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PDB ID	:	6EXV
EMDB ID	:	EMD-3981
Title	:	Structure of mammalian RNA polymerase II elongation complex inhibited by
		Alpha-amanitin
Authors	:	Liu, X.; Farnung, L.; Wigge, C.; Cramer, P.
Deposited on	:	2017-11-09
Resolution	:	3.60 Å(reported)
This is	a I	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 (i) 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 (i)) were used in the production of this report:

EMDB validation analysis	:	0.0.1. dev 43
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 3.60 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f EM} {f structures} \ (\#{f Entries})$
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 $\geq=3, 2, 1$ 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 o	of chain		
		1050	9%				
	А	1970		61%	11%	2	28%
			13%				
2	В	1167		83%			14% •
			6%				
3	С	275		9% 7%			
				90%			
4	D	142		65%		25%	10%
			9%				
5	Ε	210		90%			9%
			14%				
6	\mathbf{F}	127		57%	8%	35%	
				87%			-
7	G	172		79%			20% •



Mol	Chain	Length		Quality of ch	ain	
8	Н	150	14%	87%		11% ••
9	Ι	125	32%	78%		14% 9%
10	J	67	—	84%		16%
11	Κ	117	6%	84%		15% •
12	L	58	10%		21%	24%
13	М	8	38%	25%		38%
14	Ν	43	33% 53%	5%		42%
15	Р	20	25% 50%	10%	10%	30%
16	Т	43	44%	81%		• 16%



2 Entry composition (i)

There are 18 unique types of molecules in this entry. The entry contains 32717 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	А	1428	Total 11317	C 7120	N 2025	O 2100	S 72	0	0

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	526	VAL	-	insertion	UNP I3LJR4
А	527	THR	-	insertion	UNP I3LJR4
А	528	PRO	-	insertion	UNP I3LJR4
А	529	GLN	-	insertion	UNP I3LJR4
А	1299	GLN	-	insertion	UNP I3LJR4
А	1300	GLY	-	insertion	UNP I3LJR4
А	1301	ILE	-	insertion	UNP I3LJR4
А	1302	GLU	-	insertion	UNP I3LJR4
А	1303	GLN	-	insertion	UNP I3LJR4
А	1304	ILE	-	insertion	UNP I3LJR4
А	1305	SER	-	insertion	UNP I3LJR4
А	1308	TYR	SER	conflict	UNP I3LJR4
А	1309	MET	ARG	conflict	UNP I3LJR4
А	1310	HIS	SER	conflict	UNP I3LJR4
А	1313	GLN	ALA	conflict	UNP I3LJR4

• Molecule 2 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB2.

Mol	Chain	Residues		Α	AltConf	Trace			
2	В	1134	Total 9062	C 5732	N 1595	O 1671	S 64	0	0

• Molecule 3 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB3.

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



• Molecule 4 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	128	Total 1005	C 632	N 172	0 197	$\frac{S}{4}$	0	0

• Molecule 5 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUB-UNIT RPABC1.

Mol	Chain	Residues		Ate	AltConf	Trace			
5	Е	209	Total 1720	C 1089	N 300	O 323	S 8	0	0

• Molecule 6 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUB-UNIT RPABC1.

Mol	Chain	Residues		At	oms	AltConf	Trace		
6	F	82	Total 657	C 418	N 113	0 121	${ m S}{ m 5}$	0	0

• Molecule 7 is a protein called DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB7.

Mol	Chain	Residues	Atoms				AltConf	Trace	
7	G	171	Total 1334	C 867	N 216	0 243	S 8	0	0

• Molecule 8 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUB-UNIT RPABC3.

Mol	Chain	Residues		At	oms			AltConf	Trace
8	Н	148	Total 1186	C 750	N 194	0 237	${f S}{5}$	0	0

• Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms				AltConf	Trace	
9	Ι	114	Total 927	C 571	N 166	0 179	S 11	0	0

• Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

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



• Molecule 11 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC4.

Mol	Chain	Residues	Atoms				AltConf	Trace	
11	K	115	Total 920	C 593	N 152	0 173	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 12 is a protein called DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC4.

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

• Molecule 13 is a protein called AMATOXIN.

Mol	Chain	Residues	Atoms				AltConf	Trace	
13	М	8	Total 64	C 39	N 10	0 14	S 1	0	0

• Molecule 14 is a DNA chain called DNA (25-MER).

Mol	Chain	Residues	Atoms				AltConf	Trace	
14	Ν	25	Total 516	C 247	N 95	0 149	Р 25	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace	
15	Р	14	Total 301	C 135	N 59	O 93	Р 14	0	0

• Molecule 16 is a DNA chain called DNA (36-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Т	36	Total 735	C 352	N 131	0 216	Р 36	0	0

• Molecule 17 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
17	А	2	Total Zn 2 2	0
			Continued or	n next page

Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf
17	В	1	Total Zn 1 1	0
17	С	1	Total Zn 1 1	0
17	Ι	2	Total Zn 2 2	0
17	J	1	Total Zn 1 1	0
17	L	1	Total Zn 1 1	0

• Molecule 18 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Ator	\mathbf{ns}	AltConf
18	А	1	Total 1	Mg 1	0



3 Residue-property plots (i)

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

• Molecule 1: DNA-DIRECTED RNA POLYMERASE II SUBUNIT RPB1











• Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5











4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	134512	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	35	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT $(4k \ge 4k)$	Depositor
Maximum map value	0.447	Depositor
Minimum map value	-0.309	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.0577	Depositor
Map size (Å)	273.92, 273.92, 273.92	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles $(^{\circ})$	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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: MG, ZN, HYP, CSX, ILX, 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).

