



wwPDB EM Validation Summary Report ⓘ

Apr 16, 2024 – 10:32 am BST

PDB ID : 8OVA
EMDB ID : EMD-17208
Title : CRYO-EM STRUCTURE OF TRYPANOSOMA BRUCEI PROCYCLIC
FORM 80S RIBOSOME : PARENTAL STRAIN
Authors : Rajan, K.S.; Yonath, A.
Deposited on : 2023-04-25
Resolution : 2.47 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev92
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 : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

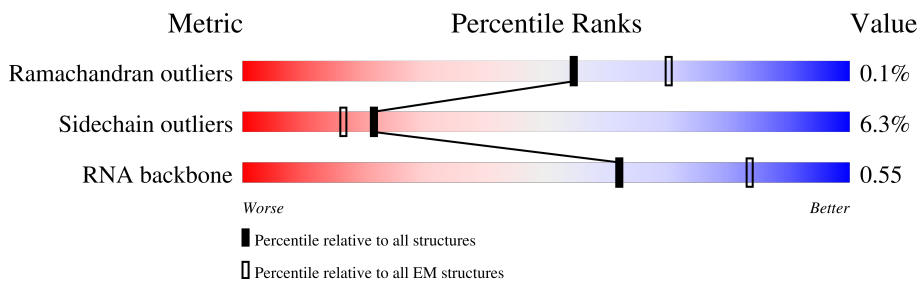
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.47 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)
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 ≥ 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	BA	1920	
2	AA	2282	
3	BB	1536	
4	BH	136	
5	BG	183	
6	BF	78	
7	BE	216	
8	BD	119	
9	BC	209	

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Mol	Chain	Length	Quality of chain
10	AB	19	
11	AQ	117	
12	A8	57	
13	A9	153	
14	Az	279	
15	AH	144	
16	AI	152	
17	AJ	130	
18	AK	149	
19	AM	153	
20	AO	167	
21	AP	266	
22	AR	194	
23	AS	143	
24	AT	137	
25	AU	113	
26	AV	111	
27	AW	86	
28	AX	214	
29	AY	66	
30	AZ	103	
31	AL	142	
32	A0	256	
33	A1	273	
34	A2	190	

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Mol	Chain	Length	Quality of chain
35	A3	250	89% 6% 5%
36	A4	202	88% 10%
37	A5	220	79% 6% 15%
38	A6	190	89% 5% 6%
39	A7	318	90% 8%
40	AC	277	72% 25%
41	AD	172	53% 5% 42%
42	AE	174	83% 5% 12%
43	AG	151	95% 5%
44	Bh	188	77% 6% 17%
45	Ba	133	89% 11%
46	Bb	145	94% 5%
47	Bc	146	95% ..
48	Bd	71	89% 6% 6%
49	Be	260	95% ..
50	Bz	34	94% 6%
51	Bg	105	82% 6% 12%
52	Bf	429	89% 8%
53	BI	193	95% ..
54	Bj	170	66% 32%
55	BK	213	85% 6% 9%
56	Bk	127	91% 6%
57	BL	194	78% 7% 14%
58	Bl	149	94% ..
59	Bm	109	86% 10%



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Mol	Chain	Length	Quality of chain
60	BN	218	96%
61	Bn	84	90%
62	BO	222	98%
63	Bo	93	92%
64	Bp	82	84%
65	Bq	51	94%
66	BQ	221	89%
67	BR	166	88%
68	Br	374	95%
69	BS	179	96%
70	Bs	128	36%
71	BT	260	72%
72	Bt	106	85%
73	BU	159	86%
74	Bu	308	76%
75	BV	130	83%
76	Bv	192	69%
77	BW	139	94%
78	BX	164	67%
79	Bw	257	88%
80	Bx	276	79%
81	BY	125	49%
82	By	189	93%
83	BZ	143	81%
84	Bi	132	98%

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Mol	Chain	Length	Quality of chain
85	BP	189	 73% 7% 20%
86	AF	144	 72% 8% 20%

2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 209127 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 RNA chain called LSUa rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	BA	1604	34346	15345	6216	11181	1604	0	0

- Molecule 2 is a RNA chain called SSU rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	AA	1919	40964	18316	7328	13401	1919	0	0

- Molecule 3 is a RNA chain called LSUb rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	BB	1119	23918	10699	4282	7818	1119	0	0

- Molecule 4 is a RNA chain called SrRNA-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	BH	119	2538	1131	451	837	119	0	0

- Molecule 5 is a RNA chain called SrRNA-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	BG	183	3919	1746	708	1282	183	0	0

- Molecule 6 is a RNA chain called SrRNA-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	BF	69	1444	646	239	490	69	0	0

- Molecule 7 is a RNA chain called SrRNA-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	BE	188	3981	1780	692	1321	188	0	0

- Molecule 8 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	BD	119	2533	1131	449	835	118	0	0

- Molecule 9 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
9	BC	160	3411	1529	610	1113	159	0	0

- Molecule 10 is a RNA chain called E-SITE TRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
10	AB	19	404	181	76	129	18	0	0

- Molecule 11 is a protein called Ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AQ	100	800	501	152	144	3	0	0

- Molecule 12 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	A8	56	461	284	97	75	5	0	0

- Molecule 13 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	A9	70	569	361	109	92	7	0	1

- Molecule 14 is a protein called RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	Az	100	807	504	154	148	1	0	0

- Molecule 15 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	AH	134	992	607	193	183	9	0	0

- Molecule 16 is a protein called 40S ribosomal protein S15, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	AI	119	966	614	188	161	3	0	0

- Molecule 17 is a protein called 40S ribosomal protein S15a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	AJ	129	1018	645	191	174	8	0	0

- Molecule 18 is a protein called 40S ribosomal protein S16, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	AK	142	1140	728	215	194	3	0	0

- Molecule 19 is a protein called 40S ribosomal protein S18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	AM	141	1143	713	227	198	5	0	0

- Molecule 20 is a protein called Ribosomal protein S19, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	AO	154	1220	770	242	199	9	0	0

- Molecule 21 is a protein called 40S ribosomal protein S2, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	AP	218	1688	1078	298	303	9	0	0

- Molecule 22 is a protein called 40S ribosomal protein S21, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	AR	89	666	415	119	129	3	0	0

- Molecule 23 is a protein called 40S ribosomal protein S23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	AS	140	1096	696	213	185	2	0	0

- Molecule 24 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	AT	129	1034	659	202	170	3	0	0

- Molecule 25 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	AU	73	575	365	105	100	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	AV	103	830	512	175	135	8	0	0

- Molecule 27 is a protein called 40S ribosomal protein S27, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	AW	85	660	411	124	116	9	0	0

- Molecule 28 is a protein called 40S ribosomal protein S3, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	AX	208	1652	1036	310	294	12	0	0

- Molecule 29 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	AY	55	448	283	93	71	1	0	0

- Molecule 30 is a protein called 40S ribosomal protein S33, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	AZ	58	449	271	94	80	4	0	0

- Molecule 31 is a protein called 40S ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	AL	122	945	600	184	156	5	0	0

- Molecule 32 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	A0	220	1789	1129	336	316	8	0	0

- Molecule 33 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	A1	262	2062	1306	388	359	9	0	0

- Molecule 34 is a protein called 40S ribosomal protein S5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	A2	183	1464	915	282	262	5	0	0

- Molecule 35 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	A3	238	1871	1161	383	323	4	0	0

- Molecule 36 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	A4	198	1602	1023	308	266	5	0	0

- Molecule 37 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	A5	187	1471	927	291	251	2	0	0

- Molecule 38 is a protein called Probable 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	A6	179	1477	929	297	243	8	0	0

- Molecule 39 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	A7	309	2371	1483	418	458	12	0	0

- Molecule 40 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	AC	208	1648	1049	297	291	11	0	0

- Molecule 41 is a protein called 40S ribosomal protein S10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	AD	99	814	531	140	139	4	0	0

- Molecule 42 is a protein called 40S ribosomal proteins S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	AE	153	1249	782	253	209	5	0	0

- Molecule 43 is a protein called 40S ribosomal protein S13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	AG	150	1203	756	236	203	8	0	0

- Molecule 44 is a protein called 60S ribosomal subunit protein L31, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	Bh	156	1249	785	253	207	4	0	0

- Molecule 45 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	Ba	132	1085	688	219	175	3	0	0

- Molecule 46 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	Bb	144	1137	717	228	186	6	0	0

- Molecule 47 is a protein called 60S ribosomal protein L28, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	Bc	144	1162	723	234	197	8	0	0

- Molecule 48 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	Bd	67	547	335	123	88	1	0	0

- Molecule 49 is a protein called 60S ribosomal protein L2, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	Be	254	1907	1189	394	312	12	1	0

- Molecule 50 is a protein called Ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	Bz	32	284	172	74	36	2	0	0

- Molecule 51 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	Bg	92	708	441	128	134	5	0	0

- Molecule 52 is a protein called Ribosomal protein L3, mitochondrial, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	Bf	396	3174	2001	626	534	13	0	0

- Molecule 53 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	BI	191	1517	950	313	246	8	0	0

- Molecule 54 is a protein called 60S ribosomal protein L34, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	Bj	116	959	593	214	148	4	0	0

- Molecule 55 is a protein called 60S ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	BK	194	1588	1002	314	260	12	0	0

- Molecule 56 is a protein called 60S ribosomal protein L35, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	Bk	123	1010	634	217	156	3	0	0

- Molecule 57 is a protein called 60S ribosomal protein L11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	BL	166	1325	836	247	235	7	0	0

- Molecule 58 is a protein called 60S ribosomal protein L35A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	Bl	144	1163	728	239	193	3	0	0

- Molecule 59 is a protein called Ribosomal protein L36, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	Bm	98	786	493	164	127	2	0	0

- Molecule 60 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	BN	215	1762	1097	365	294	6	0	0

