W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

Full wwPDB EM Validation Report (i)

Feb 22, 2025 – 10:10 AM EST

PDB ID	:	7NAO
EMDB ID	:	EMD-24276
Title	:	Human PA28-20S proteasome complex
Authors	:	Zhao, J.; Makhija, S.; Huang, B.; Cheng, Y.
Deposited on	:	2021-06-22
Resolution	:	2.90 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

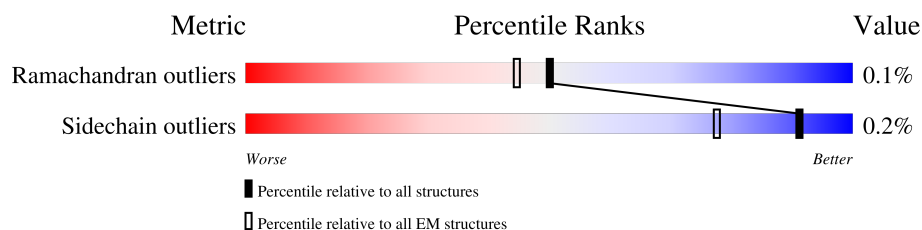|		
EMDB validation analysis	:	0.0.1.dev117
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

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.

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.
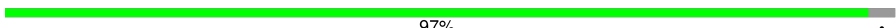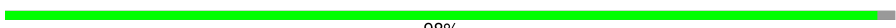
Metric	Percentile Ranks	Value
Ramachandran outliers		0.1%
Sidechain outliers		0.2%

Worse   *Better*

∎ Percentile relative to all structures

▯ Percentile relative to all EM structures
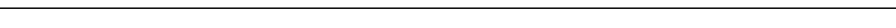
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	234	98% •
1	O	234	98% •
2	B	261	95% 5%
2	P	261	96% •
3	C	248	95% 5%
3	Q	248	95% 5%
4	D	241	99% •
4	R	241	97% •
5	E	263	91% 9%
5	S	263	90% 10%

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Mol	Chain	Length	Quality of chain
6	F	255	94% 6%
6	T	255	94% 6%
7	G	246	97% ·
7	U	246	98% ·
8	H	277	79% · 20%
8	V	277	80% 20%
9	I	205	99% ·
9	W	205	99%
10	J	201	98% ·
10	X	201	98% ·
11	K	263	76% 24%
11	Y	263	76% 24%
12	L	241	88% 12%
12	Z	241	88% 12%
13	M	264	81% 19%
13	a	264	81% 19%
14	N	239	85% 15%
14	b	239	85% 15%
15	d	239	91% 9%
15	f	239	88% 12%
15	h	239	90% 10%
15	i	239	90% 9%
16	c	249	85% 15%
16	e	249	85% 15%
16	g	249	85% 15%

2 Entry composition ⓘ

There are 16 unique types of molecules in this entry. The entry contains 58083 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 Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	229	Total	C	N	O	S	0	0
			1696	1101	294	295	6		
1	O	229	Total	C	N	O	S	0	0
			1678	1089	290	293	6		

- Molecule 2 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	249	Total	C	N	O	S	0	0
			1793	1146	318	319	10		
2	P	251	Total	C	N	O	S	0	0
			1843	1174	328	331	10		

- Molecule 3 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	235	Total	C	N	O	S	0	0
			1703	1082	314	302	5		
3	Q	236	Total	C	N	O	S	0	0
			1723	1095	320	303	5		

- Molecule 4 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	241	Total	C	N	O	S	0	0
			1751	1116	301	322	12		
4	R	235	Total	C	N	O	S	0	0
			1693	1076	292	314	11		

- Molecule 5 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	239	Total 1810	C 1144	N 331	O 324	S 11	0	0
5	S	237	Total 1759	C 1119	N 329	O 301	S 10	0	0

- Molecule 6 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	240	Total 1785	C 1145	N 313	O 316	S 11	0	0
6	T	239	Total 1784	C 1143	N 314	O 317	S 10	0	0

