wwPDB EM Validation Summary Report (i)

Mar 22, 2026 – 02:55 PM UTC

PDB ID	:	8ATM / pdb_00008atm
EMDB ID	:	EMD-15653
Title	:	Structure of the giant inhibitor of apoptosis, BIRC6 (composite map)
Authors	:	Dietz, L.; Elliott, P.R.
Deposited on	:	2022-08-23
Resolution	:	3.30 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 (i) symbol.

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

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

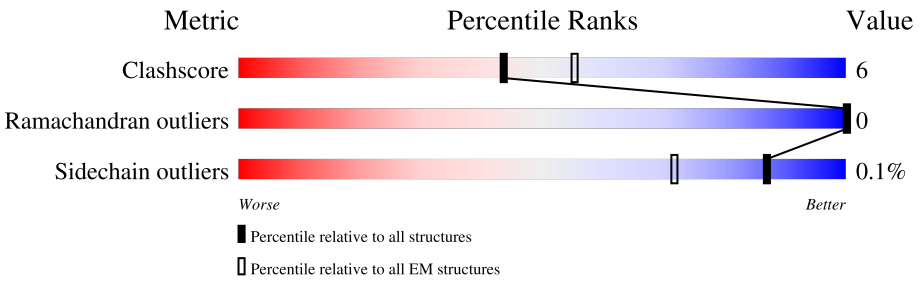
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

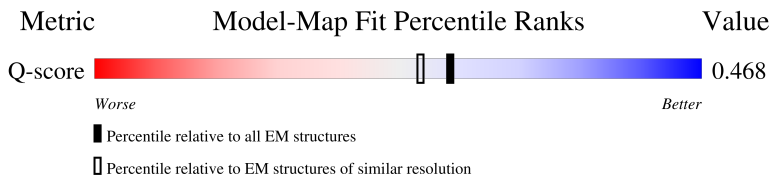
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	A	4859	35% 7% 58%
1	B	4859	34% 6% 60%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 30885 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 Baculoviral IAP repeat-containing protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	2035	15729	10066	2671	2876	116	0	0
1	B	1963	15156	9705	2568	2772	111	0	0

There are 4 discrepancies between the modelled and reference sequences:

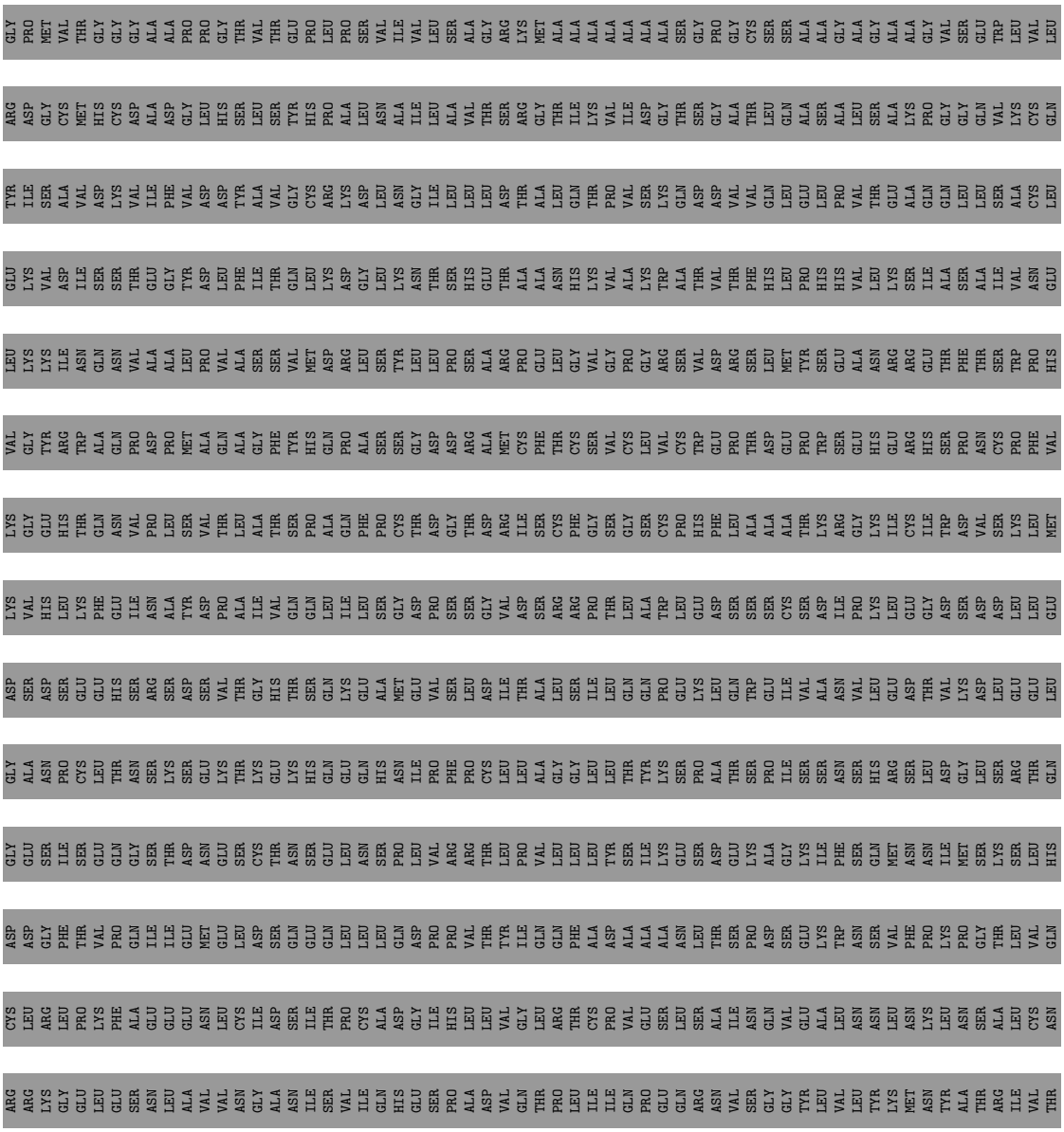
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q9NR09
A	0	PRO	-	expression tag	UNP Q9NR09
B	-1	GLY	-	expression tag	UNP Q9NR09
B	0	PRO	-	expression tag	UNP Q9NR09

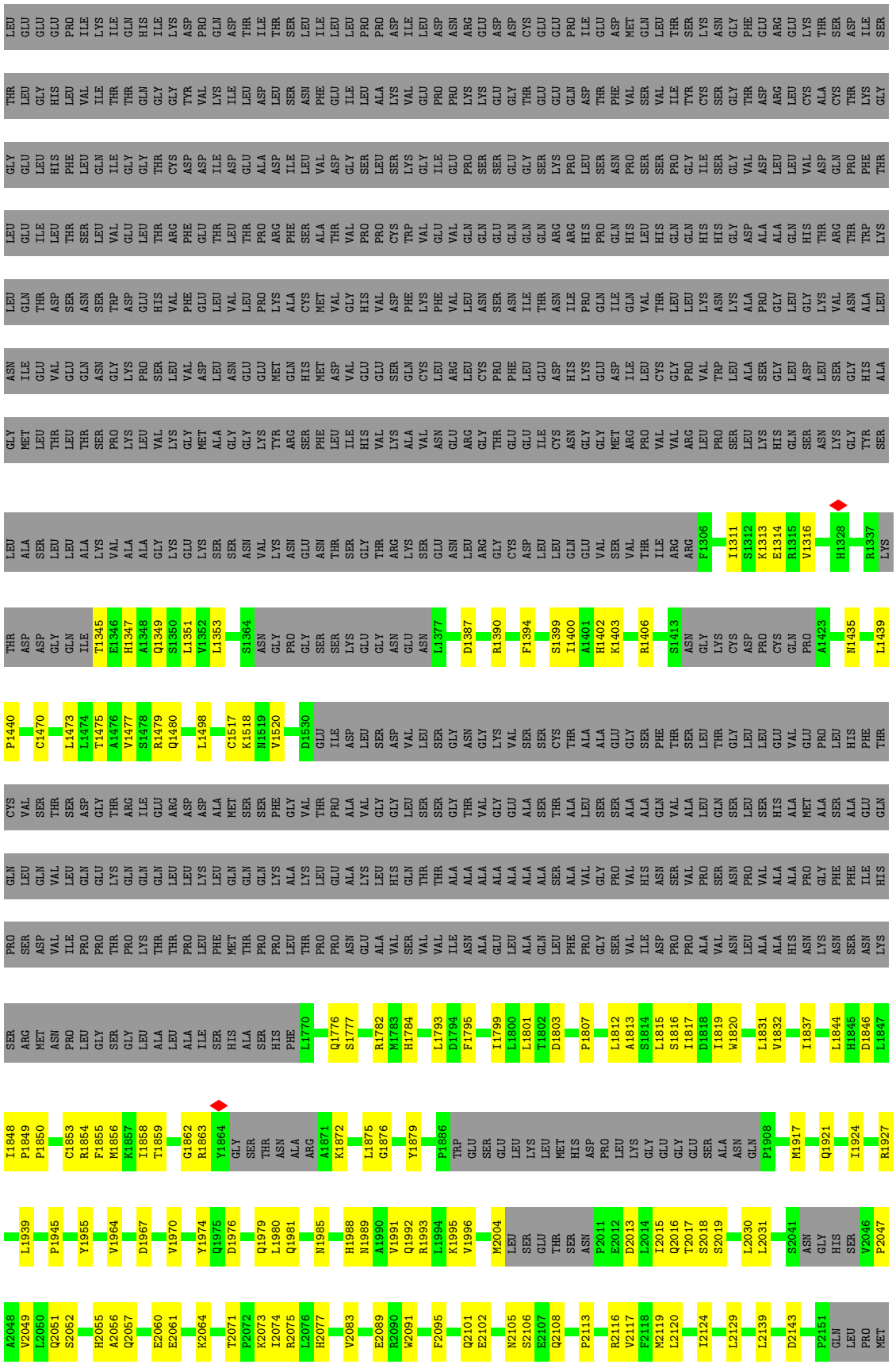
3 Residue-property plots (i)