- Molecule 61 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	Bn	80	676	410	157	103	6	0	0

- Molecule 62 is a protein called 60S ribosomal protein L13a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	BO	221	1801	1141	364	289	7	0	0

- Molecule 63 is a protein called 60S ribosomal protein L37a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	Bo	89	699	434	144	115	6	0	0

- Molecule 64 is a protein called 60S ribosomal protein L38, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	Bp	77	626	393	125	104	4	0	0

- Molecule 65 is a protein called 60S ribosomal protein L39, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
65	Bq	50	457	297	98	62	0	0

- Molecule 66 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	BQ	203	1716	1077	370	264	5	0	0

- Molecule 67 is a protein called 60S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	BR	151	1219	767	242	202	8	0	0

- Molecule 68 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	Br	367	2882	1802	575	488	17	0	0

- Molecule 69 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	BS	178	1465	926	289	243	7	0	0

- Molecule 70 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bs	50	Total	C	N	O	S	0	0
			394	247	80	60	7		

- Molecule 71 is a protein called 60S ribosomal protein L19, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BT	196	Total	C	N	O	S	0	0
			1590	974	349	259	8		

- Molecule 72 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bt	97	Total	C	N	O	S	0	0
			801	507	159	130	5		

- Molecule 73 is a protein called 60S ribosomal protein L21E, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BU	157	Total	C	N	O	S	0	0
			1247	793	245	203	6		

- Molecule 74 is a protein called 60S ribosomal protein L5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bu	247	Total	C	N	O	S	0	0
			1964	1234	378	347	5		

- Molecule 75 is a protein called 60S ribosomal protein L22, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BV	122	Total	C	N	O	S	0	0
			979	629	179	168	3		

- Molecule 76 is a protein called 60S ribosomal protein L6, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Bv	143	Total	C	N	O	S	0	0
			1101	699	202	197	3		

- Molecule 77 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	BW	136	1029	651	195	178	5	0	0

- Molecule 78 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	BX	120	982	624	185	171	2	0	0

- Molecule 79 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
79	Bw	230	1872	1190	362	312	8	0	0

- Molecule 80 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
80	Bx	235	1874	1178	369	321	6	0	0

- Molecule 81 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
81	BY	64	550	358	108	79	5	0	0

- Molecule 82 is a protein called 60S ribosomal protein L9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
82	By	186	1515	961	281	269	4	0	0

- Molecule 83 is a protein called 60S ribosomal protein L26, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
83	BZ	122	993	614	210	164	5	0	0

- Molecule 84 is a protein called 60S ribosomal protein L32, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
84	Bi	131	1075	678	217	176	4	0	0

- Molecule 85 is a protein called 40S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
85	BP	152	1237	784	240	209	4	0	0

- Molecule 86 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
86	AF	115	868	531	156	173	8	0	0

- Molecule 87 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
87	BA	67	67	67	0
87	AA	88	88	88	0
87	BB	61	61	61	0
87	BG	5	5	5	0
87	BE	1	1	1	0
87	BD	1	1	1	0
87	BC	1	1	1	0
87	AH	1	1	1	0
87	AO	2	2	2	0
87	A0	1	1	1	0
87	Be	2	2	2	0
87	Bf	1	1	1	0

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Mol	Chain	Residues	Atoms	AltConf
87	BN	1	Total Mg 1 1	0
87	BR	1	Total Mg 1 1	0
87	BW	1	Total Mg 1 1	0

- Molecule 88 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
88	BA	8	Total K 8 8	0
88	AA	25	Total K 25 25	0
88	BB	12	Total K 12 12	0
88	AH	1	Total K 1 1	0
88	BZ	1	Total K 1 1	0

- Molecule 89 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	AltConf
89	BA	10	Total Na 10 10	0
89	AA	14	Total Na 14 14	0
89	BB	14	Total Na 14 14	0
89	A3	1	Total Na 1 1	0
89	BK	1	Total Na 1 1	0

- Molecule 90 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
90	A9	1	Total Zn 1 1	0
90	Bn	1	Total Zn 1 1	0

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Mol	Chain	Residues	Atoms		AltConf
90	Bo	1	Total 1	Zn 1	0
90	Bs	1	Total 1	Zn 1	0

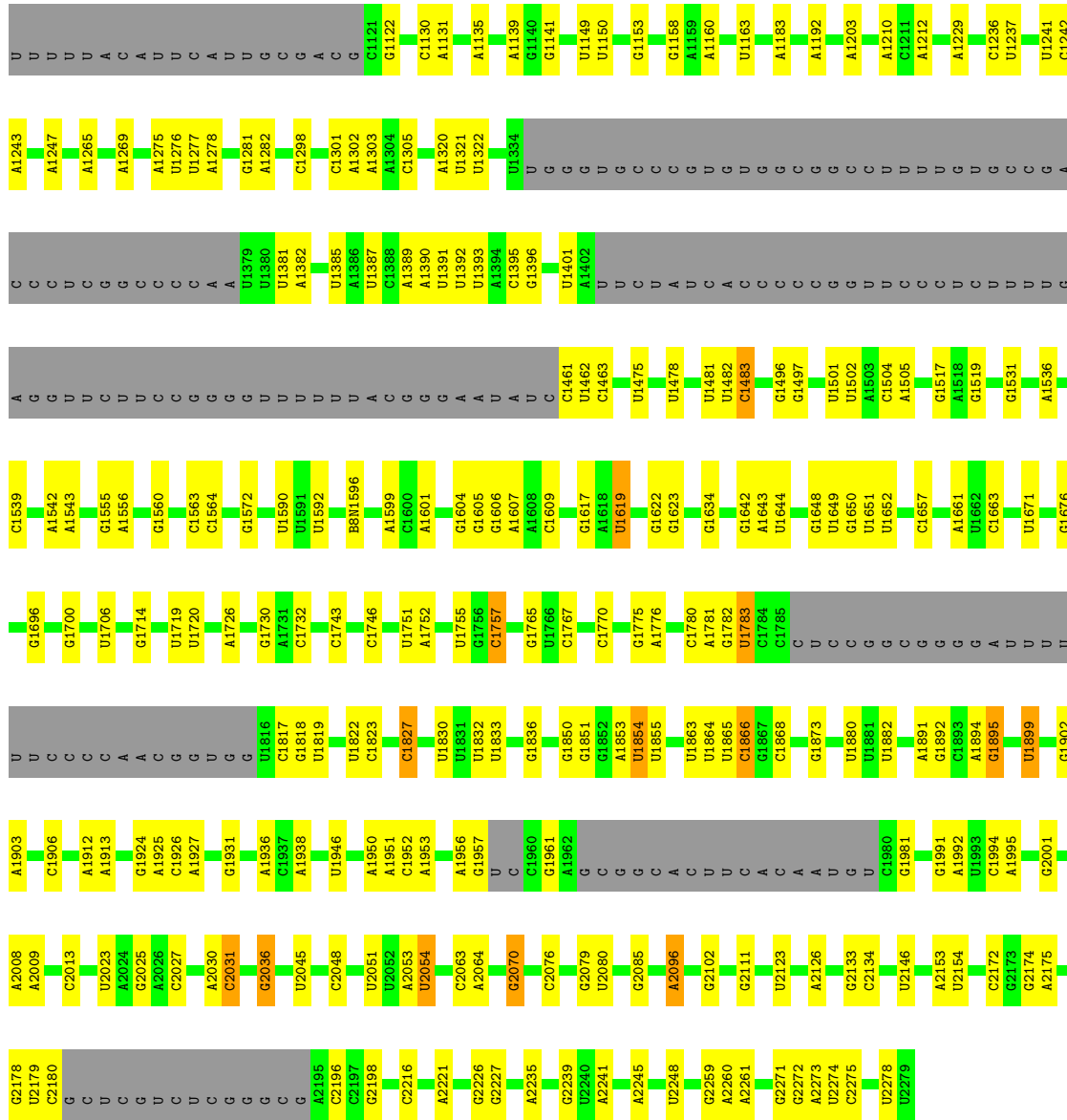
- Molecule 91 is water.

Mol	Chain	Residues	Atoms		AltConf
91	BA	53	Total 53	O 53	0
91	AA	40	Total 40	O 40	0
91	BB	61	Total 61	O 61	0
91	BH	2	Total 2	O 2	0
91	BG	4	Total 4	O 4	0
91	BE	1	Total 1	O 1	0
91	BC	1	Total 1	O 1	0
91	A8	1	Total 1	O 1	0
91	AH	1	Total 1	O 1	0
91	AK	1	Total 1	O 1	0
91	AV	3	Total 3	O 3	0
91	A2	1	Total 1	O 1	0
91	AG	1	Total 1	O 1	0
91	Bb	3	Total 3	O 3	0
91	Bd	1	Total 1	O 1	0
91	Be	7	Total 7	O 7	0
91	Bj	1	Total 1	O 1	0

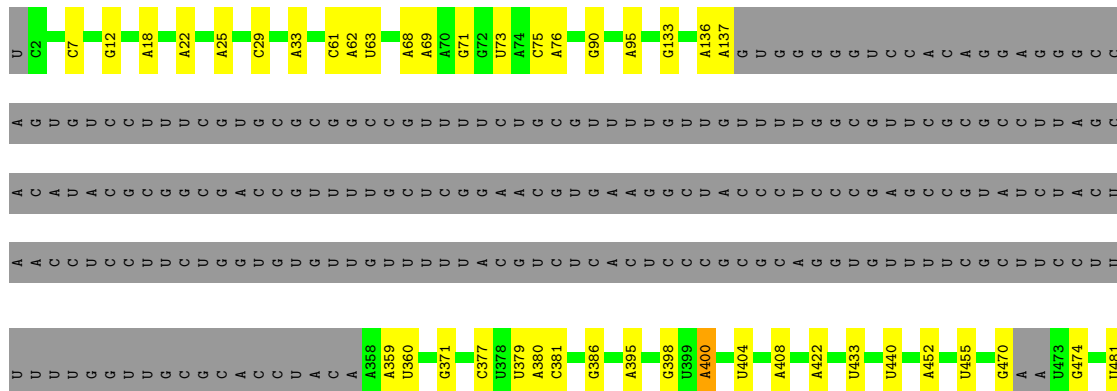
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Mol	Chain	Residues	Atoms		AltConf
91	BK	1	Total 1	O 1	0
91	BN	1	Total 1	O 1	0
91	Bn	1	Total 1	O 1	0
91	BQ	2	Total 2	O 2	0
91	Br	1	Total 1	O 1	0
91	Bi	1	Total 1	O 1	0

