



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:19 PM UTC

PDB ID : 3J0S / pdb_00003j0s
EMDB ID : EMD-5354
Title : Remodeling of actin filaments by ADF cofilin proteins
Authors : Galkin, V.E.; Orlova, A.; Kudryashov, D.S.; Solodukhin, A.; Reisler, E.;
Schroeder, G.F.; Egelman, E.H.
Deposited on : 2011-11-24
Resolution : 9.00 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

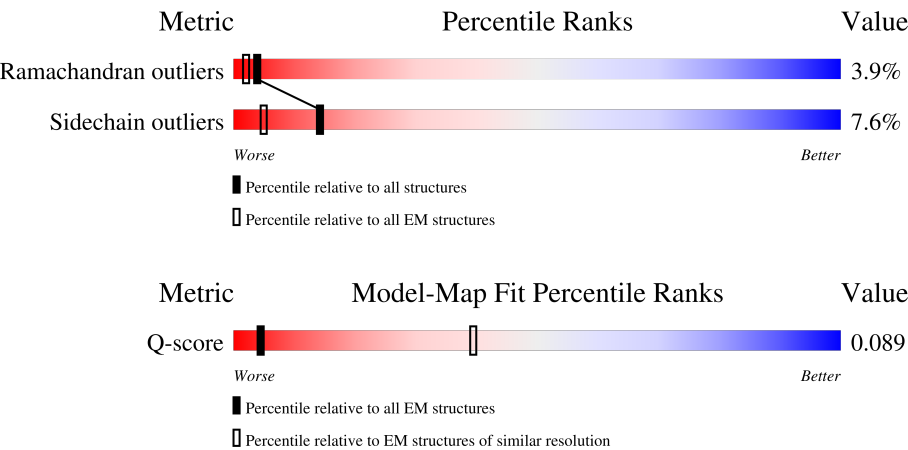
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.00 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.



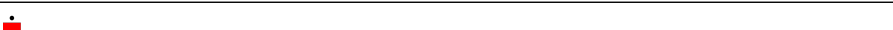
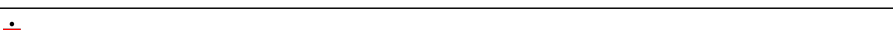
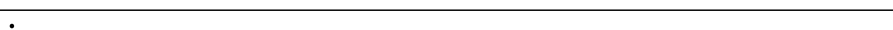
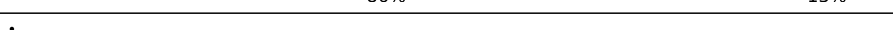
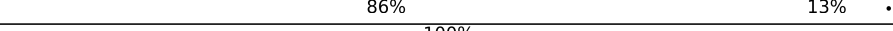
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	257 (8.50 - 9.50)

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 $\leq 5\%$. 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	A	374	51% 90% 9% .
1	B	374	90% 9% .
1	C	374	90% 9% .
1	D	374	90% 9% .
1	E	374	90% 9% .

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Mol	Chain	Length	Quality of chain
1	F	374	 90% 9% .
1	G	374	 90% 9% .
1	H	374	 90% 9% .
1	I	374	 90% 9% .
1	J	374	 51% 90% 9% .
1	K	374	 100% 90% 9% .
1	L	374	 100% 90% 9% .
2	M	166	 100% 86% 13% .
2	N	166	 86% 13% .
2	O	166	 54% 86% 13% .
2	P	166	 86% 13% .
2	Q	166	 86% 13% .
2	R	166	 86% 13% .
2	S	166	 86% 13% .
2	T	166	 86% 13% .
2	U	166	 86% 13% .
2	V	166	 50% 86% 13% .
2	W	166	 86% 13% .
2	X	166	 100% 86% 13% .

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 50556 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 Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	B	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	C	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	D	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	E	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	F	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	G	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	H	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	I	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	J	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	K	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
1	L	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		

- Molecule 2 is a protein called Cofilin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	166	Total	C	N	O	S	0	0
			1296	826	211	251	8		
2	O	166	Total	C	N	O	S	0	0
			1296	826	211	251	8		
2	N	166	Total	C	N	O	S	0	0
			1296	826	211	251	8		

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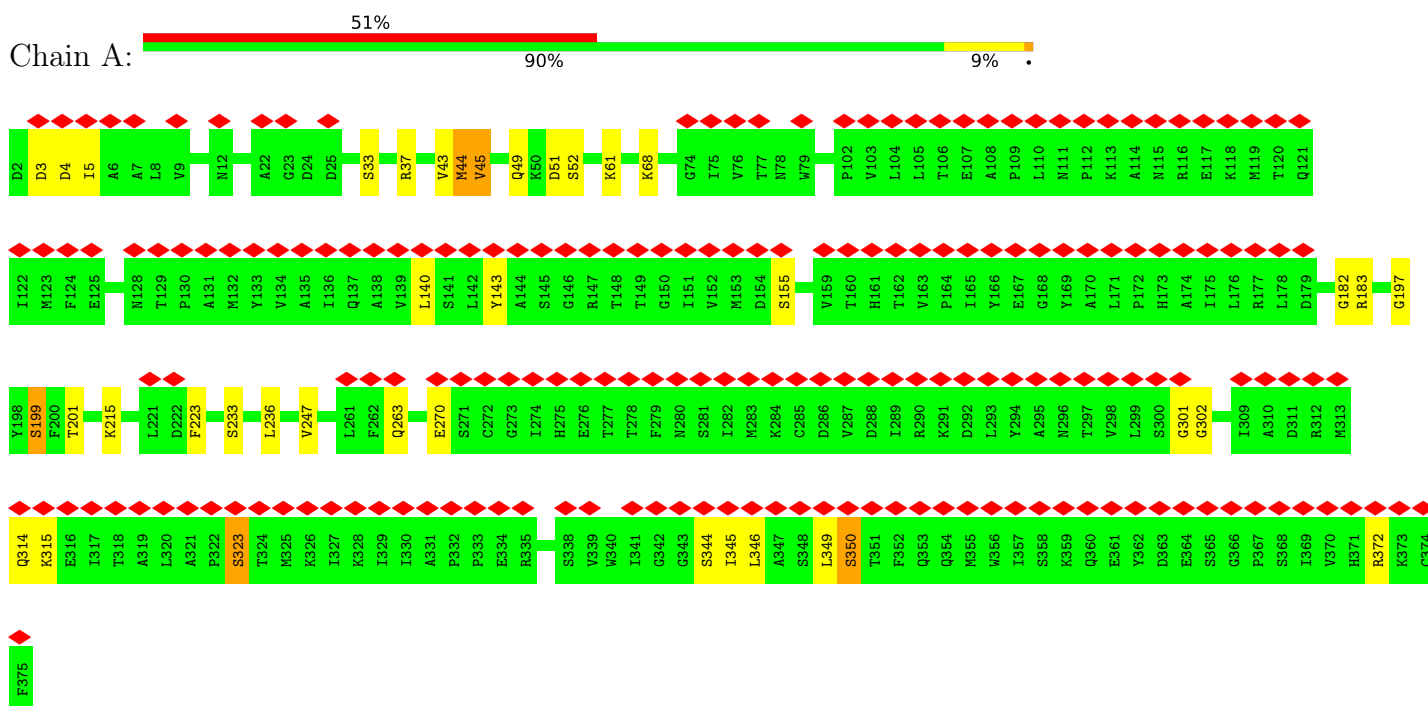
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Q	166	Total 1296	C 826	N 211	O 251	S 8	0	0
2	P	166	Total 1296	C 826	N 211	O 251	S 8	0	0
2	S	166	Total 1296	C 826	N 211	O 251	S 8	0	0
2	R	166	Total 1296	C 826	N 211	O 251	S 8	0	0
2	U	166	Total 1296	C 826	N 211	O 251	S 8	0	0
2	T	166	Total 1296	C 826	N 211	O 251	S 8	0	0
2	W	166	Total 1296	C 826	N 211	O 251	S 8	0	0
2	V	166	Total 1296	C 826	N 211	O 251	S 8	0	0
2	X	166	Total 1296	C 826	N 211	O 251	S 8	0	0

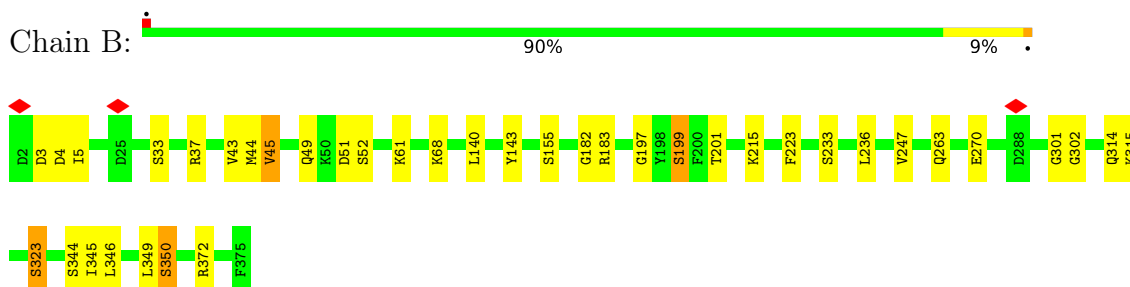
3 Residue-property plots

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.