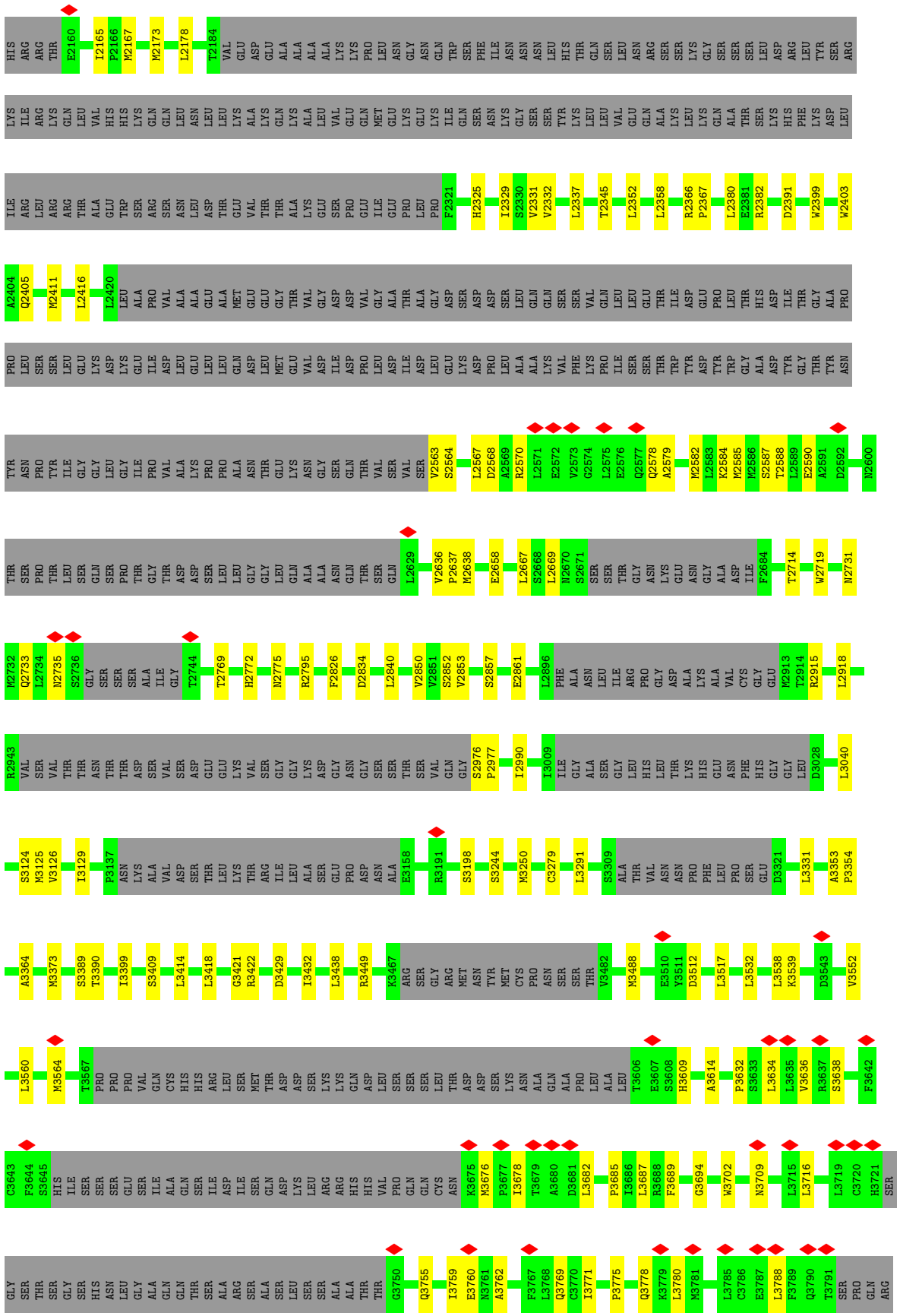
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

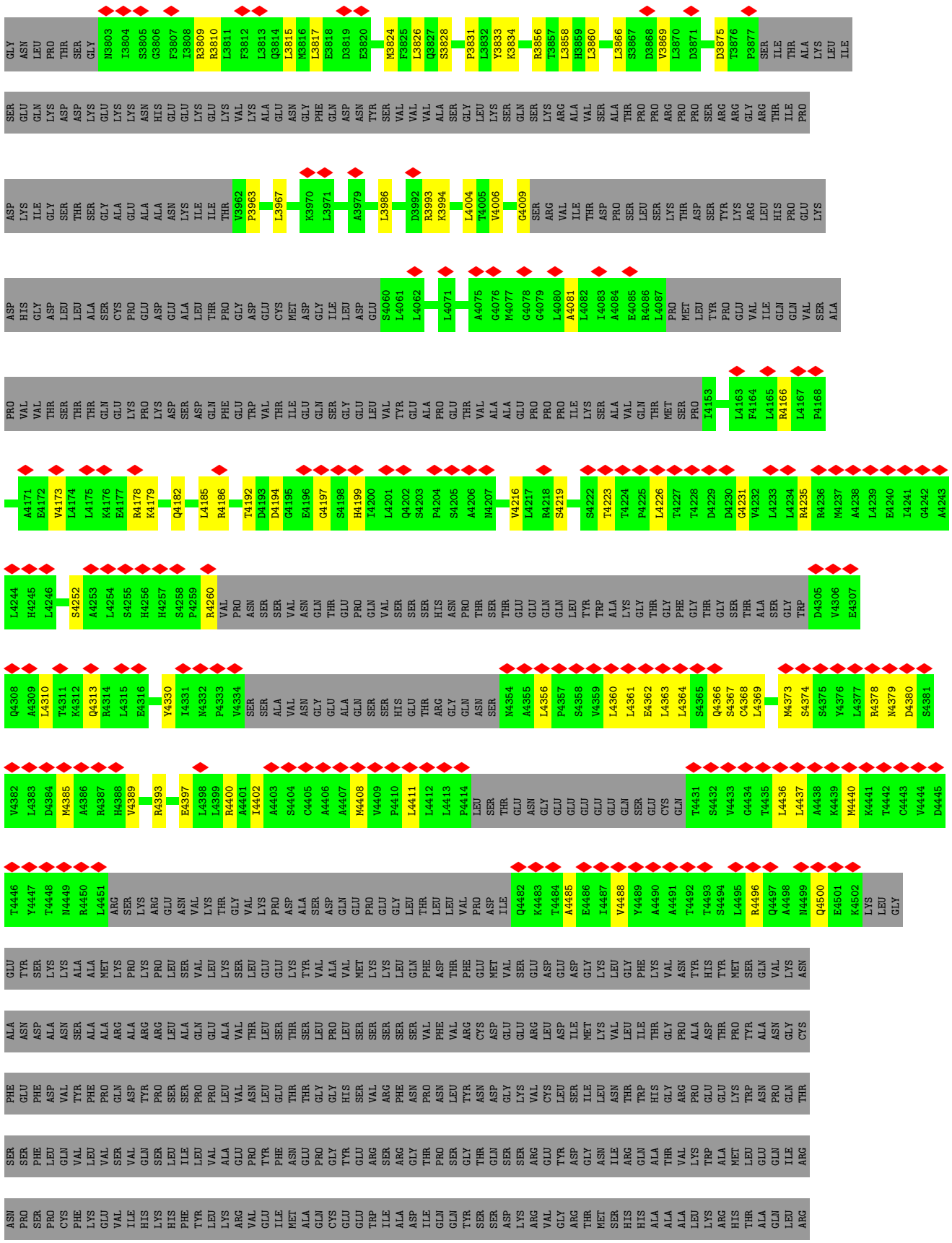
- Molecule 1: Baculoviral IAP repeat-containing protein 6

Chain A:




A2048 V2049 L2050 Q2051 S2052 H2055 A2056 Q2057 E2060 E2061 K2064 T2071 P2072 K2073 I2074 R2075 L2076 H2077 V2083 E2089 R2090 W2091 F2095 Q2101 E2102 N2105 S2106 E2107 Q2108 P2113 R2116 V2117 F2118 M2119 L2120 I2124 L2129 L2139 D2143 P2151 GLN LEU PRO MET
L1939 P1945 Y1955 V1964 D1967 V1970 Y1974 Q1975 D1976 Q1979 L1980 Q1981 N1985 H1988 N1989 A1990 V1991 Q1992 R1993 L1994 K1995 V1996 M2004 LEU SER GLU THR SER ASN P2011 E2012 D2013 L2014 I2015 Q2016 T2017 S2018 S2019 L2030 L2031 S2041 ASN GLY HIS SER V2046 P2047
I1848 P1849 P1850 C1853 R1854 F1855 M1856 K1857 I1858 T1859 G1862 R1863 Y1864 GLY SER THR ASN ALA ARG A1871 K1872 L1875 G1876 Y1879 P1886 TRP GLU SER GLU LEU LYS LEU MET HIS ASP PRO LEU GLY GLU GLU GLY GLU P1908 M1917 Q1921 I1924 R1927
SER ARG MET ASN PRO LEU GLY SER GLY LEU ALA LEU ALA ILE SER HIS ALA SER HIS PHE L1770 Q1776 S1777 R1782 M1783 H1784 L1793 D1794 F1795 I1799 L1800 L1801 T1802 D1803 P1807 L1812 A1813 S1814 L1815 S1816 I1817 D1818 I1819 W1820 L1831 V1832 T1837 L1844 H1845 D1846 L1847
PRO SER ASP VAL ILE PRO PRO THR PRO THR PRO LYS THR LEU THR PRO PHE MET THR PRO PRO LEU THR PRO PRO ASN GLU ALA VAL PRO ILE ASN ALA VAL SER VAL VAL THR PRO GLU LEU ALA ALA ALA ALA SER SER ALA VAL GLY PRO VAL HIS ASN SER VAL PRO PRO ALA VAL ASN LEU PRO LYS ASN LYS PRO SER LEU ALA HIS ASN LYS
GLN LEU GLN VAL LEU GLN GLU LYS GLN GLN GLN LEU LEU LYS LEU GLN GLN GLN LYS ALA LYS LEU GLU ALA ALA LYS LEU ALA ALA ALA ALA ALA ALA ALA SER ALA VAL GLY PRO VAL HIS GLN THR THR ALA ALA ALA ALA ALA ALA SER ALA VAL SER SER ALA ALA ALA GLN VAL ALA LEU GLN SER LEU SER HIS ALA MET ALA PHE PHE ILE HIS
CYS VAL SER THR SER ASP GLY THR ARG ILE GLU ARG ASP ASP ALA MET SER SER PHE GLY VAL THR PRO ALA VAL GLY GLY LEU SER SER GLY THR VAL GLY GLU ALA SER THR ALA LEU SER SER SER ALA ALA GLN VAL ALA LEU THR GLY LEU LEU GLU VAL PHE THR GLN
P1440 C1470 L1473 L1474 T1475 A1476 V1477 S1478 R1479 Q1480 L1498 C1517 K1518 N1519 V1520 D1530 GLU ILE ASP LEU SER ASP VAL LEU SER GLY ASN GLY LYS VAL SER SER CYS THR ALA GLU GLY PHE THR SER LEU THR GLY LEU LEU GLU VAL PRO LEU HIS PHE THR
THR ASP ASP GLY GLN ILE T1345 E1346 H1347 A1348 Q1349 S1350 L1351 V1352 L1353 S1364 ASN GLY PRO GLY SER SER LYS GLU GLY ASN GLU ASN L1377 D1387 R1390 F1394 S1399 I1400 A1401 H1402 K1403 R1406 S1413 ASN GLY LYS CYS ASP PRO CYS GLN PRO A1423 N1435 L1439
LEU ALA SER LEU LEU ALA LYS VAL ALA ALA GLY LYS GLU LYS SER SER ASN VAL LYS ASN GLU ASN THR SER GLY THR ARG LYS SER GLU ASN LEU ARG GLY THR GLU GLU ASP LEU LEU GLN GLU VAL SER VAL THR ILE ARG ARG F1306 I1311 S1312 K1313 E1314 R1315 V1316 H1328 R1337 LYS
GLY MET LEU THR LEU THR SER PRO LYS LEU VAL LYS GLY MET ALA GLY GLY LYS TYR ARG SER PHE LEU ILE HIS VAL LYS ALA VAL ASN GLU GLU ARG GLY THR GLU GLU ILE CYS ASN GLY GLY MET ARG PRO VAL VAL ARG LEU PRO VAL TRP LEU ALA SER GLY HIS GLN SER ASN LYS GLY TYR SER
ASN ILE GLU VAL GLU GLN ASN GLY LYS PRO SER LEU VAL ASP LEU ASN GLU GLU GLU MET GLN HIS MET MET VAL GLY HIS VAL GLU GLU SER GLN LEU ARG LEU CYS PRO SER LEU ILE GLU ASP HIS LYS GLU ASP ILE GLN LEU VAL LEU LYS ASN LYS ALA SER GLY HIS ALA
LEU GLN THR ASP SER ASN SER TRP ASP GLU HIS VAL PHE GLU LEU VAL LEU PRO LYS ALA CYS MET MET VAL GLY HIS VAL ASP PHE LYS PHE VAL LEU ASN SER ASN ILE PRO GLN ILE THR ASN ILE PRO GLN HIS LEU HIS GLN GLN HIS HIS GLY ASP ALA PRO GLY LEU HIS THR ARG THR LYS LEU
LEU GLU ILE LEU THR SER LEU VAL GLU LEU THR ARG PHE GLU THR LEU THR PRO ARG PHE SER ALA THR VAL PRO PRO CYS TRP VAL GLU VAL LEU GLN GLU GLU GLN GLN GLN GLN ARG HIS HIS HIS GLN GLN HIS HIS GLY ALA ALA GLN HIS THR THR TRP LYS
GLY GLU LEU HIS PHE LEU GLN ILE GLY GLY THR CYS ASP ASP ILE ASP GLU ALA ASP ILE LEU VAL ASP GLY SER LEU SER LYS GLY ILE GLU PRO SER SER GLY GLY SER LYS PRO LEU SER ASN PRO SER SER PRO GLY ILE SER GLY VAL ASP ARG LEU LEU VAL ASP GLN PRO PHE THR
THR LEU GLY HIS LEU VAL ILE THR THR GLN GLY GLY TYR VAL LYS ILE LEU ASP LEU SER ASN PHE GLU ILE GLU ILE LEU LEU PRO PRO LYS LYS GLN GLU GLU GLN GLN ASP THR PHE VAL SER VAL ILE TYR CYS SER GLY THR ASP ARG LEU CYS ALA CYS THR LYS GLY
LEU GLU GLU PRO PRO ILE LYS ILE GLN HIS ILE LYS ASP PRO GLN ASP THR ILE THR SER SER LEU ILE LEU LEU PRO PRO ASP ILE LEU ASP ASN ARG GLU ASP ASP CYS GLU GLU PRO ILE GLU ASP MET GLN LEU THR SER LYS ASN GLY PHE GLU ARG GLU LYS THR SER ASP ILE SER