- Molecule 7 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	239	Total 1769	C 1133	N 305	O 319	S 12	0	0
7	U	242	Total 1789	C 1146	N 307	O 323	S 13	0	0

- Molecule 8 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	222	Total 1609	C 1023	N 276	O 299	S 11	0	0
8	V	222	Total 1612	C 1023	N 274	O 304	S 11	0	0

- Molecule 9 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	204	Total 1564	C 1003	N 264	O 278	S 19	0	0
9	W	204	Total 1559	C 1000	N 264	O 277	S 18	0	0

- Molecule 10 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	197	Total 1544	C 998	N 265	O 272	S 9	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	X	196	Total	C	N	O	S	0	0
			1535	990	264	273	8		

- Molecule 11 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	200	Total	C	N	O	S	0	0
			1525	968	273	275	9		
11	Y	200	Total	C	N	O	S	0	0
			1532	970	272	281	9		

- Molecule 12 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	213	Total	C	N	O	S	0	0
			1599	1022	279	288	10		
12	Z	213	Total	C	N	O	S	0	0
			1593	1022	281	280	10		

- Molecule 13 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	215	Total	C	N	O	S	0	0
			1643	1043	289	299	12		
13	a	215	Total	C	N	O	S	0	0
			1624	1034	288	290	12		

- Molecule 14 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	202	Total	C	N	O	S	0	0
			1491	939	258	282	12		
14	b	202	Total	C	N	O	S	0	0
			1478	934	258	274	12		

- Molecule 15 is a protein called Proteasome activator complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	d	217	Total	C	N	O	S	0	0
			1686	1094	284	304	4		
15	f	211	Total	C	N	O	S	0	0
			1648	1069	279	297	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
15	h	216	Total	C	N	O	S	0	0
			1677	1087	285	301	4		
15	i	217	Total	C	N	O	S	0	0
			1695	1099	287	305	4		

- Molecule 16 is a protein called Proteasome activator complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	c	212	Total	C	N	O	S	0	0
			1626	1049	282	291	4		
16	e	211	Total	C	N	O	S	0	0
			1641	1059	282	295	5		
16	g	211	Total	C	N	O	S	0	0
			1626	1050	281	289	6		

3 Residue-property plots ⓘ

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

- Molecule 1: Proteasome subunit alpha type-2

Chain A:

- Molecule 1: Proteasome subunit alpha type-2

Chain O:

- Molecule 2: Proteasome subunit alpha type-4

Chain B:

- Molecule 2: Proteasome subunit alpha type-4

Chain P:

- Molecule 3: Proteasome subunit alpha type-7

Chain C:

- Molecule 3: Proteasome subunit alpha type-7

Chain Q:

MET S2 V50 E237 GLU ASN GLU LYS LYS GLN LYS LYS ALA SER

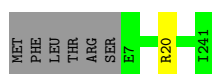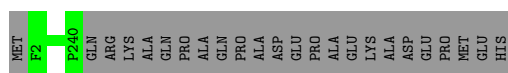• Molecule 4: Proteasome subunit alpha type-5

