



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 06:50 AM UTC

PDB ID : 8OF0 / pdb_00008of0
EMDB ID : EMD-16840
Title : Structure of the mammalian Pol II-SPT6-Elongin complex, Structure 1
Authors : Chen, Y.; Kokic, G.; Dienemann, C.; Dybkov, O.; Urlaub, H.; Cramer, P.
Deposited on : 2023-03-13
Resolution : 3.05 Å(reported)

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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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

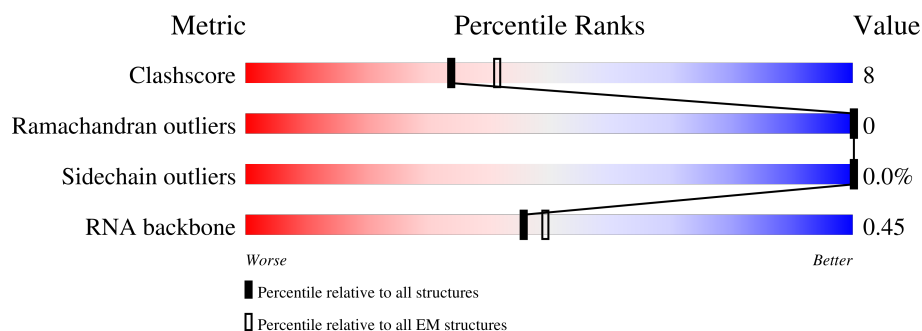
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.05 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	A	1970	58% (green), 14% (yellow), 28% (grey)
2	B	1251	73% (green), 17% (yellow), 10% (grey)
3	C	275	79% (green), 15% (yellow), 6% (grey)
4	D	184	48% (green), 16% (yellow), 36% (grey)
5	E	210	85% (green), 14% (yellow)
6	F	127	54% (green), 8% (yellow), 39% (grey)
7	G	172	76% (green), 23% (yellow), . (grey)

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Mol	Chain	Length	Quality of chain
8	H	150	 83% 15% .
9	I	125	 64% 29% 7%
10	J	67	 87% 12% .
11	K	117	 80% 18% .
12	L	58	 55% 21% 24%
13	N	48	 40% 12% 48%
14	P	46	 20% 7% . 72%
15	T	48	 58% 19% 23%
16	Q	118	 59% 15% 25%
17	M	801	 14% . 83%
18	O	112	 63% 27% 10%
19	S	1729	 34% 13% 53%

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 41700 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1409	Total	C	N	O	S	0	0
			11159	7024	2000	2064	71		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1131	Total	C	N	O	S	0	0
			9047	5721	1592	1670	64		

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	258	Total	C	N	O	S	0	0
			2072	1300	356	410	6		

- Molecule 4 is a protein called RNA polymerase II subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	118	Total	C	N	O	S	0	0
			967	608	167	188	4		

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	209	Total	C	N	O	S	0	0
			1721	1089	300	324	8		

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	78	Total	C	N	O	S	0	0
			626	401	106	114	5		

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1347	872	218	249	8		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	116	Total	C	N	O	S	0	0
			932	577	165	179	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	66	Total	C	N	O	S	0	0
			524	339	88	91	6		

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB11-a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	115	Total	C	N	O	S	0	0
			920	593	152	173	2		

- Molecule 12 is a protein called RNA polymerase II subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	44	Total	C	N	O	S	0	0
			367	228	69	64	6		

- Molecule 13 is a DNA chain called Non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	25	Total	C	N	O	P	0	0
			527	245	112	145	25		

- Molecule 14 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	13	Total	C	N	O	P	0	0
			280	125	54	88	13		

- Molecule 15 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	37	Total	C	N	O	P	0	0
			750	356	127	230	37		

- Molecule 16 is a protein called Elongin-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	88	Total	C	N	O	S	0	0
			696	437	121	135	3		

- Molecule 17 is a protein called Elongin-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	140	Total	C	N	O	S	0	0
			1149	724	214	204	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	SER	-	expression tag	UNP Q14241
M	-1	ASN	-	expression tag	UNP Q14241
M	0	ALA	-	expression tag	UNP Q14241

- Molecule 18 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	101	Total	C	N	O	S	0	0
			792	506	127	153	6		