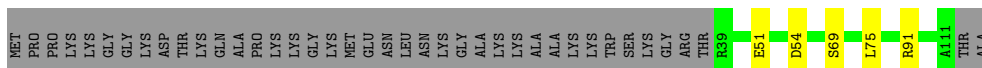


● Molecule 3: LSub rRNA





- Molecule 25: 40S ribosomal protein S25



- Molecule 26: 40S ribosomal protein S26



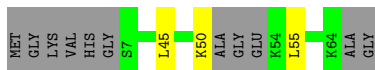
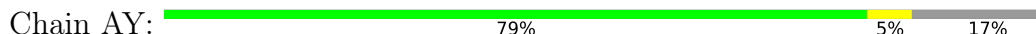
- Molecule 27: 40S ribosomal protein S27, putative



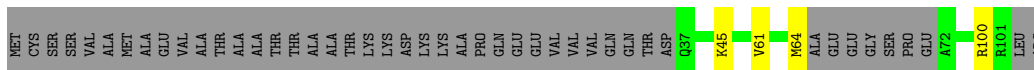
- Molecule 28: 40S ribosomal protein S3, putative



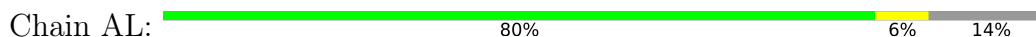
- Molecule 29: 40S ribosomal protein S30

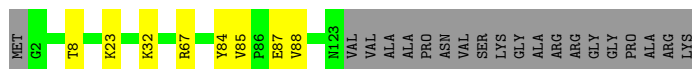


- Molecule 30: 40S ribosomal protein S33, putative

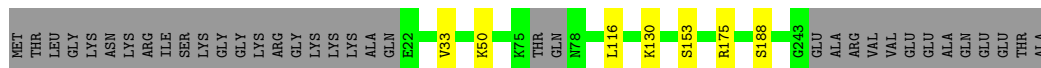
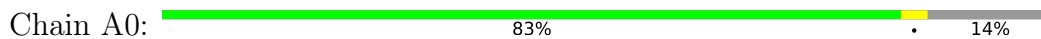


- Molecule 31: 40S ribosomal protein S17, putative





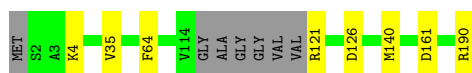
- Molecule 32: 40S ribosomal protein S3a



- Molecule 33: 40S ribosomal protein S4



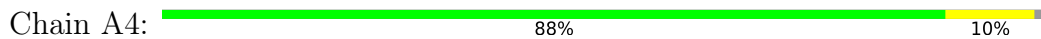
- Molecule 34: 40S ribosomal protein S5, putative



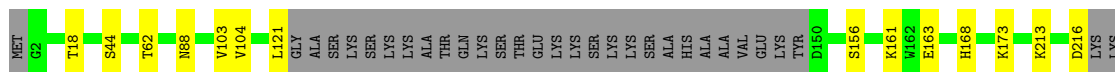
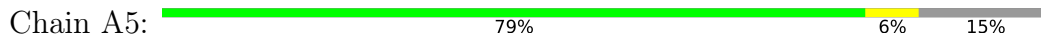
- Molecule 35: 40S ribosomal protein S6



- Molecule 36: 40S ribosomal protein S7



- Molecule 37: 40S ribosomal protein S8

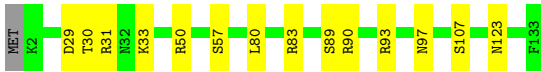


- Molecule 38: Probable 40S ribosomal protein S9



- Molecule 45: 60S ribosomal protein L27

Chain Ba: 89% 11%



- Molecule 46: 60S ribosomal protein L27a

Chain Bb: 94% 5%



- Molecule 47: 60S ribosomal protein L28, putative

Chain Bc: 95%



- Molecule 48: 60S ribosomal protein L29

Chain Bd: 89% 6% 6%



- Molecule 49: 60S ribosomal protein L2, putative

Chain Be: 95%



- Molecule 50: Ribosomal protein L41

Chain Bz: 94% 6%

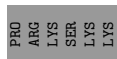
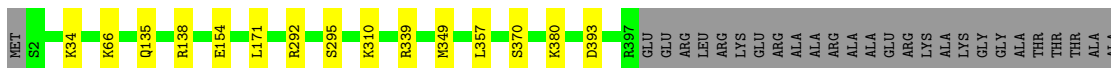
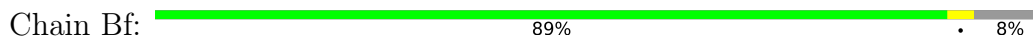


- Molecule 51: 60S ribosomal protein L30

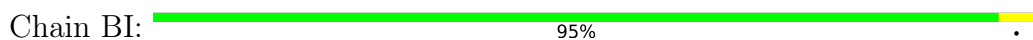
Chain Bg: 82% 6% 12%



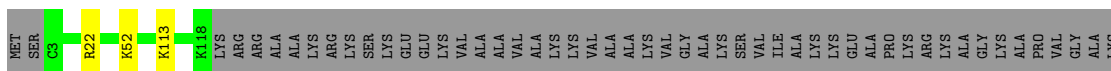
- Molecule 52: Ribosomal protein L3, mitochondrial, putative



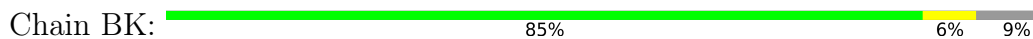
- Molecule 53: 60S ribosomal protein L18



- Molecule 54: 60S ribosomal protein L34, putative



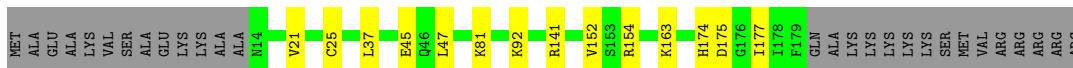
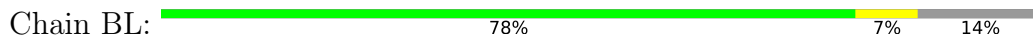
- Molecule 55: 60S ribosomal protein L10, putative



- Molecule 56: 60S ribosomal protein L35, putative



- Molecule 57: 60S ribosomal protein L11, putative



- Molecule 58: 60S ribosomal protein L35A, putative

Chain Bl:  94%



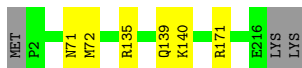
- Molecule 59: Ribosomal protein L36, putative

Chain Bm:  86%



- Molecule 60: 60S ribosomal protein L13

Chain BN:  96%



- Molecule 61: Ribosomal protein L37

Chain Bn:  90%



- Molecule 62: 60S ribosomal protein L13a, putative

Chain BO:  98%




- Molecule 63: 60S ribosomal protein L37a, putative

Chain Bo:  92%



- Molecule 64: 60S ribosomal protein L38, putative

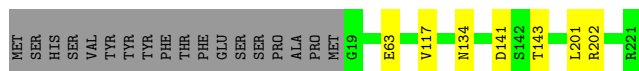
Chain Bp:  84%



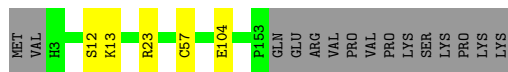
- Molecule 65: 60S ribosomal protein L39, putative



• Molecule 66: Ribosomal protein L15



• Molecule 67: 60S ribosomal protein L17, putative



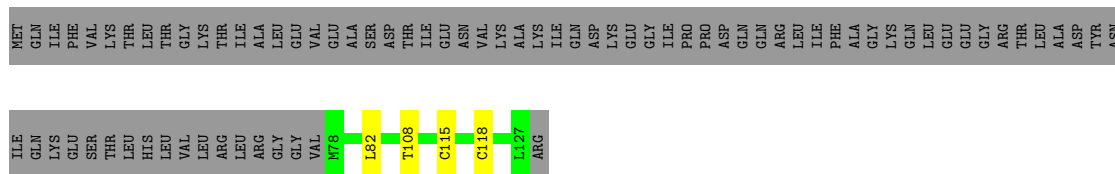
• Molecule 68: 60S ribosomal protein L4



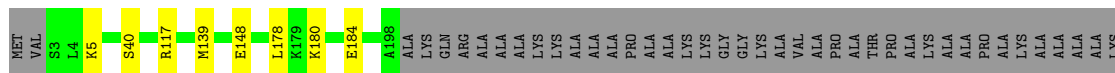
• Molecule 69: 60S ribosomal protein L18a



• Molecule 70: Ubiquitin-60S ribosomal protein L40

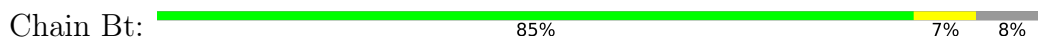


• Molecule 71: 60S ribosomal protein L19, putative



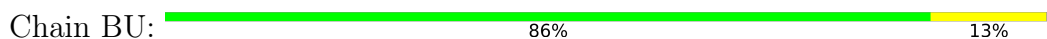
VAL
ALA
PRO
ALA
LYS
ALA
ALA
PRO
ALA
ALA
ALA
ALA
SER
PRO
ALA
GLY
LYS
LYS
ALA
ALA
GLY
LYS
LYS

