I:97:MET:N	2.46	0.48
19:m:1170:VAL:HG12	19:m:1184:THR:HG22	1.95	0.48
19:m:1365:GLU:O	19:m:1369:ASN:ND2	2.46	0.48
21:q:816:LEU:HD13	21:q:865:ILE:HA	1.95	0.48
30:j:586:ILE:HD12	30:j:628:MET:SD	2.52	0.48
1:A:819:MET:O	1:A:823:GLU:HG2	2.14	0.48
2:B:759:PRO:HD2	2:B:1046:PRO:HB3	1.94	0.48
14:N:-51:DG:H2''	14:N:-50:DT:C7	2.37	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:-2:G:N2	15:P:-1:G:N7	2.61	0.48
19:m:725:GLU:OE2	19:m:728:ARG:NH2	2.45	0.48
20:n:163:LEU:HD22	20:n:197:ILE:HD13	1.96	0.48
21:q:320:LEU:O	21:q:324:GLU:HG2	2.14	0.48
24:v:89:LYS:O	24:v:93:SER:N	2.46	0.48
24:v:304:ASP:OD2	24:v:340:LYS:NZ	2.45	0.48
4:D:157:ILE:HG23	4:D:164:ALA:HB2	1.95	0.48
18:W:603:GLN:HG3	18:W:609:VAL:HG22	1.95	0.48
19:m:933:HIS:HB3	19:m:936:LEU:HD12	1.94	0.48
23:u:202:GLU:HB3	24:v:210:VAL:HB	1.96	0.48
5:E:213:CYS:SG	5:E:214:LEU:N	2.87	0.48
12:L:70:ASP:HB3	18:W:784:ASN:HB3	1.95	0.48
19:m:823:ILE:HB	19:m:873:VAL:HG22	1.95	0.48
19:m:1279:ARG:NH1	19:m:1315:SER:O	2.47	0.48
19:m:1425:LYS:HE3	19:m:1428:PRO:HA	1.96	0.48
28:g:83:LEU:C	30:j:865:PHE:CD1	2.92	0.48
29:h:42:LEU:HD22	29:h:51:ILE:HG13	1.95	0.48
29:d:95:VAL:HG13	29:d:99:LEU:HD12	1.95	0.48
31:k:108:ARG:NH2	31:k:127:ASN:HD22	2.11	0.48
1:A:472:ASN:O	1:A:475:VAL:HG22	2.14	0.48
1:A:673:ASP:OD1	1:A:673:ASP:N	2.44	0.48
1:A:823:GLU:OE1	2:B:506:GLN:NE2	2.46	0.48
2:B:314:PHE:O	2:B:317:GLN:NE2	2.46	0.48
23:u:204:ASN:OD1	23:u:205:GLU:N	2.47	0.48
25:x:311:GLY:HA3	25:x:330:VAL:HG12	1.96	0.48
16:T:37:DC:H2''	16:T:38:DA:C8	2.49	0.48
21:q:312:GLU:O	21:q:316:LYS:HG3	2.14	0.48
21:q:607:LYS:HB2	21:q:610:LEU:HB2	1.96	0.48
22:r:493:ASN:HB2	22:r:502:ILE:HD11	1.96	0.48
24:v:73:ASN:HB3	24:v:76:ARG:HE	1.79	0.48
1:A:106:ILE:HD13	1:A:215:ILE:HD11	1.95	0.47
1:A:486:ASP:OD1	15:P:10:C:O2'	2.20	0.47
5:E:91:THR:HA	5:E:94:ASN:ND2	2.29	0.47
5:E:93:ARG:HA	5:E:122:MET:HE1	1.96	0.47
16:T:-38:DC:H5'	16:T:-38:DC:C6	2.49	0.47
19:m:1003:ALA:O	19:m:1007:THR:HG23	2.14	0.47
21:q:185:LYS:O	21:q:189:LEU:HG	2.14	0.47
1:A:504:GLN:OE1	6:F:90:ARG:NH1	2.38	0.47
1:A:976:ASP:O	1:A:979:LYS:NZ	2.48	0.47
3:C:17:VAL:HG12	3:C:240:ALA:HB1	1.97	0.47
3:C:105:GLU:N	3:C:105:GLU:OE1	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:W:260:TYR:CE1	18:W:277:ARG:HG3	2.49	0.47
19:m:1202:ASP:OD2	19:m:1204:ARG:NE	2.44	0.47
27:b:75:HIS:CD2	29:d:93:THR:HG21	2.49	0.47
1:A:1426:GLY:O	1:A:1430:ASN:ND2	2.40	0.47
15:P:-5:C:H1'	18:W:748:ARG:HD3	1.96	0.47
21:q:710:LEU:HD11	21:q:748:LEU:HD11	1.96	0.47
22:r:366:GLU:O	22:r:369:GLU:HG2	2.14	0.47
28:g:29:ARG:HG3	28:g:32:ARG:HH21	1.79	0.47
28:g:41:GLU:HB2	29:h:84:SER:HB2	1.95	0.47
2:B:303:LEU:O	2:B:307:LYS:HG2	2.15	0.47
13:M:65:GLN:N	13:M:68:ASP:OD2	2.44	0.47
19:m:381:VAL:HG13	19:m:414:LEU:HD22	1.97	0.47
23:u:173:TRP:NE1	23:u:179:SER:OG	2.36	0.47
1:A:363:ASP:HB3	1:A:509:PRO:HD3	1.97	0.47
1:A:983:LEU:HD13	1:A:1041:ARG:HA	1.97	0.47
3:C:4:GLU:HB3	3:C:5:PRO:HD3	1.96	0.47
18:W:599:HIS:HB3	18:W:677:LEU:HD21	1.96	0.47
2:B:101:PRO:HG2	2:B:172:LEU:HD11	1.97	0.47
2:B:365:THR:O	2:B:368:THR:OG1	2.29	0.47
2:B:896:ASP:OD2	12:L:31:TYR:OH	2.32	0.47
17:V:41:SER:HB2	17:V:45:THR:HB	1.96	0.47
19:m:681:VAL:HG13	19:m:708:TRP:HE1	1.78	0.47
19:m:1427:ASN:OD1	19:m:1430:SER:N	2.47	0.47
4:D:139:PRO:HA	4:D:142:ILE:HD12	1.97	0.47
11:K:62:LYS:HE3	11:K:64:GLU:OE2	2.15	0.47
17:V:91:PRO:HD2	17:V:94:ILE:HB	1.95	0.47
21:q:309:GLU:OE1	21:q:311:TYR:OH	2.20	0.47
22:r:206:PHE:HB2	22:r:227:MET:HE1	1.96	0.47
22:r:263:SER:OG	22:r:264:LYS:N	2.47	0.47
24:v:199:HIS:O	24:v:328:ALA:N	2.47	0.47
26:a:93:GLN:O	26:a:97:GLU:HG3	2.15	0.47
30:j:593:PRO:HG2	31:k:177:TYR:CE2	2.48	0.47
2:B:865:ARG:HD3	2:B:871:VAL:HG12	1.95	0.47
7:G:123:PRO:HA	7:G:128:PRO:HB3	1.97	0.47
19:m:1426:LEU:HD13	19:m:1469:ARG:HH21	1.80	0.47
22:r:408:ASP:OD2	24:v:134:VAL:HG23	2.15	0.47
30:j:644:LYS:HE2	30:j:648:GLU:OE2	2.15	0.47
1:A:580:SER:HB3	1:A:612:LYS:HA	1.97	0.47
2:B:273:PRO:HG2	2:B:276:ILE:HD12	1.97	0.47
14:N:-44:DG:OP2	23:u:273:ARG:NH2	2.44	0.47
19:m:306:LEU:HD13	19:m:314:ARG:HH21	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:q:374:ALA:HA	21:q:377:LEU:HD12	1.96	0.47
29:h:89:ARG:O	29:h:93:THR:HG23	2.15	0.47
31:k:116:GLN:OE1	31:k:125:ASN:ND2	2.47	0.47
2:B:220:ALA:O	2:B:252:ARG:NH2	2.47	0.47
2:B:788:ARG:O	2:B:967:ARG:NH1	2.47	0.47
2:B:885:LEU:HD23	2:B:936:ASP:HB2	1.97	0.47
19:m:1002:ARG:HH11	19:m:1052:TYR:HH	1.62	0.47
19:m:1426:LEU:HD21	19:m:1465:MET:HE2	1.97	0.47
1:A:649:ASN:O	1:A:653:VAL:HG23	2.16	0.46
10:J:6:ARG:HD3	10:J:13:VAL:HG22	1.97	0.46
22:r:212:SER:HA	22:r:215:TRP:HD1	1.79	0.46
23:u:170:ILE:HD11	24:v:200:PHE:CD1	2.50	0.46
2:B:421:ILE:HD11	2:B:441:VAL:HG12	1.97	0.46
18:W:491:LEU:HB3	18:W:494:LEU:HD12	1.98	0.46
18:W:666:GLU:HA	18:W:705:VAL:HG12	1.96	0.46
21:q:4:LEU:HB2	24:v:103:HIS:CE1	2.49	0.46
21:q:489:PHE:HE1	21:q:533:VAL:HG21	1.80	0.46
2:B:792:MET:HE2	2:B:857:ARG:NH2	2.28	0.46
14:N:38:DG:H5''	28:c:44:GLY:HA2	1.97	0.46
15:P:-6:A:H2'	15:P:-5:C:O4'	2.15	0.46
18:W:534:PHE:HB3	18:W:554:ILE:HD13	1.97	0.46
19:m:965:VAL:HG22	19:m:989:ILE:HG13	1.96	0.46
23:u:90:LEU:HB2	24:v:362:MET:HE1	1.96	0.46
27:f:75:HIS:HD2	29:h:93:THR:HG21	1.81	0.46
1:A:215:ILE:O	1:A:231:ARG:NH2	2.46	0.46
2:B:497:ARG:NH2	16:T:24:DT:OP2	2.49	0.46
5:E:96:CYS:SG	5:E:126:VAL:HG23	2.56	0.46
16:T:-41:DG:C6	16:T:-40:DG:C6	3.04	0.46
20:n:208:LEU:HD13	20:n:250:HIS:CE1	2.50	0.46
21:q:155:TYR:HB2	21:q:164:ALA:HB2	1.96	0.46
24:v:310:HIS:NE2	24:v:316:ASP:OD2	2.48	0.46
29:d:73:GLU:OE2	29:d:76:ARG:NH1	2.48	0.46
28:g:29:ARG:HG3	28:g:32:ARG:NH2	2.30	0.46
1:A:1192:PRO:HA	1:A:1243:ARG:HH12	1.79	0.46
2:B:1103:ILE:O	2:B:1122:ARG:NH1	2.49	0.46
5:E:98:ARG:NH1	5:E:102:LYS:HG3	2.31	0.46
19:m:380:GLU:HG2	19:m:978:CYS:HB2	1.97	0.46
1:A:564:PRO:HG2	1:A:567:LEU:HD23	1.98	0.46
2:B:463:LYS:NZ	2:B:464:LYS:HE2	2.31	0.46
2:B:505:ARG:NH1	2:B:524:GLN:O	2.32	0.46
2:B:995:ARG:NH1	2:B:997:GLU:OE2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:q:241:LEU:HD11	21:q:252:LYS:HG2	1.98	0.46
21:q:713:PHE:HB3	21:q:736:ALA:HB2	1.97	0.46
22:r:345:MET:O	22:r:348:SER:OG	2.31	0.46
28:c:42:ARG:O	29:d:85:THR:HA	2.16	0.46
31:k:141:ASN:HD21	31:k:256:LYS:HD3	1.80	0.46
2:B:25:PHE:HZ	2:B:534:LEU:HG	1.80	0.46
2:B:266:PRO:HG3	2:B:352:GLU:O	2.16	0.46
2:B:1176:LYS:HZ1	18:W:598:LEU:HB3	1.80	0.46
3:C:21:LEU:HD22	11:K:101:LEU:HD11	1.98	0.46
7:G:51:GLY:HA2	7:G:54:ILE:HD11	1.98	0.46
21:q:320:LEU:HD13	22:r:514:LEU:HD11	1.97	0.46
22:r:346:LYS:O	22:r:350:SER:N	2.48	0.46
27:b:38:ALA:HB1	27:b:43:VAL:HB	1.98	0.46
26:e:82:LEU:HD23	26:e:82:LEU:HA	1.78	0.46
1:A:1065:MET:SD	1:A:1439:MET:HB2	2.56	0.46
2:B:557:GLU:OE2	2:B:584:ARG:NH2	2.49	0.46
6:F:74:ILE:HG23	6:F:78:GLU:HG3	1.97	0.46
21:q:710:LEU:HD13	21:q:740:PHE:HB2	1.97	0.46
26:a:62:ILE:O	26:a:93:GLN:NE2	2.48	0.46
26:e:54:TYR:HB3	27:f:40:ARG:HB2	1.98	0.46
31:k:10:PHE:HB2	31:k:78:ASP:OD1	2.16	0.46
4:D:170:ASN:HB3	4:D:173:ARG:HG2	1.97	0.46
5:E:117:PRO:O	5:E:121:LYS:HG2	2.17	0.46
12:L:49:ARG:HG2	22:r:339:VAL:HG11	1.98	0.46
19:m:561:SER:HA	19:m:696:ILE:HG23	1.97	0.46
21:q:4:LEU:HD22	24:v:105:ASP:HB2	1.96	0.46
21:q:561:ILE:HD12	21:q:579:LEU:HD22	1.98	0.46
22:r:300:ASP:O	22:r:304:ARG:HG2	2.16	0.46
1:A:409:ASP:OD1	1:A:410:ASN:N	2.49	0.45
2:B:27:GLU:OE1	2:B:678:TRP:HB3	2.16	0.45
2:B:318:ASP:OD1	2:B:319:LYS:N	2.48	0.45
2:B:875:GLU:OE2	2:B:915:THR:OG1	2.26	0.45
15:P:2:G:H1	16:T:33:DC:H42	1.63	0.45
16:T:-43:DT:OP1	28:c:17:ARG:HB2	2.17	0.45
18:W:216:LEU:HD22	19:m:229:LEU:HG	1.98	0.45
19:m:387:HIS:NE2	19:m:1021:SER:OG	2.42	0.45
26:e:73:GLU:OE1	27:f:25:ASN:HB2	2.16	0.45
1:A:1061:HIS:O	1:A:1064:GLU:HG2	2.17	0.45
18:W:539:HIS:CE1	18:W:553:LEU:HD21	2.51	0.45
1:A:684:ILE:HG21	1:A:802:GLU:HG3	1.99	0.45
1:A:912:ASP:OD1	1:A:912:ASP:N	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1448:ILE:HD11	1:A:1453:LEU:HD11	1.97	0.45
2:B:322:ALA:O	2:B:326:ILE:HG12	2.15	0.45
19:m:1220:ILE:HA	19:m:1232:LEU:HD23	1.98	0.45
21:q:403:SER:OG	24:v:56:LYS:NZ	2.50	0.45
1:A:1390:HIS:O	1:A:1394:ARG:HD3	2.17	0.45
5:E:46:CYS:HB3	5:E:50:GLY:HA2	1.99	0.45
8:H:110:LYS:HE2	8:H:112:LYS:HE3	1.99	0.45
16:T:32:DA:H1'	16:T:33:DC:H5''	1.98	0.45
19:m:477:GLN:OE1	19:m:477:GLN:N	2.42	0.45
14:N:-22:DA:C6	14:N:-21:DA:N1	2.85	0.45
19:m:1286:PHE:HA	19:m:1308:ILE:HB	1.98	0.45
21:q:107:PHE:O	21:q:111:LEU:HG	2.17	0.45
2:B:250:TYR:HE2	2:B:262:LYS:HB2	1.82	0.45
19:m:1072:ASP:O	19:m:1076:MET:HG2	2.16	0.45
26:a:113:HIS:CG	26:e:126:LEU:HD22	2.51	0.45
30:j:503:ILE:CD1	30:j:907:PRO:HG3	2.47	0.45
14:N:-44:DG:H2''	14:N:-43:DT:H71	1.99	0.45
19:m:1218:ALA:HB1	19:m:1232:LEU:HB3	1.99	0.45
17:V:46:VAL:O	17:V:50:THR:N	2.43	0.45
23:u:106:TRP:CD1	23:u:217:LYS:HB2	2.52	0.45
26:e:106:ASP:OD2	26:e:131:ARG:NH2	2.42	0.45
27:f:64:ASN:HA	27:f:67:ARG:NH1	2.32	0.45
27:f:92:ARG:NH2	29:h:98:LEU:HD13	2.32	0.45
7:G:113:ARG:NH1	18:W:563:GLU:OE1	2.49	0.45
19:m:590:LYS:HD2	19:m:706:ASP:HB2	1.99	0.45
19:m:782:VAL:HG11	19:m:905:ILE:HG13	1.99	0.45
21:q:479:TYR:HD1	24:v:30:LEU:HB3	1.82	0.45
21:q:641:ALA:HB2	21:q:658:GLN:HB2	1.99	0.45
24:v:349:VAL:HA	24:v:352:VAL:HB	1.98	0.45
25:x:173:LEU:HA	25:x:177:LYS:HD2	1.98	0.45
18:W:451:GLN:HG3	18:W:458:THR:HA	1.98	0.45
19:m:521:TYR:HA	19:m:524:ILE:HD12	1.97	0.45
24:v:29:LEU:HB2	25:x:147:ARG:HB3	1.98	0.45
24:v:31:LYS:HA	25:x:147:ARG:HH12	1.82	0.45
2:B:387:ASP:H	9:I:91:ARG:NH2	2.14	0.44
2:B:778:MET:HE2	2:B:1094:ARG:HD3	1.99	0.44
7:G:81:PRO:HG3	7:G:106:LEU:HD22	1.99	0.44
16:T:-29:DC:H2''	16:T:-28:DT:H71	1.99	0.44
19:m:336:GLU:OE1	19:m:458:ARG:NH2	2.50	0.44
19:m:968:PRO:HA	19:m:971:ALA:HB3	1.99	0.44
19:m:1039:MET:SD	19:m:1039:MET:N	2.90	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:640:ASP:OD1	2:B:640:ASP:N	2.50	0.44
14:N:-44:DG:OP2	23:u:277:ARG:NH2	2.44	0.44
14:N:28:DA:H2"	14:N:29:DG:C8	2.53	0.44
19:m:1105:LEU:HD11	19:m:1128:LYS:HE2	1.98	0.44
21:q:868:GLN:O	21:q:872:GLU:HG2	2.17	0.44
30:j:622:SER:CB	30:j:628:MET:HE2	2.48	0.44
1:A:452:HIS:CE1	1:A:454:MET:HB2	2.52	0.44
1:A:880:GLU:O	1:A:957:PRO:HA	2.18	0.44
3:C:79:MET:HE1	3:C:96:VAL:HG23	2.00	0.44
16:T:-10:DC:H5"	31:k:234:ARG:HB3	2.00	0.44
18:W:763:TYR:HB3	18:W:766:LYS:HD3	2.00	0.44
19:m:603:ILE:HD13	19:m:708:TRP:HZ3	1.82	0.44
30:j:738:PRO:CG	30:j:745:LYS:HE2	2.48	0.44
1:A:779:GLY:HA3	2:B:509:ASN:HB2	1.99	0.44
1:A:1041:ARG:O	1:A:1044:PHE:N	2.50	0.44
9:I:100:PHE:HB3	9:I:109:THR:HG23	1.99	0.44
19:m:640:TYR:HB3	19:m:1256:ASP:HB3	2.00	0.44
19:m:685:TYR:O	19:m:689:LYS:N	2.41	0.44
21:q:40:ASP:CG	21:q:42:ASN:HD22	2.25	0.44
21:q:178:ASN:HA	24:v:91:PHE:CE2	2.52	0.44
21:q:489:PHE:CE1	21:q:533:VAL:HG21	2.51	0.44
23:u:117:ASN:HB3	23:u:151:ARG:HG2	2.00	0.44
25:x:314:PHE:HD2	25:x:335:ILE:HD11	1.82	0.44
28:g:83:LEU:O	30:j:865:PHE:CD1	2.71	0.44
2:B:221:ALA:O	2:B:223:SER:N	2.46	0.44
3:C:258:VAL:HG21	11:K:42:LEU:HD21	2.00	0.44
17:V:78:GLN:OE1	17:V:79:PRO:HD2	2.16	0.44
19:m:536:ILE:HG12	19:m:700:TRP:CZ3	2.53	0.44
24:v:307:PHE:HE1	24:v:335:GLY:HA3	1.83	0.44
31:k:223:VAL:HG23	31:k:308:VAL:HG11	2.00	0.44
1:A:958:LEU:HD13	1:A:1023:LEU:HD22	1.99	0.44
1:A:975:LEU:HD13	1:A:1039:LEU:HA	1.99	0.44
2:B:254:ASP:H	2:B:259:ARG:NH2	2.13	0.44
2:B:1050:LEU:HD12	24:v:127:PHE:CG	2.52	0.44
19:m:654:ASP:OD2	19:m:933:HIS:NE2	2.50	0.44
19:m:1358:ASP:OD1	19:m:1361:GLU:N	2.33	0.44
21:q:357:LYS:NZ	21:q:361:ASP:OD1	2.50	0.44
21:q:435:GLN:HG3	21:q:441:ILE:HD11	1.98	0.44
1:A:948:VAL:O	5:E:200:ARG:NH1	2.48	0.44
2:B:886:LYS:HG2	2:B:890:TYR:OH	2.18	0.44
3:C:15:ASP:OD1	3:C:15:ASP:N	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:11:LEU:HD21	5:E:57:MET:HE1	2.00	0.44
11:K:56:VAL:HG22	11:K:77:THR:HG22	2.00	0.44
29:h:105:LYS:HB2	29:h:105:LYS:HE3	1.84	0.44
1:A:100:LYS:NZ	1:A:104:GLU:OE2	2.49	0.44
14:N:-22:DA:H61	16:T:22:DT:H3	1.65	0.44
19:m:1029:PRO:O	19:m:1033:ARG:NH1	2.50	0.44
30:j:730:ILE:HG21	30:j:750:GLN:HE21	1.83	0.44
2:B:691:ASP:OD1	2:B:691:ASP:N	2.41	0.44
4:D:88:GLU:HA	4:D:91:LYS:HE3	2.00	0.44
21:q:215:ASP:OD1	21:q:217:ARG:NH1	2.47	0.44
21:q:559:ARG:NH2	24:v:24:PRO:O	2.51	0.44
5:E:99:ILE:HG13	5:E:131:ILE:HD11	2.00	0.43
10:J:63:ASN:OD1	10:J:64:PRO:HD2	2.18	0.43
19:m:305:ASP:OD1	19:m:1014:THR:OG1	2.33	0.43
19:m:999:LEU:HD23	19:m:1025:ILE:HD11	1.99	0.43
20:n:200:ARG:HG2	20:n:202:ASN:OD1	2.18	0.43
21:q:217:ARG:HA	21:q:220:ILE:HD12	2.00	0.43
27:f:49:LEU:CD2	30:j:727:LEU:CD1	2.94	0.43
14:N:-47:DC:H2''	14:N:-46:DT:C5	2.53	0.43
28:c:50:TYR:O	28:c:54:VAL:HG23	2.18	0.43
19:m:735:LEU:HB3	19:m:937:LEU:HD21	1.99	0.43
19:m:955:ASN:HD21	19:m:978:CYS:HB3	1.83	0.43
21:q:53:LEU:O	21:q:57:GLU:HG2	2.19	0.43
21:q:511:VAL:HG11	21:q:519:LEU:HD12	2.01	0.43
22:r:370:GLU:HG3	23:u:251:VAL:HA	2.01	0.43
23:u:116:ILE:HD13	23:u:150:VAL:HB	1.99	0.43
26:e:60:LEU:HD22	26:e:93:GLN:HG2	2.00	0.43
2:B:257:THR:OG1	2:B:258:GLY:N	2.50	0.43
17:V:67:TRP:NE1	18:W:217:LEU:O	2.51	0.43
19:m:622:THR:O	19:m:626:LYS:N	2.41	0.43
20:n:157:ASP:HA	20:n:210:ASN:HD21	1.83	0.43
20:n:167:MET:HE3	20:n:219:TRP:CD2	2.53	0.43
20:n:195:LYS:HE3	20:n:199:LEU:HD11	2.00	0.43
29:h:51:ILE:HG22	29:h:52:SER:O	2.18	0.43
1:A:636:ARG:HH12	1:A:878:GLN:CD	2.25	0.43
1:A:889:GLY:O	1:A:941:ARG:NH2	2.51	0.43
1:A:1389:ARG:O	1:A:1393:ASN:HB2	2.18	0.43
2:B:733:SER:HB3	2:B:736:HIS:CE1	2.54	0.43
8:H:25:ARG:HD3	8:H:41:ASP:OD1	2.18	0.43
14:N:1:DC:H2''	14:N:2:DG:C8	2.54	0.43
