

wwPDB EM Validation Summary Report (i)

Sep 21, 2024 - 10:48 am BST

PDB ID	:	8PJ6
EMDB ID	:	EMD-17701
Title	:	Structure of human 48S translation initiation complex with initiator tRNA,
		eIF1A and eIF3 (off-pathway)
Authors	:	Petrychenko, V.; Yi, SH.; Liedtke, D.; Peng, B.Z.; Rodnina, M.V.; Fischer,
		N.
Deposited on	:	2023-06-22
Resolution	:	2.90 Å(reported)

This is a wwPDB EM Validation Summary 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 (1)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev112
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	FAILED
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.38.2

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 2.90 Å.

There are no overall percentile quality scores available for this entry.

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.



2 Entry composition (i)

There are 52 unique types of molecules in this entry. The entry contains 106921 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 Eukaryotic translation initiation factor 3 subunit B.

Mol	Chain	Residues		Ate	oms			AltConf	Trace
1	1	588	Total 3258	C 1986	N 633	0 634	${ m S}{ m 5}$	0	0

• Molecule 2 is a protein called Eukaryotic translation initiation factor 3 subunit I.

Mol	Chain	Residues		Ato	\mathbf{ms}		AltConf	Trace
9	0	204	Total	С	Ν	Ο	0	0
	Δ	304	1493	885	304	304	0	0

• Molecule 3 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues		Ato	ms		AltConf	Trace
3	3	213	Total 1057	C 631	N 213	O 213	0	0

• Molecule 4 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues		Ato	ms		AltConf	Trace
4	4	257	Total 1272	C 757	N 257	O 258	0	0

• Molecule 5 is a protein called Eukaryotic translation initiation factor 3 subunit L.

Mol	Chain	Residues		Ato	ms		AltConf	Trace
л	Б	310	Total	С	Ν	Ο	0	0
5	5	519	1581	943	319	319	0	0

• Molecule 6 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues		Ate	\mathbf{oms}			AltConf	Trace
6	6	350	Total 1917	C 1159	N 376	O 380	${ m S} { m 2}$	0	0



• Molecule 7 is a RNA chain called mRNA.

Mol	Chain	Residues		A	toms			AltConf	Trace
7	7	56	Total 1196	C 537	N 226	0 377	Р 56	0	0

• Molecule 8 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues		Ato	ms		AltConf	Trace
8	8	317	Total 1571	C 936	N 317	0 318	0	0

• Molecule 9 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues		Atc	\mathbf{ms}		Atoms					
9	9	24	Total 230	C 139	N 62	O 26	${ m S} { m 3}$	0	0			

• Molecule 10 is a RNA chain called 18S rRNA.

Mol	Chain	Residues		I	Atoms			AltConf	Trace
10	А	1719	Total 36678	C 16385	N 6575	O 12000	Р 1718	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	1248	B8N	U	conflict	GB NR_046235.3

• Molecule 11 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues		At	oms	AltConf	Trace		
11	В	142	Total 1166	С 743	N 218	0 199	${ m S}{ m 6}$	0	0

• Molecule 12 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues		Ate	AltConf	Trace			
12	С	256	Total 2035	C 1302	N 378	0 347	S 8	0	0

• Molecule 13 is a protein called 40S ribosomal protein S9.



Mol	Chain	Residues		At	oms	AltConf	Trace		
13	D	177	Total 1477	C 941	N 295	O 239	${ m S} { m 2}$	0	0

• Molecule 14 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues		At	oms	AltConf	Trace		
14	Е	140	Total 1087	C 687	N 215	0 182	${ m S} { m 3}$	0	0

• Molecule 15 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues		Ate	oms	AltConf	Trace		
15	F	59	Total 468	C 290	N 102	O 75	S 1	0	0

• Molecule 16 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	177	Total 1430	C 917	N 260	O 252	S 1	0	0

• Molecule 17 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues		At	oms	AltConf	Trace		
17	Н	81	Total 631	C 397	N 116	0 111	S 7	0	0

• Molecule 18 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues		At	oms	AltConf	Trace		
18	Ι	150	Total 1208	С 773	N 229	O 205	S 1	0	0

• Molecule 19 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues		At	oms	AltConf	Trace		
19	J	129	Total 1034	C 659	N 193	0 176	S 6	0	0

• Molecule 20 is a protein called 40S ribosomal protein S21.