- Molecule 72: 60S ribosomal protein L44



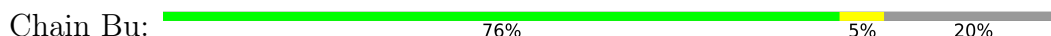
MET
V2
E15
K32
K61
S75
N76
C77
R87
K98
THR
GLY
LYS
ASN
LYS
ASP
PRO
THR
TRP

- Molecule 73: 60S ribosomal protein L21E, putative



MET
V2
C9
K21
V24
N33
V64
K87
C90
K98
F115
K119
K120
L125
K128
K129
V130
K141
K142
V145
R149
D152
M156
I157
P158
TYR

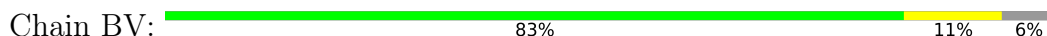
- Molecule 74: 60S ribosomal protein L5, putative



MET
THR
PHE
VAL
K45
R36
E73
S80
T93
L113
K170
K199
K215
Q216
N224
PRO
ASP
GLU
LYS
THR
CYS
GLN
PHE
SER
LYS
PHE
ILE
ALA
ALA
LYS
V240
S241
M248
T261
K262
R263
K266
LYS
GLU
ARG
PRO
ALA
GLU
LYS
PRO
LYS

TYR
ASN
THR
VAL
LEU
THR
GLY
ALA
GLU
LYS
LYS
ALA
ALA
LYS
ALA
VAL
ALA
VAL
ILE
GLU
ARG
ILE
ASP
ARG
ALA
LYS

- Molecule 75: 60S ribosomal protein L22, putative



MET
V2
R15
Q16
R17
V25
C30
S35
S66
M72
N75
S78
I79
T80
T81
T82
L93
D102
M123
ILE
GLN
ASP
GLN
GLU
GLU
ALA

- Molecule 76: 60S ribosomal protein L6, putative



MET
PRO
ALA
THR
LYS
ALA
VAL
GLU
LYS
LYS
LYS
K15
V16
S17
S24
T34
K56
T86
R87
V88
D89
L90
K104
R105
E106
LYS
LYS
GLU
LYS
LYS
ARG
VAL
LYS
SER
GLU
GLU
GLY
PHE
MET
GLY
LYS
ASP
ASP
LYS
LYS
LYS
ALA
GLU
SER
LYS
LYS

THR
SER
LYS
ALA
ALA
PRO
LYS
GLY
T142
V178
K191
W192

- Molecule 77: 60S ribosomal protein L23, putative




MET
GLY
LYS
D4
K5
A6
N7
T31
T133
V139

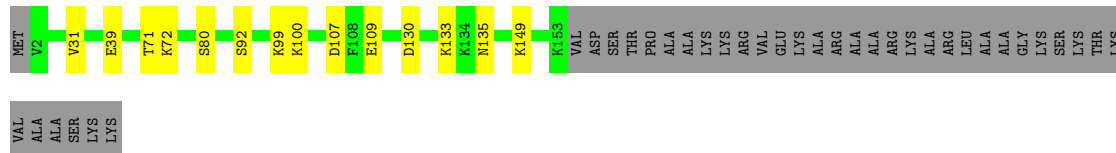
- Molecule 84: 60S ribosomal protein L32, putative

Chain Bi:  98%



- Molecule 85: 40S ribosomal protein L14, putative

Chain BP:  73% 7% 20%



- Molecule 86: 40S ribosomal protein S12

Chain AF:  72% 8% 20%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	459985	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 ($e^-/\text{\AA}^2$)	1.17	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	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: 7MG, 5MC, PSU, NA, K, B8N, A2M, OMG, OMU, ZN, OMC, MG, 1MA, MA6

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	BA	0.41	0/37519	0.85	40/58462 (0.1%)
2	AA	0.49	0/44961	0.90	88/70031 (0.1%)
3	BB	0.44	0/25592	0.85	18/39885 (0.0%)
4	BH	0.39	0/2833	0.83	3/4410 (0.1%)
5	BG	0.41	0/4383	0.83	4/6835 (0.1%)
6	BF	0.35	0/1604	0.89	2/2487 (0.1%)
7	BE	0.41	0/4442	0.91	11/6910 (0.2%)
8	BD	0.36	0/2830	0.74	0/4410
9	BC	0.36	0/3662	0.78	0/5700
10	AB	0.41	0/450	0.95	0/698
11	AQ	0.28	0/809	0.60	0/1091
12	A8	0.27	0/468	0.55	0/619
13	A9	0.30	0/582	0.59	0/773
14	Az	0.29	0/820	0.62	0/1100
15	AH	0.29	0/1006	0.61	0/1349
16	AI	0.29	0/986	0.51	0/1321
17	AJ	0.29	0/1035	0.53	0/1386
18	AK	0.29	0/1161	0.55	0/1561
19	AM	0.27	0/1161	0.55	0/1554
20	AO	0.27	0/1245	0.52	0/1665
21	AP	0.30	0/1723	0.52	0/2328
22	AR	0.27	0/676	0.48	0/919
23	AS	0.28	0/1117	0.54	0/1495
24	AT	0.28	0/1050	0.52	0/1395
25	AU	0.27	0/581	0.57	1/776 (0.1%)
26	AV	0.33	0/846	0.64	0/1132
27	AW	0.30	0/674	0.58	0/904
28	AX	0.27	0/1674	0.54	0/2236
29	AY	0.29	0/453	0.52	0/596
30	AZ	0.29	0/448	0.62	0/595
31	AL	0.26	0/957	0.50	0/1282
32	A0	0.28	0/1815	0.54	0/2440

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	A1	0.28	0/2096	0.56	1/2819 (0.0%)
34	A2	0.27	0/1486	0.51	0/1997
35	A3	0.27	0/1893	0.61	1/2533 (0.0%)
36	A4	0.27	0/1634	0.52	0/2208
37	A5	0.28	0/1494	0.57	0/2004
38	A6	0.28	0/1507	0.54	0/2023
39	A7	0.26	0/2428	0.52	0/3311
40	AC	0.30	0/1682	0.50	0/2275
41	AD	0.29	0/837	0.49	0/1129
42	AE	0.30	0/1274	0.56	0/1714
43	AG	0.28	0/1225	0.53	0/1642
44	Bh	0.26	0/1270	0.57	0/1696
45	Ba	0.29	0/1105	0.55	0/1472
46	Bb	0.26	0/1165	0.53	0/1554
47	Bc	0.25	0/1179	0.52	0/1573
48	Bd	0.25	0/558	0.52	0/747
49	Be	0.29	0/1948	0.57	0/2621
50	Bz	0.28	0/288	0.70	0/374
51	Bg	0.28	0/718	0.48	0/969
52	Bf	0.27	0/3244	0.54	0/4360
53	BI	0.25	0/1543	0.55	0/2059
54	Bj	0.26	0/977	0.59	0/1304
55	BK	0.27	0/1620	0.56	0/2171
56	Bk	0.26	0/1018	0.57	0/1346
57	BL	0.28	0/1346	0.53	0/1800
58	Bl	0.28	0/1187	0.57	0/1592
59	Bm	0.26	0/796	0.59	1/1057 (0.1%)
60	BN	0.26	0/1793	0.55	0/2391
61	Bn	0.27	0/690	0.64	0/920
62	BO	0.26	0/1832	0.53	0/2446
63	Bo	0.30	0/711	0.58	0/946
64	Bp	0.27	0/635	0.55	0/844
65	Bq	0.26	0/471	0.53	0/626
66	BQ	0.27	0/1755	0.59	0/2346
67	BR	0.26	0/1244	0.52	0/1669
68	Br	0.25	0/2936	0.54	0/3941
69	BS	0.28	0/1500	0.54	0/2018
70	Bs	0.29	0/400	0.58	0/531
71	BT	0.27	0/1607	0.59	0/2130
72	Bt	0.27	0/815	0.53	0/1077
73	BU	0.28	0/1276	0.55	0/1716
74	Bu	0.28	0/1999	0.56	0/2684
75	BV	0.29	0/995	0.60	0/1329

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Bv	0.27	0/1120	0.51	0/1511
77	BW	0.29	0/1046	0.54	0/1408
78	BX	0.26	0/999	0.55	0/1343
79	Bw	0.27	0/1907	0.51	0/2556
80	Bx	0.25	0/1901	0.54	0/2557
81	BY	0.30	0/570	0.58	0/766
82	By	0.27	0/1536	0.55	0/2065
83	BZ	0.26	0/1006	0.61	0/1340
84	Bi	0.27	0/1097	0.55	0/1468
85	BP	0.27	0/1256	0.50	0/1683
86	AF	0.26	0/870	0.53	0/1169
All	All	0.38	0/221048	0.76	170/324175 (0.1%)

There are no bond length outliers.