Mal	Chain	Bond	lengths	Bond angles	
		RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.40	0/11525	0.65	6/15559~(0.0%)
2	В	0.41	0/9243	0.63	6/12475~(0.0%)
3	С	0.44	0/2102	0.62	1/2857~(0.0%)
4	D	0.26	0/1019	0.52	0/1374
5	Е	0.36	0/1751	0.59	0/2366
6	F	0.39	0/667	0.61	0/901
7	G	0.28	0/1365	0.61	0/1853
8	Н	0.42	0/1207	0.65	0/1628
9	Ι	0.33	0/948	0.56	0/1284
10	J	0.53	0/542	0.70	0/730
11	Κ	0.41	0/939	0.67	1/1271~(0.1%)
12	L	0.36	0/377	0.58	0/500
13	М	0.44	0/22	1.00	0/26
14	Ν	0.59	0/578	1.01	0/888
15	Р	0.58	0/337	0.92	1/523~(0.2%)
16	Т	0.70	0/823	0.98	1/1267~(0.1%)
All	All	0.41	0/33445	0.66	16/45502~(0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	А	0	1
5	Е	0	1
All	All	0	2

There are no bond length outliers.

All (16) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
11	Κ	80	ASP	CB-CG-OD1	8.88	126.29	118.30
1	А	503	LEU	CA-CB-CG	7.51	132.57	115.30
16	Т	23	DC	O4'-C4'-C3'	-7.33	101.57	104.50
1	А	813	ASP	CB-CG-OD1	6.23	123.91	118.30
2	В	225	LEU	CA-CB-CG	5.76	128.55	115.30
1	А	1049	LEU	CA-CB-CG	5.62	128.22	115.30
3	С	259	LEU	CB-CG-CD1	-5.54	101.58	111.00
2	В	751	LEU	CA-CB-CG	5.47	127.87	115.30
1	А	1029	LEU	CA-CB-CG	5.43	127.79	115.30
2	В	1157	LEU	CA-CB-CG	5.39	127.71	115.30
1	А	1158	LEU	CA-CB-CG	5.26	127.40	115.30
2	В	1087	GLY	N-CA-C	5.25	126.24	113.10
1	А	1486	ILE	C-N-CD	5.25	139.43	128.40
2	В	526	LEU	CA-CB-CG	5.25	127.38	115.30
2	В	863	ASP	CB-CG-OD1	5.21	122.99	118.30
15	Р	12	А	P-O3'-C3'	5.21	125.95	119.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	538	VAL	Peptide
5	Е	54	ARG	Peptide

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	А	11317	0	11439	144	0
2	В	9062	0	9109	108	0
3	С	2059	0	2009	22	0
4	D	1005	0	964	24	0
5	Е	1720	0	1737	12	0
6	F	657	0	684	7	0
7	G	1334	0	1333	23	0
8	Н	1186	0	1147	14	0
9	Ι	927	0	862	13	0
10	J	533	0	555	8	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	K	920	0	942	12	0
12	L	372	0	378	7	0
13	М	64	0	51	3	0
14	N	516	0	285	2	0
15	Р	301	0	153	1	0
16	Т	735	0	408	0	0
17	А	2	0	0	0	0
17	В	1	0	0	0	0
17	С	1	0	0	0	0
17	Ι	2	0	0	0	0
17	J	1	0	0	0	0
17	Ĺ	1	0	0	0	0
18	A	1	0	0	0	0
All	All	32717	0	32056	346	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 5.

All (346) 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:A:792:ASN:N	1:A:792:ASN:HD22	1.62	0.96
2:B:591:ARG:NH2	2:B:663:GLU:OE2	2.02	0.92
4:D:84:ARG:O	4:D:88:LEU:HB2	1.74	0.87
7:G:99:THR:O	7:G:106:CYS:HB3	1.74	0.86
4:D:104:CYS:SG	4:D:138:ARG:NH1	2.47	0.86
7:G:97:LEU:HB2	7:G:108:ILE:O	1.80	0.81
1:A:11:SER:N	2:B:1135:TYR:HH	1.79	0.81
2:B:344:GLN:OE1	2:B:345:LYS:NZ	2.14	0.80
1:A:540:ASP:HB2	2:B:790:GLN:HE21	1.52	0.75
1:A:321:GLU:OE2	1:A:340:LYS:NZ	2.20	0.75
3:C:36:ARG:HH12	11:K:40:HIS:HB2	1.50	0.75
3:C:253:LYS:NZ	11:K:102:GLU:OE1	2.20	0.74
1:A:358:ARG:HH12	2:B:1076:GLU:HG2	1.53	0.72
1:A:792:ASN:N	1:A:792:ASN:ND2	2.33	0.71
1:A:792:ASN:HD22	1:A:792:ASN:H	1.37	0.69
4:D:95:PHE:O	4:D:99:CYS:HB2	1.92	0.69
4:D:65:LEU:O	4:D:69:ALA:HB3	1.93	0.68
1:A:532:ARG:NH1	1:A:647:THR:OG1	2.27	0.68
1:A:1190:GLN:O	1:A:1194:ASN:HB2	1.93	0.68
1:A:230:ASP:OD1	1:A:244:ARG:NH1	2.27	0.68



