



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 01:50 AM UTC

PDB ID : 8WAW / pdb_00008waw
EMDB ID : EMD-37407
Title : De novo transcribing complex 13 (TC13), the early elongation complex with Pol II positioned 13nt downstream of TSS
Authors : Chen, X.; Liu, W.; Wang, Q.; Wang, X.; Ren, Y.; Qu, X.; Li, W.; Xu, Y.
Deposited on : 2023-09-08
Resolution : 3.02 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

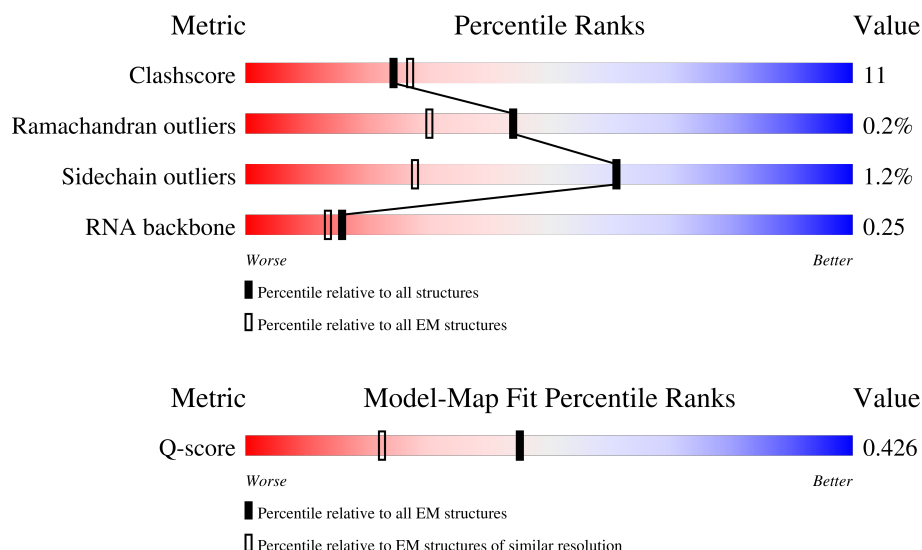
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.02 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	13913 (2.52 - 3.52)

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	N	8	
2	S	517	
3	T	249	

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Mol	Chain	Length	Quality of chain
4	X	99	
5	Y	99	
6	Z	13	
7	o	1970	
8	p	1174	
9	q	275	
10	r	142	
11	s	210	
12	t	127	
13	u	172	
14	v	150	
15	w	125	
16	x	67	
17	y	117	
18	z	58	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 35768 atoms, of which 30 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 Alpha-amanitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	N	8	Total	C	H	N	O	S	
			94	39	30	10	14	1	
								0	0

- Molecule 2 is a protein called General transcription factor IIF subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	S	138	Total	C	N	O	S		
			1138	719	208	208	3		
								0	0

- Molecule 3 is a protein called General transcription factor IIF subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	T	103	Total	C	N	O	S		
			789	492	142	154	1		
								0	0

- Molecule 4 is a DNA chain called non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	X	43	Total	C	N	O	P		
			874	416	154	261	43		
								0	0

- Molecule 5 is a DNA chain called template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Y	54	Total	C	N	O	P		
			1116	528	213	321	54		
								0	0

- Molecule 6 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Z	13	Total	C	N	O	P		
			281	123	45	98	15		
								0	0

- Molecule 7 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	o	1452	Total	C	N	O	S	0	0
			11510	7235	2056	2146	73		

- Molecule 8 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	p	1146	Total	C	N	O	S	0	0
			9149	5782	1610	1693	64		

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	q	257	Total	C	N	O	S	0	0
			2059	1294	351	408	6		

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	r	128	Total	C	N	O	S	0	0
			1050	656	178	212	4		

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	s	209	Total	C	N	O	S	0	0
			1720	1089	300	323	8		

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	t	82	Total	C	N	O	S	0	0
			657	418	113	121	5		

- Molecule 13 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	u	171	Total	C	N	O	S	0	0
			1351	875	219	249	8		

- Molecule 14 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	v	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

- Molecule 15 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	w	114	Total	C	N	O	S	0	0
			927	571	166	179	11		

- Molecule 16 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	x	67	Total	C	N	O	S	0	0
			533	345	90	92	6		

- Molecule 17 is a protein called DNA-directed RNA polymerase II subunit RPB11-a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	y	115	Total	C	N	O	S	0	0
			920	593	152	173	2		

- Molecule 18 is a protein called RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	z	44	Total	C	N	O	S	0	0
			372	231	72	63	6		

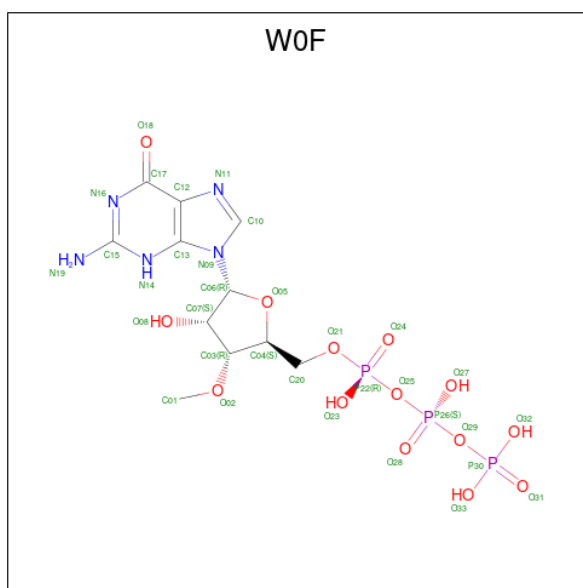
- Molecule 19 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
19	o	2	Total	Zn	0
			2	2	
19	p	1	Total	Zn	0
			1	1	
19	q	1	Total	Zn	0
			1	1	
19	w	2	Total	Zn	0
			2	2	
19	x	1	Total	Zn	0
			1	1	
19	z	1	Total	Zn	0
			1	1	

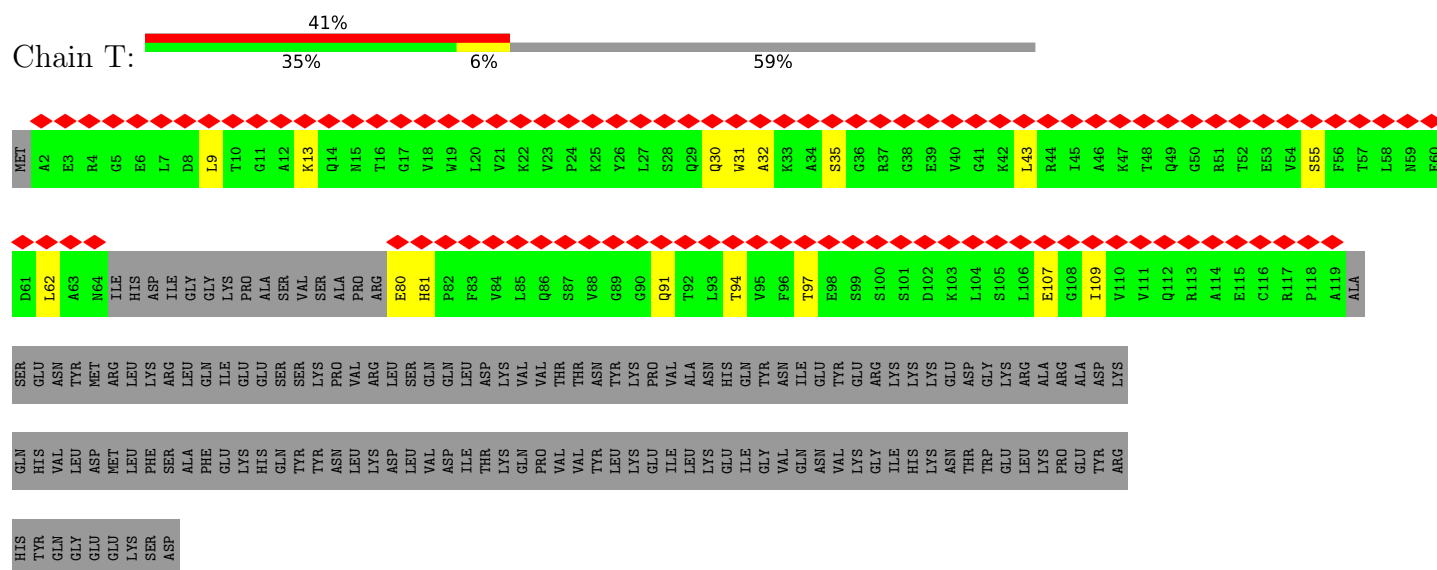
- Molecule 20 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
20	o	1	Total	Mg	0
			1	1	

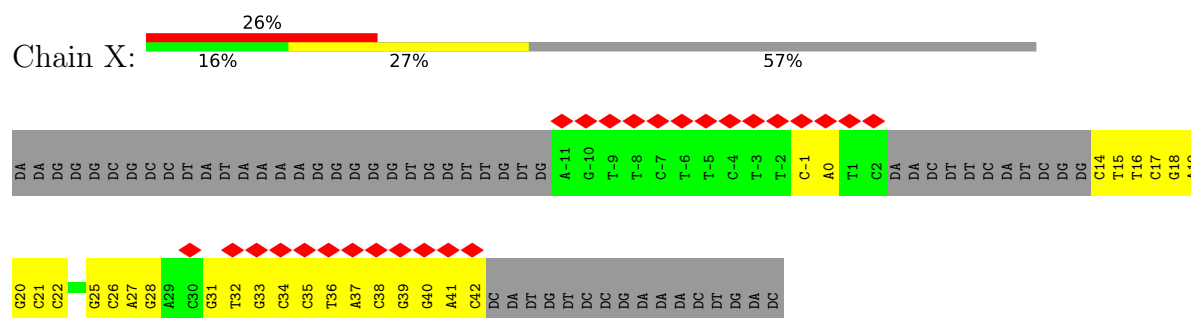
- Molecule 21 is [[(2 {S},3 {R},4 {S},5 {R})-5-(2-azanyl-6-oxidanylidene-3 {H}-purin-9-yl)-3-methoxy-4-oxidanyl-oxolan-2-yl]methoxy-oxidanyl-phosphoryl] phosphono hydrogen phosphate (CCD ID: W0F) (formula: C₁₁H₁₈N₅O₁₄P₃) (labeled as "Ligand of Interest" by depositor).



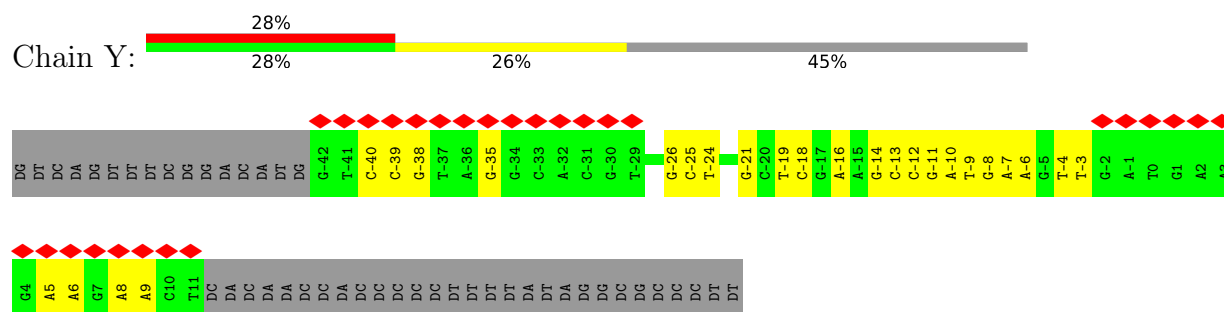
Mol	Chain	Residues	Atoms					AltConf
21	p	1	Total	C	N	O	P	0
			33	11	5	14	3	



- Molecule 4: non-template DNA



- Molecule 5: template DNA



- Molecule 6: RNA



- Molecule 7: DNA-directed RNA polymerase subunit

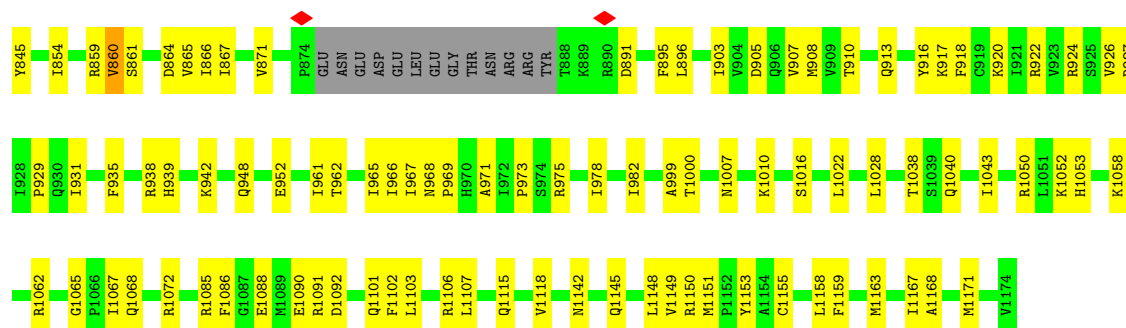




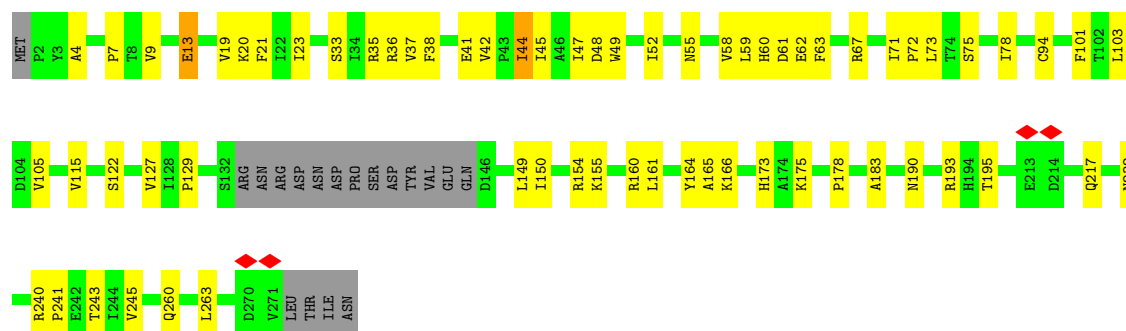


- Molecule 8: DNA-directed RNA polymerase subunit beta

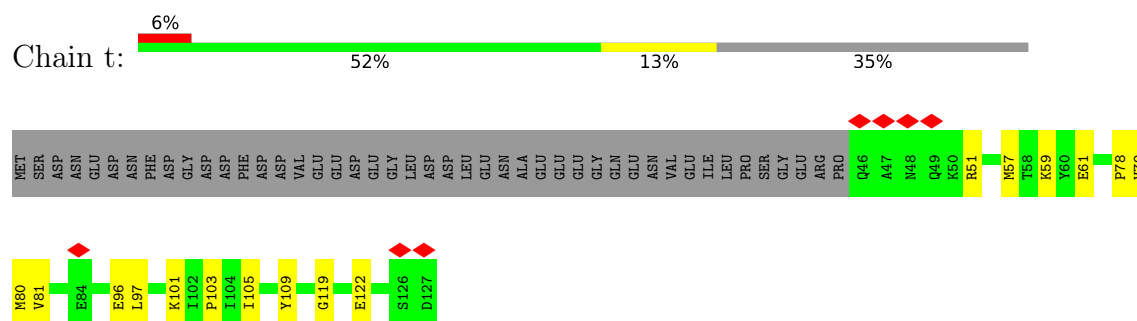




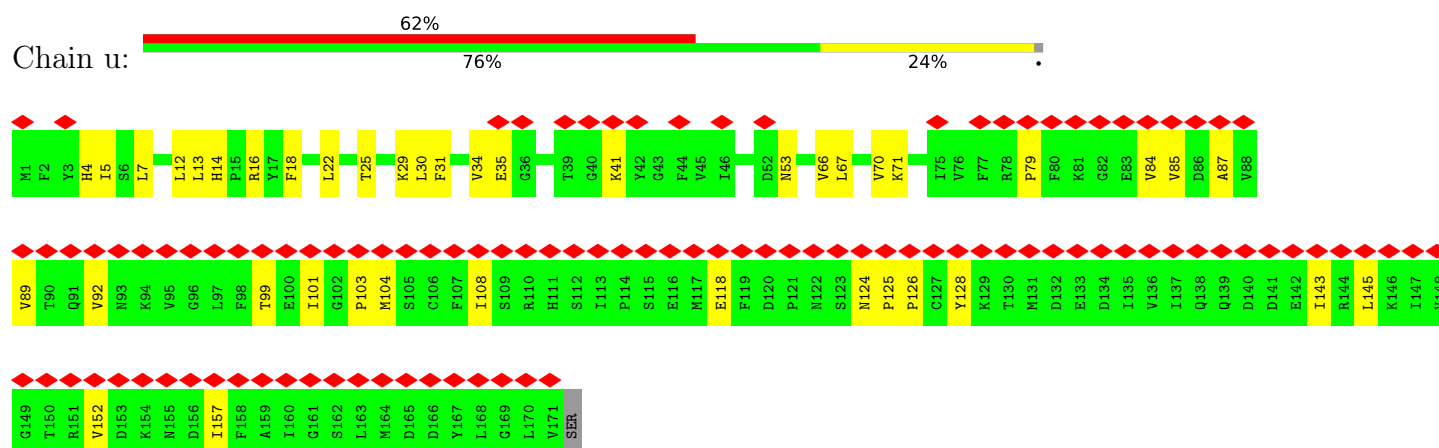
• Molecule 9: DNA-directed RNA polymerase II subunit RPB3