The worst 5 of 170 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	BB	515	G	P-O3'-C3'	-9.67	108.09	119.70
3	BB	528	U	P-O3'-C3'	-9.66	108.11	119.70
2	AA	878	U	P-O3'-C3'	-9.57	108.21	119.70
3	BB	514	G	P-O3'-C3'	-8.94	108.98	119.70
1	BA	74	C	C2-N1-C1'	8.83	128.52	118.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
11	AQ	98/117 (84%)	96 (98%)	2 (2%)	0	100	100
12	A8	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
13	A9	66/153 (43%)	61 (92%)	5 (8%)	0	100	100
14	Az	98/279 (35%)	84 (86%)	13 (13%)	1 (1%)	15	26
15	AH	132/144 (92%)	118 (89%)	14 (11%)	0	100	100
16	AI	115/152 (76%)	112 (97%)	3 (3%)	0	100	100
17	AJ	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
18	AK	140/149 (94%)	134 (96%)	6 (4%)	0	100	100
19	AM	139/153 (91%)	134 (96%)	5 (4%)	0	100	100
20	AO	152/167 (91%)	147 (97%)	5 (3%)	0	100	100
21	AP	216/266 (81%)	203 (94%)	12 (6%)	1 (0%)	29	46
22	AR	87/194 (45%)	85 (98%)	2 (2%)	0	100	100
23	AS	138/143 (96%)	128 (93%)	10 (7%)	0	100	100
24	AT	127/137 (93%)	118 (93%)	9 (7%)	0	100	100
25	AU	71/113 (63%)	67 (94%)	4 (6%)	0	100	100
26	AV	101/111 (91%)	94 (93%)	7 (7%)	0	100	100
27	AW	83/86 (96%)	80 (96%)	3 (4%)	0	100	100
28	AX	206/214 (96%)	196 (95%)	10 (5%)	0	100	100
29	AY	51/66 (77%)	50 (98%)	1 (2%)	0	100	100
30	AZ	54/103 (52%)	52 (96%)	2 (4%)	0	100	100
31	AL	120/142 (84%)	115 (96%)	5 (4%)	0	100	100
32	A0	216/256 (84%)	211 (98%)	5 (2%)	0	100	100
33	A1	260/273 (95%)	245 (94%)	15 (6%)	0	100	100
34	A2	179/190 (94%)	177 (99%)	2 (1%)	0	100	100
35	A3	236/250 (94%)	228 (97%)	8 (3%)	0	100	100
36	A4	196/202 (97%)	187 (95%)	9 (5%)	0	100	100
37	A5	183/220 (83%)	176 (96%)	7 (4%)	0	100	100
38	A6	177/190 (93%)	173 (98%)	4 (2%)	0	100	100
39	A7	305/318 (96%)	294 (96%)	11 (4%)	0	100	100
40	AC	206/277 (74%)	200 (97%)	6 (3%)	0	100	100
41	AD	97/172 (56%)	94 (97%)	3 (3%)	0	100	100
42	AE	151/174 (87%)	143 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	AG	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
44	Bh	152/188 (81%)	142 (93%)	10 (7%)	0	100	100
45	Ba	130/133 (98%)	129 (99%)	1 (1%)	0	100	100
46	Bb	142/145 (98%)	136 (96%)	6 (4%)	0	100	100
47	Bc	142/146 (97%)	139 (98%)	3 (2%)	0	100	100
48	Bd	65/71 (92%)	63 (97%)	2 (3%)	0	100	100
49	Be	253/260 (97%)	247 (98%)	6 (2%)	0	100	100
50	Bz	30/34 (88%)	30 (100%)	0	0	100	100
51	Bg	90/105 (86%)	90 (100%)	0	0	100	100
52	Bf	394/429 (92%)	388 (98%)	6 (2%)	0	100	100
53	BI	189/193 (98%)	183 (97%)	6 (3%)	0	100	100
54	Bj	114/170 (67%)	111 (97%)	3 (3%)	0	100	100
55	BK	190/213 (89%)	182 (96%)	8 (4%)	0	100	100
56	Bk	121/127 (95%)	115 (95%)	5 (4%)	1 (1%)	19	33
57	BL	164/194 (84%)	155 (94%)	9 (6%)	0	100	100
58	Bl	142/149 (95%)	136 (96%)	6 (4%)	0	100	100
59	Bm	96/109 (88%)	95 (99%)	1 (1%)	0	100	100
60	BN	213/218 (98%)	202 (95%)	11 (5%)	0	100	100
61	Bn	78/84 (93%)	76 (97%)	2 (3%)	0	100	100
62	BO	219/222 (99%)	218 (100%)	1 (0%)	0	100	100
63	Bo	87/93 (94%)	83 (95%)	4 (5%)	0	100	100
64	Bp	75/82 (92%)	71 (95%)	4 (5%)	0	100	100
65	Bq	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
66	BQ	201/221 (91%)	197 (98%)	4 (2%)	0	100	100
67	BR	149/166 (90%)	147 (99%)	2 (1%)	0	100	100
68	Br	365/374 (98%)	352 (96%)	13 (4%)	0	100	100
69	BS	176/179 (98%)	170 (97%)	6 (3%)	0	100	100
70	Bs	48/128 (38%)	46 (96%)	2 (4%)	0	100	100
71	BT	194/260 (75%)	186 (96%)	8 (4%)	0	100	100
72	Bt	95/106 (90%)	91 (96%)	4 (4%)	0	100	100
73	BU	155/159 (98%)	143 (92%)	11 (7%)	1 (1%)	25	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
74	Bu	243/308 (79%)	234 (96%)	9 (4%)	0	100	100
75	BV	120/130 (92%)	111 (92%)	8 (7%)	1 (1%)	19	33
76	Bv	139/192 (72%)	134 (96%)	5 (4%)	0	100	100
77	BW	134/139 (96%)	132 (98%)	2 (2%)	0	100	100
78	BX	118/164 (72%)	114 (97%)	4 (3%)	0	100	100
79	Bw	228/257 (89%)	223 (98%)	5 (2%)	0	100	100
80	Bx	231/276 (84%)	220 (95%)	11 (5%)	0	100	100
81	BY	62/125 (50%)	60 (97%)	2 (3%)	0	100	100
82	By	184/189 (97%)	175 (95%)	9 (5%)	0	100	100
83	BZ	120/143 (84%)	118 (98%)	2 (2%)	0	100	100
84	Bi	129/132 (98%)	125 (97%)	4 (3%)	0	100	100
85	BP	150/189 (79%)	144 (96%)	6 (4%)	0	100	100
86	AF	111/144 (77%)	107 (96%)	3 (3%)	1 (1%)	17	29
All	All	11215/13146 (85%)	10789 (96%)	420 (4%)	6 (0%)	54	71

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	Az	169	THR
56	Bk	6	LYS
73	BU	33	ASN
75	BV	17	ARG
86	AF	122	SER

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	
11	AQ	90/104 (86%)	82 (91%)	8 (9%)	9	17
12	A8	49/50 (98%)	48 (98%)	1 (2%)	55	77
13	A9	62/126 (49%)	58 (94%)	4 (6%)	17	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	Az	86/216 (40%)	73 (85%)	13 (15%)	3	4
15	AH	101/112 (90%)	95 (94%)	6 (6%)	19	35
16	AI	100/128 (78%)	93 (93%)	7 (7%)	15	27
17	AJ	108/109 (99%)	102 (94%)	6 (6%)	21	38
18	AK	117/124 (94%)	106 (91%)	11 (9%)	8	15
19	AM	123/133 (92%)	116 (94%)	7 (6%)	20	37
20	AO	127/137 (93%)	123 (97%)	4 (3%)	40	64
21	AP	181/204 (89%)	169 (93%)	12 (7%)	16	30
22	AR	73/150 (49%)	69 (94%)	4 (6%)	21	39
23	AS	115/118 (98%)	105 (91%)	10 (9%)	10	18
24	AT	108/116 (93%)	104 (96%)	4 (4%)	34	57
25	AU	64/94 (68%)	60 (94%)	4 (6%)	18	32
26	AV	90/97 (93%)	87 (97%)	3 (3%)	38	61
27	AW	74/75 (99%)	71 (96%)	3 (4%)	30	53
28	AX	176/180 (98%)	167 (95%)	9 (5%)	24	42
29	AY	47/53 (89%)	44 (94%)	3 (6%)	17	31
30	AZ	49/84 (58%)	45 (92%)	4 (8%)	11	20
31	AL	96/122 (79%)	88 (92%)	8 (8%)	11	20
32	A0	190/218 (87%)	183 (96%)	7 (4%)	34	57
33	A1	221/231 (96%)	206 (93%)	15 (7%)	16	28
34	A2	157/160 (98%)	149 (95%)	8 (5%)	24	42
35	A3	191/207 (92%)	175 (92%)	16 (8%)	11	19
36	A4	173/187 (92%)	152 (88%)	21 (12%)	5	8
37	A5	147/180 (82%)	133 (90%)	14 (10%)	8	15
38	A6	159/166 (96%)	149 (94%)	10 (6%)	18	32
39	A7	260/267 (97%)	236 (91%)	24 (9%)	9	16
40	AC	183/243 (75%)	174 (95%)	9 (5%)	25	44
41	AD	87/131 (66%)	79 (91%)	8 (9%)	9	16
42	AE	137/156 (88%)	128 (93%)	9 (7%)	16	30
43	AG	130/131 (99%)	123 (95%)	7 (5%)	22	40
44	Bh	133/162 (82%)	122 (92%)	11 (8%)	11	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	Ba	115/117 (98%)	101 (88%)	14 (12%)	5	8
46	Bb	115/116 (99%)	108 (94%)	7 (6%)	18	34
47	Bc	128/130 (98%)	123 (96%)	5 (4%)	32	55
48	Bd	56/59 (95%)	52 (93%)	4 (7%)	14	26
49	Be	191/204 (94%)	185 (97%)	6 (3%)	40	64
50	Bz	29/31 (94%)	29 (100%)	0	100	100
51	Bg	81/92 (88%)	75 (93%)	6 (7%)	13	25
52	Bf	337/360 (94%)	322 (96%)	15 (4%)	27	48
53	BI	163/165 (99%)	156 (96%)	7 (4%)	29	50
54	Bj	99/137 (72%)	96 (97%)	3 (3%)	41	65
55	BK	169/185 (91%)	157 (93%)	12 (7%)	14	26
56	Bk	104/114 (91%)	97 (93%)	7 (7%)	16	29
57	BL	142/167 (85%)	128 (90%)	14 (10%)	8	13
58	Bl	122/126 (97%)	118 (97%)	4 (3%)	38	61
59	Bm	81/90 (90%)	78 (96%)	3 (4%)	34	57
60	BN	185/188 (98%)	179 (97%)	6 (3%)	39	63
61	Bn	68/71 (96%)	64 (94%)	4 (6%)	19	35
62	BO	194/195 (100%)	191 (98%)	3 (2%)	65	83
63	Bo	72/76 (95%)	69 (96%)	3 (4%)	30	51
64	Bp	72/77 (94%)	64 (89%)	8 (11%)	6	10
65	Bq	46/47 (98%)	44 (96%)	2 (4%)	29	50
66	BQ	176/193 (91%)	169 (96%)	7 (4%)	31	53
67	BR	129/144 (90%)	124 (96%)	5 (4%)	32	55
68	Br	304/310 (98%)	293 (96%)	11 (4%)	35	58
69	BS	159/160 (99%)	152 (96%)	7 (4%)	28	49
70	Bs	41/111 (37%)	37 (90%)	4 (10%)	8	14
71	BT	153/198 (77%)	145 (95%)	8 (5%)	23	41
72	Bt	87/95 (92%)	80 (92%)	7 (8%)	12	21
73	BU	132/134 (98%)	113 (86%)	19 (14%)	3	5
74	Bu	199/247 (81%)	185 (93%)	14 (7%)	15	27
75	BV	100/116 (86%)	87 (87%)	13 (13%)	4	7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
76	Bv	119/160 (74%)	108 (91%)	11 (9%)	9 16
77	BW	106/108 (98%)	101 (95%)	5 (5%)	26 46
78	BX	107/136 (79%)	97 (91%)	10 (9%)	9 15
79	Bw	193/213 (91%)	188 (97%)	5 (3%)	46 70
80	Bx	199/229 (87%)	182 (92%)	17 (8%)	10 19
81	BY	57/102 (56%)	54 (95%)	3 (5%)	22 40
82	By	169/172 (98%)	158 (94%)	11 (6%)	17 31
83	BZ	108/125 (86%)	102 (94%)	6 (6%)	21 38
84	Bi	116/117 (99%)	114 (98%)	2 (2%)	60 81
85	BP	132/158 (84%)	118 (89%)	14 (11%)	6 12
86	AF	93/120 (78%)	83 (89%)	10 (11%)	6 11
All	All	9652/11066 (87%)	9040 (94%)	612 (6%)	21 32