		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
8:H:71:ASP:N	8:H:71:ASP:OD1	2.24	0.68
1:A:546:ARG:HH12	1:A:550:LYS:NZ	1.93	0.67
2:B:1088:GLU:HB2	2:B:1091:ARG:NH1	2.10	0.67
7:G:6:SER:HB3	7:G:71:LYS:NZ	2.10	0.66
2:B:718:GLN:HG2	2:B:720:PRO:HD2	1.78	0.66
1:A:1416:ARG:NH1	1:A:1433:GLU:OE2	2.29	0.65
2:B:592:ARG:NE	2:B:663:GLU:OE1	2.30	0.65
8:H:71:ASP:OD2	8:H:142:TYR:OH	2.07	0.65
1:A:659:GLU:OE2	1:A:985:ARG:NH1	2.29	0.65
1:A:1211:LEU:HD11	1:A:1258:ARG:HE	1.63	0.64
4:D:105:PRO:HG2	4:D:131:LEU:HD21	1.80	0.64
8:H:30:CYS:HB2	8:H:39:LEU:HB3	1.78	0.64
1:A:125:LYS:O	1:A:129:ILE:HB	1.98	0.64
1:A:546:ARG:HH12	1:A:550:LYS:HZ1	1.46	0.63
7:G:6:SER:HB3	7:G:71:LYS:HZ3	1.63	0.63
7:G:44:PHE:HB2	7:G:77:PHE:HB3	1.78	0.63
1:A:395:THR:HG23	1:A:397:PHE:H	1.62	0.62
2:B:803:ARG:NH1	10:J:8:PHE:O	2.31	0.62
1:A:358:ARG:NH1	2:B:1076:GLU:HG2	2.15	0.61
1:A:1399:ALA:O	1:A:1403:ASP:HB2	2.00	0.61
1:A:1487:PRO:HG2	6:F:78:PRO:HA	1.82	0.61
1:A:1375:ARG:NH1	1:A:1379:GLU:OE1	2.33	0.60
1:A:379:GLY:HA2	1:A:475:ARG:O	2.00	0.60
1:A:864:LEU:HD23	1:A:1414:ILE:HG21	1.84	0.60
1:A:487:SER:OG	1:A:673:GLN:NE2	2.35	0.60
11:K:7:PHE:HB2	11:K:11:LEU:HD13	1.83	0.60
1:A:111:CYS:SG	1:A:188:GLN:NE2	2.74	0.60
1:A:620:HIS:CE1	8:H:98:ARG:HH12	2.20	0.60
2:B:387:HIS:NE2	2:B:671:GLU:OE2	2.33	0.60
7:G:106:CYS:SG	7:G:107:PHE:N	2.76	0.59
2:B:237:VAL:HG11	2:B:369:VAL:HG22	1.84	0.58
7:G:11:ILE:HD11	7:G:30:LEU:HD23	1.84	0.58
5:E:13:ILE:HD11	5:E:132:GLN:HG3	1.85	0.58
1:A:904:GLN:NE2	1:A:980:PRO:O	2.37	0.58
12:L:16:ILE:HD11	12:L:25:GLU:HB3	1.83	0.58
2:B:17:ILE:HG23	2:B:19:PRO:HD3	1.86	0.58
2:B:1038:THR:HA	3:C:195:THR:HA	1.84	0.58
1:A:1430:CYS:HB2	1:A:1435:THR:HG23	1.85	0.58
1:A:1244:ASN:O	1:A:1259:ILE:HA	2.03	0.57
2:B:313:GLU:HB3	2:B:316:VAL:HG12	1.87	0.57
1:A:526:VAL:HA	1:A:533:PRO:HA	1.87	0.57



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:1038:THR:O	1:A:1042:ASN:ND2	2.38	0.57
1:A:421:ARG:NH2	1:A:437:ASP:OD2	2.38	0.56
1:A:791:GLN:HG3	13:M:1:ILX:HA	1.86	0.56
1:A:1130:ILE:HG12	1:A:1413:ALA:HB2	1.87	0.56
2:B:907:VAL:HG22	2:B:921:ILE:HG12	1.87	0.56
7:G:101:ILE:HG23	7:G:104:MET:HB3	1.87	0.56
2:B:65:ILE:HD11	2:B:86:LEU:HG	1.87	0.56
2:B:320:PHE:O	2:B:324:ARG:NH1	2.38	0.56
1:A:265:VAL:HG22	1:A:271:ARG:HG2	1.88	0.56
1:A:1130:ILE:HG21	1:A:1411:LEU:HB3	1.87	0.56
7:G:127:CYS:SG	7:G:128:TYR:N	2.77	0.56
2:B:713:PHE:HB3	2:B:716:HIS:HD2	1.71	0.56
12:L:36:CYS:SG	12:L:37:ARG:N	2.78	0.56
1:A:376:ASP:HB2	1:A:666:ARG:HD2	1.87	0.56
4:D:96:GLU:OE2	4:D:121:ARG:NH1	2.39	0.56
11:K:35:ILE:HB	11:K:71:ILE:HG22	1.89	0.55
1:A:1428:MET:HB2	1:A:1456:GLU:OE2	2.05	0.55
3:C:36:ARG:NH1	11:K:40:HIS:HB2	2.20	0.55
9:I:68:ILE:HG13	9:I:122:ARG:HD2	1.87	0.55
1:A:116:LYS:HZ1	1:A:183:GLY:H	1.55	0.55
7:G:89:VAL:HA	7:G:99:THR:HA	1.87	0.55
2:B:274:ARG:NH2	2:B:281:ASP:OD1	2.40	0.55
4:D:95:PHE:O	4:D:99:CYS:CB	2.55	0.54
2:B:953:ASP:OD1	3:C:36:ARG:NH2	2.41	0.54
1:A:1475:LEU:HB2	7:G:59:ILE:HD11	1.89	0.54
2:B:623:ARG:NH1	2:B:625:LEU:HD21	2.22	0.54
4:D:125:GLU:O	4:D:129:GLN:HB2	2.08	0.54
1:A:1173:THR:HG22	1:A:1214:VAL:HG22	1.90	0.54
2:B:50:PHE:HB2	2:B:397:GLY:HA2	1.90	0.53
1:A:358:ARG:NH1	2:B:1076:GLU:HA	2.22	0.53
8:H:32:SER:HB3	8:H:37:MET:H	1.73	0.53
1:A:689:ILE:HD11	2:B:985:LEU:HD22	1.91	0.53
5:E:195:ARG:HH12	5:E:205:THR:HG21	1.72	0.53
2:B:285:LEU:HA	2:B:288:ILE:HG22	1.90	0.53
2:B:1022:LEU:HD12	2:B:1023:ARG:HG2	1.91	0.53
1:A:1408:ARG:O	5:E:172:ARG:NH1	2.41	0.53
2:B:795:ILE:HB	2:B:966:ILE:HB	1.90	0.53
2:B:1062:ARG:HH12	2:B:1074:PRO:HB3	1.73	0.53
4:D:65:LEU:O	4:D:69:ALA:CB	2.57	0.53
5:E:24:ARG:HH12	5:E:184:GLY:HA3	1.74	0.53
9:I:15:ARG:HB3	9:I:24:LEU:HD12	1.91	0.53