14:N:3:DC:H2''	14:N:4:DG:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:W:344:LEU:HD12	18:W:349:GLU:HB2	1.99	0.43
19:m:1309:ARG:NH2	19:m:1319:THR:HG21	2.34	0.43
23:u:83:GLY:HA2	24:v:358:ALA:HB3	2.01	0.43
25:x:226:LYS:HB2	25:x:248:LEU:HD21	2.00	0.43
2:B:330:GLY:HA3	2:B:344:TYR:HE2	1.84	0.43
7:G:115:ILE:HG23	7:G:163:ILE:HD11	2.01	0.43
18:W:250:ARG:NH2	18:W:284:ASP:OD2	2.50	0.43
21:q:261:ASP:O	21:q:265:ASN:ND2	2.36	0.43
21:q:261:ASP:HB2	24:v:58:ASN:ND2	2.34	0.43
21:q:611:GLU:HG2	21:q:615:HIS:CD2	2.54	0.43
24:v:41:LYS:HB3	24:v:45:LYS:HE3	2.01	0.43
1:A:38:PRO:HA	1:A:271:LEU:HD23	2.01	0.43
1:A:1343:GLY:HA2	5:E:182:PRO:HD2	2.00	0.43
16:T:-38:DC:H5'	16:T:-38:DC:H6	1.84	0.43
19:m:960:ASP:HB2	19:m:1024:TYR:CZ	2.54	0.43
22:r:206:PHE:H	22:r:229:LEU:HD21	1.82	0.43
1:A:318:LYS:HE3	16:T:35:DC:N3	2.34	0.43
1:A:844:LYS:HD2	1:A:844:LYS:HA	1.79	0.43
21:q:122:ARG:HB2	21:q:126:PHE:CE2	2.54	0.43
28:g:31:HIS:CE1	28:g:35:ARG:HH12	2.37	0.43
1:A:252:ALA:HA	1:A:258:GLN:HA	2.00	0.43
1:A:815:PHE:O	1:A:819:MET:HG3	2.19	0.43
2:B:283:VAL:HG13	2:B:283:VAL:O	2.18	0.43
3:C:248:ILE:HG21	11:K:102:ASP:HB2	2.01	0.43
18:W:322:ARG:NE	18:W:343:VAL:H	2.17	0.43
26:a:65:LEU:HG	26:a:69:ARG:NH1	2.34	0.43
28:g:31:HIS:CD2	28:g:35:ARG:HH12	2.37	0.43
1:A:203:LEU:HD23	1:A:203:LEU:HA	1.90	0.43
2:B:262:LYS:HB3	2:B:271:ASP:HB3	2.01	0.43
21:q:526:ASN:O	21:q:530:VAL:HG23	2.18	0.43
22:r:245:VAL:HG23	22:r:298:GLU:HG2	2.01	0.43
29:h:76:ARG:HG2	29:h:80:TYR:CE2	2.54	0.43
30:j:593:PRO:HG2	31:k:177:TYR:HE2	1.83	0.43
1:A:473:LEU:HD21	2:B:835:GLN:HB2	2.00	0.42
20:n:208:LEU:HD22	20:n:250:HIS:CD2	2.54	0.42
25:x:222:MET:HE3	25:x:222:MET:HB3	1.84	0.42
27:b:32:PRO:O	27:b:36:ARG:HG3	2.18	0.42
2:B:862:GLN:HB3	2:B:963:PHE:HD1	1.85	0.42
5:E:104:PHE:HZ	21:q:925:TRP:HZ3	1.66	0.42
16:T:-43:DT:OP1	28:c:17:ARG:N	2.23	0.42
18:W:490:GLU:CD	20:n:229:PRO:HA	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:W:543:ILE:HD11	18:W:581:ILE:HG13	2.01	0.42
28:c:100:VAL:HG12	27:f:96:THR:HB	2.00	0.42
29:h:108:VAL:O	29:h:112:THR:HG23	2.19	0.42
2:B:592:THR:HG23	23:u:226:PHE:CZ	2.54	0.42
3:C:36:MET:HE3	3:C:176:ILE:HD13	2.01	0.42
6:F:103:MET:HE1	7:G:65:SER:O	2.19	0.42
7:G:11:LEU:HD23	7:G:11:LEU:HA	1.94	0.42
12:L:60:LYS:HB3	12:L:60:LYS:HE3	1.87	0.42
14:N:33:DT:H2''	14:N:34:DC:C6	2.53	0.42
17:V:12:CYS:HA	17:V:50:THR:HA	2.01	0.42
19:m:1399:SER:HA	19:m:1407:HIS:CE1	2.54	0.42
22:r:277:PRO:HB2	22:r:305:GLU:HB3	2.00	0.42
27:f:38:ALA:HB1	27:f:43:VAL:HB	2.02	0.42
5:E:42:ARG:HG3	5:E:46:CYS:SG	2.59	0.42
18:W:468:LEU:HD11	19:m:283:VAL:HG13	2.01	0.42
19:m:538:ASN:HB3	19:m:541:GLN:HB2	2.01	0.42
1:A:1221:VAL:HG21	1:A:1274:ILE:HD12	2.01	0.42
2:B:279:ARG:NH1	2:B:316:ILE:O	2.52	0.42
2:B:756:ILE:HG12	2:B:770:GLN:HG2	2.02	0.42
14:N:-43:DT:H71	14:N:-43:DT:OP2	2.20	0.42
14:N:11:DC:H2''	14:N:12:DG:C8	2.55	0.42
19:m:1005:LEU:HA	19:m:1010:LEU:HD12	2.01	0.42
2:B:299:ASP:OD2	2:B:385:ARG:NH1	2.30	0.42
2:B:837:ASP:CG	2:B:1020:ARG:HH22	2.28	0.42
4:D:54:SER:OG	4:D:121:CYS:SG	2.61	0.42
5:E:176:ARG:HD3	5:E:214:LEU:HD11	2.02	0.42
16:T:-5:DA:H2''	16:T:-4:DC:C5	2.54	0.42
17:V:13:MET:HE2	17:V:51:SER:HB2	2.01	0.42
18:W:518:ILE:HD13	20:n:185:ILE:HD13	2.00	0.42
19:m:708:TRP:CZ2	19:m:712:LEU:HD21	2.54	0.42
19:m:955:ASN:ND2	19:m:978:CYS:HB3	2.35	0.42
24:v:352:VAL:O	24:v:355:THR:OG1	2.37	0.42
1:A:421:ARG:HB3	1:A:424:ASP:HB2	2.01	0.42
2:B:479:TYR:CE2	2:B:778:MET:HG2	2.55	0.42
2:B:793:ALA:HB3	2:B:856:PHE:HB2	2.02	0.42
2:B:807:GLN:OE1	24:v:129:ARG:NH1	2.51	0.42
2:B:1156:ASP:O	2:B:1197:PRO:HA	2.19	0.42
18:W:539:HIS:HB2	18:W:584:THR:HA	2.02	0.42
19:m:306:LEU:O	19:m:311:GLN:NE2	2.51	0.42
20:n:161:GLN:O	20:n:165:LEU:HG	2.19	0.42
21:q:830:LEU:HD22	21:q:846:LEU:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:v:202:PRO:HG2	24:v:382:TYR:OH	2.19	0.42
31:k:258:GLN:OE1	31:k:260:LYS:HE2	2.20	0.42
1:A:1201:ARG:HA	1:A:1238:LEU:HD12	2.01	0.42
14:N:-51:DG:C2'	14:N:-50:DT:C7	2.93	0.42
19:m:750:ALA:HB2	19:m:1139:ARG:HB2	2.02	0.42
19:m:821:ASP:HA	19:m:850:ILE:HD13	2.01	0.42
19:m:1246:LEU:HB3	19:m:1248:VAL:HG23	2.01	0.42
21:q:29:PRO:HA	21:q:36:VAL:HG12	2.02	0.42
21:q:189:LEU:HB3	21:q:194:LYS:HB2	2.01	0.42
31:k:257:ILE:HD11	31:k:286:LEU:HD11	2.01	0.42
31:k:269:PRO:HB3	31:k:302:ARG:HH21	1.85	0.42
2:B:279:ARG:NH2	2:B:286:ASP:OD1	2.51	0.42
2:B:606:VAL:HG22	2:B:621:THR:HG22	2.02	0.42
3:C:74:GLU:O	3:C:246:ARG:NH2	2.39	0.42
9:I:29:CYS:SG	9:I:30:ARG:N	2.92	0.42
19:m:656:TYR:CE2	19:m:660:ILE:HD11	2.54	0.42
19:m:1000:VAL:HB	19:m:1004:HIS:ND1	2.35	0.42
21:q:841:TYR:HB2	21:q:846:LEU:HD21	2.01	0.42
2:B:85:SER:OG	2:B:114:PRO:HD2	2.19	0.42
2:B:1152:MET:HE3	2:B:1152:MET:HB3	1.91	0.42
6:F:99:LEU:HG	6:F:103:MET:HE2	2.02	0.42
7:G:165:GLU:H	7:G:168:LEU:HD12	1.85	0.42
18:W:329:LYS:HB2	18:W:434:ASN:HA	2.02	0.42
18:W:480:PRO:HA	18:W:498:VAL:HG12	2.02	0.42
19:m:597:LEU:HD13	19:m:708:TRP:HE3	1.84	0.42
20:n:177:ASN:HD21	20:n:186:PHE:HE2	1.67	0.42
21:q:562:TYR:CZ	21:q:566:LEU:HD11	2.55	0.42
28:c:61:GLU:O	28:c:65:LEU:HG	2.20	0.42
1:A:691:VAL:HG11	1:A:795:PRO:HG3	2.02	0.41
6:F:97:ARG:HA	6:F:97:ARG:HD2	1.78	0.41
14:N:-21:DA:H61	16:T:21:DT:H3	1.68	0.41
15:P:8:C:C2	16:T:28:DG:C2	3.08	0.41
17:V:80:GLY:HA2	18:W:244:LEU:HD21	2.02	0.41
21:q:189:LEU:HD13	21:q:197:GLN:HB2	2.02	0.41
21:q:284:LEU:HD11	21:q:297:LEU:HD22	2.01	0.41
21:q:638:ALA:HB1	21:q:642:ARG:HH22	1.84	0.41
5:E:36:GLN:HE21	5:E:36:GLN:HB3	1.69	0.41
11:K:25:SER:O	25:x:307:GLN:NE2	2.53	0.41
18:W:422:TYR:HB3	18:W:427:TYR:CE1	2.55	0.41
19:m:423:ASP:O	19:m:427:ILE:HG23	2.21	0.41
19:m:773:GLY:N	19:m:777:ASP:OD2	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:m:1002:ARG:NH2	19:m:1023:VAL:O	2.47	0.41
22:r:208:ARG:HA	22:r:211:MET:HE3	2.02	0.41
22:r:432:LEU:HD12	22:r:433:ARG:HD2	2.02	0.41
25:x:345:GLN:O	25:x:349:GLN:HG3	2.20	0.41
8:H:6:PHE:HB3	8:H:59:LEU:HB2	2.03	0.41
13:M:39:ASP:HB3	13:M:44:ILE:HG13	2.03	0.41
15:P:-5:C:C6	18:W:748:ARG:HB2	2.55	0.41
18:W:349:GLU:HA	18:W:431:ARG:HA	2.02	0.41
19:m:1279:ARG:NH2	19:m:1344:ALA:O	2.51	0.41
21:q:9:TYR:OH	24:v:106:ASP:OD2	2.20	0.41
27:f:46:ILE:HG22	27:f:47:SER:O	2.20	0.41
1:A:1210:THR:HG22	1:A:1212:ASN:H	1.86	0.41
2:B:33:GLN:HG2	2:B:34:GLN:N	2.36	0.41
2:B:1153:GLU:OE1	2:B:1153:GLU:N	2.53	0.41
21:q:66:SER:O	21:q:70:VAL:HG23	2.20	0.41
21:q:673:ASP:OD1	25:x:157:ARG:NH2	2.47	0.41
22:r:408:ASP:OD2	24:v:133:TYR:HB2	2.20	0.41
1:A:473:LEU:CD2	2:B:835:GLN:HB2	2.50	0.41
1:A:914:ILE:HG13	1:A:917:ALA:HB2	2.01	0.41
2:B:293:ILE:HD13	2:B:375:VAL:HG11	2.02	0.41
2:B:764:SER:OG	2:B:765:PRO:HD3	2.19	0.41
14:N:31:DT:H2''	14:N:32:DG:C8	2.55	0.41
16:T:-34:DG:OP1	29:d:84:SER:N	2.46	0.41
19:m:780:LEU:HD12	19:m:780:LEU:HA	1.90	0.41
23:u:168:SER:HB2	24:v:200:PHE:HB3	2.02	0.41
26:a:73:GLU:OE1	27:b:25:ASN:HB2	2.20	0.41
1:A:1218:ILE:HG12	1:A:1270:MET:HE1	2.03	0.41
9:I:94:ASP:OD1	9:I:94:ASP:N	2.49	0.41
16:T:29:DA:H2'	16:T:30:DA:C8	2.56	0.41
19:m:283:VAL:HG12	19:m:284:PHE:CD1	2.56	0.41
19:m:764:ARG:N	19:m:821:ASP:OD2	2.48	0.41
19:m:1175:VAL:HA	19:m:1180:MET:HG3	2.03	0.41
19:m:1255:TRP:HD1	19:m:1257:ILE:HG12	1.85	0.41
21:q:278:ARG:NH2	22:r:507:ASP:O	2.53	0.41
28:g:21:ALA:HB2	29:h:118:TYR:HB2	2.02	0.41
2:B:350:GLN:HE22	2:B:361:GLU:HG2	1.86	0.41
2:B:763:GLN:HG2	2:B:765:PRO:HD2	2.01	0.41
3:C:135:ARG:HE	3:C:136:ASP:CG	2.29	0.41
3:C:149:ASN:OD1	3:C:149:ASN:N	2.54	0.41
5:E:3:ASP:HA	5:E:6:ARG:HG2	2.01	0.41
18:W:614:ARG:NH2	18:W:616:GLN:HE21	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:m:313:TYR:HB3	19:m:422:LEU:HD11	2.03	0.41
19:m:1092:ASP:OD1	19:m:1092:ASP:N	2.48	0.41
20:n:171:ALA:HB2	20:n:219:TRP:CD1	2.55	0.41
22:r:316:LEU:HD23	22:r:316:LEU:HA	1.83	0.41
24:v:205:SER:O	24:v:379:ARG:NH2	2.50	0.41
1:A:109:ASN:HB2	1:A:168:CYS:SG	2.61	0.41
2:B:575:VAL:O	2:B:578:VAL:HG22	2.20	0.41
9:I:29:CYS:HB3	9:I:32:CYS:SG	2.59	0.41
21:q:350:VAL:HA	21:q:380:ARG:NH1	2.36	0.41
21:q:410:GLY:HA2	21:q:423:ALA:HA	2.03	0.41
21:q:905:ARG:NE	21:q:909:GLU:OE2	2.30	0.41
25:x:301:ASP:OD1	25:x:303:GLN:NE2	2.54	0.41
27:f:51:TYR:O	27:f:55:ARG:HG3	2.20	0.41
1:A:3:GLN:OE1	1:A:3:GLN:N	2.46	0.41
1:A:471:LEU:HD23	1:A:475:VAL:HG23	2.03	0.41
1:A:701:ASN:CG	9:I:96:ASN:HD21	2.26	0.41
1:A:1295:PRO:HD3	1:A:1301:TYR:CE1	2.56	0.41
1:A:1314:ILE:HB	1:A:1337:GLU:OE1	2.21	0.41
2:B:439:LEU:HD11	23:u:264:LEU:HB3	2.03	0.41
2:B:766:ARG:HA	2:B:766:ARG:HD3	1.79	0.41
3:C:259:LEU:HD13	11:K:91:CYS:HB2	2.03	0.41
4:D:53:LEU:HD13	4:D:147:SER:HB3	2.02	0.41
14:N:-42:DG:C8	14:N:-41:DT:C7	3.04	0.41
14:N:20:DG:C2	14:N:21:DG:C4	3.09	0.41
14:N:36:DA:H2''	14:N:37:DC:C6	2.55	0.41
15:P:-1:G:H2'	15:P:0:G:H8	1.86	0.41
16:T:16:DA:H2''	16:T:17:DA:H8	1.86	0.41
18:W:540:VAL:HG11	18:W:554:ILE:HD11	2.02	0.41
19:m:314:ARG:HD3	19:m:320:TYR:CE1	2.56	0.41
19:m:674:LEU:HD12	19:m:675:PRO:HD2	2.02	0.41
19:m:743:PHE:O	19:m:747:ILE:HG12	2.20	0.41
20:n:241:ILE:HG23	20:n:246:ILE:HD12	2.03	0.41
21:q:861:LEU:HD23	21:q:861:LEU:HA	1.95	0.41
22:r:275:ALA:HB2	22:r:281:GLU:HA	2.01	0.41
23:u:121:PHE:CE2	23:u:123:PRO:HG3	2.56	0.41
2:B:71:ILE:HG12	2:B:127:ILE:HG22	2.02	0.41
2:B:86:ARG:NH2	22:r:369:GLU:OE1	2.54	0.41
2:B:285:PRO:HB2	9:I:11:ASN:HD22	1.86	0.41
2:B:425:MET:O	2:B:429:ILE:HG13	2.21	0.41
8:H:8:ASP:OD1	8:H:9:ILE:N	2.48	0.41
16:T:-30:DG:H2''	16:T:-29:DC:OP2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:636:ARG:HG3	1:A:880:GLU:OE2	2.21	0.40
1:A:945:ARG:HG3	1:A:1301:TYR:OH	2.21	0.40
8:H:38:LEU:HD13	8:H:124:LEU:HD13	2.03	0.40
18:W:492:ASN:OD1	18:W:493:HIS:N	2.54	0.40
19:m:588:ALA:HA	19:m:591:GLN:HG2	2.03	0.40
21:q:756:TRP:HB3	21:q:772:ALA:HB2	2.03	0.40
28:c:29:ARG:NH1	29:d:32:GLU:HB3	2.36	0.40
30:j:730:ILE:CG2	30:j:750:GLN:HE21	2.34	0.40
1:A:883:THR:HA	1:A:954:HIS:O	2.21	0.40
1:A:985:ILE:N	1:A:986:PRO:HD2	2.36	0.40
2:B:632:ILE:HD11	2:B:688:GLU:HB3	2.03	0.40
3:C:146:LYS:NZ	10:J:57:GLU:OE2	2.55	0.40
14:N:-22:DA:N6	16:T:22:DT:H3	2.20	0.40
14:N:21:DG:H2'	14:N:22:DT:C6	2.56	0.40
16:T:-27:DC:H2''	16:T:-26:DT:H71	2.03	0.40
16:T:-14:DA:H2''	16:T:-13:DA:H8	1.84	0.40
19:m:524:ILE:O	19:m:530:TYR:HB2	2.22	0.40
19:m:884:TYR:CE1	19:m:890:SER:HB3	2.56	0.40
19:m:1136:ARG:HD2	19:m:1137:GLU:O	2.21	0.40
19:m:1268:ILE:O	19:m:1272:ARG:HG3	2.21	0.40
21:q:341:ARG:NH2	24:v:47:SER:O	2.54	0.40
21:q:520:SER:O	21:q:524:HIS:ND1	2.52	0.40
22:r:432:LEU:HD11	22:r:433:ARG:NH1	2.36	0.40
24:v:136:ASP:N	24:v:136:ASP:OD1	2.54	0.40
27:b:39:ARG:NH1	27:b:43:VAL:O	2.53	0.40
28:c:20:ARG:HD3	29:d:122:LYS:O	2.22	0.40
1:A:390:THR:O	1:A:394:ARG:HG2	2.21	0.40
2:B:1174:ASN:OD1	2:B:1177:LYS:HB2	2.21	0.40
3:C:262:LEU:HD11	11:K:87:LEU:HD23	2.03	0.40
11:K:55:ASP:OD2	11:K:89:ARG:NH2	2.54	0.40
18:W:524:GLU:HB2	20:n:232:GLN:HE22	1.85	0.40
19:m:586:TYR:CE2	19:m:703:LEU:HD12	2.56	0.40
19:m:709:LYS:HA	19:m:712:LEU:HD12	2.02	0.40
21:q:609:ASP:O	21:q:613:GLN:HG3	2.20	0.40
1:A:995:LEU:HD22	1:A:1048:LEU:HD22	2.03	0.40
1:A:1150:SER:OG	1:A:1198:GLU:OE1	2.29	0.40
3:C:251:LEU:HD12	3:C:251:LEU:HA	1.92	0.40
12:L:66:MET:HE1	18:W:804:TRP:HZ2	1.86	0.40
14:N:18:DG:H2''	14:N:19:DC:C6	2.57	0.40
16:T:20:DT:C6	16:T:21:DT:H73	2.56	0.40
19:m:397:ASN:HB3	19:m:401:ASN:HA	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:m:1290:LYS:H	19:m:1293:GLU:HB2	1.87	0.40
26:a:65:LEU:HB3	26:a:66:PRO:HD3	2.03	0.40
26:a:118:THR:HA	27:b:45:ARG:O	2.21	0.40
27:b:97:LEU:HD21	27:b:100:PHE:CD2	2.56	0.40
31:k:157:LYS:HD3	31:k:166:THR:HG21	2.02	0.40
1:A:231:ARG:HB3	1:A:234:TRP:CD2	2.56	0.40
3:C:135:ARG:NE	3:C:136:ASP:OD2	2.50	0.40
12:L:33:CYS:SG	12:L:34:GLY:N	2.95	0.40
21:q:224:PHE:CD1	21:q:229:ASN:HB3	2.56	0.40
21:q:341:ARG:NH2	24:v:50:LEU:HB2	2.36	0.40
26:e:65:LEU:HD23	26:e:65:LEU:HA	1.97	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	1392/1743 (80%)	1353 (97%)	38 (3%)	1 (0%)	48	79
2	B	1154/1227 (94%)	1118 (97%)	36 (3%)	0	100	100
3	C	261/304 (86%)	259 (99%)	2 (1%)	0	100	100
4	D	170/186 (91%)	167 (98%)	3 (2%)	0	100	100
5	E	211/214 (99%)	205 (97%)	6 (3%)	0	100	100
6	F	82/155 (53%)	80 (98%)	2 (2%)	0	100	100
7	G	169/171 (99%)	167 (99%)	2 (1%)	0	100	100
8	H	129/145 (89%)	125 (97%)	4 (3%)	0	100	100
9	I	109/115 (95%)	106 (97%)	3 (3%)	0	100	100
10	J	65/72 (90%)	65 (100%)	0	0	100	100
11	K	111/118 (94%)	110 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	L	43/72 (60%)	41 (95%)	2 (5%)	0	100	100
13	M	62/113 (55%)	62 (100%)	0	0	100	100
17	V	104/108 (96%)	100 (96%)	4 (4%)	0	100	100
18	W	527/911 (58%)	508 (96%)	19 (4%)	0	100	100
19	m	1179/1503 (78%)	1158 (98%)	21 (2%)	0	100	100
20	n	137/417 (33%)	136 (99%)	1 (1%)	0	100	100
21	q	928/1084 (86%)	922 (99%)	6 (1%)	0	100	100
22	r	260/544 (48%)	254 (98%)	6 (2%)	0	100	100
23	u	206/459 (45%)	204 (99%)	2 (1%)	0	100	100
24	v	341/396 (86%)	327 (96%)	14 (4%)	0	100	100
25	x	201/395 (51%)	200 (100%)	1 (0%)	0	100	100
26	a	74/139 (53%)	70 (95%)	4 (5%)	0	100	100
26	e	91/139 (66%)	90 (99%)	1 (1%)	0	100	100
27	b	81/106 (76%)	78 (96%)	3 (4%)	0	100	100
27	f	76/106 (72%)	73 (96%)	3 (4%)	0	100	100
28	c	101/133 (76%)	100 (99%)	1 (1%)	0	100	100
28	g	68/133 (51%)	66 (97%)	2 (3%)	0	100	100
29	d	93/129 (72%)	89 (96%)	4 (4%)	0	100	100
29	h	91/129 (70%)	90 (99%)	1 (1%)	0	100	100
30	j	467/956 (49%)	454 (97%)	12 (3%)	1 (0%)	43	73
31	k	423/531 (80%)	410 (97%)	12 (3%)	1 (0%)	43	73
All	All	9406/12953 (73%)	9187 (98%)	216 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	960	VAL
30	j	543	LYS
31	k	147	ARG