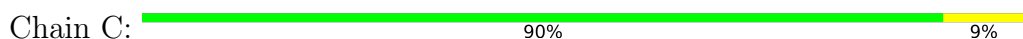
- Molecule 1: Actin, cytoplasmic 1

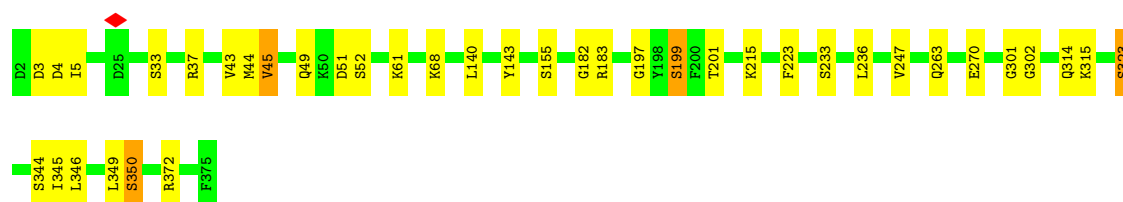


- Molecule 1: Actin, cytoplasmic 1

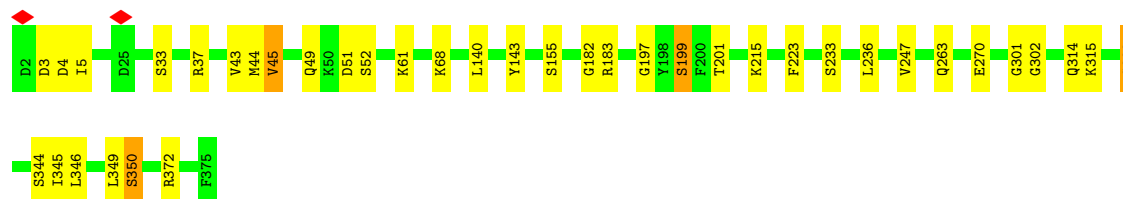


- Molecule 1: Actin, cytoplasmic 1

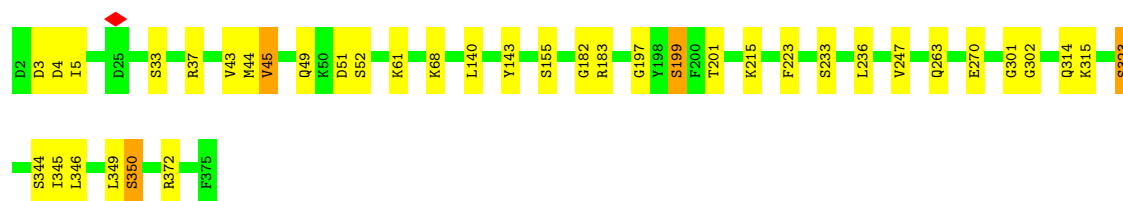
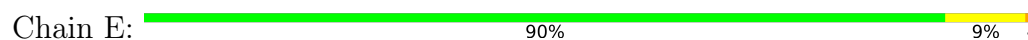




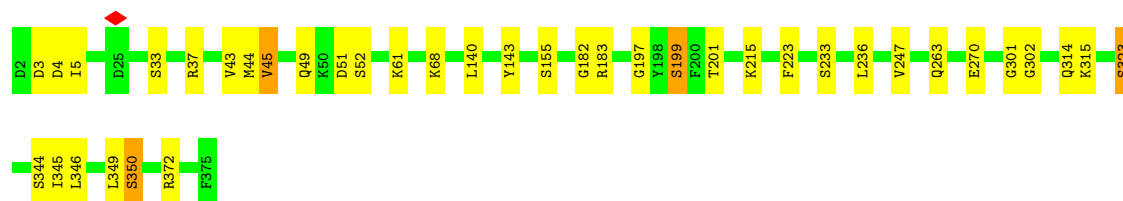
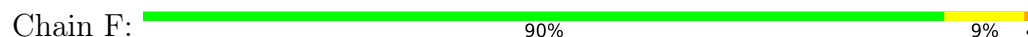
- Molecule 1: Actin, cytoplasmic 1



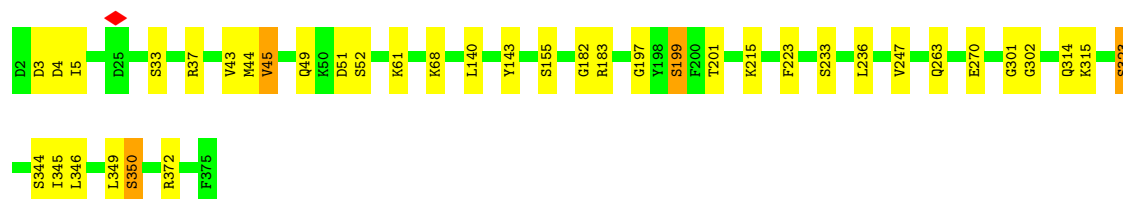
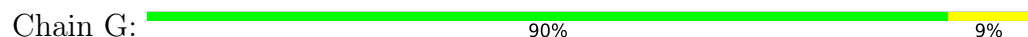
- Molecule 1: Actin, cytoplasmic 1



- Molecule 1: Actin, cytoplasmic 1



- Molecule 1: Actin, cytoplasmic 1

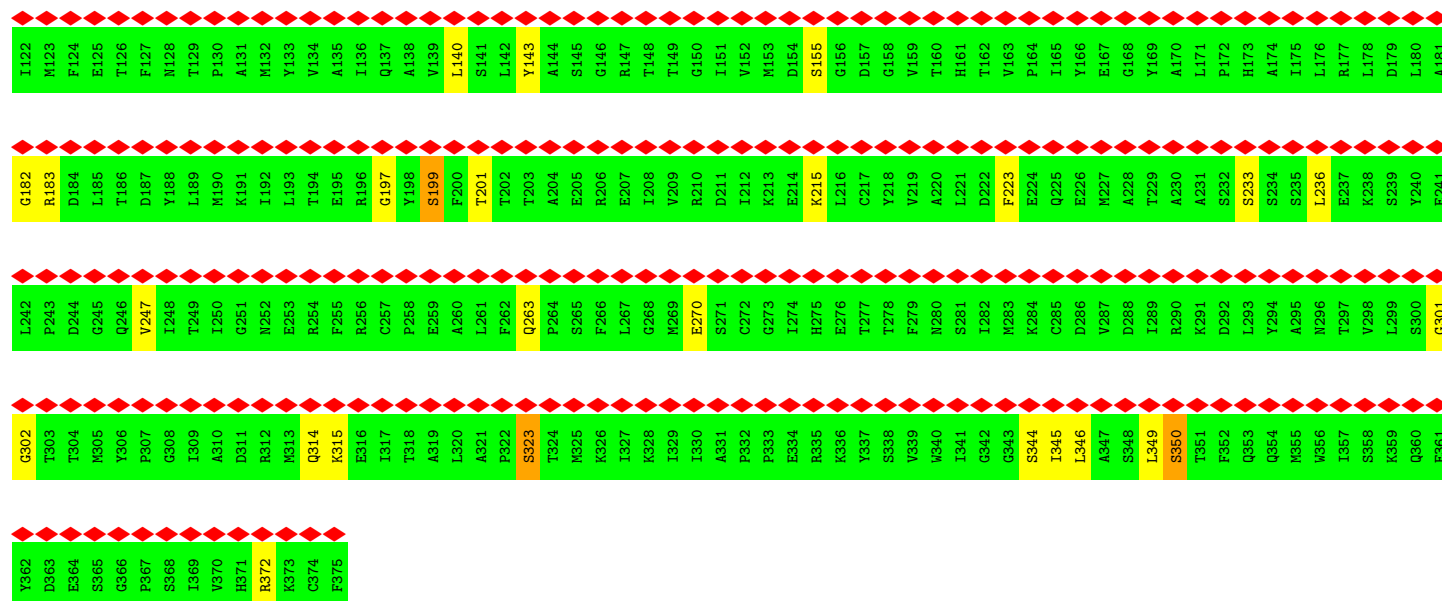


- Molecule 1: Actin, cytoplasmic 1

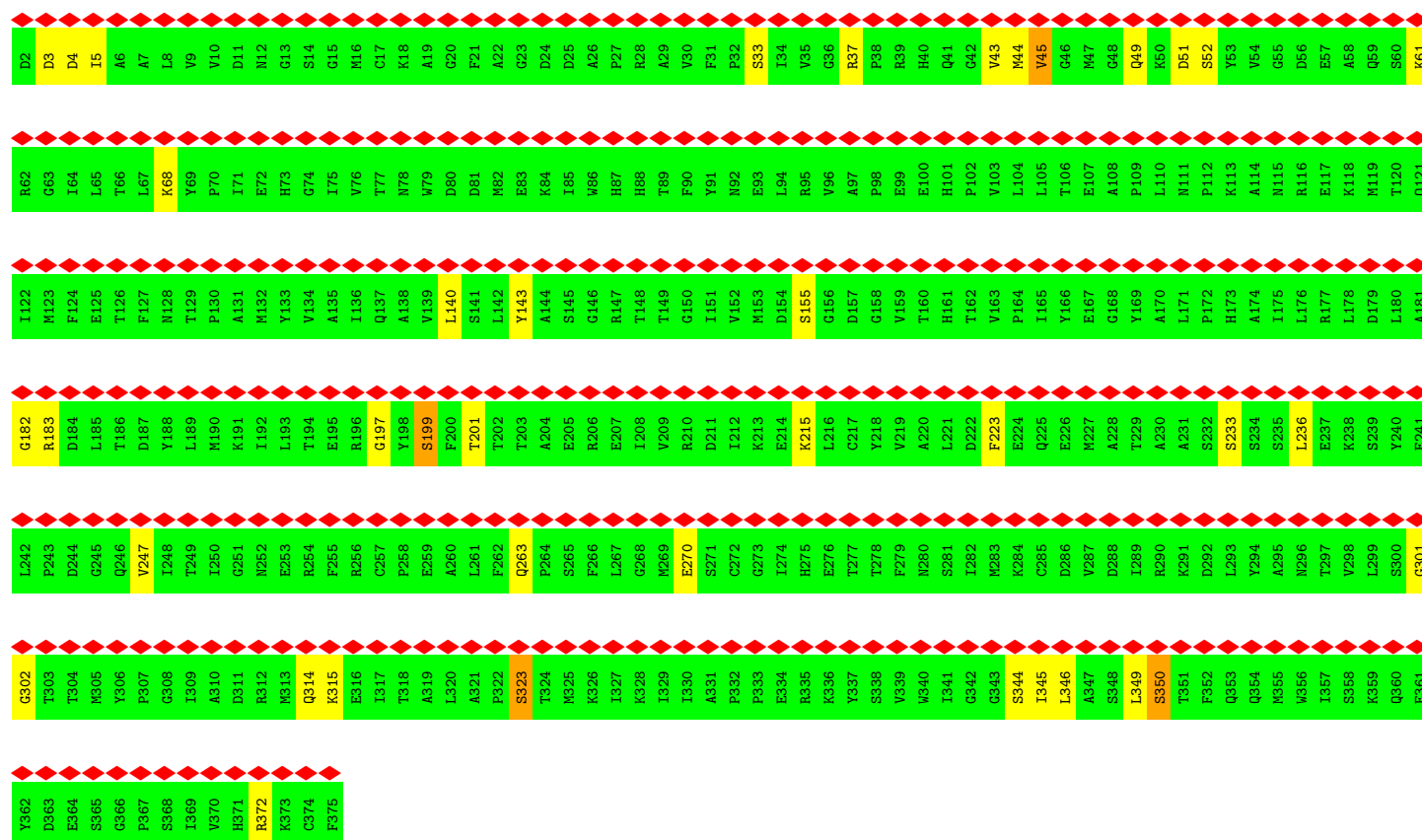
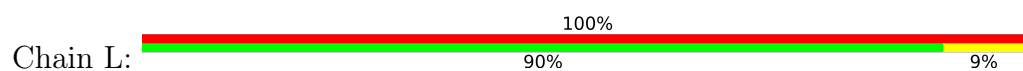
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- 
- Q314
K315
S323
S344
I345
L346
L349
S350
R372
F375