5 of 612 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
71	BT	180	LYS
82	By	82	VAL
73	BU	87	LYS
71	BT	178	LEU
76	Bv	34	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
46	Bb	116	GLN
59	Bm	66	GLN
77	BW	30	ASN
38	A6	64	ASN
36	A4	115	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	BA	1585/1920 (82%)	300 (18%)	9 (0%)
10	AB	17/19 (89%)	7 (41%)	1 (5%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	AA	1899/2282 (83%)	424 (22%)	13 (0%)
3	BB	1113/1536 (72%)	209 (18%)	5 (0%)
4	BH	116/136 (85%)	27 (23%)	0
5	BG	182/183 (99%)	30 (16%)	1 (0%)
6	BF	66/78 (84%)	17 (25%)	1 (1%)
7	BE	185/216 (85%)	47 (25%)	4 (2%)
8	BD	118/119 (99%)	15 (12%)	0
9	BC	157/209 (75%)	22 (14%)	0
All	All	5438/6698 (81%)	1098 (20%)	34 (0%)

5 of 1098 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	BA	8	G
1	BA	28	A
1	BA	33	C
1	BA	42	A
1	BA	45	A

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	BF	56	A
7	BE	123	U
7	BE	186	U
2	AA	324	A
2	AA	291	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	A2M	BB	646	3	18,25,26	3.63	7 (38%)	18,36,39	3.76	4 (22%)
3	OMU	BB	1093	3	19,22,23	3.01	8 (42%)	26,31,34	1.73	5 (19%)
2	OMU	AA	57	2	19,22,23	2.96	8 (42%)	26,31,34	1.72	5 (19%)
1	PSU	BA	1129	1	18,21,22	4.43	7 (38%)	22,30,33	1.82	5 (22%)
1	OMC	BA	1006	1	19,22,23	2.91	8 (42%)	26,31,34	0.74	0
3	OMU	BB	73	3	19,22,23	2.96	8 (42%)	26,31,34	1.69	5 (19%)
3	PSU	BB	1398	87,3	18,21,22	4.41	8 (44%)	22,30,33	1.86	6 (27%)
1	A2M	BA	743	1,3	18,25,26	3.62	8 (44%)	18,36,39	3.92	4 (22%)
3	OMG	BB	1062	3	18,26,27	2.51	8 (44%)	19,38,41	1.56	4 (21%)
1	PSU	BA	1086	1,87,88	18,21,22	4.38	7 (38%)	22,30,33	1.83	5 (22%)
2	PSU	AA	1619	2,13	18,21,22	4.38	8 (44%)	22,30,33	1.64	4 (18%)
2	OMG	AA	1700	2	18,26,27	2.43	8 (44%)	19,38,41	1.65	5 (26%)
3	PSU	BB	680	87,3	18,21,22	4.39	7 (38%)	22,30,33	1.83	5 (22%)
1	PSU	BA	737	1,87	18,21,22	4.39	7 (38%)	22,30,33	1.77	5 (22%)
2	OMU	AA	36	2	19,22,23	2.95	8 (42%)	26,31,34	1.86	5 (19%)
9	OMG	BC	75	9	18,26,27	2.55	8 (44%)	19,38,41	1.56	4 (21%)
2	B8N	AA	1596	2	24,29,30	3.01	6 (25%)	29,42,45	1.72	5 (17%)
2	A2M	AA	2096	2	18,25,26	3.62	7 (38%)	18,36,39	3.87	5 (27%)
3	PSU	BB	1076	3	18,21,22	4.41	7 (38%)	22,30,33	1.94	5 (22%)
1	PSU	BA	1609	1	18,21,22	4.44	7 (38%)	22,30,33	1.84	5 (22%)
2	A2M	AA	56	2,89	18,25,26	3.63	7 (38%)	18,36,39	3.72	4 (22%)
2	PSU	AA	61	2	18,21,22	4.46	7 (38%)	22,30,33	1.87	5 (22%)
2	OMG	AA	1531	2	18,26,27	2.42	8 (44%)	19,38,41	1.60	4 (21%)
3	OMU	BB	685	3	19,22,23	2.98	8 (42%)	26,31,34	1.73	5 (19%)
9	OMU	BC	7	1,9	19,22,23	2.99	8 (42%)	26,31,34	1.72	5 (19%)
9	A2M	BC	43	9	18,25,26	3.59	7 (38%)	18,36,39	3.72	4 (22%)
3	A2M	BB	588	1,3	18,25,26	3.63	8 (44%)	18,36,39	3.78	5 (27%)
2	OMG	AA	1931	2,89	18,26,27	2.51	8 (44%)	19,38,41	1.62	5 (26%)
2	OMU	AA	2054	2	19,22,23	2.97	8 (42%)	26,31,34	1.73	4 (15%)
9	A2M	BC	41	9	18,25,26	3.62	8 (44%)	18,36,39	3.77	4 (22%)
2	MA6	AA	2261	2	18,26,27	1.17	1 (5%)	19,38,41	3.01	2 (10%)
2	OMU	AA	1652	2	19,22,23	2.99	8 (42%)	26,31,34	1.72	5 (19%)
3	A2M	BB	622	1,3	18,25,26	3.59	7 (38%)	18,36,39	3.76	4 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMG	AA	1895	2,87	18,26,27	2.49	8 (44%)	19,38,41	1.55	4 (21%)
1	OMG	BA	1267	1	18,26,27	2.49	8 (44%)	19,38,41	1.63	5 (26%)
3	OMU	BB	578	3,89	19,22,23	2.95	8 (42%)	26,31,34	1.73	4 (15%)
1	PSU	BA	1009	1	18,21,22	4.39	7 (38%)	22,30,33	1.85	5 (22%)
1	OMC	BA	1608	1	19,22,23	2.95	8 (42%)	26,31,34	0.96	2 (7%)
1	OMU	BA	1742	1	19,22,23	2.96	8 (42%)	26,31,34	1.71	4 (15%)
1	OMC	BA	760	1	19,22,23	2.91	8 (42%)	26,31,34	0.72	0
3	A2M	BB	609	3	18,25,26	3.62	7 (38%)	18,36,39	3.67	4 (22%)
3	PSU	BB	522	3	18,21,22	4.42	7 (38%)	22,30,33	1.77	5 (22%)
2	OMG	AA	1517	2	18,26,27	2.53	8 (44%)	19,38,41	1.57	4 (21%)
3	PSU	BB	644	3	18,21,22	4.41	7 (38%)	22,30,33	1.82	5 (22%)
3	PSU	BB	1160	3	18,21,22	4.46	7 (38%)	22,30,33	1.83	5 (22%)
3	OMG	BB	1269	3	18,26,27	2.48	8 (44%)	19,38,41	1.54	5 (26%)
2	OMG	AA	1676	2,88	18,26,27	2.51	8 (44%)	19,38,41	1.56	4 (21%)
1	PSU	BA	452	1	18,21,22	4.46	7 (38%)	22,30,33	1.78	5 (22%)
1	A2M	BA	996	1,89	18,25,26	3.62	7 (38%)	18,36,39	3.68	4 (22%)
3	A2M	BB	545	87,3	18,25,26	3.69	8 (44%)	18,36,39	3.89	5 (27%)
3	OMG	BB	1245	3	18,26,27	2.51	8 (44%)	19,38,41	1.54	4 (21%)
1	A2M	BA	254	1	18,25,26	3.61	8 (44%)	18,36,39	3.77	4 (22%)
3	PSU	BB	615	3	18,21,22	4.42	7 (38%)	22,30,33	1.82	5 (22%)
1	1MA	BA	742	1,87	16,25,26	3.96	4 (25%)	18,37,40	1.75	3 (16%)