Chain D: 99%

M1 R5 S6 I241

• Molecule 4: Proteasome subunit alpha type-5

Chain R: 97%

MET PHE LEU THR ARG SER E7 R20 I241

• Molecule 5: Proteasome subunit alpha type-1

Chain E: 91%   9%

MET F2 P240 GLN ARG LYS ALA GLN PRO ALA GLN PRO ALA ASP GLU PRO ALA GLU LYS ALA ASP GLU PRO MET GLU HIS

• Molecule 5: Proteasome subunit alpha type-1

Chain S: 90%   10%

MET PHE ARG N4 K61 P240 GLN ARG LYS ALA GLN PRO ALA GLN PRO ALA ASP GLU PRO ALA GLU LYS ALA ASP GLU PRO MET GLU HIS

• Molecule 6: Proteasome subunit alpha type-3

Chain F: 94%   6%

MET SER SER ILE GLY T5 M181 K244 GLU GLU ASP GLU SER ASP ASP ASP ASN MET

• Molecule 6: Proteasome subunit alpha type-3

Chain T: 94%   6%

MET SER SER ILE GLY THR G6 K244 GLU GLU ASP GLU SER ASP ASP ASP ASN MET

• Molecule 7: Proteasome subunit alpha type-6

Chain G: 97%

MET SER ARG GLY SER A7 D120 R245 ASP

• Molecule 7: Proteasome subunit alpha type-6

Chain U:
98%

MET SER ARG G4 C154 R245 ASP

• Molecule 8: Proteasome subunit beta type-7

Chain H:
79%   20%

MET ALA ALA VAL SER VAL TYR ALA PRO PRO VAL GLY GLY PHE SER PHE ASP ASN CYS ARG ARG ASN ALA VAL LEU GLU ALA ASP PHE ALA LYS ARG GLY TYR LYS LEU PRO LYS VAL ARG LYS THR GLY T1 S171 K182 R187 P188 E222 VAL LEU GLU GLU THR VAL GLN

THR MET ASP THR SER

• Molecule 8: Proteasome subunit beta type-7

Chain V:
80%   20%

MET ALA ALA VAL SER VAL TYR ALA PRO PRO VAL GLY GLY PHE SER PHE ASP ASN CYS ARG ARG ASN ALA VAL LEU GLU ALA ASP PHE ALA LYS ARG GLY TYR LYS LEU PRO LYS VAL ARG LYS THR GLY T1 K182 E222 VAL LEU GLU GLU THR VAL GLN THR MET ASP THR SER

• Molecule 9: Proteasome subunit beta type-3

Chain I:
99%

MET S1 A31 R98 D204

• Molecule 9: Proteasome subunit beta type-3

Chain W:
99%

MET S1 R98 D204

• Molecule 10: Proteasome subunit beta type-2

Chain J:
98%

M1 P197 LYS GLN GLY SER

• Molecule 10: Proteasome subunit beta type-2

Chain X:

98%

.

M1 F196 PRO LYS GLN GLY SER
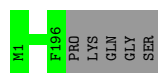
• Molecule 11: Proteasome subunit beta type-5

Chain K:

76%   24%

MET ALA LEU ALA SER VAL LEU GLU ARG PRO LEU PRO VAL ASN GLN ARG GLY PHE PHE GLY LEU GLY GLY ARG ALA ASP LEU LEU ASP LEU GLY PRO GLY SER LEU SER ASP GLY LEU SER LEU ALA ALA PRO GLY TRP GLY VAL PRO GLU GLU PRO GLY ILE GLU MET LEU HIS GLY T1

S200 GLY SER THR PRO
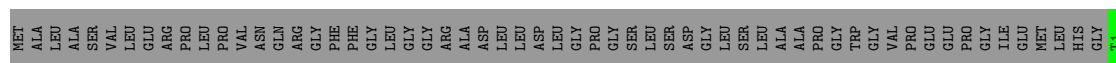
• Molecule 11: Proteasome subunit beta type-5

Chain Y:

76%   24%

MET ALA LEU ALA SER VAL LEU GLU ARG PRO LEU PRO VAL ASN GLN ARG GLY PHE PHE GLY LEU GLY GLY ARG ALA ASP LEU LEU ASP LEU GLY PRO GLY SER LEU SER ASP GLY LEU SER LEU ALA ALA PRO GLY TRP GLY VAL PRO GLU GLU PRO GLY ILE GLU MET LEU HIS GLY T1

S200 GLY SER THR PRO

• Molecule 12: Proteasome subunit beta type-1

Chain L:

88%   12%

MET LEU SER SER THR ALA MET TYR SER ALA PRO GLY ARG ASP LEU GLY MET GLU PRO HIS ARG ALA ALA GLY PRO LEU GLN LEU R1 D213
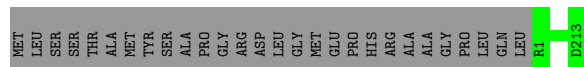
• Molecule 12: Proteasome subunit beta type-1

Chain Z:

88%   12%

MET LEU SER SER THR ALA MET TYR SER ALA PRO GLY ARG ASP LEU GLY MET GLU PRO HIS ARG ALA ALA GLY PRO LEU GLN LEU R1 D213
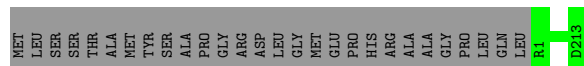
• Molecule 13: Proteasome subunit beta type-4

Chain M:

81%   19%

MET GLU ALA PHE LEU GLY SER ARG SER GLY LEU TRP ALA GLY GLY PRO ALA PRO GLY GLN PHE TYR ARG ILE PRO SER THR PRO ASP SER PHE MET ASP PRO ALA SER ALA LEU TYR ARG GLY PRO ILE THR ARG T1 D73 I215 SER GLY PHE GLU
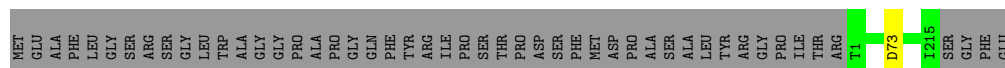
• Molecule 13: Proteasome subunit beta type-4

Chain a:

81%   19%

MET GLU ALA PHE LEU GLY SER ARG SER GLY LEU TRP ALA GLY GLY PRO ALA PRO GLY GLN PHE TYR ARG ILE PRO SER THR PRO ASP SER PHE MET ASP PRO ALA SER ALA LEU TYR ARG GLY PRO ILE THR ARG **T1** **R100** **I215** SER GLY PHE GLU
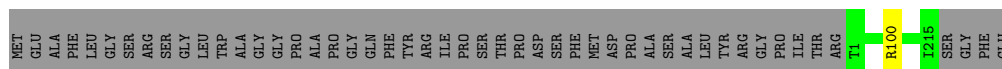
- Molecule 14: Proteasome subunit beta type-6

Chain N: 85%   15%

MET ALA ALA THR LEU LEU ALA ALA ARG GLY ALA GLY PRO ALA PRO ALA TRP GLY PRO GLU ALA PHE THR PRO ASP TRP GLU SER ARG GLU VAL SER THR GLY **T1** **L202** PRO PRO ALA
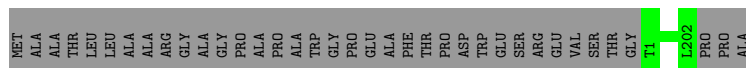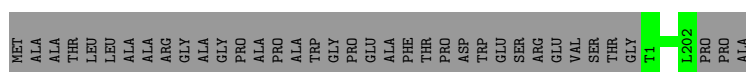
- Molecule 14: Proteasome subunit beta type-6

Chain b: 85%   15%

MET ALA ALA THR LEU LEU ALA ALA ARG GLY ALA GLY PRO ALA PRO ALA TRP GLY PRO GLU ALA PHE THR PRO ASP TRP GLU SER ARG GLU VAL SER THR GLY **T1** **L202** PRO PRO ALA

- Molecule 15: Proteasome activator complex subunit 2

Chain d: 91%   9%

MET ALA LYS PRO CYS GLY **V7** **P72** PRO LYS ASP ASP GLU MET GLU THR ASP LYS GLN GLU LYS LYS GLU VAL **H89** **Y239**
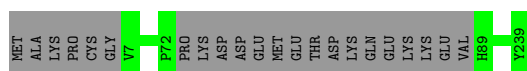
- Molecule 15: Proteasome activator complex subunit 2