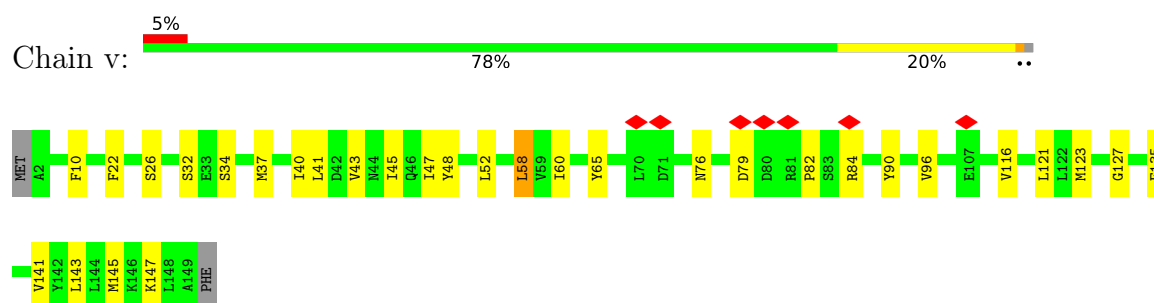
- Molecule 12: DNA-directed RNA polymerase II subunit F



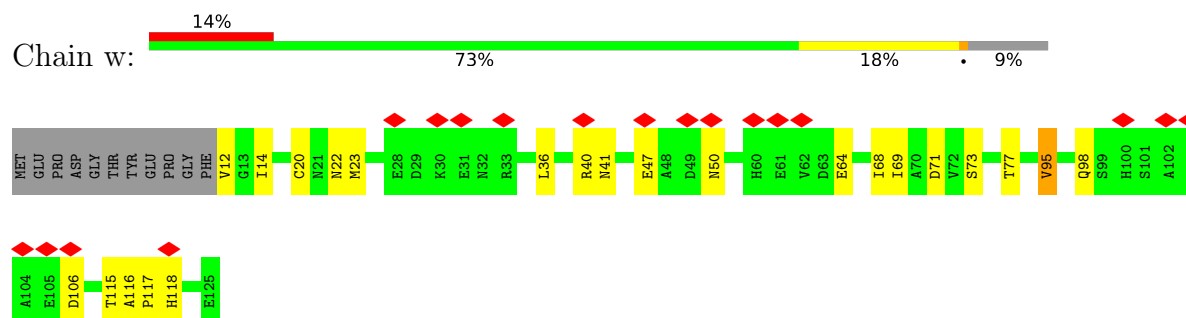
- Molecule 13: DNA-directed RNA polymerase II subunit RPB7



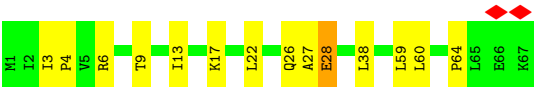
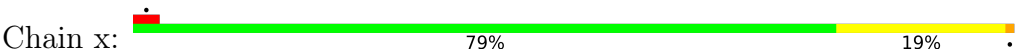
- Molecule 14: DNA-directed RNA polymerases I, II, and III subunit RPABC3



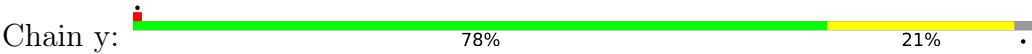
- Molecule 15: DNA-directed RNA polymerase II subunit RPB9



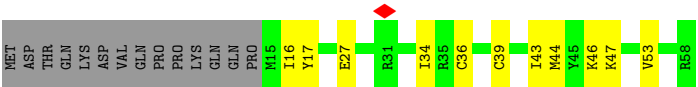
- Molecule 16: DNA-directed RNA polymerases I, II, and III subunit RPABC5



• Molecule 17: DNA-directed RNA polymerase II subunit RPB11-a



• Molecule 18: RPB12



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	108001	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	6.074	Depositor
Minimum map value	-3.419	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.7	Depositor
Map size ($\text{\AA}$)	426.88, 426.88, 426.88	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.334, 1.334, 1.334	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: W0F, ILX, HYP, ATP, CSX, G2L, ZN, MG, TRX

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	N	0.41	0/22	0.99	0/26
2	S	0.09	0/1167	0.23	0/1576
3	T	0.09	0/799	0.26	0/1077
4	X	0.29	0/976	0.62	0/1500
5	Y	0.30	0/1254	0.56	0/1935
6	Z	0.22	0/250	0.52	0/385
7	o	0.18	0/11723	0.35	0/15830
8	p	0.20	0/9332	0.38	1/12598 (0.0%)
9	q	0.19	0/2102	0.36	0/2857
10	r	0.10	0/1064	0.22	0/1428
11	s	0.17	0/1751	0.33	1/2366 (0.0%)
12	t	0.17	0/667	0.26	0/901
13	u	0.12	0/1382	0.31	0/1874
14	v	0.17	0/1207	0.34	0/1628
15	w	0.16	0/948	0.33	0/1284
16	x	0.16	0/542	0.31	0/730
17	y	0.18	0/939	0.31	0/1271
18	z	0.16	0/377	0.34	0/500
All	All	0.19	0/36502	0.37	2/49766 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	p	355	ASP	CB-CA-C	-5.55	110.19	116.63
11	s	46	ASP	CB-CA-C	-5.39	109.89	117.23

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	N	64	30	51	5	0
2	S	1138	0	1103	19	0
3	T	789	0	795	10	0
4	X	874	0	486	34	0
5	Y	1116	0	606	30	0
6	Z	281	0	138	4	0
7	o	11510	0	11616	272	0
8	p	9149	0	9178	246	0
9	q	2059	0	2007	61	0
10	r	1050	0	1033	18	0
11	s	1720	0	1737	40	0
12	t	657	0	684	13	0
13	u	1351	0	1358	26	0
14	v	1186	0	1147	22	0
15	w	927	0	859	19	0
16	x	533	0	553	12	0
17	y	920	0	942	18	0
18	z	372	0	378	9	0
19	o	2	0	0	0	0
19	p	1	0	0	0	0
19	q	1	0	0	0	0
19	w	2	0	0	0	0
19	x	1	0	0	0	0
19	z	1	0	0	0	0
20	o	1	0	0	0	0
21	p	33	0	0	6	0
All	All	35738	30	34671	750	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 11.