HIS ARG ARG THR E2160 I2165 P2166 M2167 M2173 L2178 T2184 VAL GLU ASP GLU ALA ALA ALA ALA ALA LYS LYS PRO LEU ASN GLY ASN GLN TRP SER PHE ILE ASN ASN ASN LEU HIS THR GLN SER LEU ASN ARG SER SER LYS GLY SER SER SER LEU ASP ARG LEU TYR SER ARG
LYS ILE ARG LYS GLN LEU VAL HIS HIS LYS GLN GLN LEU ASN LEU LEU LYS ALA LYS GLN LYS ALA ALA VAL GLU GLN MET GLU LYS GLU LYS ILE GLN SER ASN LYS GLY SER SER TYR LYS LEU LEU VAL GLU GLN ALA LYS LEU LYS GLN ALA THR SER LYS HIS PHE LYS ASP LEU
ILE ARG LEU ARG ARG THR ALA GLU TRP SER ARG SER ASN LEU ASP THR GLU VAL THR THR ALA LYS GLU SER PRO GLU ILE GLU PRO LEU PRO F2321 H2325 I2329 S2330 V2331 V2332 L2337 T2345 L2352 L2358 R2366 P2367 L2380 E2381 R2382 D2391 W2399 W2403
A2404 Q2405 M2411 L2416 L2420 LEU ALA PRO VAL ALA ALA GLU ALA MET GLU GLU GLY THR VAL GLY ASP ASP VAL GLY ALA THR ALA GLY ASP SER ASP ASP SER LEU GLN GLN GLN SER SER VAL GLN LEU LEU GLU THR ILE ASP GLU PRO LEU THR HIS ASP ILE THR GLY ALA PRO
PRO LEU SER SER LEU GLU LYS ASP LYS GLU ILE ASP LEU GLU LEU LEU GLN ASP LEU MET GLU VAL ASP ILE ASP PRO LEU ASP ILE ASP LEU GLU LYS ASP PRO LEU ALA ALA LYS VAL PHE LYS PRO ILE SER SER THR TRP TYR ASP TYR TRP GLY ALA ASP TYR GLY THR TYR ASN
TYR ASN PRO TYR ILE GLY GLY LEU GLY ILE PRO VAL ALA LYS PRO PRO ALA ASN THR GLU GLU LYS ASN GLY SER GLN THR VAL SER VAL SER V2563 S2564 L2567 D2568 A2569 R2570 L2571 E2572 V2573 G2574 L2575 E2576 Q2577 Q2578 A2579 M2582 L2583 K2584 M2585 M2586 S2587 T2588 L2589 E2590 A2591 D2592 N2600
THR SER PRO THR LEU SER GLN SER PRO THR GLY THR ASP ASP SER LEU LEU GLY GLY LEU GLN ALA ALA ASN GLN THR SER GLN L2629 V2636 P2637 M2638 E2658 L2667 S2668 L2669 N2670 S2671 SER SER THR GLY ASN LYS GLU ASN GLY ALA ASP ILE F2684 T2714 W2719 N2731
M2732 Q2733 L2734 N2735 S2736 GLY SER SER SER ALA ILE GLY T2744 T2769 H2772 N2775 R2795 F2826 D2834 L2840 V2850 V2851 S2852 V2853 S2857 E2861 L2896 PHE ALA ASN LEU ILE ARG PRO GLY ASP ALA LYS ALA VAL CYS GLY GLU M2913 T2914 R2915 L2918
R2943 VAL SER VAL THR THR ASN THR THR ASP SER VAL SER ASP GLU GLU LYS VAL SER GLY GLY LYS ASP GLY ASN GLY SER SER THR SER VAL GLN GLY S2976 P2977 I2990 I3009 ILE GLY ALA SER GLY LEU HIS LEU THR LYS HIS GLU ASN PHE HIS GLY GLY LEU D3028 L3040
S3124 M3125 V3126 I3129 P3137 ASN LYS ALA VAL ASP SER THR LEU LYS THR ARG ILE LEU LEU ALA SER GLU PRO ASP ASN ALA E3158 R3191 S3198 S3244 M3250 C3279 L3291 S3309 ALA THR VAL ASN ASN PRO PHE LEU PRO SER GLU D3321 L3331 A3353 P3354
A3364 M3373 S3389 T3390 I3399 S3409 L3414 L3418 G3421 R3422 D3429 I3432 L3438 R3449 K3467 ARG SER GLY ARG MET ASN TYR MET CYS PRO ASN SER SER THR V3482 M3488 E3510 Y3511 D3512 L3517 L3532 L3538 K3539 D3543 V3552
L3560 M3564 T3567 PRO PRO PRO VAL GLN CYS HIS HIS ARG LEU SER MET THR ASP ASP SER LYS LYS GLN ASP LEU SER SER SER LEU THR ASP ASP SER LYS ASN ALA GLN ALA PRO LEU ALA LEU T3606 E3607 S3608 H3609 A3614 P3632 S3633 L3634 L3635 V3636 R3637 S3638 F3642
C3643 F3644 S3645 HIS ILE SER SER SER GLU SER ILE ALA GLN SER ILE ASP ILE SER GLN ASP ASP LYS LEU ARG ARG HIS HIS VAL PRO GLN GLN CYS ASN K3675 M3676 P3677 I3678 T3679 A3680 D3681 L3682 P3685 I3686 L3687 R3688 F3689 G3694 W3702 N3709 L3715 L3716 L3719 C3720 H3721 SER
GLY SER THR SER GLY SER HIS ASN LEU GLY ALA GLN GLN THR SER ALA ARG SER ALA SER LEU SER SER ALA ALA THR THR G3750 Q3755 I3759 E3760 N3761 A3762 F3767 L3768 G3769 C3770 I3771 P3775 Q3778 K3779 L3780 M3781 L3785 C3786 E3787 L3788 F3789 Q3790 T3791 SER PRO GLN ARG