- Chain J:
-
- 51% 90% 9%
- D2 D3 D4 D5 D6 D7 D8 D9 D10 D11 D12 D13 D14 D15 D16 D17 D18 D19 D20 D21 D22 D23 D24 D25 D26 D27 D28 D29 D30 D31 D32 D33 D34 D35 D36 D37 D38 D39 D40 D41 D42 D43 D44 D45 D46 D47 D48 D49 D50 D51 D52 D53 D54 D55 D56 D57 D58 D59 D60 D61 D62 D63
- 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250
- K191 K192 K193 K194 K195 K196 K197 K198 K199 K200 K201 K202 K203 K204 K205 K206 K207 K208 K209 K210 K211 K212 K213 K214 K215 K216 K217 K218 K219 K220 K221 K222 K223 K224 K225 K226 K227 K228 K229 K230 K231 K232 K233 K234 K235 K236 K237 K238 K239 K240 K241 K242 K243 K244 K245 K246 K247 K248 K249 K250
- G251 G252 G253 G254 G255 G256 G257 G258 G259 G260 G261 G262 G263 G264 G265 G266 G267 G268 G269 G270 G271 G272 G273 G274 G275 G276 G277 G278 G279 G280 G281 G282 G283 G284 G285 G286 G287 G288 G289 G290 G291 G292 G293 G294 G295 G296 G297 G298 G299 G300 G301 G302 G303 G304 G305 G306 G307 G308 G309 G310 G311 G312 G313 G314 G315 G316 G317 G318 G319 G320 G321 G322 G323 G324 G325 G326 G327 G328 G329 G330 G331 G332 G333 G334 G335 G336 G337 G338 G339 G340 G341 G342 G343 G344 G345 G346 G347 G348 G349 G350 G351 G352 G353 G354 G355 G356 G357 G358 G359 G360 G361 G362 G363 G364 G365 G366 G367 G368 G369 G370 G371 G372 G373 G374 G375 G376 G377 G378 G379 G380 G381 G382 G383 G384 G385 G386 G387 G388 G389 G390 G391 G392 G393 G394 G395 G396 G397 G398 G399 G400 G401 G402 G403 G404 G405 G406 G407 G408 G409 G410 G411 G412 G413 G414 G415 G416 G417 G418 G419 G420 G421 G422 G423 G424 G425 G426 G427 G428 G429 G430 G431 G432 G433 G434 G435 G436 G437 G438 G439 G440 G441 G442 G443 G444 G445 G446 G447 G448 G449 G450 G451 G452 G453 G454 G455 G456 G457 G458 G459 G460 G461 G462 G463 G464 G465 G466 G467 G468 G469 G470 G471 G472 G473 G474 G475 G476 G477 G478 G479 G480 G481 G482 G483 G484 G485 G486 G487 G488 G489 G490 G491 G492 G493 G494 G495 G496 G497 G498 G499 G500 G501 G502 G503 G504 G505 G506 G507 G508 G509 G510 G511 G512 G513 G514 G515 G516 G517 G518 G519 G520 G521 G522 G523 G524 G525 G526 G527 G528 G529 G530 G531 G532 G533 G534 G535 G536 G537 G538 G539 G540 G541 G542 G543 G544 G545 G546 G547 G548 G549 G550 G551 G552 G553 G554 G555 G556 G557 G558 G559 G560 G561 G562 G563 G564 G565 G566 G567 G568 G569 G570 G571 G572 G573 G574 G575 G576 G577 G578 G579 G580 G581 G582 G583 G584 G585 G586 G587 G588 G589 G590 G591 G592 G593 G594 G595 G596 G597 G598 G599 G600 G601 G602 G603 G604 G605 G606 G607 G608 G609 G610 G611 G612 G613 G614 G615 G616 G617 G618 G619 G620 G621 G622 G623 G624 G625 G626 G627 G628 G629 G630 G631 G632 G633 G634 G635 G636 G637 G638 G639 G640 G641 G642 G643 G644 G645 G646 G647 G648 G649 G650 G651 G652 G653 G654 G655 G656 G657 G658 G659 G660 G661 G662 G663 G664 G665 G666 G667 G668 G669 G670 G671 G672 G673 G674 G675 G676 G677 G678 G679 G680 G681 G682 G683 G684 G685 G686 G687 G688 G689 G690 G691 G692 G693 G694 G695 G696 G697 G698 G699 G700 G701 G702 G703 G704 G705 G706 G707 G708 G709 G710 G711 G712 G713 G714 G715 G716 G717 G718 G719 G720 G721 G722 G723 G724 G725 G726 G727 G728 G729 G730 G731 G732 G733 G734 G735 G736 G737 G738 G739 G740 G741 G742 G743 G744 G745 G746 G747 G748 G749 G750 G751 G752 G753 G754 G755 G756 G757 G758 G759 G760 G761 G762 G763 G764 G765 G766 G767 G768 G769 G770 G771 G772 G773 G774 G775 G776 G777 G778 G779 G780 G781 G782 G783 G784 G785 G786 G787 G788 G789 G790 G791 G792 G793 G794 G795 G796 G797 G798 G799 G800 G801 G802 G803 G804 G805 G806 G807 G808 G809 G810 G811 G812 G813 G814 G815 G816 G817 G818 G819 G820 G821 G822 G823 G824 G825 G826 G827 G828 G829 G830 G831 G832 G833 G834 G835 G836 G837 G838 G839 G840 G841 G842 G843 G844 G845 G846 G847 G848 G849 G850 G851 G852 G853 G854 G855 G856 G857 G858 G859 G860 G861 G862 G863 G864 G865 G866 G867 G868 G869 G870 G871 G872 G873 G874 G875 G876 G877 G878 G879 G880 G881 G882 G883 G884 G885 G886 G887 G888 G889 G890 G891 G892 G893 G894 G895 G896 G897 G898 G899 G900 G901 G902 G903 G904 G905 G906 G907 G908 G909 G910 G911 G912 G913 G914 G915 G916 G917 G918 G919 G920 G921 G922 G923 G924 G925 G926 G927 G928 G929 G930 G931 G932 G933 G934 G935 G936 G937 G938 G939 G940 G941 G942 G943 G944 G945 G946 G947 G948 G949 G950 G951 G952 G953 G954 G955 G956 G957 G958 G959 G960 G961 G962 G963 G964 G965 G966 G967 G968 G969 G970 G971 G972 G973 G974 G975 G976 G977 G978 G979 G980 G981 G982 G983 G984 G985 G986 G987 G988 G989 G990 G991 G992 G993 G994 G995 G996 G997 G998 G999

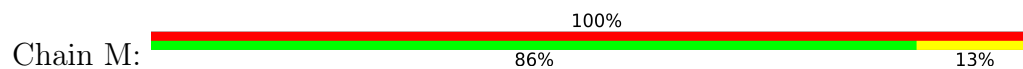
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|---------|--------|------------|
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| Chain K | Yellow | 9% |
| Chain K | Red | 1% |

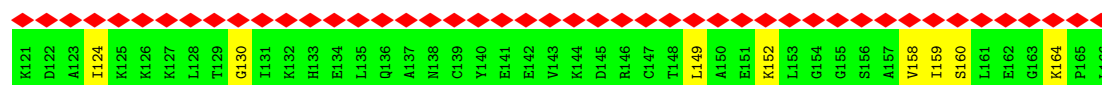
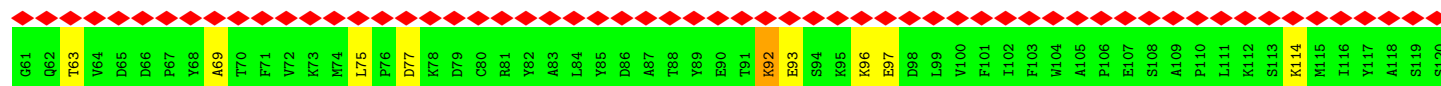


• Molecule 1: Actin, cytoplasmic 1

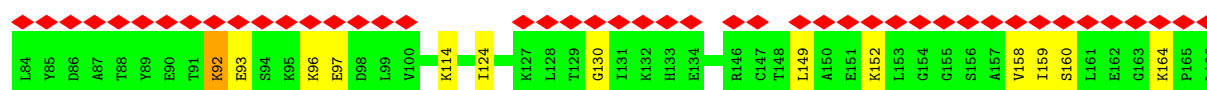
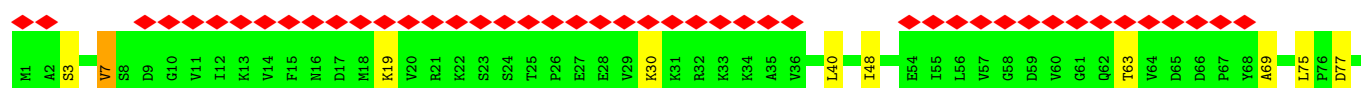
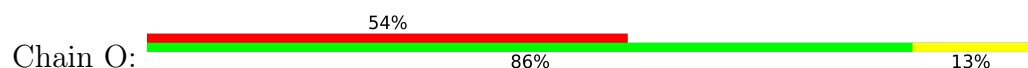


