



Full wwPDB EM Validation Report ⓘ

Jul 26, 2021 – 12:21 pm BST

PDB ID : 7O4I
EMDB ID : EMD-12719
Title : Yeast RNA polymerase II transcription pre-initiation complex with initial transcription bubble
Authors : Schilbach, S.; Aibara, S.; Dienemann, C.; Grabbe, F.; Cramer, P.
Deposited on : 2021-04-06
Resolution : 3.20 Å(reported)
Based on initial model : 5OQJ

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

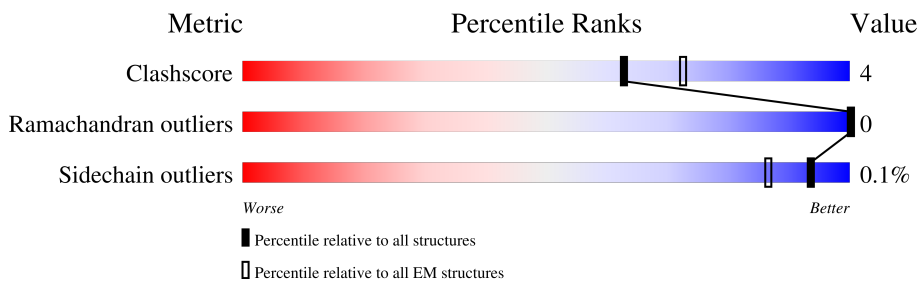
EMDB validation analysis : 0.0.0.dev84
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.22

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	0	778	
2	1	645	
3	2	517	
4	3	324	
5	4	341	
6	5	76	
7	6	464	
8	7	843	

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Mol	Chain	Length	Quality of chain
9	A	1733	75% 8% 17%
10	B	1224	88% 9%
11	C	347	69% 7% 23%
12	D	221	65% 11% 24%
13	E	215	87% 12%
14	F	155	50% 5% 45%
15	G	177	84% 12%
16	H	146	88% 8%
17	I	122	85% 10% 5%
18	J	70	91% 7%
19	K	120	87% 9%
20	L	70	59% 6% 36%
21	M	352	79% 9% 13%
22	N	106	14% 45% 18% 37%
23	O	247	63% 11% 27%
24	Q	738	8% 26% 70%
25	R	400	8% 59% 8% 33%
26	T	106	13% 48% 15% 37%
27	U	171	9% 54% 9% 37%
28	V	129	9% 74% 7% 19%
29	W	492	9% 53% 10% 37%
30	X	328	10% 57% 8% 35%

2 Entry composition i

There are 35 unique types of molecules in this entry. The entry contains 73949 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 General transcription and DNA repair factor IIIH helicase subunit XPD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	752	6091	3882	1029	1142	38	0	0

- Molecule 2 is a protein called General transcription and DNA repair factor IIIH subunit TFB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	522	4214	2660	734	798	22	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	-2	GLY	-	expression tag	UNP P32776
1	-1	GLY	-	expression tag	UNP P32776
1	0	SER	-	expression tag	UNP P32776

- Molecule 3 is a protein called General transcription and DNA repair factor IIIH subunit TFB2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	445	3597	2327	591	663	16	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	-3	GLY	-	expression tag	UNP Q02939
2	-2	PRO	-	expression tag	UNP Q02939
2	-1	GLY	-	expression tag	UNP Q02939
2	0	SER	-	expression tag	UNP Q02939

- Molecule 4 is a protein called RNA polymerase II transcription factor B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	131	1089	692	180	209	8	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	-2	GLY	-	expression tag	UNP Q03290
3	-1	PRO	-	expression tag	UNP Q03290
3	0	HIS	-	expression tag	UNP Q03290

- Molecule 5 is a protein called General transcription and DNA repair factor IIH subunit TFB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	293	2274	1454	377	429	14	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	-2	SER	-	expression tag	UNP Q12004
4	-1	ASN	-	expression tag	UNP Q12004
4	0	ALA	-	expression tag	UNP Q12004

- Molecule 6 is a protein called General transcription and DNA repair factor IIH subunit TFB5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	65	514	326	90	95	3	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	-3	GLY	-	expression tag	UNP Q3E7C1
5	-2	PRO	-	expression tag	UNP Q3E7C1
5	-1	GLY	-	expression tag	UNP Q3E7C1
5	0	SER	-	expression tag	UNP Q3E7C1

- Molecule 7 is a protein called General transcription and DNA repair factor IIH subunit SSL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	6	356	2794	1771	482	513	28	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	-2	GLY	-	expression tag	UNP Q04673
6	-1	GLY	-	expression tag	UNP Q04673
6	0	SER	-	expression tag	UNP Q04673

- Molecule 8 is a protein called General transcription and DNA repair factor IIIH helicase subunit XPB.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	7	615	Total	C	N	O	S	0	0
			4954	3153	860	914	27		

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	A	1430	Total	C	N	O	S	0	0
			11254	7088	1967	2137	62		

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	B	1180	Total	C	N	O	S	0	0
			9404	5946	1643	1760	55		

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	C	266	Total	C	N	O	S	0	0
			2092	1315	348	416	13		

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-28	MET	-	initiating methionine	UNP P16370
C	-27	GLY	-	expression tag	UNP P16370
C	-26	SER	-	expression tag	UNP P16370
C	-25	HIS	-	expression tag	UNP P16370
C	-24	HIS	-	expression tag	UNP P16370
C	-23	HIS	-	expression tag	UNP P16370
C	-22	HIS	-	expression tag	UNP P16370
C	-21	HIS	-	expression tag	UNP P16370
C	-20	HIS	-	expression tag	UNP P16370

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-19	SER	-	expression tag	UNP P16370
C	-18	ASN	-	expression tag	UNP P16370
C	-17	SER	-	expression tag	UNP P16370
C	-16	GLY	-	expression tag	UNP P16370
C	-15	LEU	-	expression tag	UNP P16370
C	-14	ASN	-	expression tag	UNP P16370
C	-13	ASP	-	expression tag	UNP P16370
C	-12	ILE	-	expression tag	UNP P16370
C	-11	PHE	-	expression tag	UNP P16370
C	-10	GLU	-	expression tag	UNP P16370
C	-9	ALA	-	expression tag	UNP P16370
C	-8	GLN	-	expression tag	UNP P16370
C	-7	LYS	-	expression tag	UNP P16370
C	-6	ILE	-	expression tag	UNP P16370
C	-5	GLU	-	expression tag	UNP P16370
C	-4	TRP	-	expression tag	UNP P16370
C	-3	HIS	-	expression tag	UNP P16370
C	-2	GLU	-	expression tag	UNP P16370
C	-1	ASP	-	expression tag	UNP P16370
C	0	THR	-	expression tag	UNP P16370
C	1	GLY	-	expression tag	UNP P16370
C	2	SER	-	expression tag	UNP P16370
C	3	SER	-	expression tag	UNP P16370

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	D	167	1343	829	242	270	2	0	0

- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	E	214	1752	1111	309	321	11	0	0

- Molecule 14 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	F	86	697	445	118	131	3	0	0

- Molecule 15 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	G	171	1339	861	222	248	8	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	172	HIS	-	expression tag	UNP P34087
G	173	HIS	-	expression tag	UNP P34087
G	174	HIS	-	expression tag	UNP P34087
G	175	HIS	-	expression tag	UNP P34087
G	176	HIS	-	expression tag	UNP P34087
G	177	HIS	-	expression tag	UNP P34087

- Molecule 16 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	H	140	1120	704	188	224	4	0	0

- Molecule 17 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	I	116	944	581	172	181	10	0	0

- Molecule 18 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	J	69	569	362	101	100	6	0	0

- Molecule 19 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	K	115	924	593	157	172	2	0	0

- Molecule 20 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	L	45	359	221	71	63	4	0	0

- Molecule 21 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	M	308	2360	1489	406	447	18	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	346	LYS	-	expression tag	UNP P29055
M	347	HIS	-	expression tag	UNP P29055
M	348	HIS	-	expression tag	UNP P29055
M	349	HIS	-	expression tag	UNP P29055
M	350	HIS	-	expression tag	UNP P29055
M	351	HIS	-	expression tag	UNP P29055
M	352	HIS	-	expression tag	UNP P29055

- Molecule 22 is a DNA chain called Non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
22	N	67	1374	657	246	404	67	0	0

- Molecule 23 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	O	181	1422	925	243	248	6	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	241	LYS	-	expression tag	UNP P13393
O	242	HIS	-	expression tag	UNP P13393
O	243	HIS	-	expression tag	UNP P13393
O	244	HIS	-	expression tag	UNP P13393
O	245	HIS	-	expression tag	UNP P13393
O	246	HIS	-	expression tag	UNP P13393
O	247	HIS	-	expression tag	UNP P13393

- Molecule 24 is a protein called Transcription initiation factor IIF subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Q	221	1871	1179	346	339	7	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	-2	GLY	-	expression tag	UNP P41895
Q	-1	PRO	-	expression tag	UNP P41895
Q	0	GLY	-	expression tag	UNP P41895

- Molecule 25 is a protein called Transcription initiation factor IIF subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	R	268	2230	1409	392	419	10	0	0

- Molecule 26 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
26	T	67	1370	656	250	398	66	0	0

- Molecule 27 is a protein called Transcription initiation factor IIA large subunit, Transcription initiation factor IIA large subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	U	107	885	559	147	176	3	0	0

- Molecule 28 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	V	104	815	511	136	164	4	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	123	LYS	-	expression tag	UNP P32774
V	124	HIS	-	expression tag	UNP P32774

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Chain	Residue	Modelled	Actual	Comment	Reference
V	125	HIS	-	expression tag	UNP P32774
V	126	HIS	-	expression tag	UNP P32774
V	127	HIS	-	expression tag	UNP P32774
V	128	HIS	-	expression tag	UNP P32774
V	129	HIS	-	expression tag	UNP P32774

- Molecule 29 is a protein called Transcription initiation factor IIE subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	W	312	2532	1595	442	488	7	0	0

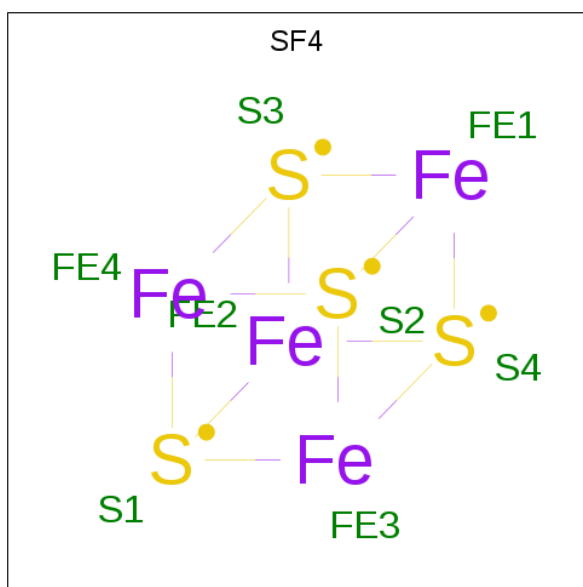
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	483	ALA	-	expression tag	UNP P36100
W	484	ALA	-	expression tag	UNP P36100
W	485	ALA	-	expression tag	UNP P36100
W	486	LEU	-	expression tag	UNP P36100
W	487	GLU	-	expression tag	UNP P36100
W	488	HIS	-	expression tag	UNP P36100
W	489	HIS	-	expression tag	UNP P36100
W	490	HIS	-	expression tag	UNP P36100
W	491	HIS	-	expression tag	UNP P36100
W	492	HIS	-	expression tag	UNP P36100

- Molecule 30 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	X	213	1708	1091	292	319	6	0	0

- Molecule 31 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).

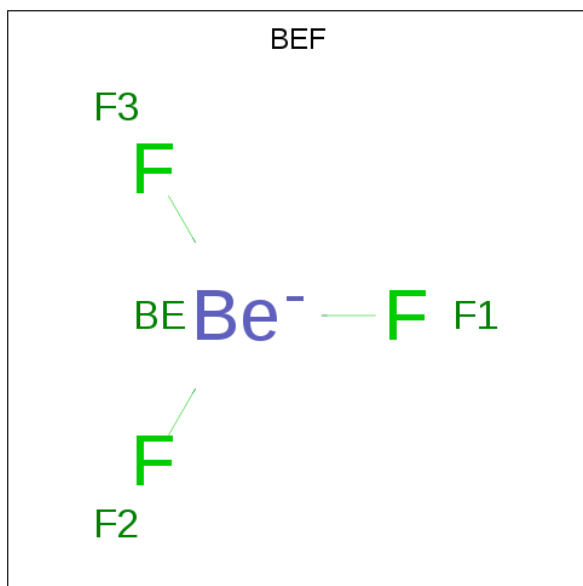


Mol	Chain	Residues	Atoms		AltConf
			Total	Fe S	
31	0	1	8	4 4	0

- Molecule 32 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
32	3	2	2	2	0
32	4	1	1	1	0
32	6	4	4	4	0
32	A	2	2	2	0
32	B	1	1	1	0
32	C	1	1	1	0
32	I	2	2	2	0
32	J	1	1	1	0
32	L	1	1	1	0
32	M	1	1	1	0
32	W	1	1	1	0

- Molecule 33 is BERYLLIUM TRIFLUORIDE ION (three-letter code: BEF) (formula: BeF₃).

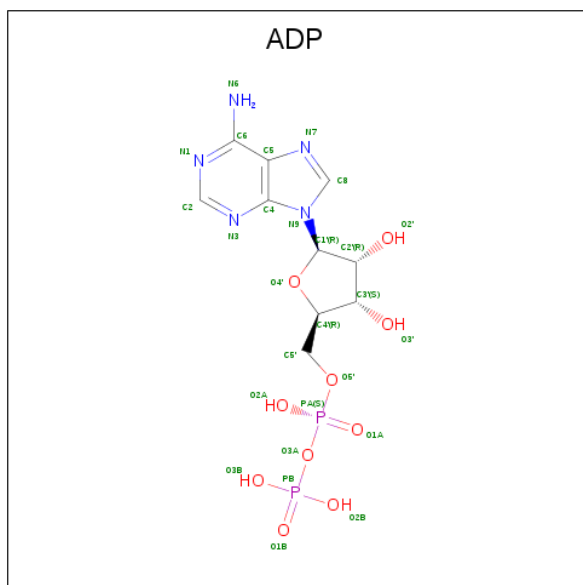


Mol	Chain	Residues	Atoms			AltConf
			Total	Be	F	
33	7	1	4	1	3	0

- Molecule 34 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
34	7	1	1	1	0
34	A	1	1	1	0