3	OMG	BB	71	3	18,26,27	2.52	8 (44%)	19,38,41	1.58	4 (21%)
3	OMC	BB	377	3	19,22,23	2.98	8 (42%)	26,31,34	0.71	0
1	PSU	BA	1248	1	18,21,22	4.44	7 (38%)	22,30,33	1.84	6 (27%)
2	OMU	AA	2154	2	19,22,23	2.98	8 (42%)	26,31,34	1.74	5 (19%)
3	PSU	BB	1409	3	18,21,22	4.47	7 (38%)	22,30,33	1.74	5 (22%)
3	5MC	BB	542	87,3	18,22,23	3.41	7 (38%)	26,32,35	1.08	2 (7%)
1	OMC	BA	1329	1	19,22,23	3.03	8 (42%)	26,31,34	0.78	0
1	PSU	BA	258	1	18,21,22	4.49	7 (38%)	22,30,33	1.78	5 (22%)
1	A2M	BA	927	1	18,25,26	3.62	7 (38%)	18,36,39	3.66	4 (22%)
3	OMC	BB	1264	3	19,22,23	2.95	8 (42%)	26,31,34	0.82	0
3	A2M	BB	1400	87,3	18,25,26	3.61	8 (44%)	18,36,39	3.76	4 (22%)
1	A2M	BA	1024	1	18,25,26	3.58	7 (38%)	18,36,39	3.70	4 (22%)
2	OMC	AA	46	2	19,22,23	2.86	8 (42%)	26,31,34	0.77	0
1	OMG	BA	1605	1	18,26,27	2.52	8 (44%)	19,38,41	1.61	4 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	OMU	BB	1375	3	19,22,23	2.96	8 (42%)	26,31,34	1.71	5 (19%)
3	PSU	BB	455	88,87,3	18,21,22	4.41	7 (38%)	22,30,33	1.84	5 (22%)
2	OMG	AA	2227	2	18,26,27	2.49	8 (44%)	19,38,41	1.56	4 (21%)
9	PSU	BC	74	9	18,21,22	4.49	7 (38%)	22,30,33	1.88	5 (22%)
3	A2M	BB	1201	3	18,25,26	3.61	8 (44%)	18,36,39	3.72	4 (22%)
1	OMU	BA	46	1	19,22,23	2.96	8 (42%)	26,31,34	1.78	5 (19%)
2	PSU	AA	131	2	18,21,22	4.41	7 (38%)	22,30,33	1.74	3 (13%)
1	OMU	BA	916	1	19,22,23	2.96	8 (42%)	26,31,34	1.77	5 (19%)
3	PSU	BB	1429	3	18,21,22	4.37	7 (38%)	22,30,33	1.87	5 (22%)
2	A2M	AA	2153	2	18,25,26	3.64	9 (50%)	18,36,39	3.90	4 (22%)
3	OMC	BB	1175	3	19,22,23	2.95	8 (42%)	26,31,34	0.78	0
2	OMU	AA	1899	2	19,22,23	3.00	8 (42%)	26,31,34	1.78	5 (19%)
2	OMU	AA	2123	2	19,22,23	2.87	7 (36%)	26,31,34	1.81	4 (15%)
3	OMC	BB	1413	3	19,22,23	2.92	8 (42%)	26,31,34	0.76	0
9	A2M	BC	163	1,9	18,25,26	3.59	7 (38%)	18,36,39	3.79	4 (22%)
3	OMG	BB	552	3	18,26,27	2.46	8 (44%)	19,38,41	1.50	4 (21%)
1	PSU	BA	1258	1	18,21,22	4.41	7 (38%)	22,30,33	1.84	5 (22%)
2	MA6	AA	2260	2	18,26,27	1.14	1 (5%)	19,38,41	3.21	2 (10%)
1	OMG	BA	925	1	18,26,27	2.50	8 (44%)	19,38,41	1.54	3 (15%)
2	OMC	AA	2134	2	19,22,23	2.84	8 (42%)	26,31,34	0.72	0
3	PSU	BB	1319	3	18,21,22	4.46	8 (44%)	22,30,33	1.83	6 (27%)
2	PSU	AA	942	2	18,21,22	4.41	7 (38%)	22,30,33	1.68	5 (22%)
3	OMG	BB	1247	3	18,26,27	2.52	8 (44%)	19,38,41	1.52	4 (21%)
1	A2M	BA	1620	1,87,3	18,25,26	3.61	8 (44%)	18,36,39	3.75	4 (22%)
2	PSU	AA	2045	2	18,21,22	4.39	7 (38%)	22,30,33	1.81	5 (22%)
1	OMU	BA	1181	1	19,22,23	2.97	8 (42%)	26,31,34	1.80	5 (19%)
3	PSU	BB	629	3	18,21,22	4.40	7 (38%)	22,30,33	1.79	5 (22%)
3	A2M	BB	400	3	18,25,26	3.62	8 (44%)	18,36,39	3.71	4 (22%)
3	A2M	BB	95	3	18,25,26	3.60	8 (44%)	18,36,39	3.72	4 (22%)
3	OMG	BB	1094	3	18,26,27	2.50	8 (44%)	19,38,41	1.64	4 (21%)
1	A2M	BA	762	1	18,25,26	3.60	7 (38%)	18,36,39	3.79	4 (22%)
1	A2M	BA	746	1	18,25,26	3.65	7 (38%)	18,36,39	3.74	4 (22%)
1	OMU	BA	1448	1	19,22,23	2.97	8 (42%)	26,31,34	1.74	4 (15%)
1	PSU	BA	1614	1,3	18,21,22	4.43	7 (38%)	22,30,33	1.79	5 (22%)
3	OMC	BB	601	3	19,22,23	2.91	8 (42%)	26,31,34	0.71	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PSU	BB	1280	3	18,21,22	4.41	7 (38%)	22,30,33	1.86	6 (27%)
2	A2M	AA	721	2,87	18,25,26	3.64	8 (44%)	18,36,39	3.82	4 (22%)
3	PSU	BB	611	3	18,21,22	4.37	8 (44%)	22,30,33	1.65	4 (18%)
2	PSU	AA	2146	2	18,21,22	4.39	7 (38%)	22,30,33	1.70	4 (18%)
2	OMC	AA	66	2	19,22,23	2.93	8 (42%)	26,31,34	0.77	0
3	OMG	BB	673	3	18,26,27	2.52	8 (44%)	19,38,41	1.61	4 (21%)
2	PSU	AA	1592	2	18,21,22	4.39	7 (38%)	22,30,33	1.85	5 (22%)
1	OMG	BA	1028	1	18,26,27	2.50	8 (44%)	19,38,41	1.52	4 (21%)
2	PSU	AA	1276	2	18,21,22	4.37	7 (38%)	22,30,33	1.87	5 (22%)
3	A2M	BB	1388	3	18,25,26	3.64	7 (38%)	18,36,39	3.88	4 (22%)
3	OMU	BB	1435	3	19,22,23	2.98	8 (42%)	26,31,34	1.72	5 (19%)
1	OMG	BA	1709	1	18,26,27	2.53	8 (44%)	19,38,41	1.56	4 (21%)
1	OMG	BA	1621	1,3	18,26,27	2.46	8 (44%)	19,38,41	1.52	5 (26%)
3	PSU	BB	1210	3	18,21,22	4.45	7 (38%)	22,30,33	1.78	5 (22%)
2	7MG	AA	2070	2	22,26,27	4.14	10 (45%)	29,39,42	2.05	9 (31%)
1	OMG	BA	915	1	18,26,27	2.51	8 (44%)	19,38,41	1.59	4 (21%)
3	OMG	BB	659	3	18,26,27	2.50	8 (44%)	19,38,41	1.61	5 (26%)
3	PSU	BB	1334	3	18,21,22	4.38	7 (38%)	22,30,33	1.80	5 (22%)
3	5MC	BB	1324	3	18,22,23	3.51	7 (38%)	26,32,35	1.10	1 (3%)
1	A2M	BA	1665	1,3	18,25,26	3.61	8 (44%)	18,36,39	3.70	4 (22%)
1	PSU	BA	1169	1	18,21,22	4.43	7 (38%)	22,30,33	1.87	5 (22%)
2	OMU	AA	714	2	19,22,23	2.94	8 (42%)	26,31,34	1.71	5 (19%)