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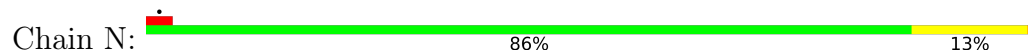




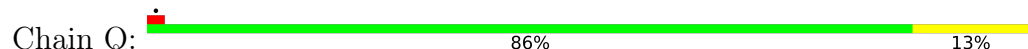
● Molecule 2: Cofilin-2



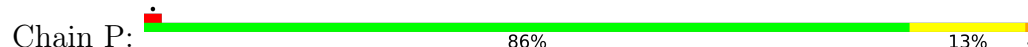
● Molecule 2: Cofilin-2



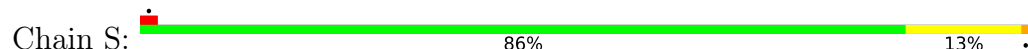
● Molecule 2: Cofilin-2

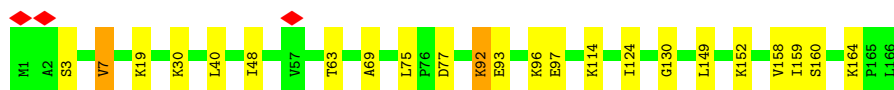


● Molecule 2: Cofilin-2

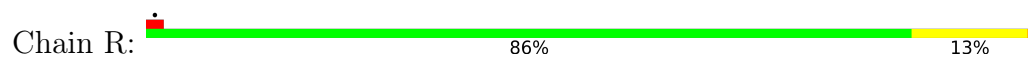


● Molecule 2: Cofilin-2

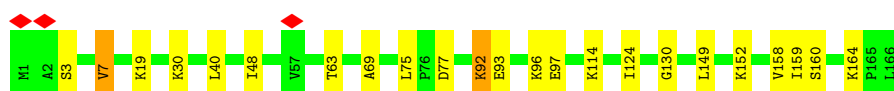
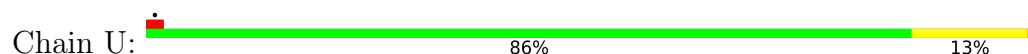




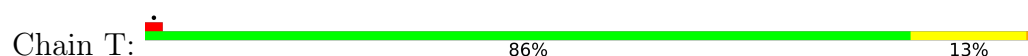
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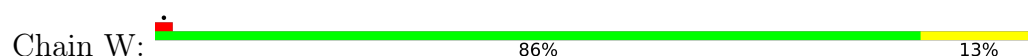
• Molecule 2: Cofilin-2



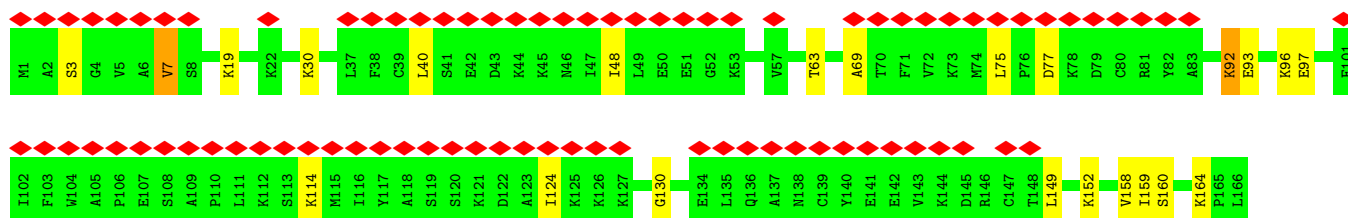
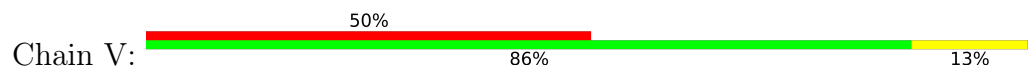
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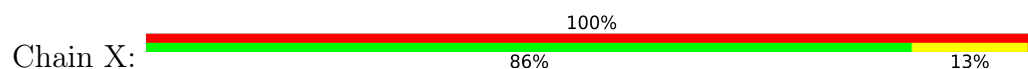
• Molecule 2: Cofilin-2



• Molecule 2: Cofilin-2



• Molecule 2: Cofilin-2



A	K121	M1	G61	B	K122	A2	Q62	C	A123	S3	T63	D	I124	G4	V64	E	K125	D65	F	K126	A6	D66	G	L127	P67	K127	V7	S8	V68	H	L128	P68	I	L129	A69	T70	J	G130	G10	T71	K	I131	V11	F71	L	K132	I12	V72	M	L133	K13	V73	N	E134	V14	M74	O	L135	F15	L75	P	K136	N16	P76	Q	L137	D17	A77	R	M138	M18	K78	S	K139	K19	D79	T	Y140	V20	C90	U	E141	R21	C81	V	E142	K22	Y92	W	V143	S23	A83	X	K144	S24	L84	Y	D145	T25	Y85	Z	R146	P26	D86	AA	C147	E27	A87	AB	T148	E28	T98	AC	L149	V29	Y89	AD	A150	K30	E90	AE	E151	K31	T91	AF	K152	K32	C92	AG	L153	K33	E93	AH	G154	K34	S94	AI	G155	A35	K95	AJ	S156	V36	K96	AK	A157	L37	E97	AL	V158	F38	D98	AM	I159	C39	L99	AN	S160	L40	V100	AO	L161	S41	F101	AP	E162	F42	I102	AQ	G163	D43	I103	AR	K164	K44	V104	AS	P165	A45	A105	AT	L166	N46	P106	AU	AV	AW	AX	AY	AZ	BA	BB	BC	BD	BE	BF	BG	BH	BI	BJ	BK	BL	BM	BN	BO	BP	BQ	BR	BS	BT	BU	BV	BW	BX	BY	BZ	CA	CB	CC	CD	CE	CF	CG	CH	CI	CJ	CK	CL	CM	CN	CO	CP	CQ	CR	CS	CT	CU	CV	CW	CX	CY	CZ	DA	DB	DC	DD	DE	DF	DG	DH	DI	DJ	DK	DL	DM	DN	DO	DP	DQ	DR	DS	DT	DU	DV	DW	DX	DY	DZ	EA	EB	EC	ED	EE	EF	EG	EH	EI	EJ	EK	EL	EM	EN	EO	EP	EQ	ER	ES	ET	EU	EV	EW	EX	EY	EZ	FA	FB	FC	FD	FE	FF	FG	FH	FI	FJ	FK	FL	FM	FN	FO	FP	FQ	FR	FS	FT	FU	FV	FW	FX	FY	FZ	GA	GB	GC	GD	GE	GF	GG	GH	GI	GJ	GK	GL	GM	GN	GO	GP	GQ	GR	GS	GT	GU	GV	GW	GX	GY	GZ	HA	HB	HC	HD	HE	HF	HG	HH	HI	HJ	HK	HL	HM	HN	HO	HP	HQ	HR	HS	HT	HU	HV	HW	HX	HY	HZ	IA	IB	IC	ID	IE	IF	IG	IH	II	IJ	IK	IL	IM	IN	IO	IP	IQ	IR	IS	IT	IU	IV	IW	IX	IY	IZ	JA	JB	JC	JD	JE	JF	JG	JH	JI	JJ	JK	JL	JM	JN	JO	JP	JQ	JR	JS	JT	JU	JV	JW	JX	JY	JZ	KA	KB	KC	KD	KE	KF	KG	KH	KI	KJ	KK	KL	KM	KN	KO	KP	KQ	KR	KS	KT	KU	KV	KW	KX	KY	KZ	LA	LB	LC	LD	LE	LF	LG	LH	LI	LJ	LK	LM	LN	LO	LP	LQ	LR	LS	LT	LU	LV	LW	LX	LY	LZ	MA	MB	MC	MD	ME	MF	MG	MH	MI	MJ	MK	ML	MN	MO	MP	MQ	MR	MS	MT	MU	MV	MW	MX	MY	MZ	NA	NB	NC	ND	NE	NF	NG	NH	NI	NJ	NK	NL	NM	NO	NP	NQ	NR	NS	NT	NU	NV	NW	NX	NY	NZ	OA	OB	OC	OD	OE	OF	OG	OH	OI	OJ	OK	OL	OM	ON	OO	OP	OQ	OR	OS	OT	OU	OV	OW	OX	OY	OZ	PA	PB	PC	PD	PE	PF	PG	PH	PI	PJ	PK	PL	PM	PN	PO	PP	PQ	PR	PS	PT	PU	PV	PW	PX	PY	PZ	QA	QB	QC	QD	QE	QF	QG	QH	QI	QJ	QK	QL	QM	QN	QO	QP	QQ	QR	QS	QT	QU	QV	QW	QX	QY	QZ	RA	RB	RC	RD	RE	RF	RG	RH	RI	RJ	RK	RL	RM	RN	RO	RP	RQ	RR	RS	RT	RU	RV	RW	RX	RY	RZ	SA	SB	SC	SD	SE	SF	SG	SH	SI	SJ	SK	SL	SM	SN	SO	SP	SQ	SR	SS	ST	SU	SV	SW	SX	SY	SZ	TA	TB	TC	TD	TE	TF	TG	TH	TI	TJ	TK	TL	TM	TN	TO	TP	TQ	TR	TS	TT	TU	TV	TW	TX	TY	TZ	UA	UB	UC	UD	UE	UF	UG	UH	UI	UJ	UK	UL	UM	UN	UO	UP	UQ	UR	US	UT	UU	UV	UW	UX	UY	UZ	VA	VB	VC	VD	VE	VF	VG	VH	VI	VJ	VK	VL	VM	VN	VO	VP	VQ	VR	VS	VT	VU	VV	VW	VX	VY	VZ	WA	WB	WC	WD	WE	WF	WG	WH	WI	WJ	WK	WL	WM	WN	WO	WP	WQ	WR	WS	WT	WU	WV	WW	WX	WY	WZ	XA	XB	XC	XD	XE	XF	XG	XH	XI	XJ	XK	XL	XM	XN	XO	XP	XQ	XR	XS	XT	XU	XV	XW	XX	XY	XZ	YA	YB	YC	YD	YE	YF	YG	YH	YI	YJ	YK	YL	YM	YN	YO	YP	YQ	YR	YS	YT	YU	YV	YW	YX	YY	YZ	ZA	ZB	ZC	ZD	ZE	ZF	ZG	ZH	ZI	ZJ	ZK	ZL	ZM	ZN	ZO	ZP	ZQ	ZR	ZS	ZT	ZU	ZV	ZW	ZX	ZY	ZZ
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4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=162.1°, rise=27.6 Å, axial sym=C1	Depositor
Number of segments used	Not provided	
Resolution determination method	FSC	Depositor
CTF correction method	each EM	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{Å}^2$)	Not provided	
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	5300	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.237	Depositor
Minimum map value	-0.082	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.043	Depositor
Map size (Å)	250.0, 250.0, 250.0	wwPDB
Map dimensions	100, 100, 100	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.5, 2.5, 2.5	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	0.70	0/2980	1.11	11/4035 (0.3%)
1	B	0.71	0/2980	1.11	10/4035 (0.2%)
1	C	0.71	0/2980	1.11	10/4035 (0.2%)
1	D	0.70	0/2980	1.11	10/4035 (0.2%)
1	E	0.70	0/2980	1.11	10/4035 (0.2%)
1	F	0.70	0/2980	1.11	10/4035 (0.2%)
1	G	0.70	0/2980	1.11	10/4035 (0.2%)
1	H	0.71	0/2980	1.11	10/4035 (0.2%)
1	I	0.71	0/2980	1.11	10/4035 (0.2%)
1	J	0.71	0/2980	1.11	10/4035 (0.2%)
1	K	0.70	0/2980	1.11	10/4035 (0.2%)
1	L	0.70	0/2980	1.11	10/4035 (0.2%)
2	M	0.77	1/1315 (0.1%)	1.14	2/1762 (0.1%)
2	N	0.77	1/1315 (0.1%)	1.14	2/1762 (0.1%)
2	O	0.77	1/1315 (0.1%)	1.14	2/1762 (0.1%)
2	P	0.77	1/1315 (0.1%)	1.14	2/1762 (0.1%)
2	Q	0.77	1/1315 (0.1%)	1.14	2/1762 (0.1%)
2	R	0.77	1/1315 (0.1%)	1.14	2/1762 (0.1%)
2	S	0.77	1/1315 (0.1%)	1.14	2/1762 (0.1%)
2	T	0.77	1/1315 (0.1%)	1.14	2/1762 (0.1%)
2	U	0.77	1/1315 (0.1%)	1.14	2/1762 (0.1%)
2	V	0.77	1/1315 (0.1%)	1.14	2/1762 (0.1%)
2	W	0.77	1/1315 (0.1%)	1.14	2/1762 (0.1%)
2	X	0.77	1/1315 (0.1%)	1.14	2/1762 (0.1%)
All	All	0.73	12/51540 (0.0%)	1.12	145/69564 (0.2%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	S	7	VAL	N-CA	5.38	1.53	1.46
2	V	7	VAL	N-CA	5.32	1.53	1.46
2	N	7	VAL	N-CA	5.31	1.52	1.46
2	T	7	VAL	N-CA	5.29	1.52	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	7	VAL	N-CA	5.29	1.52	1.46