- Molecule 35 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

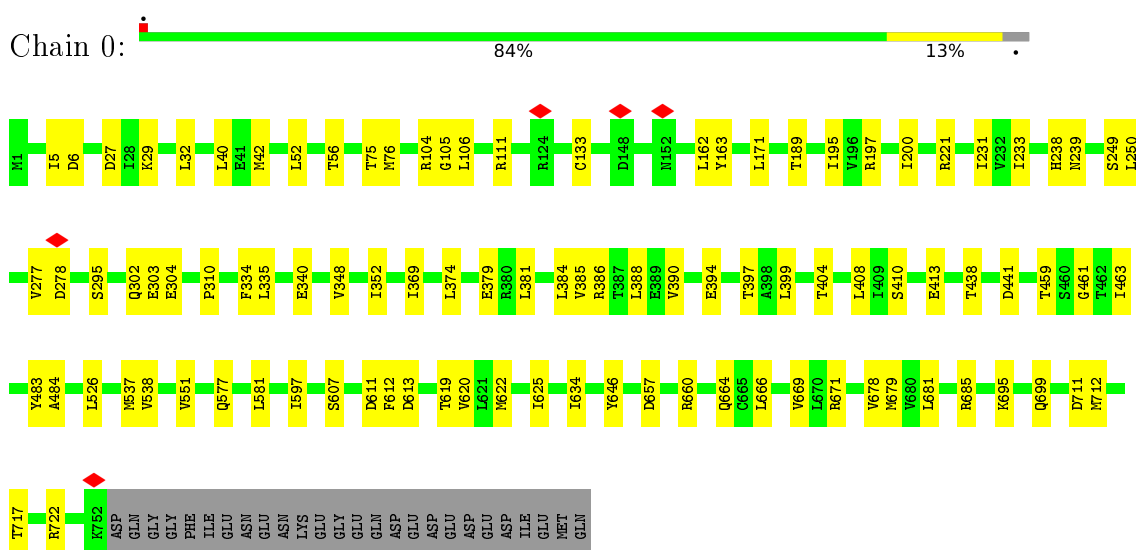


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
35	7	1	27	10	5	10	2	0

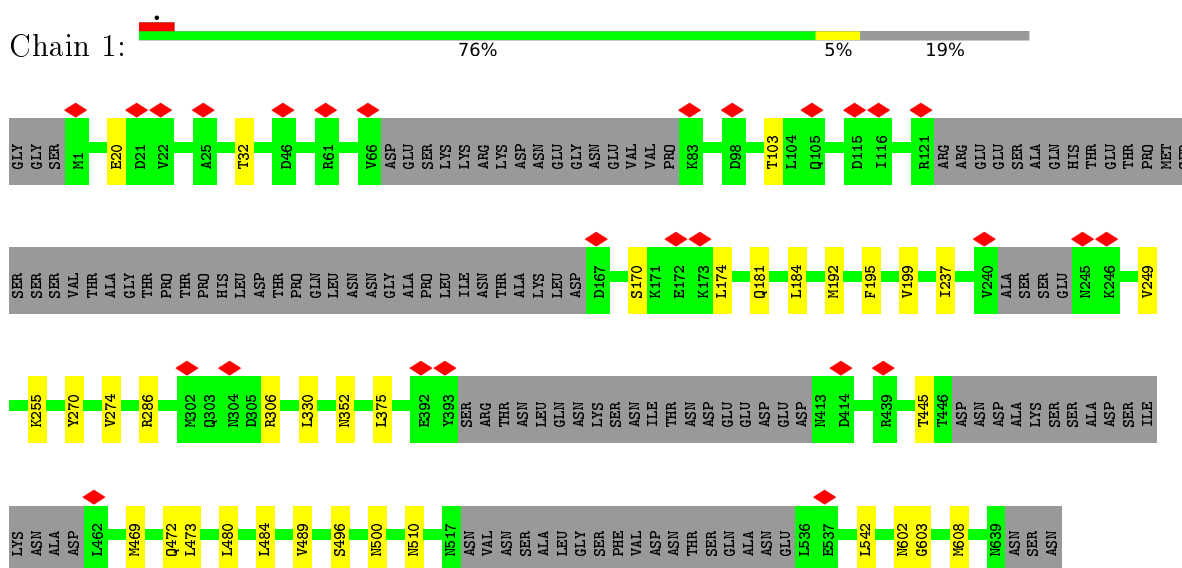
3 Residue-property plots

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

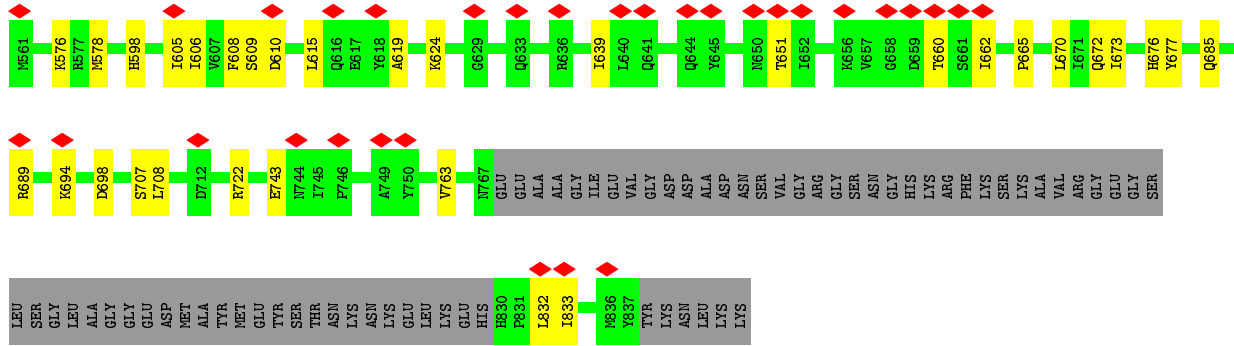
- Molecule 1: General transcription and DNA repair factor IIIH helicase subunit XPD



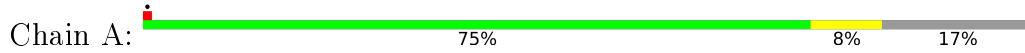
- Molecule 2: General transcription and DNA repair factor IIIH subunit TFB1



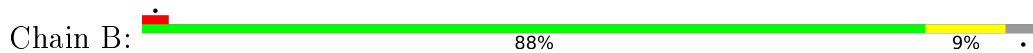
- Molecule 3: General transcription and DNA repair factor IIIH subunit TFB2

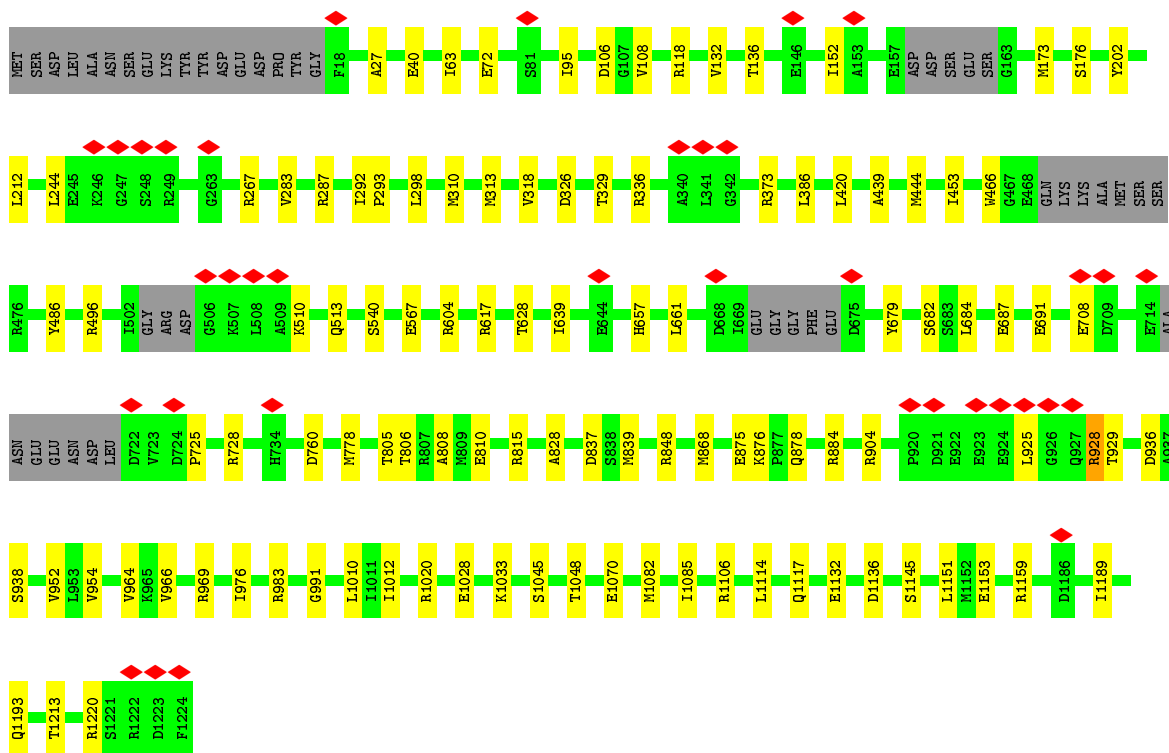


• Molecule 9: DNA-directed RNA polymerase II subunit RPB1

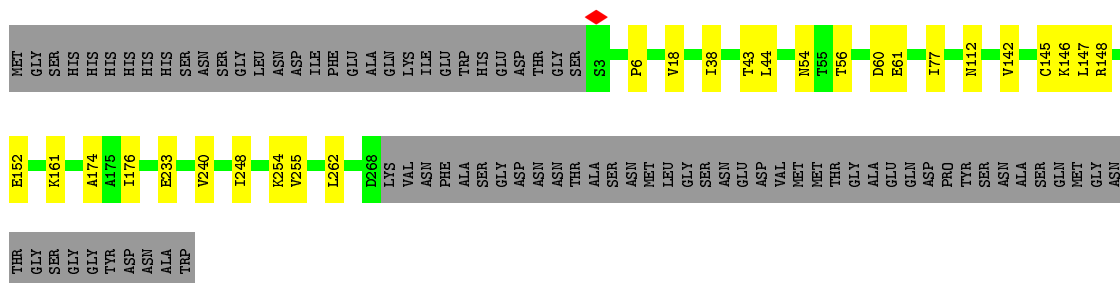


• Molecule 10: DNA-directed RNA polymerase II subunit RPB2

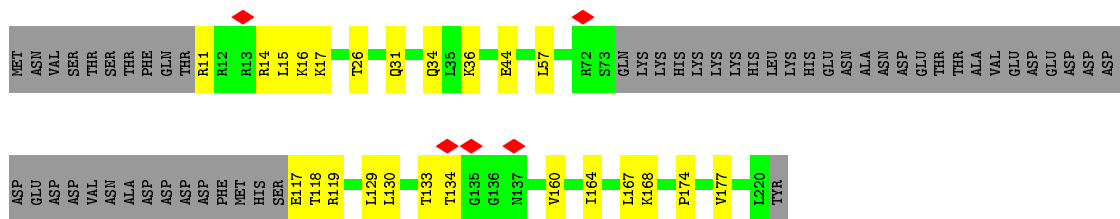




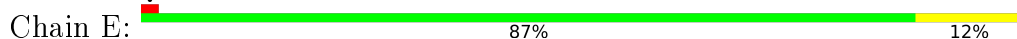
• Molecule 11: DNA-directed RNA polymerase II subunit RPB3

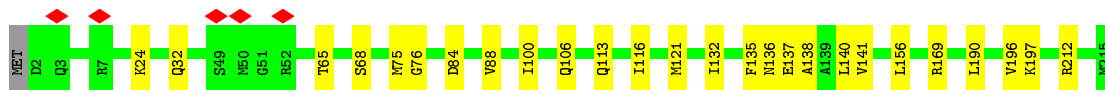


• Molecule 12: DNA-directed RNA polymerase II subunit RPB4



• Molecule 13: DNA-directed RNA polymerases I, II, and III subunit RPABC1

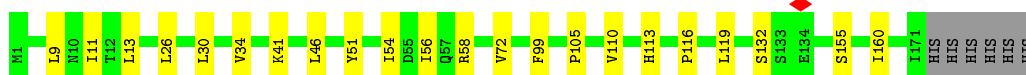
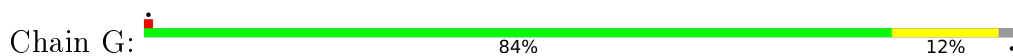




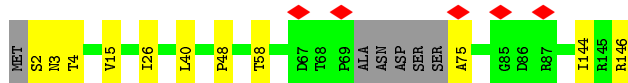
- Molecule 14: DNA-directed RNA polymerases I, II, and III subunit RPABC2



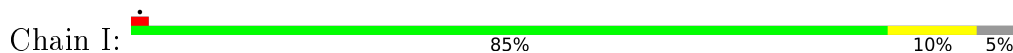
- Molecule 15: DNA-directed RNA polymerase II subunit RPB7



- Molecule 16: DNA-directed RNA polymerases I, II, and III subunit RPABC3



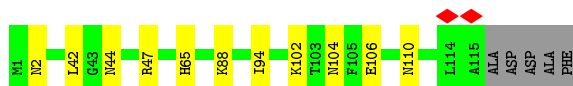
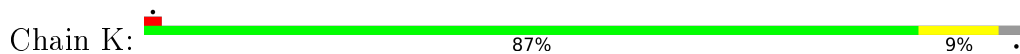
- Molecule 17: DNA-directed RNA polymerase II subunit RPB9



- Molecule 18: DNA-directed RNA polymerases I, II, and III subunit RPABC5



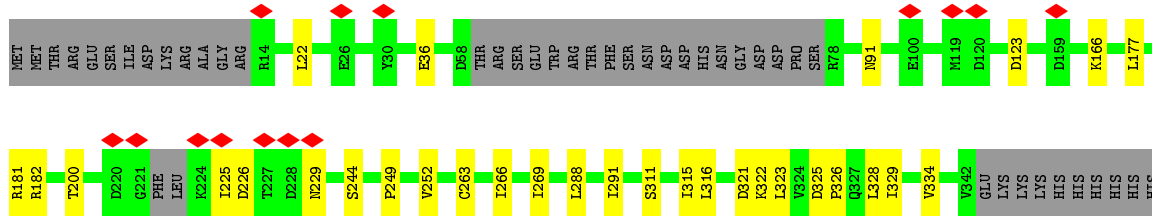
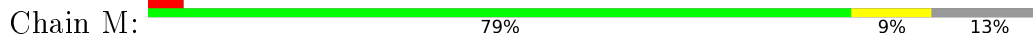
- Molecule 19: DNA-directed RNA polymerase II subunit RPB11



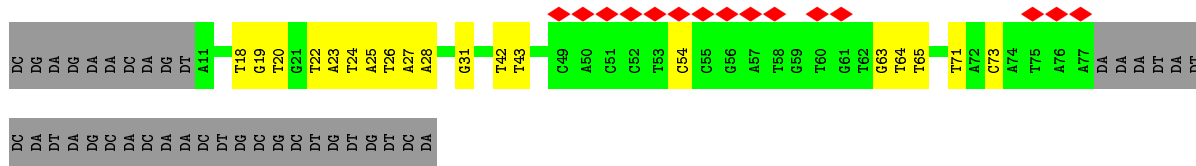
• Molecule 20: DNA-directed RNA polymerases I, II, and III subunit RPABC4



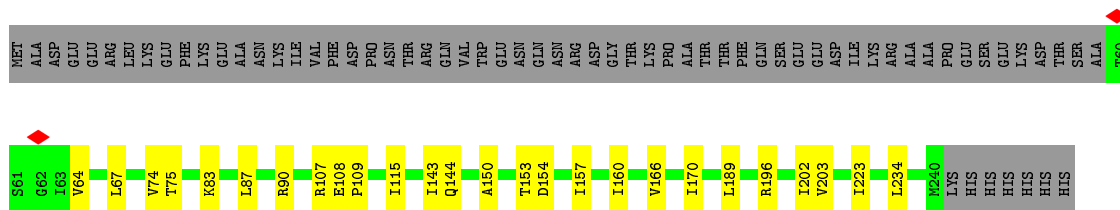
• Molecule 21: Transcription initiation factor IIB