GLY ASN LEU PRO THR SER GLY N3803 I3804 S3805 G3806 F3807 I3808 R3809 R3810 L3811 F3812 L3813 Q3814 L3815 M3816 L3817 E3818 D3819 E3820 M3824 F3825 L3826 Q3827 S3828 P3831 L3832 Y3833 K3834 R3856 T3857 L3858 H3859 L3860 L3866 S3867 D3868 V3869 L3870 D3871 D3875 T3876 P3877 SER ILE THR ALA LYS LEU ILE
SER GLU GLN LYS ASP ASP LYS GLU LYS LYS ASN HIS GLU GLU LYS GLU LYS VAL LYS ALA GLU ASN GLY PHE GLN ASP ASN TYR SER VAL VAL ALA SER GLY LEU LYS SER GLN SER LYS ARG ALA VAL SER ALA THR PRO PRO ARG PRO PRO SER ARG ARG GLY ARG THR ILE PRO
ASP LYS ILE GLY SER THR SER GLY ALA GLU ALA ALA ASN LYS ILE ILE THR V3962 P3963 L3967 K3970 L3971 A3979 L3986 D3992 R3993 K3994 L4004 T4005 V4006 G4009 SER ARG VAL ILE THR ASP PRO SER LEU SER LYS THR ASP SER TYR LYS ARG LEU HIS PRO GLU LYS
ASP HIS GLY ASP LEU LEU ALA SER CYS PRO GLU ASP GLU ALA LEU THR PRO GLY ASP GLU CYS MET ASP GLY ILE LEU ASP GLU S4060 L4061 L4062 L4071 A4075 G4076 M4077 G4078 G4079 L4080 A4081 L4082 I4083 A4084 E4085 R4086 L4087 PRO MET LEU TYR PRO GLU VAL ILE GLN GLN VAL SER ALA
PRO VAL VAL THR SER THR THR GLN GLU LYS PRO LYS ASP SER ASP GLN PHE GLU TRP VAL THR ILE GLU GLN SER GLY GLU LEU VAL TYR GLU ALA PRO GLU THR VAL ALA ALA GLU PRO PRO PRO ILE LYS SER ALA VAL GLN THR MET SER PRO I4153 L4163 F4164 L4165 R4166 L4167 P4168
A4171 E4172 V4173 L4174 L4175 K4176 E4177 R4178 K4179 Q4182 L4185 R4186 T4192 D4193 D4194 G4195 E4196 G4197 S4198 H4199 I4200 L4201 Q4202 S4203 P4204 S4205 A4206 N4207 V4216 L4217 R4218 S4219 S4222 T4223 T4224 P4225 L4226 T4227 T4228 D4229 D4230 G4231 V4232 L4233 L4234 R4235 R4236 M4237 A4238 L4239 E4240 I4241 G4242 A4243
L4244 H4245 L4246 S4252 A4253 L4254 S4255 H4256 H4257 S4258 P4259 R4260 VAL PRO ASN SER SER SER VAL ASN GLN THR GLU PRO GLN VAL SER SER SER HIS ASN PRO THR SER THR GLU GLU GLN GLN LEU TYR TRP ALA LYS GLY THR GLY PHE GLY THR GLY SER THR ALA SER GLY TRP D4305 V4306 E4307
Q4308 A4309 L4310 T4311 K4312 Q4313 R4314 L4315 E4316 Y4330 I4331 N4332 P4333 V4334 SER SER ALA VAL ASN GLY GLU ALA GLN SER SER HIS GLU THR ARG GLY GLN ASN SER N4354 A4355 L4356 P4357 S4358 V4359 L4360 L4361 E4362 L4363 L4364 S4365 Q4366 S4367 C4368 L4369 M4373 S4374 S4375 Y4376 L4377 R4378 N4379 D4380 S4381
V4382 L4383 D4384 M4385 A4386 R4387 H4388 V4389 R4393 E4397 L4398 L4399 R4400 A4401 I4402 A4403 S4404 C4405 A4406 A4407 M4408 V4409 P4410 L4411 L4412 L4413 P4414 LEU SER THR GLU ASN GLY GLU GLU GLU GLU GLN SER GLU CYS GLN T4431 S4432 V4433 G4434 T4435 L4436 L4437 A4438 K4439 M4440 K4441 T4442 C4443 V4444 D4445
T4446 Y4447 T4448 N4449 R4450 L4451 ARG SER LYS ARG GLU ASN VAL LYS THR GLY VAL LYS PRO ASP ALA SER ASP GLU GLU LEU THR LEU LEU VAL PRO ASP ILE Q4482 K4483 T4484 A4485 E4486 T4487 V4488 Y4489 A4490 A4491 T4492 T4493 S4494 L4495 R4496 Q4497 A4498 N4499 Q4500 E4501 K4502 LYS LEU GLY
GLU TYR SER LYS LYS ALA ALA MET LYS PRO LYS PRO LEU SER VAL LEU LYS SER LEU LEU GLU GLU LYS TYR VAL ALA VAL MET LYS LYS GLU LEU GLN PHE ASP THR PHE GLU MET VAL SER GLU ASP GLU ASP GLY LYS LEU GLY PHE LYS VAL ASN TYR HIS TYR MET SER GLN VAL LYS ASN
ALA ASN ASP ALA ASN SER ALA ARG ALA ARG ARG LEU ALA GLN GLU ALA VAL THR LEU SER THR SER LEU PRO LEU SER SER SER SER SER VAL PHE VAL ARG CYS ASP GLU GLU ARG LEU ASP ILE MET LYS VAL LEU ILE THR GLY PRO ALA ASP THR PRO TYR ALA ASN GLY CYS
PHE GLU PHE ASP VAL TYR PHE PRO GLN ASP TYR PRO SER SER LEU VAL ASN LEU GLU THR THR GLY GLY HIS SER VAL ARG PHE ASN PRO ASN LEU TYR ASN ASP GLY LYS VAL CYS LEU SER ILE LEU ASN THR TRP HIS GLY ARG PRO GLU GLU LYS TRP ASN PRO GLN THR
SER SER PHE LEU GLN VAL LEU VAL SER VAL GLN SER LEU SER ILE LEU VAL ALA GLU PRO TYR PHE ASN GLU PRO GLY TYR GLU ARG SER ARG GLY THR PRO SER GLY THR GLN GLN TYR SER SER ASP LYS ARG VAL GLY ARG THR MET SER HIS HIS ALA ALA ALA LEU LYS ARG HIS THR ALA GLN GLN LEU ARG
ASN PRO SER PRO CYS PHE LYS GLU VAL ILE HIS LYS HIS PHE TYR LEU LYS ARG VAL GLU ILE MET ALA GLN CYS GLU GLU TRP ILE ALA ASP ILE GLN GLN TYR SER SER ASP LYS ARG VAL GLY ARG THR MET SER HIS HIS ALA ALA ALA LEU LYS ARG HIS THR ALA GLN GLN LEU ARG

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

- Molecule 1: Baculoviral IAP repeat-containing protein 6

Chain B: 34% 6% 60%

GLY PRO MET VAL THR GLY GLY GLY ALA ALA PRO PRO GLY THR VAL THR GLU PRO LEU PRO SER VAL ILE VAL LEU SER ALA GLY ARG LYS MET ALA ALA ALA ALA ALA ALA ALA SER GLY PRO GLY CYS SER SER ALA ALA GLY ALA GLY ALA ALA GLY VAL GLU GLU LYS TRP LEU VAL LEU

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

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

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

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

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

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

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

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

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

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

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

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

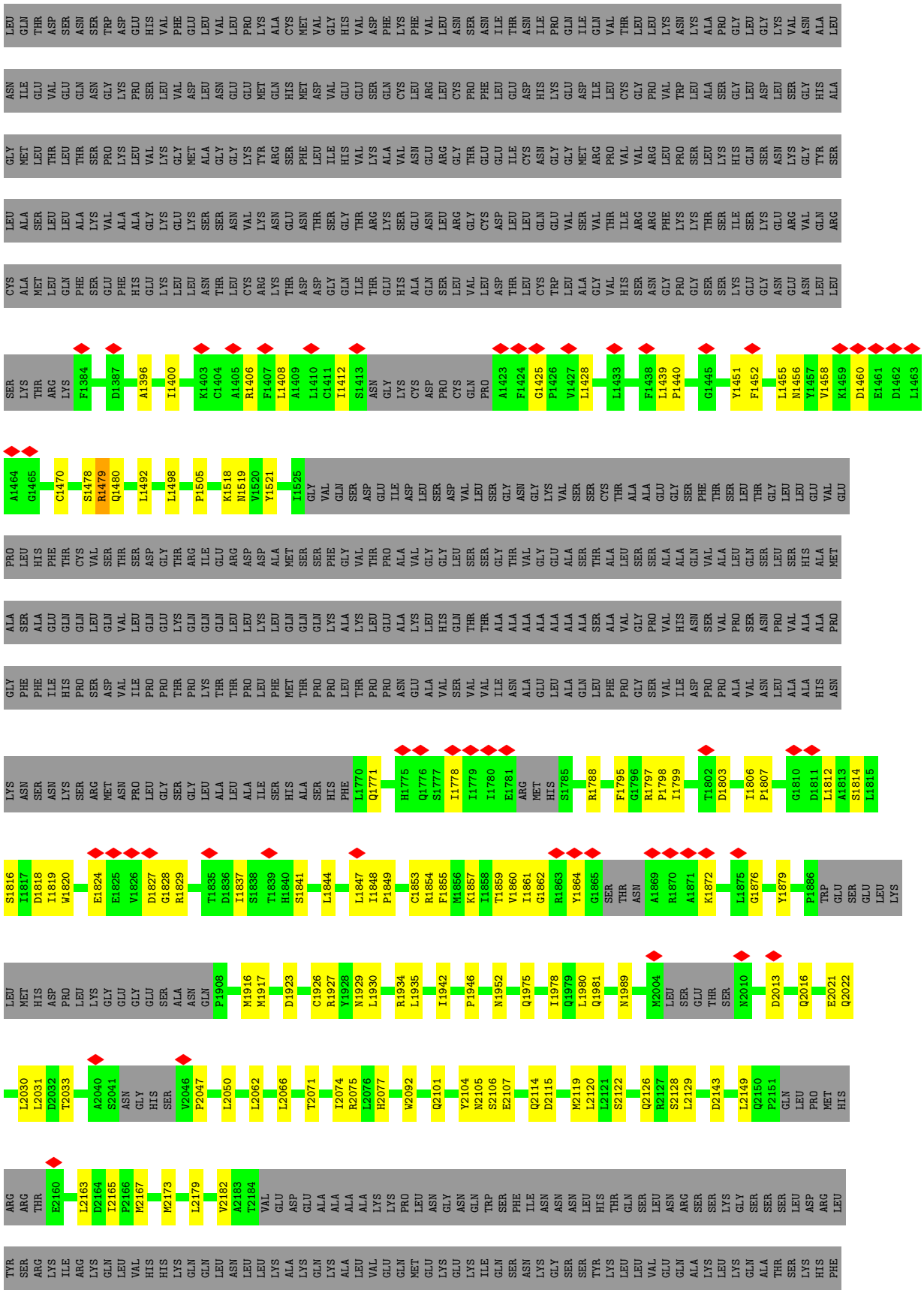
ARG ARG LYS GLY GLU LEU GLU GLU SER ASN LEU ALA VAL VAL ASN GLY ALA ASN SER VAL ILE GLN HIS GLU SER PRO ALA ASP VAL GLN THR PRO LEU ILE ILE GLN PRO GLU GLN ARG ASN VAL SER GLY GLY TYR LEU VAL LEU TYR LYS MET ASN TYR ALA THR ARG ILE ILE THR