	has pagetti	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
8:H:32:SER:OG	8:H:33:GLU:N	2.41	0.53
8:H:128:ASP:OD1	8:H:131:ASN:ND2	2.42	0.53
7:G:12:LEU:HD23	7:G:67:LEU:HB3	1.90	0.52
12:L:19:CYS:SG	12:L:20:GLY:N	2.81	0.52
2:B:111:ASN:HD21	2:B:742:VAL:HG11	1.74	0.52
1:A:342:ARG:NE	2:B:1161:GLU:OE2	2.42	0.52
1:A:340:LYS:HG3	1:A:1436:VAL:HG11	1.90	0.52
1:A:873:VAL:HG22	1:A:879:VAL:HG22	1.92	0.52
2:B:230:ARG:HH11	2:B:409:LYS:HD2	1.75	0.52
4:D:90:LYS:HE2	4:D:130:ILE:HD11	1.90	0.52
1:A:32:LYS:HE3	1:A:89:GLU:OE2	2.10	0.52
1:A:955:GLU:OE2	1:A:1010:VAL:HG22	2.09	0.52
2:B:319:ASN:O	2:B:323:SER:HB2	2.10	0.52
4:D:61:PHE:O	4:D:65:LEU:HB2	2.10	0.52
4:D:107:THR:HG23	4:D:110:GLU:H	1.75	0.51
6:F:61:GLU:OE2	6:F:108:ARG:NH1	2.44	0.51
1:A:576:GLN:HE21	1:A:580:LEU:HD21	1.76	0.51
1:A:721:HIS:HD2	9:I:110:LEU:HD13	1.74	0.51
1:A:1016:LEU:HD11	1:A:1072:ILE:HB	1.92	0.51
1:A:1281:ASP:HA	1:A:1284:PHE:HB3	1.93	0.51
3:C:78:ILE:HD11	3:C:127:VAL:HG23	1.91	0.51
10:J:14:VAL:HG13	10:J:49:LEU:HD12	1.92	0.51
1:A:606:HIS:HB3	1:A:626:THR:HG23	1.92	0.51
2:B:114:ARG:NH2	2:B:184:TYR:OH	2.43	0.51
1:A:137:PRO:HA	1:A:140:ARG:HE	1.75	0.51
1:A:1472:ASP:N	1:A:1472:ASP:OD1	2.43	0.51
1:A:1374:VAL:O	1:A:1378:LEU:HB2	2.10	0.51
1:A:619:LYS:NZ	1:A:627:LYS:HE3	2.26	0.50
1:A:129:ILE:HD11	1:A:143:HIS:HB3	1.93	0.50
1:A:511:THR:HA	1:A:514:GLU:HG2	1.94	0.50
1:A:546:ARG:NH1	1:A:550:LYS:NZ	2.59	0.50
1:A:864:LEU:HD21	1:A:1128:ILE:HD12	1.94	0.50
9:I:81:THR:HG22	9:I:83:ASP:H	1.76	0.50
1:A:322:LEU:HD22	1:A:325:LEU:HD12	1.93	0.50
2:B:1062:ARG:NH1	2:B:1074:PRO:HB3	2.27	0.50
7:G:90:THR:HA	7:G:139:GLN:HE22	1.77	0.50
2:B:438:ARG:O	2:B:442:ASP:HB2	2.11	0.50
3:C:264:SER:O	3:C:268:GLN:HB2	2.11	0.49
4:D:132:ASP:O	4:D:136:THR:CB	2.60	0.49
2:B:196:ALA:HA	2:B:394:ASP:O	2.12	0.49
4:D:84:ARG:O	4:D:88:LEU:CB	2.54	0.49