Mol	Chain	Residues		At	oms	AltConf	Trace		
20	K	81	Total 617	C 380	N 114	0 118	${ m S}{ m 5}$	0	0

• Molecule 21 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues		At	AltConf	Trace			
21	L	220	Total 1707	C 1104	N 292	O 301	S 10	0	0

• Molecule 22 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	М	131	Total 1064	C 668	N 198	0 194	${S \atop 4}$	0	0

• Molecule 23 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues		Ate		AltConf	Trace		
23	Ν	207	Total 1633	C 1040	N 288	O 297	S 8	0	0

• Molecule 24 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues		At	AltConf	Trace			
24	О	211	Total 1715	C 1088	N 307	O 306	S 14	0	0

• Molecule 25 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues		At	oms			AltConf	Trace
25	Р	133	Total 997	C 610	N 196	0 185	S 6	0	0

• Molecule 26 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues		At	oms	AltConf	Trace		
26	Q	99	Total 792	C 492	N 165	0 130	${S \atop 5}$	0	0

• Molecule 27 is a protein called 40S ribosomal protein S8.



Mol	Chain	Residues		At	oms			AltConf	Trace
27	R	198	Total 1627	C 1021	N 322	O 279	${ m S}{ m 5}$	0	0

• Molecule 28 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues		Ate	AltConf	Trace			
28	S	230	Total 1862	C 1164	N 371	O 320	${ m S} 7$	0	0

• Molecule 29 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Т	125	Total 1015	C 642	N 199	0 169	${ m S}{ m 5}$	0	0

• Molecule 30 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues		At	oms	AltConf	Trace		
30	V	184	Total 1461	C 914	N 276	0 264	${f S}7$	0	0

• Molecule 31 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues		At	oms	AltConf	Trace		
31	Y	141	Total 1124	C 715	N 212	0 194	${ m S} { m 3}$	0	0

• Molecule 32 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues		At		AltConf	Trace		
32	Z	227	Total 1765	C 1125	N 317	0 315	S 8	0	0

• Molecule 33 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues		At	oms	AltConf	Trace		
33	a	99	Total 834	C 544	N 149	0 135	S 6	0	0

• Molecule 34 is a protein called 40S ribosomal protein S15.



Mol	Chain	Residues		At	AltConf	Trace			
34	b	131	Total 1072	C 682	N 201	O 182	${ m S} 7$	0	0

• Molecule 35 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues		At	AltConf	Trace			
35	с	313	Total 2436	C 1535	N 424	O 465	S 12	0	0

• Molecule 36 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues		At	AltConf	Trace			
36	d	142	Total 1105	C 692	N 213	0 197	${ m S} { m 3}$	0	0

• Molecule 37 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues		Ato	\mathbf{ms}	AltConf	Trace		
27	0	66	Total	С	Ν	Ο	S	0	0
57	е	00	523	338	93	91	1	0	0

• Molecule 38 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues		At	oms	AltConf	Trace		
38	f	149	Total 1227	C 770	N 249	O 207	S 1	0	0

• Molecule 39 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues		At	oms	AltConf	Trace		
39	h	103	Total 817	C 511	N 155	0 147	${f S}$ 4	0	0

• Molecule 40 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
40	i	50	Total 419	C 262	N 85	O 67	${f S}{5}$	0	0

• Molecule 41 is a protein called Ubiquitin.



Mol	Chain	Residues		At	oms			AltConf	Trace
41	k	68	Total 554	C 349	N 103	O 95	${ m S} 7$	0	0

• Molecule 42 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues		At	oms	AltConf	Trace		
42	m	122	Total 950	C 596	N 168	0 177	${f S}$ 9	0	0

• Molecule 43 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues		Ate	\mathbf{oms}			AltConf	Trace
43	n	63	Total 498	C 302	N 101	O 93	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 44 is a protein called Eukaryotic translation initiation factor 3 subunit G.