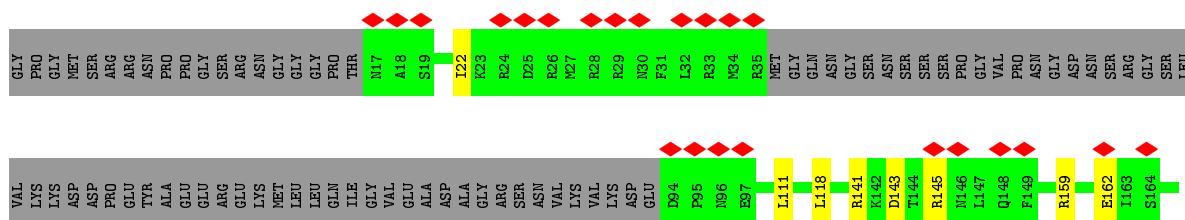
• Molecule 22: Non-template DNA

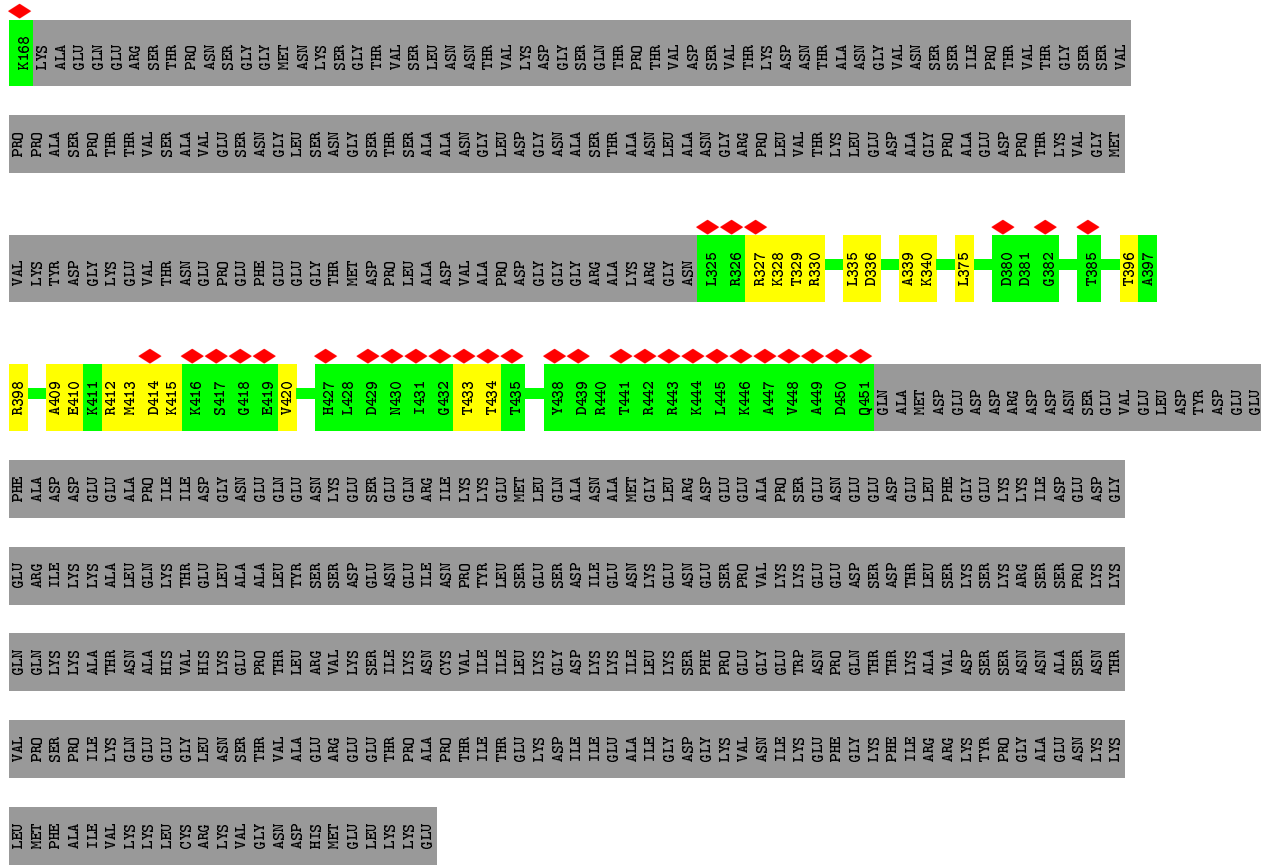


• Molecule 23: TATA-box-binding protein

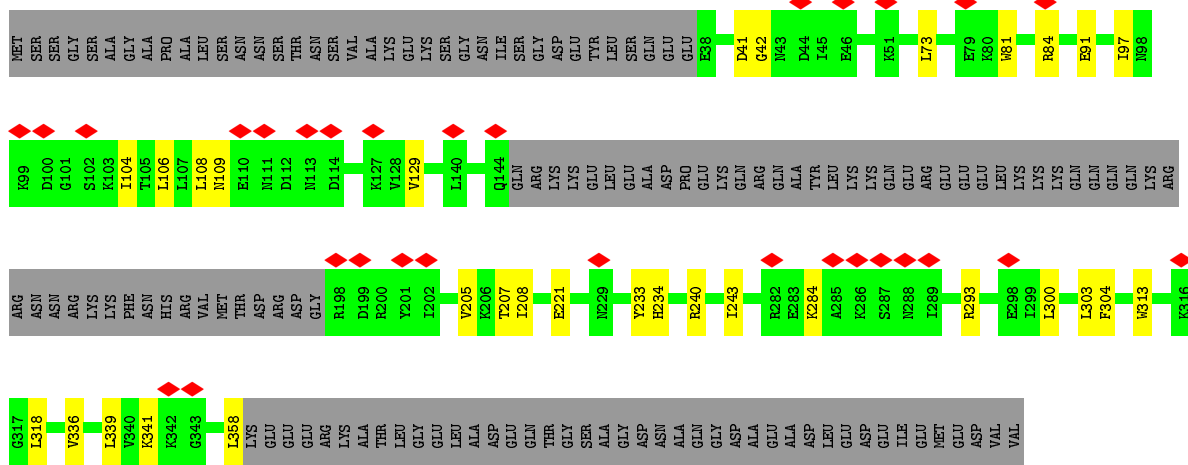


• Molecule 24: Transcription initiation factor IIF subunit alpha





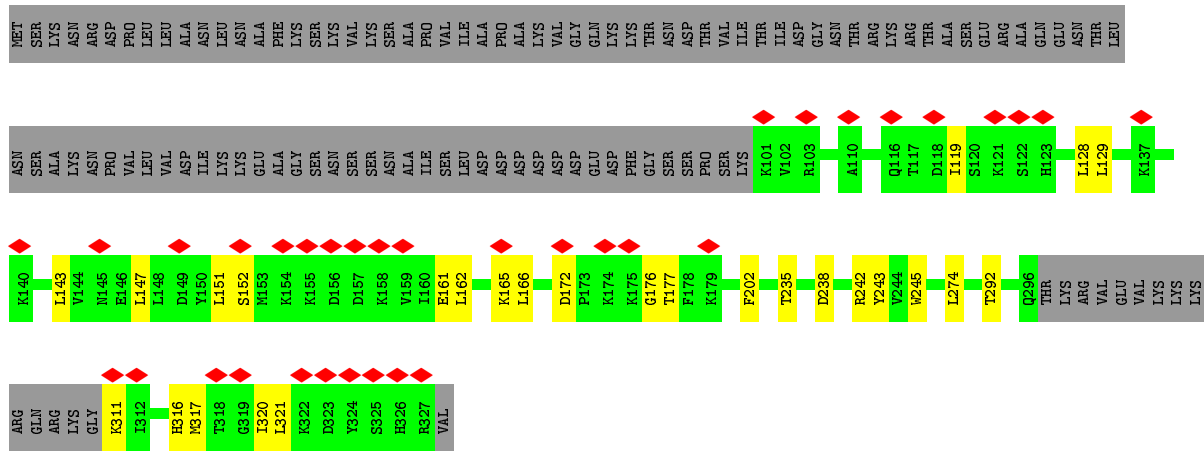
• Molecule 25: Transcription initiation factor IIF subunit beta



• Molecule 26: Template DNA



● Molecule 30: Transcription initiation factor IIE subunit beta



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16495	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.233	Depositor
Minimum map value	-0.110	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.011	Depositor
Map size (Å)	398.99997, 398.99997, 398.99997	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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: ADP, SF4, MG, ZN, BEF

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	0	0.25	0/6209	0.41	0/8384
2	1	0.24	0/4277	0.38	0/5755
3	2	0.24	0/3664	0.39	0/4952
4	3	0.24	0/1109	0.38	0/1492
5	4	0.25	0/2312	0.42	0/3127
6	5	0.23	0/520	0.39	0/701
7	6	0.24	0/2851	0.40	0/3856
8	7	0.24	0/5059	0.41	0/6841
9	A	0.24	0/11455	0.41	0/15490
10	B	0.25	0/9589	0.42	0/12934
11	C	0.24	0/2130	0.41	0/2887
12	D	0.24	0/1351	0.40	0/1811
13	E	0.25	0/1788	0.40	0/2406
14	F	0.24	0/709	0.40	0/956
15	G	0.26	0/1367	0.42	0/1844
16	H	0.24	0/1139	0.43	0/1544
17	I	0.26	0/962	0.44	0/1295
18	J	0.25	0/578	0.39	0/775
19	K	0.25	0/942	0.41	0/1272
20	L	0.24	0/361	0.44	0/478
21	M	0.25	0/2387	0.40	0/3211
22	N	0.57	0/1540	0.98	1/2375 (0.0%)
23	O	0.26	0/1449	0.44	0/1952
24	Q	0.25	0/1907	0.44	0/2556
25	R	0.24	0/2270	0.43	0/3052
26	T	0.58	0/1537	0.94	0/2370
27	U	0.23	0/898	0.41	0/1212
28	V	0.23	0/822	0.41	0/1109
29	W	0.24	0/2575	0.39	0/3473
30	X	0.24	0/1740	0.39	0/2343
All	All	0.27	0/75497	0.45	1/102453 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	N	22	DT	N3-C4-O4	5.34	123.10	119.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	6091	0	6155	65	0
2	1	4214	0	4288	30	0
3	2	3597	0	3687	40	0
4	3	1089	0	1069	9	0
5	4	2274	0	2332	35	0
6	5	514	0	541	2	0
7	6	2794	0	2815	29	0
8	7	4954	0	4946	63	0
9	A	11254	0	11319	91	0
10	B	9404	0	9398	82	0
11	C	2092	0	2050	20	0
12	D	1343	0	1366	15	0
13	E	1752	0	1776	17	0
14	F	697	0	720	6	0
15	G	1339	0	1357	18	0
16	H	1120	0	1086	6	0
17	I	944	0	899	9	0
18	J	569	0	585	5	0
19	K	924	0	934	9	0
20	L	359	0	381	3	0
21	M	2360	0	2467	23	0
22	N	1374	0	759	16	0
23	O	1422	0	1500	19	0
24	Q	1871	0	1883	19	0
25	R	2230	0	2254	24	0
26	T	1370	0	758	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	U	885	0	866	11	0
28	V	815	0	822	8	0
29	W	2532	0	2529	37	0
30	X	1708	0	1752	19	0
31	0	8	0	0	0	0
32	3	2	0	0	0	0
32	4	1	0	0	0	0
32	6	4	0	0	0	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	W	1	0	0	0	0
33	7	4	0	0	0	0
34	7	1	0	0	0	0
34	A	1	0	0	0	0
35	7	27	0	12	0	0
All	All	73949	0	73306	645	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 4.

