WORLDWIDE PDB
PROTEIN DATA BANK

wwPDB EM Validation Summary Report (i)

Dec 18, 2022 – 04:52 am GMT

PDB ID	:	6ZYM
EMDB ID	:	EMD-11569
Title	:	Human C Complex Spliceosome - High-resolution CORE
Authors	:	Bertram, K.; Kastner, B.
Deposited on	:	2020-08-02
Resolution	:	3.40 Å(reported)

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 3.40 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
Clashscore		7
Ramachandran outliers		0.0%
Sidechain outliers		0.2%
RNA backbone		0.39

Worse   *Better*

▮ Percentile relative to all structures

▯ Percentile relative to all EM structures
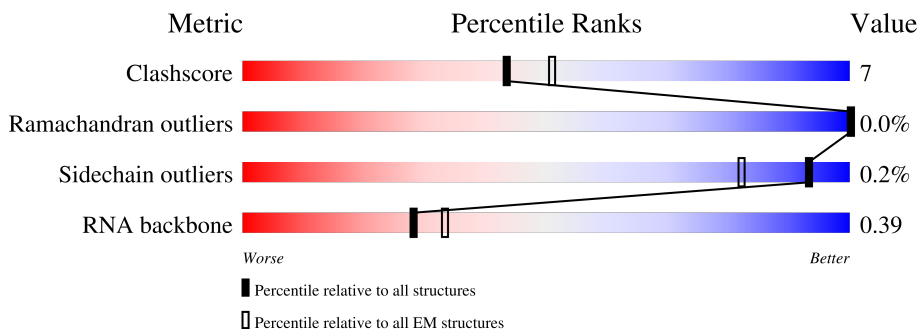
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	2	188	5% 6% • 86%
2	5	116	50% 11% • 36%
3	6	79	56% 42% •
4	9	450	• • 97%
5	A	1755	81% 16% • •
6	B	952	75% 18% • 6%
7	C	536	36% 5% 58%

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	D	514	46% 14% 39%
9	E	579	11% 87%
10	F	357	62% 21% 16%
11	L	802	23% 75%
12	O	848	25% 5% 70%
13	P	218	72% 16% 11%
14	Q	144	85% 10%
15	R	229	32% 6% 62%
16	S	2752	99%
17	T	908	19% 78%
18	V	166	81% 17%
19	Y	324	7% 87%
19	Z	324	96%
20	p	654	48% 50%
21	r	1227	97%
22	s	285	7% 93%
23	t	425	13% 87%
24	u	178	83% 5% 12%
25	x	258	12% 88%

2 Entry composition (i)

There are 29 unique types of molecules in this entry. The entry contains 48271 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 U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	27	575	257	99	192	27	0	0

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	5	74	1548	693	256	525	74	0	0

- Molecule 3 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	6	79	1690	756	312	543	79	0	0

- Molecule 4 is a protein called Corepressor interacting with RBPJ 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	9	14	112	68	21	22	1	0	0

- Molecule 5 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A	1722	14270	9190	2521	2494	65	0	0

- Molecule 6 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	B	895	6953	4447	1163	1309	34	0	0

- Molecule 7 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	224	Total 1703	C 1074	N 308	O 312	S 9	0	0

- Molecule 8 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	315	Total 2481	C 1565	N 451	O 458	S 7	0	0

- Molecule 9 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	78	Total 629	C 400	N 107	O 118	S 4	0	0

- Molecule 10 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	299	Total 2230	C 1407	N 381	O 430	S 12	0	0

- Molecule 11 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	202	Total 1611	C 1012	N 297	O 296	S 6	0	0

- Molecule 12 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	252	Total 2108	C 1345	N 381	O 377	S 5	0	0

- Molecule 13 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	195	Total 1577	C 991	N 279	O 290	S 17	0	0

- Molecule 14 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	142	Total 1162	C 733	N 216	O 202	S 11	0	0

- Molecule 15 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	87	Total 681	C 421	N 134	O 125	S 1	0	0

- Molecule 16 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	30	Total 230	C 140	N 49	O 40	S 1	0	0

- Molecule 17 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	203	Total 1669	C 1071	N 278	O 307	S 13	0	0

- Molecule 18 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	163	Total 1081	C 677	N 200	O 199	S 5	0	0

- Molecule 19 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Y	41	Total 873	C 391	N 155	O 286	P 41	0	0
19	Z	13	Total 276	C 123	N 50	O 90	P 13	0	0

- Molecule 20 is a protein called WD repeat-containing protein 70.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	p	325	Total 2372	C 1493	N 421	O 442	S 16	0	0

- Molecule 21 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase

PRP16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	r	35	Total 259	C 157	N 50	O 51	S 1	0	0

- Molecule 22 is a protein called Pre-mRNA-splicing factor ISY1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	s	20	Total 158	C 96	N 33	O 28	S 1	0	0

- Molecule 23 is a protein called Pre-mRNA-splicing factor CWC25 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	t	56	Total 418	C 259	N 80	O 79	0	0

- Molecule 24 is a protein called Splicing factor YJU2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	u	157	Total 1286	C 819	N 226	O 231	S 10	0	0

- Molecule 25 is a protein called Protein FRG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	x	30	Total 239	C 149	N 49	O 40	S 1	0	0

- Molecule 26 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
26	6	5	Total 5	Mg 5	0

- Molecule 27 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$).

IHP
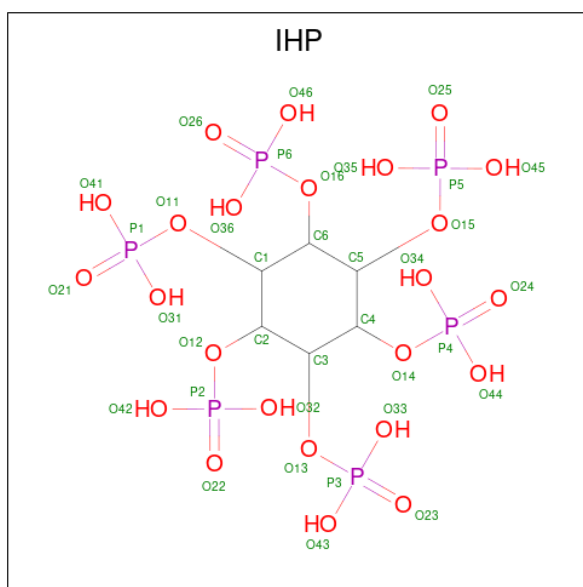
Mol	Chain	Residues	Atoms				AltConf
27	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 28 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

GTP
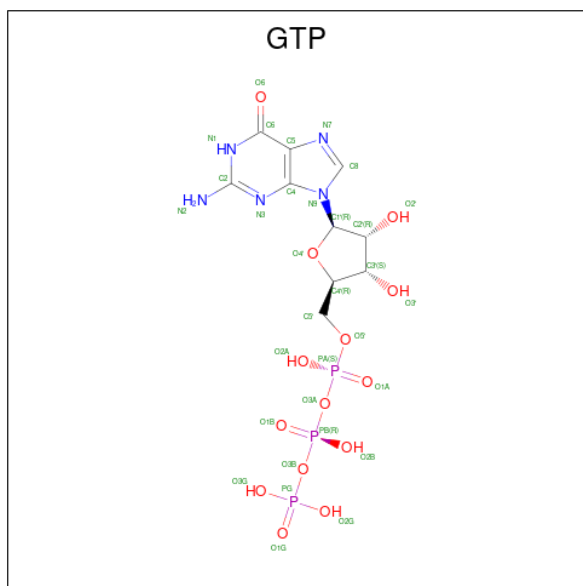
Mol	Chain	Residues	Atoms					AltConf
28	B	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 29 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
29	P	3	Total 3	Zn 3	0
29	Q	3	Total 3	Zn 3	0
29	u	1	Total 1	Zn 1	0

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 and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: U2 snRNA

Chain 2: 5% 6% · 86%

- Molecule 2: U5 snRNA

Chain 5: 50% 11% · 36%

- Molecule 3: U6 snRNA

Chain 6: 56% 42% ·

- Molecule 4: Corepressor interacting with RBPJ 1

Chain 9: ·· 97%

ASN VAL ARG CYS ILE LYS CYS HIS LYS TRP GLY HIS VAL ASN THR ASP ARG GLU CYS PRO LEU PHE GLY LEU SER GLY ILE ASN ALA SER SER VAL PRO THR ASP GLY SER GLY PRO SER MET HIS PRO SER GLU LEU ILE ALA GLU MET ARG ASN SER GLY PHE ALA LEU LYS ARG ASN

VAL LEU GLY ARG ASN LEU THR ALA ASN ASP PRO SER GLN GLU TYR VAL ALA SER GLU GLY GLU GLU GLU ASP PRO GLU VAL PHE GLU LYS SER LEU THR THR LYS GLN LYS GLN LYS LEU LEU LEU ARG LYS LEU ASP ARG LEU GLU LYS LYS LYS LYS ASP ARG LYS LYS

PHE GLN LYS ARG SER HIS LYS HIS LYS SER SER SER SER SER SER SER SER SER THR GLU THR GLU GLU SER SER SER GLU GLU SER GLU ASN ASN LYS GLU LYS LYS ILE GLN ARG LYS ARG LYS LYS ASN ASN CYS SER GLY HIS ASN ASN

SER ASP SER GLU LYS SER LYS HIS LYS ARG LEU HIS GLU LEU SER SER HIS ASN GLU LYS LYS GLU LYS PRO ARG PHE LEU HIS GLU SER SER ARG ASP SER LYS TRP SER SER ASP ASP LYS SER ARG THR HIS LYS HIS

SER PRO GLU ARG GLY GLU ARG GLU GLY SER SER HIS GLY ARG GLU GLU ARG SER ARG SER ARG SER ARG GLY PRO TYR LYS GLN ARG GLU THR ARG LYS ARG ALA GLN ARG ASN PRO GLY GLU GLU GLN SER ARG ASN ASP ARG SER ARG SER HIS

GLY THR ASP LEU TYR ARG GLY GLU LYS MET TYR ARG GLU GLU HIS PRO GLY GLY THR HIS LYS THR VAL THR GLN ARG GLU

• Molecule 5: Pre-mRNA-processing-splicing factor 8

Chain A:

S1648 K1649 D1650 D1653 Y1660 R1667 D1670 S1673 K1683 D1690 S1693 V1701 I1705 Y1715 G1716 N1717 W1718 F1719 K1723 I1726 A1729 I1733 R1746 K1749 Q1752 S1755

• Molecule 6: 116 kDa U5 small nuclear ribonucleoprotein component

Chain B:

75%   18%   • 6%

MET ASP THR ASP LEU TYR ASP GLU PHE GLY ASN TYR ILE GLY PRO GLU LEU ASP ASP SER ASP GLU ASP ASP GLU LEU GLY ARG GLU THR LYS ASP LEU ASP GLU MET ASP ASP ASP ASP ASP ASP VAL GLY ASP HIS ASP HIS PRO GLY MET GLU VAL **V58** **A69**

I80 P92 I93 L109 **P110** V111 T112 D124 I129 R130 L134 H137 H140 C148 T153 I157 R158 C166 Y167 T168 D169 I170 L171 E174 I181 K182 S183 V186 V189 D192 T193 L199 F200 N201 I202 M203 **D204** G207 **E214** V215

T216 R220 G224 V235 M236 L237 N238 T239 **L242** I243 V255 K259 I260 D261 R262 L263 L269 P270 P271 K277 V282 D283 E284 V285 L300 S301 P302 L303 L304 **I316** L320 K325 E338 K341 R342 K359 S365 **Q366** R367 S368 F369 V370 E371

F372 I373 D389 T404 E407 L408 R413 L416 R417 C420 D432 V435 Q436 H437 I438 K448 I449 E450 H451 T452 **M465** L474 M475 C476 I501 L516 Q523 I524 C525 T526 L530 A535 R536 Y537 P545 I552 P558 K561 T564

I565 T566 E567 Q575 I576 F577 R578 P579 L580 S598 E599 L600 D605 R608 Y614 E622 H627 L637 V640 R645 E650 F662 C663 E664 T678 P679 N680 I688 L696 I700 V705 F717 F718 Q719 W724 I732 W733 P737

G741 L745 V746 **E753** K763 L779 F789 K790 A797 H802 R803 Q807 T811 L827 M828 E829 Y832 F833 V834 D841 C842 V846 R854 D860 P864 I871 K872 I875 P876 D879 L887 S899 V900 F901 H902 H903 W904 Q905 I906

L929 E932 K936 T937 R938 L943 F952

• Molecule 7: SNW domain-containing protein 1

Chain C:

36%   5%   58%

MET ALA LEU THR SER PHE LEU PRO ALA PRO THR GLN SER GLN LEU SER GLN ASP GLN GLN LEU GLU GLU ALA GLU GLU LYS ALA ARG SER GLN ARG SER ARG GLN THR SER LEU VAL SER SER ARG GLU PRO PRO TYR GLY TYR ARG LYS GLY TRP ILE PRO ARG LEU GLU ASP PHE GLY ASP

GLY GLY ALA PHE PRO GLU **I67** R78 L86 I101 Q104 **S107** Y113 S114 K115 L119 N126 A127 D128 L132 Q133 R134 E142 K146 V155 **S156** **Q157** **A161** **P164** V165 R166 **A167** **A168** **D169** K170 **L171** **A172** **P173** N189 R195 V196 **I197** R198