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
4:D:114:LEU:HD22	7:G:84:VAL:HG21	1.94	0.49
1:A:394:VAL:HG22	1:A:402:LEU:HD13	1.94	0.49
1:A:65:ILE:CG2	1:A:271:ARG:HH12	2.26	0.49
1:A:832:THR:OG1	1:A:835:GLU:OE1	2.30	0.49
2:B:580:PRO:O	2:B:584:MET:HB2	2.12	0.49
2:B:341:GLU:O	2:B:345:LYS:HB2	2.12	0.49
9:I:80:ARG:HB3	9:I:93:GLU:OE2	2.13	0.49
7:G:1:MET:N	7:G:78:ARG:O	2.44	0.49
1:A:922:PHE:HB2	1:A:1052:ARG:HB2	1.94	0.49
3:C:259:LEU:HD11	11:K:42:LEU:HD21	1.95	0.49
1:A:554:PHE:HB3	1:A:585:LEU:HD23	1.95	0.48
1:A:1122:PRO:HA	1:A:1125:LYS:HG2	1.95	0.48
2:B:917:LYS:NZ	12:L:34:ILE:HD11	2.28	0.48
3:C:93:PHE:HE1	3:C:166:LYS:HZ3	1.61	0.48
3:C:259:LEU:O	3:C:263:LEU:HB3	2.13	0.48
2:B:628:VAL:HG22	2:B:633:LEU:HD23	1.95	0.48
1:A:604:ARG:HH21	1:A:643:LYS:HE2	1.77	0.48
3:C:197:TYR:HD2	3:C:217:GLN:HE21	1.60	0.48
1:A:860:ILE:HD11	1:A:1125:LYS:HB3	1.96	0.48
1:A:1365:ILE:HG23	1:A:1369:LEU:HD12	1.95	0.48
1:A:1416:ARG:O	1:A:1420:ASN:HB2	2.12	0.48
1:A:137:PRO:HB3	1:A:140:ARG:HH21	1.79	0.48
1:A:555:LEU:HD12	1:A:591:ILE:HG13	1.95	0.48
3:C:7:PRO:HA	3:C:24:GLU:O	2.13	0.48
2:B:306:ASP:OD1	9:I:25:TYR:OH	2.29	0.48
1:A:1468:THR:HG23	6:F:64:ARG:HB2	1.96	0.48
2:B:623:ARG:HH12	2:B:625:LEU:HD21	1.79	0.48
2:B:794:VAL:HG22	2:B:967:ILE:HG22	1.96	0.48
4:D:132:ASP:O	4:D:136:THR:HB	2.14	0.48
2:B:159:THR:HA	2:B:164:ASN:HD22	1.78	0.47
12:L:18:ILE:HD11	12:L:47:LYS:NZ	2.30	0.47
2:B:225:LEU:HB3	2:B:349:PRO:HB2	1.96	0.47
3:C:9:VAL:HG11	11:K:105:PHE:HD1	1.78	0.47
1:A:823:VAL:HG22	1:A:835:GLU:HG3	1.96	0.47
4:D:19:GLN:HG3	4:D:21:ILE:HG12	1.96	0.47
1:A:648:SER:OG	1:A:651:SER:OG	2.32	0.47
2:B:344:GLN:O	2:B:361:LYS:NZ	2.47	0.47
1:A:1220:HIS:HB3	1:A:1224:ARG:HH12	1.79	0.47
7:G:59:ILE:HG12	7:G:66:VAL:HG22	1.96	0.47
1:A:11:SER:N	2:B:1135:TYR:OH	2.43	0.47
1:A:466:LYS:HE3	2:B:1097:HIS:CD2	2.49	0.47



	h h	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:B:311:ILE:HG23	2:B:316:VAL:HG13	1.95	0.47
4:D:60:VAL:O	4:D:64:THR:CB	2.63	0.47
4:D:109:GLU:O	4:D:113:ALA:HB2	2.14	0.47
5:E:55:ARG:HA	5:E:58:LEU:HD12	1.97	0.47
1:A:865:ILE:HG12	2:B:1092:ASP:OD2	2.14	0.47
4:D:44:ARG:NH2	7:G:35:GLU:OE2	2.48	0.47
1:A:1032:GLN:OE1	1:A:1036:ASN:ND2	2.48	0.47
5:E:24:ARG:NH1	5:E:184:GLY:HA3	2.30	0.47
14:N:35:DA:OP2	14:N:35:DA:H8	1.98	0.47
1:A:1205:ALA:HB1	1:A:1267:ASN:HB2	1.97	0.47
1:A:201:GLU:HG3	1:A:213:LYS:HG2	1.97	0.46
1:A:1440:MET:HG2	2:B:1167:ILE:HD11	1.98	0.46
1:A:130:LEU:HD21	1:A:235:VAL:HG12	1.96	0.46
2:B:177:CYS:HG	2:B:738:THR:HG1	1.53	0.46
1:A:364:ARG:NH1	1:A:502:ASN:OD1	2.45	0.46
7:G:151:ARG:HH11	7:G:158:PHE:HE1	1.63	0.46
1:A:1307:VAL:HG22	1:A:1338:THR:HG22	1.98	0.46
2:B:759:VAL:HG12	2:B:999:ALA:HB2	1.97	0.46
7:G:11:ILE:O	7:G:67:LEU:HA	2.14	0.46
7:G:112:SER:HB3	7:G:163:LEU:H	1.81	0.46
1:A:477:LEU:HB2	1:A:483:ARG:HH21	1.81	0.46
1:A:387:ASN:ND2	2:B:1061:SER:OG	2.47	0.46
1:A:922:PHE:HA	1:A:1052:ARG:HD3	1.98	0.46
2:B:474:THR:OG1	2:B:732:ALA:O	2.33	0.46
10:J:1:MET:HA	10:J:55:LEU:HB2	1.97	0.46
11:K:38:GLU:OE2	11:K:42:LEU:HD13	2.16	0.46
1:A:545:VAL:HG23	1:A:676:ILE:HG21	1.98	0.46
1:A:1004:LEU:HD13	1:A:1062:GLY:HA2	1.98	0.46
1:A:1281:ASP:O	1:A:1285:LEU:HB2	2.15	0.45
1:A:1218:ARG:HA	1:A:1221:MET:HB2	1.98	0.45
1:A:1218:ARG:NH2	1:A:1253:GLU:OE1	2.41	0.45
9:I:25:TYR:O	9:I:37:TYR:HA	2.16	0.45
1:A:621:ILE:HD11	8:H:124:ARG:HB2	1.97	0.45
2:B:473:LEU:HD13	2:B:731:GLN:HA	1.98	0.45
1:A:393:ILE:HD11	6:F:74:ALA:HB1	1.98	0.45
2:B:206:TYR:O	2:B:219:GLY:HA2	2.16	0.45
1:A:510:GLU:OE2	6:F:71:LEU:HD13	2.17	0.45
1:A:620:HIS:HB2	8:H:115:TYR:HE2	1.82	0.45
2:B:509:VAL:HG11	2:B:524:LYS:HD2	1.96	0.45
2:B:567:ILE:HD11	2:B:577:HIS:HB2	1.98	0.45
1:A:33:ARG:HE	2:B:1139:GLY:HA2	1.82	0.45