Chain f: 88%   12%

MET ALA LYS PRO CYS GLY **V7** **P72** PRO LYS ASP ASP GLU MET GLU THR ASP LYS GLN GLU LYS LYS GLU VAL **H89** **E233** GLU LYS PRO SER MET TYR
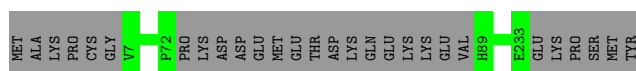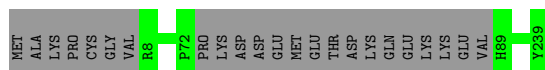
- Molecule 15: Proteasome activator complex subunit 2

Chain h: 90%   10%

MET ALA LYS PRO CYS GLY VAL **R8** **P72** PRO LYS ASP ASP GLU MET GLU THR ASP LYS GLN GLU LYS LYS GLU VAL **H89** **Y239**

- Molecule 15: Proteasome activator complex subunit 2

Chain i: 90%   9%

MET ALA LYS PRO CYS GLY **V7** **P72** PRO LYS ASP ASP GLU MET GLU THR ASP LYS GLN GLU LYS LYS GLU VAL **H89** **C118** **Y239**
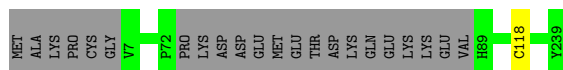
- Molecule 16: Proteasome activator complex subunit 1

Chain c: 85%   15%

MET ALA MET LEU ARG V6 D67 PRO VAL LYS GLU LYS LYS GLU LYS GLU GLU ARG LYS LYS GLN GLN GLU GLU LYS GLU ASP LYS GLU LYS LYS LYS GLY GLU ASP GLU ASP LYS GLY PRO P100 Y249

• Molecule 16: Proteasome activator complex subunit 1

Chain e:　　　　　　　85%　　　　　　15%

MET ALA MET LEU ARG VAL Q7 D67 PRO VAL LYS GLU LYS GLU GLU LYS GLU GLU ARG LYS LYS GLN GLN GLU GLU LYS GLU ASP LYS GLU LYS LYS LYS GLY GLU ASP GLU ASP LYS GLY PRO P100 Y249

• Molecule 16: Proteasome activator complex subunit 1

Chain g:　　　　　　　85%　　　　　　15%

MET ALA MET LEU ARG VAL Q7 D67 PRO VAL LYS GLU LYS GLU GLU LYS GLU GLU ARG LYS LYS GLN GLN GLU GLU LYS GLU ASP LYS GLU LYS LYS LYS GLY GLU ASP GLU ASP LYS GLY PRO P100 Y249

4　Experimental information　ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	135937	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	A	0.34	0/1735	0.55	0/2362
1	O	0.34	0/1717	0.51	0/2339
2	B	0.31	0/1821	0.52	0/2477
2	P	0.30	0/1872	0.54	0/2541
3	C	0.32	0/1729	0.57	0/2356
3	Q	0.31	0/1749	0.60	1/2380 (0.0%)
4	D	0.31	0/1780	0.54	0/2417
4	R	0.29	0/1720	0.49	0/2336
5	E	0.31	0/1845	0.58	0/2504
5	S	0.31	0/1794	0.58	0/2437
6	F	0.35	0/1820	0.54	0/2464
6	T	0.32	0/1819	0.53	0/2463
7	G	0.33	0/1802	0.54	1/2449 (0.0%)
7	U	0.33	0/1823	0.51	0/2478
8	H	0.32	0/1636	0.58	0/2223
8	V	0.32	0/1639	0.58	0/2228
9	I	0.33	0/1593	0.55	0/2149
9	W	0.33	0/1588	0.53	0/2144
10	J	0.34	0/1577	0.55	0/2138
10	X	0.34	0/1567	0.55	0/2124
11	K	0.33	0/1556	0.56	0/2104
11	Y	0.33	0/1563	0.59	0/2115
12	L	0.33	0/1629	0.56	0/2201
12	Z	0.33	0/1623	0.56	0/2192
13	M	0.33	0/1676	0.61	1/2272 (0.0%)
13	a	0.32	0/1657	0.59	0/2250
14	N	0.34	0/1517	0.55	0/2056
14	b	0.33	0/1504	0.54	0/2038
15	d	0.30	0/1720	0.51	0/2338
15	f	0.30	0/1680	0.50	0/2281
15	h	0.30	0/1710	0.51	0/2322
15	i	0.30	0/1729	0.52	0/2349
16	c	0.30	0/1657	0.49	0/2250
16	e	0.30	0/1672	0.52	0/2265