E201 D205 E208 P209 P210 R211 P222 V229 **M230** H231 S232 Q242 Q243 E244 P248 D265 LYS ARG ALA ALA ASP GLY ARG GLY LEU GLN THR V278 GLU V302 MET ARG ALA GLN VAL GLU ARG LYS MET ALA GLN LYS GLU LYS GLU LYS HIS GLU LEU GLU ARG ASN GLU

ARG GLU MET ALA GLN LYS ALA ALA ARG GLU ARG ALA GLY ILE LYS THR HIS VAL GLU LYS GLU ASP GLU GLY ALA ALA ARG GLU GLU GLU ARG ALA LEU ALA ALA PRO ASP LYS ARG GLU SER LYS LEU GLU LYS GLU ARG ASN GLU

ASN ARG ASP ILE SER GLU VAL ILE ALA LEU GLY VAL PRO ASN PRO THR SER ASN GLU VAL GLN ASP TYR ASP ASP ASP ILE LYS MET TYR ASP VAL TYR ASP ALA TRP PRO ARG GLY GLY LYS ASP ASP MET ALA

GLN SER ILE TYR ARG PRO SER LYS ASN LEU ASP ASP LYS MET TYR GLY ASP ASP ILE LYS ALA ARG ILE LYS THR ASN ARG PHE VAL PRO ASP ARG SER GLU PHE SER GLY SER ASP ARG GLN GLN GLY PRO VAL GLN LEU GLU ILE ARG ASN GLU

LEU GLU GLU ALA LYS GLN HIS GLY SER LYS ARG PRO SER ASP SER ARG PRO LYS GLU HIS GLU GLY HIS GLU GLY LYS LYS ARG ARG LYS GLU

• Molecule 8: Pleiotropic regulator 1

Chain D: 46% 14% • 39%

MET VAL GLU GLU VAL GLN LYS HIS SER VAL HIS THR LEU VAL PHE ARG SER LEU LYS ARG THR HIS ASP MET PHE VAL ALA ASP ASN GLY LYS PRO VAL PRO LEU ASP GLU GLU SER HIS LYS ARG MET ALA ILE LYS LEU ARG ASN GLU TYR GLY PRO VAL LEU HIS MET PRO THR

SER LYS GLU GLN ASN LEU LYS GLU LYS GLY LYS PRO GLN ASN ALA THR ASP SER THR TYR VAL HIS LYS GLN ILE TYR PRO ALA ASN GLN GLY GLU VAL GLU TYR PHE VAL ALA GLY THR HIS PRO TYR PRO PRO GLY PRO GLY VAL ALA LEU THR ALA ASP THR LYS ILE ARG MET PRO SER GLU

SER ALA ALA GLN SER LEU VAL ALA LEU PRO LEU GLN THR LYS ALA ASP ALA ASN ARG THR ALA PRO SER GLY SER GLU GLU TYR ARG HIS PRO GLY ALA ASP SER ASP ARG PRO GLN ASN PRO THR ALA MET ASN SER ILE VAL MET GLU THR GLY TYR ASN THR LYS ASN SER ALA ALA LEU MET ALA LYS

LYS ALA PRO THR MET P186 L196 I200 E213 P214 W218 F219 V220 L240 I246 V249 V254 S255 T256 R257 Y260 L261 F262 S263 C264 G265 E266 D267 C272 W273 D274 L275 E276 R282 H287 A290 V291 L294 D301 C306 S307 R308 D309

R313 I314 H324 V333 A334 H350 D351 T352 T353 I354 D358 R365 T369 K372 V375 H381 P382 R383 K399 F400 P401 D402 L409 L419 D424 G425 V426 L427 W439 R442 T443 G444 Q455 P456 G457 S458 L459 E462 S473 E474 S475

L478 E481 T485 I486 K487 V488 D492 T496 E497 E498 T499 H500 PRO VAL SER TRP LYS GLU ILE ILE LYS PRO ARG ARG ARG PHE

• Molecule 9: Pre-mRNA-processing factor 17

Chain E: 11% • 87%

MET SER ALA ALA ILE ALA ALA LEU ALA ALA SER TYR GLY SER GLY SER GLY SER GLU ASP SER SER ASP SER GLU SER GLY SER ARG CYS PRO LEU PRO ALA ALA ASP SER LEU MET HIS LEU THR LYS SER PRO SER LYS PRO SER LEU PRO SER LEU ALA VAL ALA VAL ASP SER ARG ALA PRO GLU VAL

ALA VAL LYS GLU ASP LEU GLU LEU THR GLY V70 A90 P91 E92 N97 P98 T101 R108 L111 I120 M124 Q128 L139 N145 H146 Q147 VAL SER ALA LYS TYR ILE GLY SER VAL GLU GLU GLU ALA GLU LYS SER ASN GLN GLY LEU THR VAL PHE GLU GLU THR GLY GLN

LYS LYS THR GLU LYS ARG LYS LYS PHE LYS GLU ASN VAL LYS GLU MET TYR ASP TYR GLN GLY ARG SER ILE ASP GLY PHE LEU GLY PRO TRP ALA LYS TYR TYR VAL ASP GLU ASP LYS VAL VAL GLY ASN LEU ILE ARG SER THR MET PRO GLU GLU GLN GLU LEU GLU ASP GLU ILE THR ALA LYS ARG GLN GLN LYS GLY LYS LYS GLN GLU GLU

LYS PRO GLY GLU GLU GLU LYS SER THR ILE LEU GLU HIS VAL LYS GLU MET TYR ASP TYR GLN GLY ARG SER ARG PHE LEU VAL PRO TRP GLU VAL TYR GLU GLU GLY ASP ARG CYS LEU GLU ARG THR PHE ILE GLY HIS SER LYS ALA VAL ARG ASP ILE CYS PHE ASN THR ALA GLY THR PHE LEU LEU SER ALA ALA TYR

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

ASP ARG TYR LEU LYS LEU TRP ASP THR GLU THR GLY TYR GLN THR GLY GLN LYS ILE SER VAL MET ASP ALA CYS MET SER ASP LYS LYS ILE PHE VAL LYS GLY HIS SER LYS ALA VAL ARG ASP ILE CYS PHE ASN THR PHE GLU ALA LYS LEU ARG TRP SER ASP ASP ILE ARG SER GLY ILE VAL GLN

GLU TYR ASP ARG HIS LEU GLY ALA VAL ASN THR ILE VAL PHE VAL ASP ASN ARG PHE VAL SER THR SER ASP ASP LYS LEU ILE PHE LYS TYR ALA GLU MET SER ASP LYS LYS ILE ALA GLU PRO SER MET HIS SER MET PRO ALA VAL THR LEU SER ARG ASN GLU TYR ASP ARG HIS LEU GLY ALA VAL ASN THR ILE VAL PHE VAL ASP ASN ARG PHE VAL SER THR SER ASP ASP LYS LEU ILE ARG VAL GLY ILE LEU VAL GLN

GLY LYS TRP LEU ALA CYS GLN SER SER MET ASP ASN GLN ILE LEU ILE PHE GLY ALA GLN ASN ARG PHE LYS ARG ASP LYS ASN LYS LYS ILE PHE LYS GLY HIS MET VAL ALA GLY TYR ALA CYS GLN LEU ASP LEU THR CYS GLY LYS TRP LEU ALA SER GLY SER GLU ASP ARG SER VAL TYR VAL TRP ILE SER ASP GLY ASN GLY LYS LEU

ASN ILE TRP ASP TRP LYS THR LYS LEU TYR SER ARG ALA HIS ASP HIS LEU PHE VAL ALA CYS SER VAL ILE CYS GLY ALA VAL TRP HIS PRO HIS GLU THR SER LYS VAL ILE THR CYS GLY TRP ASP GLY LEU ILE LYS LEU TRP ASP

• Molecule 10: U5 small nuclear ribonucleoprotein 40 kDa protein

Chain F:

62%   21%   •   16%

• Molecule 11: Cell division cycle 5-like protein

Chain L:

23%   •   75%

• Molecule 12: Crooked neck-like protein 1

Chain O:

25%   5%   70%

MET THR ALA THR VAL GLU ASN LEU THR PHE GLN LYS ASP THR LEU GLY ASN ALA VAL ASP LYS ASN THR SER SER ARG LEU GLU ARG SER TYR SER LEU ALA GLY ARG HIS GLY SER THR GLU PRO LEU VAL LEU ALA TRP SER SER GLN PHE ARG ARG LEU THR TRP GLY CYS ALA LEU

ASP ALA LEU HIS ARG SER CYS VAL ALA ALA SER GLN HIS GLY VAL THR HIS LEU ILE ARG SER SER ARG THR PRO HIS SER THR ARG CYS SER ARG LYS GLU ASP ALA GLN PRO GLY HIS GLY GLY ASN GLY ALA ALA SER VAL THR ALA GLN ALA ARG GLY GLN ARG SER VAL LEU GLN

VAL PRO LEU PRO VAL PRO ARG SER CYS LEU PHE SER GLU SER PHE VAL VAL SER VAL SER SER GLN SER ARG PHE LEU ALA SER VAL PRO GLY THR GLY VAL GLN ARG SER THR ALA ALA ASP MET ALA ALA SER THR ALA ALA GLY LYS ARG ILE PRO LYS VAL ALA LYS **V179** **K180**

N181 **E202** **L203** GLU LEU LEU PRO PRO PRO GLN GLN LYS ILE **T215** **K227** **R228** **E232** **I235** **R236** **K237** **I242** **W251** **E252** **I258** **Q259** **R260** **A261** **R262** **R267** **D270** **V271** **D272** **L278** **Y282** **M285** **E286** **Q291** **V292** **N293** **R296** **W299** **D300** **R301** **A302**

I303 **T317** **E321** **N325** **M337** **E343** **W346** **H347** **D360** **R363** **H373** **P374** **D375** **N378** **V403** **E409** **D412** **V416** **D441** ARG ILE SER LYS GLN ASP ALA GLN GLU LEU PHE LYS ASN TYR THR ILE PHE GLU LYS LYS PHE GLY ASP ARG ARG GLY

ILE GLU ASP ILE ILE VAL SER LYS ARG ARG PHE GLN TYR GLU GLU VAL LYS ALA ASN PRO HIS ASN TYR ASP ALA TRP PHE ASP TYR LEU ARG LEU ILE ASN VAL TYR GLN LEU ARG LEU ALA SER LEU GLU LEU GLU ASP ALA GLU GLU VAL ARG GLU VAL TYR GLU ARG ALA ILE ALA ASN VAL PRO PRO ILE GLN GLU GLU LYS

ARG HIS TRP LYS ARG TYR ILE LEU TYR LEU TRP ILE ASN ALA LEU GLU TYR GLU GLU ALA LYS ASP PRO GLU ARG THR ARG GLN VAL VAL LEU TYR GLN TYR GLN ALA SER LEU GLU LEU ILE PRO HIS LYS LYS PHE THR PHE ALA LYS MET TRP ILE LEU TYR ALA GLN PHE GLU ILE ARG GLN LYS

ASN LEU SER LEU ALA ARG ARG ALA LEU GLY THR SER ILE GLY LYS CYS PRO LYS ASN LYS LEU PHE LYS VAL TYR ILE GLU LEU GLU LEU GLN LEU ARG GLU GLU PHE ASP CYS ARG LYS LEU TYR GLU VAL PHE LEU GLU ALA GLY PRO GLU GLN ALA ASN CYS THR SER TRP ILE LYS PHE ALA

GLU LEU GLU THR ILE LEU GLY ASP ILE ASP ARG ALA ARG ALA ILE TYR GLU LEU ALA ILE SER GLN PRO ARG ASP MET PRO GLU VAL VAL LEU GLN LEU TRP LYS SER TYR ILE ASP PHE GLU ILE GLU GLU GLU THR GLU ARG THR ARG ASN LEU TYR ARG ARG LEU LEU GLN ARG THR GLN

HIS VAL LYS VAL TRP ILE SER PHE ALA GLN PHE GLU GLU SER SER GLY LYS LYS ARG ARG LYS VAL GLN ILE LEU THR LYS CYS ARG GLN ILE TYR GLU GLU ALA LYS THR MET LEU LEU GLU SER TRP ARG ASN SER PHE GLU GLU GLN PHE GLY THR

ALA SER ASP LYS GLU ARG VAL ALA VAL ASP LYS LEU LEU MET PRO GLU LYS VAL LYS ARG ARG LYS VAL GLN GLU GLU THR TRP ILE LYS PHE ALA GLN GLN GLU PHE GLY THR

GLN GLN GLN GLU LYS GLU GLU ASP ALA GLU HIS HIS PRO ASP GLU ASP VAL ALA VAL ASP GLU SER GLU SER

• Molecule 13: Pre-mRNA-splicing factor RBM22

Chain P:

72%   16% • 11%

MET ALA THR SER LEU GLY SER ASN THR TYR ASN ARG GLN ALA ASN **W15** **E16** **F20** **P21** **I22** **G29** **E30** **N31** **P32** **M36** **Y41** **C45** **K46** **W57** **K66** **K67** **T68** **C71** **Q72** **V80** **C81** **Q82** **E89** **L92** **P93** **I94** **Q95** **V96** **R123** **T131** **R132** **P133** VAL

GLY MET LEU GLY LYS ALA THR SER **T143** **S144** **D145** **M146** **L147** **L150** **P162** **R175** **R182** **H183** **E184** **D191** **P192** **L193** **Q196** **D207** **P208** **V209** **L213** **S218**

• Molecule 14: Protein BUD31 homolog

Chain Q:

85%   10%   • •

MET PRO K3 K9 A10 G14 L17 K42 S45 L46 L63 I79 A84 Q95 C101 C102 C105 C117 R120 C134 C137 G138 C139 C142 S143 G144

• Molecule 15: Spliceosome-associated protein CWC15 homolog

Chain R:

32% 6% 62%

MET THR THR ALA ARG PRO THR PHE GLU PRO ALA GLY ARG GLY GLY LYS GLU GLY GLY ASP L23 L26 Y30 L35 I41 E52 R55 N56 R57 E62 N75 ARG ASP ARG PRO THR ARG GLU GLU HIS THR THR SER SER VAL SER LYS LYS PRO ARG

LEU ASP GLN ILE PRO ALA ALA ASN LEU ASP ALA ASP ASP ASP PRO LEU THR ASP ASP GLU GLU ASP ASP PHE GLU GLU GLU SER ASP ASP ASP ASP THR ALA LEU LEU LEU ALA GLU LEU GLU LYS ILE LYS LYS GLU ARG ALA GLU GLN GLN ALA ARG LYS GLU GLN LYS GLU GLN LYS ALA GLU

GLU GLU ARG ILE ARG MET GLU ASN ILE LEU SER GLY PRO LEU LEU ASN LEU THR GLY PRO SER GLN PRO GLN ALA ASN PHE LYS VAL LYS ARG ARG TRP ASP ASP VAL VAL PHE LYS N196 C197 A198 K199 G200 V201 D202 D203 Q204 K205 K206 D207 D213 T214 L215 R216 K222

K229

• Molecule 16: Serine/arginine repetitive matrix protein 2

Chain S: 99%

M1 I5 R11 V19 S24 R29 R30 GLY GLU ARG PRO ASP TYR LYS GLY GLU GLU GLU LEU ARG ARG LEU GLU ALA LEU VAL LYS ARG PRO ASN PRO ASP ILE LEU ASP HIS GLU ARG LYS ARG ARG VAL GLU LEU ARG CYS LEU GLU LEU GLU GLU MET MET GLU

GLU GLN GLY TYR GLU GLU GLN ILE GLN GLU LYS VAL ALA THR PHE ARG LEU MET LEU LEU GLU GLU LYS ASP VAL ASN PRO GLY GLY LYS GLU GLU THR PRO GLY GLN GLN ARG PRO ALA VAL THR GLU HIS GLN LEU ALA LEU ASN LEU LYS LYS LYS ASN GLU ARG ARG ALA ALA

PHE GLY ILE SER ASP SER TYR VAL ASP GLY SER SER PHE ASP PRO GLN ARG ARG ARG GLU ALA ALA LYS GLN GLN PRO ALA PRO GLU PRO LYS GLU GLU TYR SER LEU VAL ARG GLU SER SER ARG SER PRO THR PRO LYS GLN LYS LYS LYS LYS LYS LYS LYS LYS ASP ARG GLY ARG

ARG SER GLU SER SER SER PRO ARG ARG GLU GLU ARG LYS SER SER SER LYS LYS HIS ARG SER GLU LEU SER GLU LYS SER HIS ARG ARG SER PRO THR PRO LYS SER ARG SER GLU THR PRO ALA PRO LYS LYS SER ARG

ARG ALA HIS ARG SER THR SER ALA ASP SER ALA SER SER ASP THR ARG SER ARG SER ARG SER ALA ALA ALA LYS THR HIS THR ALA LEU GLY ARG SER PRO THR PRO LYS SER ARG SER GLU GLU SER PRO ALA SER GLY GLU ASP ALA PRO PHE SER GLU PRO GLY THR GLY THR SER THR

GLN ARG PRO SER PRO GLU THR ALA THR LYS GLN GLU PRO SER SER PRO THR TYR GLU ASP LYS ASP LYS SER ASP THR ARG ASP SER PRO PRO ALA THR PRO SER GLU ARG SER SER THR GLY SER PRO ALA PRO LYS HIS GLY SER PRO

GLN PRO LEU ALA THR THR PRO LEU SER GLN GLU PRO LYS VAL ASN PRO PRO SER GLU ALA THR ARG ASP SER ARG ARG LYS SER GLU LYS LEU LEU PRO GLN ARG SER PRO GLU ARG SER SER GLU THR SER ARG PRO ALA GLU LEU ALA GLU ARG HIS GLY GLY SER PRO

GLU SER PRO LYS PRO ALA PRO ALA PRO GLY SER HIS ARG GLU ILE SER SER SER PRO THR SER LYS ASN ARG SER HIS GLY ILE ARG ALA ALA LYS ASP LYS SER HIS SER THR PRO SER ARG ARG GLN PRO ALA THR ALA LYS ARG GLY ARG SER ARG SER ARG MET GLY SER ARG SER SER PRO ALA SER GLN SER ARG ALA THR ARG ALA LYS ARG GLY ARG SER ARG SER ARG

THR PRO THR LYS ARG GLY HIS SER ARG SER SER PRO GLN TRP ARG ARG SER ARG SER ALA GLN ARG TRP GLY ARG SER ARG PRO GLN ARG ARG GLY ARG SER ARG PRO GLN ARG ARG GLY PRO GLY TRP SER SER ARG ARG ASN THR GLN ARG ARG GLY ARG SER ARG SER ALA ARG

ARG GLY ARG SER HIS SER ARG SER PRO ALA THR ARG ARG SER GLY ARG SER SER ARG PRO ALA ARG ARG GLY SER SER ARG SER ARG SER ARG PRO ALA ARG ARG GLY ARG SER SER ARG SER ALA ARG

GLY TYR HIS SER ARG SER PRO ALA ARG GLN GLU SER SER ARG SER THR SER SER ARG ARG ARG GLY ARG SER ARG THR PRO PRO THR THR SER ARG LYS ARG SER SER ARG ARG THR SER PRO ALA PRO TRP LYS ARG SER SER SER ARG ALA SER PRO ALA THR HIS ARG ARG SER ARG SER

ARG THR PRO LEU ILE SER ARG ARG SER ARG SER ARG THR SER PRO VAL SER ARG ARG SER ARG SER THR SER VAL THR ARG ARG SER ARG SER ARG THR PRO VAL THR ARG ARG SER ARG SER ARG THR PRO VAL THR ARG ARG SER ARG ARG

THR PRO THR ARG ARG SER ARG ARG SER THR PRO VAL THR ARG ARG SER ARG SER THR PRO VAL THR ARG ARG SER ARG SER THR PRO ILE THR ARG ARG SER ARG SER THR PRO VAL THR ARG ARG SER SER ARG THR

SER PRO VAL THR ARG ARG SER ARG SER THR PRO VAL THR ARG ARG SER ARG SER ARG THR PRO ALA ILE ARG ARG SER ARG SER THR PRO LEU LEU ARG LYS ARG SER ARG SER PRO LEU ILE ARG ARG SER ARG SER ARG THR

PRO ARG THR ALA ARG GLY LYS ARG SER LEU THR ARG SER PRO PRO ALA ILE ARG ARG SER SER ALA GLY SER SER ASP ARG SER ARG ALA THR PRO PRO ALA THR ASN HIS GLY SER ARG THR PRO VAL ALA LEU ASN SER ARG MET CYS PHE SER

ARG PRO SER MET SER PRO THR PRO LEU ASP ARG CYS SER PRO GLY MET LEU GLU PRO LEU GLY SER SER ARG THR PRO MET SER VAL LEU GLN ALA GLY GLY SER MET MET ASP GLY PRO GLY PRO ARG ILE PRO HIS GLN ARG THR SER VAL PRO GLU HIS ALA GLN

SER ARG ILE ALA LEU ALA LEU ALA ILE SER LEU GLY THR ALA ARG PRO PRO SER MET SER ALA GLY LEU ALA ARG MET GLN VAL PRO ALA PRO VAL PRO LEU MET SER LEU ARG THR ALA PRO ALA ASN LEU SER ARG ILE ALA SER ALA ALA

ALA MET ASN LEU ALA SER ALA ARG THR PRO ALA ILE PRO THR ALA VAL ASN LEU ALA ASP SER ARG THR PRO ALA ALA ALA MET ASN LEU ALA SER PRO ARG THR ALA VAL ALA PRO ALA VAL ASN LEU ALA SER PRO ARG THR PRO ALA VAL ASN LEU ALA

GLY ALA ARG THR PRO ALA ALA LEU ALA LEU SER LEU THR GLY SER GLY THR PRO PRO THR ALA ALA ASN TYR PRO SER SER ARG THR PRO GLN ALA PRO ALA SER ALA ASN LEU VAL GLY PRO ARG SER ALA HIS THR ALA PRO VAL ASN ILE ALA GLY SER ARG THR ALA

ALA ALA LEU ALA PRO ALA SER LEU THR SER ALA ARG MET ALA PRO ALA LEU SER GLY ALA ASN LEU THR SER PRO ARG VAL PRO LEU SER ALA TYR GLU VAL GLY ARG THR SER PRO LEU LEU ASP ARG ALA ARG SER ARG THR PRO SER ALA PRO SER GLN SER ARG

MET THR SER GLU ARG ALA PRO SER PRO SER ARG MET GLY GLN ALA PRO SER GLN SER LEU PRO ALA GLN ASP GLN PRO ARG SER PRO VAL SER ALA PHE SER ASP GLN SER ARG CYS LEU ILE ALA GLN THR THR PRO VAL ALA GLY SER GLN SER LEU SER GLY

ALA VAL ALA THR THR SER SER ALA GLY ASP HIS ASN GLY MET SER VAL PRO ALA PRO GLY VAL PRO HIS SER ASP VAL GLY SER GLU PRO ALA SER THR GLY ALA GLN GLN PRO ALA LEU ALA LEU GLN PRO ALA LYS GLU ARG SER SER SER SER SER

SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER GLY SER SER SER SER ASP SER GLU GLY SER SER LEU PRO VAL GLN PRO GLU VAL ALA LEU LYS ARG VAL PRO SER PRO THR PRO ALA LYS GLU ALA VAL GLU GLY ARG SER SER SER SER PRO

THR PRO ALA LYS ARG ARG SER ARG SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER SER PRO SER PRO ALA LYS PRO GLY PRO GLN ALA

LEU PRO LYS PRO ALA SER PRO LYS LYS SER PRO PRO GLY GLU ARG SER ARG SER PRO ARG LYS PRO ILE ASP LEU ARG ASP SER ARG ARG LEU SER TYR SER PRO VAL GLU ARG ARG PRO SER GLN PRO SER ARG ASP GLN SER SER SER GLU ARG GLY

SER ARG ARG GLY GLN ARG GLY ASP SER ARG SER PRO ARG HIS LYS ARG ARG GLU THR PRO SER PRO ARG PRO MET ARG HIS ARG SER SER ARG PRO

• Molecule 17: Pre-mRNA-splicing factor CWC22 homolog

Chain T:　████████████ 19%　·　　　　　　78%

MET LYS SER SER VAL ALA GLN ILE LYS PRO SER SER GLY HIS ASP ARG ARG GLU GLN ASN LEU LEU ASN SER SER PRO GLU ARG TYR GLN GLU GLU GLN GLU ARG SER PRO ARG ASP ALA SER ALA GLU ASP TYR PHE ASP TYR SER ARG ARG ASP SER ARG GLY ARG

SER TYR ASP SER GLU MET GLU SER ARG ASN ARG ASP ARG ARG GLU LYS ARG GLU GLU ARG ASP ALA ASP THR ASP SER ASP LYS ARG ASP ARG ARG SER ARG SER PRO ARG SER PRO GLY ARG ARG ASN PRO GLU THR GLU VAL THR GLN SER SER ALA GLN GLU GLU PRO ALA THR LYS LYS LYS ASP

GLU LEU ASP PRO LEU LEU THR ARG THR GLY GLY ALA TYR ILE PRO PRO ALA LYS LEU ARG MET MET GLN GLU ILE ILE THR ASP LYS ASN SER LEU ALA TYR GLN ARG MET SER TRP GLU ALA LEU LYS LYS SER ILE ASN GLY LEU ILE ASN LYS VAL ASN ILE SER ASN ILE SER ILE

ILE ILE GLN GLU LEU LEU GLN GLU ASN ILE ILE VAL ARG GLY ARG GLY LEU LEU LEU SER ARG SER VAL LEU LEU GLN GLN ALA GLN ALA SER ALA PRO ILE PHE THR HIS VAL TYR ALA ALA LEU VAL ALA ILE ILE ILE ASN SER LYS PHE PRO GLN ILE GLY LEU ILE LEU LEU LYS ARG LEU ILE LEU ASN

PHE ARG LYS GLY TYR ARG ARG ASN ASP LYS LEU GLN LEU CYS LEU THR ALA SER LYS PHE VAL ALA HIS LEU ILE LEU ASN GLN ASN VAL ALA HIS GLU VAL VAL LEU LEU CYS LEU GLU MET LEU THR LEU LEU LEU GLU ARG PRO THR ASP SER VAL GLU VAL ALA ILE GLY PHE LEU LYS GLU CYS

GLY LEU LYS THR GLN VAL SER PRO ARG GLY ILE ALA ILE GLU ARG ARG ASN LEU HIS SER GLU ASP LYS ARG VAL GLN TYR MET ILE GLU VAL MET PHE ALA VAL ARG LYS ASP PHE SER HIS PRO ILE LEU LEU GLU GLY GLY LEU ASP LEU VAL

GLU GLU ASP GLN PHE HIS MET PRO LEU ASP ASP PRO ASP ASP VAL LEU ASN VAL PHE LYS MET ASP PRO ASN PHE MET GLU GLU GLU LYS TYR LYS ILE LYS GLU VAL ALA ILE LYS LYS ILE ASP GLY ASP SER SER THR ASP GLN ASP ASP ALA GLY