The worst 5 of 145 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	301	GLY	N-CA-C	6.93	120.72	112.33
1	G	301	GLY	N-CA-C	6.92	120.71	112.33
1	A	301	GLY	N-CA-C	6.92	120.70	112.33
1	I	301	GLY	N-CA-C	6.91	120.69	112.33
1	B	301	GLY	N-CA-C	6.90	120.68	112.33

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2917	0	2879	0	0
1	B	2917	0	2879	0	0
1	C	2917	0	2879	0	0
1	D	2917	0	2879	0	0
1	E	2917	0	2879	0	0
1	F	2917	0	2879	0	0
1	G	2917	0	2879	0	0
1	H	2917	0	2879	0	0
1	I	2917	0	2879	0	0
1	J	2917	0	2879	0	0
1	K	2917	0	2879	0	0
1	L	2917	0	2879	0	0
2	M	1296	0	1345	0	0
2	N	1296	0	1345	0	0
2	O	1296	0	1345	0	0
2	P	1296	0	1345	0	0
2	Q	1296	0	1345	0	0
2	R	1296	0	1345	0	0
2	S	1296	0	1345	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	T	1296	0	1345	0	0
2	U	1296	0	1345	0	0
2	V	1296	0	1345	0	0
2	W	1296	0	1345	0	0
2	X	1296	0	1345	0	0
All	All	50556	0	50688	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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	372/374 (100%)	349 (94%)	10 (3%)	13 (4%)	3	20
1	B	372/374 (100%)	349 (94%)	10 (3%)	13 (4%)	3	20
1	C	372/374 (100%)	348 (94%)	11 (3%)	13 (4%)	3	20
1	D	372/374 (100%)	349 (94%)	10 (3%)	13 (4%)	3	20
1	E	372/374 (100%)	349 (94%)	10 (3%)	13 (4%)	3	20
1	F	372/374 (100%)	349 (94%)	10 (3%)	13 (4%)	3	20
1	G	372/374 (100%)	349 (94%)	10 (3%)	13 (4%)	3	20
1	H	372/374 (100%)	349 (94%)	10 (3%)	13 (4%)	3	20
1	I	372/374 (100%)	349 (94%)	10 (3%)	13 (4%)	3	20
1	J	372/374 (100%)	349 (94%)	10 (3%)	13 (4%)	3	20
1	K	372/374 (100%)	349 (94%)	10 (3%)	13 (4%)	3	20
1	L	372/374 (100%)	349 (94%)	10 (3%)	13 (4%)	3	20
2	M	164/166 (99%)	141 (86%)	15 (9%)	8 (5%)	1	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	N	164/166 (99%)	141 (86%)	15 (9%)	8 (5%)	1	16
2	O	164/166 (99%)	141 (86%)	15 (9%)	8 (5%)	1	16
2	P	164/166 (99%)	141 (86%)	15 (9%)	8 (5%)	1	16
2	Q	164/166 (99%)	141 (86%)	15 (9%)	8 (5%)	1	16
2	R	164/166 (99%)	141 (86%)	15 (9%)	8 (5%)	1	16
2	S	164/166 (99%)	141 (86%)	15 (9%)	8 (5%)	1	16
2	T	164/166 (99%)	141 (86%)	15 (9%)	8 (5%)	1	16
2	U	164/166 (99%)	141 (86%)	15 (9%)	8 (5%)	1	16
2	V	164/166 (99%)	141 (86%)	15 (9%)	8 (5%)	1	16
2	W	164/166 (99%)	141 (86%)	15 (9%)	8 (5%)	1	16
2	X	164/166 (99%)	141 (86%)	15 (9%)	8 (5%)	1	16
All	All	6432/6480 (99%)	5879 (91%)	301 (5%)	252 (4%)	4	19

5 of 252 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	ASP
1	A	5	ILE
1	A	43	VAL
1	A	49	GLN
1	A	302	GLY

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	317/317 (100%)	296 (93%)	21 (7%)	15	37
1	B	317/317 (100%)	296 (93%)	21 (7%)	15	37
1	C	317/317 (100%)	296 (93%)	21 (7%)	15	37
1	D	317/317 (100%)	296 (93%)	21 (7%)	15	37
1	E	317/317 (100%)	296 (93%)	21 (7%)	15	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	317/317 (100%)	296 (93%)	21 (7%)	15	37
1	G	317/317 (100%)	296 (93%)	21 (7%)	15	37
1	H	317/317 (100%)	296 (93%)	21 (7%)	15	37
1	I	317/317 (100%)	296 (93%)	21 (7%)	15	37
1	J	317/317 (100%)	296 (93%)	21 (7%)	15	37
1	K	317/317 (100%)	296 (93%)	21 (7%)	15	37
1	L	317/317 (100%)	296 (93%)	21 (7%)	15	37
2	M	144/144 (100%)	130 (90%)	14 (10%)	8	24
2	N	144/144 (100%)	130 (90%)	14 (10%)	8	24
2	O	144/144 (100%)	130 (90%)	14 (10%)	8	24
2	P	144/144 (100%)	130 (90%)	14 (10%)	8	24
2	Q	144/144 (100%)	130 (90%)	14 (10%)	8	24
2	R	144/144 (100%)	130 (90%)	14 (10%)	8	24
2	S	144/144 (100%)	130 (90%)	14 (10%)	8	24
2	T	144/144 (100%)	130 (90%)	14 (10%)	8	24
2	U	144/144 (100%)	130 (90%)	14 (10%)	8	24
2	V	144/144 (100%)	130 (90%)	14 (10%)	8	24
2	W	144/144 (100%)	130 (90%)	14 (10%)	8	24
2	X	144/144 (100%)	130 (90%)	14 (10%)	8	24
All	All	5532/5532 (100%)	5112 (92%)	420 (8%)	14	33

5 of 420 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	4	ASP
2	N	93	GLU
2	V	96	LYS
1	L	140	LEU
2	M	114	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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](#)

There are no ligands in this entry.

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.