- Molecule 19 is a protein called Transcription elongation factor SPT6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	818	Total	C	N	O	S	0	0
			6629	4221	1144	1232	32		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	-2	SER	-	expression tag	UNP Q7KZ85
S	-1	ASN	-	expression tag	UNP Q7KZ85
S	0	ALA	-	expression tag	UNP Q7KZ85

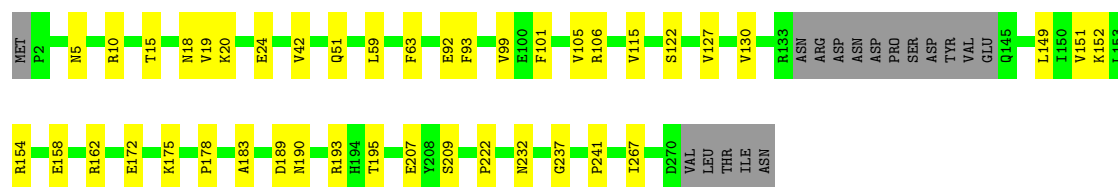
- Molecule 20 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
20	A	1	Total Mg 1 1	0

- Molecule 21 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

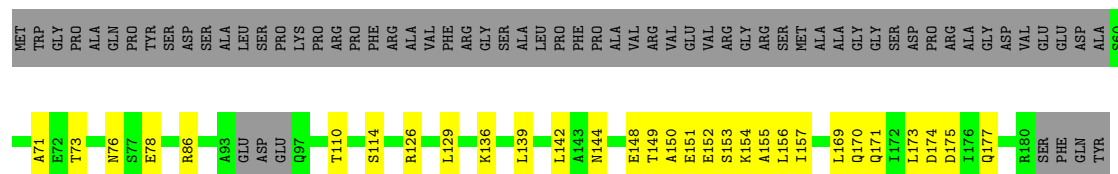
Mol	Chain	Residues	Atoms	AltConf
21	A	2	Total Zn 2 2	0
21	B	1	Total Zn 1 1	0
21	C	1	Total Zn 1 1	0
21	I	2	Total Zn 2 2	0
21	J	1	Total Zn 1 1	0
21	L	1	Total Zn 1 1	0

Chain C:  79% 15% 6%



• Molecule 4: RNA polymerase II subunit D

Chain D:  48% 16% 36%



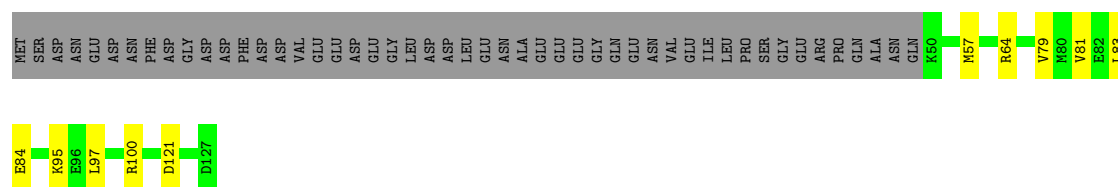
• Molecule 5: DNA-directed RNA polymerase II subunit E

Chain E:  85% 14%



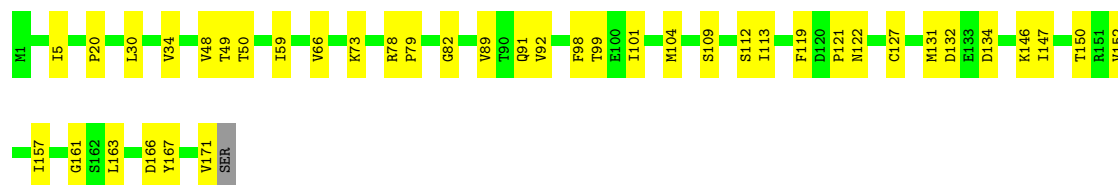
• Molecule 6: DNA-directed RNA polymerase II subunit F

Chain F:  54% 8% 39%



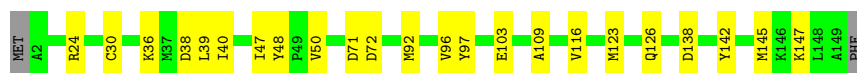
• Molecule 7: DNA-directed RNA polymerase II subunit RPB7