Mol	Chain	Residues		Ato	ms		AltConf	Trace
44	О	77	Total 616	C 389	N 111	O 116	0	0

• Molecule 45 is a protein called Eukaryotic translation initiation factor 1A, X-chromosomal.

Mol	Chain	Residues		At	AltConf	Trace			
45	q	112	Total 902	$\begin{array}{c} \mathrm{C} \\ 560 \end{array}$	N 173	O 165	${S \atop 4}$	0	0

• Molecule 46 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues		At	oms			AltConf	Trace
46	u	706	Total 5383	C 3379	N 982	0 999	S 23	1	0

• Molecule 47 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues		At	oms			AltConf	Trace
47	V	384	Total 2635	C 1657	N 477	0 489	S 12	0	0

• Molecule 48 is a RNA chain called Initiator Met-tRNA-i.



Mol	Chain	Residues		A	toms			AltConf	Trace
48	W	73	Total 1562	C 698	N 290	O 502	Р 72	0	0

• Molecule 49 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues		Ate	AltConf	Trace			
49	x	420	Total 2826	C 1743	N 520	0 554	S 9	0	0

• Molecule 50 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues		At	AltConf	Trace			
50	У	531	Total 4305	С 2711	N 764	O 797	S 33	0	0

• Molecule 51 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
51	А	82	TotalMg8282	0
51	V	1	Total Mg 1 1	0
51	d	1	Total Mg 1 1	0
51	f	1	Total Mg 1 1	0
51	i	2	Total Mg 2 2	0

• Molecule 52 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
52	Q	1	Total Zn 1 1	0
52	k	1	Total Zn 1 1	0

MolProbity failed to run properly - this section is therefore empty.



3 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55368	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 $(e^-/\text{\AA}^2)$	45	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.091	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0102	Depositor
Map size (Å)	417.59998, 417.59998, 417.59998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^{\circ}$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor



4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

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

29 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	Tiple	Bo	ond leng	$_{\rm sths}$	B	ond ang	les
MOI	туре	Unam	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
10	A2M	А	27	10,51	18,25,26	4.32	7 (38%)	18,36,39	3.84	4 (22%)
10	A2M	А	668	10,51	18,25,26	4.21	8 (44%)	18,36,39	3.89	5 (27%)
10	A2M	A	159	10	18,25,26	4.26	8 (44%)	18,36,39	3.96	5 (27%)



Mol	Type	Chain	Ros	Link	Bo	ond leng	ths	Bond angles			
WIOI	Type	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2	
10	MA6	А	1850	10	18,26,27	1.32	2 (11%)	19,38,41	3.11	2 (10%)	
10	OMC	А	517	10	19,22,23	0.59	0	26,31,34	0.66	0	
10	OMU	А	121	10	19,22,23	2.95	6 (31%)	26,31,34	1.63	5 (19%)	
10	PSU	А	1081	10	18,21,22	1.04	1 (5%)	22,30,33	1.83	5 (22%)	
10	PSU	А	1243	10	18,21,22	1.06	1 (5%)	22,30,33	1.80	4 (18%)	
10	6MZ	А	1832	10,51	18,25,26	1.77	2 (11%)	16,36,39	2.59	5 (31%)	
10	PSU	А	612	10	18,21,22	1.00	1 (5%)	22,30,33	1.79	5 (22%)	
10	OMG	А	683	10	18,26,27	1.20	2 (11%)	19,38,41	0.89	1 (5%)	
10	PSU	А	822	10	18,21,22	1.03	1 (5%)	22,30,33	1.86	6 (27%)	
10	5MC	А	1374	10	18,22,23	0.65	0	26,32,35	0.60	0	
10	OMU	А	116	10	19,22,23	2.97	5 (26%)	26,31,34	1.58	5 (19%)	
10	OMG	А	509	10,51	18,26,27	1.20	2 (11%)	19,38,41	0.89	1 (5%)	
10	OMC	А	1703	10	19,22,23	0.61	0	26,31,34	0.77	1 (3%)	
10	A2M	А	1678	$10,\!51$	$18,\!25,\!26$	4.39	8 (44%)	18,36,39	3.88	4 (22%)	
10	A2M	А	1031	10	18,25,26	4.38	8 (44%)	18,36,39	3.85	4 (22%)	
10	A2M	А	484	10	18,25,26	4.24	9 (50%)	18,36,39	3.89	5 (27%)	
10	OMC	А	174	10,51	19,22,23	0.57	0	26,31,34	0.71	1 (3%)	
10	B8N	А	1248	10	24,29,30	0.30	0	29,42,45	0.73	1 (3%)	
10	OMG	А	644	10	18,26,27	1.19	2 (11%)	19,38,41	0.85	1 (5%)	
10	UR3	А	1830	10	19,22,23	2.76	7 (36%)	26,32,35	1.51	4 (15%)	
10	PSU	А	823	10	18,21,22	1.08	1 (5%)	22,30,33	1.77	4 (18%)	
10	PSU	А	119	10	18,21,22	0.99	1 (5%)	22,30,33	1.59	4 (18%)	
10	A2M	А	166	10	18,25,26	4.35	7 (38%)	18,36,39	3.82	5 (27%)	
10	MA6	А	1851	10	18,26,27	1.33	2 (11%)	19,38,41	3.17	2 (10%)	
10	JMH	А	1219	10	18,22,23	0.25	0	21,32,35	0.25	0	
10	5MU	А	814	10	19,22,23	0.48	0	28,32,35	0.93	2 (7%)	