All (750) 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)
3:T:91:GLN:HB2	8:p:555:GLU:HG3	1.57	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Z:13:G2L:H4'	7:o:499:ASP:OD1	1.75	0.85
8:p:866:ILE:HG22	8:p:867:ILE:HG13	1.60	0.84
8:p:975:ARG:NH2	21:p:1201:W0F:O32	2.11	0.83
8:p:926:VAL:HG21	9:q:62:GLU:HG3	1.63	0.81
8:p:597:ILE:HG23	8:p:601:VAL:HB	1.62	0.81
7:o:948:ILE:HG12	7:o:1007:ILE:HD11	1.63	0.79
4:X:21:DC:N4	5:Y:-21:DG:O6	2.17	0.78
7:o:497:ASP:OD2	21:p:1201:W0F:O33	2.02	0.77
7:o:1458:ILE:HD12	8:p:1091:ARG:HH21	1.50	0.76
7:o:922:PHE:H	7:o:1052:ARG:HD2	1.51	0.75
9:q:20:LYS:HG3	9:q:232:ASN:HD22	1.51	0.75
8:p:118:LEU:HD22	8:p:913:GLN:HG3	1.68	0.75
9:q:190:ASN:ND2	9:q:195:THR:O	2.20	0.74
8:p:1142:ASN:HD21	8:p:1145:GLN:HB2	1.52	0.74
9:q:60:HIS:HD2	9:q:62:GLU:HG2	1.53	0.73
5:Y:-13:DC:O2	21:p:1201:W0F:N19	2.21	0.73
9:q:42:VAL:HB	9:q:178:PRO:HG3	1.71	0.73
7:o:375:ILE:HD11	7:o:669:TYR:HB2	1.72	0.72
4:X:16:DT:H4'	4:X:17:DC:H5'	1.71	0.72
4:X:17:DC:H2''	4:X:18:DG:C8	2.25	0.71
8:p:274:ARG:NH1	8:p:311:ILE:O	2.22	0.71
10:r:16:ASP:H	10:r:21:ILE:HB	1.55	0.71
10:r:25:GLU:HG3	13:u:41:LYS:HE2	1.71	0.71
8:p:910:THR:HG22	18:z:43:ILE:HA	1.72	0.70
7:o:204:HIS:HA	7:o:211:GLU:HB3	1.73	0.70
7:o:1148:ALA:HB1	7:o:1333:GLU:HB2	1.72	0.70
9:q:193:ARG:HH12	9:q:217:GLN:HB3	1.56	0.70
17:y:45:ILE:HG22	17:y:94:LEU:HD13	1.74	0.70
17:y:7:PHE:HB2	17:y:11:LEU:HD12	1.74	0.70
9:q:48:ASP:HB3	9:q:166:LYS:HE2	1.75	0.69
9:q:67:ARG:NH2	16:x:3:ILE:O	2.26	0.69
7:o:358:ARG:NH2	8:p:1068:GLN:OE1	2.25	0.69
8:p:108:MET:HE2	8:p:118:LEU:HD12	1.74	0.69
2:S:115:LYS:NZ	2:S:117:GLY:O	2.27	0.68
8:p:193:VAL:HG21	8:p:470:LEU:HD13	1.75	0.68
8:p:744:MET:HE3	8:p:922:ARG:HB2	1.73	0.68
5:Y:-8:DG:H2'	5:Y:-7:DA:C8	2.28	0.68
5:Y:-26:DG:H1'	5:Y:-25:DC:H5'	1.76	0.68
8:p:407:MET:HE1	8:p:444:LEU:HG	1.76	0.68
5:Y:-12:DC:H2'	5:Y:-11:DG:C8	2.28	0.68
7:o:784:VAL:HG22	8:p:978:ILE:HD11	1.74	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:s:171:PRO:HB2	11:s:207:ARG:HD3	1.75	0.67
5:Y:-4:DT:H3	6:Z:5:A:H61	1.42	0.67
7:o:560:VAL:HG22	7:o:591:ILE:HD11	1.77	0.67
8:p:505:LEU:HD22	8:p:509:VAL:HB	1.76	0.67
4:X:35:DC:H2"	4:X:36:DT:H71	1.76	0.67
1:N:1:ILX:HG23	7:o:791:GLN:NE2	2.09	0.67
7:o:26:LEU:HG	8:p:1168:ALA:HB2	1.77	0.67
7:o:358:ARG:HA	8:p:1085:ARG:HA	1.77	0.67
8:p:80:GLU:O	8:p:82:PRO:HD3	1.94	0.67
8:p:1062:ARG:HE	8:p:1065:GLY:H	1.43	0.67
10:r:33:LEU:HD12	10:r:80:ILE:HG23	1.77	0.67
7:o:636:ILE:HG22	7:o:637:MET:HG2	1.77	0.67
8:p:827:GLU:HG2	8:p:871:VAL:HG22	1.77	0.67
7:o:1213:ARG:NH1	7:o:1215:GLU:OE2	2.27	0.66
5:Y:-12:DC:O2	6:Z:13:G2L:N2	2.24	0.66
7:o:141:LEU:HD13	7:o:1445:HIS:HE1	1.59	0.66
8:p:1115:GLN:HB3	8:p:1148:LEU:HD11	1.77	0.66
8:p:665:ILE:HG23	8:p:669:GLU:HB3	1.78	0.66
18:z:16:ILE:HG12	18:z:27:GLU:HG2	1.78	0.66
1:N:1:ILX:HG23	7:o:791:GLN:HE22	1.60	0.66
7:o:527:THR:HB	7:o:534:VAL:HG22	1.77	0.66
8:p:544:PHE:HB2	8:p:596:ILE:HD13	1.77	0.66
8:p:567:ILE:HA	8:p:612:ILE:HG22	1.78	0.66
7:o:733:LEU:HB3	15:w:106:ASP:HB2	1.78	0.65
14:v:26:SER:HB3	14:v:45:ILE:HD11	1.77	0.65
8:p:566:LYS:HA	8:p:576:ILE:HG22	1.79	0.64
4:X:33:DG:H2"	4:X:34:DC:C5	2.32	0.64
7:o:792:ASN:HD21	7:o:1108:HIS:CE1	2.16	0.64
7:o:121:SER:HA	7:o:126:ILE:HG21	1.80	0.64
11:s:8:TYR:CZ	11:s:12:LYS:HD2	2.33	0.64
7:o:576:GLN:O	7:o:590:GLN:NE2	2.31	0.64
7:o:1262:MET:HB3	7:o:1265:ASP:HB3	1.78	0.64
4:X:19:DA:H2"	4:X:20:DG:C8	2.34	0.63
7:o:98:GLY:HA3	7:o:1440:MET:HE2	1.79	0.63
8:p:37:LYS:HB3	8:p:41:ARG:HG3	1.80	0.63
8:p:761:THR:H	8:p:764:MET:HE3	1.62	0.63
11:s:17:ILE:HD13	11:s:74:VAL:HG11	1.80	0.63
2:S:170:VAL:HG23	7:o:1279:MET:HG3	1.81	0.63
8:p:718:GLN:HG2	8:p:720:PRO:HD2	1.78	0.63
12:t:81:VAL:HG22	12:t:101:LYS:HD3	1.81	0.63
7:o:1485:GLU:HB3	12:t:78:PRO:HB3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:o:478:PRO:O	7:o:483:ARG:NH2	2.31	0.62
8:p:387:HIS:CD2	8:p:504:THR:HG21	2.34	0.62
18:z:17:TYR:HB3	18:z:44:MET:HB3	1.81	0.62
5:Y:8:DA:H2''	5:Y:9:DA:C8	2.34	0.62
8:p:403:LEU:HD23	8:p:444:LEU:HD23	1.81	0.62
7:o:924:TYR:OH	7:o:953:GLU:OE2	2.18	0.62
4:X:27:DA:H2''	4:X:28:DG:C8	2.34	0.62
3:T:94:THR:HG22	3:T:109:ILE:HG22	1.81	0.61
8:p:387:HIS:HD2	8:p:504:THR:HG21	1.65	0.61
8:p:924:ARG:HH11	9:q:60:HIS:HB2	1.66	0.61
11:s:82:VAL:HG23	11:s:106:VAL:HG13	1.82	0.61
8:p:540:PRO:HB2	8:p:596:ILE:HG23	1.82	0.61
8:p:572:CYS:O	8:p:574:VAL:HG23	1.99	0.61
8:p:917:LYS:HG3	18:z:34:ILE:HD11	1.82	0.61
9:q:19:VAL:HG23	9:q:241:PRO:HB2	1.83	0.60
7:o:1128:ILE:HG23	7:o:1414:ILE:HB	1.83	0.60
9:q:9:VAL:HG11	17:y:105:PHE:HD1	1.66	0.60
7:o:201:GLU:HG2	7:o:203:LYS:H	1.67	0.60
7:o:461:GLN:NE2	8:p:1090:GLU:OE2	2.35	0.60
11:s:82:VAL:HB	11:s:110:MET:HG2	1.84	0.60
2:S:167:ARG:O	8:p:248:LYS:NZ	2.34	0.60
8:p:157:ARG:NH2	8:p:177:CYS:O	2.34	0.60
8:p:516:GLU:HA	8:p:520:VAL:HG22	1.83	0.60
8:p:1062:ARG:NE	8:p:1065:GLY:H	2.00	0.60
12:t:105:ILE:HG22	12:t:119:GLY:HA2	1.84	0.60
11:s:18:MET:HE2	11:s:32:GLU:HB3	1.84	0.60
14:v:58:LEU:HD11	14:v:143:LEU:HD11	1.84	0.60
7:o:549:THR:HG21	7:o:640:LEU:HD12	1.82	0.60
5:Y:-13:DC:H2'	5:Y:-12:DC:C6	2.37	0.59
7:o:1268:LYS:HD3	7:o:1275:VAL:HG13	1.84	0.59
5:Y:-4:DT:H2''	5:Y:-3:DT:H5''	1.84	0.59
7:o:760:LEU:HD11	7:o:781:ILE:HG21	1.84	0.59
8:p:285:LEU:HD11	8:p:305:LEU:HD11	1.84	0.59
13:u:99:THR:HG21	13:u:143:ILE:HD11	1.85	0.59
7:o:322:LEU:HB3	7:o:325:LEU:HD12	1.83	0.59
4:X:15:DT:H2''	4:X:16:DT:H2'	1.85	0.59
8:p:834:ARG:HD2	8:p:840:MET:HE2	1.84	0.59
13:u:89:VAL:HA	13:u:99:THR:HG22	1.82	0.59
7:o:370:ASP:HB2	7:o:483:ARG:HB3	1.84	0.59
8:p:905:ASP:HB2	8:p:924:ARG:HG3	1.85	0.59
15:w:69:ILE:HG22	15:w:71:ASP:H	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Y:-3:DT:H5''	5:Y:-3:DT:H6	1.68	0.59
8:p:591:ARG:HH22	8:p:592:ARG:HE	1.50	0.59
14:v:96:VAL:HG22	14:v:116:VAL:HG22	1.85	0.59
8:p:50:PHE:HB2	8:p:397:GLY:HA2	1.85	0.58
10:r:60:VAL:HG13	13:u:103:PRO:HB3	1.85	0.58
8:p:545:LEU:HB3	8:p:550:MET:HG3	1.85	0.58
7:o:1474:LEU:HB2	12:t:105:ILE:HG13	1.86	0.58
4:X:21:DC:N3	5:Y:-21:DG:N1	2.45	0.58
7:o:367:ILE:HG21	7:o:501:MET:HG3	1.86	0.58
7:o:996:ILE:HD13	7:o:1060:LEU:HA	1.86	0.58
8:p:550:MET:SD	8:p:577:HIS:HB2	2.44	0.58
11:s:45:GLY:HA3	11:s:52:ARG:HB2	1.85	0.58
13:u:30:LEU:HD22	13:u:70:VAL:HG11	1.86	0.58
7:o:508:SER:HB3	7:o:511:THR:HG22	1.85	0.58
5:Y:-4:DT:H2''	5:Y:-3:DT:C5'	2.34	0.57
9:q:4:ALA:HB2	17:y:93:ASP:HB3	1.86	0.57
9:q:37:VAL:HG13	9:q:41:GLU:HB2	1.86	0.57
16:x:3:ILE:HD12	16:x:4:PRO:HD2	1.84	0.57
4:X:16:DT:H1'	4:X:17:DC:C6	2.40	0.57
7:o:555:LEU:HD12	7:o:591:ILE:HD12	1.86	0.57
8:p:91:ILE:HD12	8:p:126:VAL:HG22	1.86	0.57
8:p:636:LYS:H	8:p:639:HIS:HD2	1.52	0.57
8:p:709:SER:HB2	8:p:767:LEU:HD11	1.86	0.57
17:y:49:GLN:HB2	17:y:94:LEU:HD21	1.85	0.57
4:X:38:DC:H2''	4:X:39:DG:C8	2.40	0.57
7:o:721:HIS:HE1	15:w:98:GLN:HE21	1.51	0.57
2:S:168:ASN:HA	8:p:248:LYS:HD3	1.85	0.57
8:p:403:LEU:HD21	8:p:447:SER:OG	2.03	0.57
7:o:62:GLN:HG3	7:o:84:HIS:O	2.05	0.56
4:X:14:DC:O2	5:Y:-14:DG:N2	2.38	0.56
8:p:627:ILE:HD11	8:p:663:GLU:HB2	1.87	0.56
7:o:1130:ILE:HD13	7:o:1411:LEU:HB3	1.86	0.56
7:o:1471:PHE:CZ	12:t:61:GLU:HA	2.41	0.56
8:p:860:VAL:HG12	8:p:864:ASP:HB2	1.88	0.56
9:q:78:ILE:HD11	9:q:127:VAL:HG23	1.87	0.56
7:o:375:ILE:HD11	7:o:669:TYR:CB	2.36	0.56
8:p:392:ARG:NE	8:p:617:ASP:OD2	2.32	0.56
8:p:859:ARG:HG2	8:p:903:ILE:HG12	1.88	0.56
7:o:894:ASP:O	7:o:1022:ILE:HD13	2.06	0.56
7:o:1386:ILE:HD12	7:o:1398:LEU:HD21	1.87	0.56
9:q:105:VAL:HG11	9:q:115:VAL:HG22	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Y:-16:DA:N3	7:o:1416:ARG:NH2	2.54	0.56
8:p:747:LEU:HD23	8:p:810:PHE:CE1	2.41	0.56
4:X:21:DC:H2"	4:X:22:DC:C5	2.41	0.55
7:o:1147:SER:HA	7:o:1153:ARG:HB2	1.88	0.55
8:p:65:ILE:HB	8:p:86:LEU:HB2	1.88	0.55
9:q:260:GLN:HB2	17:y:91:ILE:HG21	1.89	0.55
8:p:952:GLU:HB2	9:q:36:ARG:HG3	1.87	0.55
7:o:545:VAL:HG22	7:o:676:ILE:HG12	1.87	0.55
7:o:111:CYS:SG	7:o:114:CYS:HB3	2.45	0.55
7:o:671:ASN:O	7:o:675:VAL:HG13	2.06	0.55
7:o:867:SER:HB3	7:o:1414:ILE:HG23	1.89	0.55
7:o:413:TYR:O	7:o:449:HIS:HD2	1.89	0.55
7:o:706:ILE:HD13	7:o:824:GLU:HB2	1.87	0.55
7:o:938:LEU:HD22	7:o:1005:HIS:HD1	1.70	0.55
7:o:1211:LEU:HD11	7:o:1258:ARG:HB3	1.87	0.55
7:o:1206:ARG:HB2	7:o:1267:ASN:HB2	1.89	0.55
13:u:53:ASN:HD22	13:u:71:LYS:HE3	1.71	0.55
8:p:811:TYR:CE2	8:p:924:ARG:HG2	2.42	0.55
7:o:693:ILE:HD13	7:o:828:LEU:HD21	1.89	0.54
9:q:44:ILE:HG12	9:q:45:ILE:H	1.72	0.54
11:s:87:ILE:HD12	11:s:114:ALA:HB1	1.89	0.54
4:X:17:DC:H2"	4:X:18:DG:H8	1.73	0.54
8:p:754:PRO:HB2	8:p:773:PRO:HG2	1.88	0.54
7:o:847:LEU:HD11	8:p:720:PRO:HB3	1.90	0.54
7:o:1258:ARG:HH22	7:o:1260:ARG:HH21	1.56	0.54
7:o:545:VAL:HG11	7:o:645:LEU:HD12	1.90	0.54
7:o:864:LEU:HD23	7:o:1414:ILE:HG21	1.90	0.54
7:o:1189:ASP:HA	7:o:1192:TRP:CE2	2.43	0.54
7:o:1347:LEU:HB3	11:s:137:ILE:HD12	1.90	0.54
15:w:115:THR:HG22	15:w:116:ALA:H	1.73	0.53
8:p:260:LEU:HB2	8:p:263:ILE:HD12	1.90	0.53
8:p:752:TYR:CE2	8:p:807:ARG:HD2	2.43	0.53
7:o:601:ASN:ND2	7:o:989:ASN:OD1	2.40	0.53
11:s:26:TYR:HB3	11:s:62:VAL:HG12	1.91	0.53
14:v:58:LEU:HD12	14:v:145:MET:HG2	1.90	0.53
8:p:587:LEU:HB3	8:p:603:MET:SD	2.48	0.53
5:Y:-24:DT:H5"	11:s:112:PRO:HB3	1.90	0.53
7:o:427:ILE:HD13	7:o:437:ASP:HB3	1.91	0.53
8:p:625:LEU:HD13	8:p:675:LEU:HD21	1.90	0.53
8:p:759:VAL:HG12	8:p:999:ALA:HB2	1.89	0.53
9:q:52:ILE:HD12	9:q:61:ASP:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:o:1403:ASP:O	7:o:1407:CYS:HB2	2.08	0.53
8:p:495:LEU:HG	8:p:497:LYS:H	1.74	0.53
7:o:1479:LYS:HD2	12:t:103:PRO:HA	1.91	0.53
8:p:565:THR:H	8:p:610:ARG:HB3	1.73	0.53
21:p:1201:W0F:C01	21:p:1201:W0F:C20	2.85	0.53
8:p:545:LEU:O	8:p:550:MET:HG2	2.08	0.53
11:s:192:LYS:HE3	11:s:204:ILE:HD13	1.91	0.52
18:z:36:CYS:HB2	18:z:44:MET:HE1	1.91	0.52
7:o:1163:HIS:CE1	7:o:1297:THR:HG23	2.44	0.52
9:q:7:PRO:HB2	17:y:101:LEU:HD13	1.92	0.52
13:u:108:ILE:HD11	13:u:145:LEU:HD22	1.91	0.52
8:p:557:SER:N	8:p:558:PRO:HD2	2.24	0.52
13:u:13:LEU:HB3	13:u:66:VAL:HG12	1.91	0.52
16:x:17:LYS:HB3	16:x:38:LEU:HD13	1.91	0.52
13:u:92:VAL:HB	13:u:126:PRO:HB2	1.91	0.52
8:p:187:ILE:HD13	8:p:448:LEU:HB3	1.91	0.52
8:p:86:LEU:HD22	8:p:431:LEU:HD21	1.91	0.52
7:o:1381:GLU:O	7:o:1385:VAL:HG13	2.09	0.52
11:s:55:ARG:HE	11:s:76:PHE:HB3	1.75	0.52
8:p:384:ASP:O	8:p:390:ASN:ND2	2.43	0.52
7:o:577:PRO:HG2	7:o:580:LEU:HD23	1.92	0.52
7:o:912:SER:HB2	7:o:1327:GLU:HG2	1.91	0.52
7:o:1230:GLN:HG2	7:o:1234:LYS:HE3	1.91	0.52
7:o:823:VAL:HG11	7:o:831:LEU:HD22	1.90	0.51
7:o:901:VAL:HB	7:o:978:VAL:HG12	1.92	0.51
8:p:616:THR:O	8:p:616:THR:OG1	2.24	0.51
9:q:52:ILE:HG21	9:q:55:ASN:HB2	1.92	0.51
9:q:58:VAL:HG11	16:x:59:LEU:HB3	1.91	0.51
7:o:626:THR:OG1	7:o:627:LYS:N	2.42	0.51
8:p:298:MET:HE3	15:w:14:ILE:HB	1.91	0.51
8:p:388:TYR:CZ	8:p:505:LEU:HD21	2.46	0.51
10:r:20:LEU:HD12	10:r:121:ARG:HH22	1.74	0.51
8:p:50:PHE:O	8:p:51:ILE:C	2.52	0.51
8:p:569:VAL:O	8:p:571:GLY:N	2.44	0.51
7:o:565:MET:HE1	17:y:74:ARG:HB2	1.93	0.51
7:o:1262:MET:HB3	7:o:1265:ASP:CB	2.41	0.51
7:o:1472:ASP:HB2	12:t:109:TYR:HE2	1.74	0.51
2:S:114:LYS:HB3	8:p:356:PHE:CZ	2.45	0.51
8:p:747:LEU:HD23	8:p:810:PHE:HE1	1.76	0.51
3:T:97:THR:OG1	3:T:107:GLU:OE2	2.25	0.51
10:r:32:LEU:HD11	13:u:4:HIS:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:164:TRP:CZ2	2:S:167:ARG:HD3	2.46	0.51
7:o:548:PHE:HE1	7:o:555:LEU:HD11	1.76	0.51
7:o:1082:HIS:CD2	12:t:59:LYS:HE3	2.46	0.51
8:p:192:LYS:NZ	8:p:449:ALA:O	2.39	0.51
8:p:789:ASN:O	8:p:968:ASN:HB2	2.11	0.51
11:s:13:ILE:HD11	11:s:132:GLN:HG3	1.93	0.51
9:q:49:TRP:HB3	9:q:164:TYR:HB2	1.93	0.51
7:o:1212:LEU:HD23	7:o:1259:ILE:HD12	1.93	0.51
9:q:154:ARG:HB2	16:x:60:LEU:HD22	1.93	0.51
4:X:39:DG:H1	5:Y:-39:DC:H42	1.59	0.50
7:o:93:PRO:HD2	7:o:219:GLU:HG2	1.92	0.50
8:p:472:ARG:NH1	8:p:737:ILE:HD11	2.25	0.50
8:p:567:ILE:O	8:p:567:ILE:HG13	2.11	0.50
8:p:604:ILE:O	8:p:612:ILE:HA	2.11	0.50
7:o:344:LYS:O	7:o:1435:THR:HG21	2.12	0.50
7:o:916:PHE:HE2	7:o:960:ARG:HG2	1.75	0.50
7:o:1005:HIS:HD2	7:o:1007:ILE:HB	1.76	0.50
7:o:1161:LEU:HD22	7:o:1346:VAL:HG22	1.93	0.50
7:o:1427:LEU:HB2	7:o:1456:GLU:HG2	1.94	0.50
8:p:570:ASN:OD1	8:p:616:THR:N	2.36	0.50
11:s:21:CYS:SG	11:s:62:VAL:HG11	2.50	0.50
11:s:21:CYS:SG	11:s:26:TYR:HB2	2.51	0.50
14:v:79:ASP:O	14:v:82:PRO:HD2	2.11	0.50
2:S:169:LYS:HD2	2:S:173:HIS:CD2	2.46	0.50
8:p:565:THR:HA	8:p:610:ARG:O	2.11	0.50
8:p:631:GLN:NE2	8:p:691:SER:O	2.41	0.50
7:o:201:GLU:HB2	7:o:213:LYS:HG2	1.94	0.50
7:o:788:VAL:HG21	7:o:831:LEU:HD21	1.93	0.50
8:p:961:ILE:HG23	16:x:9:THR:HG21	1.92	0.50
8:p:1072:ARG:HD2	8:p:1153:TYR:CE1	2.46	0.50
9:q:183:ALA:HB3	9:q:232:ASN:HB3	1.93	0.50
7:o:460:ARG:HB2	7:o:501:MET:SD	2.52	0.50
7:o:689:ILE:HD11	8:p:982:ILE:HA	1.94	0.50
8:p:924:ARG:NH1	9:q:60:HIS:HB2	2.26	0.50
13:u:30:LEU:O	13:u:34:VAL:HG22	2.12	0.50
14:v:40:ILE:O	14:v:123:MET:HA	2.12	0.50
7:o:802:PHE:HD2	8:p:671:GLU:HG2	1.76	0.50
8:p:49:GLU:O	8:p:50:PHE:C	2.54	0.50
4:X:17:DC:P	4:X:17:DC:H3'	2.51	0.50
7:o:581:LYS:HG2	7:o:582:PRO:HA	1.94	0.50
8:p:794:VAL:HG22	8:p:967:ILE:HG22	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:o:350:VAL:O	7:o:355:MET:HG2	2.11	0.50
7:o:769:MET:HE1	8:p:969:PRO:HB2	1.94	0.50
9:q:101:PHE:HZ	9:q:127:VAL:HG12	1.77	0.50
9:q:13:GLU:HB2	9:q:20:LYS:HB2	1.94	0.49
7:o:460:ARG:HD3	7:o:492:TYR:O	2.12	0.49
7:o:525:ILE:HG12	7:o:535:MET:HE3	1.94	0.49
8:p:570:ASN:ND2	8:p:616:THR:O	2.45	0.49
8:p:40:VAL:HG11	8:p:482:LEU:HD13	1.94	0.49
8:p:569:VAL:HG12	8:p:572:CYS:HB2	1.93	0.49
8:p:564:ALA:HB3	8:p:580:PRO:HD3	1.94	0.49
11:s:60:VAL:HG12	11:s:62:VAL:HG23	1.93	0.49
2:S:116:GLY:HA2	8:p:356:PHE:HD2	1.77	0.49
7:o:601:ASN:HA	7:o:630:VAL:O	2.13	0.49
7:o:756:ALA:HB2	7:o:786:ALA:HB2	1.94	0.49
7:o:1181:PRO:HG3	7:o:1207:ILE:HG21	1.94	0.49
8:p:550:MET:HE1	8:p:577:HIS:ND1	2.28	0.49
9:q:9:VAL:HG22	9:q:23:ILE:HG12	1.95	0.49
9:q:103:LEU:HB3	9:q:161:LEU:HG	1.94	0.49
7:o:936:GLU:HA	7:o:939:VAL:HG12	1.95	0.49
10:r:34:ASN:O	10:r:68:THR:OG1	2.31	0.49
15:w:22:ASN:ND2	15:w:41:ASN:HD22	2.11	0.49
2:S:142:ASN:OD1	2:S:143:TRP:N	2.45	0.49
9:q:154:ARG:HD3	16:x:64:PRO:HD3	1.95	0.49
7:o:554:PHE:HZ	14:v:121:LEU:HD11	1.77	0.49
7:o:1234:LYS:NZ	7:o:1298:LEU:O	2.45	0.49
8:p:69:ALA:H	8:p:82:PRO:HD2	1.76	0.49
8:p:854:ILE:O	8:p:907:VAL:HG21	2.13	0.49
9:q:63:PHE:CE1	9:q:67:ARG:HD2	2.47	0.49
5:Y:-13:DC:H2'	5:Y:-12:DC:H6	1.78	0.49
7:o:909:LEU:O	7:o:910:LYS:HB2	2.12	0.49
7:o:972:THR:HA	7:o:1320:ILE:HG13	1.94	0.49
8:p:85:LEU:HB2	8:p:131:THR:OG1	2.13	0.49
9:q:263:LEU:HD22	17:y:87:PHE:HD2	1.78	0.49
7:o:1443:ALA:HB2	8:p:1167:ILE:HG23	1.94	0.48
8:p:561:ILE:O	8:p:610:ARG:NH1	2.46	0.48
5:Y:-11:DG:H5''	8:p:1085:ARG:HG3	1.95	0.48
7:o:76:GLY:HA2	7:o:81:CYS:HB2	1.95	0.48
8:p:561:ILE:HB	8:p:610:ARG:HH11	1.78	0.48
5:Y:5:DA:H2''	5:Y:6:DA:C8	2.48	0.48
7:o:527:THR:HG22	7:o:532:ARG:O	2.14	0.48
8:p:77:GLU:HA	8:p:80:GLU:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:s:106:VAL:HG21	11:s:110:MET:HG3	1.95	0.48
16:x:27:ALA:O	16:x:28:GLU:HB2	2.13	0.48
3:T:31:TRP:HD1	3:T:62:LEU:HD21	1.78	0.48
4:X:40:DG:H1	5:Y:40:DC:H42	1.59	0.48
5:Y:12:DC:H2'	5:Y:11:DG:H8	1.75	0.48
7:o:46:THR:HG22	7:o:47:THR:HG23	1.95	0.48
7:o:909:LEU:C	7:o:911:PRO:HD2	2.39	0.48
11:s:14:ARG:O	11:s:18:MET:HG2	2.12	0.48
2:S:161:GLU:O	2:S:165:GLU:HG2	2.14	0.48
8:p:1088:GLU:O	8:p:1091:ARG:HG2	2.13	0.48
9:q:67:ARG:NH1	9:q:149:LEU:O	2.47	0.48
11:s:118:LEU:HD22	11:s:127:LEU:HB2	1.96	0.48
4:X:18:DG:H2''	4:X:19:DA:O5'	2.13	0.48
7:o:675:VAL:HG22	7:o:676:ILE:HD12	1.96	0.48
15:w:64:GLU:O	15:w:68:ILE:HG12	2.12	0.48
7:o:931:ARG:HG2	7:o:939:VAL:HG11	1.95	0.48
8:p:236:TRP:HB2	8:p:259:THR:HB	1.96	0.48
11:s:160:LEU:HD11	11:s:167:GLU:HG2	1.94	0.48
7:o:388:MET:HE1	7:o:503:LEU:HD23	1.94	0.48
7:o:913:ASN:OD1	7:o:963:ARG:NH1	2.47	0.48
7:o:1347:LEU:HB3	11:s:137:ILE:CD1	2.43	0.48
8:p:761:THR:HG23	8:p:1000:THR:HA	1.96	0.48
8:p:185:PHE:HB2	8:p:187:ILE:HD11	1.96	0.48
8:p:427:LYS:HG3	8:p:428:ASP:H	1.78	0.48
8:p:818:GLU:HG2	8:p:917:LYS:HB3	1.96	0.48
10:r:57:LEU:HD13	10:r:61:PHE:CE1	2.48	0.48
8:p:50:PHE:O	8:p:54:SER:N	2.38	0.47
15:w:12:VAL:HG23	15:w:50:ASN:HD21	1.79	0.47
7:o:983:LEU:HD12	7:o:1044:HIS:CD2	2.49	0.47
9:q:9:VAL:HG11	17:y:105:PHE:CD1	2.47	0.47
8:p:472:ARG:CZ	8:p:737:ILE:HD11	2.44	0.47
7:o:865:ILE:HG21	8:p:1092:ASP:CG	2.39	0.47
8:p:117:ASN:HA	8:p:189:GLY:HA3	1.96	0.47
8:p:515:PRO:HG3	8:p:523:VAL:HB	1.95	0.47
7:o:471:GLY:O	7:o:521:VAL:HG23	2.14	0.47
8:p:677:MET:CE	8:p:700:PRO:HB3	2.44	0.47
8:p:929:PRO:HB3	8:p:935:PHE:HZ	1.79	0.47
8:p:1028:LEU:HD11	8:p:1043:ILE:HD11	1.96	0.47
10:r:90:LYS:HE2	10:r:130:ILE:HD11	1.97	0.47
7:o:852:VAL:HG13	8:p:494:LYS:HB3	1.97	0.47
7:o:886:VAL:HG11	7:o:889:LEU:HD23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:p:631:GLN:HE22	8:p:691:SER:C	2.22	0.47
7:o:668:PHE:CZ	7:o:672:ILE:HD11	2.50	0.47
7:o:1105:ASN:HB3	7:o:1107:PHE:CD2	2.50	0.47
7:o:1208:SER:HB3	7:o:1260:ARG:HB3	1.96	0.47
7:o:1261:ILE:HG22	7:o:1262:MET:H	1.80	0.47
7:o:1321:ILE:HD12	7:o:1331:LEU:HD12	1.97	0.47
8:p:446:TYR:CD2	8:p:456:GLN:HG2	2.49	0.47
8:p:561:ILE:HG21	8:p:610:ARG:HB2	1.96	0.47
8:p:674:MET:HG2	15:w:77:THR:HA	1.97	0.47
9:q:101:PHE:CE2	9:q:122:SER:HB3	2.49	0.47
12:t:57:MET:HE1	12:t:97:LEU:HD11	1.96	0.47
7:o:1263:ASN:OD1	7:o:1263:ASN:N	2.46	0.47