Chain G:  76% 23%



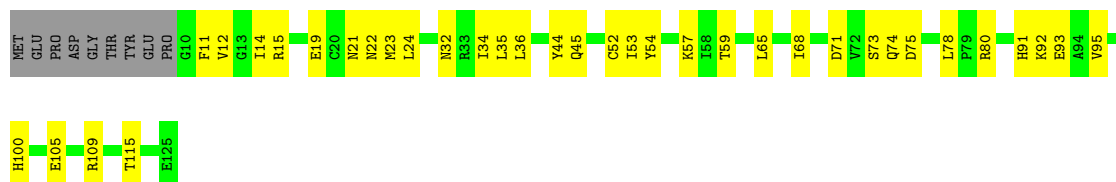
• Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H:  83% 15%



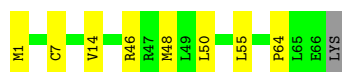
- Molecule 9: DNA-directed RNA polymerase II subunit RPB9

Chain I: 64% 29% 7%



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

Chain J: 87% 12%



- Molecule 11: DNA-directed RNA polymerase II subunit RPB11-a

Chain K: 80% 18%



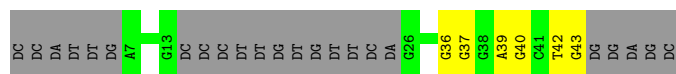
- Molecule 12: RNA polymerase II subunit K