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	1219/1528 (80%)	1219 (100%)	0	100	100
2	B	1018/1077 (94%)	1018 (100%)	0	100	100
3	C	236/264 (89%)	236 (100%)	0	100	100
4	D	149/160 (93%)	149 (100%)	0	100	100
5	E	196/197 (100%)	196 (100%)	0	100	100
6	F	75/137 (55%)	75 (100%)	0	100	100
7	G	148/148 (100%)	148 (100%)	0	100	100
8	H	120/130 (92%)	120 (100%)	0	100	100
9	I	106/109 (97%)	106 (100%)	0	100	100
10	J	61/66 (92%)	61 (100%)	0	100	100
11	K	104/109 (95%)	104 (100%)	0	100	100
12	L	38/56 (68%)	38 (100%)	0	100	100
13	M	61/99 (62%)	61 (100%)	0	100	100
17	V	90/92 (98%)	90 (100%)	0	100	100
18	W	480/796 (60%)	480 (100%)	0	100	100
19	m	1087/1354 (80%)	1087 (100%)	0	100	100
20	n	125/361 (35%)	125 (100%)	0	100	100
21	q	824/962 (86%)	824 (100%)	0	100	100
22	r	239/485 (49%)	239 (100%)	0	100	100
23	u	192/406 (47%)	192 (100%)	0	100	100
24	v	325/369 (88%)	325 (100%)	0	100	100
25	x	190/354 (54%)	190 (100%)	0	100	100
26	a	64/112 (57%)	64 (100%)	0	100	100
26	e	79/112 (70%)	79 (100%)	0	100	100
27	b	68/81 (84%)	68 (100%)	0	100	100
27	f	63/81 (78%)	63 (100%)	0	100	100
28	c	82/102 (80%)	82 (100%)	0	100	100
28	g	54/102 (53%)	54 (100%)	0	100	100
29	d	81/107 (76%)	81 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	h	79/107 (74%)	79 (100%)	0	100	100
30	j	422/864 (49%)	422 (100%)	0	100	100
31	k	392/474 (83%)	392 (100%)	0	100	100
All	All	8467/11401 (74%)	8467 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (79) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	109	ASN
1	A	260	GLN
1	A	265	HIS
1	A	291	ASN
1	A	295	GLN
1	A	364	GLN
1	A	491	HIS
1	A	1021	GLN
1	A	1056	GLN
2	B	157	HIS
2	B	215	GLN
2	B	350	GLN
2	B	388	GLN
2	B	438	ASN
2	B	736	HIS
2	B	887	HIS
2	B	1074	ASN
3	C	11	ASN
3	C	13	GLN
3	C	25	ASN
3	C	150	HIS
4	D	130	ASN
5	E	31	GLN
5	E	36	GLN
7	G	24	GLN
8	H	44	ASN
9	I	11	ASN
10	J	52	HIS
13	M	32	ASN
18	W	242	GLN
18	W	283	ASN