All (645) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:438:THR:HG21	1:0:634:ILE:HD12	1.41	1.01
10:B:326:ASP:OD1	10:B:329:THR:OG1	1.89	0.91
29:W:284:LYS:NZ	29:W:288:ASN:OD1	2.04	0.91
22:N:63:DG:OP1	30:X:311:LYS:N	2.06	0.88
8:7:673:ILE:HG22	8:7:708:LEU:HD12	1.55	0.86
9:A:584:ASN:O	9:A:637:LYS:NZ	2.08	0.86
2:1:472:GLN:NE2	5:4:41:ASP:OD2	2.10	0.85
21:M:181:ARG:O	21:M:229:ASN:ND2	2.09	0.85
23:O:153:THR:HG22	23:O:154:ASP:H	1.41	0.84
10:B:875:GLU:OE2	20:L:42:ARG:NH1	2.12	0.83
29:W:17:VAL:HG21	29:W:29:LEU:HD13	1.59	0.83
1:0:335:LEU:HD21	1:0:399:LEU:HD12	1.59	0.82
9:A:469:ARG:NH2	10:B:991:GLY:O	2.13	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:595:THR:OG1	9:A:603:ASN:OD1	1.97	0.81
29:W:21:TYR:OH	29:W:64:ASP:OD2	1.98	0.81
1:0:384:LEU:O	1:0:388:LEU:HD23	1.81	0.80
2:1:473:LEU:HD11	5:4:34:PRO:HB3	1.63	0.80
5:4:90:SER:OG	7:6:402:ASP:OD2	1.99	0.78
10:B:679:TYR:OH	10:B:687:GLU:OE1	2.01	0.78
1:0:385:VAL:HG13	1:0:390:VAL:HG21	1.66	0.77
10:B:373:ARG:NE	10:B:567:GLU:OE2	2.18	0.77
9:A:840:ARG:NH1	9:A:1106:ASN:OD1	2.18	0.77
7:6:450:ASN:C	7:6:450:ASN:HD22	1.88	0.77
9:A:500:GLU:OE1	10:B:1145:SER:OG	2.01	0.76
10:B:496:ARG:NH2	10:B:540:SER:O	2.18	0.76
10:B:287:ARG:NH1	10:B:292:ILE:O	2.18	0.76
23:O:115:ILE:HD13	23:O:143:ILE:HD11	1.67	0.75
30:X:235:THR:OG1	30:X:238:ASP:O	2.03	0.75
2:1:237:ILE:HD11	2:1:255:LYS:HD3	1.69	0.75
9:A:1198:ASP:OD2	9:A:1201:ALA:N	2.18	0.74
23:O:90:ARG:NE	27:U:228:ASP:O	2.20	0.74
2:1:32:THR:OG1	29:W:211:ASN:OD1	2.06	0.73
15:G:119:LEU:HD23	15:G:132:SER:HB2	1.70	0.73
5:4:51:ILE:O	5:4:55:GLU:OE1	2.07	0.72
8:7:498:PHE:O	8:7:501:VAL:HG22	1.89	0.71
10:B:336:ARG:NH1	24:Q:410:GLU:OE1	2.23	0.71
16:H:48:PRO:O	16:H:146:ARG:NH2	2.24	0.71
9:A:407:ARG:NH1	9:A:413:ILE:HD11	2.06	0.70
10:B:876:LYS:O	10:B:878:GLN:NE2	2.24	0.70
29:W:292:GLU:OE2	29:W:296:GLN:NE2	2.25	0.70
10:B:928:ARG:NH1	10:B:929:THR:O	2.25	0.69
3:2:139:SER:HB2	3:2:272:THR:HG21	1.71	0.69
15:G:11:ILE:HD12	15:G:72:VAL:HG21	1.74	0.69
22:N:25:DA:OP1	23:O:196:ARG:NH2	2.26	0.69
13:E:76:GLY:N	13:E:106:GLN:OE1	2.26	0.69
11:C:152:GLU:OE1	18:J:69:ARG:NH1	2.26	0.69
10:B:617:ARG:NH2	17:I:61:ASP:OD2	2.25	0.69
8:7:342:ASP:OD2	8:7:345:ASN:ND2	2.26	0.69
10:B:267:ARG:NH2	10:B:313:MET:SD	2.66	0.69
10:B:657:HIS:O	10:B:661:LEU:HD23	1.93	0.69
2:1:20:GLU:OE2	2:1:286:ARG:NH1	2.26	0.68
5:4:165:LYS:NZ	7:6:439:ASP:OD1	2.21	0.68
17:I:58:VAL:HG11	17:I:109:ILE:HD11	1.73	0.68
25:R:233:TYR:O	25:R:234:HIS:ND1	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:I:102:VAL:HG22	17:I:109:ILE:HG12	1.74	0.68
1:0:613:ASP:OD2	1:0:671:ARG:NE	2.25	0.68
19:K:44:ASN:OD1	19:K:47:ARG:NH2	2.27	0.67
3:2:250:LEU:HD12	3:2:259:VAL:HG11	1.77	0.67
27:U:13:ILE:HG12	28:V:51:THR:HG21	1.76	0.67
8:7:241:ILE:CG1	8:7:245:LEU:HD13	2.25	0.67
9:A:1384:VAL:HG12	9:A:1384:VAL:O	1.95	0.67
8:7:130:ARG:NH1	8:7:198:ASP:O	2.27	0.67
15:G:46:LEU:HD21	15:G:105:PRO:HG3	1.77	0.67
3:2:272:THR:HG22	3:2:273:LYS:H	1.59	0.66
29:W:272:ALA:O	29:W:276:LEU:HD23	1.95	0.66
1:0:310:PRO:HB3	1:0:404:THR:HG23	1.78	0.66
9:A:5:GLN:O	10:B:1159:ARG:NH2	2.27	0.66
9:A:1386:ARG:NH1	9:A:1404:GLU:OE2	2.28	0.66
8:7:356:LEU:HD22	8:7:360:THR:HG21	1.76	0.66
25:R:300:LEU:HD11	30:X:129:LEU:HD23	1.78	0.66
1:0:695:LYS:NZ	1:0:699:GLN:OE1	2.28	0.66
3:2:369:ARG:HG3	3:2:374:VAL:HG22	1.78	0.65
8:7:469:ASP:O	8:7:473:VAL:HG23	1.95	0.65
17:I:65:ASP:OD2	17:I:67:THR:OG1	2.12	0.65
1:0:348:VAL:HG11	1:0:352:ILE:HD12	1.79	0.65
3:2:104:PHE:CE2	3:2:108:LEU:HD11	2.30	0.65
9:A:189:ARG:NH1	26:T:51:DC:OP2	2.29	0.65
13:E:88:VAL:HB	13:E:116:ILE:HG22	1.77	0.65
27:U:5:GLU:OE1	28:V:58:SER:OG	2.15	0.65
8:7:677:TYR:HB3	22:N:73:DC:OP1	1.97	0.64
5:4:85:TYR:OH	7:6:405:SER:O	2.09	0.64
8:7:324:GLU:OE2	8:7:499:ARG:NE	2.25	0.64
8:7:832:LEU:HD23	9:A:1263:ILE:HG22	1.79	0.64
10:B:72:GLU:OE2	24:Q:330:ARG:NE	2.30	0.64
6:5:53:GLU:OE2	6:5:56:ARG:NH2	2.30	0.64
9:A:1287:TYR:OH	9:A:1307:GLU:OE2	2.15	0.64
21:M:166:LYS:NZ	26:T:76:DC:OP1	2.30	0.64
21:M:311:SER:O	21:M:315:ILE:HD12	1.97	0.64
8:7:444:GLU:N	8:7:444:GLU:OE1	2.31	0.64
9:A:928:LEU:HD11	9:A:984:LYS:HE2	1.80	0.64
10:B:639:ILE:HD11	10:B:691:GLU:HB2	1.78	0.64
30:X:147:LEU:O	30:X:151:LEU:HD23	1.97	0.64
3:2:217:ASP:O	3:2:221:VAL:HG23	1.98	0.63
10:B:954:VAL:HG12	10:B:964:VAL:HG12	1.79	0.63
3:2:357:ILE:HG12	3:2:374:VAL:HG21	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:95:THR:OG1	4:3:97:ASP:OD1	2.14	0.63
8:7:608:PHE:CE2	8:7:670:LEU:HD11	2.33	0.63
8:7:665:PRO:O	8:7:694:LYS:N	2.32	0.63
10:B:604:ARG:NH2	10:B:691:GLU:OE2	2.31	0.63
1:0:607:SER:O	1:0:664:GLN:NE2	2.32	0.62
5:4:50:ILE:O	5:4:54:LEU:HD23	1.99	0.62
5:4:89:GLU:O	7:6:407:GLN:NE2	2.32	0.62
29:W:133:GLN:O	29:W:137:VAL:HG23	1.99	0.62
4:3:44:ASP:O	4:3:48:SER:OG	2.06	0.62
13:E:24:LYS:NZ	13:E:32:GLN:OE1	2.32	0.62
25:R:205:VAL:HG13	25:R:207:THR:HG23	1.80	0.62
7:6:450:ASN:O	7:6:450:ASN:ND2	2.24	0.62
22:N:31:DG:OP1	25:R:293:ARG:HG3	2.00	0.61
2:1:249:VAL:CG1	29:W:262:ILE:HG22	2.30	0.61
8:7:662:ILE:O	8:7:689:ARG:NH1	2.33	0.61
9:A:1209:MET:SD	9:A:1236:LEU:HD11	2.39	0.61
14:F:145:ASP:OD2	15:G:58:ARG:NH1	2.33	0.61
29:W:17:VAL:CG2	29:W:29:LEU:HD13	2.30	0.61
10:B:63:ILE:CD1	10:B:95:ILE:HD12	2.31	0.61
3:2:211:ILE:CD1	3:2:221:VAL:HG21	2.29	0.61
3:2:200:LEU:HD11	3:2:258:LEU:HD11	1.82	0.61
5:4:34:PRO:O	5:4:38:THR:HG23	2.00	0.61
22:N:27:DA:H2'	22:N:28:DA:C8	2.36	0.61
2:1:469:MET:O	2:1:473:LEU:HD13	2.01	0.61
10:B:837:ASP:OD1	10:B:1020:ARG:NH2	2.32	0.61
3:2:221:VAL:HG22	3:2:249:MET:CE	2.31	0.61
5:4:91:THR:HG22	5:4:91:THR:O	2.01	0.61
29:W:37:VAL:HG12	29:W:88:TYR:HB3	1.83	0.61
1:0:163:TYR:OH	1:0:302:GLN:OE1	2.19	0.61
9:A:514:PRO:HG2	9:A:1067:LEU:HD11	1.83	0.60
2:1:472:GLN:OE1	5:4:38:THR:HG22	2.01	0.60
7:6:149:ILE:HD12	7:6:235:VAL:HG11	1.82	0.60
10:B:884:ARG:NH1	21:M:36:GLU:OE1	2.34	0.60
9:A:690:VAL:O	9:A:694:THR:HG23	2.00	0.60
12:D:130:LEU:HD12	12:D:134:THR:HG21	1.83	0.60
2:1:445:THR:N	5:4:280:GLY:O	2.34	0.60
9:A:107:CYS:SG	9:A:171:GLN:NE2	2.75	0.60
10:B:728:ARG:NH2	10:B:1048:THR:O	2.34	0.60
24:Q:412:ARG:HG3	24:Q:420:VAL:HG22	1.83	0.60
5:4:32:ILE:HG22	5:4:50:ILE:HD11	1.83	0.60
9:A:116:ASP:OD2	9:A:164:ARG:NH1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:86:LEU:HD11	3:2:104:PHE:CD2	2.37	0.59
8:7:673:ILE:HG22	8:7:708:LEU:CD1	2.31	0.59
4:3:129:THR:O	4:3:133:LEU:HD23	2.03	0.59
29:W:360:TYR:CZ	29:W:364:LEU:HD11	2.38	0.59
8:7:130:ARG:O	8:7:202:LYS:NZ	2.29	0.58
29:W:18:ARG:NH2	29:W:30:ASP:OD2	2.36	0.58
7:6:124:ARG:NH1	7:6:305:VAL:O	2.35	0.58
9:A:860:LEU:HD11	9:A:1393:ASN:O	2.02	0.58
7:6:440:CYS:O	7:6:444:ILE:HD12	2.03	0.58
8:7:360:THR:HG22	8:7:427:TRP:HE3	1.68	0.58
3:2:357:ILE:HD13	3:2:369:ARG:HH11	1.69	0.58
24:Q:143:ASP:OD2	24:Q:145:ARG:NE	2.37	0.58
9:A:362:ASP:OD2	9:A:459:ARG:NE	2.32	0.58
10:B:976:ILE:HG22	10:B:976:ILE:O	2.02	0.58
3:2:144:GLU:OE2	3:2:148:HIS:NE2	2.37	0.58
5:4:276:CYS:SG	5:4:277:TYR:N	2.75	0.58
23:O:144:GLN:NE2	23:O:150:ALA:O	2.36	0.58
10:B:27:ALA:N	10:B:708:GLU:OE2	2.37	0.57
14:F:97:ARG:NE	14:F:124:GLU:OE1	2.29	0.57
25:R:97:ILE:HG13	25:R:104:ILE:HG23	1.86	0.57
1:0:249:SER:O	1:0:250:LEU:HD22	2.03	0.57
2:1:192:MET:SD	29:W:357:LEU:HD12	2.43	0.57
12:D:57:LEU:HD12	12:D:160:VAL:HG21	1.87	0.57
12:D:117:GLU:N	12:D:117:GLU:OE1	2.37	0.57
5:4:27:THR:HB	5:4:176:LEU:HD23	1.86	0.57
25:R:300:LEU:HD23	25:R:304:PHE:CE2	2.40	0.56
26:T:77:DT:H2 ⁺	26:T:78:DA:H8	1.70	0.56
1:0:463:ILE:HG23	1:0:463:ILE:O	2.05	0.56
21:M:91:ASN:ND2	21:M:123:ASP:OD2	2.36	0.56
7:6:334:THR:OG1	7:6:355:LYS:NZ	2.27	0.56
11:C:142:VAL:HG11	18:J:5:VAL:HG13	1.88	0.56
13:E:169:ARG:HH12	14:F:74:ILE:HD11	1.71	0.56
8:7:660:THR:OG1	8:7:685:GLN:OE1	2.09	0.56
1:0:5:ILE:HG22	1:0:6:ASP:H	1.70	0.56
5:4:68:ASN:OD1	5:4:69:SER:N	2.38	0.56
1:0:666:LEU:HD22	1:0:679:MET:HB3	1.87	0.56
13:E:84:ASP:O	13:E:113:GLN:NE2	2.39	0.56
23:O:153:THR:HG22	23:O:154:ASP:N	2.18	0.56
1:0:335:LEU:HD21	1:0:399:LEU:CD1	2.32	0.56
8:7:241:ILE:HG12	8:7:245:LEU:HD13	1.87	0.56
8:7:424:PHE:CE2	8:7:452:LEU:HD13	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:26:THR:HG22	12:D:26:THR:O	2.06	0.55
8:7:639:ILE:HD13	30:X:321:LEU:HD11	1.89	0.55
9:A:694:THR:HG22	9:A:714:PHE:CE1	2.42	0.55
9:A:1260:LEU:HD23	9:A:1263:ILE:HD11	1.88	0.55
29:W:49:ILE:HD11	29:W:54:LEU:CD1	2.36	0.55
8:7:241:ILE:HG13	8:7:245:LEU:HD13	1.87	0.55
11:C:56:THR:HG22	11:C:147:LEU:CD2	2.36	0.55
27:U:7:SER:OG	27:U:53:THR:O	2.12	0.55
9:A:260:ASP:OD1	9:A:261:ASP:N	2.39	0.55
11:C:6:PRO:O	19:K:104:ASN:ND2	2.38	0.55
3:2:211:ILE:HD13	3:2:221:VAL:HG21	1.88	0.55
6:5:17:LYS:HE3	6:5:21:LEU:HD11	1.89	0.55
9:A:1446:ASP:HB2	14:F:133:VAL:HG13	1.89	0.55
29:W:61:LEU:HD13	29:W:67:ILE:HD12	1.89	0.55
1:0:413:GLU:N	1:0:413:GLU:OE1	2.40	0.55
5:4:220:GLU:N	5:4:220:GLU:OE1	2.39	0.55
14:F:109:VAL:HG23	14:F:127:GLU:OE1	2.07	0.55
8:7:239:ALA:O	8:7:242:LEU:HG	2.07	0.55
10:B:868:MET:SD	21:M:182:ARG:NH1	2.80	0.55
28:V:47:VAL:O	28:V:51:THR:HG22	2.07	0.55
12:D:16:LYS:NZ	12:D:17:LYS:O	2.39	0.54
10:B:173:MET:O	10:B:176:SER:OG	2.15	0.54
3:2:219:VAL:O	3:2:223:HIS:ND1	2.38	0.54
4:3:18:THR:HG23	4:3:18:THR:O	2.06	0.54
11:C:77:ILE:HD11	11:C:161:LYS:HB3	1.89	0.54
27:U:30:ILE:CG1	27:U:34:THR:HG21	2.38	0.54
1:0:111:ARG:NE	1:0:133:CYS:SG	2.79	0.54
9:A:839:ARG:NH1	10:B:1132:GLU:OE1	2.41	0.54
3:2:272:THR:HG22	3:2:273:LYS:N	2.22	0.53
7:6:181:LEU:HD13	7:6:220:LEU:HD11	1.90	0.53
22:N:26:DT:H2'	22:N:27:DA:C8	2.43	0.53
8:7:330:CYS:HA	8:7:333:ILE:HG22	1.90	0.53
10:B:63:ILE:HD12	10:B:95:ILE:HD12	1.89	0.53
15:G:113:HIS:NE2	29:W:120:ASN:OD1	2.41	0.53
1:0:722:ARG:NH1	7:6:266:LEU:O	2.38	0.53
22:N:42:DT:H2'	22:N:43:DT:H72	1.89	0.53
13:E:116:ILE:HD11	13:E:121:MET:CE	2.38	0.53
1:0:581:LEU:HD21	2:1:330:LEU:HA	1.91	0.53
8:7:186:VAL:HG13	8:7:186:VAL:O	2.09	0.53
10:B:904:ARG:NH2	20:L:66:GLN:O	2.41	0.53
30:X:119:ILE:HG21	30:X:152:SER:H	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:326:ARG:NH2	9:A:1407:GLU:OE2	2.42	0.52
9:A:1038:THR:HG22	9:A:1039:LYS:N	2.24	0.52
9:A:326:ARG:HG3	9:A:1406:VAL:HG21	1.92	0.52
24:Q:409:ALA:O	24:Q:413:MET:HG3	2.09	0.52
10:B:969:ARG:NH1	11:C:61:GLU:OE1	2.41	0.52
7:6:328:ILE:HG22	7:6:346:GLY:O	2.10	0.52
25:R:129:VAL:HG21	25:R:221:GLU:HG3	1.91	0.52
25:R:339:LEU:HD11	25:R:341:LYS:CE	2.40	0.52
29:W:49:ILE:HD11	29:W:54:LEU:HD13	1.89	0.52
9:A:1148:ILE:HD11	9:A:1198:ASP:HB2	1.92	0.52
9:A:1312:ASN:ND2	9:A:1315:GLU:OE1	2.43	0.52
10:B:1010:LEU:CD2	10:B:1012:ILE:HG23	2.39	0.52
15:G:30:LEU:HD12	15:G:72:VAL:HG11	1.92	0.52
15:G:160:ILE:HG22	29:W:137:VAL:HG21	1.91	0.52
10:B:639:ILE:HD11	10:B:691:GLU:CB	2.40	0.52
21:M:263:CYS:SG	21:M:269:ILE:HG21	2.49	0.52
21:M:266:ILE:HB	21:M:269:ILE:HG22	1.91	0.52
25:R:73:LEU:HD21	25:R:81:TRP:CE3	2.45	0.52
25:R:313:TRP:HE1	25:R:318:LEU:HA	1.74	0.52
1:0:303:GLU:OE2	1:0:386:ARG:NE	2.43	0.52
5:4:64:HIS:O	5:4:71:ASN:ND2	2.43	0.52
13:E:88:VAL:CB	13:E:116:ILE:HG22	2.40	0.52
30:X:143:LEU:HD23	30:X:177:THR:HG22	1.92	0.52
2:1:473:LEU:HD11	5:4:34:PRO:CB	2.37	0.51
7:6:450:ASN:C	7:6:450:ASN:ND2	2.62	0.51
1:0:385:VAL:CG1	1:0:390:VAL:HG21	2.39	0.51
10:B:983:ARG:NH2	10:B:1028:GLU:OE2	2.37	0.51
9:A:335:ARG:HH22	10:B:1114:LEU:HD21	1.75	0.51
10:B:40:GLU:OE1	10:B:682:SER:N	2.43	0.51
8:7:493:VAL:N	8:7:494:PRO:CD	2.74	0.51
16:H:15:VAL:HG12	16:H:26:ILE:HG22	1.92	0.51
21:M:200:THR:CG2	23:O:189:LEU:HD22	2.40	0.51
29:W:198:THR:HG22	29:W:199:PHE:N	2.26	0.51
29:W:349:GLU:HB3	29:W:352:GLU:OE1	2.09	0.51
1:0:526:LEU:HD11	1:0:597:ILE:HD11	1.93	0.51
8:7:832:LEU:HD22	9:A:1266:THR:HG21	1.92	0.51
9:A:474:VAL:HG22	9:A:474:VAL:O	2.11	0.51
23:O:166:VAL:HG21	23:O:170:ILE:HD11	1.92	0.51
1:0:40:LEU:HD12	1:0:483:TYR:HE1	1.76	0.51
5:4:33:ALA:HB3	5:4:36:LEU:HD12	1.91	0.51
30:X:172:ASP:O	30:X:176:GLY:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Q:111:LEU:HD21	25:R:84:ARG:NH1	2.26	0.51
2:1:602:ASN:OD1	2:1:603:GLY:N	2.42	0.51
3:2:221:VAL:HG22	3:2:249:MET:HE2	1.93	0.51
7:6:113:LYS:HA	7:6:388:THR:HG21	1.91	0.51
2:1:510:ASN:ND2	5:4:266:ASN:O	2.39	0.50
8:7:605:ILE:HB	8:7:651:THR:HG22	1.93	0.50
5:4:273:ARG:NH2	7:6:326:THR:HG23	2.25	0.50
8:7:624:LYS:C	30:X:316:HIS:HE2	2.14	0.50
1:0:5:ILE:HG21	1:0:29:LYS:HD3	1.93	0.50
1:0:620:VAL:HG21	1:0:669:VAL:CG2	2.42	0.50
10:B:839:MET:HG2	10:B:1012:ILE:HG22	1.92	0.50
10:B:1010:LEU:HD21	10:B:1012:ILE:HG23	1.94	0.50
11:C:54:ASN:ND2	11:C:60:ASP:OD1	2.45	0.50
2:1:270:TYR:CZ	2:1:274:VAL:HG21	2.47	0.50
9:A:1116:LEU:HD23	9:A:1329:THR:HG23	1.94	0.50
21:M:321:ASP:OD1	21:M:322:LYS:N	2.45	0.50
26:T:82:DT:H2'	26:T:83:DA:C8	2.46	0.50
29:W:61:LEU:HD13	29:W:67:ILE:CD1	2.42	0.50
5:4:254:ILE:HG12	5:4:262:ILE:HG21	1.93	0.50
16:H:2:SER:OG	16:H:3:ASN:N	2.39	0.50
3:2:221:VAL:HG22	3:2:249:MET:HE1	1.94	0.50
26:T:77:DT:H2''	26:T:78:DA:C8	2.47	0.50
29:W:93:HIS:NE2	29:W:196:GLU:OE2	2.45	0.50
9:A:62:ASP:OD1	9:A:63:ARG:N	2.45	0.50
9:A:1215:ARG:O	9:A:1219:THR:HG23	2.12	0.50
24:Q:396:THR:OG1	24:Q:398:ARG:NH1	2.45	0.50
8:7:743:GLU:N	8:7:743:GLU:OE1	2.45	0.50
10:B:108:VAL:HG23	21:M:244:SER:HB2	1.92	0.50
13:E:137:GLU:O	13:E:141:VAL:HG23	2.11	0.50
9:A:1230:GLU:N	9:A:1230:GLU:OE1	2.45	0.49
23:O:83:LYS:HE3	23:O:87:LEU:HD11	1.93	0.49
1:0:711:ASP:OD1	1:0:712:MET:N	2.45	0.49
3:2:231:LEU:HD22	3:2:237:TYR:CE1	2.48	0.49
13:E:65:THR:HG23	13:E:68:SER:H	1.77	0.49
1:0:52:LEU:HD11	1:0:459:THR:HG21	1.94	0.49
10:B:806:THR:HG23	10:B:1045:SER:HA	1.94	0.49
13:E:156:LEU:HD11	13:E:197:LYS:HB2	1.94	0.49
29:W:37:VAL:HG11	29:W:199:PHE:CD1	2.47	0.49
9:A:1029:ARG:NH1	9:A:1033:GLN:OE1	2.45	0.49
27:U:17:VAL:HG22	28:V:47:VAL:HG21	1.95	0.49
8:7:519:ARG:NH2	8:7:521:ASP:OD2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Q:336:ASP:N	24:Q:336:ASP:OD1	2.45	0.49
2:1:542:LEU:HD23	2:1:608:MET:SD	2.52	0.49
12:D:167:LEU:HB3	12:D:177:VAL:HG23	1.95	0.49
11:C:174:ALA:N	11:C:233:GLU:O	2.41	0.49
1:0:162:LEU:CD2	1:0:195:ILE:HD11	2.43	0.49
1:0:334:PHE:CE2	1:0:369:ILE:HG23	2.47	0.49
15:G:160:ILE:CG2	29:W:137:VAL:HG21	2.43	0.49
2:1:489:VAL:HG22	5:4:55:GLU:HG2	1.94	0.48
1:0:197:ARG:HA	1:0:200:ILE:HD12	1.95	0.48
1:0:295:SER:N	1:0:379:GLU:OE2	2.46	0.48
20:L:40:LEU:HD11	20:L:56:LEU:CD1	2.43	0.48
5:4:65:LEU:O	5:4:117:ARG:NH2	2.47	0.48
29:W:116:ASN:O	29:W:116:ASN:ND2	2.46	0.48
1:0:657:ASP:OD1	1:0:660:ARG:NH2	2.46	0.48
1:0:27:ASP:OD2	1:0:483:TYR:OH	2.15	0.48
1:0:340:GLU:HG3	4:3:78:VAL:HG21	1.96	0.48
1:0:484:ALA:HB1	1:0:699:GLN:HE22	1.79	0.48
5:4:80:SER:HG	5:4:144:SER:HG	1.62	0.48
9:A:1002:GLY:HA3	9:A:1007:ILE:HG21	1.95	0.48
10:B:805:THR:HG23	24:Q:22:ILE:HD12	1.95	0.48
27:U:42:TRP:O	27:U:46:LEU:HD23	2.13	0.48
16:H:40:LEU:HD21	16:H:144:ILE:HD11	1.96	0.47
29:W:360:TYR:CE2	29:W:364:LEU:HD11	2.48	0.47
1:0:611:ASP:OD2	1:0:671:ARG:NH2	2.47	0.47
8:7:385:VAL:HA	8:7:514:THR:O	2.13	0.47
24:Q:414:ASP:OD1	24:Q:415:LYS:N	2.47	0.47
2:1:170:SER:O	2:1:174:LEU:HD23	2.15	0.47
9:A:526:ASP:OD1	9:A:657:LEU:CD2	2.62	0.47
29:W:409:LEU:HD23	29:W:409:LEU:O	2.14	0.47
30:X:161:GLU:O	30:X:165:LYS:HG3	2.15	0.47
5:4:86:LEU:HD23	5:4:125:LEU:HD12	1.96	0.47
7:6:427:TYR:O	7:6:436:PHE:N	2.41	0.47
9:A:1227:ILE:HD11	9:A:1239:ARG:HH11	1.78	0.47
10:B:283:VAL:HG21	10:B:318:VAL:HA	1.95	0.47
1:0:394:GLU:O	1:0:397:THR:HG22	2.14	0.47
1:0:551:VAL:HG11	2:1:375:LEU:CD2	2.44	0.47
4:3:92:PHE:HE2	4:3:133:LEU:HD13	1.80	0.47
8:7:698:ASP:OD1	8:7:698:ASP:N	2.48	0.47
9:A:1209:MET:CG	9:A:1236:LEU:HD11	2.44	0.47
15:G:116:PRO:HD2	15:G:119:LEU:HD12	1.97	0.47
23:O:153:THR:CG2	23:O:154:ASP:H	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:T:38:DG:H2'	26:T:39:DT:H72	1.96	0.47
29:W:95:ILE:HD12	29:W:194:ILE:HD13	1.97	0.47
9:A:346:ASP:OD1	10:B:1106:ARG:NE	2.45	0.47
9:A:549:MET:HE2	9:A:577:ILE:HG21	1.97	0.47
21:M:325:ASP:HB3	21:M:328:LEU:HD13	1.97	0.47
23:O:67:LEU:CD2	23:O:223:ILE:HD13	2.45	0.47
8:7:833:ILE:O	8:7:833:ILE:HG22	2.14	0.47
9:A:1384:VAL:O	9:A:1384:VAL:CG1	2.62	0.47
10:B:925:LEU:HD22	21:M:22:LEU:HD13	1.97	0.47
15:G:56:ILE:CD1	15:G:72:VAL:HG22	2.45	0.47