8:p:1072:ARG:HB2	8:p:1153:TYR:CD2	2.50	0.47
11:s:7:THR:OG1	11:s:48:PRO:HD3	2.14	0.47
11:s:90:TYR:O	11:s:94:MET:HG2	2.14	0.47
13:u:18:PHE:HA	13:u:22:LEU:HD13	1.97	0.47
3:T:80:GLU:OE1	3:T:81:HIS:N	2.47	0.47
7:o:601:ASN:HB3	7:o:988:TRP:CE3	2.50	0.47
7:o:1429:LYS:HB2	7:o:1438:VAL:HG11	1.97	0.47
8:p:163:LEU:HA	8:p:166:LEU:HD12	1.97	0.47
8:p:297:MET:O	8:p:301:VAL:HG23	2.14	0.47
11:s:7:THR:HG21	11:s:41:LYS:HG2	1.96	0.47
7:o:530:SER:O	7:o:532:ARG:HG3	2.15	0.47
13:u:124:ASN:HB2	13:u:125:PRO:HD3	1.97	0.47
7:o:353:ASN:O	7:o:357:LYS:HE2	2.15	0.46
7:o:421:ARG:CZ	7:o:427:ILE:HD11	2.45	0.46
9:q:19:VAL:HG12	9:q:21:PHE:HD1	1.80	0.46
9:q:103:LEU:O	9:q:160:ARG:HA	2.15	0.46
11:s:114:ALA:O	11:s:117:SER:HB2	2.15	0.46
8:p:387:HIS:CD2	8:p:389:GLY:H	2.33	0.46
14:v:65:TYR:CD1	14:v:84:ARG:HG2	2.50	0.46
5:Y:-7:DA:H2"	5:Y:-6:DA:H8	1.80	0.46
7:o:585:LEU:HD12	14:v:47:ILE:HD11	1.97	0.46
8:p:491:ARG:HB3	8:p:518:HIS:HB3	1.97	0.46
3:T:32:ALA:HA	3:T:35:SER:HB2	1.96	0.46
7:o:26:LEU:HD13	7:o:31:LEU:HD21	1.97	0.46
7:o:282:ASP:O	7:o:286:ILE:HG12	2.16	0.46
7:o:971:PRO:O	7:o:972:THR:OG1	2.27	0.46
8:p:465:GLY:O	8:p:468:GLN:NE2	2.42	0.46
11:s:72:MET:HE3	11:s:72:MET:HB2	1.79	0.46
7:o:62:GLN:HE22	7:o:255:VAL:HG12	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:o:1440:MET:SD	8:p:1167:ILE:HD11	2.55	0.46
8:p:591:ARG:NH2	8:p:592:ARG:HG3	2.30	0.46
12:t:51:ARG:NH1	12:t:122:GLU:OE1	2.49	0.46
7:o:357:LYS:HD2	8:p:1107:LEU:O	2.16	0.46
7:o:377:GLN:HA	7:o:473:ARG:O	2.16	0.46
7:o:1209:PRO:HG2	7:o:1210:TRP:CD1	2.50	0.46
7:o:1477:ALA:O	7:o:1481:LYS:HG2	2.15	0.46
8:p:815:LYS:HZ2	8:p:918:PHE:HZ	1.62	0.46
14:v:37:MET:HE3	14:v:127:GLY:HA3	1.98	0.46
7:o:112:PHE:HD1	7:o:113:PHE:HD2	1.63	0.46
2:S:172:ASN:HB2	7:o:1280:ASP:OD1	2.15	0.46
8:p:403:LEU:HD22	8:p:453:TRP:CZ2	2.51	0.46
1:N:2:TRX:CE3	7:o:749:ARG:HD2	2.46	0.46
7:o:112:PHE:HD1	7:o:113:PHE:CD2	2.34	0.46
8:p:675:LEU:HD23	8:p:695:HIS:HB2	1.97	0.46
7:o:375:ILE:HG23	7:o:488:VAL:HG22	1.98	0.45
7:o:93:PRO:HB2	7:o:218:PRO:HB2	1.97	0.45
7:o:516:GLN:O	7:o:520:MET:HB2	2.15	0.45
7:o:618:TYR:HE1	14:v:40:ILE:HD13	1.81	0.45
8:p:859:ARG:HG3	18:z:53:VAL:HG11	1.98	0.45
10:r:77:ARG:HA	10:r:80:ILE:HD12	1.98	0.45
7:o:41:ILE:HG21	7:o:57:LEU:HD23	1.98	0.45
7:o:709:ALA:HB2	7:o:748:ALA:HB2	1.98	0.45
7:o:769:MET:SD	8:p:973:PRO:HG3	2.57	0.45
9:q:240:ARG:O	9:q:243:THR:HG22	2.16	0.45
7:o:343:LEU:HD22	8:p:1158:LEU:HD12	1.99	0.45
7:o:1416:ARG:HB3	7:o:1433:GLU:OE1	2.16	0.45
8:p:88:PHE:HD2	8:p:126:VAL:HG11	1.81	0.45
8:p:558:PRO:O	8:p:562:ALA:N	2.50	0.45
8:p:865:VAL:HG22	8:p:895:PHE:CE1	2.50	0.45
11:s:63:ALA:HB1	11:s:68:PRO:HA	1.98	0.45
14:v:48:TYR:OH	14:v:147:LYS:HG3	2.16	0.45
8:p:574:VAL:HG12	8:p:574:VAL:O	2.16	0.45
8:p:665:ILE:HD13	8:p:673:VAL:HG21	1.98	0.45
8:p:926:VAL:CG2	9:q:62:GLU:HG3	2.39	0.45
8:p:942:LYS:HE2	21:p:1201:W0F:O31	2.16	0.45
15:w:73:SER:HA	15:w:95:VAL:HG11	1.98	0.45
4:X:19:DA:H61	5:Y:-19:DT:H3	1.63	0.45
7:o:309:LEU:HD12	7:o:309:LEU:HA	1.84	0.45
7:o:853:LYS:HA	7:o:1104:LEU:HD21	1.98	0.45
8:p:235:ILE:HG21	8:p:348:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:q:71:ILE:HD11	9:q:150:ILE:HG12	1.97	0.45
9:q:73:LEU:HB3	9:q:127:VAL:HG13	1.98	0.45
16:x:22:LEU:O	16:x:26:GLN:HG2	2.17	0.45
7:o:569:THR:HG23	7:o:671:ASN:HD21	1.82	0.45
7:o:1208:SER:O	7:o:1260:ARG:NH1	2.50	0.45
7:o:381:PRO:HB3	7:o:480:SER:HA	1.98	0.45
8:p:713:PHE:HB3	8:p:716:HIS:CD2	2.51	0.45
9:q:72:PRO:HG3	16:x:13:ILE:HD11	1.98	0.45
10:r:37:VAL:O	10:r:41:LEU:HG	2.16	0.45
13:u:79:PRO:HG3	13:u:104:MET:SD	2.57	0.45
15:w:69:ILE:HG22	15:w:71:ASP:N	2.32	0.45
2:S:177:MET:HG2	15:w:40:ARG:O	2.17	0.45
7:o:18:ILE:HD11	8:p:1149:VAL:HG11	1.98	0.45
7:o:87:HIS:HD2	7:o:89:GLU:HG3	1.81	0.45
7:o:721:HIS:CE1	15:w:98:GLN:HE21	2.32	0.45
7:o:1318:LYS:HE2	7:o:1330:ALA:HB1	1.99	0.45
8:p:780:VAL:HA	8:p:965:ILE:O	2.15	0.45
8:p:968:ASN:OD1	8:p:969:PRO:HD2	2.17	0.45
8:p:1159:PHE:O	8:p:1163:MET:HG3	2.17	0.45
9:q:73:LEU:HD23	9:q:129:PRO:HA	1.99	0.45
5:Y:-39:DC:H2"	5:Y:-38:DG:C8	2.52	0.45
7:o:155:GLU:H	7:o:181:HIS:CD2	2.35	0.45
7:o:727:PRO:HA	7:o:736:THR:HG21	1.98	0.45
8:p:794:VAL:HG13	8:p:965:ILE:HG23	1.98	0.45
10:r:23:PRO:HG2	10:r:26:PHE:HB2	1.98	0.45
12:t:81:VAL:HG23	12:t:96:GLU:HG2	1.97	0.45
13:u:87:ALA:HB2	13:u:101:ILE:HG12	1.98	0.45
2:S:175:SER:O	2:S:179:GLN:HG2	2.17	0.44
4:X:36:DT:H2"	4:X:37:DA:C8	2.53	0.44
7:o:1458:ILE:HD12	8:p:1091:ARG:NH2	2.28	0.44
8:p:419:ALA:O	8:p:423:ILE:HG12	2.17	0.44
8:p:422:PHE:HB3	8:p:428:ASP:O	2.17	0.44
8:p:473:LEU:HD22	8:p:1052:LYS:HD3	1.98	0.44
8:p:561:ILE:HG21	8:p:610:ARG:CB	2.47	0.44
7:o:920:PHE:CD1	7:o:959:MET:HE1	2.52	0.44
7:o:1175:ILE:HG12	7:o:1212:LEU:HD12	1.99	0.44
8:p:51:ILE:O	8:p:52:GLN:C	2.58	0.44
9:q:63:PHE:HE1	9:q:67:ARG:HD2	1.82	0.44
7:o:531:ASN:HD21	7:o:1392:TYR:HE2	1.65	0.44
7:o:784:VAL:HG13	8:p:978:ILE:HD11	1.98	0.44
9:q:44:ILE:HG12	9:q:45:ILE:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:19:DA:H2''	4:X:20:DG:H8	1.81	0.44
7:o:470:MET:HB3	7:o:521:VAL:HG22	1.99	0.44
7:o:1268:LYS:HG3	7:o:1271:GLU:OE2	2.18	0.44
8:p:643:LEU:O	8:p:646:ARG:HB2	2.18	0.44
9:q:7:PRO:HD3	17:y:97:GLU:HG3	2.00	0.44
11:s:62:VAL:O	11:s:71:GLN:HA	2.17	0.44
11:s:73:PHE:HE1	11:s:99:ILE:HD13	1.82	0.44
15:w:14:ILE:HG21	15:w:23:MET:HE2	1.99	0.44
17:y:58:PHE:HB3	17:y:76:GLN:HB3	1.99	0.44
1:N:2:TRX:HE3	7:o:788:VAL:O	2.18	0.44
7:o:102:LYS:HZ1	7:o:141:LEU:HD13	1.82	0.44
7:o:631:GLU:HG2	7:o:988:TRP:HZ2	1.83	0.44
8:p:158:SER:O	8:p:164:ASN:HB2	2.18	0.44
8:p:470:LEU:HD11	8:p:478:THR:HG23	1.99	0.44
8:p:591:ARG:HH12	8:p:592:ARG:HE	1.66	0.44
9:q:59:LEU:HD13	9:q:63:PHE:CE1	2.53	0.44
9:q:72:PRO:HG3	16:x:13:ILE:CD1	2.48	0.44
11:s:94:MET:HE3	11:s:99:ILE:O	2.17	0.44
7:o:365:THR:HG22	7:o:482:PHE:CD2	2.52	0.44
7:o:733:LEU:HA	7:o:736:THR:HG22	1.99	0.44
4:X:41:DA:H2''	4:X:42:DC:C6	2.53	0.44
7:o:469:MET:HE1	8:p:1086:PHE:CZ	2.53	0.44
7:o:1458:ILE:HD11	8:p:1103:LEU:HD21	2.00	0.44
8:p:65:ILE:HG23	8:p:416:ARG:HD3	2.00	0.44
8:p:1007:ASN:HB2	8:p:1010:LYS:HG3	2.00	0.44
8:p:1038:THR:HA	9:q:195:THR:HA	2.00	0.44
12:t:80:MET:HE3	12:t:103:PRO:HG3	1.99	0.44
18:z:36:CYS:HB3	18:z:39:CYS:SG	2.58	0.44
18:z:43:ILE:O	18:z:44:MET:HE2	2.18	0.44
4:X:16:DT:H3	5:Y:-16:DA:H61	1.66	0.44
7:o:212:LYS:H	7:o:212:LYS:HD3	1.82	0.44
7:o:492:TYR:CD1	7:o:501:MET:HE1	2.53	0.44
7:o:991:GLN:HA	7:o:996:ILE:HD12	2.00	0.44
7:o:1347:LEU:C	11:s:137:ILE:HD11	2.43	0.44
7:o:1374:VAL:HG11	7:o:1411:LEU:HD21	1.99	0.44
10:r:24:LYS:HA	10:r:27:GLU:CD	2.43	0.44
4:X:25:DG:H4'	4:X:26:DC:H5'	2.00	0.44
7:o:811:ILE:HD11	8:p:690:CYS:HB2	2.00	0.44
7:o:1421:ARG:HA	7:o:1421:ARG:HD3	1.86	0.44
8:p:313:GLU:HB2	8:p:316:VAL:HG23	1.99	0.44
8:p:796:MET:HE3	8:p:948:GLN:HE21	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:q:38:PHE:CE1	9:q:245:VAL:HA	2.52	0.44
11:s:100:THR:HA	11:s:125:TYR:HD1	1.82	0.44
15:w:106:ASP:OD1	15:w:106:ASP:N	2.51	0.44
17:y:64:PRO:HG3	17:y:70:LYS:HE2	2.00	0.44
7:o:15:LEU:HD11	8:p:1150:ARG:HG3	2.00	0.43
7:o:362:SER:HA	7:o:503:LEU:O	2.18	0.43
7:o:821:GLY:HA2	7:o:838:PHE:CD2	2.53	0.43
7:o:1158:LEU:HG	7:o:1307:VAL:HB	2.00	0.43
17:y:84:GLN:O	17:y:88:THR:HG23	2.18	0.43
7:o:548:PHE:CE1	7:o:555:LEU:HD11	2.53	0.43
9:q:78:ILE:HD11	9:q:127:VAL:CG2	2.48	0.43
18:z:46:LYS:O	18:z:47:LYS:HB3	2.17	0.43
2:S:150:ALA:HB2	15:w:20:CYS:HB3	2.00	0.43
7:o:686:THR:HG21	8:p:1040:GLN:O	2.19	0.43
7:o:910:LYS:N	7:o:911:PRO:HD2	2.33	0.43
7:o:1153:ARG:O	7:o:1157:ILE:HG12	2.19	0.43
8:p:861:SER:O	8:p:896:LEU:HD12	2.19	0.43
13:u:14:HIS:CD2	13:u:16:ARG:H	2.36	0.43
14:v:60:ILE:HG21	14:v:135:PHE:CZ	2.53	0.43
7:o:210:GLN:HB2	7:o:214:ILE:HD11	1.99	0.43
7:o:1206:ARG:HA	7:o:1206:ARG:HD3	1.73	0.43
8:p:565:THR:HA	8:p:610:ARG:C	2.43	0.43
8:p:731:GLN:HG2	8:p:1052:LYS:NZ	2.33	0.43
8:p:1151:MET:HE2	8:p:1155:CYS:HB3	2.00	0.43
15:w:36:LEU:HD23	15:w:47:GLU:HA	1.99	0.43
7:o:552:ASP:OD1	14:v:22:PHE:HB3	2.17	0.43
7:o:1160:ARG:O	7:o:1300:GLY:HA2	2.17	0.43
7:o:1282:ASP:N	7:o:1282:ASP:OD1	2.51	0.43
9:q:60:HIS:CD2	9:q:62:GLU:HG2	2.43	0.43
10:r:110:GLU:O	10:r:114:LEU:HG	2.17	0.43
11:s:8:TYR:CE2	11:s:12:LYS:HD2	2.53	0.43
13:u:84:VAL:HA	13:u:145:LEU:O	2.19	0.43
7:o:1016:LEU:O	7:o:1020:LEU:HG	2.18	0.43
8:p:296:GLU:O	8:p:300:MET:HG2	2.19	0.43
8:p:415:VAL:HA	8:p:434:ALA:HB1	2.00	0.43
9:q:173:HIS:ND1	9:q:175:LYS:HB3	2.32	0.43
11:s:63:ALA:HA	11:s:71:GLN:HA	1.99	0.43
17:y:47:LYS:HD3	17:y:61:TYR:HD1	1.83	0.43
4:X:17:DC:H2''	4:X:18:DG:OP2	2.17	0.43
4:X:17:DC:C2'	4:X:18:DG:C8	3.00	0.43
5:Y:-11:DG:H5''	8:p:1085:ARG:CG	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:o:123:ASN:HD21	7:o:125:LYS:HB2	1.83	0.43
7:o:885:GLN:HE22	7:o:1408:ARG:HH12	1.65	0.43
7:o:892:GLY:HA3	7:o:1396:ARG:HH11	1.82	0.43
8:p:193:VAL:HG23	8:p:470:LEU:HB2	1.99	0.43
8:p:646:ARG:HG3	8:p:651:TYR:O	2.19	0.43
8:p:971:ALA:O	8:p:975:ARG:HD2	2.18	0.43
8:p:1142:ASN:ND2	8:p:1145:GLN:HB2	2.27	0.43
13:u:5:ILE:HD12	13:u:7:LEU:HD21	2.01	0.43
7:o:34:MET:HE2	7:o:34:MET:HB3	1.92	0.43
7:o:58:MET:HE3	7:o:65:ILE:HD13	2.00	0.43
8:p:43:GLN:HE21	8:p:43:GLN:HB3	1.69	0.43
8:p:567:ILE:HA	8:p:612:ILE:CG2	2.48	0.43
8:p:713:PHE:HB3	8:p:716:HIS:HD2	1.83	0.43
8:p:860:VAL:HB	8:p:896:LEU:HD11	2.01	0.43
13:u:31:PHE:O	13:u:35:GLU:HB2	2.19	0.43
7:o:379:GLY:O	7:o:482:PHE:HA	2.18	0.43
7:o:472:HIS:CE1	7:o:521:VAL:HG21	2.54	0.43
7:o:916:PHE:CE2	7:o:960:ARG:HG2	2.53	0.43
8:p:237:VAL:HG11	8:p:369:VAL:HG22	2.01	0.43
8:p:789:ASN:HD22	8:p:966:ILE:HG22	1.84	0.43
10:r:121:ARG:HD3	10:r:121:ARG:HA	1.80	0.43
17:y:20:THR:OG1	17:y:34:THR:HB	2.19	0.43
1:N:1:ILX:CG2	7:o:791:GLN:HE22	2.28	0.43
4:X:-1:DC:H2"	4:X:0:DA:C8	2.54	0.43
7:o:113:PHE:CE1	7:o:186:ARG:HD2	2.53	0.43
7:o:421:ARG:NE	7:o:427:ILE:HD11	2.34	0.43
7:o:457:ILE:HG12	7:o:515:ILE:HD13	2.01	0.43
8:p:818:GLU:O	8:p:916:TYR:HB3	2.19	0.43
13:u:152:VAL:HG22	13:u:157:ILE:HG12	2.00	0.43
14:v:10:PHE:CE2	14:v:32:SER:HB3	2.53	0.43
14:v:60:ILE:HG23	14:v:141:VAL:HG13	2.01	0.43
7:o:510:GLU:O	7:o:514:GLU:HG3	2.19	0.42
7:o:552:ASP:CG	14:v:22:PHE:HB3	2.43	0.42
7:o:1161:LEU:HD21	7:o:1349:GLU:HG3	2.01	0.42
9:q:190:ASN:HD22	9:q:217:GLN:NE2	2.16	0.42
14:v:41:LEU:HG	14:v:43:VAL:HG23	1.99	0.42
7:o:87:HIS:CD2	7:o:89:GLU:HG3	2.54	0.42
7:o:1289:GLU:O	7:o:1293:LEU:HG	2.19	0.42
8:p:712:PRO:HD3	8:p:938:ARG:HD2	2.01	0.42
8:p:712:PRO:O	8:p:939:HIS:HE1	2.01	0.42
10:r:134:ILE:O	10:r:138:ARG:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:s:18:MET:HE3	11:s:28:VAL:HG13	2.01	0.42
14:v:52:LEU:HD23	14:v:52:LEU:HA	1.78	0.42
7:o:1245:CYS:HB3	7:o:1257:LEU:HD11	2.01	0.42
8:p:407:MET:HE3	8:p:407:MET:HB2	1.77	0.42
8:p:719:SER:OG	8:p:720:PRO:HD3	2.19	0.42
2:S:43:ASN:OD1	2:S:44:GLN:N	2.52	0.42
4:X:15:DT:H2''	4:X:16:DT:C2'	2.49	0.42
5:Y:-35:DG:OP2	5:Y:-35:DG:H8	2.03	0.42
8:p:564:ALA:HA	8:p:610:ARG:HD2	2.01	0.42
17:y:105:PHE:CE2	17:y:109:ILE:HD11	2.54	0.42
7:o:255:VAL:HG22	7:o:280:LEU:HD22	2.00	0.42
7:o:1095:LEU:HD13	7:o:1401:LEU:HD22	1.99	0.42
8:p:404:PHE:HA	8:p:407:MET:HE2	2.02	0.42
8:p:473:LEU:HD23	8:p:731:GLN:HA	2.02	0.42
9:q:49:TRP:CE3	9:q:164:TYR:HD2	2.37	0.42
7:o:535:MET:O	7:o:669:TYR:OH	2.31	0.42
7:o:1118:THR:HG21	7:o:1135:LYS:HB2	2.02	0.42
8:p:561:ILE:HB	8:p:610:ARG:NH1	2.34	0.42
11:s:24:ARG:HH12	11:s:103:LEU:HD21	1.85	0.42
8:p:918:PHE:CE2	8:p:920:LYS:HE3	2.55	0.42
10:r:41:LEU:HD22	10:r:61:PHE:CE2	2.55	0.42
14:v:37:MET:HE2	14:v:37:MET:HB3	1.78	0.42
7:o:456:VAL:HG21	7:o:503:LEU:HD11	2.02	0.42
7:o:792:ASN:HD21	7:o:1108:HIS:HE1	1.62	0.42
7:o:811:ILE:HG13	8:p:689:TYR:CE2	2.55	0.42
13:u:25:THR:O	13:u:29:LYS:HG2	2.20	0.42
7:o:952:LEU:HD21	7:o:1006:PRO:HB2	2.01	0.42
7:o:1139:LEU:HD12	7:o:1358:THR:O	2.19	0.42
7:o:1215:GLU:HG2	7:o:1256:VAL:HG22	2.02	0.42
8:p:19:PRO:C	8:p:21:LEU:H	2.27	0.42
8:p:764:MET:HE1	8:p:938:ARG:NH1	2.35	0.42
8:p:975:ARG:CZ	21:p:1201:W0F:O32	2.67	0.42
13:u:14:HIS:HD2	13:u:16:ARG:H	1.68	0.42
7:o:340:LYS:O	7:o:344:LYS:HB2	2.20	0.42
7:o:515:ILE:HD11	8:p:1102:PHE:CD1	2.55	0.42
7:o:1143:LEU:HB2	7:o:1148:ALA:HB2	2.02	0.42
8:p:369:VAL:O	8:p:373:LEU:HG	2.20	0.42
8:p:661:VAL:HG12	8:p:662:VAL:HG13	2.02	0.42
14:v:90:TYR:HB3	14:v:145:MET:HB2	2.02	0.42
2:S:111:LYS:O	2:S:146:PHE:HA	2.20	0.41
7:o:713:VAL:O	7:o:717:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:o:745:LEU:HD21	7:o:817:PRO:HB3	2.01	0.41
8:p:1028:LEU:HD23	8:p:1028:LEU:HA	1.77	0.41
9:q:33:SER:O	9:q:37:VAL:HG23	2.20	0.41
11:s:26:TYR:HA	11:s:64:HIS:HA	2.01	0.41
3:T:9:LEU:O	3:T:13:LYS:HG2	2.20	0.41
7:o:368:THR:HG21	8:p:931:ILE:O	2.20	0.41
7:o:376:ASP:N	7:o:376:ASP:OD1	2.51	0.41
7:o:589:LYS:HZ3	7:o:625:ASP:CG	2.28	0.41
7:o:687:ILE:HD13	7:o:765:ASN:HB2	2.01	0.41
8:p:1016:SER:HB2	8:p:1022:LEU:HD23	2.01	0.41
2:S:47:LEU:HD11	2:S:98:TRP:HB3	2.01	0.41
4:X:31:DG:H2''	4:X:32:DT:H72	2.01	0.41
7:o:256:PRO:HB2	7:o:260:VAL:HB	2.02	0.41
7:o:717:ILE:HG12	7:o:737:PHE:CZ	2.56	0.41
8:p:833:THR:HB	8:p:836:THR:HB	2.02	0.41
8:p:1118:VAL:HG21	8:p:1171:MET:HE3	2.02	0.41
13:u:101:ILE:HD11	13:u:145:LEU:HD11	2.02	0.41
5:Y:-19:DT:H1'	5:Y:-18:DC:H5'	2.02	0.41
7:o:526:VAL:HA	7:o:533:PRO:HA	2.02	0.41
8:p:780:VAL:HG22	8:p:965:ILE:HB	2.01	0.41
8:p:1053:HIS:HB3	8:p:1058:LYS:HE3	2.01	0.41
10:r:111:SER:HB2	10:r:131:LEU:HD21	2.02	0.41
13:u:118:GLU:O	13:u:128:TYR:HA	2.20	0.41
7:o:316:THR:HG21	7:o:328:ALA:HB3	2.01	0.41
8:p:222:ARG:HG2	8:p:234:THR:HG22	2.03	0.41
8:p:623:ARG:CZ	8:p:625:LEU:HD21	2.50	0.41
8:p:715:ASP:OD1	8:p:715:ASP:N	2.52	0.41
8:p:795:ILE:HB	8:p:966:ILE:HB	2.02	0.41
9:q:154:ARG:HG2	9:q:155:LYS:N	2.35	0.41
6:Z:8:U:H2'	6:Z:9:C:C6	2.55	0.41
7:o:360:ASP:O	8:p:1106:ARG:NH2	2.54	0.41
7:o:1207:ILE:O	7:o:1266:GLU:HG2	2.20	0.41
8:p:298:MET:HB3	15:w:14:ILE:HD12	2.03	0.41
8:p:627:ILE:HD12	8:p:660:GLY:O	2.21	0.41
8:p:1102:PHE:CE1	8:p:1106:ARG:HD3	2.56	0.41
13:u:104:MET:HE2	13:u:104:MET:HB3	1.94	0.41
3:T:43:LEU:HD12	3:T:55:SER:O	2.21	0.41
4:X:35:DC:H2''	4:X:36:DT:C7	2.47	0.41
7:o:945:ASN:HB2	7:o:948:ILE:HG13	2.01	0.41
8:p:425:ARG:HB3	8:p:427:LYS:HE3	2.02	0.41
9:q:35:ARG:HA	9:q:38:PHE:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:17:DC:H3'	4:X:17:DC:OP2	2.20	0.41
7:o:198:LEU:O	7:o:215:LEU:HD12	2.21	0.41
7:o:408:ARG:HH11	7:o:414:PRO:HB2	1.85	0.41
7:o:873:VAL:HG22	7:o:879:VAL:HG22	2.02	0.41
3:T:31:TRP:CD1	3:T:62:LEU:HD21	2.56	0.41
5:Y:-10:DA:H2'	5:Y:-9:DT:C6	2.56	0.41
7:o:123:ASN:ND2	7:o:125:LYS:HB2	2.36	0.41
7:o:194:SER:HB3	7:o:199:TYR:HE2	1.85	0.41
7:o:514:GLU:CD	8:p:1101:GLN:HB3	2.46	0.41
7:o:1434:GLU:C	7:o:1435:THR:HG1	2.26	0.41
8:p:230:ARG:O	8:p:231:PRO:C	2.64	0.41
2:S:164:TRP:CH2	2:S:167:ARG:HD3	2.56	0.41
2:S:172:ASN:O	2:S:176:ILE:HG12	2.21	0.41
4:X:18:DG:H4'	7:o:1417:HIS:CG	2.55	0.41
7:o:102:LYS:HB3	7:o:102:LYS:HE3	1.82	0.41
7:o:903:PHE:O	7:o:904:GLN:HG3	2.20	0.41
7:o:992:LYS:HD3	7:o:992:LYS:HA	1.84	0.41
8:p:52:GLN:O	8:p:53:MET:C	2.64	0.41
9:q:47:ILE:HA	9:q:165:ALA:HA	2.03	0.41
8:p:721:ARG:HA	8:p:721:ARG:HD3	1.91	0.40
13:u:12:LEU:HD11	13:u:67:LEU:HD12	2.03	0.40
7:o:53:LYS:HE3	7:o:53:LYS:HB2	1.78	0.40
7:o:491:PRO:CG	7:o:535:MET:HG2	2.51	0.40
7:o:1487:PRO:HD2	12:t:79:VAL:H	1.86	0.40
8:p:806:PHE:O	8:p:1050:ARG:NH1	2.54	0.40
8:p:839:GLY:O	8:p:891:ASP:HB2	2.21	0.40
11:s:61:LEU:HD13	11:s:73:PHE:CE1	2.56	0.40
14:v:76:ASN:HB3	14:v:79:ASP:HB2	2.03	0.40
4:X:14:DC:H2'	4:X:14:DC:OP2	2.20	0.40
4:X:38:DC:H2''	4:X:39:DG:N7	2.37	0.40
7:o:64:VAL:HG12	7:o:78:MET:HE2	2.03	0.40
7:o:1004:LEU:HD13	7:o:1062:GLY:HA2	2.03	0.40
7:o:1486:ILE:HB	7:o:1487:PRO:HD3	2.03	0.40
8:p:505:LEU:HD23	8:p:505:LEU:HA	1.83	0.40
8:p:628:VAL:HG21	8:p:683:GLN:NE2	2.35	0.40
8:p:809:VAL:HG21	9:q:60:HIS:CE1	2.57	0.40
8:p:962:THR:O	16:x:9:THR:HG23	2.21	0.40
15:w:117:PRO:HB2	15:w:118:HIS:CD2	2.57	0.40
3:T:30:GLN:O	3:T:62:LEU:HD11	2.22	0.40
7:o:18:ILE:HB	7:o:1462:GLN:HE22	1.85	0.40
7:o:226:LYS:HG2	7:o:246:GLU:OE1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:o:521:VAL:HG12	7:o:535:MET:HE1	2.04	0.40
7:o:948:ILE:HG23	7:o:1007:ILE:HG13	2.03	0.40
7:o:1194:ASN:O	7:o:1198:GLU:N	2.55	0.40
8:p:132:VAL:O	8:p:139:GLN:HA	2.22	0.40
8:p:252:ILE:HD12	8:p:255:ARG:HD3	2.04	0.40
8:p:577:HIS:CD2	8:p:578:LYS:H	2.39	0.40
7:o:1115:LYS:HD3	7:o:1337:GLU:HB3	2.02	0.40
7:o:1467:GLY:C	7:o:1469:GLY:H	2.29	0.40
8:p:831:LYS:HE3	8:p:845:TYR:O	2.21	0.40
11:s:55:ARG:HB2	11:s:78:GLU:HG2	2.02	0.40
17:y:11:LEU:HD23	17:y:11:LEU:HA	1.97	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	N	4/8 (50%)	3 (75%)	1 (25%)	0	100	100
2	S	134/517 (26%)	134 (100%)	0	0	100	100
3	T	99/249 (40%)	95 (96%)	4 (4%)	0	100	100
7	o	1448/1970 (74%)	1393 (96%)	53 (4%)	2 (0%)	48	79
8	p	1142/1174 (97%)	1072 (94%)	67 (6%)	3 (0%)	36	68
9	q	253/275 (92%)	243 (96%)	10 (4%)	0	100	100
10	r	126/142 (89%)	126 (100%)	0	0	100	100
11	s	207/210 (99%)	198 (96%)	9 (4%)	0	100	100
12	t	80/127 (63%)	80 (100%)	0	0	100	100
13	u	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
14	v	146/150 (97%)	138 (94%)	7 (5%)	1 (1%)	18	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	w	112/125 (90%)	103 (92%)	9 (8%)	0	100	100
16	x	65/67 (97%)	63 (97%)	0	2 (3%)	3	17
17	y	113/117 (97%)	112 (99%)	1 (1%)	0	100	100
18	z	42/58 (72%)	39 (93%)	3 (7%)	0	100	100
All	All	4140/5361 (77%)	3964 (96%)	168 (4%)	8 (0%)	44	75