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
10	A2M	А	27	10,51	-	1/5/27/28	0/3/3/3
10	A2M	А	668	$10,\!51$	-	2/5/27/28	0/3/3/3
10	A2M	А	159	10	-	2/5/27/28	0/3/3/3
10	MA6	А	1850	10	-	0/7/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	OMC	А	517	10	-	2/9/27/28	0/2/2/2
10	OMU	А	121	10	-	1/9/27/28	0/2/2/2
10	PSU	А	1081	10	-	1/7/25/26	0/2/2/2
10	PSU	А	1243	10	-	2/7/25/26	0/2/2/2
10	6MZ	А	1832	10,51	-	0/5/27/28	0/3/3/3
10	PSU	А	612	10	-	0/7/25/26	0/2/2/2
10	OMG	А	683	10	-	2/5/27/28	0/3/3/3
10	PSU	А	822	10	-	2/7/25/26	0/2/2/2
10	5MC	А	1374	10	-	0/7/25/26	0/2/2/2
10	OMU	А	116	10	-	1/9/27/28	0/2/2/2
10	OMG	А	509	10,51	-	1/5/27/28	0/3/3/3
10	OMC	А	1703	10	-	2/9/27/28	0/2/2/2
10	A2M	А	1678	10,51	-	0/5/27/28	0/3/3/3
10	A2M	А	1031	10	-	1/5/27/28	0/3/3/3
10	A2M	А	484	10	-	1/5/27/28	0/3/3/3
10	OMC	А	174	10,51	-	0/9/27/28	0/2/2/2
10	B8N	А	1248	10	-	7/16/34/35	0/2/2/2
10	OMG	А	644	10	-	2/5/27/28	0/3/3/3
10	UR3	А	1830	10	-	2/7/25/26	0/2/2/2
10	PSU	А	823	10	-	0/7/25/26	0/2/2/2
10	PSU	А	119	10	-	0/7/25/26	0/2/2/2
10	A2M	A	166	10	-	0/5/27/28	0/3/3/3
10	MA6	А	1851	10	-	3/7/29/30	0/3/3/3
10	JMH	А	1219	10	-	0/7/25/26	0/2/2/2
10	5MU	А	814	10	-	0/7/25/26	0/2/2/2

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The worst 5 of 91 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
10	А	1031	A2M	C3'-C2'	-12.99	1.24	1.52
10	А	1678	A2M	C3'-C2'	-12.96	1.24	1.52
10	А	166	A2M	C3'-C2'	-12.90	1.24	1.52
10	А	27	A2M	C3'-C2'	-12.85	1.24	1.52
10	А	159	A2M	C3'-C2'	-12.45	1.25	1.52

The worst 5 of 91 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
10	А	1851	MA6	N1-C6-N6	-12.38	104.03	117.06
10	А	1850	MA6	N1-C6-N6	-12.18	104.24	117.06

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Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
10	А	159	A2M	C1'-N9-C4	10.97	145.91	126.64
10	А	1678	A2M	C1'-N9-C4	10.91	145.81	126.64
10	А	484	A2M	C1'-N9-C4	10.64	145.34	126.64

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There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	А	27	A2M	C1'-C2'-O2'-CM'
10	А	116	OMU	C1'-C2'-O2'-CM2
10	А	121	OMU	C1'-C2'-O2'-CM2
10	А	159	A2M	C1'-C2'-O2'-CM'
10	А	484	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

No monomer is involved in short contacts.