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Mol	Chain	Res	Type
18	W	558	ASN
19	m	299	ASN
19	m	402	ASN
19	m	428	HIS
19	m	896	ASN
19	m	1116	HIS
19	m	1288	ASN
19	m	1338	ASN
19	m	1407	HIS
20	n	156	GLN
20	n	177	ASN
20	n	232	GLN
21	q	105	HIS
21	q	187	GLN
21	q	319	ASN
21	q	397	ASN
21	q	398	GLN
21	q	438	ASN
21	q	615	HIS
21	q	625	HIS
21	q	658	GLN
21	q	781	GLN
22	r	336	ASN
22	r	416	ASN
22	r	493	ASN
23	u	93	HIS
23	u	138	GLN
24	v	229	ASN
24	v	283	ASN
24	v	381	GLN
25	x	251	GLN
27	b	25	ASN
27	b	75	HIS
29	d	64	ASN
30	j	578	ASN
30	j	750	GLN
30	j	841	GLN
30	j	887	ASN
30	j	916	ASN
31	k	93	GLN
31	k	125	ASN
31	k	127	ASN

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Mol	Chain	Res	Type
31	k	143	ASN
31	k	148	HIS
31	k	163	HIS
31	k	303	ASN
31	k	362	GLN
31	k	420	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	P	19/19 (100%)	6 (31%)	1 (5%)