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	o	910	LYS
16	x	28	GLU
8	p	549	SER
14	v	34	SER
16	x	6	ARG
8	p	570	ASN
7	o	184	CYS
8	p	614	ILE

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	N	2/2 (100%)	2 (100%)	0	100	100
2	S	121/448 (27%)	120 (99%)	1 (1%)	73	85
3	T	85/218 (39%)	85 (100%)	0	100	100
7	o	1280/1749 (73%)	1258 (98%)	22 (2%)	53	77
8	p	1001/1027 (98%)	986 (98%)	15 (2%)	57	79
9	q	234/252 (93%)	230 (98%)	4 (2%)	53	77
10	r	118/126 (94%)	118 (100%)	0	100	100
11	s	191/192 (100%)	191 (100%)	0	100	100
12	t	71/111 (64%)	71 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	u	152/153 (99%)	151 (99%)	1 (1%)	76	85
14	v	129/131 (98%)	128 (99%)	1 (1%)	73	85
15	w	103/112 (92%)	102 (99%)	1 (1%)	68	83
16	x	56/56 (100%)	56 (100%)	0	100	100
17	y	104/106 (98%)	103 (99%)	1 (1%)	68	83
18	z	41/55 (74%)	41 (100%)	0	100	100
All	All	3688/4738 (78%)	3642 (99%)	46 (1%)	61	81