7:6:197:LYS:O	7:6:200:ARG:HG2	2.14	0.47
8:7:242:LEU:HD12	8:7:243:GLN:N	2.30	0.47
10:B:952:VAL:HG12	10:B:966:VAL:HG13	1.96	0.47
13:E:136:ASN:OD1	13:E:138:ALA:N	2.47	0.47
30:X:292:THR:HG22	30:X:292:THR:O	2.15	0.47
17:I:3:THR:HG22	17:I:3:THR:O	2.14	0.46
5:4:21:GLU:N	5:4:257:SER:HG	2.13	0.46
9:A:1219:THR:HG21	9:A:1271:ILE:HD12	1.96	0.46
9:A:1345:ARG:HG2	9:A:1372:VAL:HG12	1.98	0.46
12:D:118:THR:HG22	12:D:119:ARG:N	2.30	0.46
2:1:270:TYR:CE1	2:1:274:VAL:HG21	2.50	0.46
9:A:925:LEU:HD12	9:A:983:ILE:HB	1.97	0.46
23:O:67:LEU:HD22	23:O:160:ILE:CG2	2.46	0.46
24:Q:118:LEU:HD21	24:Q:375:LEU:HD21	1.96	0.46
1:0:56:THR:HG21	1:0:233:ILE:HD11	1.98	0.46
9:A:1342:GLU:OE2	13:E:212:ARG:NE	2.45	0.46
1:0:250:LEU:HD23	1:0:408:LEU:CD1	2.45	0.46
8:7:244:MET:HG3	8:7:245:LEU:HD12	1.97	0.46
25:R:300:LEU:CD2	25:R:304:PHE:CE2	2.98	0.46
25:R:358:LEU:HD22	30:X:162:LEU:HD22	1.97	0.46
3:2:368:ALA:HB3	3:2:375:LEU:HD21	1.98	0.46
9:A:443:LEU:HD13	9:A:501:LEU:HD11	1.98	0.46
25:R:339:LEU:HD11	25:R:341:LYS:HE3	1.97	0.46
1:0:622:MET:HB2	1:0:681:LEU:HD23	1.96	0.46
9:A:464:PRO:O	19:K:2:ASN:HB3	2.14	0.46
9:A:1428:VAL:HG13	10:B:1151:LEU:HD13	1.97	0.46
11:C:38:ILE:HG13	11:C:176:ILE:HD12	1.98	0.46
21:M:316:LEU:HD23	21:M:323:LEU:HD13	1.98	0.46
24:Q:336:ASP:OD1	24:Q:339:ALA:HB3	2.16	0.46
1:0:277:VAL:HG23	1:0:278:ASP:N	2.31	0.46
3:2:139:SER:CB	3:2:272:THR:HG21	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:258:LEU:H	5:4:258:LEU:HD23	1.81	0.46
10:B:106:ASP:N	10:B:106:ASP:OD1	2.47	0.46
3:2:143:TRP:NE1	3:2:147:LEU:HD11	2.31	0.46
8:7:356:LEU:CD2	8:7:360:THR:HG21	2.44	0.46
9:A:890:ASP:OD1	9:A:940:ARG:NH1	2.48	0.46
25:R:233:TYR:O	25:R:234:HIS:CG	2.68	0.46
3:2:67:ASN:OD1	3:2:68:SER:N	2.49	0.46
11:C:248:ILE:HG21	19:K:102:LYS:HB2	1.97	0.46
23:O:64:VAL:HG13	23:O:64:VAL:O	2.15	0.46
26:T:53:DG:C2	26:T:54:DA:C5	3.03	0.46
30:X:202:PHE:O	30:X:245:TRP:NE1	2.45	0.46
8:7:609:SER:HB3	8:7:615:LEU:HD13	1.98	0.45
10:B:628:THR:HG22	10:B:628:THR:O	2.16	0.45
11:C:112:ASN:ND2	18:J:19:GLU:OE2	2.48	0.45
11:C:262:LEU:HD23	19:K:88:LYS:HG2	1.97	0.45
23:O:157:ILE:HG21	23:O:160:ILE:HD11	1.96	0.45
10:B:132:VAL:HG11	10:B:444:MET:CE	2.47	0.45
10:B:1033:LYS:NZ	10:B:1070:GLU:OE2	2.32	0.45
29:W:5:ILE:HD13	29:W:192:SER:HB3	1.98	0.45
30:X:128:LEU:HD21	30:X:166:LEU:CD1	2.47	0.45
1:0:438:THR:HG22	2:1:352:ASN:OD1	2.17	0.45
30:X:317:MET:HA	30:X:320:ILE:HD12	1.97	0.45
3:2:117:VAL:O	3:2:117:VAL:HG22	2.17	0.45
3:2:375:LEU:HD23	3:2:375:LEU:H	1.81	0.45
7:6:172:ILE:HD11	7:6:220:LEU:HD12	1.98	0.45
9:A:227:VAL:HG12	12:D:15:LEU:HD12	1.98	0.45
9:A:992:ASP:OD1	9:A:993:LEU:N	2.50	0.45
10:B:1159:ARG:NH1	10:B:1193:GLN:OE1	2.48	0.45
15:G:51:TYR:HA	15:G:54:ILE:HD11	1.99	0.45
23:O:170:ILE:HD13	23:O:234:LEU:HD22	1.97	0.45
8:7:424:PHE:CE2	8:7:452:LEU:CD1	3.00	0.45
9:A:1143:LEU:O	9:A:1147:THR:HG22	2.17	0.45
10:B:292:ILE:N	10:B:293:PRO:CD	2.79	0.45
11:C:145:CYS:SG	11:C:146:LYS:N	2.90	0.45
12:D:174:PRO:HA	12:D:177:VAL:HG12	1.98	0.45
24:Q:335:LEU:HD11	24:Q:340:LYS:HD3	1.99	0.45
30:X:128:LEU:HD21	30:X:166:LEU:HD11	1.98	0.45
3:2:224:PHE:HZ	3:2:250:LEU:HD13	1.82	0.45
10:B:976:ILE:O	10:B:976:ILE:CG2	2.65	0.45
13:E:135:PHE:HB3	13:E:140:LEU:HD11	1.98	0.45
21:M:249:PRO:HG2	21:M:252:VAL:HG23	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:T:82:DT:C2'	26:T:83:DA:C8	3.00	0.45
2:1:103:THR:HG22	2:1:306:ARG:HH12	1.81	0.45
3:2:433:LEU:HD11	3:2:438:VAL:CG2	2.47	0.45
7:6:114:ASN:O	7:6:114:ASN:ND2	2.50	0.45
25:R:41:ASP:OD1	25:R:42:GLY:N	2.47	0.45
3:2:99:ASN:OD1	3:2:100:LEU:N	2.50	0.45
9:A:555:ASP:OD2	9:A:648:ASN:ND2	2.49	0.45
10:B:118:ARG:NH2	10:B:202:TYR:OH	2.50	0.45
15:G:155:SER:O	15:G:155:SER:OG	2.32	0.45
21:M:177:LEU:HD21	21:M:181:ARG:CZ	2.47	0.45
24:Q:433:THR:O	24:Q:434:THR:OG1	2.34	0.45
1:0:75:THR:HG22	1:0:76:MET:N	2.32	0.45
1:0:441:ASP:OD1	1:0:646:TYR:OH	2.32	0.45
10:B:1189:ILE:HD12	15:G:41:LYS:HG3	1.99	0.45
11:C:44:LEU:HB2	11:C:77:ILE:HD13	1.99	0.45
9:A:350:ARG:NE	9:A:486:GLU:OE1	2.48	0.44
12:D:129:LEU:O	12:D:133:THR:HG22	2.16	0.44
13:E:68:SER:OG	13:E:75:MET:SD	2.75	0.44
24:Q:141:ARG:O	25:R:208:ILE:N	2.44	0.44
26:T:52:DG:C2	26:T:53:DG:C6	3.05	0.44
10:B:136:THR:HG23	10:B:152:ILE:HG22	1.98	0.44
15:G:56:ILE:HD13	15:G:72:VAL:HG22	1.98	0.44
9:A:559:VAL:HG11	16:H:75:ALA:HB1	2.00	0.44
9:A:881:GLN:NE2	9:A:958:VAL:O	2.51	0.44
9:A:1227:ILE:HD11	9:A:1239:ARG:NH1	2.32	0.44
10:B:244:LEU:HD23	10:B:244:LEU:H	1.81	0.44
10:B:439:ALA:HB1	25:R:284:LYS:HD3	2.00	0.44
3:2:347:ILE:HD11	3:2:378:ILE:HD11	2.00	0.44
9:A:1279:ILE:HG23	9:A:1308:THR:CG2	2.47	0.44
15:G:9:LEU:HD22	15:G:34:VAL:CG2	2.47	0.44
3:2:250:LEU:CD1	3:2:259:VAL:HG11	2.46	0.44
8:7:410:LEU:HD12	8:7:487:LEU:CD2	2.48	0.44
22:N:54:DC:O2	24:Q:415:LYS:HE3	2.17	0.44
1:0:221:ARG:NH1	1:0:304:GLU:OE2	2.47	0.44
5:4:59:VAL:HG13	5:4:245:ILE:HD13	1.98	0.44
11:C:255:VAL:HG21	19:K:94:ILE:HG21	1.99	0.44
12:D:164:ILE:O	12:D:168:LYS:HG2	2.18	0.44
8:7:323:VAL:HA	8:7:326:VAL:HG12	1.99	0.44
9:A:886:ILE:O	9:A:944:ARG:NH1	2.51	0.44
9:A:1135:ARG:NH2	9:A:1282:VAL:O	2.51	0.44
10:B:310:MET:HG3	10:B:386:LEU:HD13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:848:ARG:NH1	18:J:8:PHE:O	2.51	0.44
9:A:356:ASP:OD2	19:K:65:HIS:NE2	2.46	0.44
25:R:339:LEU:HD11	25:R:341:LYS:HE2	1.99	0.44
9:A:590:ARG:NH1	9:A:592:ASP:OD2	2.50	0.43
10:B:954:VAL:HG12	10:B:964:VAL:CG1	2.46	0.43
15:G:13:LEU:HD11	15:G:26:LEU:HG	1.98	0.43
29:W:174:ARG:O	29:W:178:GLN:HG3	2.18	0.43
1:0:42:MET:O	1:0:461:GLY:HA2	2.18	0.43
7:6:429:CYS:O	7:6:433:LYS:N	2.43	0.43
9:A:261:ASP:OD1	9:A:316:GLN:NE2	2.46	0.43
9:A:694:THR:HG22	9:A:714:PHE:CZ	2.52	0.43
28:V:10:TYR:O	28:V:13:SER:OG	2.32	0.43
1:0:5:ILE:O	1:0:6:ASP:C	2.57	0.43
5:4:50:ILE:O	5:4:53:VAL:HG12	2.18	0.43
9:A:1197:LEU:HB2	9:A:1236:LEU:HD23	2.00	0.43
19:K:106:GLU:O	19:K:110:ASN:ND2	2.49	0.43
21:M:225:ILE:HG13	21:M:226:ASP:N	2.33	0.43
29:W:364:LEU:O	29:W:368:GLN:HG3	2.19	0.43
8:7:578:MET:HE3	8:7:677:TYR:CE1	2.53	0.43
9:A:806:ARG:NH1	10:B:725:PRO:O	2.49	0.43
10:B:1220:ARG:O	12:D:11:ARG:NH2	2.49	0.43
29:W:65:ARG:HH21	30:X:274:LEU:HD22	1.84	0.43
2:1:103:THR:HG22	2:1:306:ARG:NH1	2.34	0.43
24:Q:327:ARG:NH2	26:T:67:DG:OP1	2.51	0.43
27:U:251:VAL:HG23	27:U:260:CYS:SG	2.59	0.43
3:2:13:TYR:CE2	3:2:208:LEU:HD13	2.54	0.43
3:2:227:MET:O	3:2:231:LEU:HG	2.18	0.43
8:7:493:VAL:HG12	8:7:494:PRO:HD3	2.01	0.43
11:C:148:ARG:NH1	18:J:61:LEU:O	2.52	0.43
1:0:551:VAL:HG11	2:1:375:LEU:HD21	2.00	0.43
5:4:194:ILE:HB	5:4:195:PRO:HD3	2.01	0.43
8:7:250:VAL:HG21	8:7:329:ARG:HD3	2.00	0.43
9:A:982:THR:OG1	9:A:985:ASP:OD2	2.37	0.43
1:0:105:GLY:O	1:0:106:LEU:HD22	2.19	0.43
3:2:141:ASN:O	3:2:145:THR:HG23	2.19	0.43
8:7:384:ILE:HB	8:7:513:LEU:HD23	2.01	0.43
10:B:828:ALA:HB2	10:B:1085:ILE:HG23	2.00	0.43
11:C:18:VAL:O	11:C:18:VAL:HG13	2.19	0.43
1:0:577:GLN:O	1:0:581:LEU:HD13	2.19	0.43
8:7:217:THR:HG22	8:7:217:THR:O	2.19	0.43
9:A:709:THR:HG22	9:A:710:LEU:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1002:GLY:H	9:A:1007:ILE:HG21	1.84	0.43
9:A:1151:GLU:OE2	17:I:45:ARG:NH1	2.51	0.43
10:B:936:ASP:OD1	10:B:938:SER:N	2.50	0.43
13:E:169:ARG:NH1	14:F:142:SER:OG	2.51	0.43
15:G:54:ILE:HD12	15:G:54:ILE:H	1.84	0.43
25:R:303:LEU:HD21	25:R:318:LEU:HD11	2.00	0.43
25:R:336:VAL:HG12	30:X:129:LEU:CD2	2.48	0.43
1:0:32:LEU:HD22	1:0:231:ILE:HD12	2.01	0.43
22:N:64:DT:H2'	22:N:65:DT:H71	2.00	0.43
25:R:106:LEU:HG	25:R:108:LEU:HD12	2.01	0.43
1:0:678:VAL:HG11	1:0:717:THR:HG23	2.01	0.42
4:3:23:SER:O	4:3:26:VAL:HG12	2.19	0.42
8:7:610:ASP:OD2	8:7:676:HIS:ND1	2.52	0.42
22:N:18:DT:H2''	22:N:19:DG:C8	2.53	0.42
8:7:598:HIS:HB2	8:7:605:ILE:HD11	2.01	0.42
10:B:661:LEU:HD21	10:B:684:LEU:HD21	2.01	0.42
10:B:1153:GLU:OE1	10:B:1153:GLU:N	2.52	0.42
16:H:4:THR:HG23	16:H:58:THR:HG23	2.00	0.42
22:N:42:DT:C2'	22:N:43:DT:H72	2.49	0.42
2:1:480:LEU:HD12	2:1:484:LEU:HD12	2.01	0.42
10:B:1213:THR:O	10:B:1213:THR:OG1	2.35	0.42
4:3:92:PHE:CE2	4:3:133:LEU:HD13	2.54	0.42
22:N:23:DA:H2''	22:N:24:DT:H5'	2.01	0.42
1:0:104:ARG:NH2	1:0:171:LEU:O	2.47	0.42
1:0:625:ILE:HD12	1:0:685:ARG:HB2	2.01	0.42
22:N:26:DT:H2'	22:N:27:DA:N7	2.34	0.42
24:Q:159:ARG:HA	24:Q:162:GLU:HG2	2.02	0.42
9:A:672:ASP:OD1	9:A:675:THR:OG1	2.28	0.42
9:A:997:LEU:O	9:A:1011:GLN:NE2	2.53	0.42
10:B:510:LYS:HG3	10:B:513:GLN:HG2	2.02	0.42
1:0:238:HIS:O	1:0:660:ARG:HD2	2.20	0.42
1:0:374:LEU:HD23	1:0:410:SER:HB3	2.01	0.42
1:0:538:VAL:CG2	1:0:620:VAL:HG22	2.50	0.42
7:6:215:GLU:OE2	7:6:218:ARG:NH2	2.50	0.42
10:B:212:LEU:HD21	10:B:466:TRP:CH2	2.55	0.42
27:U:52:THR:HG22	27:U:53:THR:N	2.34	0.42
29:W:102:VAL:HG22	29:W:179:ILE:HD11	2.02	0.42
1:0:381:LEU:O	1:0:385:VAL:HG23	2.19	0.42
9:A:660:ASN:O	10:B:1082:MET:N	2.53	0.42
10:B:63:ILE:HD11	10:B:95:ILE:HD12	2.00	0.42
17:I:17:ARG:NH1	17:I:28:GLU:OE1	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:433:LEU:HD11	3:2:438:VAL:HG23	2.02	0.42
8:7:107:ASP:OD1	8:7:108:SER:N	2.51	0.42
8:7:445:MET:SD	8:7:453:VAL:HG22	2.59	0.42
9:A:726:ARG:HD3	9:A:766:GLY:HA3	2.02	0.42
9:A:989:GLY:O	9:A:992:ASP:OD1	2.38	0.42
10:B:420:LEU:HB3	10:B:453:ILE:HD13	2.02	0.42
23:O:74:VAL:HG12	23:O:75:THR:N	2.35	0.42
25:R:91:GLU:O	25:R:109:ASN:ND2	2.53	0.42
3:2:387:LEU:HD13	3:2:448:LEU:HD12	2.02	0.42
4:3:126:VAL:HG13	4:3:127:ALA:N	2.35	0.42
9:A:537:ARG:NH2	9:A:599:SER:O	2.44	0.42
11:C:254:LYS:HE3	19:K:42:LEU:HD11	2.01	0.42
15:G:99:PHE:CE1	15:G:110:VAL:HG21	2.55	0.42
17:I:72:ASP:OD1	17:I:72:ASP:N	2.48	0.42
22:N:19:DG:C8	22:N:20:DT:H72	2.55	0.42
5:4:57:LEU:O	5:4:61:LEU:HG	2.20	0.41
5:4:210:ILE:HG23	5:4:210:ILE:O	2.20	0.41
9:A:465:TYR:CG	10:B:976:ILE:HD12	2.55	0.41
9:A:694:THR:HG22	9:A:714:PHE:HE1	1.84	0.41
30:X:242:ARG:O	30:X:243:TYR:C	2.59	0.41
10:B:486:TYR:OH	10:B:778:MET:HG2	2.20	0.41
27:U:45:LYS:O	27:U:49:THR:HG23	2.21	0.41
29:W:82:VAL:HG11	29:W:84:ARG:HE	1.85	0.41
1:0:189:THR:O	1:0:189:THR:HG22	2.20	0.41
2:1:195:PHE:CE2	2:1:199:VAL:HG21	2.55	0.41
8:7:576:LYS:NZ	8:7:763:VAL:O	2.52	0.41
9:A:1176:LEU:HD12	9:A:1176:LEU:O	2.19	0.41
24:Q:328:LYS:O	24:Q:329:THR:HG23	2.21	0.41
1:0:537:MET:HG3	1:0:619:THR:HG23	2.03	0.41
2:1:195:PHE:CD2	2:1:199:VAL:HG21	2.55	0.41
3:2:189:PHE:CD2	3:2:391:ILE:HG23	2.55	0.41
7:6:347:TYR:CD1	7:6:359:LEU:HD13	2.55	0.41
8:7:598:HIS:CB	8:7:605:ILE:HD11	2.51	0.41
9:A:842:VAL:HG11	10:B:1136:ASP:OD2	2.20	0.41
11:C:18:VAL:HG12	11:C:240:VAL:CG2	2.50	0.41
26:T:54:DA:C2	26:T:55:DG:C5	3.08	0.41
1:0:40:LEU:HD12	1:0:483:TYR:CE1	2.55	0.41
8:7:490:VAL:HG21	8:7:531:ILE:HD13	2.02	0.41
9:A:227:VAL:CG1	12:D:15:LEU:HD12	2.50	0.41
9:A:1400:CYS:HB2	9:A:1405:THR:HG23	2.03	0.41
12:D:31:GLN:OE1	12:D:34:GLN:NE2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:496:SER:O	2:1:500:ASN:ND2	2.53	0.41
8:7:606:ILE:HB	8:7:670:LEU:HD12	2.03	0.41
8:7:672:GLN:OE1	8:7:722:ARG:NH1	2.54	0.41
23:O:202:ILE:HG22	23:O:203:VAL:N	2.36	0.41
25:R:240:ARG:HA	25:R:243:ILE:HD12	2.02	0.41
8:7:454:VAL:O	8:7:454:VAL:HG13	2.20	0.41
10:B:806:THR:HG22	10:B:808:ALA:H	1.84	0.41
10:B:839:MET:O	10:B:991:GLY:N	2.49	0.41
13:E:190:LEU:HD11	13:E:196:VAL:HG11	2.02	0.41
21:M:177:LEU:HD21	21:M:181:ARG:NE	2.36	0.41
21:M:288:LEU:HG	21:M:334:VAL:HG11	2.02	0.41
22:N:24:DT:H2'	22:N:25:DA:C8	2.55	0.41
23:O:108:GLU:HB3	23:O:109:PRO:HD3	2.02	0.41
27:U:13:ILE:O	27:U:17:VAL:HG23	2.20	0.41
3:2:148:HIS:HA	3:2:151:VAL:HG12	2.01	0.41
8:7:439:THR:OG1	8:7:440:SER:N	2.54	0.41
12:D:36:LYS:HB3	12:D:44:GLU:OE2	2.20	0.41
21:M:326:PRO:HA	21:M:329:ILE:HG22	2.03	0.41
23:O:107:ARG:NH2	28:V:66:LEU:O	2.53	0.41
7:6:150:ILE:HG21	7:6:200:ARG:HB3	2.03	0.41
7:6:384:MET:O	7:6:384:MET:HG3	2.21	0.41
8:7:493:VAL:N	8:7:494:PRO:HD3	2.36	0.41
9:A:471:ASN:O	9:A:474:VAL:HG12	2.20	0.41
29:W:109:LEU:HD12	29:W:175:LEU:CD2	2.51	0.41
1:0:239:ASN:O	1:0:239:ASN:ND2	2.54	0.41
1:0:612:PHE:O	1:0:669:VAL:HA	2.21	0.41
2:1:489:VAL:HG11	5:4:59:VAL:HG11	2.03	0.41
7:6:338:CYS:SG	7:6:339:HIS:CE1	3.14	0.41
8:7:519:ARG:NE	8:7:521:ASP:OD1	2.54	0.41
9:A:130:ASP:OD2	9:A:133:LYS:NZ	2.40	0.41
9:A:339:ASN:ND2	10:B:1117:GLN:OE1	2.49	0.41
10:B:298:LEU:HD12	17:I:6:PHE:CZ	2.56	0.41
1:0:620:VAL:HG21	1:0:669:VAL:HG21	2.03	0.40
3:2:208:LEU:HD23	3:2:221:VAL:HG11	2.03	0.40
8:7:490:VAL:HG21	8:7:531:ILE:CD1	2.51	0.40
8:7:707:SER:OG	8:7:722:ARG:NH2	2.54	0.40
21:M:252:VAL:HG21	21:M:291:ILE:HD11	2.03	0.40
21:M:315:ILE:HD12	21:M:315:ILE:H	1.85	0.40
2:1:181:GLN:HA	2:1:184:LEU:CD2	2.50	0.40
7:6:140:ASP:OD1	7:6:141:LEU:N	2.53	0.40
8:7:492:VAL:HG12	22:N:71:DT:OP1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:M:325:ASP:CB	21:M:328:LEU:HD13	2.51	0.40
10:B:760:ASP:N	10:B:760:ASP:OD1	2.55	0.40
28:V:34:ALA:O	28:V:38:MET:HG2	2.21	0.40
29:W:13:LEU:O	29:W:17:VAL:HG23	2.21	0.40
29:W:95:ILE:HD13	29:W:189:ILE:HG21	2.04	0.40
3:2:142:LYS:NZ	3:2:255:ASP:O	2.52	0.40
7:6:368:LEU:HD23	7:6:369:MET:O	2.21	0.40
8:7:619:ALA:HB1	8:7:624:LYS:O	2.21	0.40
9:A:924:LYS:O	9:A:927:VAL:HG22	2.20	0.40
11:C:43:THR:HG22	11:C:44:LEU:N	2.36	0.40
13:E:100:ILE:HD13	13:E:132:ILE:CD1	2.52	0.40
26:T:46:DC:H2''	26:T:47:DA:C8	2.56	0.40
3:2:356:GLN:O	3:2:360:LEU:HD13	2.21	0.40
7:6:400:SER:OG	7:6:402:ASP:OD1	2.40	0.40
10:B:810:GLU:OE1	10:B:815:ARG:NH1	2.55	0.40
26:T:75:DG:H2''	26:T:76:DC:C6	2.57	0.40
28:V:44:PHE:HA	28:V:47:VAL:HG22	2.02	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	0	750/778 (96%)	733 (98%)	17 (2%)	0	100	100
2	1	508/645 (79%)	502 (99%)	6 (1%)	0	100	100
3	2	435/517 (84%)	430 (99%)	5 (1%)	0	100	100
4	3	129/324 (40%)	127 (98%)	2 (2%)	0	100	100
5	4	287/341 (84%)	287 (100%)	0	0	100	100
6	5	63/76 (83%)	61 (97%)	2 (3%)	0	100	100
7	6	352/464 (76%)	349 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	7	609/843 (72%)	588 (97%)	21 (3%)	0	100	100
9	A	1422/1733 (82%)	1387 (98%)	35 (2%)	0	100	100
10	B	1168/1224 (95%)	1131 (97%)	37 (3%)	0	100	100
11	C	264/347 (76%)	258 (98%)	6 (2%)	0	100	100
12	D	163/221 (74%)	163 (100%)	0	0	100	100
13	E	212/215 (99%)	207 (98%)	5 (2%)	0	100	100
14	F	84/155 (54%)	82 (98%)	2 (2%)	0	100	100
15	G	169/177 (96%)	166 (98%)	3 (2%)	0	100	100
16	H	136/146 (93%)	133 (98%)	3 (2%)	0	100	100
17	I	114/122 (93%)	106 (93%)	8 (7%)	0	100	100
18	J	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
19	K	113/120 (94%)	112 (99%)	1 (1%)	0	100	100
20	L	43/70 (61%)	42 (98%)	1 (2%)	0	100	100
21	M	302/352 (86%)	294 (97%)	8 (3%)	0	100	100
23	O	179/247 (72%)	172 (96%)	7 (4%)	0	100	100
24	Q	215/738 (29%)	204 (95%)	11 (5%)	0	100	100
25	R	264/400 (66%)	256 (97%)	8 (3%)	0	100	100
27	U	101/171 (59%)	97 (96%)	4 (4%)	0	100	100
28	V	100/129 (78%)	100 (100%)	0	0	100	100
29	W	304/492 (62%)	296 (97%)	8 (3%)	0	100	100
30	X	209/328 (64%)	199 (95%)	10 (5%)	0	100	100
All	All	8762/11445 (77%)	8548 (98%)	214 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	684/707 (97%)	684 (100%)	0	100	100
2	1	483/590 (82%)	483 (100%)	0	100	100
3	2	408/470 (87%)	408 (100%)	0	100	100
4	3	125/305 (41%)	125 (100%)	0	100	100
5	4	260/302 (86%)	260 (100%)	0	100	100
6	5	59/68 (87%)	59 (100%)	0	100	100
7	6	323/419 (77%)	322 (100%)	1 (0%)	92	96
8	7	547/737 (74%)	547 (100%)	0	100	100
9	A	1251/1520 (82%)	1251 (100%)	0	100	100
10	B	1024/1061 (96%)	1023 (100%)	1 (0%)	93	98
11	C	234/299 (78%)	234 (100%)	0	100	100
12	D	149/200 (74%)	148 (99%)	1 (1%)	84	94
13	E	196/197 (100%)	196 (100%)	0	100	100
14	F	76/137 (56%)	76 (100%)	0	100	100
15	G	152/158 (96%)	152 (100%)	0	100	100
16	H	123/128 (96%)	123 (100%)	0	100	100
17	I	110/116 (95%)	110 (100%)	0	100	100
18	J	64/65 (98%)	64 (100%)	0	100	100
19	K	99/102 (97%)	99 (100%)	0	100	100
20	L	40/57 (70%)	40 (100%)	0	100	100
21	M	265/306 (87%)	265 (100%)	0	100	100
23	O	153/212 (72%)	153 (100%)	0	100	100
24	Q	204/642 (32%)	204 (100%)	0	100	100
25	R	252/363 (69%)	252 (100%)	0	100	100
27	U	99/154 (64%)	99 (100%)	0	100	100
28	V	94/115 (82%)	94 (100%)	0	100	100
29	W	281/436 (64%)	280 (100%)	1 (0%)	91	95
30	X	191/295 (65%)	191 (100%)	0	100	100
All	All	7946/10161 (78%)	7942 (100%)	4 (0%)	93	98