4.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

4.6 Ligand geometry (i)

Of 89 ligands modelled in this entry, 89 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.

4.7 Other polymers (i)

There are no such residues in this entry.



4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-17701. 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.

5.1 Orthogonal projections (i)

5.1.1 Primary map



5.1.2 Raw map



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



5.2 Central slices (i)

5.2.1 Primary map



X Index: 180



Y Index: 180



Z Index: 180

5.2.2 Raw map



X Index: 180

Y Index: 180

Z Index: 180

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



5.3 Largest variance slices (i)

5.3.1 Primary map



X Index: 147



Y Index: 216



Z Index: 174

5.3.2 Raw map



X Index: 147

Y Index: 216



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



5.4 Orthogonal standard-deviation projections (False-color) (i)

5.4.1 Primary map



5.4.2 Raw map



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



5.5 Orthogonal surface views (i)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0102. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

5.5.2 Raw map



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



Mask visualisation (i) 5.6

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

$emd_17701_msk_1.map$ (i) 5.6.1





6 Map analysis (i)

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

6.1 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.



6.2 Volume estimate (i)



The volume at the recommended contour level is 2072 nm^3 ; this corresponds to an approximate mass of 1872 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.



6.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.345 ${\rm \AA^{-1}}$



7 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.

7.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.345 $\mathrm{\AA^{-1}}$



7.2 Resolution estimates (i)

$\mathbf{B}_{\text{assolution ostimato}}(\mathbf{\hat{\lambda}})$	Estim	Estimation criterion (FSC cut-off		
Resolution estimate (A)	0.143	0.5	Half-bit	
Reported by author	2.90	-	-	
Author-provided FSC curve	3.24	4.25	3.38	
Unmasked-calculated*	3.92	7.21	4.08	

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.24 differs from the reported value 2.9 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.92 differs from the reported value 2.9 by more than 10 %



8 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-17701 and PDB model 8PJ6. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.0102 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.



8.2 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.

8.3 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 (0.0102).



8.4 Atom inclusion (i)



At the recommended contour level, 83% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.



1.0

0.0 <0.0

8.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0102) and Q-score for the entire model and for each chain.