SER SER GLU GLU ASP GLU GLU GLU GLU GLU GLU GLU GLY GLU ASP GLU GLU GLY GLN LYS VAL THR ILE HIS ASP LYS THR **E449** I450 I463 Q464 S465 S466 L467 E470 L476 L477 I493 R513 F514 C515 M516 S524 F525 I528 Y533 D534 T535 R538

S563 V564 L565 E566 C567 I568 T574 T575 Q588 E592 L596 N600 L603 L608 F611 F612 L616 P617 R618 P651 LYS VAL ILE VAL ALA GLN LYS PRO ASP VAL GLU GLN ASN LYS SER SER PRO SER SER SER ALA SER SER SER GLU SER ASP

SER SER ASP SER ASP SER ASP SER ASP SER ASP SER GLU SER ASP SER SER GLU GLU SER ASP SER SER ILE SER HIS SER SER ALA SER ALA ASN ASP VAL ARG LYS GLY HIS GLY LYS THR ARG SER LYS ASN ASP VAL ARG LYS SER LEU ILE ARG ASN GLN THR ASN ASP

ARG LYS GLN LYS GLU ARG ARG GLN GLU GLY HIS GLY HIS GLN GLU GLU THR ARG THR GLU ARG GLU ARG SER GLU GLU LYS HIS ARG ASP ASN SER GLY ASN GLY SER ASN TRP ARG ASP PRO ILE THR LYS TYR THR SER ASP LYS ASP VAL PRO SER GLU ARG ASN ASN TYR SER ARG VAL ALA

ASN ASP ARG ASP GLN GLU MET HIS ILE ASP LEU GLU ASN LYS HIS GLY ASP PRO LYS LYS ARG GLY ARG ASN SER PHE SER ASN GLU LYS HIS THR ARG LYS ASP SER GLU ASN PHE ARG ARG LYS ASP ARG SER LYS SER GLU MET ASN ARG LYS HIS

SER GLY SER ARG SER ASP GLU ASP ARG TYR GLN ASN GLY ALA GLU ARG ARG TRP GLU LYS SER SER ARG TYR SER GLU GLN SER ARG GLU SER LYS LYS ASN GLN ASP ARG ARG ARG GLU GLN LYS SER PRO ALA LYS GLN LYS

- Molecule 18: Peptidyl-prolyl cis-trans isomerase-like 1

Chain V: 81% 17%

MET ALA A3 P12 N13 V14 E17 T18 G21 I22 L25 E26 L27 Y28 F53 H54 R55 I56 D59 I62 Q63 R72 A95 L116 T119 Q120 W121 L122 R131 E146 T147 N148 D151 R152 P153 S165 GLY

- Molecule 19: pre-mRNA

Chain Y: 7% 87%

G G G A A C G G A A U U G G A A G C U G C C C A C U C U G U G G A A U C G G A A C C C G C U C C G C C U C C C A A C G G59 U60

A61 A62 G63 A64 G65 C66 C67 U68 A69 G70 C71 A72 U73 G74 U75 A76 G77 A78 A79 U U G G U U A C C U G C C A C C U U G C C A G C U G U C C U G C C U U C C C A U C C U C U A G G G C C

A G G U A G U C C C A G G G U U C C U U G A141 U142 G143 A144 U145 G146 U147 C148 A149 C152 U159 G160 U C C U C U U U U U U U C C A C A G U U C C C G U G U

U G A G G A C A A A C U U U C C U U C C G G C U U C C C G C U A U U U C C U A A C C C U U C A G G G U

A C G A G C U U A G C C C A U G C C U A G A C A C A U C U U C A U A A C U A G G A A C C U A A C C C A U C A A G

G U A C G G A A U U C U C U A G A

• Molecule 19: pre-mRNA

Chain Z: ..   96%

G G G A C A C G G A A U U C G A G C U U C G C C C A C U C U U G G A U C G G A A A C C C C U **C46 C49 C57 G58** G U A A G A G C C

U A G C A U G U A G A A C U G G G U U A C U U G C A G A C C C C A A G C U U G C C U C G C A G U C U A G G G G C

C A G G G U U C C U U G A U C A U G A U G U C C A U U A C U C U U C C C U U U U U C C A C A C A G C U C G G G G U U

G A G G A C A A A C U U C U C C G G G U C U U C C U A G U G G G A U C C G A U A C C A U C A G G G U A

C G G A C U U A G C C C A U G G C G U A C A C C A U U A G C C A U G A G U A A G A U C U C C U A C A C C A U C A G G

G U A C G G A A U U C U C U A G A

• Molecule 20: WD repeat-containing protein 70

Chain p: 48%   .   50%

MET GLU ARG SER GLY PRO SER GLU VAL THR GLY SER ASP ALA SER GLY PRO ASP GLN LEU LEU ALA VAL THR MET GLY PHE THR GLY PHE GLY LYS LYS ALA ARG THR PHE ASP LEU GLU ALA MET PHE GLU GLN THR ARG ARG THR ALA VAL GLU ARG SER ARG LYS THR LEU GLU ALA

ARG GLU LYS GLU GLU MET ASN ARG GLU GLU LYS GLU LEU ARG ARG GLN ASN GLU ILE GLU LEU ASP PRO THR SER SER ARG SER ASN VAL VAL ARG ASP CYS SER LYS SER SER SER ARG ASP THR SER SER SER GLU GLU SER GLN GLN SER SER ASP SER ASP GLU ASP GLU ILE GLY PRO

PRO LEU PRO PRO LYS MET VAL GLY LYS PRO VAL ASN PHE MET GLU ASP ILE GLY PRO LEU PRO PRO LEU ASN GLU GLU GLU GLU ALA GLU GLU GLU GLU GLU GLU GLU ASN PRO VAL HIS ILE LYS PRO ASP SER **H174** ALA **M214** LEU **C227** PRO MET **L235** PHE ARG GLU

M300 ARG **C338** SER **L346** ARG **Q352** LYS **D406** ILE **F410** ASP **M426** PRO **F431** LYS **P501** HIS LYS SER GLN ARG GLY ALA LYS LEU CYS VAL VAL LYS THR GLN ARG LYS ALA GLU THR LEU THR GLN ASP TYR ILE VAL LYS ASN ILE ALA LEU ASP LYS THR ASP PRO MET PHE ARG GLU

PRO ARG GLN ARG SER THR ARG LYS GLN LEU GLU GLU LYS ASP LEU ARG ARG LEU ASP PRO LEU LYS SER HIS LYS LYS PRO GLU PRO PRO VAL ALA GLY PRO GLY ARG GLY ARG VAL GLY THR HIS GLY GLY LEU LEU SER TYR ILE VAL LYS ASN ILE ALA LEU ASP LYS THR ASP PRO MET PHE ARG GLU

PRO ARG GLU GLU ALA ILE LEU ARG HIS ALA LYS ALA ALA ASP SER SER PRO TYR TRP VAL SER PRO ALA TYR SER LYS THR GLN LEU PRO LYS THR MET PHE ALA GLN VAL GLU SER ASP GLU GLU ALA LYS ASN GLU PRO GLU TRP LYS LYS ARG ALA LYS ILE

• Molecule 21: Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16

Chain r: .   97%

MET GLY ASP THR SER GLU ASP ALA SER ILE HIS ARG GLU LEU GLU GLY THR ASP LEU ASP CYS GLN VAL GLY LEU LEU ILE CYS LYS SER LYS SER SER ALA ALA SER GLU GLU GLN HIS VAL PHE LYS ALA PRO ALA PRO ARG PRO SER LEU LEU GLY LEU ASP LEU LEU ALA SER GLU LEU LYS ARG ARG

GLU ARG GLU GLU LYS ASP ASP GLY GLU LYS LYS LYS SER VAL VAL SER SER TYR LYS ASP TRP GLU GLU LEU SER LYS ASP SER GLN LYS ASP ALA GLU GLU GLU GLY GLY ASP ALA GLY GLU ASN ILE ARG ASP ARG HIS TYR ARG SER ALA ARG VAL GLU GLU ILE ARG ASP SER ARG PRO SER HIS

PRO GLY GLY VAL SER GLU GLU PHE TRP GLU GLY SER ARG GLN ARG ARG GLU ARG GLU GLU HIS ARG GLU VAL TYR ALA SER LEU GLU LYS ASP TRP LYS SER GLU GLN LYS SER GLU ARG ASP ASP TYR ARG GLU LYS ASP ARG ASP ARG ASP ARG SER ARG HIS SER SER

ARG SER GLU ARG ASP GLY GLY SER GLU ARG SER ARG SER ARG ARG ASN GLU PRO GLU GLU SER PRO ARG HIS PRO LYS ASP ALA ALA THR PRO SER ARG SER THR TRP GLU GLU GLU ASP SER SER GLY TYR GLY SER SER ARG SER ARG SER GLN TRP GLU GLU SER PRO THR PRO SER TYR ARG

ASP SER GLU ARG SER HIS ARG LEU SER THR ARG ASP ASP ARG ARG SER VAL ARG GLY LYS TYR SER ASP ASP THR PRO LEU PRO THR PRO SER TYR LYS TYR ASN GLU ARG TRP ALA ASP ASP ARG ARG HIS GLU LEU GLY SER ARG THR PRO ARG LEU SER ARG GLY GLU ARG GLU GLY GLY

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

LYS ARG I363 N380 D394 F397 GLU GLU ASP ASN ALA ALA LYS VAL HIS LEU MET VAL HIS ASN LEU VAL PRO PRO PHE LEU ASP GLY ARG ILE VAL PHE THR LYS GLN PRO GLU GLU PRO VAL ILE PRO VAL LYS ASP ALA THR SER ASP ALA ILE ILE ALA ARG LYS GLY SER

GLN THR VAL ARG LYS HIS ARG GLU GLN LYS GLU ARG LYS LYS ALA GLN HIS HIS LYS HIS LEU TRP GLU LEU ALA GLY THR LYS LEU GLY LEU ASP ILE MET GLY VAL LYS LYS GLU GLU PRO ASP LYS ALA VAL THR GLU ASP GLY LYS VAL ASP TYR ARG THR GLN LYS PHE ALA ASP HIS

MET LYS ARG LYS SER GLU ALA SER SER GLU PHE ALA LYS LYS LYS SER ILE LEU GLU GLN ARG GLN TYR LEU PRO ILE PHE ALA VAL GLN GLN GLU LEU LEU THR ILE ILE ARG ASP ASN SER ILE VAL VAL ILE VAL GLY GLU THR GLY SER GLY LYS THR THR GLN LEU THR GLN TYR

LEU HIS GLU ASP GLY TYR THR ASP TYR GLY MET ILE GLY CYS THR GLN PRO ARG ARG VAL ALA ALA MET SER VAL ALA LYS ARG VAL SER GLU GLU MET GLY GLY ASN LEU GLY GLU GLU VAL GLY TYR ALA ILE ARG PHE GLU ASP CYS THR SER GLU ASN THR LEU ILE LYS TYR MET

THR ASP GLY ILE LEU LEU ARG GLU SER LEU ARG GLU ALA ASP LEU ASP HIS TYR SER ALA ILE ILE MET ASP GLU ALA HIS GLU ARG SER LEU ASN THR ASP LEU LEU GLY LEU LEU LEU ARG GLU LEU LEU PHE LEU ARG GLU LEU LEU ARG SER ASP ASP GLY LYS LEU VAL THR SER ALA THR MET ASP

ALA GLU LYS PHE ALA ALA PHE PHE GLY ASN VAL PRO ILE PHE HIS ILE PRO GLY ARG THR PHE PRO VAL ASP ILE LEU PHE SER LYS THR PRO GLN GLU ASP ALA ASP ILE ALA VAL LYS SER LEU VAL HIS SER LEU ALA PRO GLY ASP ILE LEU PHE MET PRO

GLY GLN GLU ASP ILE GLU VAL THR SER ASP GLN GLY ILE LEU ARG GLU VAL ASP HIS LEU GLU GLU LEU ASN ALA PRO LEU ALA LEU PRO ILE TYR SER GLN LEU PRO SER ASP ASP LEU GLN ALA LYS ILE PHE GLN GLN LYS ALA PRO ASP GLY VAL ARG LYS CYS ILE ALA THR ASN ILE ALA

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

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

ILE LEU GLY ALA LEU ASP ASN THR GLY GLY LEU THR SER THR GLY ARG LEU MET VAL GLU PHE PRO LEU ASP PRO ALA LEU SER LYS MET LEU ILE VAL SER ASP CYS ASP MET GLY CYS SER SER GLU ILE LEU LEU ILE VAL SER MET LEU SER VAL PRO ALA ILE PHE TYR ARG PRO LYS

GLY ARG GLU GLU GLU SER ASP GLN GLN ILE ARG GLU GLY LYS PHE ALA VAL PRO GLU SER ASP HIS LEU THR TYR LEU ASN VAL TYR LEU GLN TRP LYS ASN ASN ASN TYR SER THR ILE TRP CYS ASN ASP HIS PHE ILE HIS ALA LYS ALA MET ARG LYS VAL ARG GLU VAL ARG ALA GLN LEU

LYS ASP ILE MET VAL GLN GLN ARG MET SER LEU ALA SER CYS GLY THR ASP TRP ASP ILE VAL ARG LYS CYS ILE ALA ALA TYR PHE HIS GLN ALA ALA LYS LYS GLY ILE ILE GLY LEU LYS GLY ILE TYR VAL ASN ILE ARG THR GLY MET PRO CYS HIS LEU HIS PRO THR SER SER LEU PHE