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	S	170	VAL
7	o	46	THR
7	o	48	GLU
7	o	184	CYS
7	o	227	ARG
7	o	302	VAL
7	o	488	VAL
7	o	490	THR
7	o	495	ASP
7	o	534	VAL
7	o	538	VAL
7	o	626	THR
7	o	636	ILE
7	o	675	VAL
7	o	676	ILE
7	o	689	ILE
7	o	863	ARG
7	o	909	LEU
7	o	1087	VAL
7	o	1207	ILE
7	o	1279	MET
7	o	1389	ASP
7	o	1458	ILE
8	p	42	GLN
8	p	51	ILE
8	p	59	VAL
8	p	235	ILE
8	p	279	VAL
8	p	423	ILE

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Mol	Chain	Res	Type
8	p	447	SER
8	p	466	VAL
8	p	471	ASN
8	p	598	VAL
8	p	670	GLU
8	p	860	VAL
8	p	908	MET
8	p	927	ARG
8	p	1067	ILE
9	q	13	GLU
9	q	44	ILE
9	q	75	SER
9	q	94	CYS
13	u	85	VAL
14	v	58	LEU
15	w	95	VAL
17	y	42	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (70) such sidechains are listed below:

Mol	Chain	Res	Type
2	S	44	GLN
2	S	178	GLN
3	T	59	ASN
3	T	64	ASN
7	o	62	GLN
7	o	181	HIS
7	o	301	HIS
7	o	449	HIS
7	o	531	ASN
7	o	539	GLN
7	o	599	HIS
7	o	671	ASN
7	o	721	HIS
7	o	731	ASN
7	o	780	ASN
7	o	783	GLN
7	o	791	GLN
7	o	792	ASN
7	o	804	HIS
7	o	904	GLN
7	o	1032	GLN

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Mol	Chain	Res	Type
7	o	1044	HIS
7	o	1082	HIS
7	o	1093	GLN
7	o	1163	HIS
7	o	1190	GLN
7	o	1194	ASN
7	o	1230	GLN
7	o	1410	HIS
7	o	1422	GLN
7	o	1445	HIS
7	o	1462	GLN
8	p	43	GLN
8	p	56	GLN
8	p	68	GLN
8	p	117	ASN
8	p	164	ASN
8	p	245	GLN
8	p	312	GLN
8	p	387	HIS
8	p	430	ASN
8	p	486	ASN
8	p	500	GLN
8	p	518	HIS
8	p	639	HIS
8	p	699	HIS
8	p	725	GLN
8	p	755	GLN
8	p	797	ASN
8	p	838	GLN
8	p	941	GLN
8	p	948	GLN
8	p	1071	ASN
8	p	1094	GLN
9	q	18	ASN
9	q	190	ASN
9	q	232	ASN
9	q	262	GLN
10	r	66	ASN
10	r	129	GLN
11	s	35	GLN
11	s	64	HIS
12	t	46	GLN

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Mol	Chain	Res	Type
13	u	14	HIS
13	u	53	ASN
14	v	131	ASN
15	w	41	ASN
15	w	118	HIS
17	y	49	GLN
17	y	69	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	Z	11/13 (84%)	3 (27%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	Z	3	C
6	Z	4	A
6	Z	13	G2L

There are no RNA pucker outliers to report.

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

5 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	G2L	Z	13	5,6,20	23,26,30	1.19	3 (13%)	31,38,44	2.10	7 (22%)
1	HYP	N	8	1	7,8,9	0.81	0	5,10,12	2.33	2 (40%)
1	ILX	N	1	1	8,9,10	0.65	0	8,11,13	1.39	1 (12%)
1	TRX	N	2	1	15,16,17	1.10	1 (6%)	17,22,24	0.96	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	CSX	N	6	1	3,6,7	1.05	0	1,6,8	2.10	1 (100%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	G2L	Z	13	5,6,20	-	0/9/27/31	0/3/3/3
1	HYP	N	8	1	-	0/0/11/13	0/1/1/1
1	ILX	N	1	1	-	7/11/12/14	-
1	TRX	N	2	1	-	2/5/6/8	0/2/2/2
1	CSX	N	6	1	-	2/2/5/7	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	Z	13	G2L	C5-C4	3.17	1.47	1.38
1	N	2	TRX	CD2-CE2	2.45	1.44	1.41
6	Z	13	G2L	C6-N1	-2.39	1.34	1.38
6	Z	13	G2L	C5-N7	-2.02	1.35	1.39

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	Z	13	G2L	C5-C4-N3	-6.14	118.62	128.39
6	Z	13	G2L	C2-N3-C4	5.03	120.97	112.30
6	Z	13	G2L	N9-C4-N3	4.52	134.99	125.95
1	N	8	HYP	CB-CG-CD	3.35	106.89	103.16
1	N	8	HYP	O-C-CA	-3.33	116.20	124.77
6	Z	13	G2L	C6-C5-N7	3.23	136.17	130.29
1	N	1	ILX	OD1-CD1-CG1	-3.05	104.76	111.16
6	Z	13	G2L	C3'-C2'-C1'	2.76	105.95	99.89
6	Z	13	G2L	C4-C5-N7	-2.60	106.56	110.67
1	N	6	CSX	CA-CB-SG	2.10	118.12	113.17
6	Z	13	G2L	O6-C6-C5	-2.07	121.07	126.53

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	N	1	ILX	C-CA-CB-CG2
1	N	1	ILX	OD1-CD1-CG1-CB
1	N	1	ILX	OD1-CD1-CG1-OG1
1	N	6	CSX	N-CA-CB-SG
1	N	6	CSX	C-CA-CB-SG
1	N	2	TRX	CA-CB-CG-CD2
1	N	2	TRX	CA-CB-CG-CD1
1	N	1	ILX	C-CA-CB-CG1
1	N	1	ILX	N-CA-CB-CG2
1	N	1	ILX	CG2-CB-CG1-CD1
1	N	1	ILX	CG2-CB-CG1-OG1

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	Z	13	G2L	2	0
1	N	1	ILX	3	0
1	N	2	TRX	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 9 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
21	W0F	p	1201	-	34,35,35	4.05	14 (41%)	43,55,55	3.45	17 (39%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	W0F	p	1201	-	-	3/24/40/40	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	p	1201	W0F	P26-O29	13.71	1.74	1.59
21	p	1201	W0F	C03-C04	-9.79	1.27	1.52
21	p	1201	W0F	P22-O25	8.41	1.68	1.59
21	p	1201	W0F	O05-C04	6.89	1.60	1.45
21	p	1201	W0F	O05-C06	-5.98	1.28	1.42
21	p	1201	W0F	C12-C13	5.62	1.47	1.38
21	p	1201	W0F	P26-O25	5.35	1.65	1.59
21	p	1201	W0F	C13-N09	-3.14	1.34	1.37
21	p	1201	W0F	C07-C03	-3.00	1.46	1.53
21	p	1201	W0F	C20-C04	2.58	1.59	1.51
21	p	1201	W0F	C06-N09	2.34	1.54	1.47
21	p	1201	W0F	P22-O21	2.16	1.67	1.59
21	p	1201	W0F	C12-N11	-2.09	1.34	1.39
21	p	1201	W0F	C17-N16	-2.03	1.34	1.38

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	p	1201	W0F	O05-C06-N09	-14.58	75.33	108.36
21	p	1201	W0F	C07-C06-N09	8.28	136.31	113.25
21	p	1201	W0F	O05-C04-C03	-5.77	92.75	104.92
21	p	1201	W0F	O27-P26-O25	-5.27	93.04	107.27
21	p	1201	W0F	O05-C04-C20	4.92	125.11	109.33
21	p	1201	W0F	O05-C06-C07	-4.15	97.74	106.62
21	p	1201	W0F	O21-C20-C04	3.98	122.53	108.99
21	p	1201	W0F	O32-P30-O29	3.90	117.70	104.64
21	p	1201	W0F	O33-P30-O31	-3.35	97.77	110.83
21	p	1201	W0F	C06-N09-C10	-3.23	117.55	126.73
21	p	1201	W0F	O08-C07-C06	2.82	119.81	110.10
21	p	1201	W0F	O33-P30-O29	2.66	113.56	104.64
21	p	1201	W0F	O21-P22-O24	-2.28	99.90	108.94
21	p	1201	W0F	O29-P26-O28	2.27	117.54	110.70
21	p	1201	W0F	O27-P26-O29	2.16	113.11	107.27
21	p	1201	W0F	C13-C12-N11	-2.10	106.54	109.26
21	p	1201	W0F	C10-N09-C13	2.09	108.43	106.67

There are no chirality outliers.

All (3) torsion outliers are listed below:

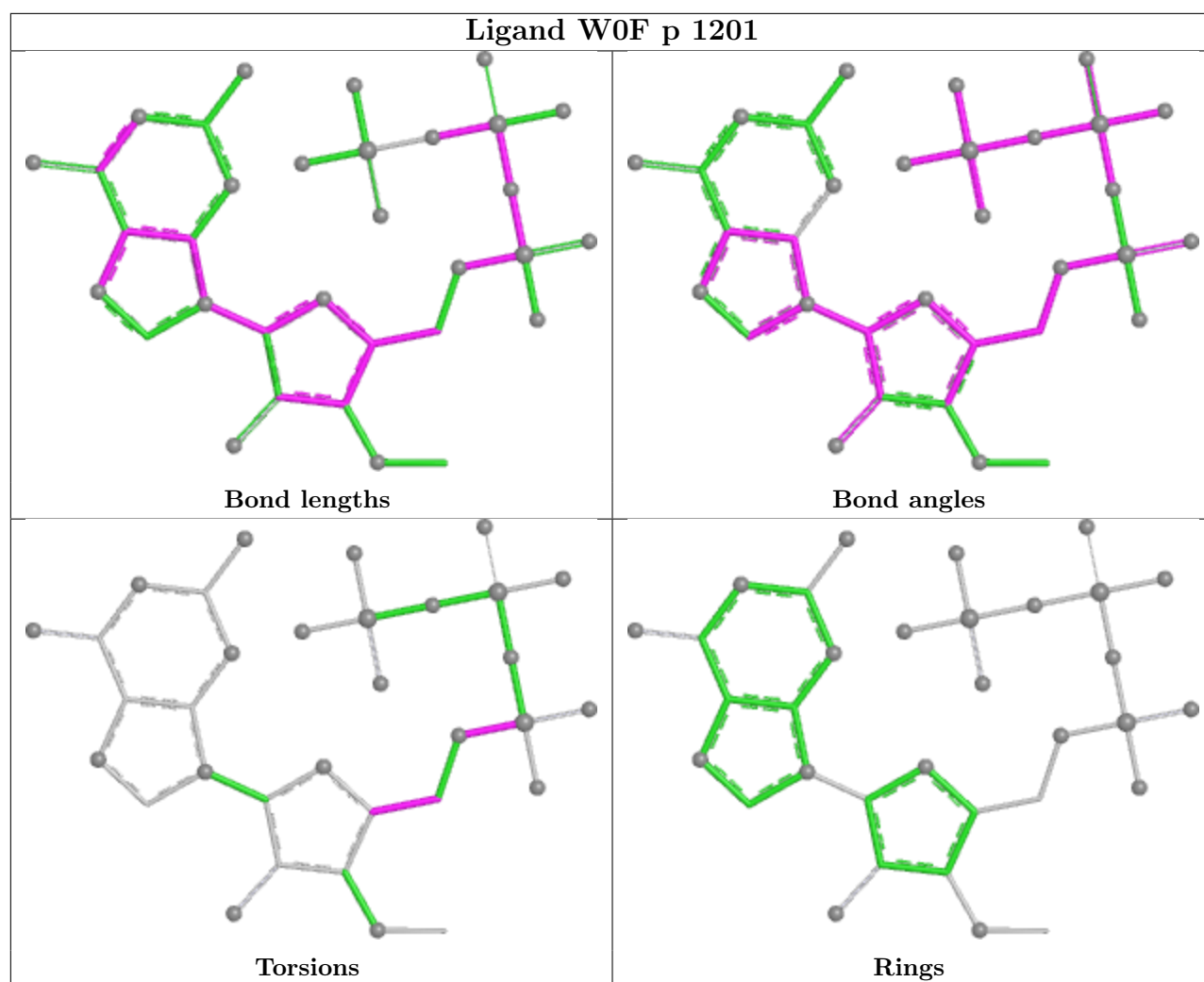
Mol	Chain	Res	Type	Atoms
21	p	1201	W0F	C20-O21-P22-O24
21	p	1201	W0F	C20-O21-P22-O25
21	p	1201	W0F	C03-C04-C20-O21

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
21	p	1201	W0F	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

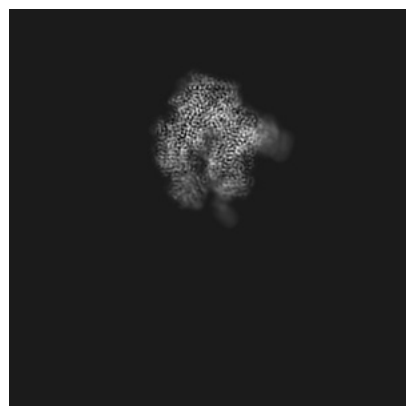
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37407. These allow visual inspection of the internal detail of the map and identification of artifacts.

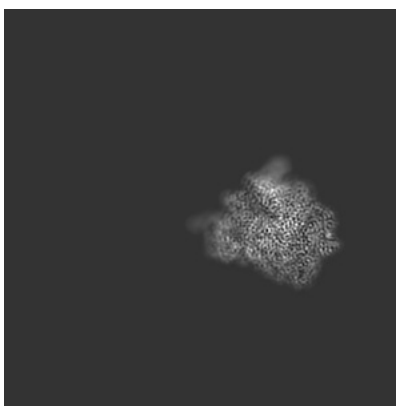
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

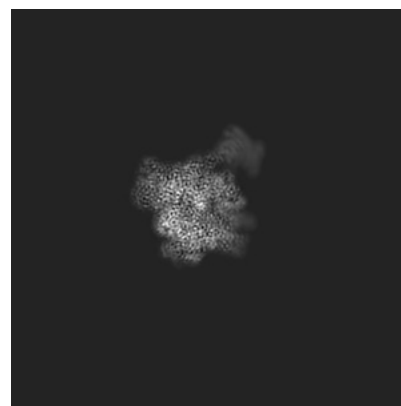
6.1.1 Primary map



X

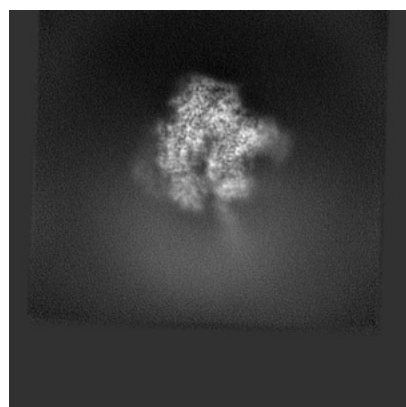


Y

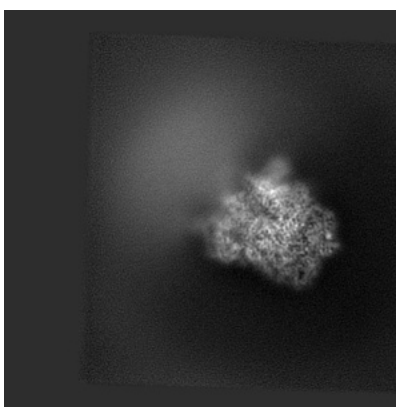


Z

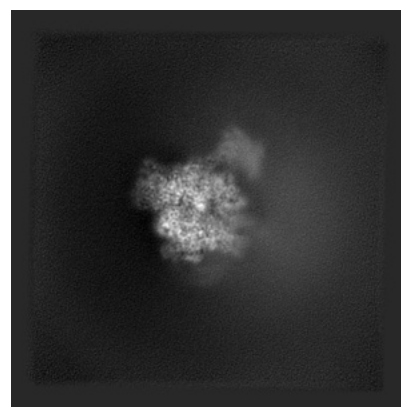
6.1.2 Raw map



X



Y

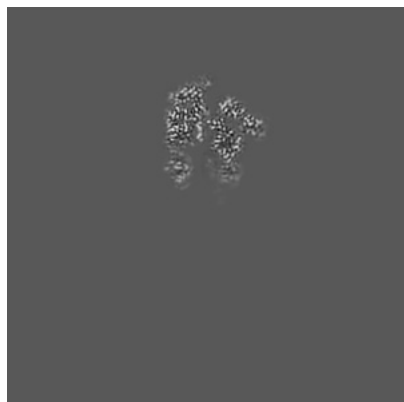


Z

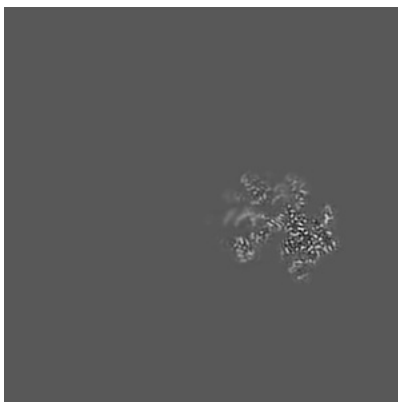
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