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
16	g	0.30	0/1657	0.51	0/2247
All	All	0.32	0/59176	0.55	3/80289 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	D	0	1
8	H	0	1
All	All	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	50	VAL	CG1-CB-CG2	7.85	123.46	110.90
13	M	73	ASP	CB-CG-OD1	5.66	123.39	118.30
7	G	120	ASP	CB-CG-OD1	5.60	123.34	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	5	ARG	Peptide
8	H	187	ARG	Peptide

5.2   Too-close contacts ⓘ

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

5.3   Torsion angles ⓘ

5.3.1   Protein backbone ⓘ

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

W O R L D W I D E
wwPDB
PROTEIN DATA BANK

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	227/234 (97%)	225 (99%)	2 (1%)	0	100	100
1	O	227/234 (97%)	225 (99%)	2 (1%)	0	100	100
2	B	247/261 (95%)	244 (99%)	3 (1%)	0	100	100
2	P	249/261 (95%)	243 (98%)	6 (2%)	0	100	100
3	C	233/248 (94%)	228 (98%)	5 (2%)	0	100	100
3	Q	234/248 (94%)	234 (100%)	0	0	100	100
4	D	239/241 (99%)	232 (97%)	6 (2%)	1 (0%)	30	60
4	R	233/241 (97%)	229 (98%)	4 (2%)	0	100	100
5	E	237/263 (90%)	233 (98%)	4 (2%)	0	100	100
5	S	235/263 (89%)	230 (98%)	4 (2%)	1 (0%)	30	60
6	F	238/255 (93%)	237 (100%)	1 (0%)	0	100	100
6	T	237/255 (93%)	235 (99%)	2 (1%)	0	100	100
7	G	237/246 (96%)	234 (99%)	3 (1%)	0	100	100
7	U	240/246 (98%)	238 (99%)	2 (1%)	0	100	100
8	H	220/277 (79%)	215 (98%)	3 (1%)	2 (1%)	14	43
8	V	220/277 (79%)	217 (99%)	3 (1%)	0	100	100
9	I	202/205 (98%)	198 (98%)	3 (2%)	1 (0%)	25	56
9	W	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
10	J	195/201 (97%)	190 (97%)	5 (3%)	0	100	100
10	X	194/201 (96%)	191 (98%)	3 (2%)	0	100	100
11	K	198/263 (75%)	197 (100%)	1 (0%)	0	100	100
11	Y	198/263 (75%)	194 (98%)	4 (2%)	0	100	100
12	L	211/241 (88%)	208 (99%)	3 (1%)	0	100	100
12	Z	211/241 (88%)	209 (99%)	2 (1%)	0	100	100
13	M	213/264 (81%)	210 (99%)	3 (1%)	0	100	100
13	a	213/264 (81%)	208 (98%)	5 (2%)	0	100	100
14	N	200/239 (84%)	198 (99%)	2 (1%)	0	100	100
14	b	200/239 (84%)	198 (99%)	2 (1%)	0	100	100
15	d	213/239 (89%)	211 (99%)	2 (1%)	0	100	100
15	f	207/239 (87%)	205 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	h	212/239 (89%)	210 (99%)	2 (1%)	0	100	100
15	i	213/239 (89%)	210 (99%)	3 (1%)	0	100	100
16	c	208/249 (84%)	207 (100%)	1 (0%)	0	100	100
16	e	207/249 (83%)	206 (100%)	1 (0%)	0	100	100
16	g	207/249 (83%)	206 (100%)	1 (0%)	0	100	100
All	All	7657/8579 (89%)	7552 (99%)	100 (1%)	5 (0%)	50	77