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

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

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

LEU GLU ILE LEU THR SER LEU VAL THR ARG PHE GLU THR LEU THR PRO ARG PHE SER ALA THR VAL PRO PRO CYS TRP VAL GLU VAL GLN GLN GLU GLN GLN GLN ARG ARG HIS PRO GLN HIS LEU HIS GLN GLN HIS HIS GLY ASP ALA ALA GLN HIS THR ARG THR TRP LYS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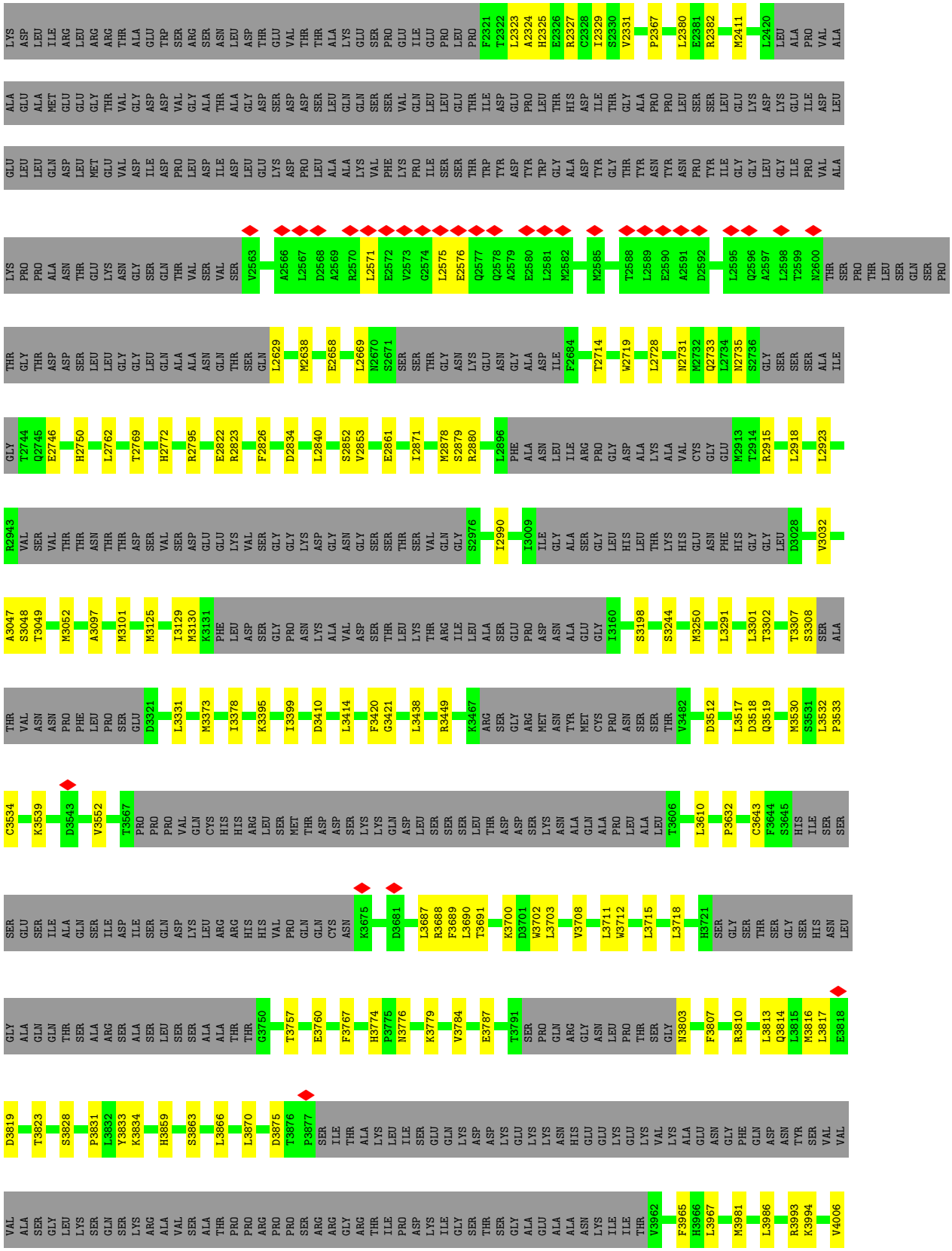
ASN ILE GLU VAL GLU GLN GLN ASN GLY LYS PRO SER LEU VAL ASP LEU ASN LEU GLU GLU MET GLN HIS MET ASP VAL GLU GLU SER GLN CYS LEU ARG LEU CYS PRO PHE LEU GLU ASP HIS LYS GLU ASP ILE LEU CYS GLY PRO VAL TRP LEU LEU ALA SER GLY LEU ASP LEU SER ALA HIS ALA
GLY MET LEU THR LEU THR SER PRO LYS LEU VAL LYS GLY MET ALA GLY GLY LYS TYR ARG SER PHE LEU ILE HIS VAL LYS ALA ALA VAL ASN GLU ARG GLY THR GLU GLU ILE CYS ASN GLY GLY MET ARG PRO VAL VAL ARG LEU PRO SER LEU LYS HIS GLN SER ASN LYS GLY TYR SER
LEU ALA SER LEU LEU ALA LYS VAL ALA ALA ALA GLY LYS GLU LYS SER SER VAL LYS ASN GLU ASN THR SER GLY THR ARG LYS SER GLU ASN LEU ARG GLY CYS ASP LEU LEU GLN GLU VAL SER VAL THR ILE ARG ARG PHE LYS LYS THR SER ILE SER LYS GLU ARG VAL GLN ARG
CYS ALA MET LEU GLN PHE SER GLU PHE HIS GLU LYS LEU LEU ASN THR LEU CYS ARG LYS THR ASP ASP GLY GLN ILE THR GLU HIS ALA GLN SER LEU VAL LEU ASP THR LEU CYS TRP LEU ALA GLY VAL HIS SER ASN GLY PRO GLY SER SER LYS GLU GLY ASN GLU ASN LEU LEU
SER LYS THR ARG LYS F1384 D1387 A1396 I1400 K1403 C1404 A1405 R1406 F1407 L1408 A1409 L1410 C1411 I1412 S1413 ASN GLY LYS CYS ASP PRO CYS GLN PRO A1423 F1424 G1425 P1426 V1427 L1428 L1433 F1438 L1439 P1440 G1445 Y1451 F1452 L1455 N1456 Y1457 V1458 K1459 D1460 E1461 D1462 L1463
A1464 G1465 C1470 S1478 R1479 Q1480 L1492 L1498 P1505 K1518 N1519 V1520 Y1521 I1525 GLY VAL GLN SER ASP GLU ILE ASP LEU SER ASP VAL LEU SER GLY ASN GLY LYS VAL SER SER CYS THR ALA ALA GLU GLY SER PHE THR SER LEU THR GLY LEU LEU GLU VAL GLU
PRO LEU HIS PHE THR CYS VAL SER THR SER ASP GLY THR ARG ILE GLU ARG ASP ASP ALA MET SER SER PHE GLY VAL THR PRO ALA VAL GLY GLY LEU SER SER GLY THR VAL GLY GLU ALA SER THR ALA LEU SER SER ALA ALA GLN VAL ALA LEU GLN SER LEU SER PHE THR HIS ALA MET
ALA SER ALA GLU GLN GLN GLN VAL LEU LEU GLN GLN GLU LYS GLN GLN GLN LEU LEU LYS LEU GLN GLN GLN LYS ALA LYS LYS LEU GLU ALA LYS LEU HIS GLN THR THR ALA ALA ALA ALA ALA ALA SER ALA VAL GLY PRO VAL HIS ASN SER VAL PRO PRO SER ASN PRO VAL ALA ALA ALA PRO
GLY PHE PHE ILE HIS PRO SER ASP VAL ILE PRO PRO THR PRO LYS THR THR PRO LEU PHE MET THR PRO PRO LEU THR PRO PRO ASN GLU ALA VAL SER VAL VAL ILE ASN ALA GLU LEU ALA GLN LEU PHE PRO GLY SER VAL ILE ASP PRO PRO ALA VAL ASN LEU ALA ALA HIS ASN
LYS ASN SER ASN LYS SER ARG MET ASN PRO LEU GLY SER GLY LEU ALA LEU ALA ILE SER HIS ALA SER HIS PHE L1770 Q1771 H1775 Q1776 S1777 I1778 I1779 I1780 E1781 ARG MET HIS S1785 R1788 F1795 G1796 R1797 P1798 I1799 T1802 D1803 I1806 P1807 G1810 D1811 L1812 A1813 S1814 L1815
S1816 I1817 D1818 I1819 W1820 E1824 E1825 V1826 D1827 G1828 R1829 T1835 D1836 I1837 S1838 T1839 H1840 S1841 L1844 L1847 I1848 P1849 C1853 R1854 F1855 M1856 K1857 I1858 T1859 V1860 I1861 G1862 R1863 Y1864 G1865 SER THR ASN A1869 R1870 A1871 K1872 L1875 G1876 Y1879 P1886 TRP GLU SER GLU LEU LYS
LEU MET HIS ASP PRO LEU LYS GLY GLU GLU SER ALA ASN GLN P1908 M1916 M1917 D1923 C1926 R1927 Y1928 N1929 L1930 R1934 L1935 I1942 P1946 N1952 Q1975 I1978 Q1979 L1980 Q1981 N1989 M2004 LEU SER GLU THR SER N2010 D2013 Q2016 E2021 Q2022
L2030 L2031 D2032 T2033 A2040 S2041 ASN GLY HIS SER V2046 P2047 L2050 L2062 L2066 T2071 I2074 R2075 L2076 H2077 W2092 Q2101 Y2104 N2105 S2106 E2107 Q2114 D2115 M2119 L2120 L2121 S2122 Q2126 R2127 S2128 L2129 D2143 L2149 Q2150 P2151 GLN LEU PRO MET HIS
ARG ARG THR E2160 L2163 D2164 I2165 P2166 M2167 M2173 L2179 V2182 A2183 T2184 VAL GLU ASP GLU ALA ALA ALA ALA LYS LYS PRO LEU ASN LYS GLY ASN GLN ILE TRP SER PHE ILE ASN ASN ASN LEU HIS THR GLN SER LEU ASN ARG SER SER LYS GLY SER SER SER LEU ASP ARG LEU
TYR SER ARG LYS ILE ARG LYS GLN LEU VAL HIS HIS LYS GLN GLN LEU ASN LEU LEU LYS ALA LYS GLN LYS ALA ALA LEU VAL GLU GLU MET GLU LYS GLU LYS ILE GLN SER ASN LYS GLY SER SER TYR LYS LEU LEU VAL GLU GLN ALA LYS LEU LYS GLN ALA THR SER LYS HIS PHE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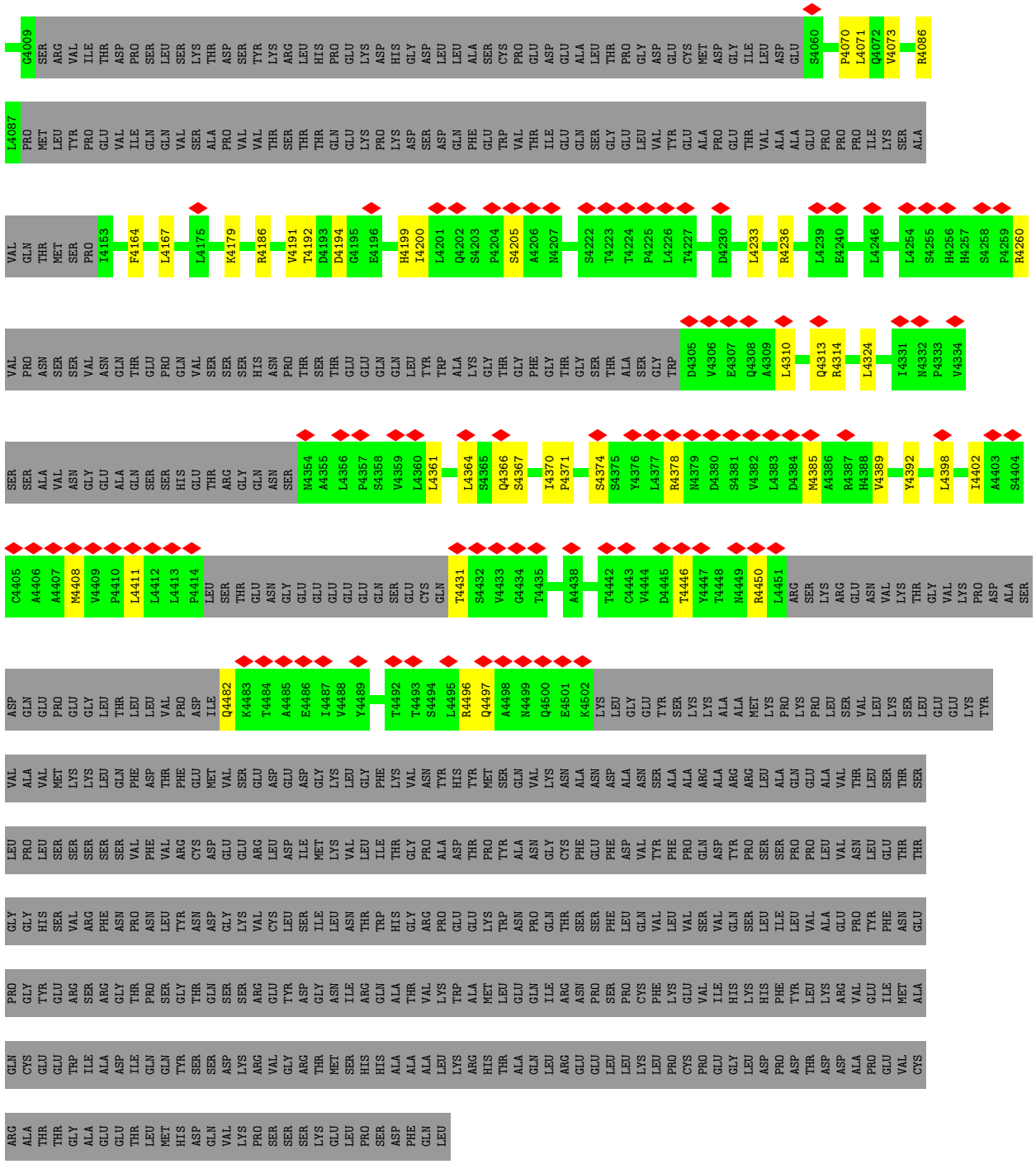
ALA GLU ALA MET GLU GLU GLY GLY VAL GLY ASP ASP VAL GLY ALA THR ALA GLY ASP SER ASP ASP SER LEU GLN GLN SER SER VAL GLN LEU LEU GLU THR ILE ASP GLU PRO LEU THR HIS ASP ILE THR GLY ALA PRO PRO LEU SER SER LEU GLU LYS ASP LYS GLU ILE ASP LEU
GLU LEU LEU GLN ASP LEU MET GLU VAL ASP ILE ASP PRO LEU ASP ILE ASP LEU GLU LYS ASP PRO LEU ALA ALA LYS VAL PHE LYS PRO ILE SER SER THR TRP TYR ASP TYR TRP GLY ALA ASP TYR GLY THR TYR ASN TYR ASN PRO TYR ILE GLY GLY GLY LEU GLY ILE PRO VAL ALA
LYS PRO PRO ALA ASN THR GLU LYS ASN GLY SER GLN THR VAL SER VAL SER V2563 A2566 L2567 D2568 A2569 R2570 L2571 E2572 V2573 G2574 L2575 E2576 Q2577 Q2578 A2579 E2580 L2581 M2582 M2585 T2588 L2589 E2590 A2591 D2592 L2595 Q2596 A2597 L2598 T2599 N2600 THR SER PRO THR LEU SER GLN SER PRO