All 0.8620 0.3740 1 0.0480 0.1230 2 0.0000 0.1160 3 0.2540 0.1220 4 0.6150 0.1240 5 0.4660 0.1170 6 0.5550 0.1380 7 0.7220 0.2430 8 0.5440 0.1010 9 1.0000 0.4250 A 0.9990 0.4610 B 0.9950 0.4940 C 0.9970 0.4780 D 0.9990 0.4640 E 0.9990 0.4890 F 0.9900 0.4890 F 0.9900 0.4840 K 0.9930 0.4890 J 0.9940 0.4840 K 0.9730 0.4710 M 0.9530 0.4080 N 0.9800 0.4530 O 0.9890 0.4390 P 0.9810	\mathbf{Chain}	Atom inclusion	$\mathbf{Q} extsf{-score}$
1 0.0480 0.1230 2 0.0000 0.1160 3 0.2540 0.1220 4 0.6150 0.1240 5 0.4660 0.1170 6 0.5550 0.1380 7 0.7220 0.2430 8 0.5440 0.1010 9 1.0000 0.4250 A 0.9990 0.4610 B 0.9950 0.4940 C 0.9970 0.4780 D 0.9990 0.4640 E 0.9990 0.4440 C 0.9970 0.4780 D 0.9990 0.4890 F 0.9760 0.4130 G 0.9930 0.4840 K 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4930 P 0.9890 0.4330 P 0.9890 0.4390 P 0.9990 0.4510 S 0.9990 0.4510 S 0.9990 0.4350 V 0.9980 0.4390 A 0.99	All	0.8620	0.3740
2 0.0000 0.1160 3 0.2540 0.1220 4 0.6150 0.1240 5 0.4660 0.1170 6 0.5550 0.1380 7 0.7220 0.2430 8 0.5440 0.1010 9 1.0000 0.4250 A 0.9990 0.4610 B 0.9950 0.4940 C 0.9970 0.4780 D 0.9990 0.4640 E 0.9990 0.4480 F 0.9760 0.4130 G 0.9430 0.3920 H 0.9760 0.4460 I 0.9860 0.4500 J 0.9940 0.4480 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4460 L 0.9730 0.4460 L 0.9730 0.4460 L 0.9930 0.4450 N 0.9890 0.4450 N 0.9800 0.4450 N 0.9800 0.4450 N 0.9800 0.4450 N 0.9980 0.4450 V 0.9880 0.4450 Y 0.9990 0.4350 V 0.9880 0.4590 Y 0.9990 0.4350 V 0.9880 0.4270 b 0.9930 0.4170	1	0.0480	0.1230
3 0.2540 0.1220 4 0.6150 0.1240 5 0.4660 0.1170 6 0.5550 0.1380 7 0.7220 0.2430 8 0.5440 0.1010 9 1.0000 0.4250 A 0.9990 0.4610 B 0.9950 0.4940 C 0.9970 0.4780 D 0.9990 0.4640 E 0.9990 0.4480 F 0.9760 0.4130 G 0.9430 0.3920 H 0.9760 0.4480 I 0.9860 0.4500 J 0.9940 0.4480 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4080 N 0.9800 0.4450 R 0.9990 0.4450 R 0.9990 0.4450 T 0.9990 0.4450 Y 0.9990 0.4450 S 0.9930 0.4450 S 0.9930 0.4450 Y 0.9990 0.4550 Y 0.9990 0.44510 S 0.9930 0.4350 V 0.9880 0.4590 Y 0.9990 0.4350 V 0.9880 0.4270 b 0.9930 0.4170	2	0.0000	0.1160
4 0.6150 0.1240 5 0.4660 0.1170 6 0.5550 0.1380 7 0.7220 0.2430 8 0.5440 0.1010 9 1.0000 0.4250 A 0.9990 0.4610 B 0.9950 0.4940 C 0.9970 0.4780 D 0.9900 0.4640 E 0.9990 0.4480 F 0.9760 0.4130 G 0.9430 0.3920 H 0.9760 0.4480 I 0.9860 0.44500 J 0.9940 0.4440 K 0.9730 0.4710 M 0.9530 0.4460 L 0.9730 0.4710 M 0.9800 0.4530 O 0.9890 0.4430 F 0.9930 0.44510 J 0.9990 0.4450 K 0.9990 0.4390 P 0.9810 0.44510 S 0.9990 0.44510 S 0.9990 0.4450 Y 0.9970 0.4770 Z 0.9650 0.4390 A 0.9830 0.4270 b 0.9930 0.4170	3	0.2540	0.1220
5 0.4660 0.1170 6 0.5550 0.1380 7 0.7220 0.2430 8 0.5440 0.1010 9 1.0000 0.4250 A 0.9990 0.4610 B 0.9950 0.4940 C 0.9970 0.4780 D 0.9900 0.4440 E 0.9990 0.4480 F 0.9900 0.4480 F 0.9760 0.4130 G 0.9430 0.3920 H 0.9760 0.4440 I 0.9860 0.4500 J 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4080 N 0.9800 0.4530 O 0.9890 0.4390 P 0.9910 0.4450 R 0.9990 0.4350 V 0.9880 0.4350 V 0.9880 0.4350 V 0.9880 0.4350 V 0.9880 0.4470 A 0.9930 0.4470 A 0.9930 0.4470	4	0.6150	0.1240
6 0.5550 0.1380 7 0.7220 0.2430 8 0.5440 0.1010 9 1.0000 0.4250 A 0.9990 0.4610 B 0.9950 0.4940 C 0.9970 0.4780 D 0.9970 0.4780 D 0.9990 0.4640 E 0.9990 0.4890 F 0.9760 0.4130 G 0.9430 0.3920 H 0.9760 0.4440 I 0.9960 0.4480 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4460 L 0.9730 0.4710 M 0.9800 0.4530 O 0.9890 0.4390 P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	5	0.4660	0.1170