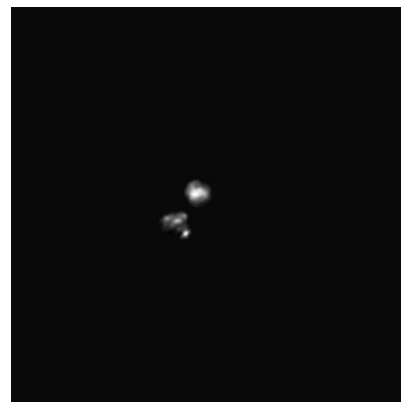
6.2.1 Primary map



X Index: 160

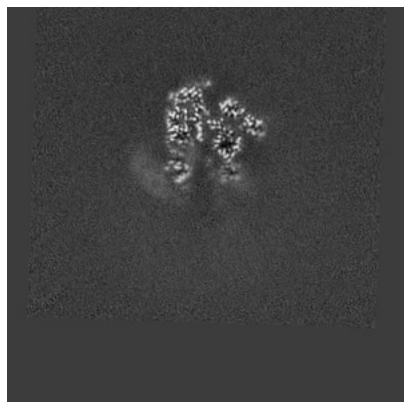


Y Index: 160

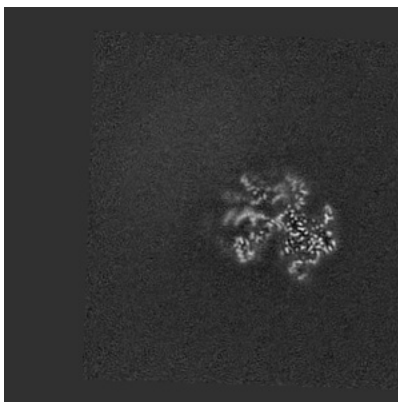


Z Index: 160

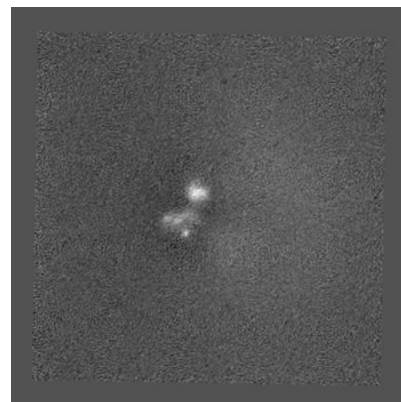
6.2.2 Raw map



X Index: 160



Y Index: 160

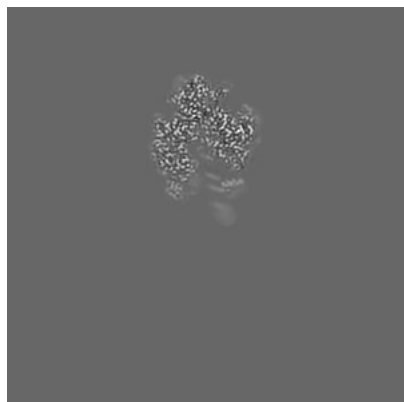


Z Index: 160

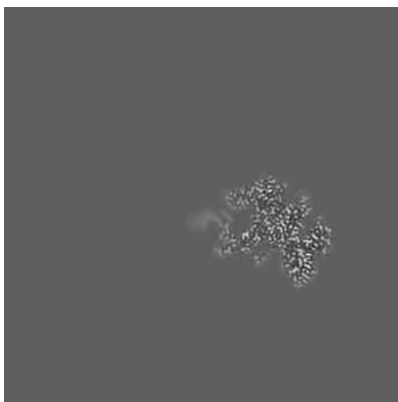
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

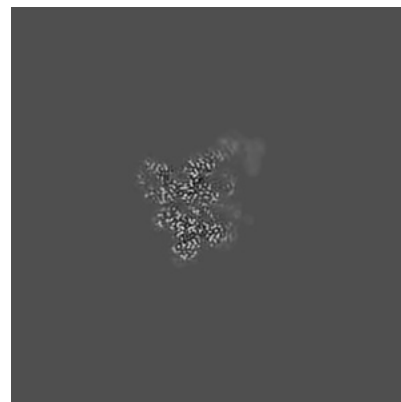
6.3.1 Primary map



X Index: 145

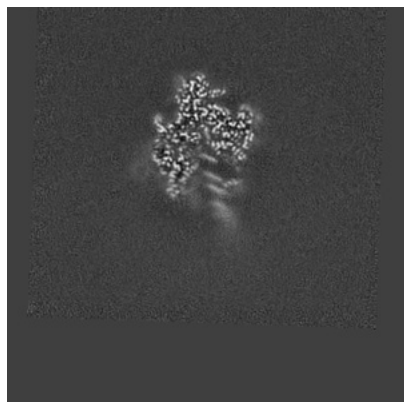


Y Index: 172

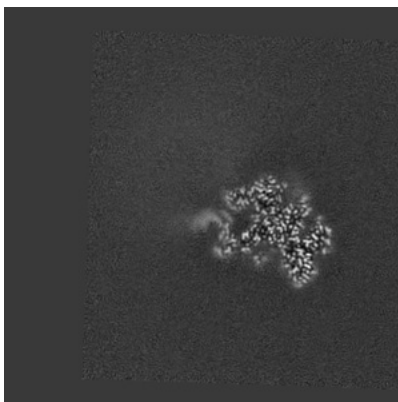


Z Index: 224

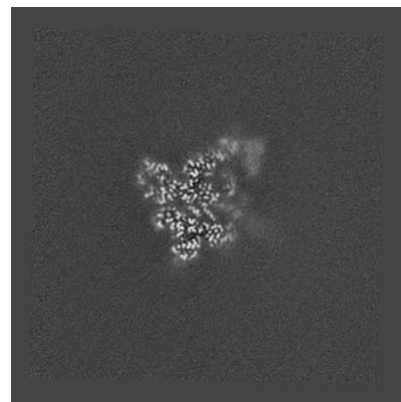
6.3.2 Raw map



X Index: 147



Y Index: 172

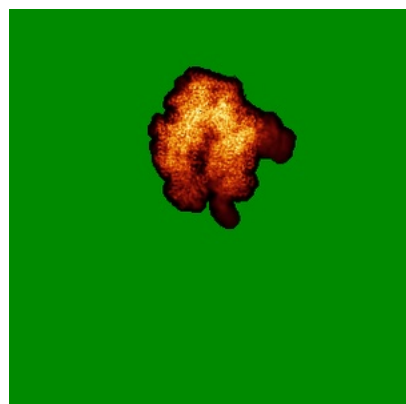


Z Index: 224

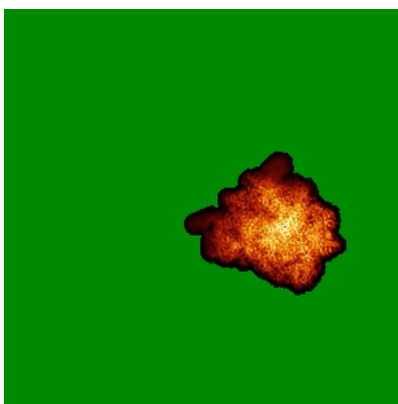
The images above show the largest variance slices of the map in three orthogonal directions.

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

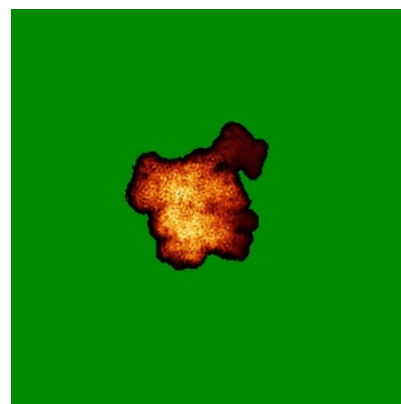
6.4.1 Primary map



X

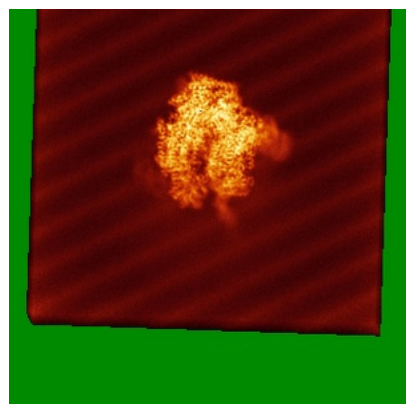


Y

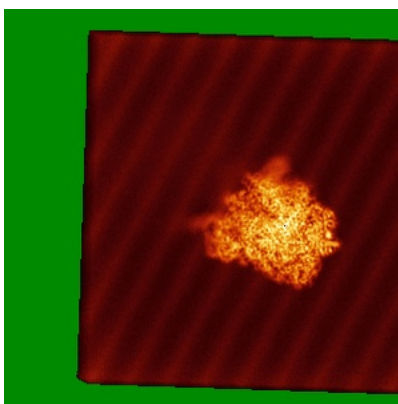


Z

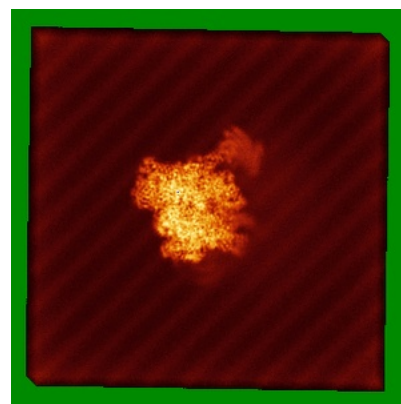
6.4.2 Raw map



X



Y

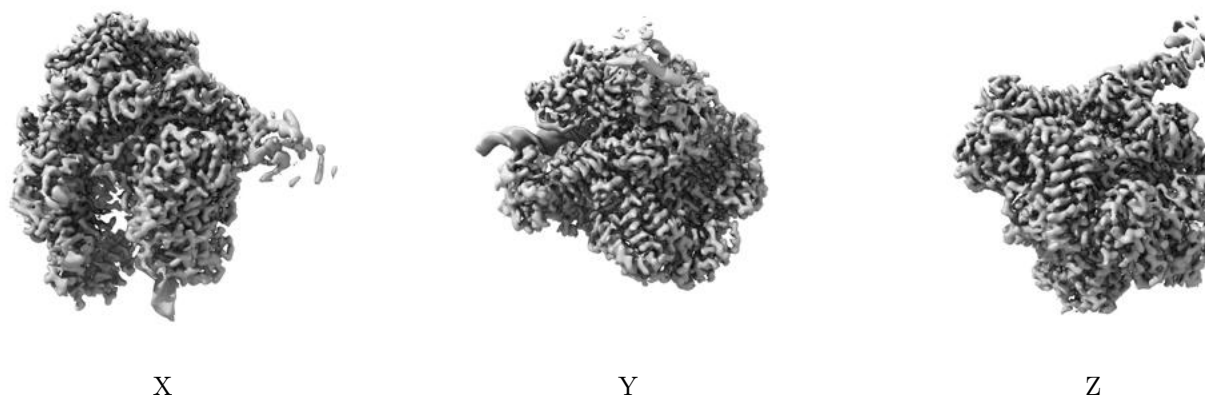


Z

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 0.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

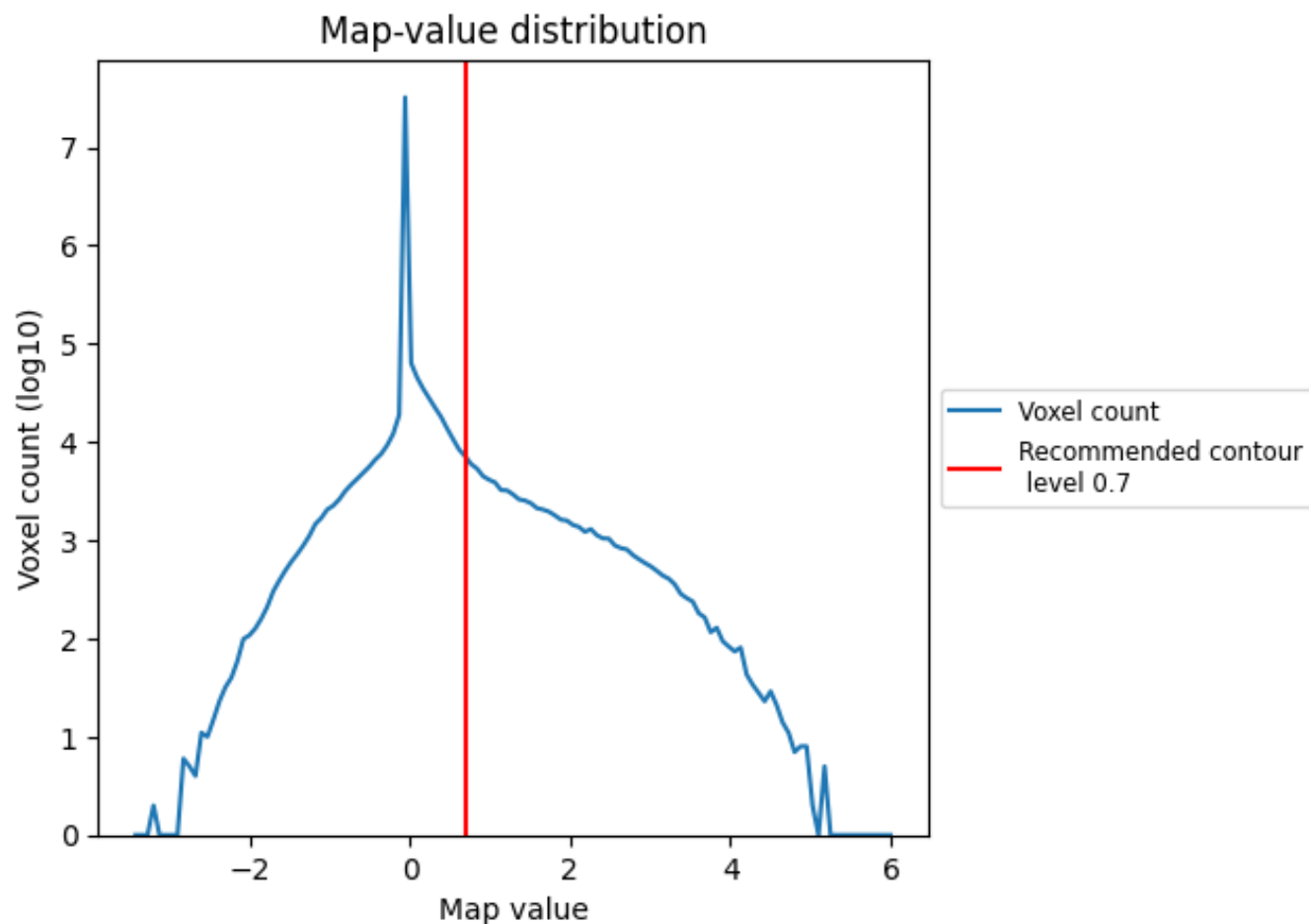
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

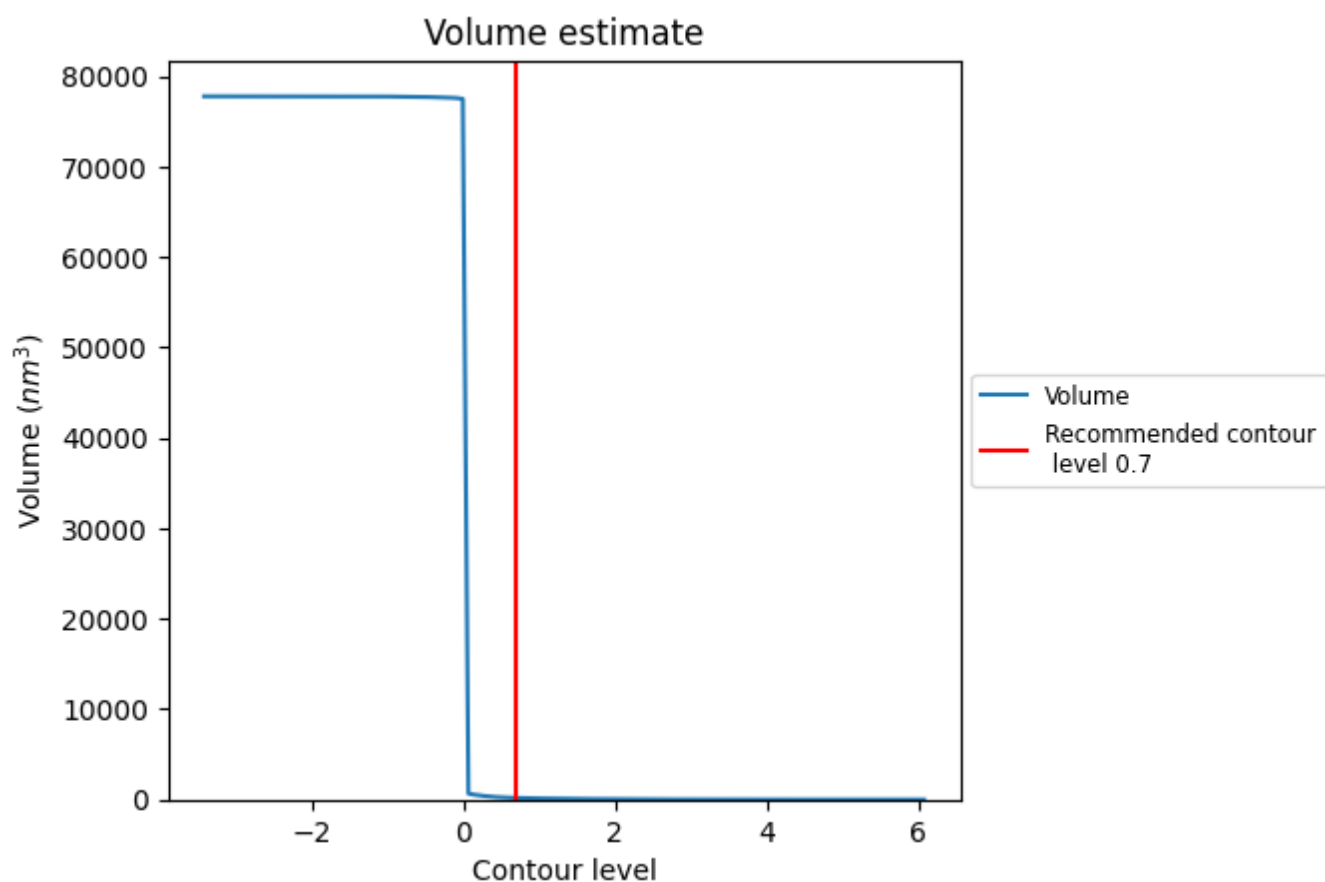
This section contains the results of statistical analysis of the map.