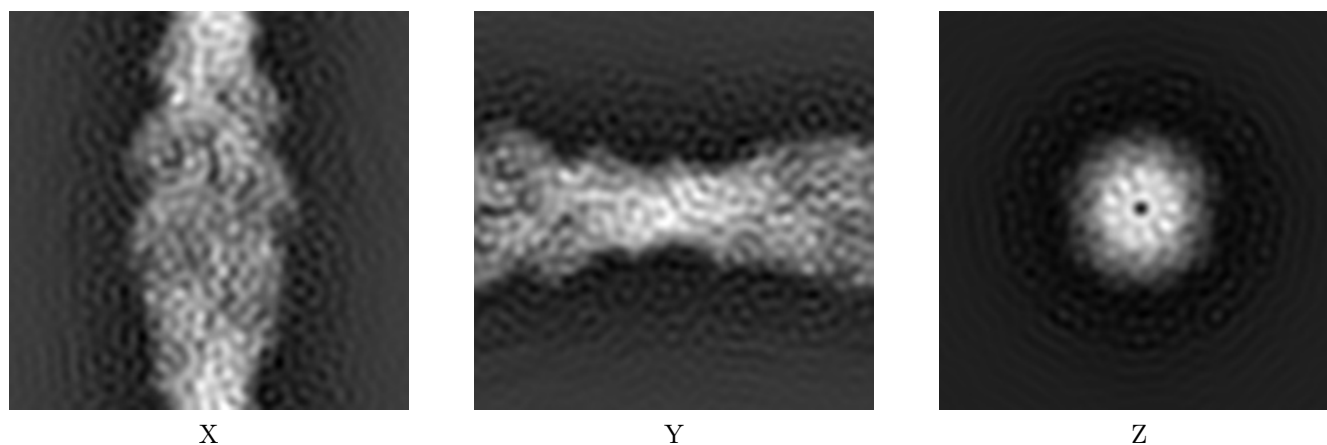
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5354. 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 [i](#)

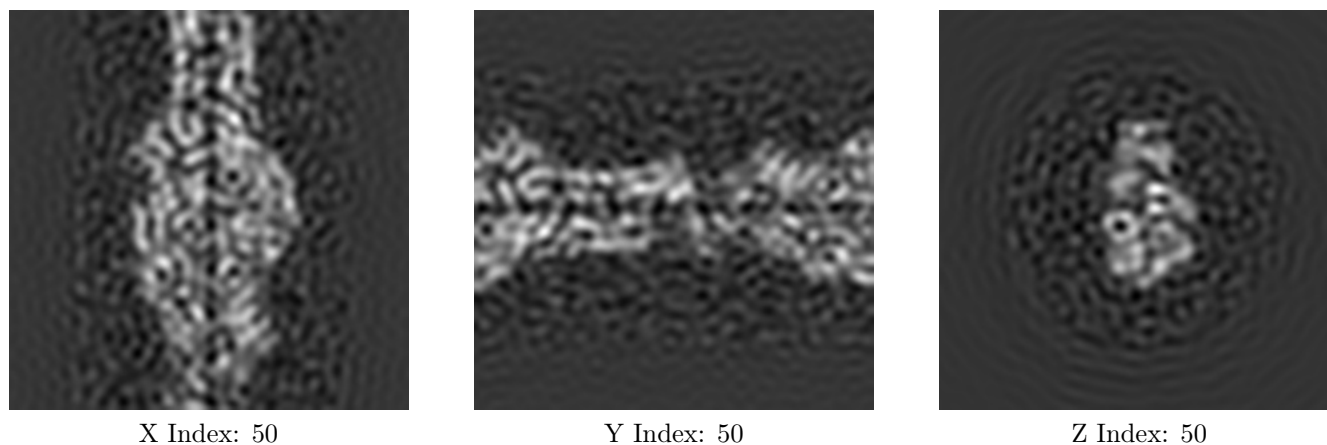
6.1.1 Primary map



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

6.2 Central slices [i](#)

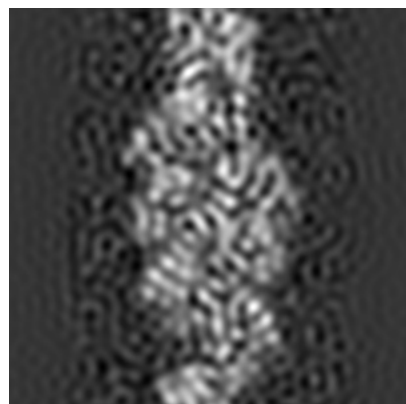
6.2.1 Primary map



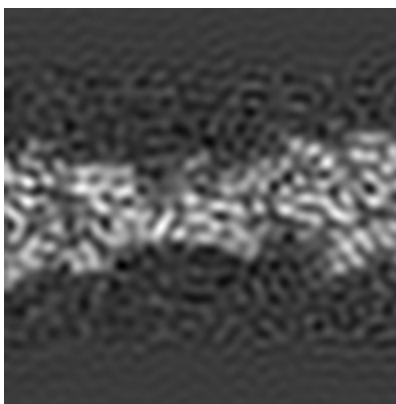
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

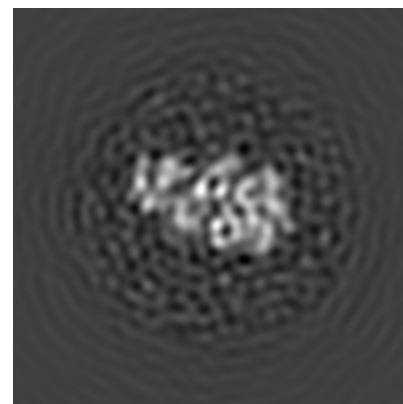
6.3.1 Primary map



X Index: 52



Y Index: 47

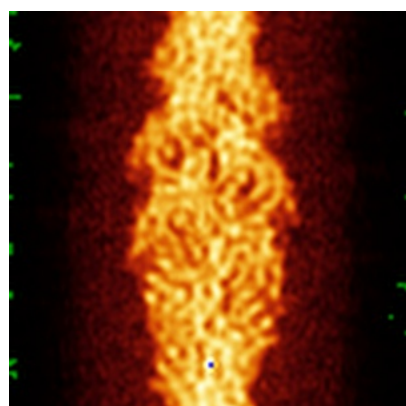


Z Index: 95

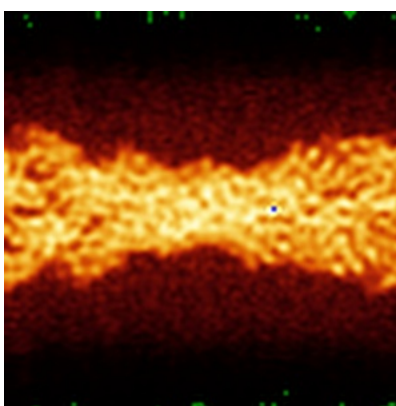
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

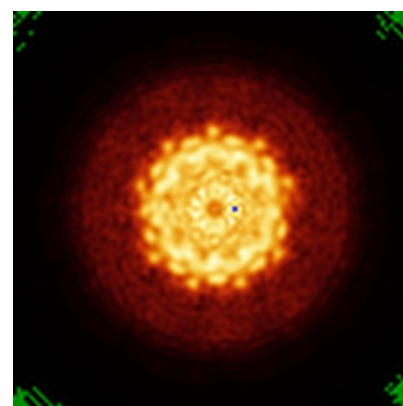
6.4.1 Primary map



X



Y

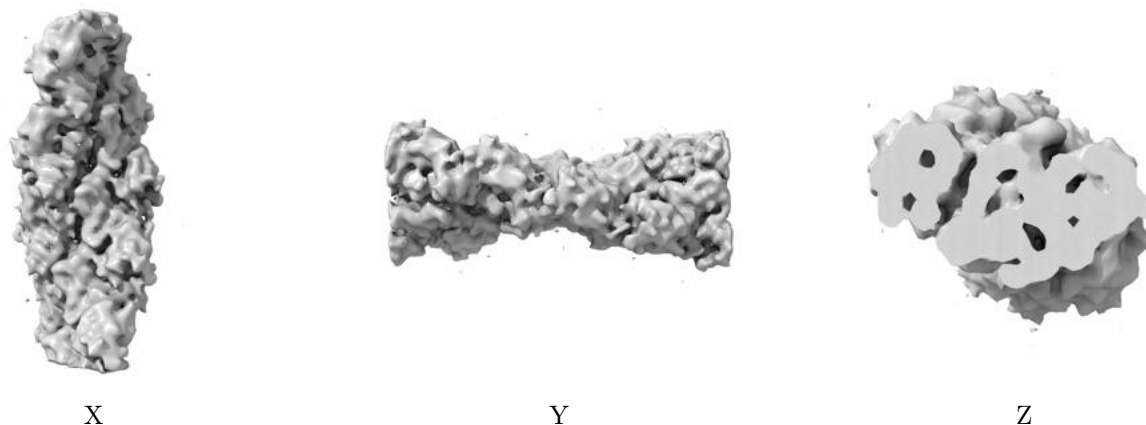


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.043. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