Chain L: 55% 21% 24%



- Molecule 13: Non-template DNA

Chain N: 40% 12% 48%



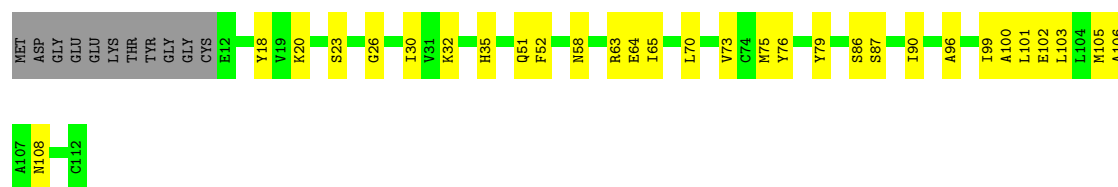
- Molecule 14: RNA

Chain P: 20% 7% 72%



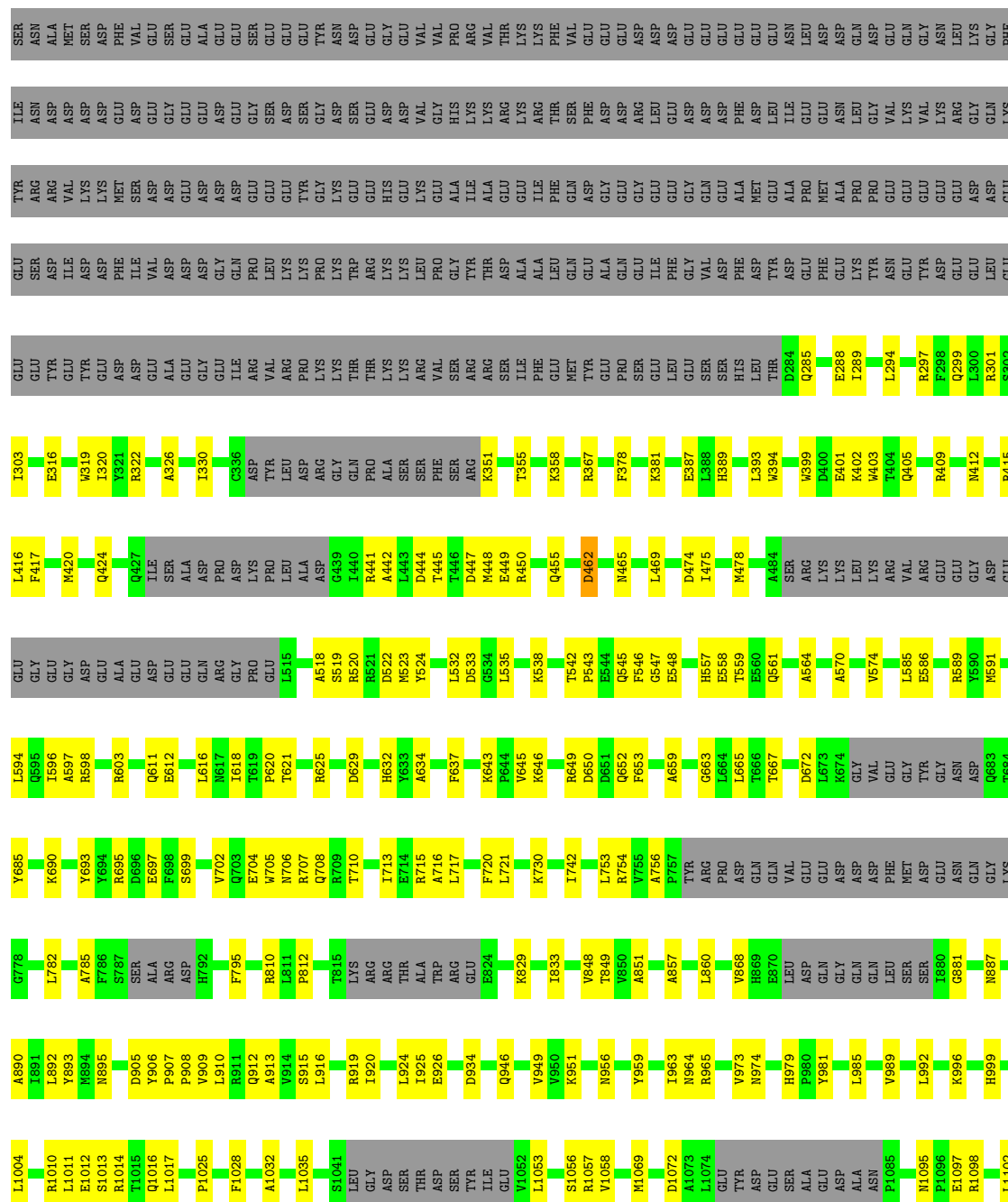
- Molecule 15: Template DNA

Chain O:  63% 27% 10%



• Molecule 19: Transcription elongation factor SPT6

Chain S:  34% 13% 53%



LEU	ARG	ALA	PRO	GLY	ALA	SER	TYR	GLN				
LEU	GLN	TYR	ALA	PRO	SER	SER	TYR	GLN				F1107
ASP	GLN	HIS	ASN	LYS	PHE	LYS	ASP	ASP				A1108
GLU	GLN	VAL	ILE	ARG	ALA	GLY	PHE	ASN				L1111
MET	PRO	PHE	ASN	ILE	ARG	GLU	ASP	ALA				L1117
ASP	LYS	PRO	LEU	GLU	ASP	ASN	ALA	PRO				G1117
ARG	SER	THR	ASP	TYR	LEU	HIS	GLU	LEU				H1120
	SER	ALA	LEU	VAL	ASN	THR	ALA	SER				I1121
ALA	HIS	GLN	THR	VAL	HIS	VAL	ASP	GLU				T1122
ALA	ALA	PRO	ARG	PRO	TYR	THR	LYS	VAL				L1123
ILE	VAL	VAL	VAL	GLY	TYR	LYS	GLN	ASN				Y1124
ASP	THR	ALA	ALA	PHE	ASP	SER	GLU	HIS				D1125
THR	GLY	PRO	LEU	ARG	CYS	ASP	ASP	PHE				G1132
LYS	LYS	LEU	PRO	TYR	SER	GLY	MET	SER				F1133
MET	MET	MET	GLN	ARG	GLY	ILE	LYS	GLY				Y1134
ALA	THR	ALA	ASN	GLY	GLY	TYR	ARG	SER				K1135
GLU	GLU	PRO	MET	GLN	ASP	GLN	LYS	CYS				D1136
THR	GLN	SER	THR	ILE	ARG	HIS	GLN	GLN				L1137
TRP	TRP	TYR	SER	PHE	LYS	VAL	GLN	GLY				R1138
LEU	SER	SER	GLN	PRO	LYS	ASP	ARG	ALA				T1139
GLN	LEU	TYR	MET	THR	LEU	VAL	THR	GLN				A1140
GLU	GLU	THR	PHE	VAL	GLU	ARG	THR	ALA				Y1141
LYS	LYS	THR	ALA	ASN	GLU	GLU	TYR	ILE				R1142
ALA	GLU	PRO	SER	GLY	LEU	GLY	ILE	L1232				S1143
ALA	ALA	SER	ILE	LEU	LEU	GLY	LYS	LYS				V1236
GLN	GLN	GLN	ALA	PHE	ILE	LYS	ARG	VAL				I1149
PRO	ARG	PRO	ALA	ARG	LYS	GLU	VAL	VAL				M1152
ILE	ARG	ILE	VAL	THR	THR	ASN	ILE	L1245				L1153
THR	THR	THR	THR	PHE	LYS	ALA	ALA	SER				A1175
GLN	GLN	GLN	PRO	ASP	GLY	PHE	HIS	ASP				HIS
PRO	LYS	PRO	GLN	ASP	LYS	SER	PRO	LYS				ARG
ARG	GLN	GLN	GLY	HIS	LYS	LEU	SER	VAL				ARG
LEU	ARG	TYR	GLN	THR	PRO	GLY	PHE	VAL				ARG
THR	THR	HIS	ASN	GLN	THR	ALA	ALA	LYS				ARG
THR	GLN	GLN	PRO	ASP	PHE	THR	ASN	ASN				PRO
PRO	PRO	PRO	ASN	PRO	ILE	LEU	ILE	P1253				GLN