7 0.7220 0.2430 8 0.5440 0.1010 9 1.0000 0.4250 A 0.9990 0.4610 B 0.9950 0.4940 C 0.9970 0.4780 D 0.9970 0.4780 D 0.9900 0.4640 E 0.9990 0.4890 F 0.9760 0.4130 G 0.9760 0.4130 G 0.9760 0.4540 I 0.9960 0.4540 J 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4460 L 0.9730 0.4460 L 0.9730 0.4450 R 0.9800 0.4530 O 0.9890 0.4390 P 0.9810 0.4610 Q 0.9920 0.4250 R 0.9990 0.4350 V 0.9880 0.4350 V 0.9880 0.4390 A 0.9930 0.4470 B 0.9930 0.4170	6	0.5550	0.1380
8 0.5440 0.1010 9 1.0000 0.4250 A 0.9990 0.4610 B 0.9950 0.4940 C 0.9970 0.4780 D 0.9970 0.4780 D 0.9900 0.4640 E 0.9990 0.4890 F 0.9760 0.4130 G 0.9430 0.3920 H 0.9760 0.4540 I 0.9860 0.4500 J 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4480 N 0.9800 0.4390 P 0.9810 0.4430 Q 0.9920 0.4390 P 0.9930 0.4450 T 0.9990 0.44510 S 0.9930 0.44770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	7	0.7220	0.2430
9 1.0000 0.4250 A 0.9990 0.4610 B 0.9950 0.4940 C 0.9970 0.4780 D 0.9900 0.4640 E 0.9990 0.4890 F 0.9760 0.4130 G 0.9430 0.3920 H 0.9760 0.44500 J 0.9940 0.4840 K 0.9780 0.4460 L 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4460 L 0.9730 0.44710 M 0.9800 0.4330 O 0.9890 0.4390 P 0.9810 0.44610 Q 0.9920 0.4920 R 0.9990 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	8	0.5440	0.1010
A 0.9990 0.4610 B 0.9950 0.4940 C 0.9970 0.4780 D 0.9900 0.4640 E 0.9990 0.4890 F 0.9760 0.4130 G 0.9760 0.4130 G 0.9760 0.4430 I 0.9760 0.4540 I 0.9940 0.4840 K 0.9780 0.4460 L 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4480 N 0.9800 0.4530 O 0.9890 0.4430 P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4350 V 0.9990 0.4350 V 0.9990 0.4350 V 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	9	1.0000	0.4250
B 0.9950 0.4940 C 0.9970 0.4780 D 0.9900 0.4640 E 0.9990 0.4890 F 0.9760 0.4130 G 0.9760 0.4130 G 0.9760 0.4430 I 0.9860 0.4500 J 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4480 N 0.9800 0.4530 O 0.9890 0.4390 P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4350 V 0.9880 0.4390 T 0.9990 0.4350 V 0.9880 0.4390 A 0.9830 0.4270 b 0.9930 0.4170	А	0.9990	0.4610
C 0.9970 0.4780 D 0.9900 0.4640 E 0.9990 0.4890 F 0.9760 0.4130 G 0.9430 0.3920 H 0.9760 0.4440 I 0.9760 0.4430 J 0.9860 0.4500 J 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9930 0.4390 P 0.9800 0.4430 Q 0.9730 0.4460 L 0.9730 0.4460 M 0.9930 0.4390 P 0.9800 0.4390 P 0.9990 0.4350 Q 0.9990 0.4350 V 0.9930 0.4270 <t< td=""><td>В</td><td>0.9950</td><td>0.4940</td></t<>	В	0.9950	0.4940
D 0.9900 0.4640 E 0.9990 0.4890 F 0.9760 0.4130 G 0.9430 0.3920 H 0.9760 0.4540 I 0.9860 0.4500 J 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4080 N 0.9800 0.4530 O 0.9890 0.4450 P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4350 V 0.9980 0.4350 V 0.9990 0.4350 V 0.9990 0.4350 V 0.9980 0.4390 A 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	C	0.9970	0.4780
E 0.9990 0.4890 F 0.9760 0.4130 G 0.9430 0.3920 H 0.9760 0.4540 I 0.9860 0.4500 J 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4080 N 0.9800 0.4530 O 0.9890 0.4390 P 0.9910 0.4610 Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4170	D	0.9900	0.4640
F 0.9760 0.4130 G 0.9430 0.3920 H 0.9760 0.4540 I 0.9860 0.4500 J 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4080 N 0.9800 0.4390 P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4350 V 0.9880 0.4350 V 0.9990 0.4350 V 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4170	Ε	0.9990	0.4890