GLY MET GLY TYR THR PRO ASP TYR ILE VAL TYR HIS GLU LEU VAL MET THR THR LYS GLU TYR MET GLN CYS VAL THR ALA VAL ASP ALA GLU TRP LEU ALA GLU LEU GLY PRO MET PHE TYR SER VAL LYS GLN ALA GLY LYS SER ARG GLN GLU ASN ARG ARG ARG ALA LYS GLU GLU

ALA SER ALA MET GLU GLU MET GLU MET ALA LEU ALA GLU GLU GLN GLN LEU ARG ALA ALA ARG GLN GLU GLN GLU LYS ARG SER ARG SER ILE LEU TYR PRO GLY GLY ARG LYS GLU GLU GLY GLY PRO MET THR THR PRO ARG ARG THR PRO ALA ARG PHE GLY LEU

• Molecule 22: Pre-mRNA-splicing factor ISY1 homolog

Chain s:

7%   93%

MET A2 R3 N4 E21 GLU GLY LYS VAL LYS GLU GLU ARG ARG PRO PHE LEU ALA SER GLU CYS THR GLU ILE ASP TRP ILE VAL ARG SER ASP TRP ILE LEU GLY LYS LEU PRO LYS ALA GLU GLU TRP ARG ARG ILE ILE GLY LEU ILE SER LYS LYS VAL ALA GLN ILE ASN GLN ASN ALA GLY LEU GLY LEU GLU PHE ARG ILE ARG ASP ASP LEU ASN ASP

GLU ILE ASN LYS LEU LEU ARG GLU GLU LYS GLY HIS TRP GLU VAL ARG ILE LYS GLU LEU GLY GLY PRO ASP TYR GLY LYS VAL GLY LYS MET LEU ASP HIS GLU GLY LYS GLU VAL PRO GLY ASN ARG GLY TYR LYS TYR PHE GLY ALA ALA LYS ASP LEU PRO GLY VAL ARG GLU LEU

PHE GLU LYS GLU PRO LEU PRO PRO PRO ARG LYS THR ARG ALA GLU LEU MET LYS ALA ILE ASP PHE GLU TYR TYR GLY TYR LEU ASP ASP GLU ASP GLY GLY VAL ILE VAL PRO LEU GLU GLN GLU TYR GLU LYS LEU ARG GLU LEU VAL GLU LYS TRP LYS ALA GLU ARG GLU ALA

ARG LEU ALA GLY GLU GLU GLU GLU GLU GLU GLU GLU GLU ILE ASN ILE TYR ALA VAL THR GLU GLU GLU SER ASP GLU GLY SER GLN GLU LYS GLY GLY ASP SER GLN GLY LYS PHE ILE ALA HIS VAL PRO VAL PRO SER GLN GLU ILE GLU GLU ALA LEU

VAL ARG ARG LYS LYS MET LEU LEU LYS TYR SER GLU LEU GLN ALA GLN ASN GLU GLU ALA ARG ARG LEU LEU GLY TYR

• Molecule 23: Pre-mRNA-splicing factor CWC25 homolog

Chain t: 13% 87%

MET G2 L8 A57 GLU ASP VAL GLY ALA VAL LYS LYS GLU LYS ASP TRP MET TYR GLN GLY PRO GLY GLY MET VAL ASN ARG ASP GLU TYR LEU LEU GLY ARG PRO ILE ASP LYS TYR VAL PHE GLU GLU MET GLU GLU LYS GLU ALA GLY CYS SER SER GLU THR

GLY LEU LEU PRO GLY SER ILE PHE ALA PRO SER GLY ALA ASN SER LEU ASP MET ALA SER LYS ILE ARG GLU ASP PRO LEU PHE ILE ILE ARG LYS GLU GLU GLU LYS ARG GLU VAL LEU ASN ASN PRO VAL MET LYS ILE LYS LEU GLN MET SER LEU

GLU LYS LYS GLU LYS LYS LYS LYS GLU LYS LYS LYS HIS LYS LYS HIS LYS ARG SER SER SER ASP ARG SER SER GLU ASP HIS SER ALA GLY ARG SER GLN LYS MET ALA ASN SER PRO VAL LEU SER LYS VAL PRO GLY TYR LEU GLN GLN VAL

ARG ASN SER ASP ARG ASN GLN GLY LEU GLN GLY PRO LEU THR ALA GLU GLN LYS ARG GLY HIS GLY MET LYS ASN HIS SER ARG SER ARG SER HIS SER PRO ARG HIS ALA SER LYS SER THR ARG GLU GLY ALA GLY SER ASP ARG ARG SER ARG SER LEU GLY ARG

ARG SER ARG SER PRO ARG SER LYS LEU HIS ASN SER LYS VAL ASN ARG GLU GLU THR GLY GLN THR ARG SER PRO SER PRO LYS GLU VAL VAL TYR GLN ARG ARG HIS ALA PRO GLY TYR THR ARG LYS LEU SER ALA GLU GLU LEU ARG LYS ARG GLN GLU GLU MET MET GLU ASN

ALA LYS TRP ARG GLU GLU ARG LEU ASN ILE LEU LYS ARG HIS ALA LYS ASP GLU GLU ARG GLU GLN GLN ARG LEU GLU LYS LEU GLU LYS ASP SER GLU ARG ASP ARG ALA ASP ARG ALA SER LYS SER LEU GLU GLU GLU ARG VAL LYS ARG ASN ILE TYR SER LEU

GLN ARG THR SER VAL ALA LEU GLU LYS ASN PHE MET LYS ARG

• Molecule 24: Splicing factor YJU2

Chain u: 83% 5% 12%

MET S2 K27 D28 C43 C46 G47 E48 C80 C83 K90 E101 Q109 ALA GLU LYS LEU LEU GLU GLU GLU GLU LYS ARG VAL GLN LYS GLU ARG GLU ASP GLU GLU L130 N131 N132 V136 R140 L178

• Molecule 25: Protein FRG1

Chain x: 12% 88%

MET ALA GLU GLU TYR SER TYR VAL LYS SER THR LYS LEU VAL LYS GLY THR LYS LYS SER LYS LYS LYS SER LYS LYS SER LYS LYS LYS SER ASP LYS ARG GLU LYS ARG GLU ASP GLU GLU THR GLN LEU ASP ILE VAL GLY ILE TRP TRP THR VAL THR ASN PHE GLY GLU ILE SER GLY THR ILE

ALA ILE GLU GLU MET ASP LYS SER GLY THR TYR ILE HIS ALA LEU ASP ASN GLY LEU PHE THR LEU GLY ALA PRO HIS LYS GLU VAL ASP GLU GLY PRO SER PRO PRO GLU GLN PHE THR ALA VAL LYS LEU SER ASP SER ARG ILE ALA LEU LYS SER GLY TYR GLY LYS TYR LEU GLY ILE ASN

SER ASP GLY LEU VAL VAL GLY ARG SER ASP ALA ILE GLY PRO ARG GLU GLN TRP GLU PRO VAL PHE GLN ASN GLY LYS MET ALA LEU LEU ALA SER ASN SER CYS PHE ILE ARG CYS ASN GLU ALA GLY ASP ILE GLU ALA LYS SER LYS THR ALA GLY GLU GLU GLU MET ILE LYS ILE

ARG SER CYS ALA GLU ARG GLU THR LYS LYS LYS ASP ASP ILE PRO GLU GLU ASP LYS GLY ASN VAL LYS GLN CYS GLU ILE ASN TYR VAL LYS LYS PHE GLN SER PHE GLN ASP HIS LYS LEU LYS ILE SER GLU ASP SER K229 D237 K258

4   Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	411539	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 $(e^-/\text{Å}^2)$	120	Depositor
Minimum defocus (nm)	-1	Depositor
Maximum defocus (nm)	-3	Depositor
Magnification	132000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.336	Depositor
Minimum map value	-0.185	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	466.39996, 466.39996, 466.39996	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5   Model quality   ⓘ

5.1   Standard geometry   ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, IHP, 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	2	0.84	1/642 (0.2%)	1.08	3/998 (0.3%)
2	5	0.77	0/1725	1.04	5/2681 (0.2%)
3	6	0.86	0/1892	0.96	2/2947 (0.1%)
4	9	0.26	0/113	0.45	0/148
5	A	0.55	4/14669 (0.0%)	0.70	23/19894 (0.1%)
6	B	0.47	2/7112 (0.0%)	0.67	9/9681 (0.1%)
7	C	0.48	1/1738 (0.1%)	0.69	4/2353 (0.2%)
8	D	0.68	2/2547 (0.1%)	0.76	4/3471 (0.1%)
9	E	0.39	0/650	0.64	1/886 (0.1%)
10	F	0.47	1/2282 (0.0%)	0.76	9/3109 (0.3%)
11	L	0.46	0/1641	0.65	1/2208 (0.0%)
12	O	0.45	0/2160	0.65	4/2920 (0.1%)
13	P	0.60	2/1613 (0.1%)	0.71	1/2174 (0.0%)
14	Q	0.81	7/1187 (0.6%)	0.96	10/1591 (0.6%)
15	R	0.55	0/690	0.71	0/922
16	S	0.56	0/233	0.70	0/312
17	T	0.50	1/1704 (0.1%)	1.08	10/2291 (0.4%)
18	V	0.33	0/1105	0.58	0/1511
19	Y	0.67	0/975	1.14	9/1514 (0.6%)
19	Z	0.89	0/307	0.87	0/476
20	p	0.48	1/2424 (0.0%)	0.77	5/3295 (0.2%)
21	r	0.36	0/262	0.55	0/356
22	s	0.38	0/158	0.50	0/209
23	t	0.59	0/424	0.74	1/570 (0.2%)
24	u	0.91	9/1312 (0.7%)	1.10	9/1764 (0.5%)
25	x	0.36	0/240	0.58	0/317
All	All	0.58	31/49805 (0.1%)	0.78	110/68598 (0.2%)

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
5	A	0	2
6	B	0	1
20	p	0	3
24	u	0	1
All	All	0	7

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	u	136	VAL	CB-CG1	-15.50	1.20	1.52
14	Q	137	CYS	CB-SG	-12.19	1.61	1.82
24	u	136	VAL	CB-CG2	-9.93	1.31	1.52
24	u	46	CYS	CB-SG	9.92	1.99	1.82
14	Q	134	CYS	CB-SG	-9.87	1.65	1.82

The worst 5 of 110 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
17	T	538	ARG	NE-CZ-NH2	-32.07	104.27	120.30
5	A	506	LEU	CB-CG-CD1	-24.98	68.54	111.00
17	T	538	ARG	NE-CZ-NH1	20.37	130.49	120.30
24	u	140	ARG	NE-CZ-NH2	-18.29	111.16	120.30
24	u	136	VAL	CG1-CB-CG2	-17.26	83.29	110.90

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	A	1649	LYS	Peptide
5	A	380	LEU	Peptide
6	B	366	GLN	Peptide
20	p	227	CYS	Peptide
20	p	352	GLN	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	2	575	0	288	7	0
2	5	1548	0	785	3	0
3	6	1690	0	855	12	0
4	9	112	0	109	3	0
5	A	14270	0	14118	188	0
6	B	6953	0	6837	109	0
7	C	1703	0	1692	28	0
8	D	2481	0	2431	52	0
9	E	629	0	572	13	0
10	F	2230	0	2087	52	0
11	L	1611	0	1588	16	0
12	O	2108	0	1963	26	0
13	P	1577	0	1543	30	0
14	Q	1162	0	1163	12	0
15	R	681	0	635	9	0
16	S	230	0	238	3	0
17	T	1669	0	1662	20	0
18	V	1081	0	929	20	0
19	Y	873	0	440	9	0
19	Z	276	0	143	2	0
20	p	2372	0	2209	0	0
21	r	259	0	213	0	0
22	s	158	0	162	0	0
23	t	418	0	379	0	0
24	u	1286	0	1274	0	0
25	x	239	0	252	0	0
26	6	5	0	0	0	0
27	A	36	0	6	4	0
28	B	32	0	12	0	0
29	P	3	0	0	0	0
29	Q	3	0	0	0	0
29	u	1	0	0	0	0
All	All	48271	0	44585	541	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 7.

The worst 5 of 541 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)
5:A:75:ASP:HA	5:A:502:ASN:HD22	1.45	0.80
13:P:96:VAL:HG21	13:P:213:LEU:HD23	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:591:MET:HG3	5:A:598:LEU:HD21	1.64	0.78
5:A:993:LEU:O	5:A:997:LEU:HB2	1.83	0.77
18:V:53:PHE:HB3	18:V:56:ILE:HD11	1.67	0.75

There are no symmetry-related clashes.

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.