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Atom-1	Atom-2	distance (Å)	overlap (Å)
4:D:118:LEU:HD23	4:D:121:ARG:HG3	1.99	0.45
15:P:11:A:H8	15:P:11:A:OP2	2.00	0.45
3:C:183:ALA:HB3	3:C:232:ASN:HB3	1.99	0.45
1:A:542:LEU:HD21	1:A:642:LYS:HB3	1.98	0.45
2:B:643:LEU:O	2:B:646:ARG:NH1	2.50	0.45
9:I:69:ILE:HG22	9:I:71:ASP:H	1.81	0.45
2:B:499:ARG:NH2	2:B:518:HIS:O	2.50	0.44
2:B:794:VAL:HG13	2:B:965:ILE:HG23	1.98	0.44
6:F:114:SER:OG	6:F:115:TYR:N	2.50	0.44
11:K:106:ARG:HA	11:K:109:ILE:HG22	1.99	0.44
1:A:585:LEU:HD22	8:H:47:ILE:HD11	1.98	0.44
2:B:473:LEU:HD11	2:B:1052:LYS:HD3	1.98	0.44
11:K:13:PHE:N	11:K:16:GLU:OE2	2.49	0.44
2:B:109:MET:HB2	2:B:112:GLU:HG2	1.99	0.44
9:I:96:PHE:HD2	9:I:110:LEU:HD11	1.83	0.44
1:A:1160:ARG:NH2	1:A:1350:LYS:O	2.50	0.44
1:A:1196:TYR:OH	1:A:1201:ASP:O	2.35	0.44
2:B:91:ILE:HD11	2:B:124:LEU:HD21	1.99	0.44
5:E:104:ILE:HD11	5:E:127:LEU:HD23	1.99	0.44
1:A:1087:VAL:HG12	1:A:1400:LEU:HD22	2.00	0.44
1:A:1141:VAL:HB	1:A:1336:LEU:HB2	1.98	0.44
10:J:46:ARG:O	10:J:50:LEU:CB	2.66	0.44
11:K:61:TYR:HA	11:K:72:ILE:O	2.17	0.44
1:A:70:ARG:HD2	1:A:75:ALA:HB1	2.00	0.44
3:C:264:SER:O	3:C:268:GLN:CB	2.66	0.44
1:A:45:GLU:HB3	1:A:53:LYS:HE2	1.99	0.44
2:B:897:ARG:HB2	2:B:900:GLU:OE2	2.17	0.44
1:A:119:VAL:HG22	1:A:151:LYS:NZ	2.33	0.43
1:A:1179:PRO:HA	1:A:1209:PRO:HB3	2.00	0.43
2:B:861:SER:OG	2:B:862:GLY:N	2.51	0.43
3:C:16:ASP:OD1	3:C:240:ARG:NE	2.51	0.43
3:C:240:ARG:NH2	3:C:242:GLU:OE2	2.51	0.43
3:C:7:PRO:HG3	11:K:97:GLU:OE2	2.17	0.43
14:N:34:DG:OP2	14:N:34:DG:H2'	2.18	0.43
2:B:438:ARG:HD3	2:B:442:ASP:OD2	2.18	0.43
2:B:565:THR:O	2:B:576:ILE:HA	2.18	0.43
2:B:1092:ASP:N	2:B:1092:ASP:OD1	2.43	0.43
1:A:1374:VAL:O	1:A:1378:LEU:CB	2.65	0.43
2:B:222:ARG:HG2	2:B:234:THR:HG22	2.00	0.43
2:B:333:GLU:HA	2:B:336:ILE:HG22	1.99	0.43
2:B:98:HIS:NE2	2:B:100:GLU:OE1	2.41	0.43



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Atom-1	Atom-2	distance (Å)	overlap (Å)
10:J:40:LEU:O	10:J:46:ARG:NH1	2.51	0.43
1:A:42:LYS:O	1:A:288:ASN:ND2	2.46	0.43
1:A:620:HIS:CE1	8:H:98:ARG:NH1	2.86	0.43
1:A:1416:ARG:HA	1:A:1432:PHE:HE2	1.83	0.43
2:B:777:ASN:O	10:J:47:ARG:NH1	2.52	0.43
1:A:589:LYS:NZ	1:A:625:ASP:OD2	2.40	0.43
2:B:284:ILE:HD13	2:B:284:ILE:HG21	1.84	0.43
2:B:873:LEU:HD12	2:B:874:PRO:HD2	2.00	0.43
1:A:26:LEU:HG	2:B:1168:ALA:HB2	2.01	0.43
3:C:19:VAL:HG23	3:C:241:PRO:HB2	2.00	0.43
3:C:75:SER:HB3	3:C:79:VAL:HG11	2.01	0.43
10:J:67:LYS:NZ	12:L:23:HIS:CE1	2.87	0.43
2:B:715:ASP:OD1	2:B:715:ASP:N	2.48	0.42
4:D:112:LYS:HD2	4:D:119:GLU:HG2	2.00	0.42
9:I:110:LEU:HD12	9:I:110:LEU:HA	1.88	0.42
1:A:1163:HIS:CE1	1:A:1302:GLU:HG3	2.54	0.42
2:B:513:GLU:HG2	2:B:525:ASN:HD22	1.85	0.42
1:A:831:LEU:H	2:B:715:ASP:HB2	1.85	0.42
12:L:17:TYR:HB3	12:L:44:MET:HB3	2.00	0.42
13:M:6:CSX:HB2	13:M:7:ASN:H	1.43	0.42
2:B:601:VAL:HG12	2:B:616:THR:HG23	2.01	0.42
2:B:626:LEU:HD23	2:B:662:VAL:HG12	2.01	0.42
1:A:466:LYS:HE3	2:B:1097:HIS:HD2	1.83	0.42
1:A:963:ARG:NH2	1:A:967:ARG:HH21	2.18	0.42
1:A:1227:THR:HG23	1:A:1229:GLU:H	1.84	0.42
2:B:24:GLU:O	2:B:28:ILE:HB	2.19	0.42
2:B:249:LYS:HA	2:B:252:ILE:HB	2.00	0.42
5:E:116:GLN:HA	5:E:119:VAL:HG22	2.02	0.42
5:E:139:ILE:H	5:E:139:ILE:HG13	1.67	0.42
1:A:358:ARG:HH12	2:B:1076:GLU:HA	1.83	0.42
2:B:629:GLU:HB3	2:B:630:LYS:H	1.64	0.42
1:A:546:ARG:NH1	1:A:550:LYS:HZ3	2.17	0.42
1:A:1429:LYS:HB2	1:A:1438:VAL:HG11	2.00	0.42
2:B:285:LEU:HD11	2:B:305:LEU:HD11	2.00	0.42
4:D:30:GLU:O	7:G:4:HIS:N	2.47	0.42
1:A:721:HIS:CD2	9:I:110:LEU:HD13	2.55	0.42
1:A:734:ARG:NH1	9:I:108:MET:HG3	2.35	0.42
1:A:823:VAL:HG13	1:A:835:GLU:OE2	2.20	0.42
1:A:551:ARG:HH12	8:H:27:ARG:HH21	1.67	0.42
2:B:622:CYS:HB3	2:B:666:ASP:HB3	2.02	0.42
1:A:1005:HIS:HA	1:A:1006:PRO:HD3	1.90	0.41