All (6) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	P	-6	A
15	P	-5	C
15	P	-4	C
15	P	-3	C
15	P	-2	G
15	P	1	U

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
15	P	-7	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 11 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

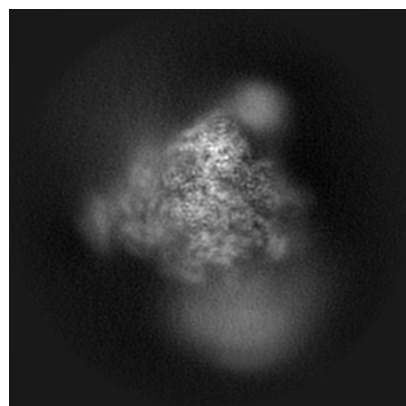
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33436. These allow visual inspection of the internal detail of the map and identification of artifacts.

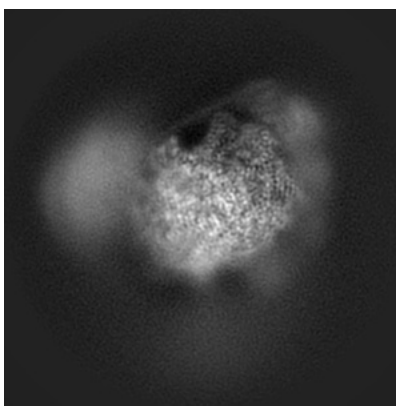
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

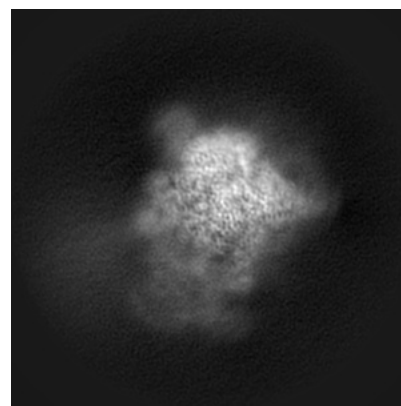
6.1.1 Primary map



X

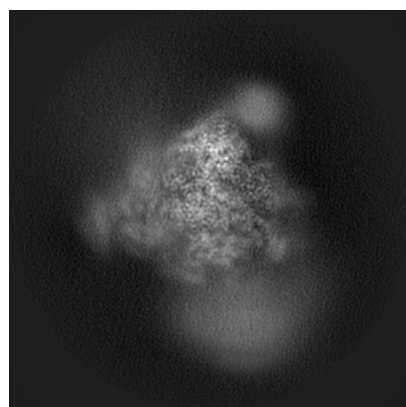


Y

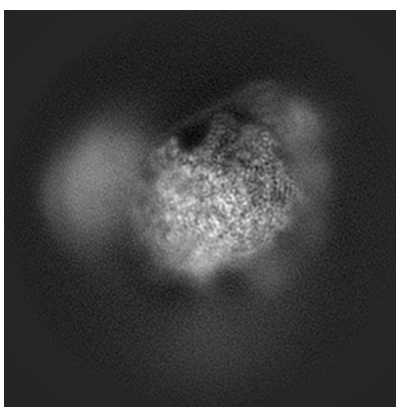


Z

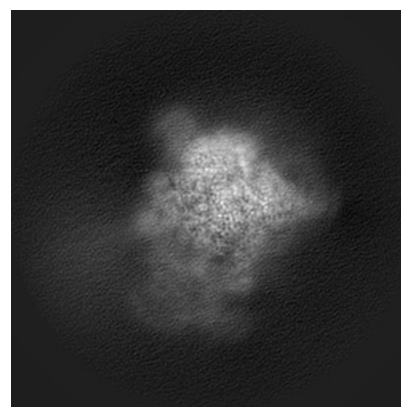
6.1.2 Raw map



X



Y

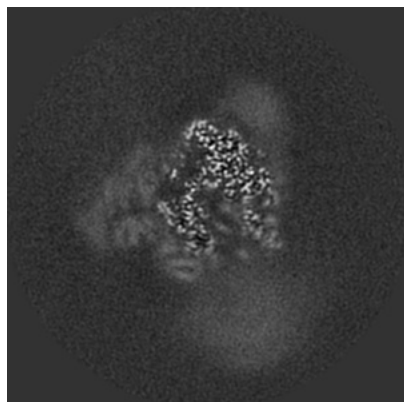


Z

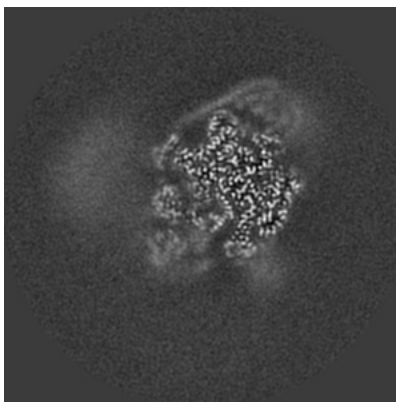
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

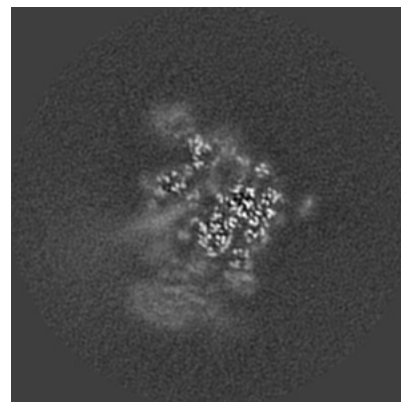
6.2.1 Primary map



X Index: 120

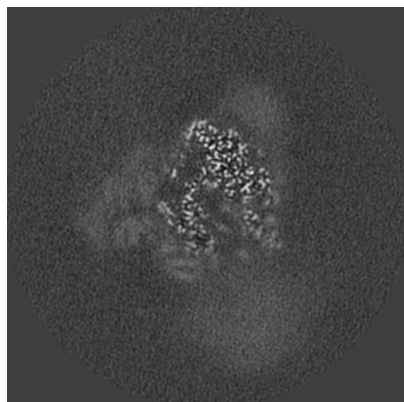


Y Index: 120

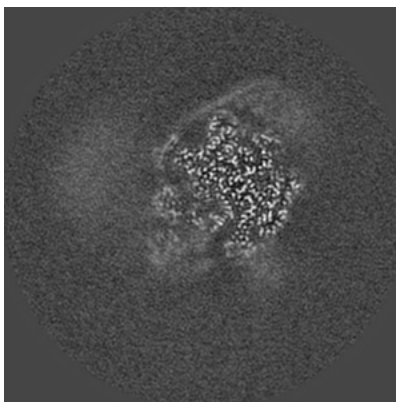


Z Index: 120

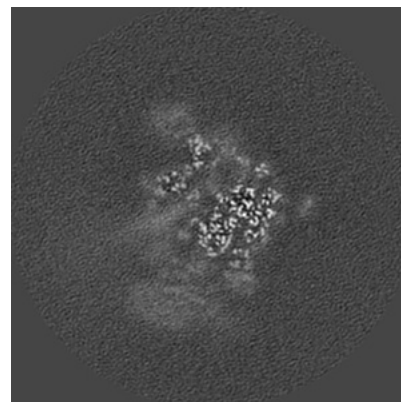
6.2.2 Raw map



X Index: 120



Y Index: 120

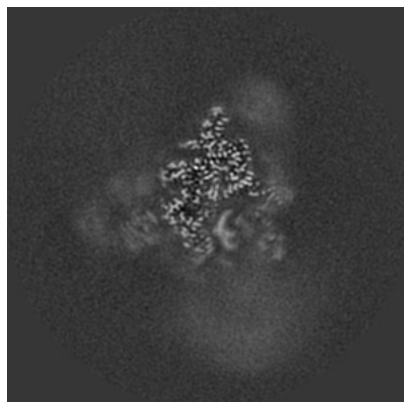


Z Index: 120

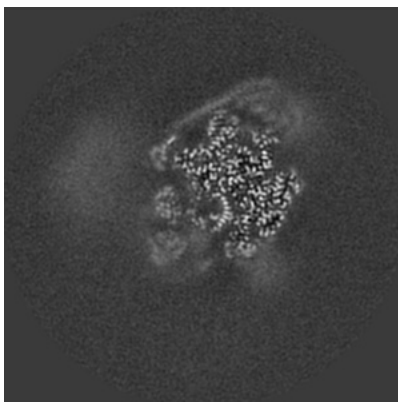
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