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	
4	9	12/450 (3%)	10 (83%)	2 (17%)	0	100	100
5	A	1718/1755 (98%)	1567 (91%)	150 (9%)	1 (0%)	51	82
6	B	893/952 (94%)	809 (91%)	84 (9%)	0	100	100
7	C	220/536 (41%)	187 (85%)	33 (15%)	0	100	100
8	D	313/514 (61%)	277 (88%)	36 (12%)	0	100	100
9	E	76/579 (13%)	66 (87%)	10 (13%)	0	100	100
10	F	297/357 (83%)	262 (88%)	35 (12%)	0	100	100
11	L	198/802 (25%)	176 (89%)	22 (11%)	0	100	100
12	O	248/848 (29%)	229 (92%)	19 (8%)	0	100	100
13	P	191/218 (88%)	175 (92%)	16 (8%)	0	100	100
14	Q	140/144 (97%)	126 (90%)	14 (10%)	0	100	100
15	R	83/229 (36%)	77 (93%)	6 (7%)	0	100	100
16	S	28/2752 (1%)	23 (82%)	5 (18%)	0	100	100
17	T	201/908 (22%)	184 (92%)	17 (8%)	0	100	100
18	V	161/166 (97%)	149 (92%)	12 (8%)	0	100	100
20	p	321/654 (49%)	273 (85%)	48 (15%)	0	100	100
21	r	33/1227 (3%)	30 (91%)	3 (9%)	0	100	100

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WORLDWIDE wwPDB PROTEIN DATA BANK

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	s	18/285 (6%)	16 (89%)	2 (11%)	0	100	100
23	t	54/425 (13%)	54 (100%)	0	0	100	100
24	u	153/178 (86%)	131 (86%)	22 (14%)	0	100	100
25	x	28/258 (11%)	26 (93%)	2 (7%)	0	100	100
All	All	5386/14237 (38%)	4847 (90%)	538 (10%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	A	803	ALA

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	
4	9	11/411 (3%)	11 (100%)	0	100	100
5	A	1528/1584 (96%)	1524 (100%)	4 (0%)	92	97
6	B	756/847 (89%)	756 (100%)	0	100	100
7	C	173/459 (38%)	173 (100%)	0	100	100
8	D	271/441 (62%)	271 (100%)	0	100	100
9	E	65/502 (13%)	65 (100%)	0	100	100
10	F	231/300 (77%)	231 (100%)	0	100	100
11	L	158/709 (22%)	158 (100%)	0	100	100
12	O	201/751 (27%)	201 (100%)	0	100	100
13	P	175/197 (89%)	175 (100%)	0	100	100
14	Q	125/130 (96%)	125 (100%)	0	100	100
15	R	64/203 (32%)	64 (100%)	0	100	100
16	S	24/2432 (1%)	24 (100%)	0	100	100
17	T	186/838 (22%)	186 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	V	87/134 (65%)	87 (100%)	0	100	100
20	p	234/572 (41%)	234 (100%)	0	100	100
21	r	23/1074 (2%)	22 (96%)	1 (4%)	29	59
22	s	14/240 (6%)	13 (93%)	1 (7%)	14	44
23	t	36/381 (9%)	36 (100%)	0	100	100
24	u	139/167 (83%)	138 (99%)	1 (1%)	84	92
25	x	23/223 (10%)	23 (100%)	0	100	100
All	All	4524/12595 (36%)	4517 (100%)	7 (0%)	93	98

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	A	617	ASN
21	r	380	ASN
24	u	136	VAL
22	s	4	ASN
5	A	409	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
20	p	480	HIS
12	O	325	ASN
8	D	287	HIS
6	B	903	HIS
9	E	128	GLN

5.3.3   RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	26/188 (13%)	13 (50%)	2 (7%)
19	Y	39/324 (12%)	23 (58%)	0
19	Z	12/324 (3%)	1 (8%)	0
2	5	73/116 (62%)	11 (15%)	1 (1%)
3	6	78/79 (98%)	22 (28%)	0
All	All	228/1031 (22%)	70 (30%)	3 (1%)

5 of 70 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	19	G
1	2	22	U
1	2	24	A
1	2	25	G
1	2	29	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	28	C
1	2	39	U
2	5	23	C

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 14 ligands modelled in this entry, 12 are monoatomic - leaving 2 for Mogul analysis.

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	#$|Z| > 2$
28	GTP	B	1001	6	26,34,34	1.35	2 (7%)	32,54,54	1.86	8 (25%)
27	IHP	A	3001	-	36,36,36	0.85	0	54,60,60	1.38	6 (11%)

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
28	GTP	B	1001	6	-	8/18/38/38	0/3/3/3
27	IHP	A	3001	-	-	7/30/54/54	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	B	1001	GTP	C5-C6	-4.92	1.37	1.47
28	B	1001	GTP	C5-C4	-2.08	1.37	1.43

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	B	1001	GTP	C3'-C2'-C1'	4.66	108.00	100.98
27	A	3001	IHP	C6-C1-C2	3.80	118.72	110.41
28	B	1001	GTP	C5-C6-N1	3.54	120.20	113.95
28	B	1001	GTP	C2-N1-C6	-3.45	118.75	125.10
27	A	3001	IHP	C5-C6-C1	3.20	117.42	110.41

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
27	A	3001	IHP	C1-O11-P1-O21
27	A	3001	IHP	C2-O12-P2-O22
27	A	3001	IHP	C4-O14-P4-O24
27	A	3001	IHP	C5-O15-P5-O25
28	B	1001	GTP	C5'-O5'-PA-O3A

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
27	A	3001	IHP	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GTP B 1001

Bond lengths

Bond angles

Torsions

Rings

Ligand IHP A 3001

Bond lengths

Bond angles

Torsions

Rings
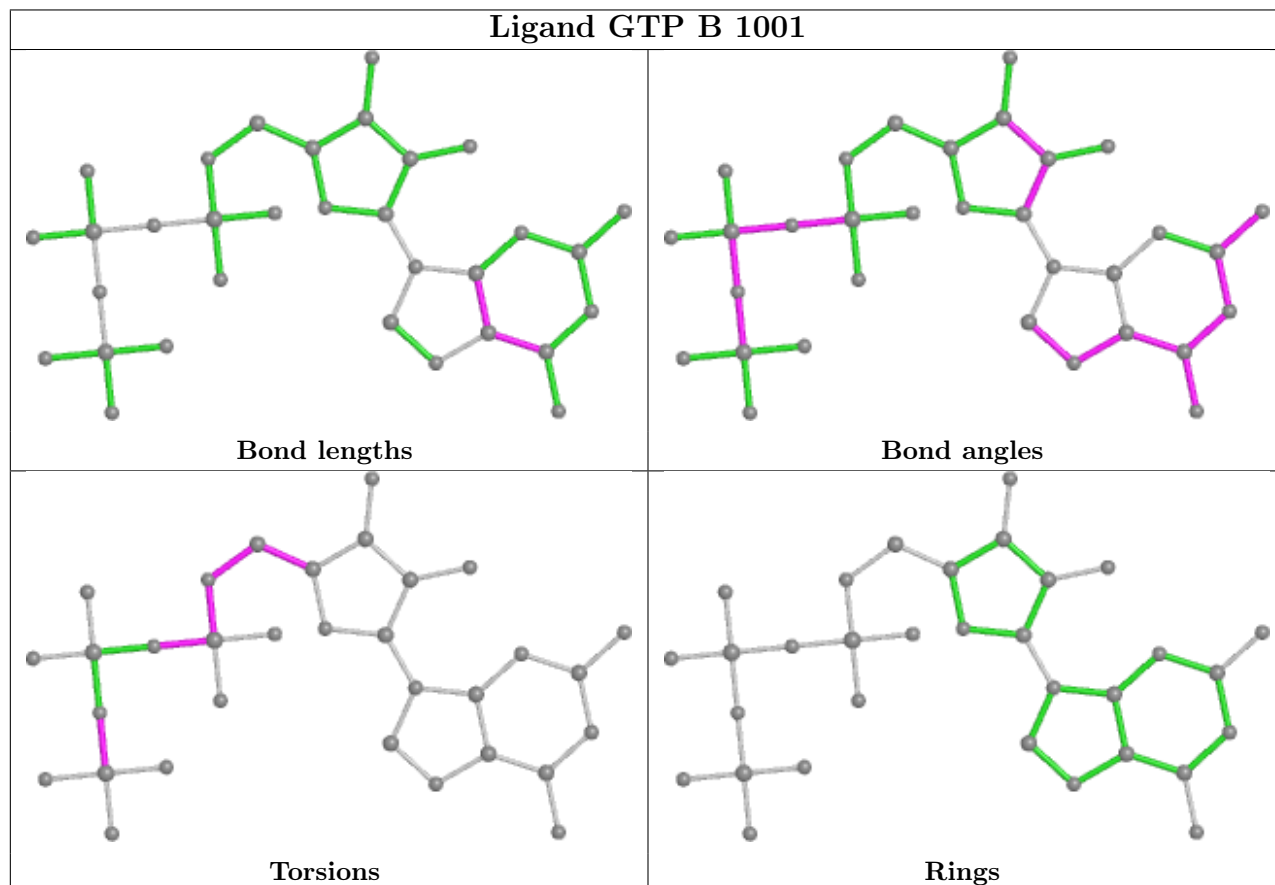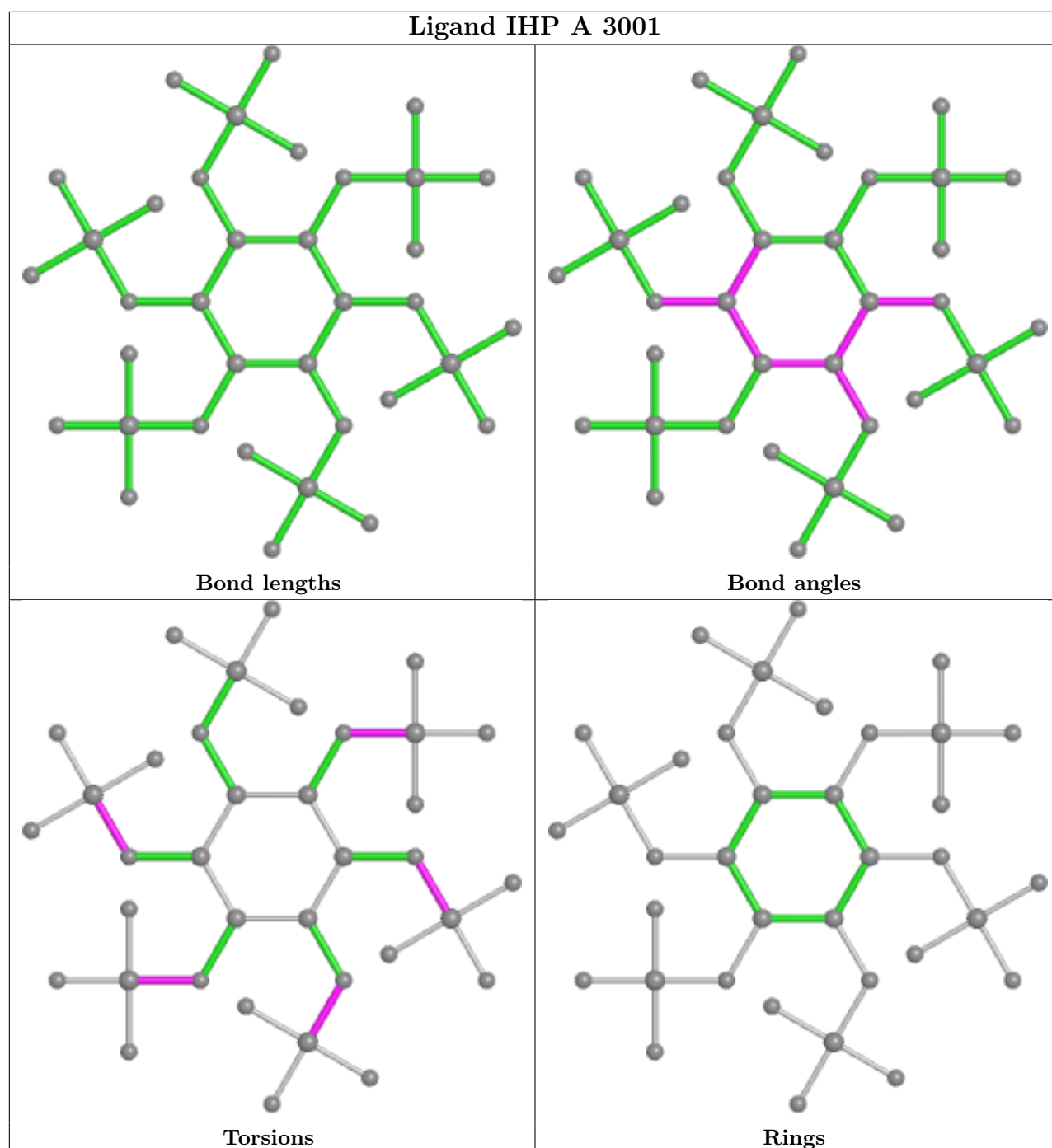
5.7 Other polymers ⓘ

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-11569. 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 ⓘ

6.1.1 Primary map

| X | Y | Z |
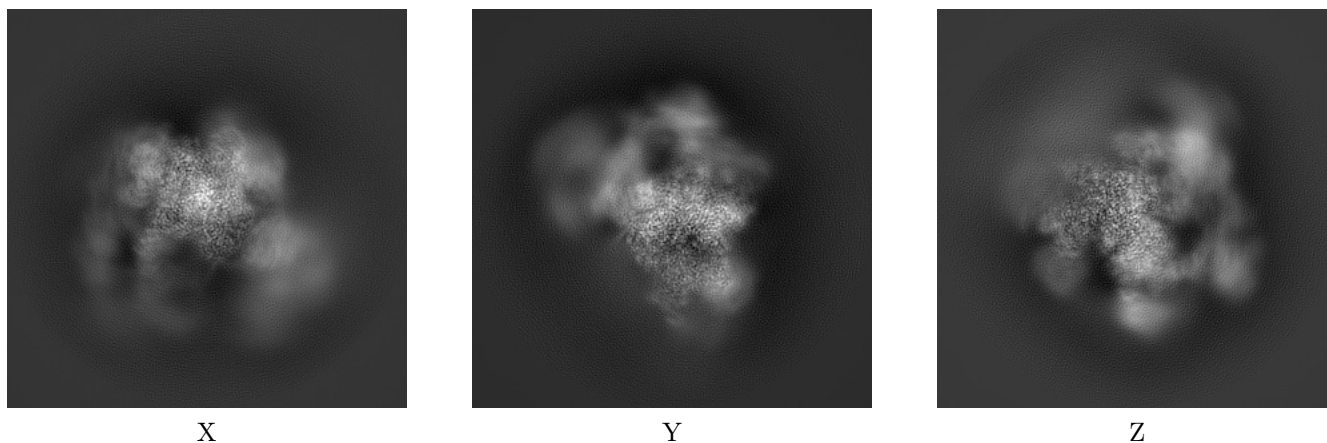
The images above show the map projected in three orthogonal directions.