Atom-1	Atom-2	Interatomic	Clash
1100111-1	1100111-2	distance (Å)	overlap (Å)
6:F:125:ILE:HG22	6:F:127:ASP:H	1.85	0.41
7:G:137:ILE:HG23	7:G:141:ASP:OD2	2.20	0.41
1:A:184:CYS:SG	1:A:185:GLY:N	2.93	0.41
2:B:86:LEU:HA	2:B:129:THR:O	2.20	0.41
9:I:86:CYS:SG	9:I:87:GLN:N	2.93	0.41
1:A:461:GLN:NE2	2:B:1090:GLU:OE2	2.54	0.41
1:A:928:ARG:HE	8:H:106:THR:HB	1.86	0.41
2:B:177:CYS:SG	2:B:738:THR:OG1	2.64	0.41
2:B:937:SER:OG	2:B:938:ARG:N	2.53	0.41
3:C:259:LEU:O	3:C:263:LEU:CB	2.69	0.41
1:A:365:THR:OG1	1:A:366:VAL:N	2.53	0.41
2:B:82:PRO:HA	2:B:133:ILE:O	2.21	0.41
2:B:213:SER:OG	2:B:214:LYS:N	2.53	0.41
2:B:1088:GLU:HB2	2:B:1091:ARG:HH12	1.84	0.41
1:A:792:ASN:HD21	13:M:8:HYP:HA	1.85	0.41
1:A:892:GLY:HA3	1:A:1396:ARG:HH11	1.85	0.41
2:B:905:ASP:OD2	2:B:922:ARG:NH2	2.25	0.41
2:B:1126:ALA:HB3	2:B:1146:ILE:HD11	2.03	0.41
1:A:139:LYS:HA	1:A:142:THR:HG22	2.03	0.41
5:E:177:ASP:OD1	5:E:177:ASP:N	2.54	0.41
5:E:194:ILE:HG12	5:E:204:ILE:HG12	2.02	0.41
8:H:20:LYS:NZ	8:H:45:ILE:HD12	2.35	0.41
1:A:408:ARG:HH21	1:A:412:GLN:HB3	1.86	0.41
1:A:1052:ARG:NE	1:A:1056:GLU:OE1	2.49	0.41
5:E:102:ALA:HB3	5:E:127:LEU:HG	2.03	0.41
7:G:60:GLN:HE22	7:G:65:PHE:HB2	1.86	0.41
1:A:41:ILE:HB	1:A:88:ILE:HG12	2.03	0.41
2:B:244:GLY:H	2:B:249:LYS:NZ	2.19	0.41
3:C:67:ARG:NH1	10:J:2:ILE:HG23	2.35	0.41
2:B:799:SER:O	2:B:803:ARG:NH1	2.54	0.40
1:A:52:PRO:HB2	1:A:60:PRO:HD3	2.04	0.40
2:B:225:LEU:HD23	2:B:229:SER:HB3	2.03	0.40
1:A:290:LEU:HD11	1:A:307:VAL:HG22	2.04	0.40
4:D:80:ILE:HA	4:D:83:VAL:HG12	2.04	0.40
1:A:806:THR:O	2:B:503:ASN:ND2	2.54	0.40
2:B:386:ASP:OD2	2:B:497:LYS:HG3	2.21	0.40
2:B:634:LEU:HB3	2:B:661:VAL:HG12	2.03	0.40
2:B:1137:CYS:SG	2:B:1138:ARG:N	2.94	0.40
2:B:407:MET:SD	2:B:443:GLY:HA3	2.61	0.40

There are no symmetry-related clashes.



5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
1	А	1418/1970~(72%)	1287 (91%)	129 (9%)	2~(0%)	51	83
2	В	1128/1167~(97%)	1027 (91%)	101 (9%)	0	100	100
3	С	253/275~(92%)	227 (90%)	26 (10%)	0	100	100
4	D	126/142~(89%)	114 (90%)	12 (10%)	0	100	100
5	Е	207/210~(99%)	194 (94%)	13 (6%)	0	100	100
6	F	80/127~(63%)	77 (96%)	3 (4%)	0	100	100
7	G	169/172~(98%)	154 (91%)	15 (9%)	0	100	100
8	Н	146/150~(97%)	136 (93%)	10 (7%)	0	100	100
9	Ι	112/125~(90%)	93 (83%)	19 (17%)	0	100	100
10	J	65/67~(97%)	58 (89%)	7 (11%)	0	100	100
11	К	113/117~(97%)	108 (96%)	5 (4%)	0	100	100
12	L	42/58~(72%)	40 (95%)	2 (5%)	0	100	100
13	М	4/8~(50%)	3 (75%)	1 (25%)	0	100	100
All	All	3863/4588 (84%)	3518 (91%)	343 (9%)	2(0%)	54	83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	539	GLN
1	А	540	ASP