THR GLY THR ASP ASP SER LEU LEU GLY LEU GLN ALA ALA ASN GLN THR SER GLN L2629 M2638 E2658 L2669 N2670 S2671 SER SER THR GLY ASN LYS GLU ASN GLY ALA ASP ILE F2684 T2714 W2719 L2728 N2731 M2732 Q2733 L2734 N2735 S2736 GLY SER SER SER ALA ILE
GLY T2744 Q2745 E2746 H2750 L2762 T2769 H2772 R2795 E2822 R2823 F2826 D2834 L2840 S2852 V2853 E2861 I2871 M2878 S2879 R2880 L2896 PHE ALA ASN LEU ILE ARG PRO GLY ASP ALA LYS ALA VAL CYS GLY GLU M2913 T2914 R2915 L2918 L2923
R2943 VAL SER VAL THR THR ASN THR THR ASP SER VAL SER ASP GLU GLU LYS VAL SER GLY GLY LYS ASP GLY ASN GLY SER SER THR SER VAL GLN GLY S2976 I2990 I3009 ILE GLY ALA SER GLY LEU HIS LEU THR LYS HIS GLU ASN PHE HIS GLY GLY LEU D3028 V3032
A3047 S3048 T3049 M3052 A3097 M3101 M3125 I3129 M3130 K3131 PHE LEU ASP SER GLY PRO ASN LYS ALA VAL ASP SER THR LEU LYS THR ARG ILE LEU ALA SER GLU PRO ASP ASN ALA GLU GLY I3160 S3198 S3244 M3250 L3291 L3301 T3302 T3307 S3308 SER ALA
THR VAL ASN ASN PRO PHE LEU PRO SER GLU D3321 L3331 M3373 I3378 K3395 I3399 D3410 L3414 F3420 G3421 L3438 R3449 K3467 ARG SER GLY ARG MET ASN TYR MET CYS PRO ASN SER SER THR V3462 D3512 L3517 D3518 Q3519 M3530 S3531 L3532 P3533
C3534 K3539 D3543 V3552 T3567 PRO PRO PRO VAL GLN CYS HIS HIS ARG LEU SER MET THR ASP ASP SER LYS LYS GLN ASP LEU SER SER SER LEU THR ASP ASP SER LYS ASN ALA GLN ALA PRO LEU ALA LEU T3606 L3610 P3632 C3643 F3644 S3645 HIS ILE SER SER
SER GLU SER ILE ALA GLN SER ILE ASP ILE SER GLN ASP LYS LEU ARG ARG HIS HIS VAL PRO GLN GLN CYS ASN K3675 D3681 L3687 R3688 F3689 L3690 T3691 K3700 D3701 W3702 L3703 V3708 L3711 W3712 L3715 L3718 H3721 SER GLY SER THR SER GLY HIS ASN LEU
GLY ALA GLN GLN THR SER ALA SER ARG ALA SER LEU SER SER ALA ALA THR THR G3750 T3757 E3760 F3767 H3774 P3775 N3776 K3779 V3784 E3787 T3791 SER PRO GLN ARG GLY ASN LEU PRO THR SER GLY N3803 F3807 R3810 L3813 Q3814 L3815 M3816 L3817 E3818
D3819 T3823 S3828 P3831 L3832 Y3833 K3834 H3859 S3863 L3866 L3870 D3875 T3876 P3877 SER ILE THR ALA LYS LEU ILE SER GLU GLN LYS ASP ASP LYS GLU LYS LYS ASN HIS GLU GLU GLU LYS LYS GLU LYS VAL LYS ALA GLU ASN GLY PHE GLN ASP ASN TYR SER VAL VAL
VAL ALA SER GLY LEU LYS SER GLN SER LYS ARG ALA VAL SER ALA THR PRO PRO ARG PRO PRO SER ARG ARG GLY ARG THR ILE PRO ASP LYS ILE GLY SER THR SER GLY ALA GLU ALA ALA ASN LYS ILE ILE THR V3962 F3965 H3966 L3967 M3981 L3986 R3993 K3994 V4006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L4087 PRO MET LEU TYR PRO GLU VAL ILE GLN GLN VAL SER ALA PRO VAL VAL THR SER THR THR GLN GLU LYS PRO LYS ASP SER ASP GLN PHE GLU TRP VAL THR ILE GLU GLN SER GLY GLU LEU VAL TYR GLU ALA PRO GLU THR VAL ALA ALA GLU PRO PRO PRO ILE LYS SER ALA
VAL GLN THR MET SER PRO I4153 F4164 L4167 L4175 K4179 R4186 V4191 T4192 D4193 D4194 G4195 E4196 H4199 I4200 L4201 Q4202 S4203 P4204 S4205 A4206 M4207 S4222 T4223 T4224 P4225 L4226 T4227 D4230 L4233 R4236 L4239 E4240 L4246 L4254 S4255 H4256 H4257 S4258 P4259 R4260
VAL PRO ASN SER SER VAL ASN GLN THR GLU PRO GLN VAL SER SER SER HIS ASN PRO THR SER THR GLU GLU GLN GLN GLN LEU TYR TRP ALA LYS GLY THR GLY PHE GLY THR GLY SER THR ALA SER GLY TRP D4305 V4306 E4307 Q4308 A4309 L4310 Q4313 R4314 L4324 I4331 N4332 P4333 V4334
SER SER ALA VAL ASN GLY GLU ALA GLN SER SER HIS GLU THR ARG GLY GLN ASN SER N4354 A4355 L4356 P4357 S4358 V4359 L4360 L4361 L4364 S4365 Q4366 S4367 I4370 P4371 S4374 S4375 Y4376 L4377 R4378 N4379 D4380 S4381 V4382 L4383 D4384 M4385 A4386 R4387 H4388 V4389 Y4392 L4398 I4402 A4403 S4404
C4405 A4406 A4407 M4408 V4409 P4410 L4411 L4412 L4413 P4414 LEU SER THR GLU ASN GLY GLU GLU GLU GLU GLU GLN SER GLU CYS GLN T4431 S4432 V4433 G4434 T4435 A4438 T4442 C4443 V4444 D4445 T4446 Y4447 T4448 N4449 R4450 L4451 ARG SER LYS ARG GLU ASN VAL LYS THR GLY VAL LYS PRO ASP ALA SER
ASP GLN GLU PRO GLU GLY LEU THR LEU LEU VAL PRO ASP ILE Q4482 K4483 T4484 A4485 E4486 I4487 V4488 Y4489 T4492 T4493 S4494 L4495 R4496 Q4497 A4498 N4499 Q4500 E4501 K4502 LYS LEU GLY GLU GLU TYR SER LYS LYS ALA ALA MET LYS PRO LYS PRO LEU SER VAL LEU LYS SER LEU GLU GLU LYS TYR
VAL ALA VAL MET LYS LYS LEU GLN PHE ASP THR PHE GLU MET VAL SER GLU ASP GLU ASP GLY LYS LEU GLY PHE LYS VAL ASN TYR HIS TYR MET SER GLN VAL LYS ASN ALA ASN ASP ALA ASN SER ALA ALA ARG ALA ARG ARG LEU ALA GLN GLU ALA VAL THR LEU SER THR SER
LEU PRO LEU SER SER SER SER SER VAL PHE VAL ARG CYS ASP GLU GLU ARG LEU ASP ILE MET LYS VAL LEU ILE THR GLY PRO ALA ASP THR PRO TYR ALA ASN GLY CYS PHE GLU PHE ASP VAL TYR PHE PRO GLN ASP TYR PRO SER SER PRO PRO LEU VAL ASN LEU GLU THR THR
GLY GLY HIS SER VAL ARG PHE ASN PRO ASN LEU TYR ASN ASP GLY LYS VAL CYS LEU SER ILE LEU ASN THR TRP HIS GLY ARG PRO GLU GLU LYS TRP ASN PRO GLN THR SER SER PHE LEU GLN VAL LEU VAL SER VAL GLN SER LEU ILE LEU VAL ALA GLU PRO TYR LEU LYS ASN LEU GLU THR ASN GLU
PRO GLY TYR GLU ARG SER ARG GLY THR PRO SER GLY THR GLN SER SER ARG GLU TYR ASP GLY ASN ILE ARG GLN ALA THR VAL LYS TRP ALA MET LEU GLU GLN ILE ARG ASN PRO SER PRO CYS PHE LYS GLU VAL ILE HIS LYS HIS PHE TYR LEU LYS ARG VAL GLU ILE MET ALA
GLN CYS GLU GLU TRP ILE ALA ASP ILE GLN GLN TYR SER SER ASP LYS ARG VAL GLY ARG THR MET SER HIS HIS ALA ALA ALA LEU LYS ARG HIS THR ALA GLN LEU ARG GLU GLU GLU LEU LEU LEU LYS LEU PRO CYS PRO GLU GLY LEU ASP PRO ASP THR ASP ASP ALA PRO GLU VAL CYS
ARG ALA THR THR GLY ALA GLU GLU THR LEU MET HIS ASP GLN VAL LYS PRO SER SER SER LYS GLU LEU PRO SER ASP PHE GLN LEU