ARG	ARG	GLN	ALA	VAL	VAL	THR	ASN	ASN				GLY
PRO	PRO	ALA	THR	PRO	THR	ILE	PHE	F1275				GLU
SER	SER	SER	PRO	GLY	PHE	ASN	LYS	LYS				SER
PRO	PRO	THR	ALA	THR	ILE	SER	GLN	R1282				TYR
SER	SER	THR	GLN	THR	THR	SER	ALA	THR				ASP
PRO	PRO	PRO	TRP	PRO	ALA	GLU	GLU	GLU				GLN
MET	MET	GLN	ALA	SER	CYS	PHE	LYS	ASP				ALA
ILE	ILE	SER	SER	SER	LYS	GLU	MET	LEU				ILE
GLU	GLU	ALA	SER	SER	GLU	ASP	MET	MET				ARG
SER	SER	GLN	GLN	SER	LEU	LEU	GLU	GLU				ASN
THR	THR	ALA	TYR	ARG	PRO	ASP	THR	ARG				ASP
PRO	PRO	GLN	GLY	THR	LYS	GLU	MET	ASN				THR
MET	MET	GLN	TYR	ARG	ILE	ILE	ASP	ASN				GLY
ILE	ILE	PRO	GLY	THR	PHE	VAL	GLN	GLU				LEU
ALA	SER	SER	SER	ALA	LEU	ARG	ASP	LYS				TRP
GLY	GLY	SER	GLY	TYR	LEU	THR	VAL	LYS				GLN
ASP	ASP	SER	GLY	ILE	GLY	TYR	VAL	ILE				PRO
ALA	ALA	SER	GLY	ILE	GLY	GLN	ILE	LYS				CYS
ALA	ALA	SER	GLY	ASN	GLN	GLN	ILE	LYS				PRO
THR	THR	CTR	SER	ALA	PRO	PRO	ARG	THR				PHE
PRO	PRO	CTR	SER	CTR	CTR	MET	PRO	CTR				CYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	72087	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 ($e^-/\text{\AA}^2$)	40.09	Depositor
Minimum defocus (nm)	350	Depositor
Maximum defocus (nm)	7500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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	0.25	0/11360	0.47	1/15328 (0.0%)
2	B	0.28	0/9227	0.48	1/12454 (0.0%)
3	C	0.27	0/2115	0.42	0/2873
4	D	0.30	0/979	0.59	0/1312
5	E	0.25	0/1752	0.51	0/2366
6	F	0.26	0/636	0.52	0/859
7	G	0.22	0/1378	0.51	0/1870
8	H	0.24	0/1207	0.44	0/1628
9	I	0.23	0/954	0.51	0/1293
10	J	0.29	0/533	0.46	0/719
11	K	0.27	0/939	0.44	0/1271
12	L	0.25	0/372	0.49	0/493
13	N	0.20	0/594	0.35	0/915
14	P	0.17	0/313	0.21	0/486
15	T	0.27	0/836	0.45	0/1287
16	Q	0.22	0/707	0.62	0/952
17	M	0.30	0/1172	0.61	0/1578
18	O	0.24	0/810	0.62	0/1097
19	S	0.22	0/6750	0.52	0/9096
All	All	0.25	0/42634	0.49	2/57877 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
18	O	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	478	PRO	CA-C-O	-5.85	116.88	121.38
2	B	430	VAL	N-CA-C	-5.62	107.26	112.43