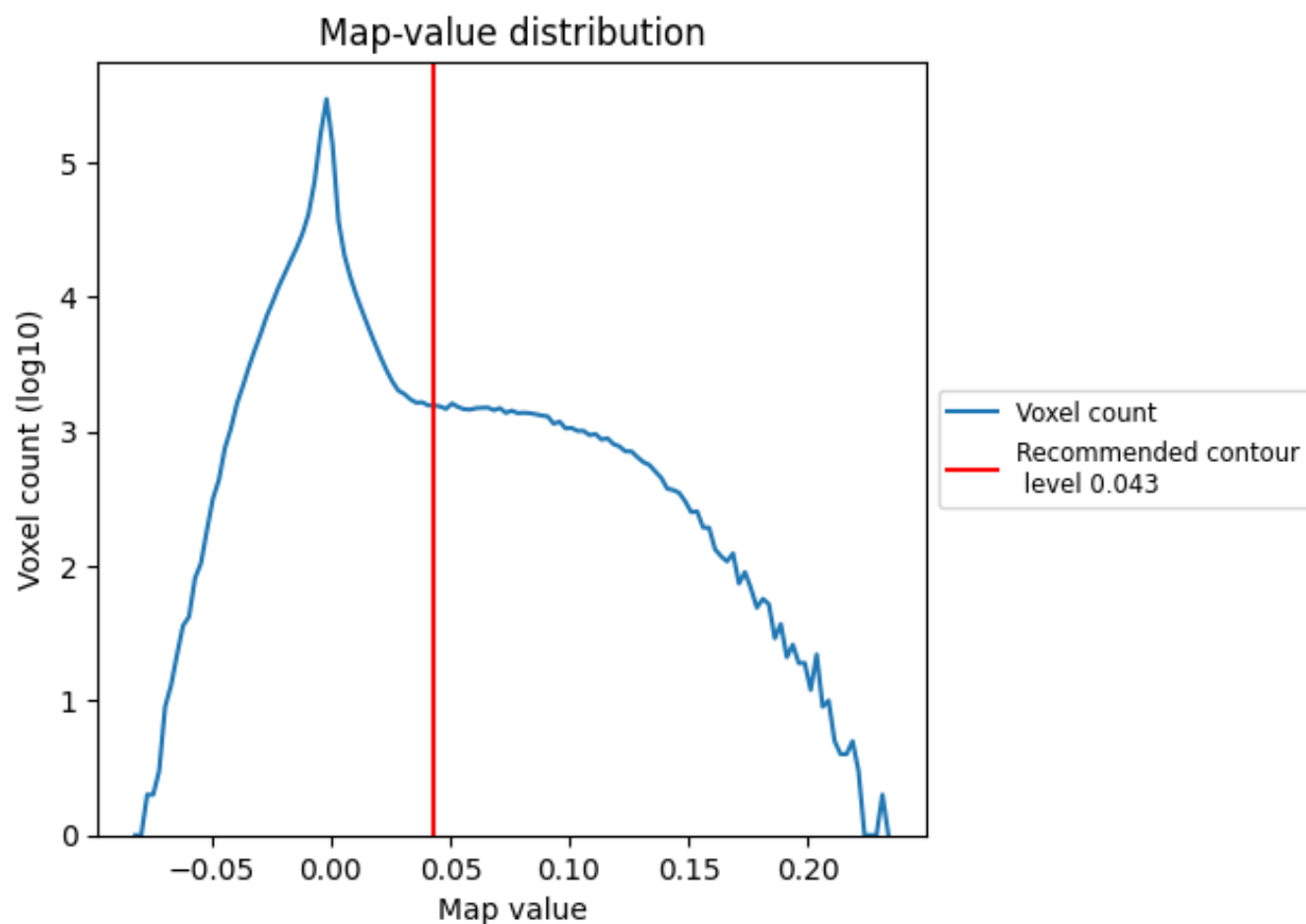
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

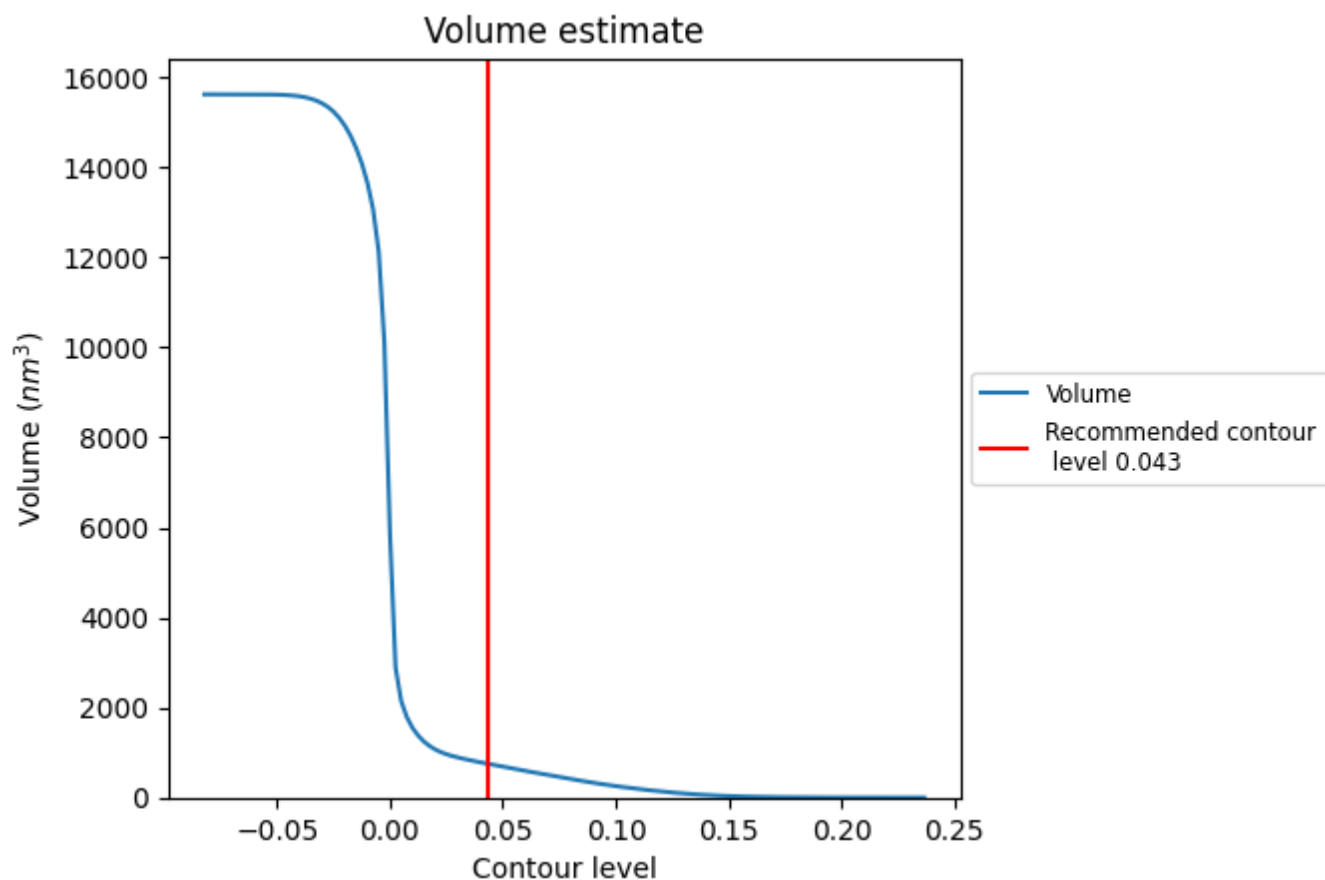
This section contains the results of statistical analysis of the map.

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.

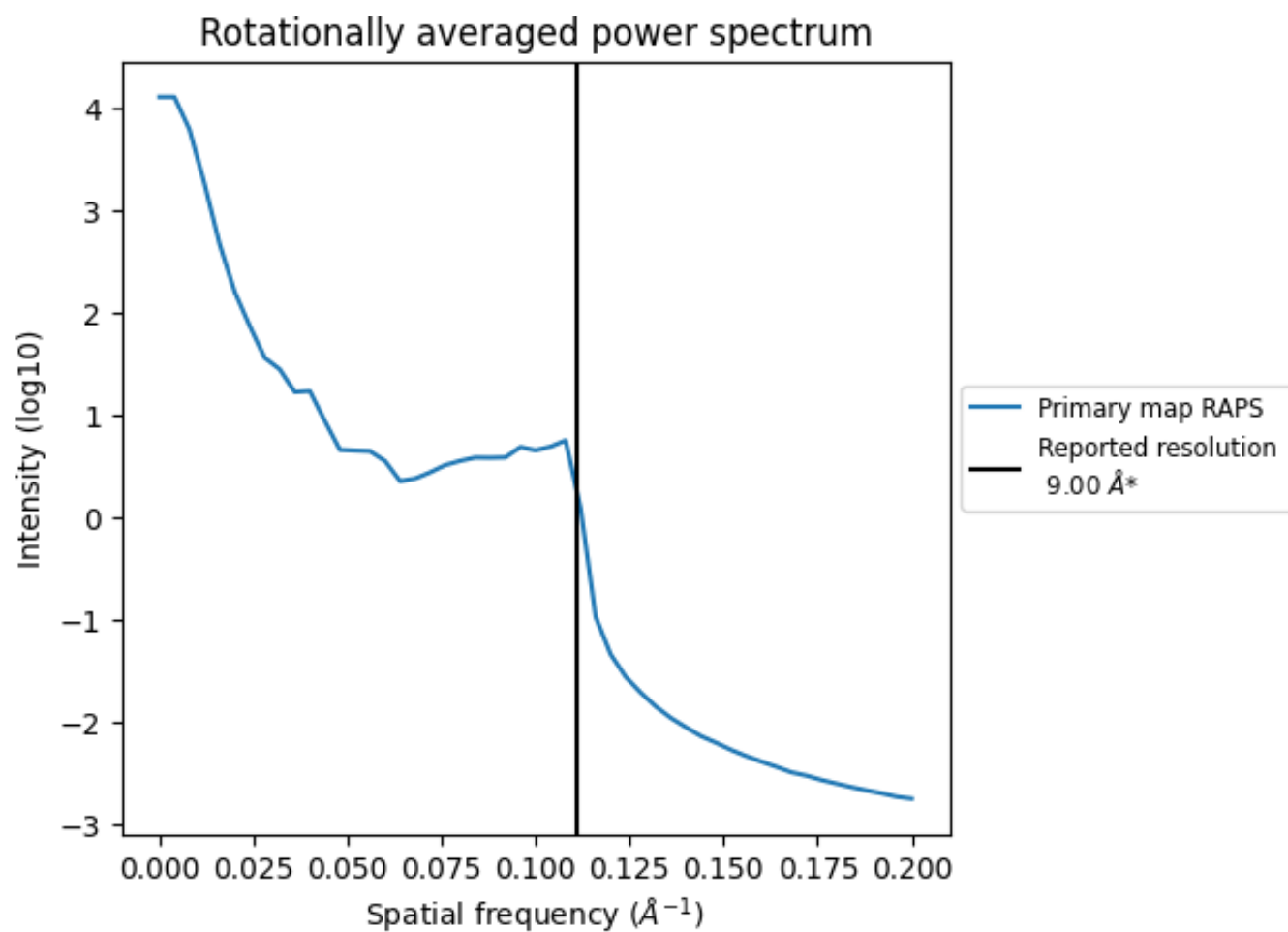
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 753 nm³; this corresponds to an approximate mass of 681 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 0.111 Å⁻¹