6.2 Central slices ⓘ

6.2.1 Primary map

| X Index: 220 | Y Index: 220 | Z Index: 220 |
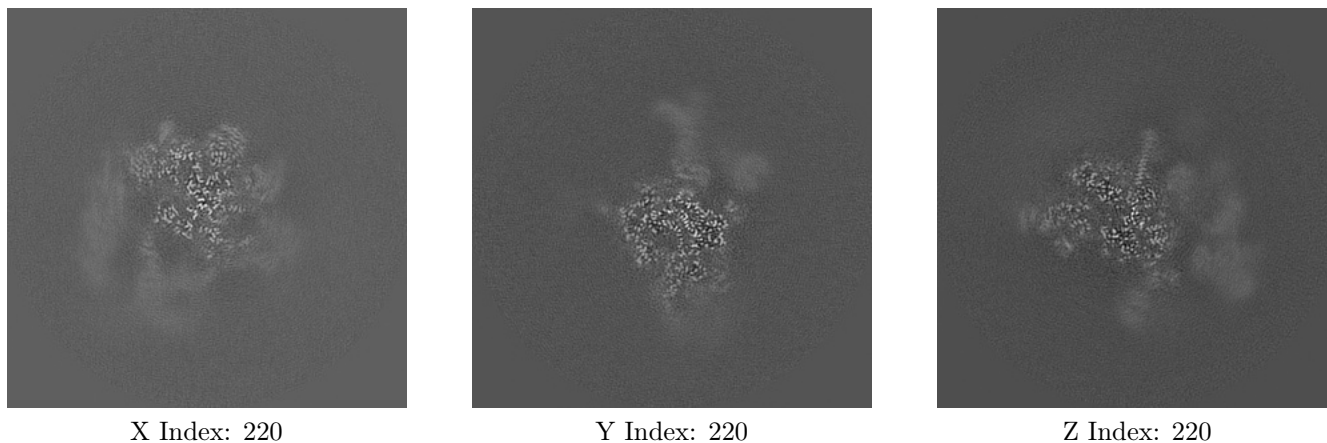
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map
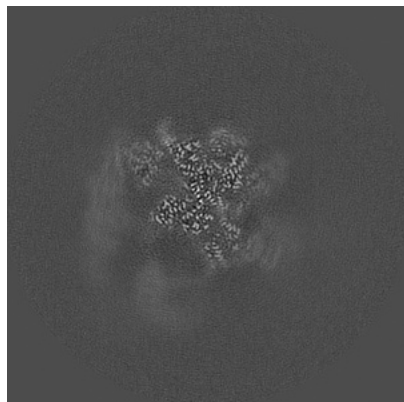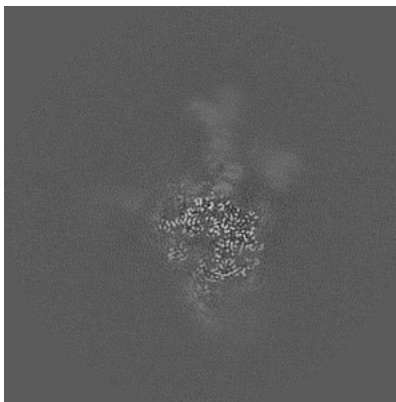
| X Index: 213 | Y Index: 216 | Z Index: 227 |
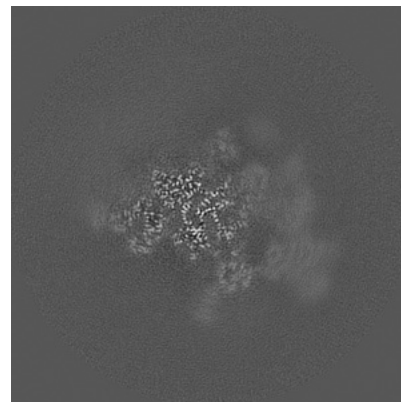
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map
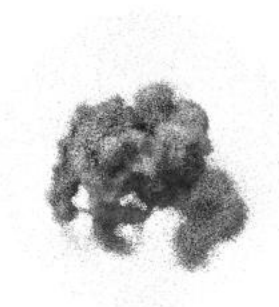
| X | Y | Z |

The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5 Mask visualisation ⓘ

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

7   Map analysis (i)

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

7.1   Map-value distribution (i)
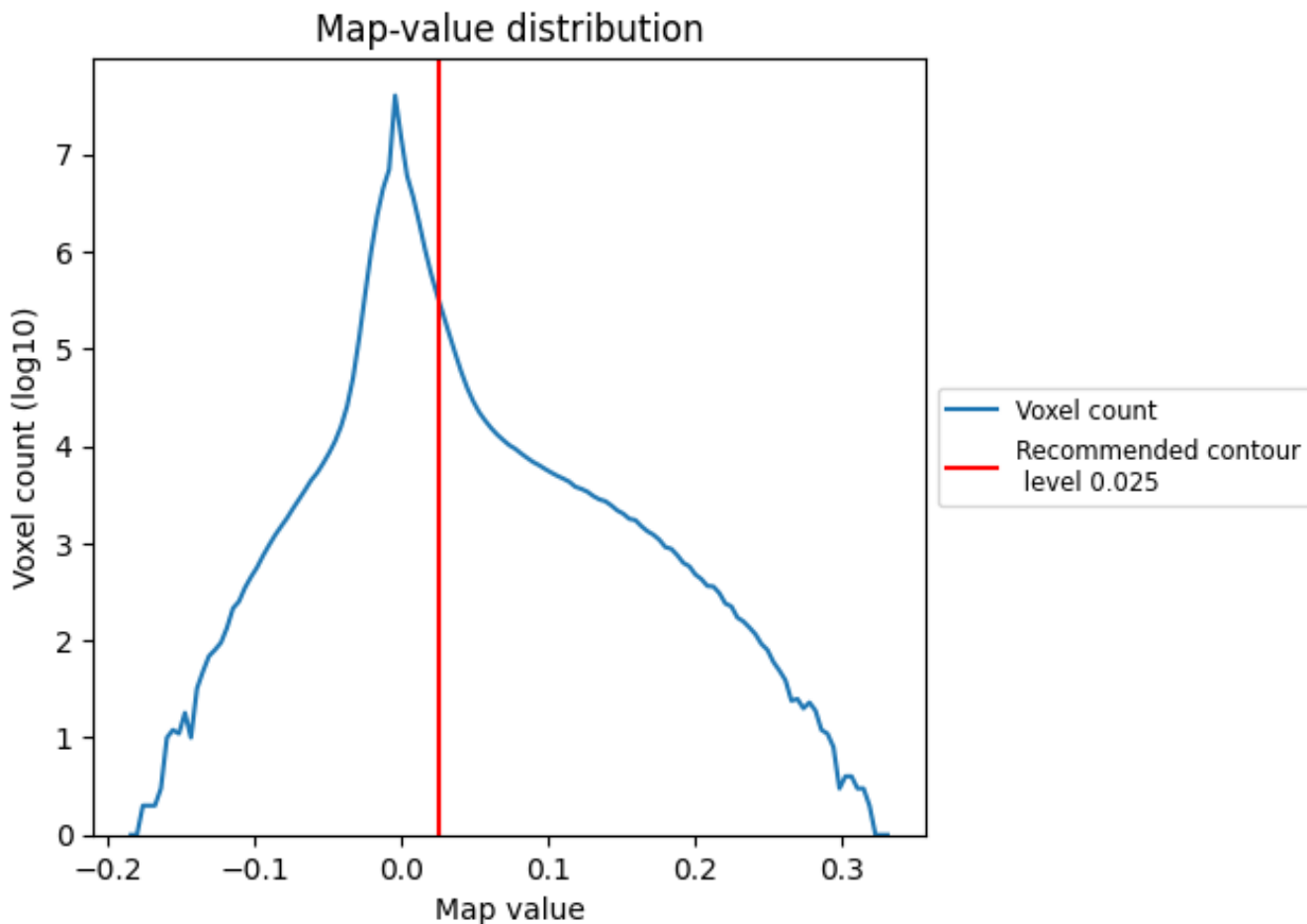
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate ⓘ
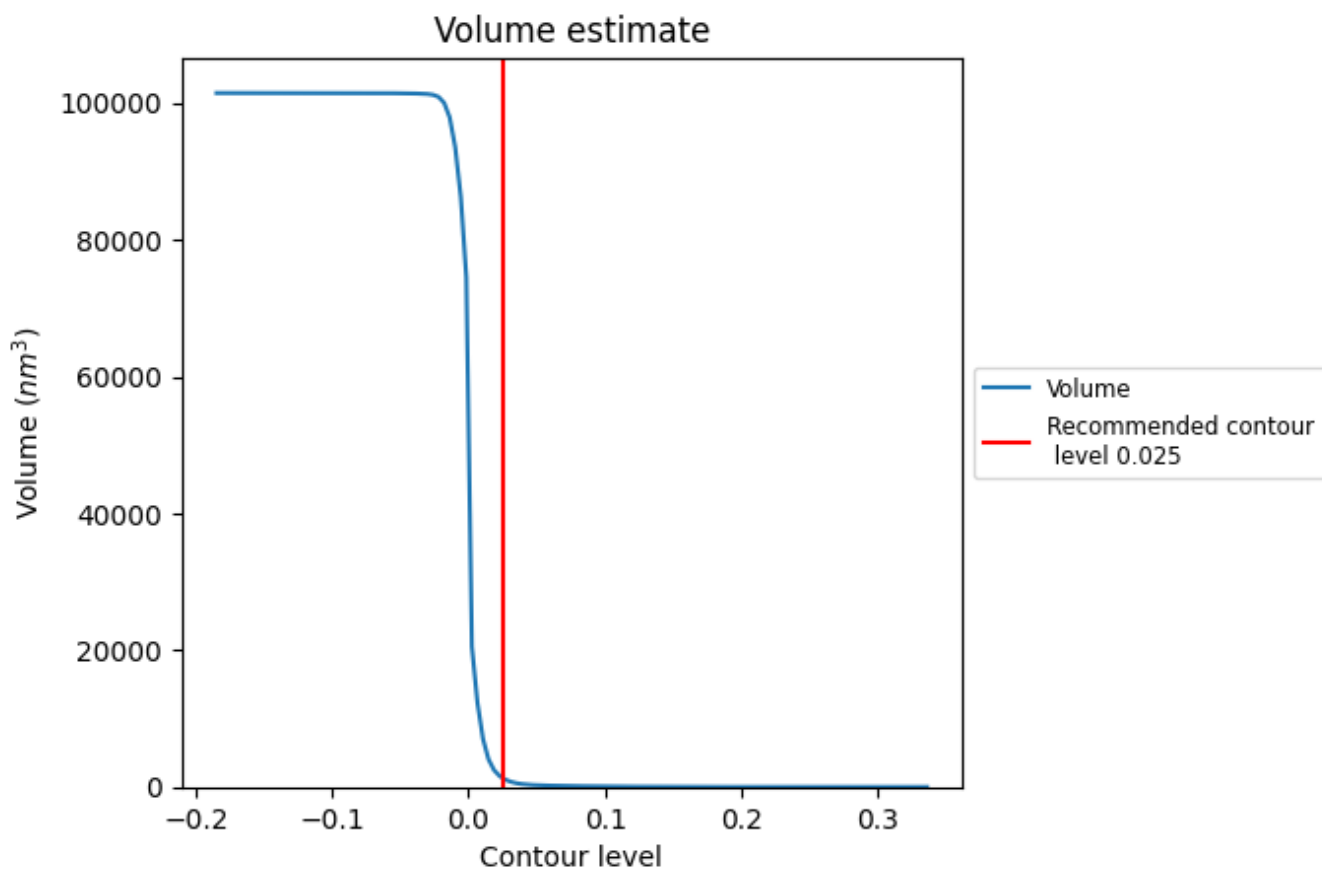
The volume at the recommended contour level is 1311 nm^3; this corresponds to an approximate mass of 1184 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ
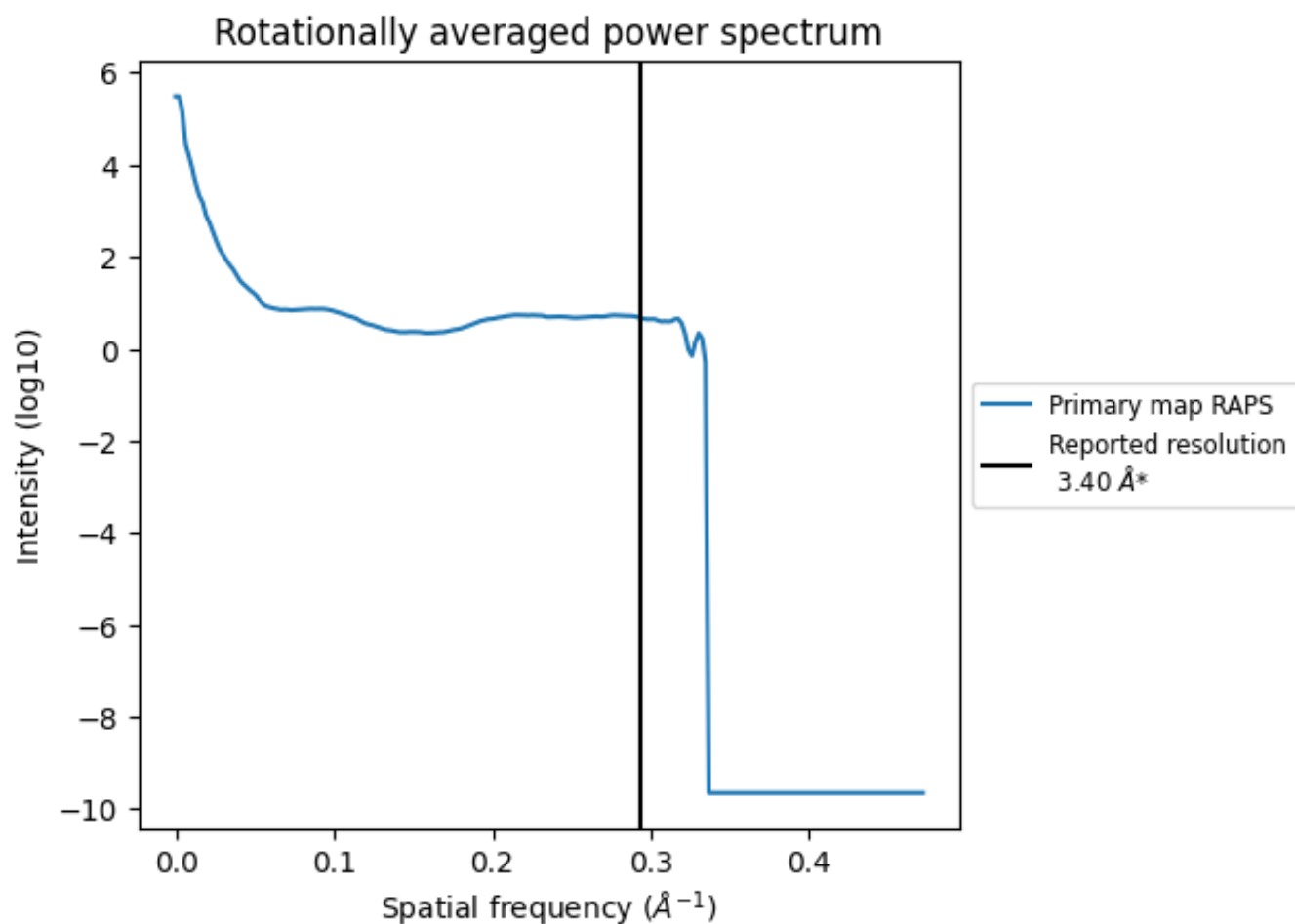
*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8 Fourier-Shell correlation (i)