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	538	VAL	Peptide
18	O	90	ILE	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11159	0	11304	179	0
2	B	9047	0	9080	139	0
3	C	2072	0	2019	28	0
4	D	967	0	973	38	0
5	E	1721	0	1737	20	0
6	F	626	0	657	6	0
7	G	1347	0	1347	41	0
8	H	1186	0	1147	15	0
9	I	932	0	856	28	0
10	J	524	0	540	7	0
11	K	920	0	942	14	0
12	L	367	0	367	9	0
13	N	527	0	278	3	0
14	P	280	0	142	3	0
15	T	750	0	418	7	0
16	Q	696	0	694	13	0
17	M	1149	0	1127	26	0
18	O	792	0	774	21	0
19	S	6629	0	6583	166	0
20	A	1	0	0	0	0
21	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	B	1	0	0	0	0
21	C	1	0	0	0	0
21	I	2	0	0	0	0
21	J	1	0	0	0	0
21	L	1	0	0	0	0
All	All	41700	0	40985	672	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 672 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:132:ASP:O	19:S:416:LEU:HD21	1.45	1.15
4:D:148:GLU:HG2	19:S:519:SER:HB2	1.13	1.12
4:D:149:THR:OG1	4:D:152:GLU:HB2	1.62	0.99
4:D:148:GLU:CG	19:S:519:SER:HB2	1.96	0.96
7:G:134:ASP:OD1	19:S:475:ILE:HG23	1.66	0.95

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1395/1970 (71%)	1357 (97%)	38 (3%)	0	100	100
2	B	1123/1251 (90%)	1089 (97%)	34 (3%)	0	100	100
3	C	254/275 (92%)	249 (98%)	5 (2%)	0	100	100
4	D	114/184 (62%)	104 (91%)	10 (9%)	0	100	100
5	E	207/210 (99%)	201 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	76/127 (60%)	74 (97%)	2 (3%)	0	100	100
7	G	169/172 (98%)	157 (93%)	12 (7%)	0	100	100
8	H	146/150 (97%)	143 (98%)	3 (2%)	0	100	100
9	I	114/125 (91%)	107 (94%)	7 (6%)	0	100	100
10	J	64/67 (96%)	64 (100%)	0	0	100	100
11	K	113/117 (97%)	109 (96%)	4 (4%)	0	100	100
12	L	42/58 (72%)	41 (98%)	1 (2%)	0	100	100
16	Q	86/118 (73%)	73 (85%)	13 (15%)	0	100	100
17	M	136/801 (17%)	126 (93%)	10 (7%)	0	100	100
18	O	99/112 (88%)	92 (93%)	7 (7%)	0	100	100
19	S	792/1729 (46%)	762 (96%)	30 (4%)	0	100	100
All	All	4930/7466 (66%)	4748 (96%)	182 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	1239/1749 (71%)	1239 (100%)	0	100	100
2	B	991/1084 (91%)	991 (100%)	0	100	100
3	C	235/252 (93%)	235 (100%)	0	100	100
4	D	109/160 (68%)	109 (100%)	0	100	100
5	E	191/192 (100%)	191 (100%)	0	100	100
6	F	68/111 (61%)	68 (100%)	0	100	100
7	G	151/153 (99%)	151 (100%)	0	100	100
8	H	129/131 (98%)	129 (100%)	0	100	100
9	I	102/112 (91%)	102 (100%)	0	100	100
10	J	55/56 (98%)	55 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	K	104/106 (98%)	104 (100%)	0	100	100
12	L	40/55 (73%)	40 (100%)	0	100	100
16	Q	75/103 (73%)	75 (100%)	0	100	100
17	M	121/706 (17%)	121 (100%)	0	100	100
18	O	88/96 (92%)	88 (100%)	0	100	100
19	S	710/1524 (47%)	709 (100%)	1 (0%)	88	89
All	All	4408/6590 (67%)	4407 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	S	462	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
9	I	41	ASN
19	S	405	GLN
9	I	67	GLN
17	M	665	GLN
19	S	577	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	P	12/46 (26%)	2 (16%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
14	P	36	G
14	P	37	G

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-16840. 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.