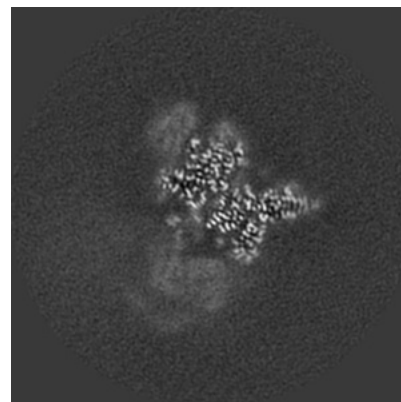
6.3.1 Primary map



X Index: 127

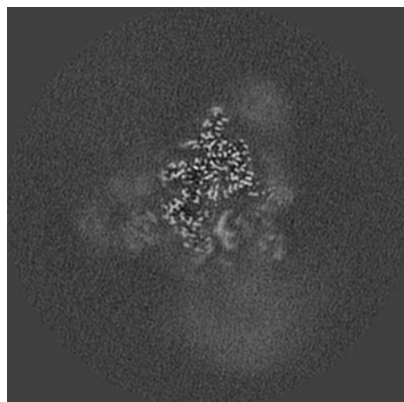


Y Index: 121

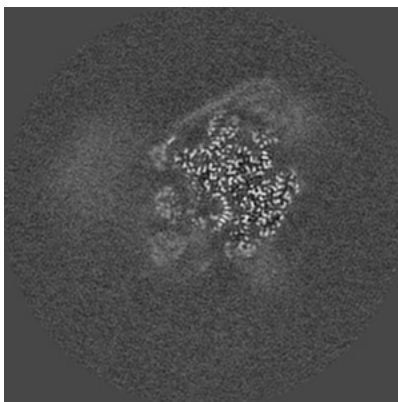


Z Index: 129

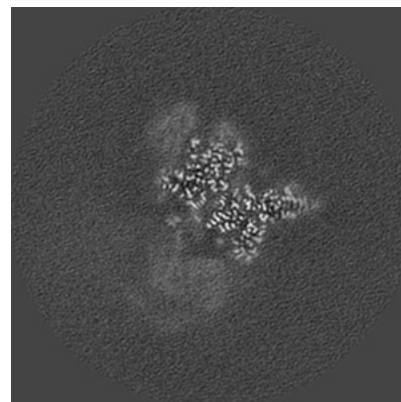
6.3.2 Raw map



X Index: 127



Y Index: 121

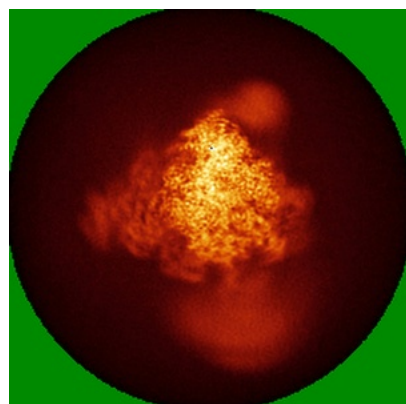


Z Index: 129

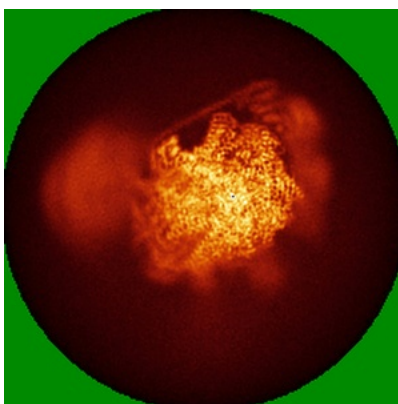
The images above show the largest variance slices of the map in three orthogonal directions.

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

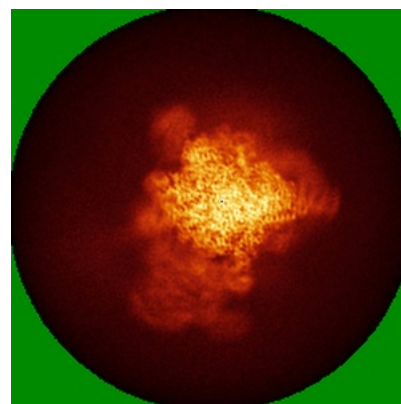
6.4.1 Primary map



X

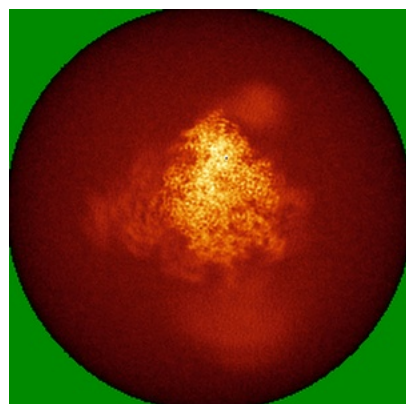


Y

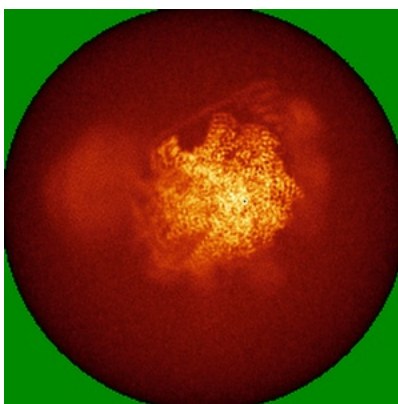


Z

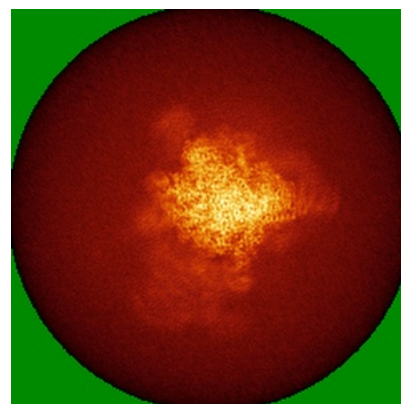
6.4.2 Raw map



X



Y

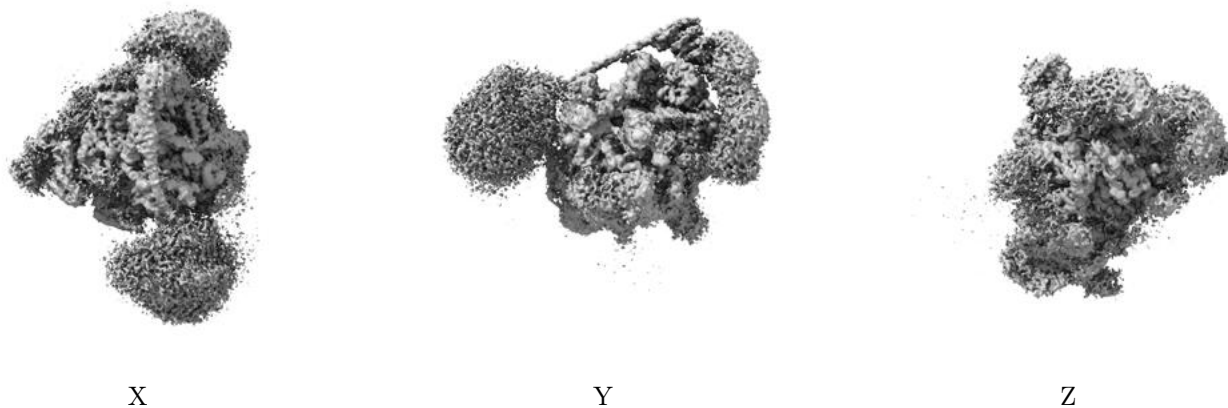


Z

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.

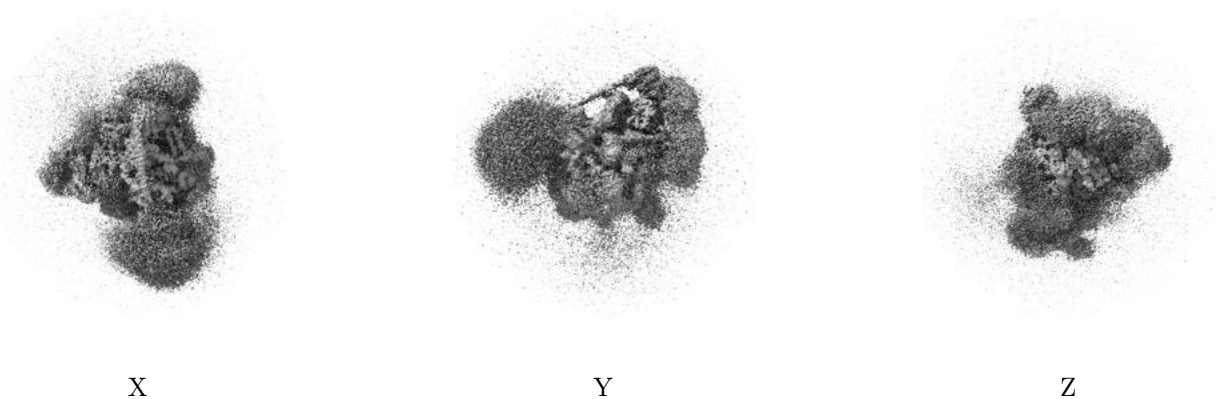
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.013. 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.