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	127710	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	49.9	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	18.896	Depositor
Minimum map value	-7.641	Depositor
Average map value	-0.020	Depositor
Map value standard deviation	0.841	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	258.0, 258.0, 258.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	0.15	0/16012	0.30	0/21743
1	B	0.16	0/15429	0.31	0/20963
All	All	0.16	0/31441	0.30	0/42706

There are no bond length outliers.

There are no bond angle outliers.

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	15729	0	16117	228	0
1	B	15156	0	15536	195	0
All	All	30885	0	31653	405	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 6.

The worst 5 of 405 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)
1:B:1820:TRP:O	1:B:1855:PHE:HB2	1.66	0.96
1:A:2031:LEU:HD22	1:A:2077:HIS:HB3	1.56	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1927:ARG:HB3	1:B:1980:LEU:HD11	1.62	0.81
1:A:4437:LEU:HA	1:A:4440:MET:HE3	1.62	0.80
1:A:2101:GLN:HA	1:A:2167:MET:HE1	1.67	0.76

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	1971/4859 (41%)	1901 (96%)	70 (4%)	0	100	100
1	B	1901/4859 (39%)	1835 (96%)	66 (4%)	0	100	100
All	All	3872/9718 (40%)	3736 (96%)	136 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1783/4217 (42%)	1783 (100%)	0	100	100
1	B	1717/4217 (41%)	1715 (100%)	2 (0%)	88	90
All	All	3500/8434 (42%)	3498 (100%)	2 (0%)	87	90

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1478	SER
1	B	1479	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	3069	GLN
1	B	4482	GLN
1	B	3184	GLN
1	B	3776	ASN
1	A	3695	ASN

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.

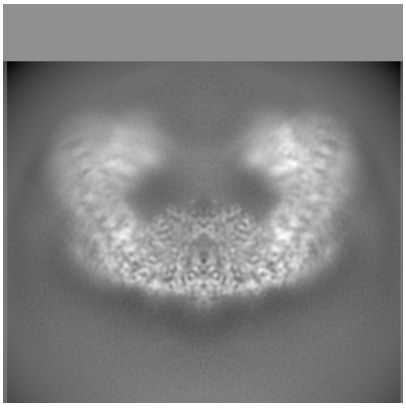
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-15653. These allow visual inspection of the internal detail of the map and identification of artifacts.

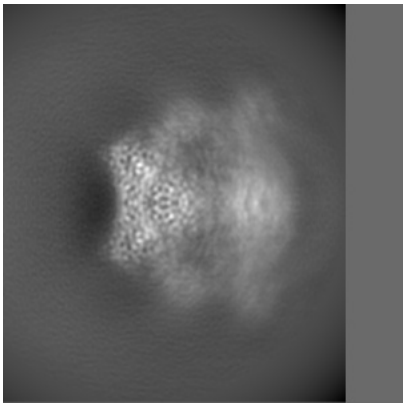
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

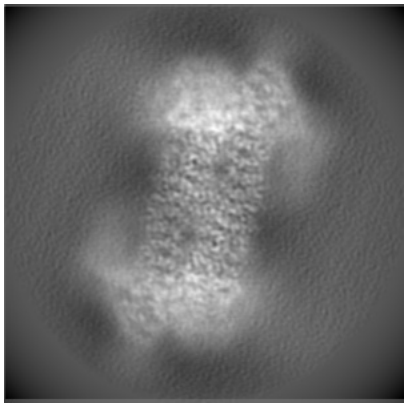
6.1.1 Primary map



X



Y

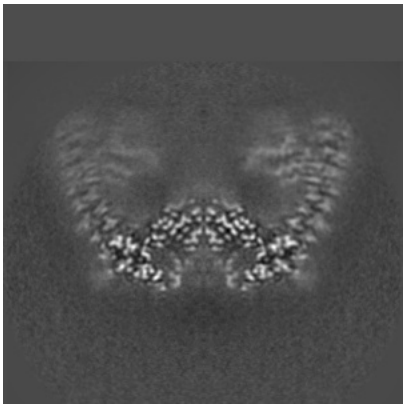


Z

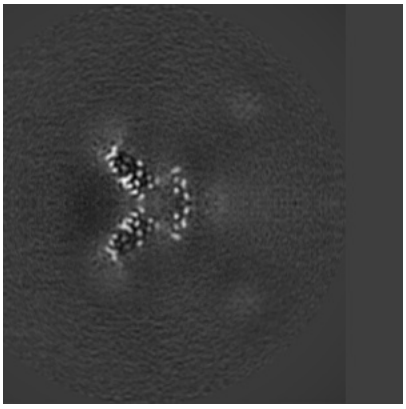
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

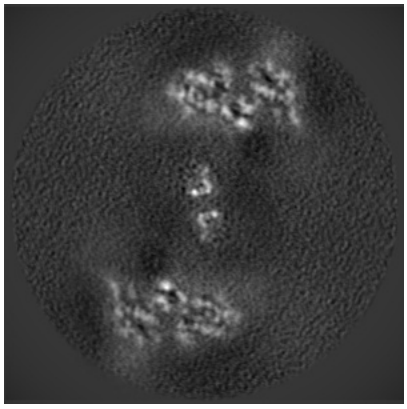
6.2.1 Primary map



X Index: 150



Y Index: 150

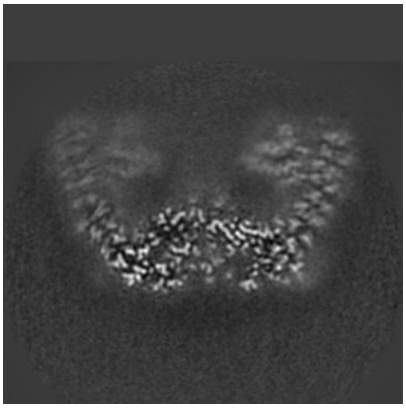


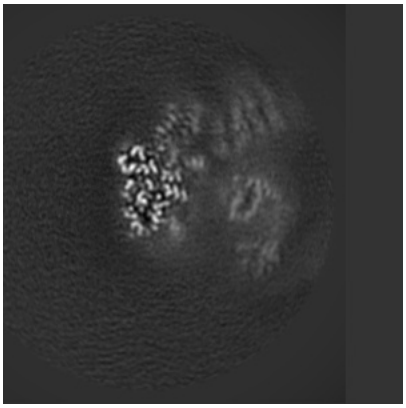
Z Index: 150

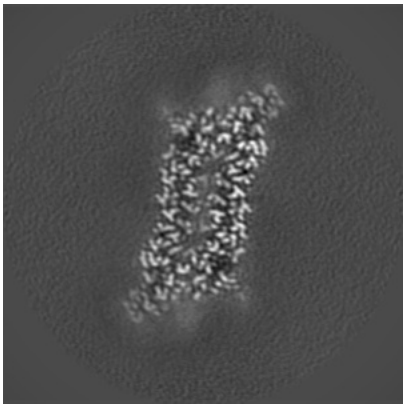
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map


X Index: 154

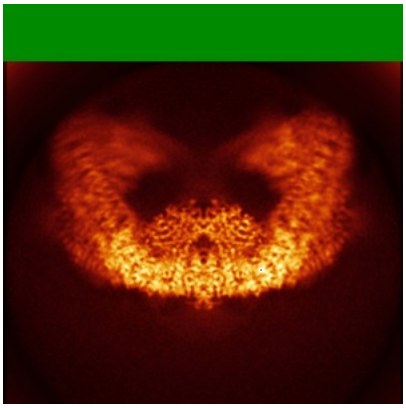

Y Index: 207

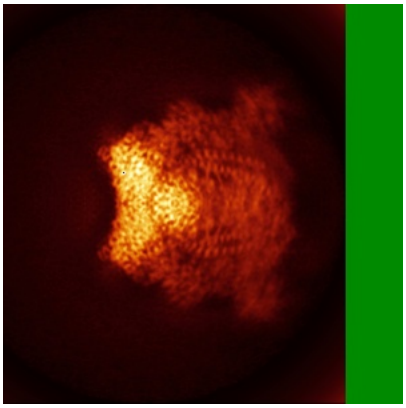

Z Index: 101

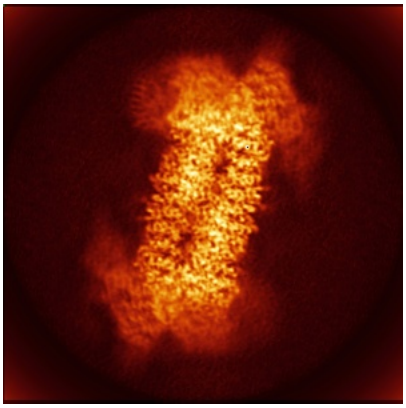
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map


X

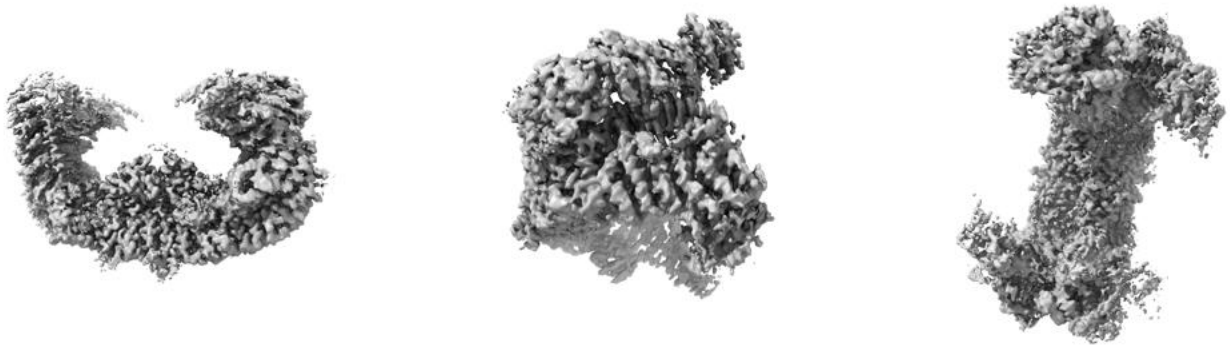

Y


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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