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

9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-11569 and PDB model 6ZYM. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay (i)

| X | Y | Z |
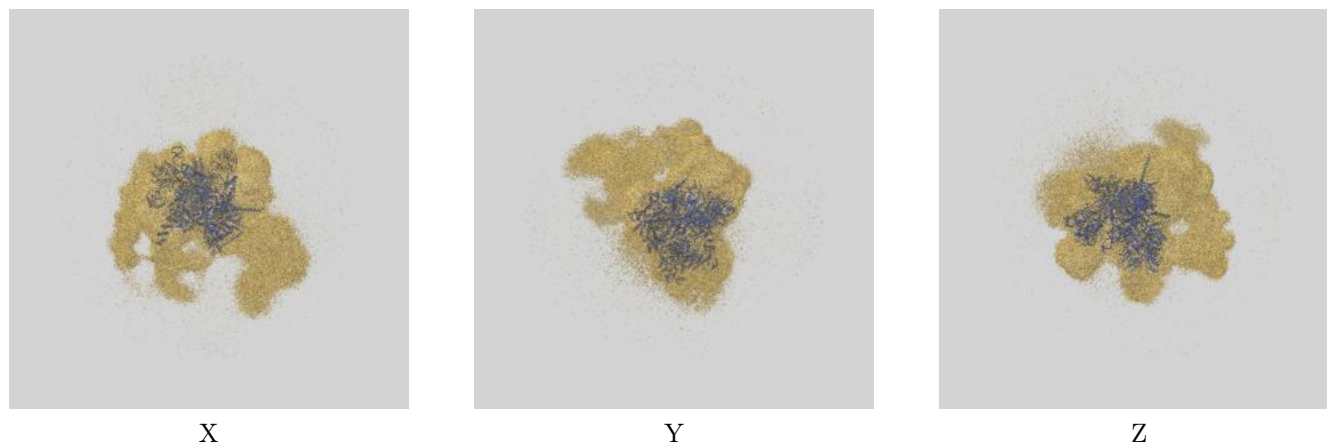
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2   Q-score mapped to coordinate model ⓘ

X   Y   Z
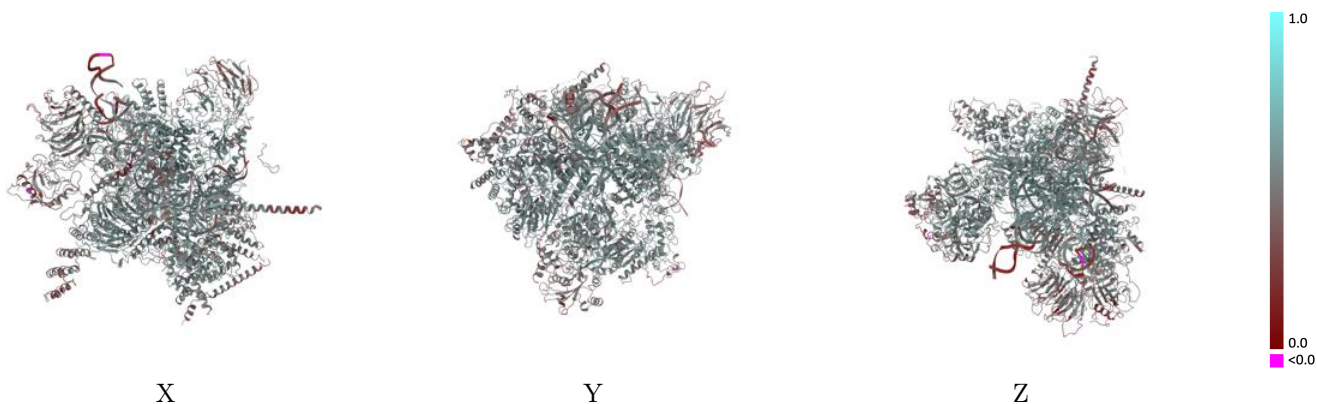
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3   Atom inclusion mapped to coordinate model ⓘ

X   Y   Z
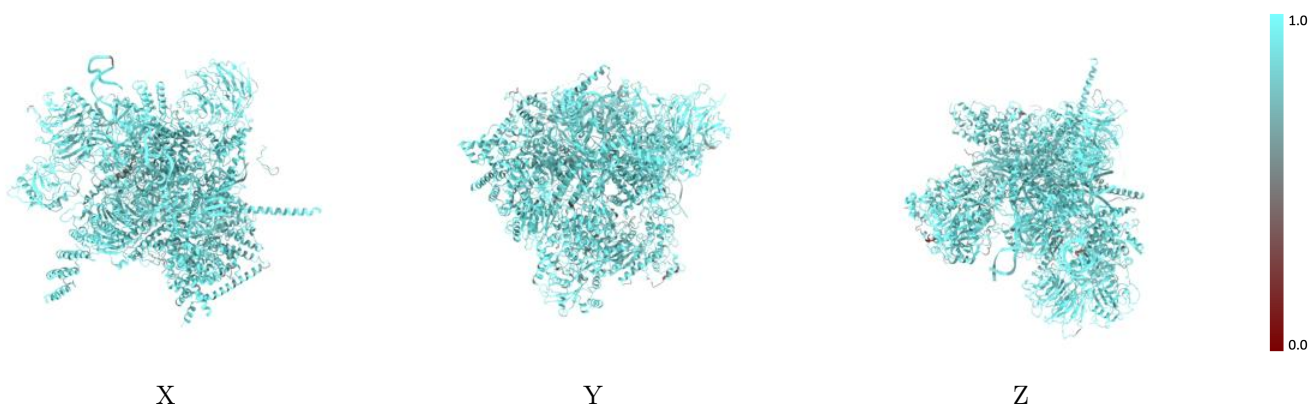
The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.025).

9.4　Atom inclusion ⓘ
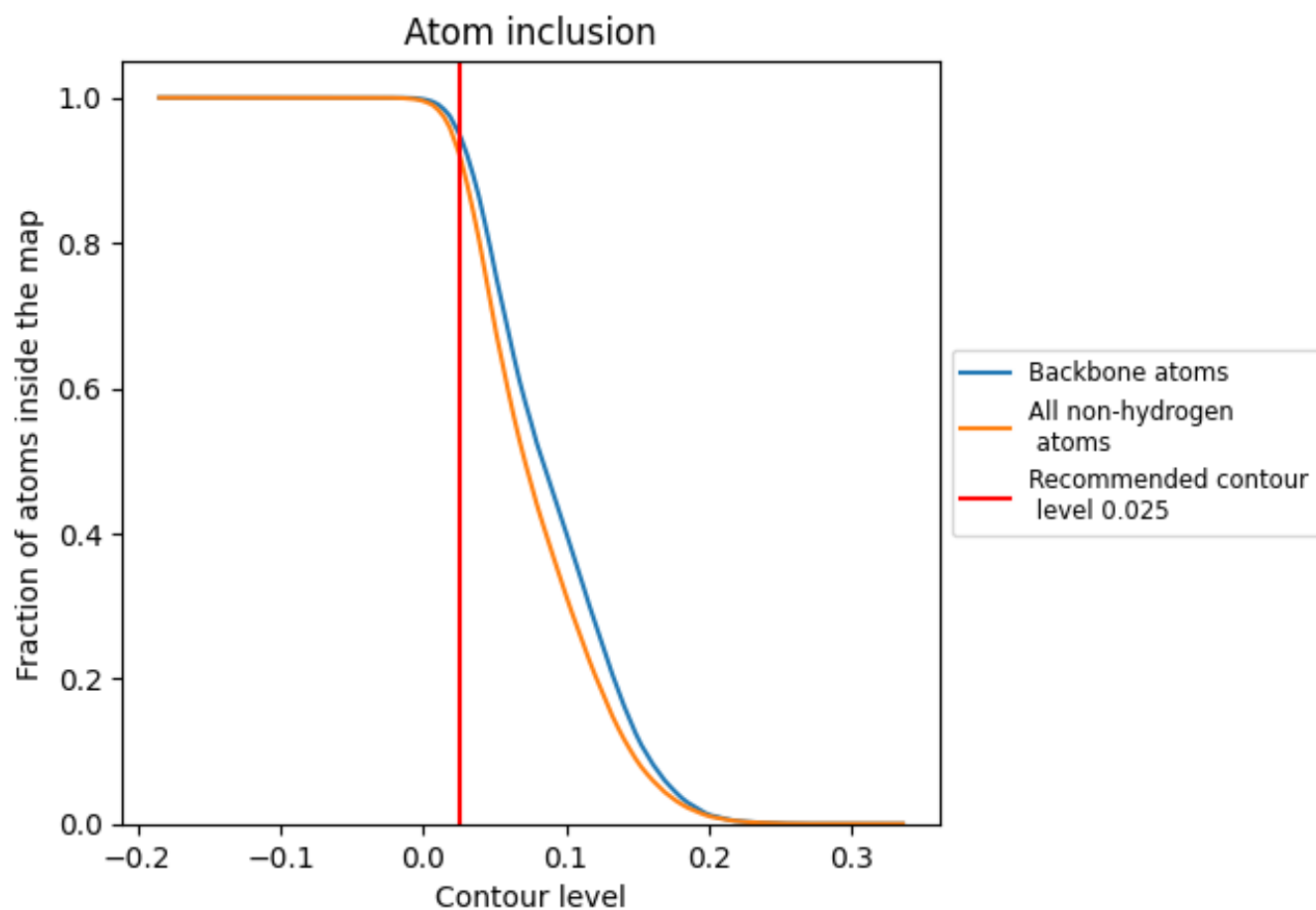
At the recommended contour level, 95% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5   Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.025) and Q-score
for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9241	0.4980
2	0.9043	0.4570
5	0.9348	0.4550
6	0.9499	0.4720
9	0.6789	0.4240
A	0.9350	0.5390
B	0.9223	0.4880
C	0.8898	0.4710
D	0.9567	0.5520
E	0.9058	0.4900
F	0.9257	0.4340
L	0.8908	0.4840
O	0.9078	0.4660
P	0.9154	0.5070
Q	0.9487	0.5260
R	0.8845	0.4980
S	0.9083	0.5290
T	0.9035	0.4820
V	0.9287	0.4170
Y	0.9267	0.4580
Z	0.9457	0.5490
p	0.9352	0.4540
r	0.8333	0.4610
s	0.9342	0.5570
t	0.8908	0.4500
u	0.8926	0.4830
x	0.8957	0.5330

1.0

0.0
<0.0