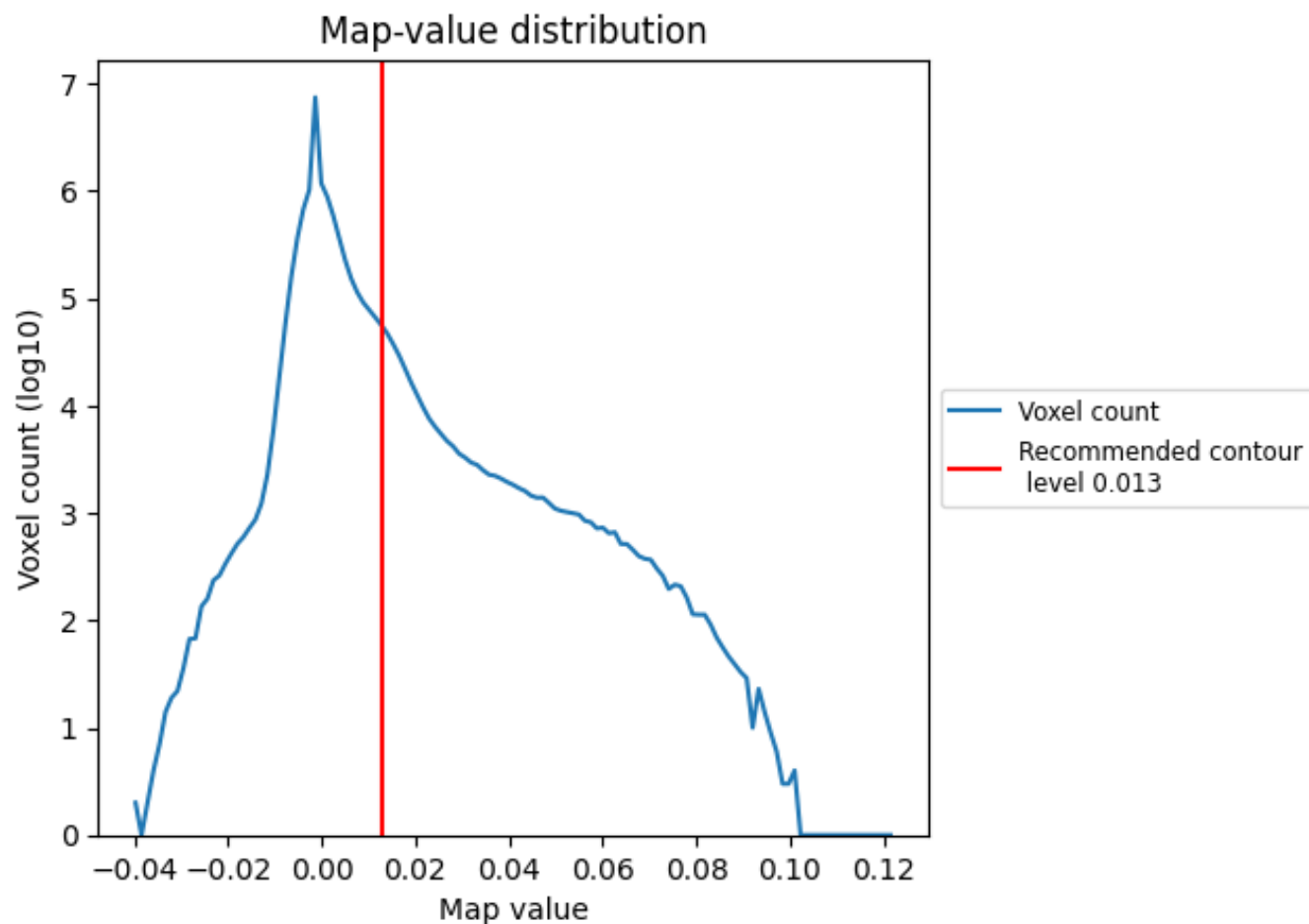
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

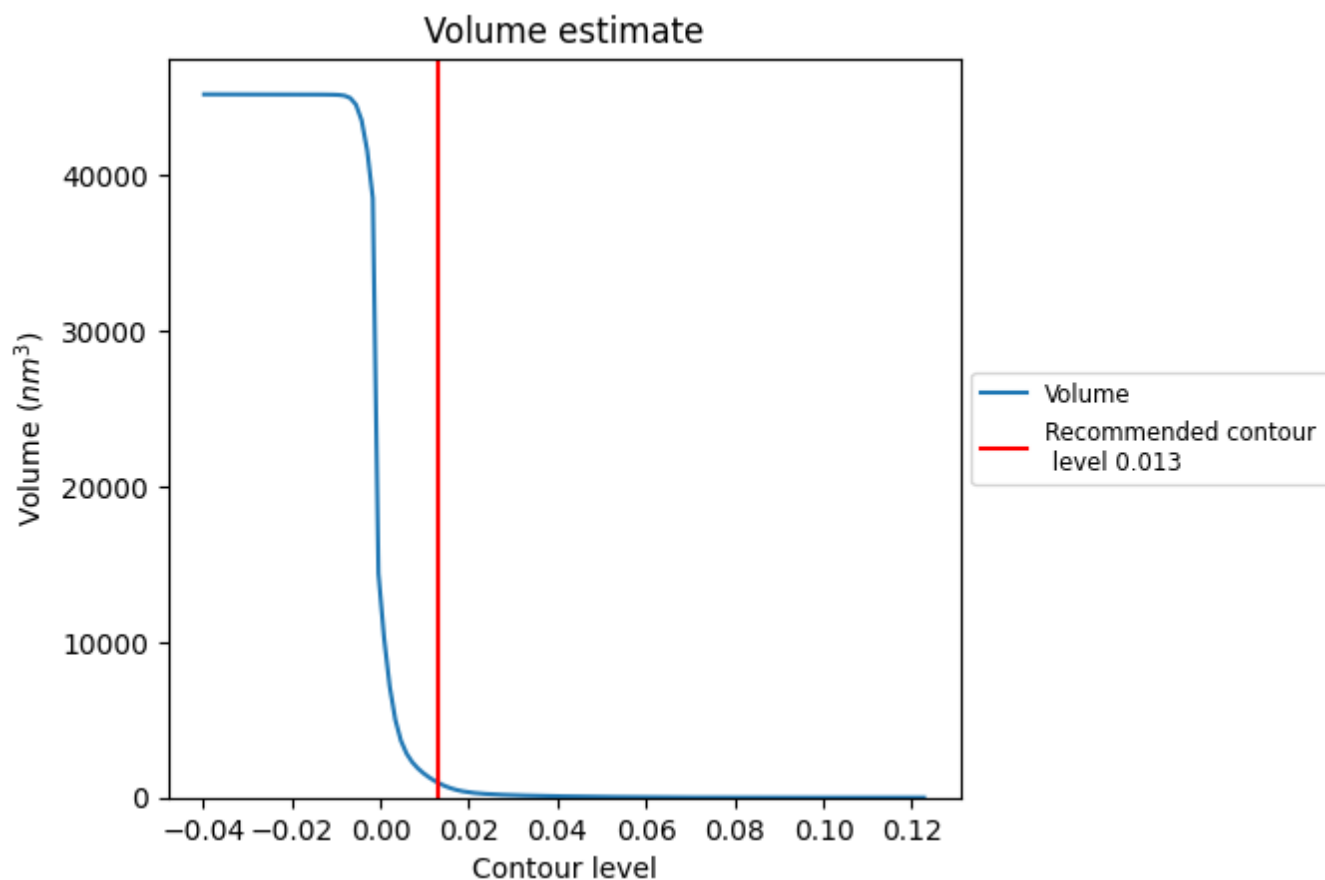
This section contains the results of statistical analysis of the map.

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.

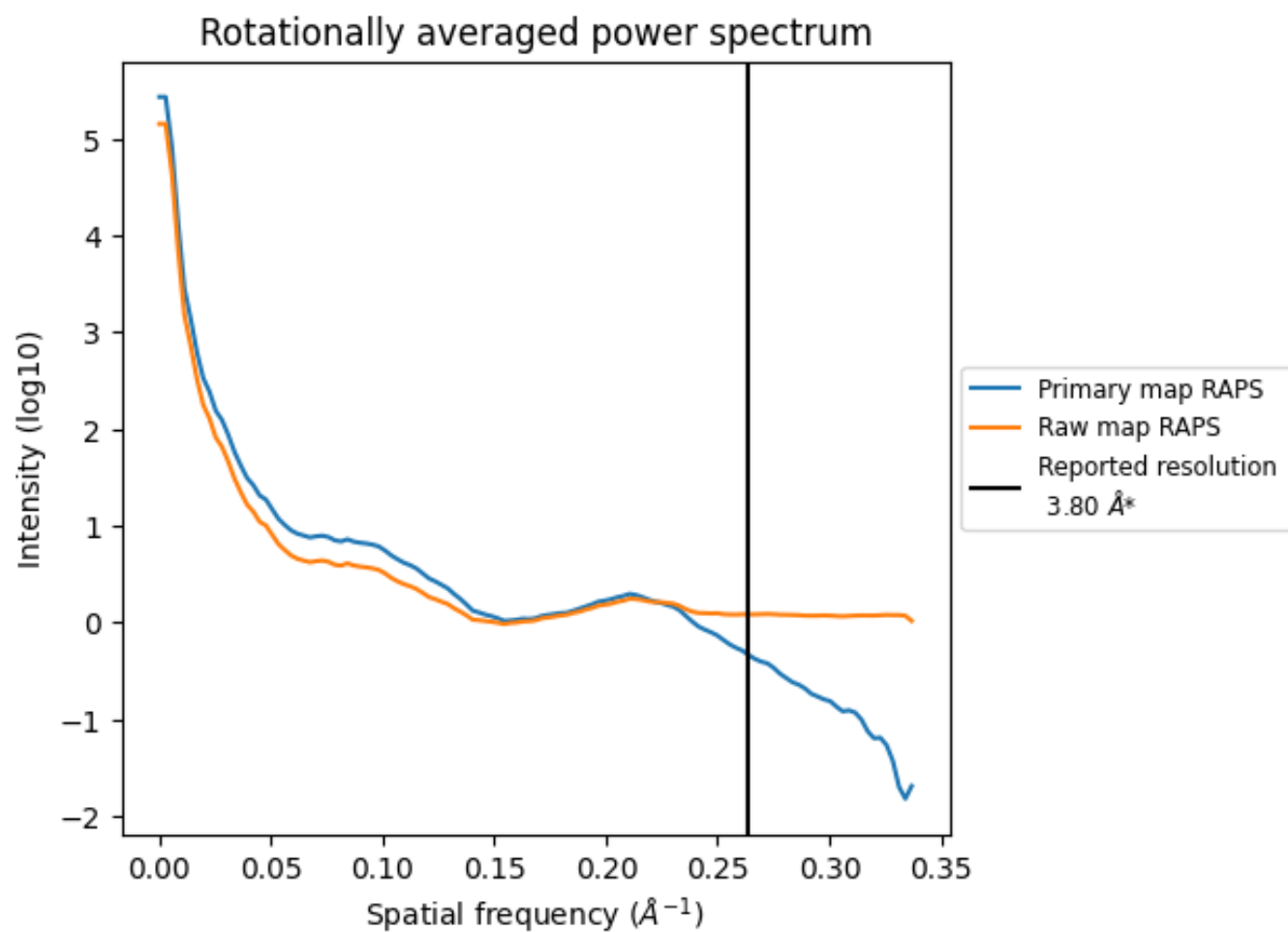
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 964 nm³; this corresponds to an approximate mass of 871 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 ⓘ