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.

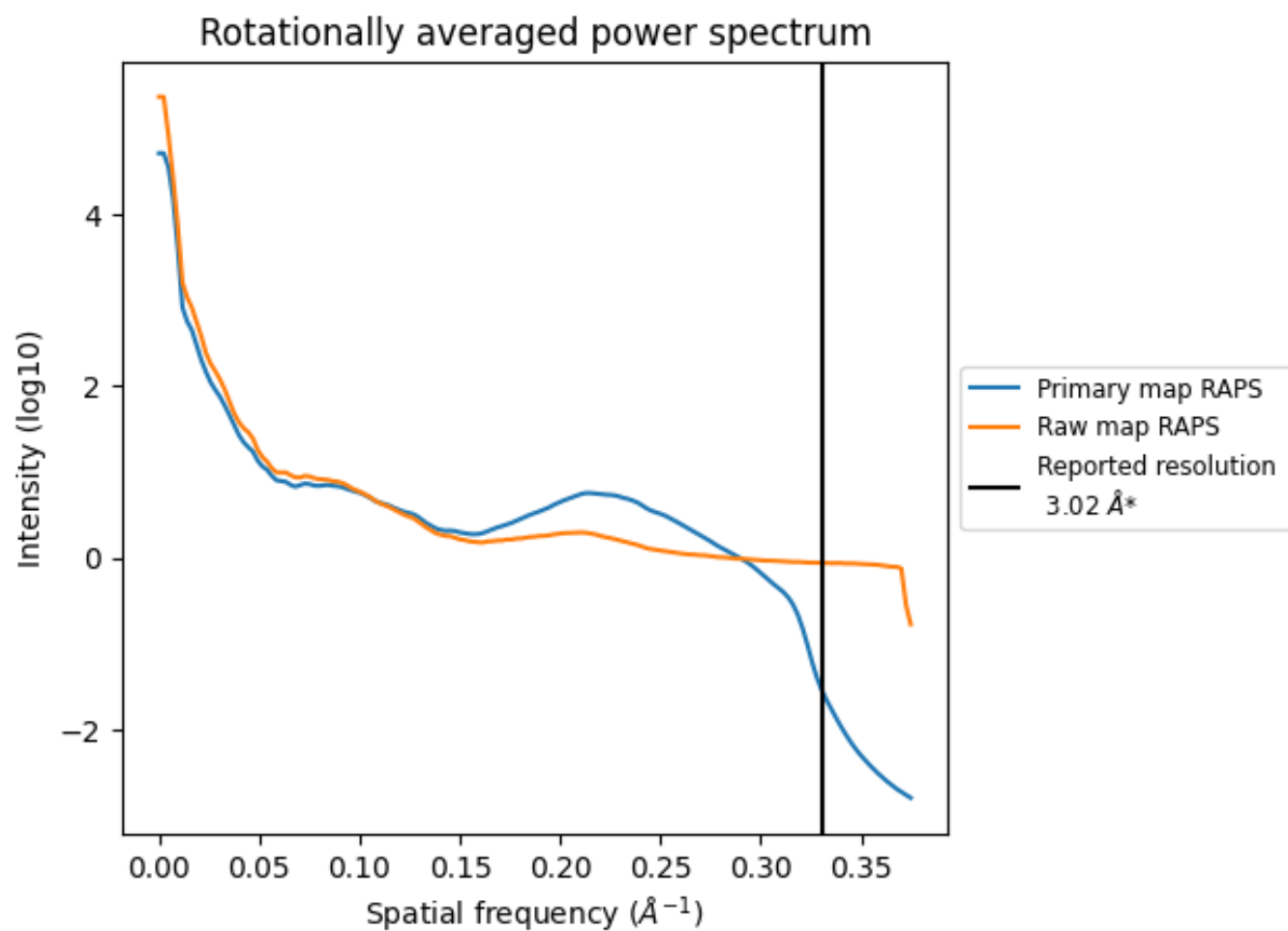
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 180 nm^3 ; this corresponds to an approximate mass of 162 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 ⓘ

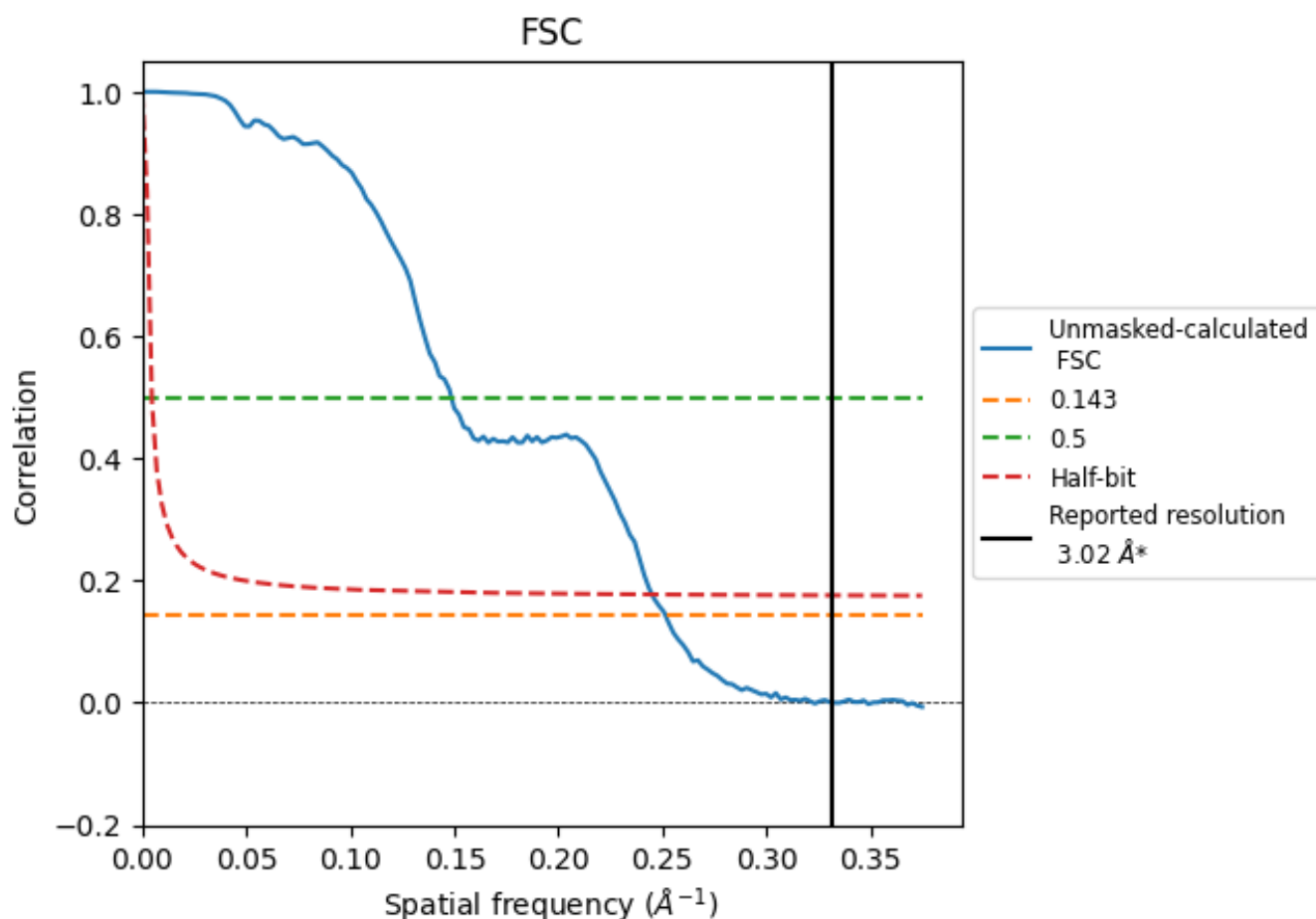


*Reported resolution corresponds to spatial frequency of 0.331 $\text{\AA}^{-1}$

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 0.331 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

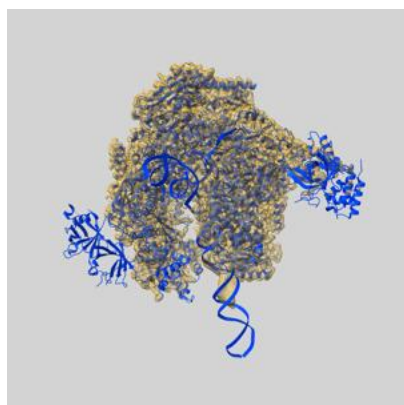
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.02	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.98	6.73	4.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.98 differs from the reported value 3.02 by more than 10 %

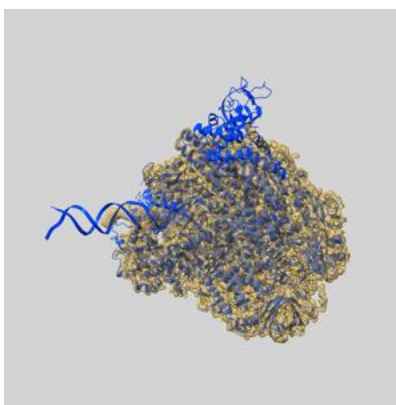
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37407 and PDB model 8WAW. Per-residue inclusion information can be found in section 3 on page 8.

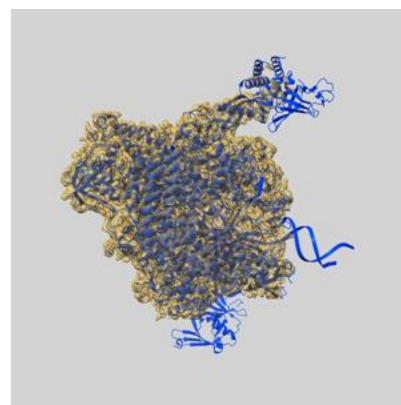
9.1 Map-model overlay [i](#)



X



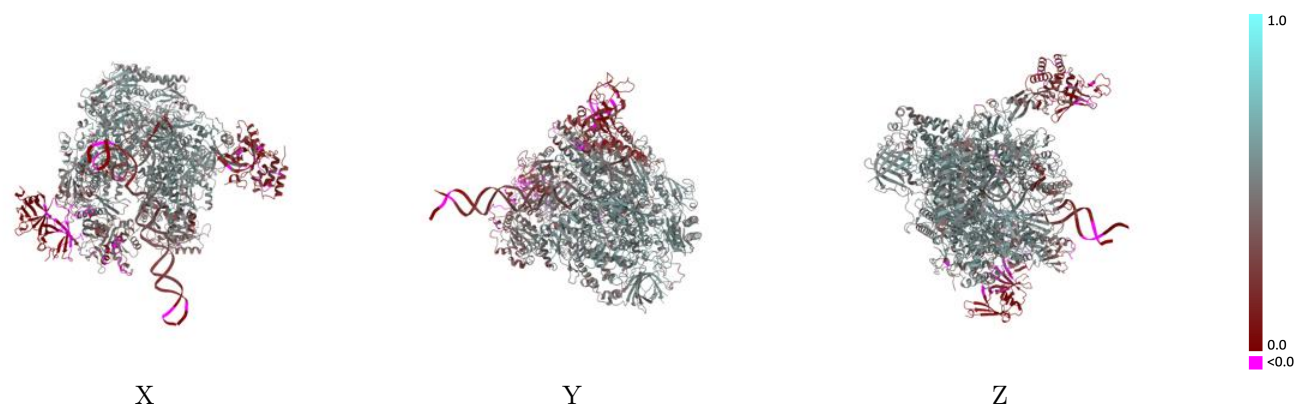
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.7 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](#)

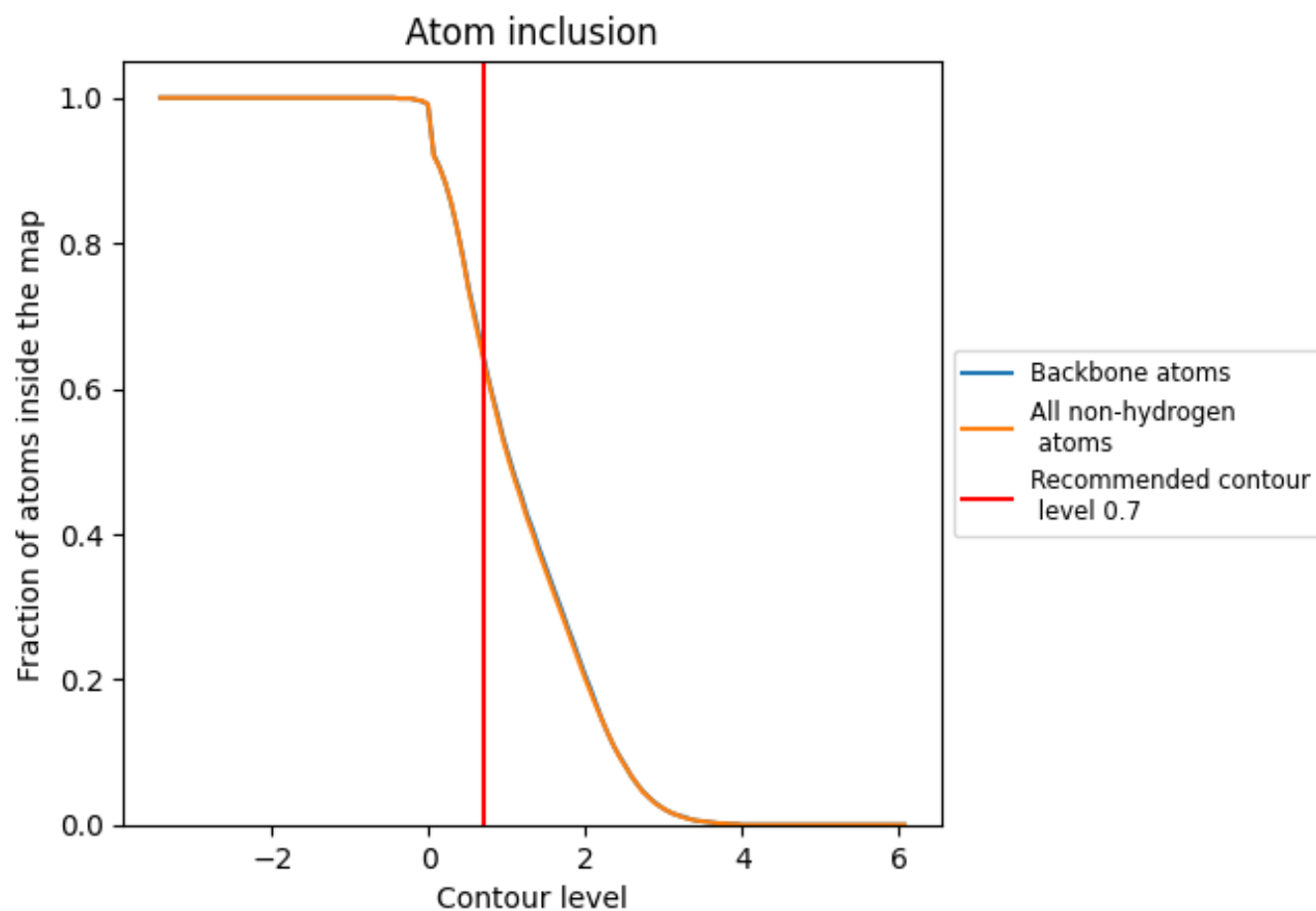


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 64% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6410	 0.4260
N	 0.8550	 0.5690
S	 0.0000	 0.0080
T	 0.0000	 -0.0080
X	 0.2640	 0.1680
Y	 0.4060	 0.2650
Z	 0.6260	 0.3860
o	 0.7370	 0.4840
p	 0.7350	 0.4820
q	 0.8220	 0.5160
r	 0.1080	 0.1730
s	 0.7370	 0.4620
t	 0.7950	 0.5080
u	 0.2910	 0.2540
v	 0.7890	 0.4850
w	 0.6680	 0.4250
x	 0.8370	 0.5260
y	 0.8300	 0.5280
z	 0.7360	 0.4620