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	Perce	ntiles
1	А	1258/1749~(72%)	1257 (100%)	1 (0%)	93	98
2	В	993/1021~(97%)	993 (100%)	0	100	100
3	С	234/252~(93%)	234 (100%)	0	100	100
4	D	106/126 (84%)	105 (99%)	1 (1%)	78	90
5	Ε	191/192~(100%)	191 (100%)	0	100	100
6	F	71/111 (64%)	71 (100%)	0	100	100
7	G	147/153~(96%)	147 (100%)	0	100	100
8	Н	129/131~(98%)	128 (99%)	1 (1%)	81	91
9	Ι	103/112~(92%)	103 (100%)	0	100	100
10	J	56/56~(100%)	56 (100%)	0	100	100
11	Κ	104/106~(98%)	104 (100%)	0	100	100
12	L	41/55~(74%)	41 (100%)	0	100	100
13	М	2/2~(100%)	2 (100%)	0	100	100
All	All	3435/4066~(84%)	3432 (100%)	3 (0%)	93	98

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	792	ASN
4	D	126	GLU
8	Н	71	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	576	GLN
1	А	673	GLN
1	А	739	ASN
1	А	792	ASN
1	А	1230	GLN
1	А	1420	ASN
2	В	111	ASN
2	В	639	HIS
2	В	790	GLN
2	В	941	GLN
2	В	970	HIS
3	С	66	HIS



Continued from previous page...

Mol	Chain	\mathbf{Res}	Type
7	G	139	GLN
9	Ι	22	ASN
9	Ι	45	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	Р	13/20~(65%)	3~(23%)	1 (7%)

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	Р	11	А
15	Р	13	G
15	Р	18	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
15	Р	12	А

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

4 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).

Mal	Turne	Chain			Dec	Dag	Dec	Tinle	Bo	ond leng	$_{\rm sths}$	E	Bond ang	gles
	туре	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2				
13	CSX	М	6	13	3,6,7	1.00	0	1,6,8	2.24	1 (100%)				
13	HYP	М	8	13	6,8,9	0.76	0	5,10,12	2.19	2 (40%)				
13	TRX	М	2	13	14,16,17	1.01	0	15,22,24	1.99	4 (26%)				
13	ILX	М	1	13	8,9,10	0.61	0	9,11,13	1.32	2 (22%)				



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
13	CSX	М	6	13	-	1/1/5/7	-
13	HYP	М	8	13	-	0/0/11/13	0/1/1/1
13	TRX	М	2	13	-	0/4/6/8	0/2/2/2
13	ILX	М	1	13	-	7/11/12/14	-

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
13	М	2	TRX	CG-CB-CA	5.73	123.38	114.53
13	М	8	HYP	O-C-CA	-3.29	116.16	124.78
13	М	8	HYP	CB-CG-CD	3.12	107.08	103.27
13	М	2	TRX	CB-CG-CD1	-2.98	124.28	127.97
13	М	1	ILX	OD1-CD1-CG1	-2.90	104.75	111.07
13	М	2	TRX	CH2-CZ2-CE2	-2.47	116.69	119.29
13	М	2	TRX	CB-CG-CD2	2.27	129.77	126.25
13	М	6	CSX	CA-CB-SG	2.24	118.24	113.36
13	М	1	ILX	CB-CA-C	-2.04	110.19	112.94

There are no chirality outliers.

All	(8)	torsion	outliers	are	listed	below:
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Mol	Chain	Res	Type	Atoms
13	М	1	ILX	C-CA-CB-CG2
13	М	1	ILX	OD1-CD1-CG1-CB
13	М	1	ILX	OD1-CD1-CG1-OG1
13	М	6	CSX	N-CA-CB-SG
13	М	1	ILX	C-CA-CB-CG1
13	М	1	ILX	CG2-CB-CG1-CD1
13	М	1	ILX	O-C-CA-CB
13	М	1	ILX	N-CA-CB-CG2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	М	6	CSX	1	0



Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	М	8	HYP	1	0
13	М	1	ILX	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (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-3981. 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



6.1.2 Raw map



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



6.2 Central slices (i)

6.2.1 Primary map



X Index: 128





Z Index: 128

6.2.2 Raw map



X Index: 128

Y Index: 128

Z Index: 128

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: 118





Z Index: 101

6.3.2 Raw map



X Index: 118

Y Index: 119



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



The images above show the 3D surface view of the map at the recommended contour level 0.0577. 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



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.



Mask visualisation (i) 6.5

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

emd_3981_msk_1.map (i) 6.5.1





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 149 $\rm nm^3;$ this corresponds to an approximate mass of 134 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 0.278 \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 0.278 $\mathrm{\AA^{-1}}$



8.2 Resolution estimates (i)

$\begin{bmatrix} Bosolution ostimato (Å) \end{bmatrix}$	Estimation criterion (FSC cut-off)			
Resolution estimate (A)	0.143	0.5	Half-bit	
Reported by author	3.60	-	-	
Author-provided FSC curve	3.42	3.73	3.45	
Unmasked-calculated*	3.68	4.13	3.73	

*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-3981 and PDB model 6EXV. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.0577 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 its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0577).



9.4 Atom inclusion (i)



At the recommended contour level, 70% of all backbone atoms, 65% of all non-hydrogen atoms, are inside the map.



9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0577) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score	
All	0.6487	0.4820	
A	0.6969	0.5100	
В	0.7256	0.5150	1 0
С	0.7671	0.5280	
D	0.0020	0.1280	
Е	0.6933	0.4950	
F	0.6520	0.5010	
G	0.0989	0.2170	
Н	0.7144	0.5060	
Ι	0.5286	0.4660	
J	0.8273	0.5500	
K	0.7555	0.5230	0.0
L	0.6517	0.4980	<0.0
М	0.9194	0.5860	
N	0.3004	0.3230]
Р	0.6113	0.4400	
Т	0.4435	0.4140	