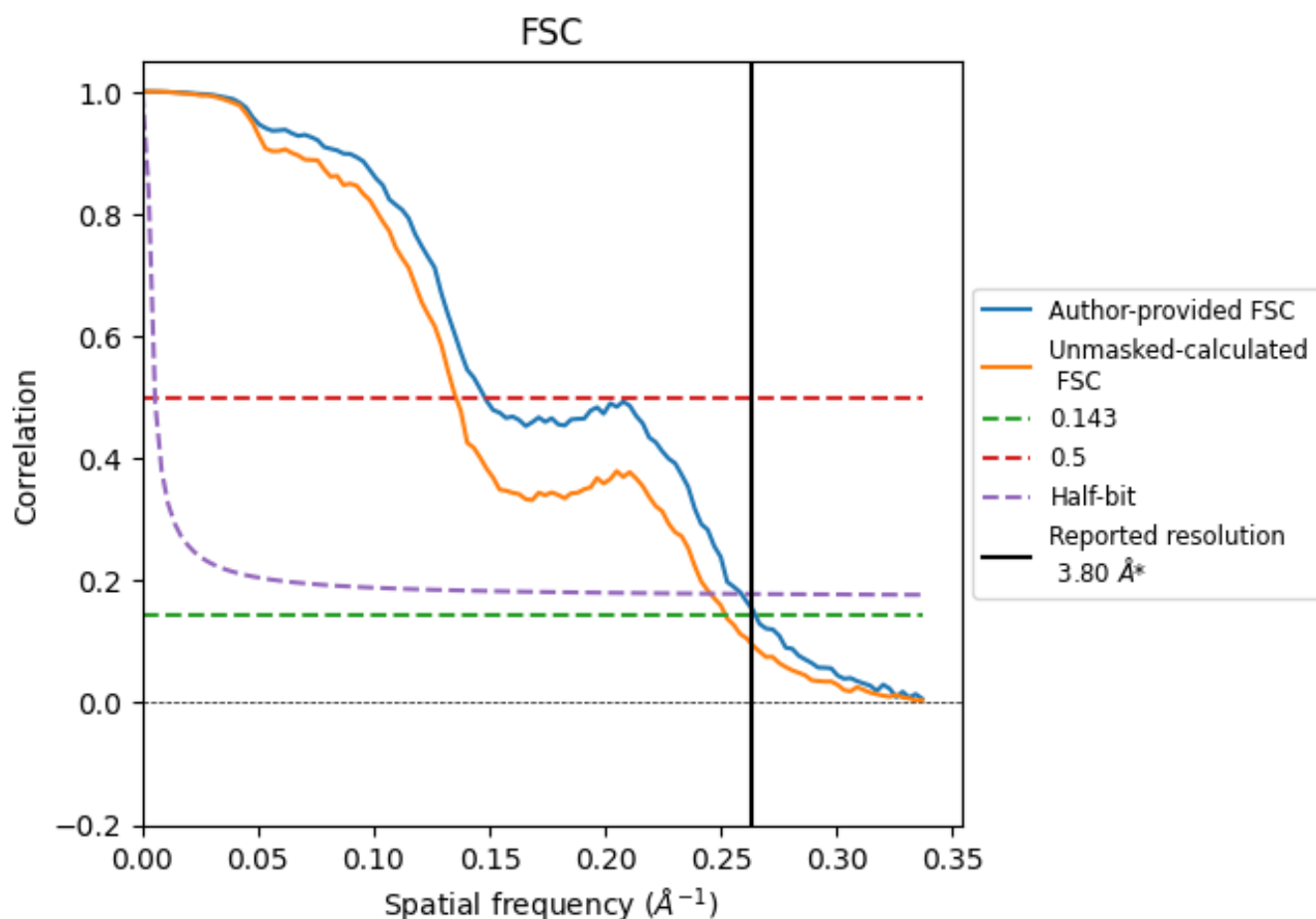


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

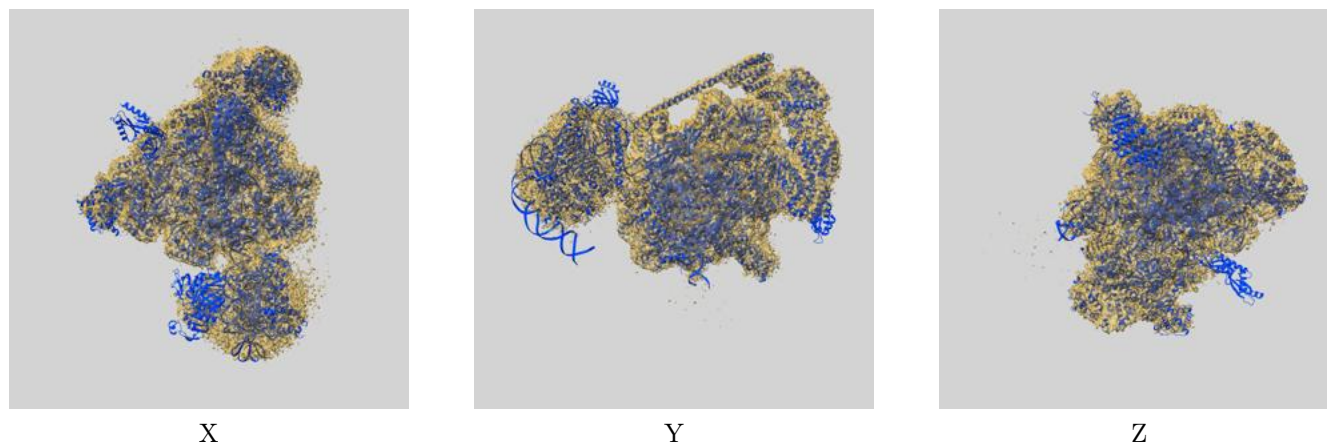
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.78	6.76	3.86
Unmasked-calculated*	3.97	7.39	4.07

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

9 Map-model fit [i](#)

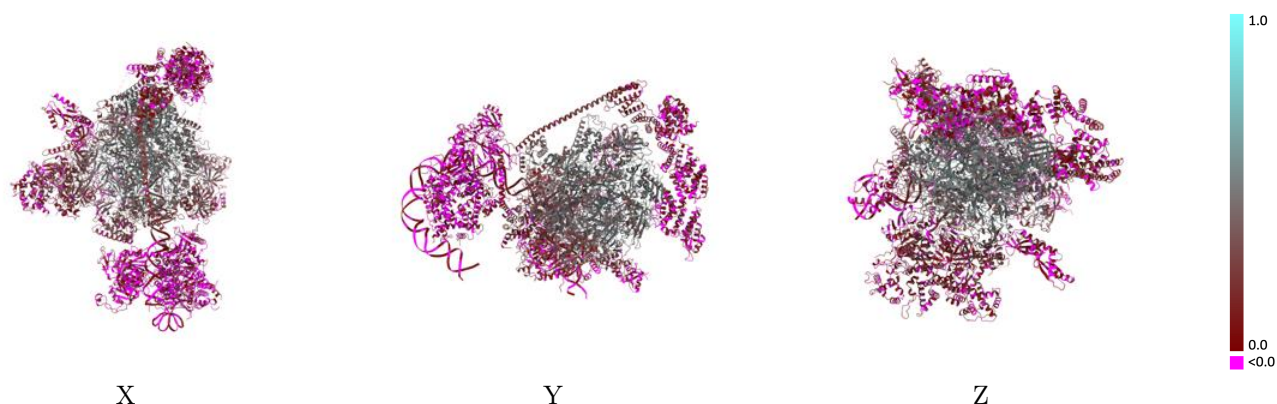
This section contains information regarding the fit between EMDB map EMD-33436 and PDB model 7XSX. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



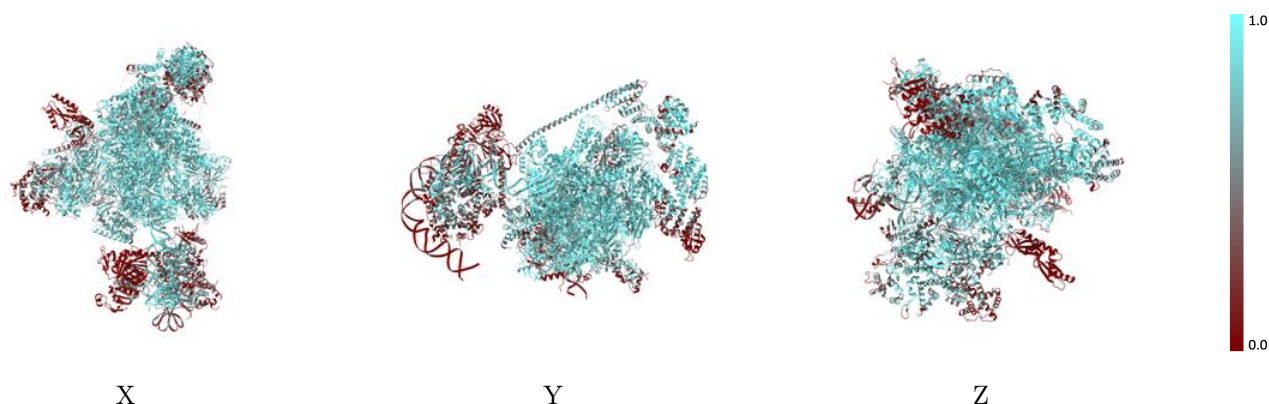
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



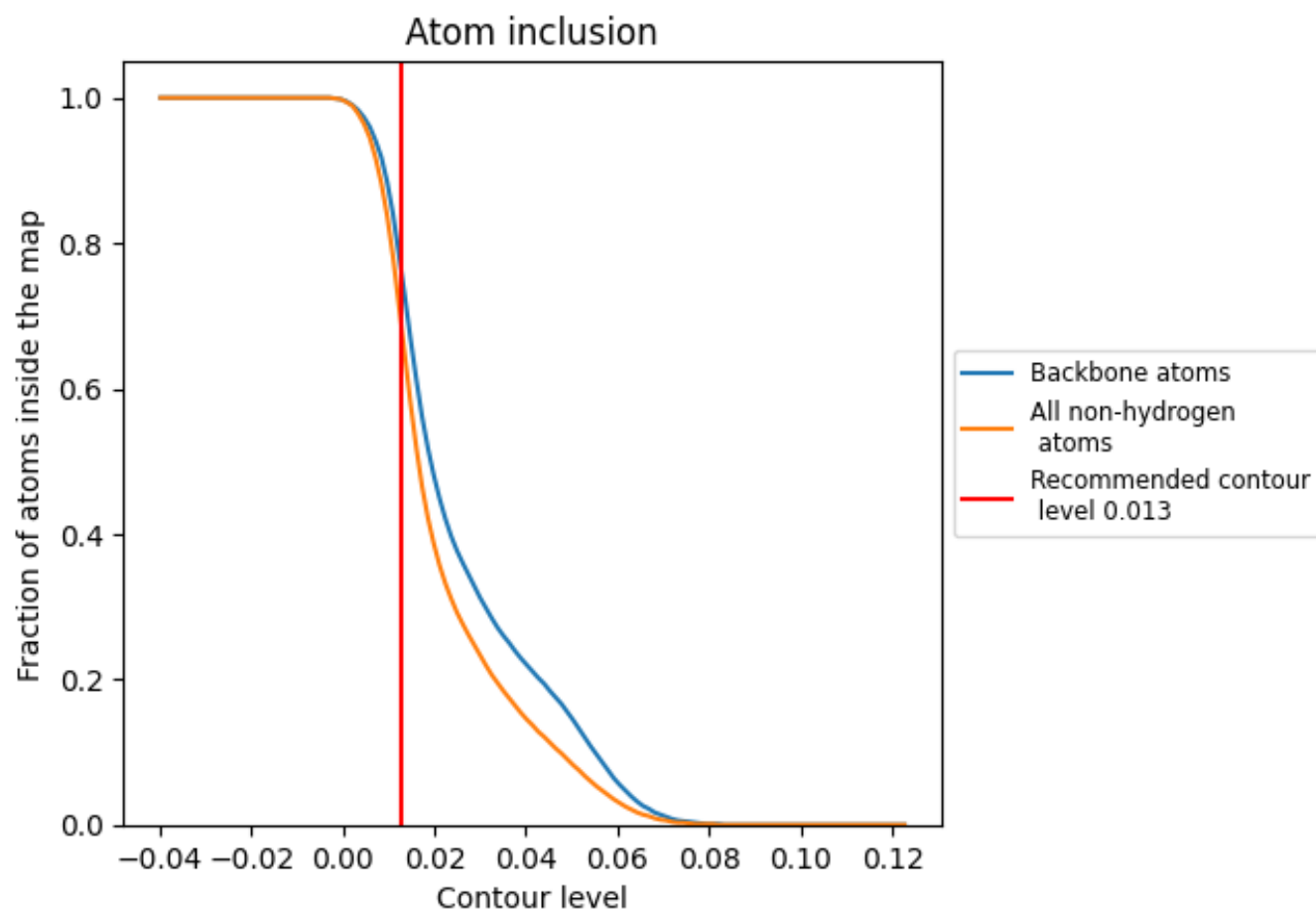
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.013).

9.4 Atom inclusion ⓘ



At the recommended contour level, 76% of all backbone atoms, 68% 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 (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6780	 0.2270
A	 0.9290	 0.4470
B	 0.9290	 0.4580
C	 0.9350	 0.4740
D	 0.7980	 0.2140
E	 0.9400	 0.4140
F	 0.9500	 0.4830
G	 0.8360	 0.3030
H	 0.9300	 0.4650
I	 0.8820	 0.3190
J	 0.9370	 0.4820
K	 0.9560	 0.4750
L	 0.9450	 0.4350
M	 0.8110	 0.1650
N	 0.5560	 0.1000
P	 0.9020	 0.3150
T	 0.5690	 0.1130
V	 0.8740	 0.1210
W	 0.7050	 0.1890
a	 0.8340	 0.0090
b	 0.7830	 -0.0210
c	 0.2020	 -0.0010
d	 0.3740	 0.0070
e	 0.4690	 0.0300
f	 0.5430	 0.0060
g	 0.4910	 0.0030
h	 0.4760	 -0.0080
j	 0.3090	 -0.0020
k	 0.1770	 0.0110
m	 0.4590	 0.1050
n	 0.7890	 0.1970
q	 0.5970	 0.0820
r	 0.4880	 0.1320
u	 0.6080	 0.1870
v	 0.5300	 0.1150
x	 0.7220	 0.2700