G 0.9430 0.3920 H 0.9760 0.4540 I 0.9860 0.4500 J 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4080 N 0.9800 0.4390 P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4350 V 0.9880 0.4390 T 0.9990 0.4350 V 0.9990 0.4350 V 0.9930 0.4390 A 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	F	0.9760	0.4130
H 0.9760 0.4540 I 0.9860 0.4500 J 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4080 N 0.9800 0.4530 O 0.9800 0.4530 P 0.9800 0.4530 Q 0.9890 0.4510 R 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4500 Y 0.9990 0.4510 S 0.9930 0.4350 Y 0.9990 0.4350 Y 0.9990 0.4350 Y 0.9990 0.4350 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	G	0.9430	0.3920
I 0.9860 0.4500 J 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4080 N 0.9800 0.4530 O 0.9800 0.4530 P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9990 0.4550 V 0.9990 0.4500 Y 0.9990 0.4350 V 0.9990 0.4350 Y 0.9990 0.4350 Y 0.9990 0.4350 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	Н	0.9760	0.4540
J 0.9940 0.4840 K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4080 N 0.9800 0.4530 O 0.9890 0.4390 P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4350 V 0.9980 0.4350 V 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	Ι	0.9860	0.4500
K 0.9780 0.4460 L 0.9730 0.4710 M 0.9530 0.4080 N 0.9800 0.4530 O 0.9800 0.4390 P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4000 T 0.9990 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	J	0.9940	0.4840
L 0.9730 0.4710 M 0.9530 0.4080 N 0.9800 0.4530 O 0.9890 0.4390 P 0.9890 0.4390 Q 0.9920 0.4610 Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4000 T 0.9990 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	К	0.9780	0.4460
M 0.9530 0.4080 N 0.9800 0.4530 O 0.9890 0.4390 P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4000 T 0.9990 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	L	0.9730	0.4710
N 0.9800 0.4530 O 0.9890 0.4390 P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4000 T 0.9990 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	М	0.9530	0.4080
O 0.9890 0.4390 P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4000 T 0.9990 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	Ν	0.9800	0.4530
P 0.9810 0.4610 Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4000 T 0.9990 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	О	0.9890	0.4390
Q 0.9920 0.4920 R 0.9990 0.4510 S 0.9930 0.4000 T 0.9990 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	Р	0.9810	0.4610
R 0.9990 0.4510 S 0.9930 0.4000 T 0.9990 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	Q	0.9920	0.4920
S 0.9930 0.4000 T 0.9990 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	R	0.9990	0.4510
T 0.9990 0.4350 V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	S	0.9930	0.4000
V 0.9880 0.4590 Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	Т	0.9990	0.4350
Y 0.9970 0.4770 Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	V	0.9880	0.4590
Z 0.9650 0.4390 a 0.9830 0.4270 b 0.9930 0.4170	Y	0.9970	0.4770
a 0.9830 0.4270 b 0.9930 0.4170	Z	0.9650	0.4390
b 0.9930 0.4170	a	0.9830	0.4270
	b	0.9930	0.4170

 $Continued \ on \ next \ page...$



Continued	from	previous	page

Chain	Atom inclusion	Q-score
С	0.9910	0.4260
d	0.9940	0.4570
е	0.9900	0.4340
f	0.9920	0.4300
h	0.9890	0.4360
i	0.9880	0.5020
k	0.9960	0.3130
m	0.9630	0.2870
n	0.9900	0.4500
0	0.9110	0.2080
q	0.9670	0.3550
u	0.5270	0.2040
V	0.5880	0.1420
W	0.9970	0.2510
Х	0.8460	0.2890
у	0.6840	0.2590