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	6	450	ASN
10	B	928	ARG
12	D	14	ARG
29	W	116	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
7	6	450	ASN
9	A	451	HIS
9	A	659	HIS
10	B	794	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 19 are monoatomic - leaving 3 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	$\# Z > 2$
35	ADP	7	903	34,33	24,29,29	0.67	0	29,45,45	0.68	0
33	BEF	7	901	35	0,3,3	0.00	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
31	SF4	0	801	1	0,12,12	0.00	-	-		

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
35	ADP	7	903	34,33	-	2/12/32/32	0/3/3/3
31	SF4	0	801	1	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

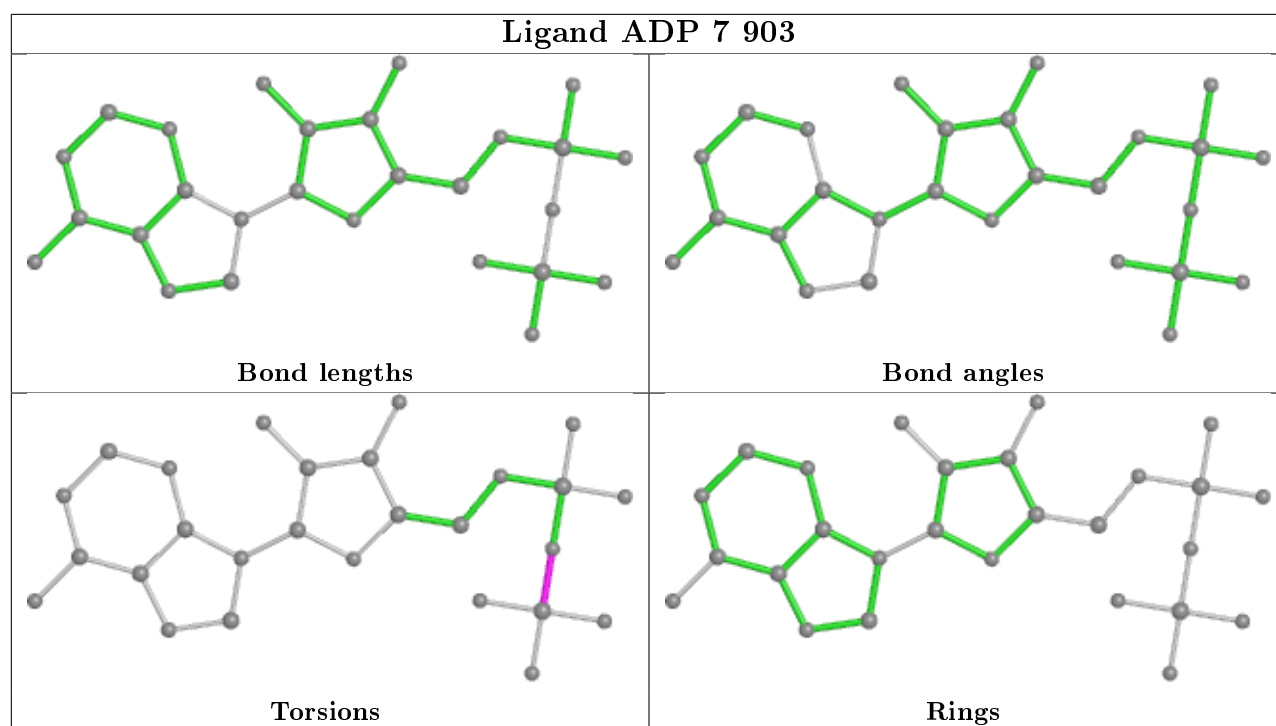
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	7	903	ADP	PA-O3A-PB-O3B
35	7	903	ADP	PA-O3A-PB-O2B

There are no ring outliers.