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
3	A2M	BB	646	3	-	0/5/27/28	0/3/3/3
3	OMU	BB	1093	3	-	0/9/27/28	0/2/2/2
2	OMU	AA	57	2	-	1/9/27/28	0/2/2/2
1	PSU	BA	1129	1	-	0/7/25/26	0/2/2/2
1	OMC	BA	1006	1	-	0/9/27/28	0/2/2/2
3	OMU	BB	73	3	-	0/9/27/28	0/2/2/2
3	PSU	BB	1398	87,3	-	1/7/25/26	0/2/2/2
1	A2M	BA	743	1,3	-	2/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OMG	BB	1062	3	-	3/5/27/28	0/3/3/3
1	PSU	BA	1086	1,87,88	-	0/7/25/26	0/2/2/2
2	PSU	AA	1619	2,13	-	2/7/25/26	0/2/2/2
2	OMG	AA	1700	2	-	0/5/27/28	0/3/3/3
3	PSU	BB	680	87,3	-	0/7/25/26	0/2/2/2
1	PSU	BA	737	1,87	-	0/7/25/26	0/2/2/2
2	OMU	AA	36	2	-	6/9/27/28	0/2/2/2
9	OMG	BC	75	9	-	1/5/27/28	0/3/3/3
2	B8N	AA	1596	2	-	5/16/34/35	0/2/2/2
2	A2M	AA	2096	2	-	2/5/27/28	0/3/3/3
3	PSU	BB	1076	3	-	0/7/25/26	0/2/2/2
1	PSU	BA	1609	1	-	0/7/25/26	0/2/2/2
2	A2M	AA	56	2,89	-	1/5/27/28	0/3/3/3
2	PSU	AA	61	2	-	0/7/25/26	0/2/2/2
2	OMG	AA	1531	2	-	1/5/27/28	0/3/3/3
3	OMU	BB	685	3	-	1/9/27/28	0/2/2/2
9	OMU	BC	7	1,9	-	1/9/27/28	0/2/2/2
9	A2M	BC	43	9	-	1/5/27/28	0/3/3/3
3	A2M	BB	588	1,3	-	1/5/27/28	0/3/3/3
2	OMG	AA	1931	2,89	-	0/5/27/28	0/3/3/3
2	OMU	AA	2054	2	-	2/9/27/28	0/2/2/2
9	A2M	BC	41	9	-	0/5/27/28	0/3/3/3
2	MA6	AA	2261	2	-	1/7/29/30	0/3/3/3
2	OMU	AA	1652	2	-	0/9/27/28	0/2/2/2
3	A2M	BB	622	1,3	-	1/5/27/28	0/3/3/3
2	OMG	AA	1895	2,87	-	1/5/27/28	0/3/3/3
1	OMG	BA	1267	1	-	0/5/27/28	0/3/3/3
3	OMU	BB	578	3,89	-	5/9/27/28	0/2/2/2
1	PSU	BA	1009	1	-	0/7/25/26	0/2/2/2
1	OMC	BA	1608	1	-	3/9/27/28	0/2/2/2
1	OMU	BA	1742	1	-	1/9/27/28	0/2/2/2
1	OMC	BA	760	1	-	1/9/27/28	0/2/2/2
3	A2M	BB	609	3	-	1/5/27/28	0/3/3/3
3	PSU	BB	522	3	-	2/7/25/26	0/2/2/2
2	OMG	AA	1517	2	-	1/5/27/28	0/3/3/3
3	PSU	BB	644	3	-	0/7/25/26	0/2/2/2
3	PSU	BB	1160	3	-	0/7/25/26	0/2/2/2
3	OMG	BB	1269	3	-	0/5/27/28	0/3/3/3
2	OMG	AA	1676	2,88	-	1/5/27/28	0/3/3/3
1	PSU	BA	452	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A2M	BA	996	1,89	-	1/5/27/28	0/3/3/3
3	A2M	BB	545	87,3	-	2/5/27/28	0/3/3/3
3	OMG	BB	1245	3	-	0/5/27/28	0/3/3/3
1	A2M	BA	254	1	-	0/5/27/28	0/3/3/3
3	PSU	BB	615	3	-	0/7/25/26	0/2/2/2
1	1MA	BA	742	1,87	-	0/3/25/26	0/3/3/3
3	OMG	BB	71	3	-	0/5/27/28	0/3/3/3
3	OMC	BB	377	3	-	0/9/27/28	0/2/2/2
1	PSU	BA	1248	1	-	0/7/25/26	0/2/2/2
2	OMU	AA	2154	2	-	1/9/27/28	0/2/2/2
3	PSU	BB	1409	3	-	0/7/25/26	0/2/2/2
3	5MC	BB	542	87,3	-	1/7/25/26	0/2/2/2
1	OMC	BA	1329	1	-	1/9/27/28	0/2/2/2
1	PSU	BA	258	1	-	0/7/25/26	0/2/2/2
1	A2M	BA	927	1	-	0/5/27/28	0/3/3/3
3	OMC	BB	1264	3	-	1/9/27/28	0/2/2/2
3	A2M	BB	1400	87,3	-	0/5/27/28	0/3/3/3
1	A2M	BA	1024	1	-	1/5/27/28	0/3/3/3
2	OMC	AA	46	2	-	0/9/27/28	0/2/2/2
1	OMG	BA	1605	1	-	2/5/27/28	0/3/3/3
3	OMU	BB	1375	3	-	1/9/27/28	0/2/2/2
3	PSU	BB	455	88,87,3	-	0/7/25/26	0/2/2/2
2	OMG	AA	2227	2	-	0/5/27/28	0/3/3/3
9	PSU	BC	74	9	-	0/7/25/26	0/2/2/2
3	A2M	BB	1201	3	-	3/5/27/28	0/3/3/3
1	OMU	BA	46	1	-	0/9/27/28	0/2/2/2
2	PSU	AA	131	2	-	2/7/25/26	0/2/2/2
1	OMU	BA	916	1	-	0/9/27/28	0/2/2/2
3	PSU	BB	1429	3	-	0/7/25/26	0/2/2/2
2	A2M	AA	2153	2	-	1/5/27/28	0/3/3/3
3	OMC	BB	1175	3	-	0/9/27/28	0/2/2/2
2	OMU	AA	1899	2	-	4/9/27/28	0/2/2/2
2	OMU	AA	2123	2	-	0/9/27/28	0/2/2/2
3	OMC	BB	1413	3	-	0/9/27/28	0/2/2/2
9	A2M	BC	163	1,9	-	1/5/27/28	0/3/3/3
3	OMG	BB	552	3	-	2/5/27/28	0/3/3/3
1	PSU	BA	1258	1	-	2/7/25/26	0/2/2/2
2	MA6	AA	2260	2	-	0/7/29/30	0/3/3/3
1	OMG	BA	925	1	-	0/5/27/28	0/3/3/3
2	OMC	AA	2134	2	-	1/9/27/28	0/2/2/2
3	PSU	BB	1319	3	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	AA	942	2	-	4/7/25/26	0/2/2/2
3	OMG	BB	1247	3	-	0/5/27/28	0/3/3/3
1	A2M	BA	1620	1,87,3	-	0/5/27/28	0/3/3/3
2	PSU	AA	2045	2	-	0/7/25/26	0/2/2/2
1	OMU	BA	1181	1	-	0/9/27/28	0/2/2/2
3	PSU	BB	629	3	-	2/7/25/26	0/2/2/2
3	A2M	BB	400	3	-	2/5/27/28	0/3/3/3
3	A2M	BB	95	3	-	1/5/27/28	0/3/3/3
3	OMG	BB	1094	3	-	0/5/27/28	0/3/3/3
1	A2M	BA	762	1	-	1/5/27/28	0/3/3/3
1	A2M	BA	746	1	-	0/5/27/28	0/3/3/3
1	OMU	BA	1448	1	-	2/9/27/28	0/2/2/2
1	PSU	BA	1614	1,3	-	2/7/25/26	0/2/2/2
3	OMC	BB	601	3	-	0/9/27/28	0/2/2/2
3	PSU	BB	1280	3	-	0/7/25/26	0/2/2/2
2	A2M	AA	721	2,87	-	3/5/27/28	0/3/3/3
3	PSU	BB	611	3	-	0/7/25/26	0/2/2/2
2	PSU	AA	2146	2	-	0/7/25/26	0/2/2/2
2	OMC	AA	66	2	-	0/9/27/28	0/2/2/2
3	OMG	BB	673	3	-	0/5/27/28	0/3/3/3
2	PSU	AA	1592	2	-	2/7/25/26	0/2/2/2
1	OMG	BA	1028	1	-	2/5/27/28	0/3/3/3
2	PSU	AA	1276	2	-	0/7/25/26	0/2/2/2
3	A2M	BB	1388	3	-	0/5/27/28	0/3/3/3
3	OMU	BB	1435	3	-	0/9/27/28	0/2/2/2
1	OMG	BA	1709	1	-	0/5/27/28	0/3/3/3
1	OMG	BA	1621	1,3	-	0/5/27/28	0/3/3/3
3	PSU	BB	1210	3	-	0/7/25/26	0/2/2/2
2	7MG	AA	2070	2	-	1/7/37/38	0/3/3/3
1	OMG	BA	915	1	-	0/5/27/28	0/3/3/3
3	OMG	BB	659	3	-	0/5/27/28	0/3/3/3
3	PSU	BB	1334	3	-	0/7/25/26	0/2/2/2
3	5MC	BB	1324	3	-	4/7/25/26	0/2/2/2
1	A2M	BA	1665	1,3	-	3/5/27/28	0/3/3/3
1	PSU	BA	1169	1	-	0/7/25/26	0/2/2/2
2	OMU	AA	714	2	-	0/9/27/28	0/2/2/2

The worst 5 of 935 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BA	742	1MA	C2-N3	14.22	1.46	1.29
1	BA	258	PSU	C6-C5	11.65	1.48	1.35
3	BB	1409	PSU	C6-C5	11.60	1.48	1.35
1	BA	452	PSU	C6-C5	11.60	1.48	1.35
9	BC	74	PSU	C6-C5	11.56	1.48	1.35

The worst 5 of 508 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AA	2260	MA6	N1-C6-N6	-12.60	103.80	117.06
2	AA	2261	MA6	N1-C6-N6	-11.59	104.85	117.06
1	BA	762	A2M	C5-C6-N6	10.89	136.89	120.35
1	BA	743	A2M	C5-C6-N6	10.71	136.62	120.35
2	AA	2096	A2M	C5-C6-N6	10.70	136.61	120.35

There are no chirality outliers.

5 of 105 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	BC	7	OMU	C1'-C2'-O2'-CM2
9	BC	43	A2M	C1'-C2'-O2'-CM'
9	BC	163	A2M	C1'-C2'-O2'-CM'
1	BA	743	A2M	C1'-C2'-O2'-CM'
1	BA	760	OMC	C1'-C2'-O2'-CM2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 325 ligands modelled in this entry, 325 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
10	AB	1
2	AA	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AB	7:A	O3'	65:G	P	16.03
1	AA	1596:B8N	O3'	1597:C	P	4.10

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-17208. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis

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

7.1 Map-value distribution

This section was not generated.

7.2 Volume estimate versus contour level

This section was not generated.

7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.