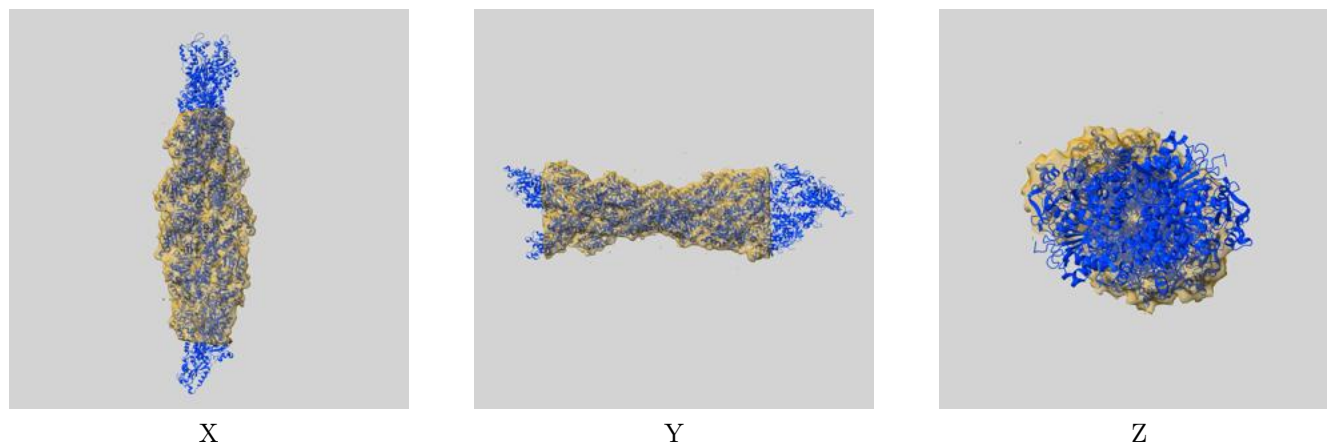
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

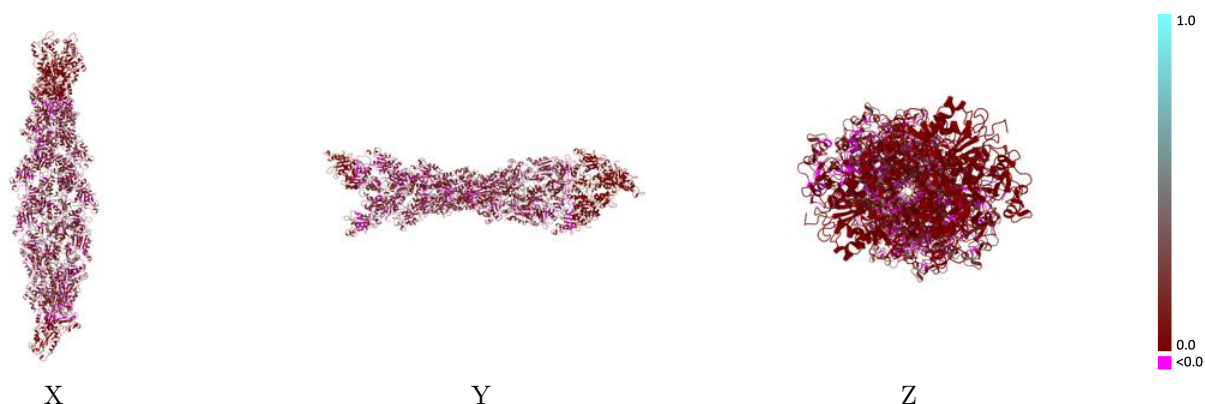
This section contains information regarding the fit between EMDB map EMD-5354 and PDB model 3J0S. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



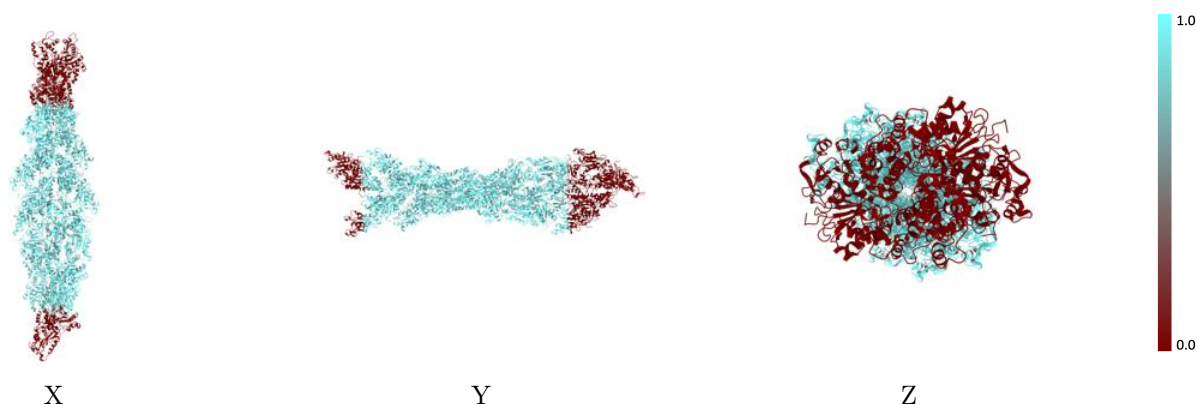
The images above show the 3D surface view of the map at the recommended contour level 0.043 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



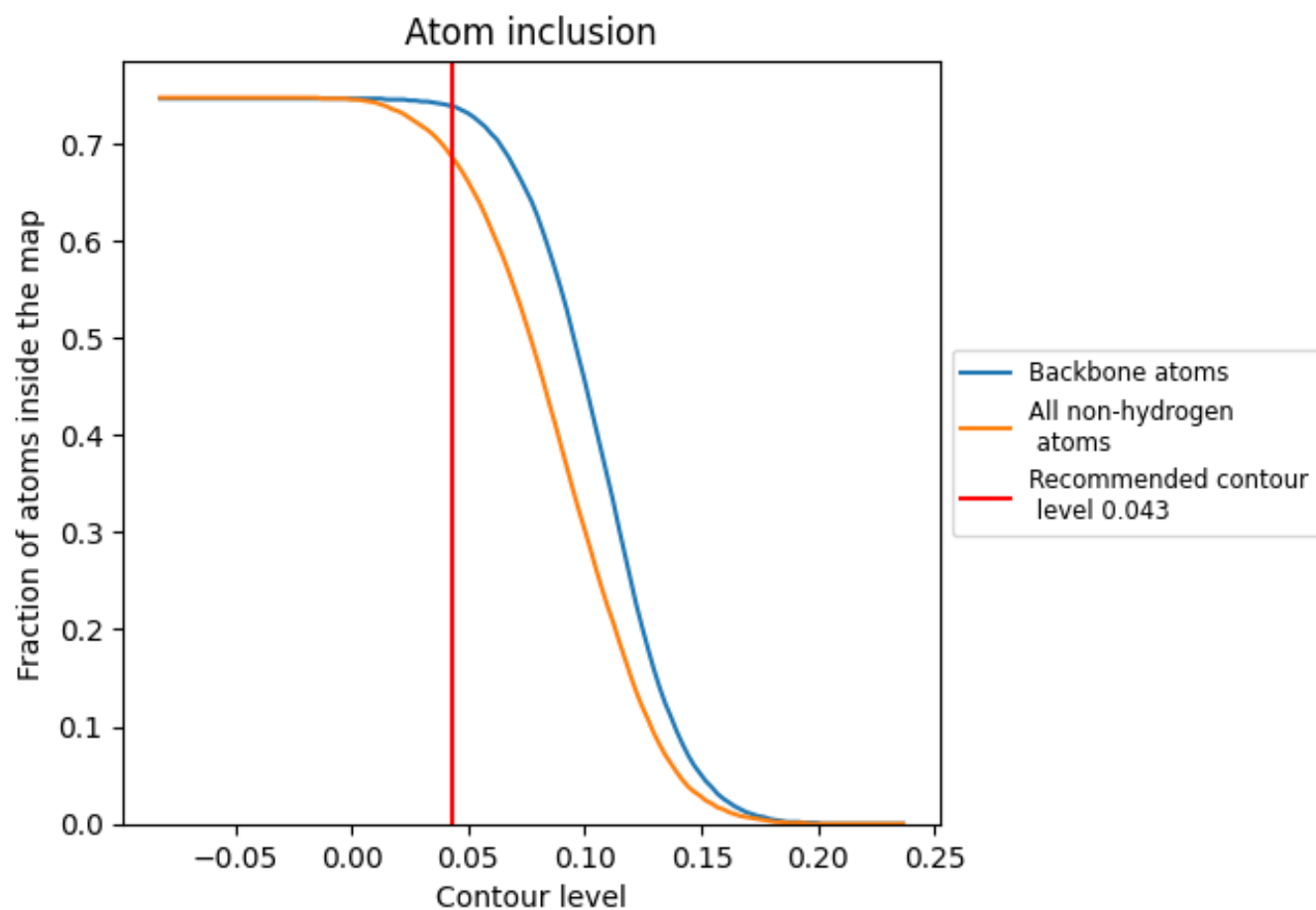
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.043).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 69% 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 (0.043) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6860	 0.0890
A	 0.4560	 0.0560
B	 0.9190	 0.1240
C	 0.9260	 0.1230
D	 0.9220	 0.1230
E	 0.9270	 0.1230
F	 0.9240	 0.1240
G	 0.9270	 0.1220
H	 0.9280	 0.1230
I	 0.9130	 0.1200
J	 0.4430	 0.0450
K	 0.0010	 -0.0010
L	 0.0000	 0.0000
M	 0.0000	 -0.0010
N	 0.8950	 0.1120
O	 0.4210	 0.0430
P	 0.9030	 0.1180
Q	 0.9110	 0.1180
R	 0.9100	 0.1180
S	 0.9060	 0.1180
T	 0.9080	 0.1210
U	 0.9090	 0.1130
V	 0.4580	 0.0510
W	 0.9060	 0.1210
X	 0.0000	 0.0000