No monomer is involved in short contacts.

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.

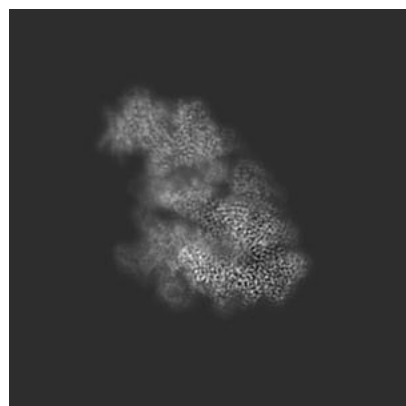
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12719. These allow visual inspection of the internal detail of the map and identification of artifacts.

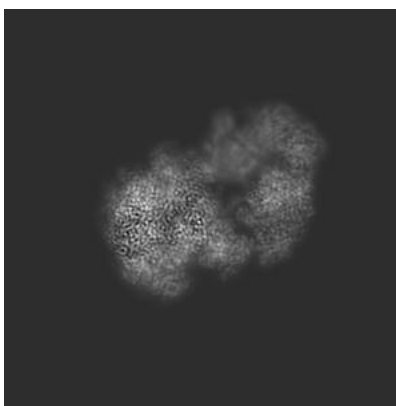
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

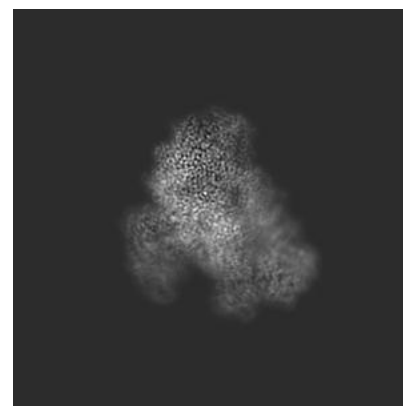
6.1.1 Primary map



X

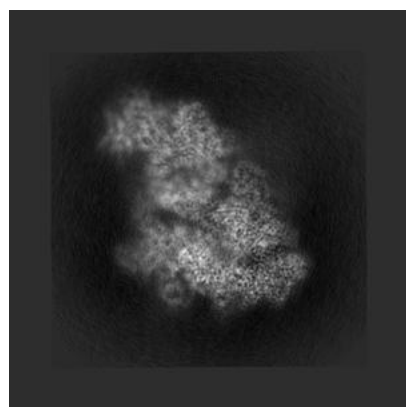


Y

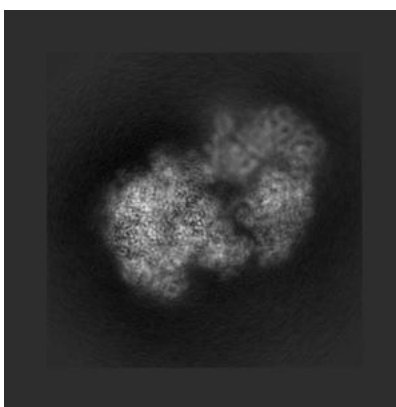


Z

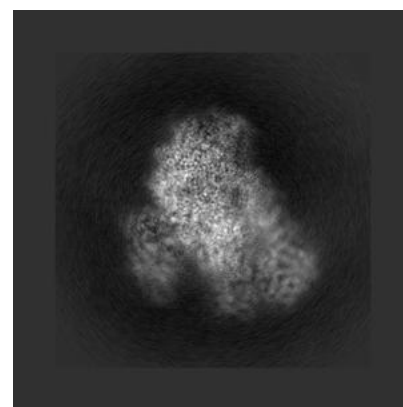
6.1.2 Raw map



X



Y

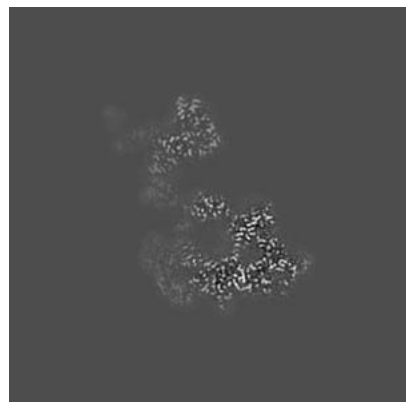


Z

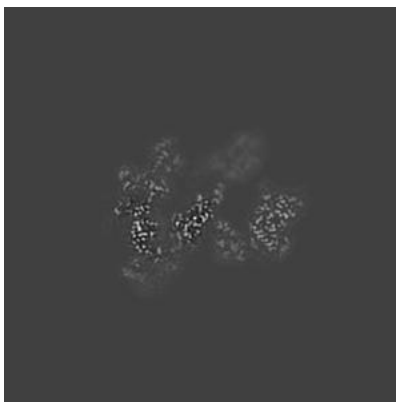
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 190

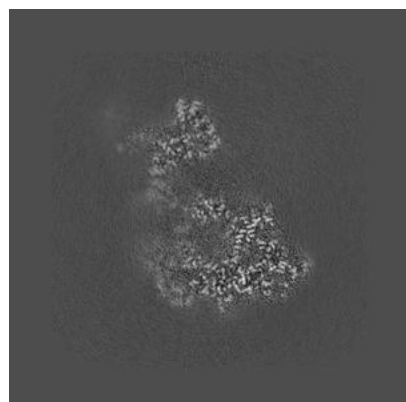


Y Index: 190

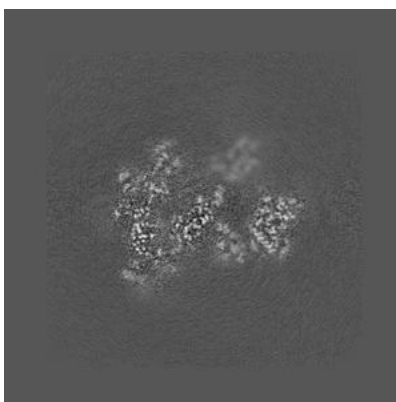


Z Index: 190

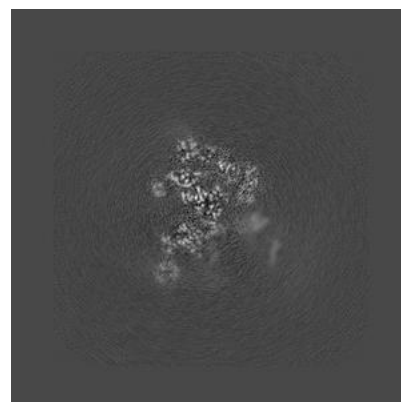
6.2.2 Raw map



X Index: 190



Y Index: 190

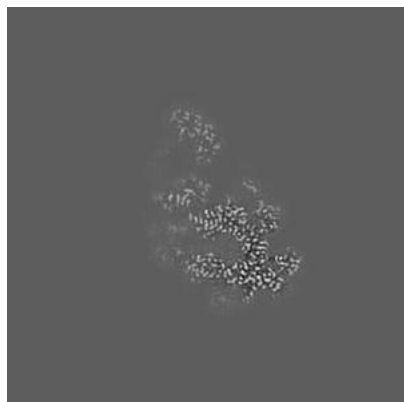


Z Index: 190

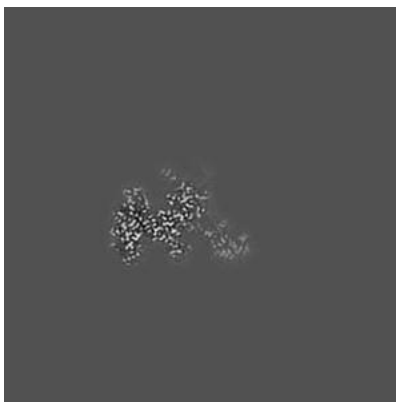
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

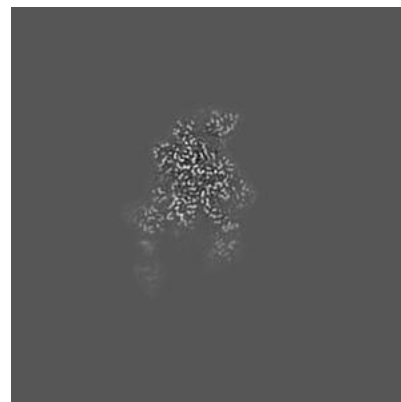
6.3.1 Primary map



X Index: 172

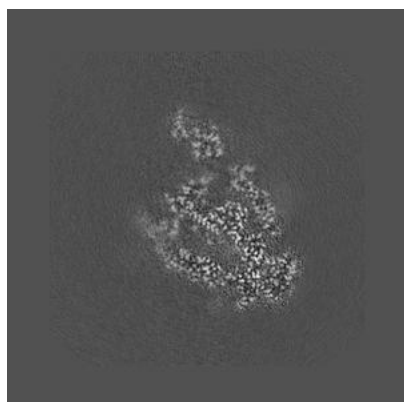


Y Index: 234

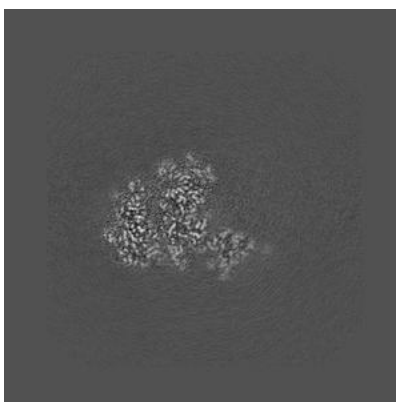


Z Index: 127

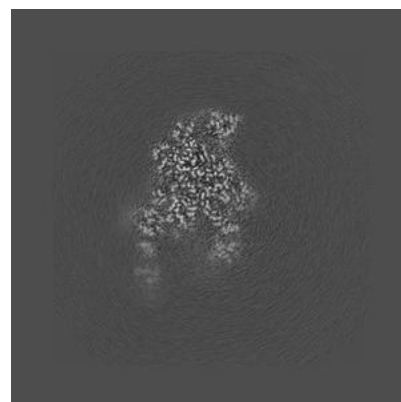
6.3.2 Raw map



X Index: 163



Y Index: 223



Z Index: 127

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

6.4 Orthogonal surface views [i](#)

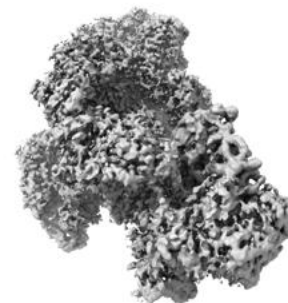
6.4.1 Primary map



X



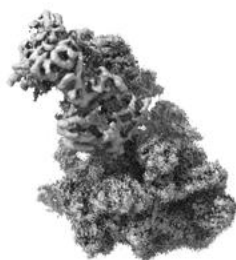
Y



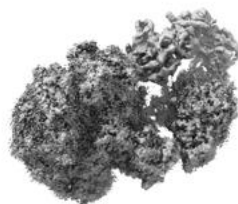
Z

The images above show the 3D surface view of the map at the recommended contour level 0.011. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

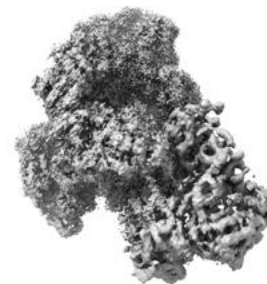
6.4.2 Raw map



X



Y



Z

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

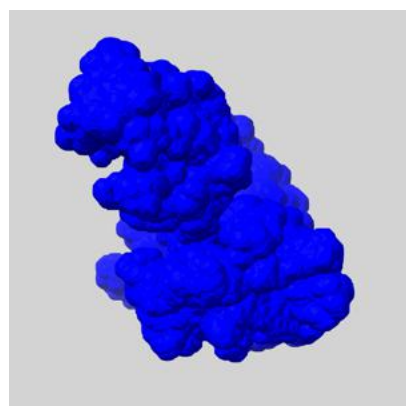
6.5 Mask visualisation [i](#)

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

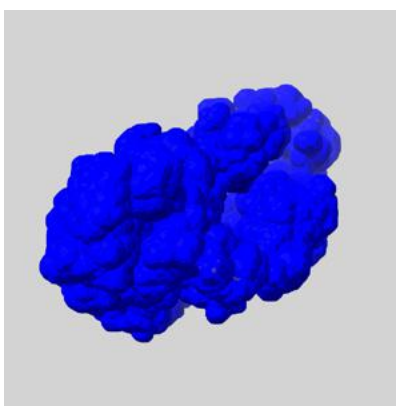
A mask typically either:

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

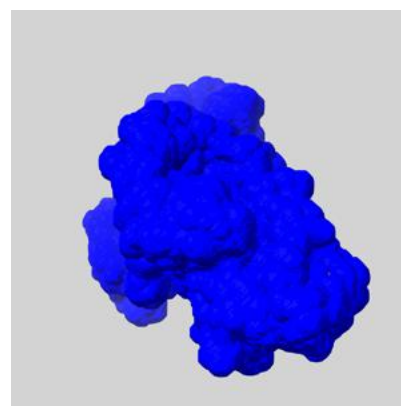
6.5.1 emd_12719_msk_1.map [i](#)