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	I	31	ALA
5	S	61	LYS
4	D	6	SER
8	H	171	SER
8	H	188	PRO

5.3.2   Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	158/191 (83%)	158 (100%)	0	100	100
1	O	155/191 (81%)	155 (100%)	0	100	100
2	B	159/221 (72%)	159 (100%)	0	100	100
2	P	171/221 (77%)	171 (100%)	0	100	100
3	C	152/211 (72%)	152 (100%)	0	100	100
3	Q	157/211 (74%)	157 (100%)	0	100	100
4	D	173/203 (85%)	173 (100%)	0	100	100
4	R	164/203 (81%)	163 (99%)	1 (1%)	84	95
5	E	181/224 (81%)	181 (100%)	0	100	100
5	S	169/224 (75%)	169 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	167/212 (79%)	166 (99%)	1 (1%)	84	95
6	T	168/212 (79%)	168 (100%)	0	100	100
7	G	175/210 (83%)	175 (100%)	0	100	100
7	U	177/210 (84%)	176 (99%)	1 (1%)	84	95
8	H	165/228 (72%)	164 (99%)	1 (1%)	84	95
8	V	166/228 (73%)	165 (99%)	1 (1%)	84	95
9	I	164/174 (94%)	163 (99%)	1 (1%)	84	95
9	W	162/174 (93%)	161 (99%)	1 (1%)	84	95
10	J	156/171 (91%)	156 (100%)	0	100	100
10	X	156/171 (91%)	156 (100%)	0	100	100
11	K	146/202 (72%)	146 (100%)	0	100	100
11	Y	147/202 (73%)	147 (100%)	0	100	100
12	L	161/199 (81%)	161 (100%)	0	100	100
12	Z	160/199 (80%)	160 (100%)	0	100	100
13	M	166/215 (77%)	166 (100%)	0	100	100
13	a	160/215 (74%)	159 (99%)	1 (1%)	84	95
14	N	149/181 (82%)	149 (100%)	0	100	100
14	b	145/181 (80%)	145 (100%)	0	100	100
15	d	174/212 (82%)	174 (100%)	0	100	100
15	f	172/212 (81%)	172 (100%)	0	100	100
15	h	173/212 (82%)	173 (100%)	0	100	100
15	i	175/212 (82%)	174 (99%)	1 (1%)	84	95
16	c	165/224 (74%)	165 (100%)	0	100	100
16	e	170/224 (76%)	170 (100%)	0	100	100
16	g	167/224 (75%)	167 (100%)	0	100	100
All	All	5725/7204 (80%)	5716 (100%)	9 (0%)	91	98

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	F	181	MET
8	H	182	LYS
9	I	98	ARG

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Mol	Chain	Res	Type
4	R	20	ARG
7	U	154	CYS
8	V	182	LYS
9	W	98	ARG
13	a	100	ARG
15	i	118	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	109	GLN
3	C	15	HIS
3	C	146	GLN
4	D	122	GLN
10	J	63	ASN
12	L	157	ASN
14	N	77	HIS
14	N	110	GLN
2	P	109	GLN
5	S	68	ASN
5	S	146	GLN
7	U	128	ASN
9	W	6	ASN
9	W	172	ASN
10	X	63	ASN
10	X	71	ASN
12	Z	108	ASN
12	Z	157	ASN
15	d	183	HIS
16	e	147	ASN
16	g	27	ASN

5.3.3   RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-24276. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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.