X



Y

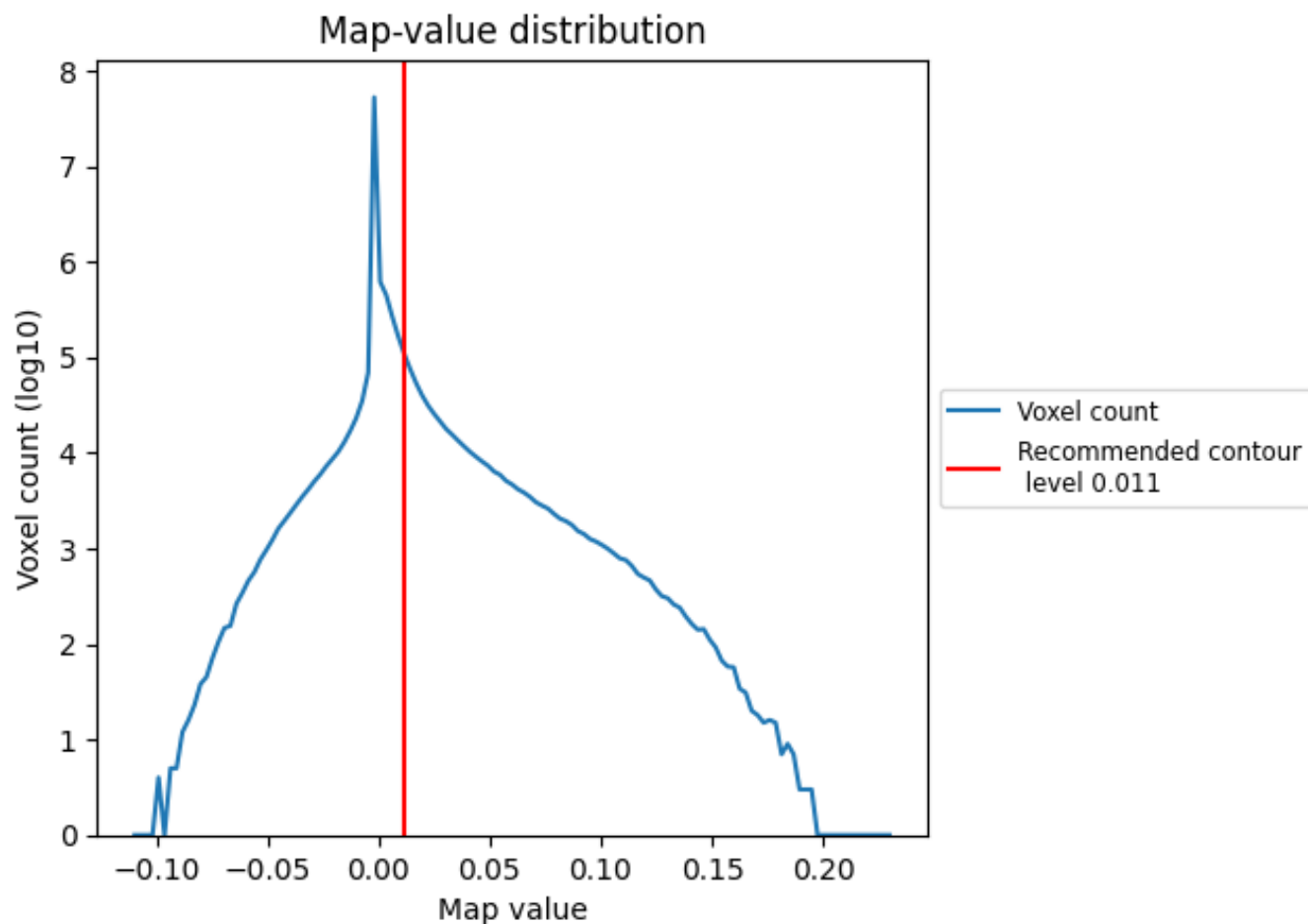


Z

7 Map analysis [i](#)

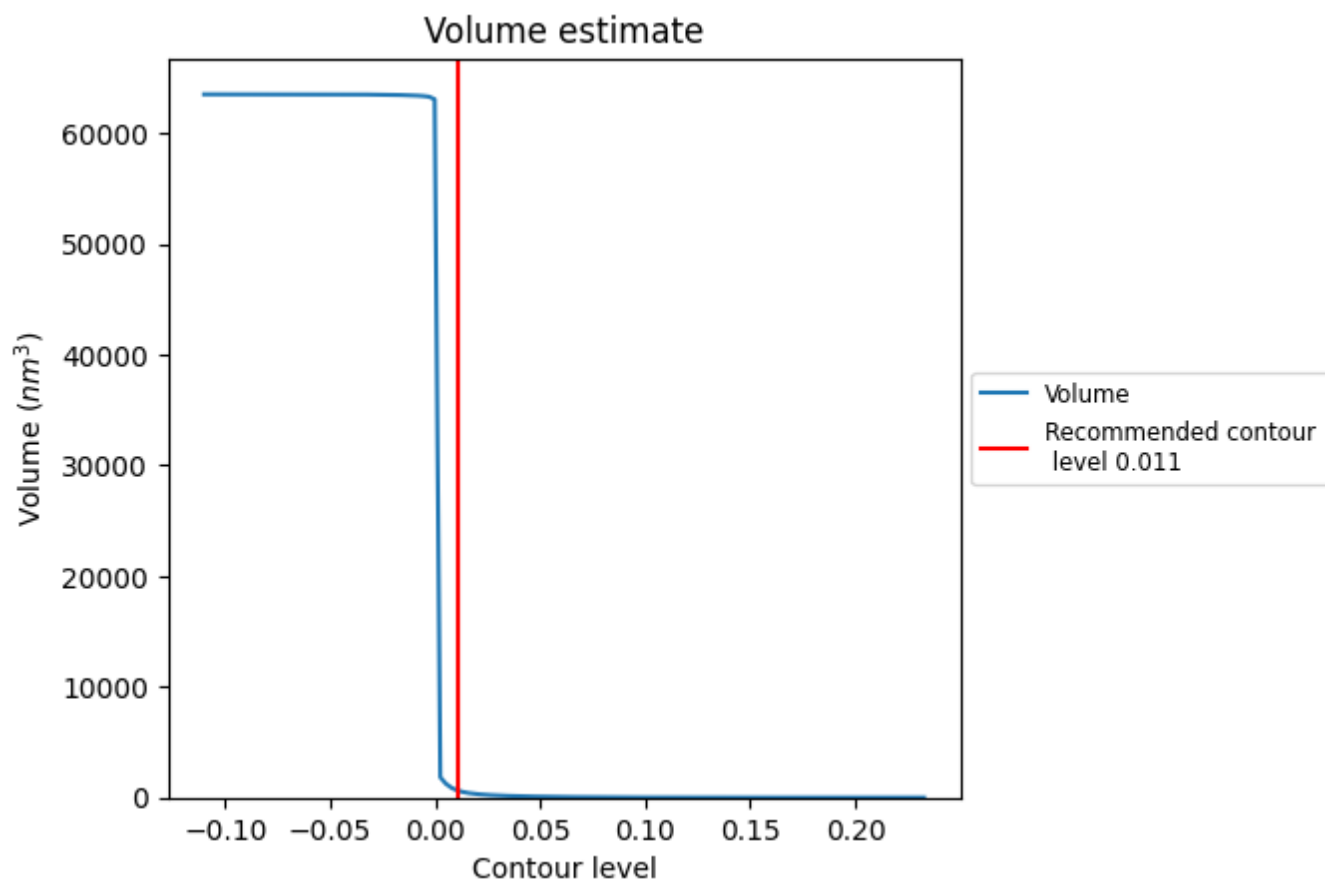
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

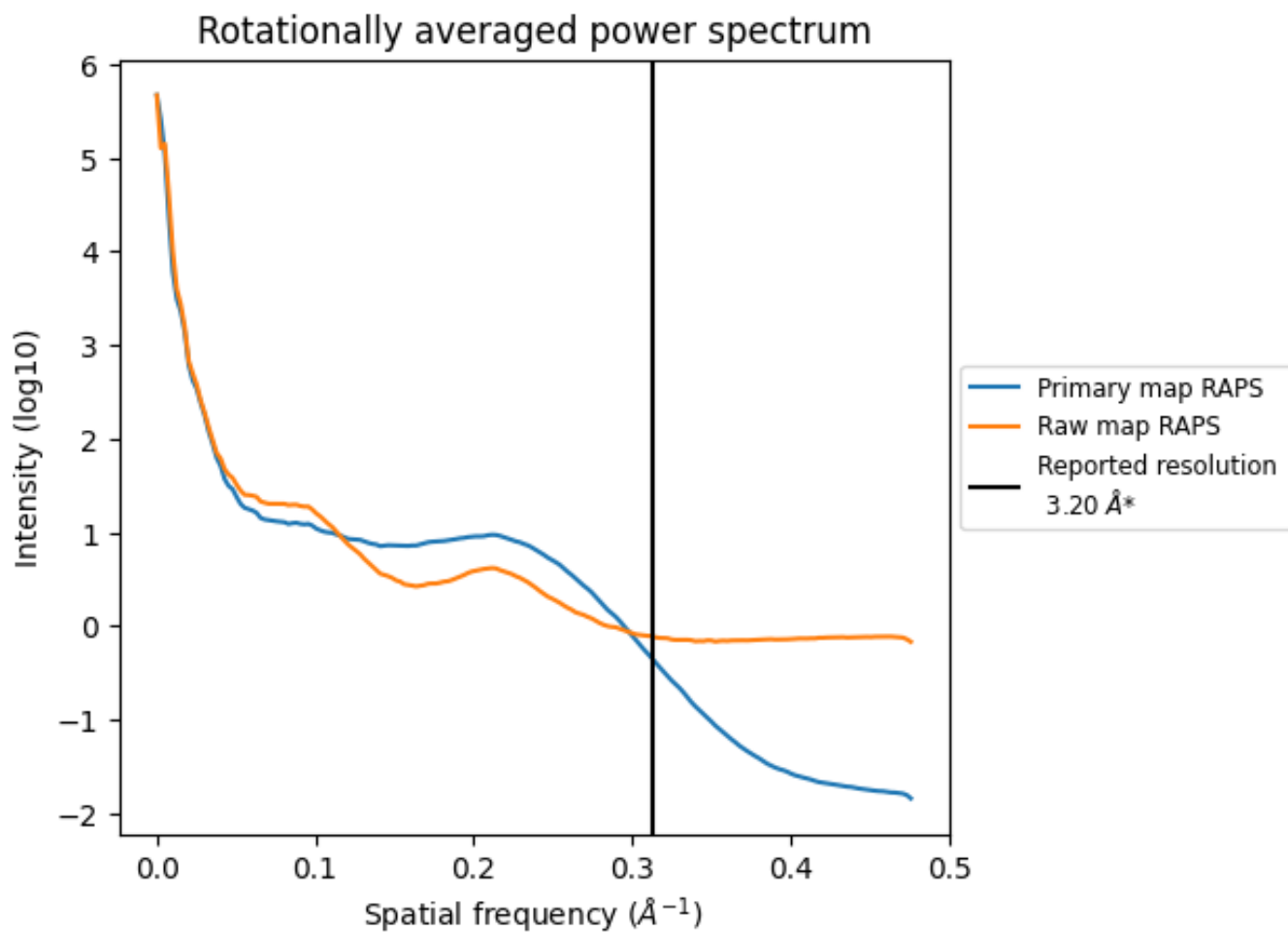
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 626 nm^3 ; this corresponds to an approximate mass of 565 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 [\(i\)](#)

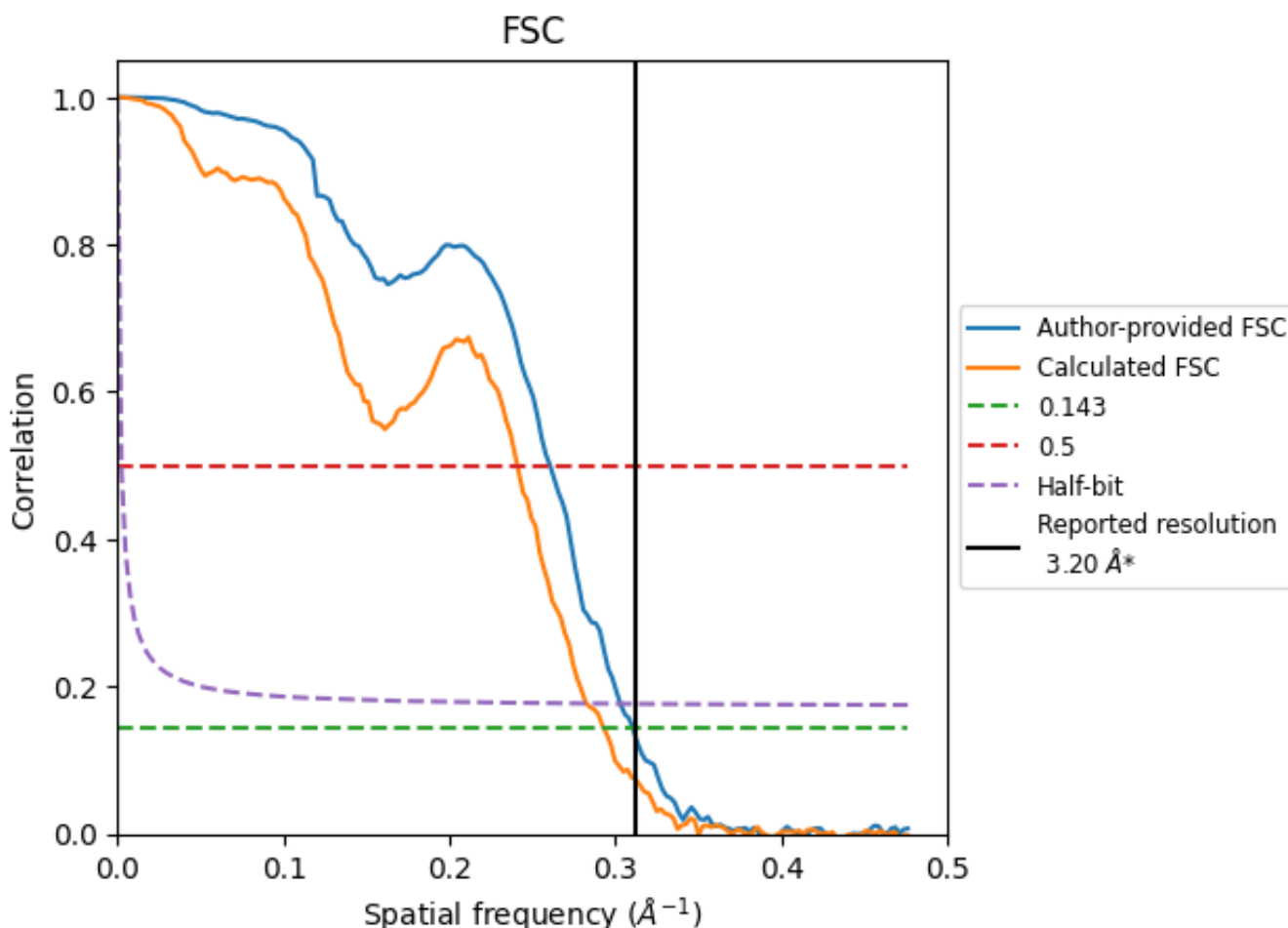


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 \AA^{-1}

8.2 Resolution estimates [i](#)

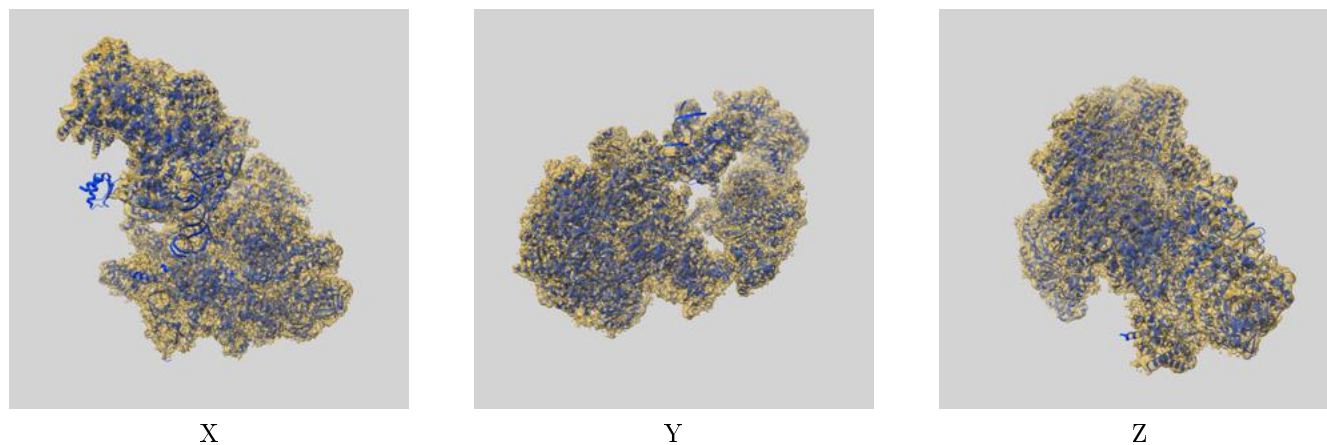
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.22	3.84	3.30
Calculated*	3.41	4.15	3.54

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

9 Map-model fit [i](#)

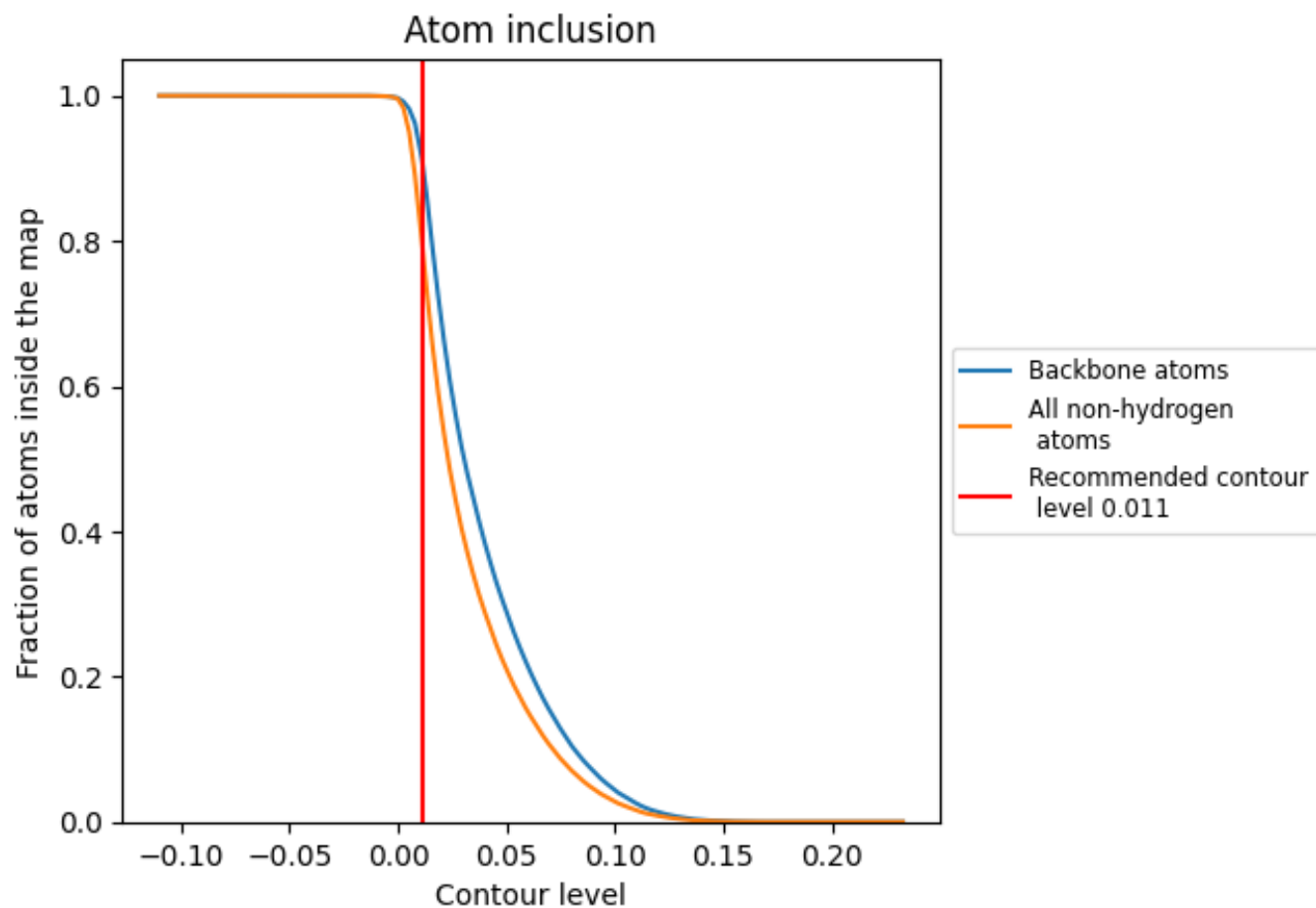
This section contains information regarding the fit between EMDB map EMD-12719 and PDB model 7O4I. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.011 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 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.