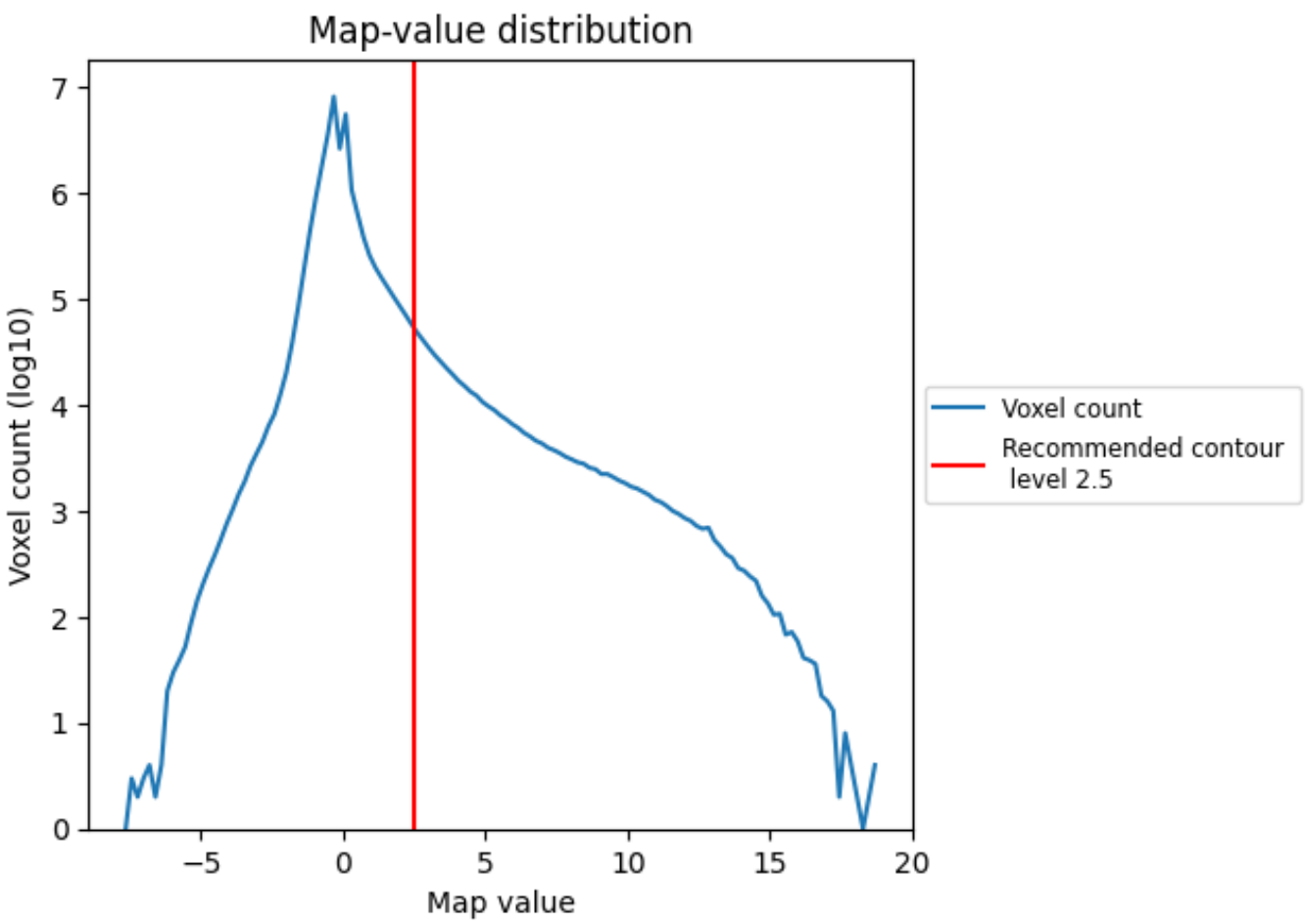
6.6 Mask visualisation (i)

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

7 Map analysis (i)

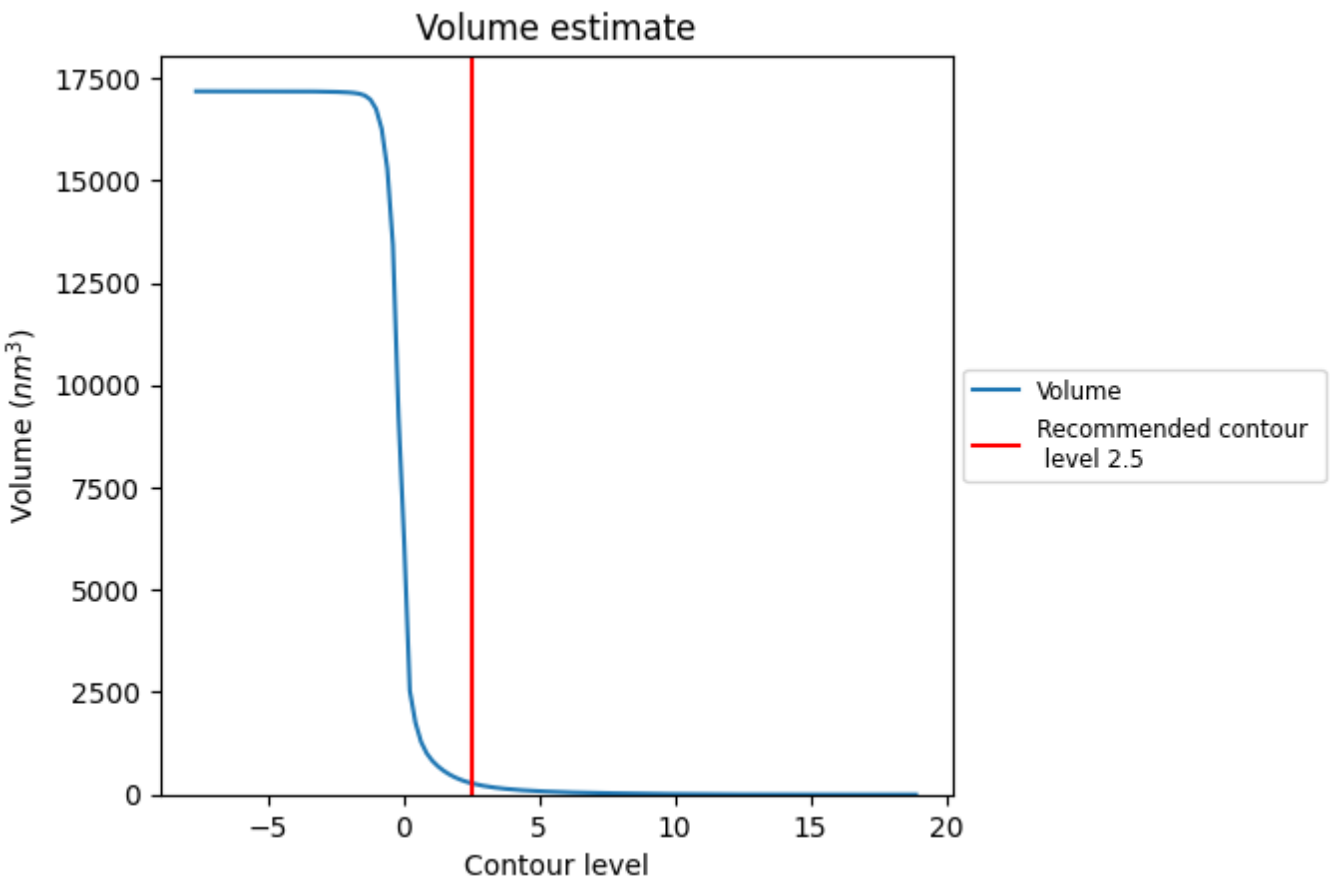
This section contains the results of statistical analysis of the map.

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.

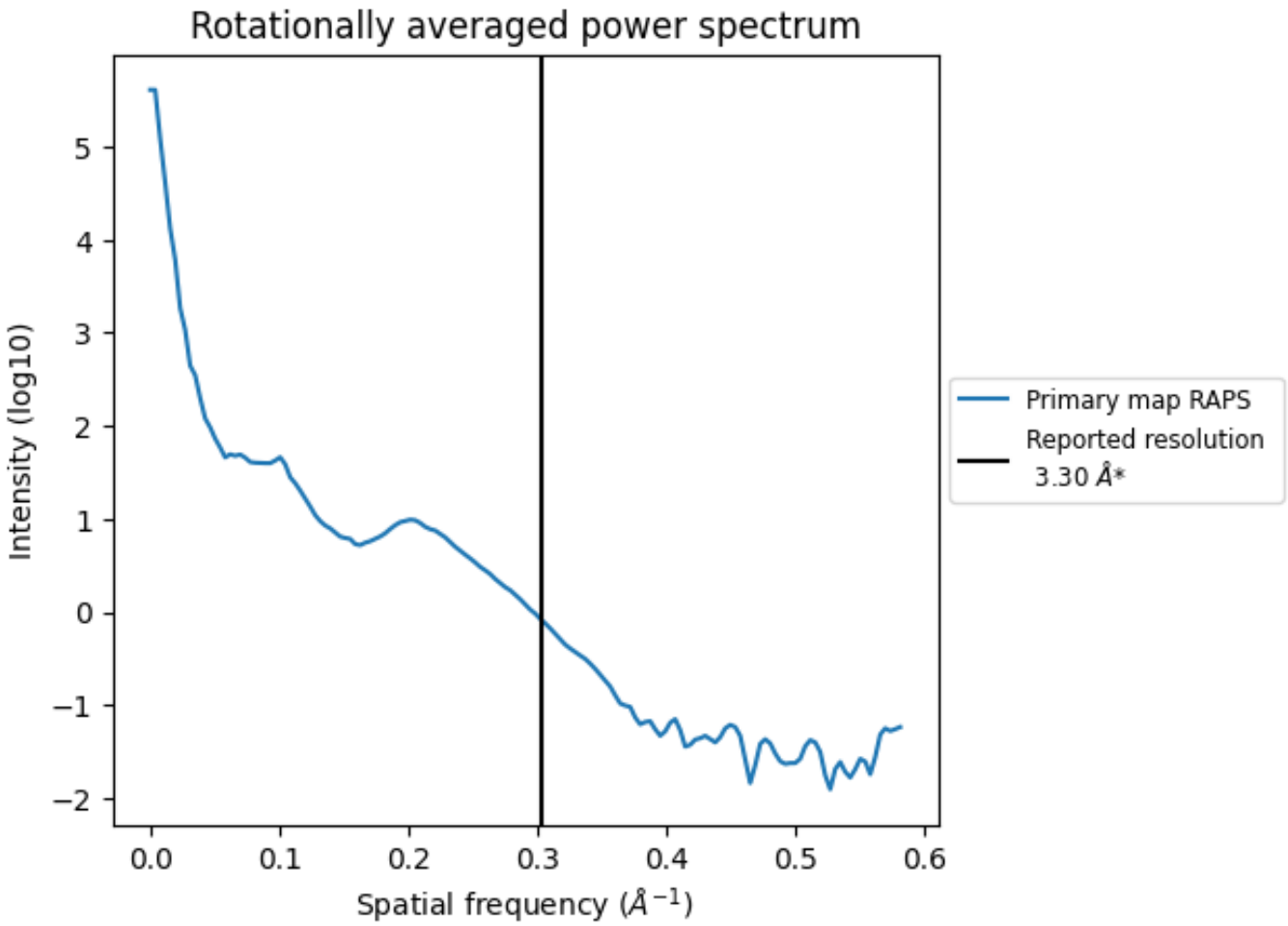
7.2 Volume estimate (i)



The volume at the recommended contour level is 279 nm^3; this corresponds to an approximate mass of 252 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 (i)



*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

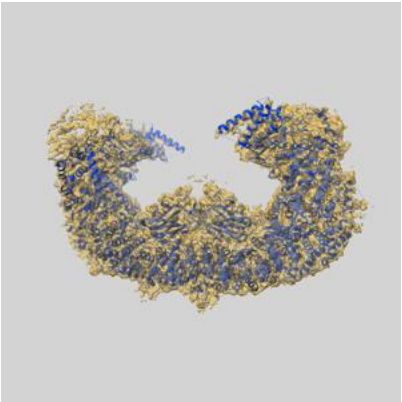
8 Fourier-Shell correlation (i)

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

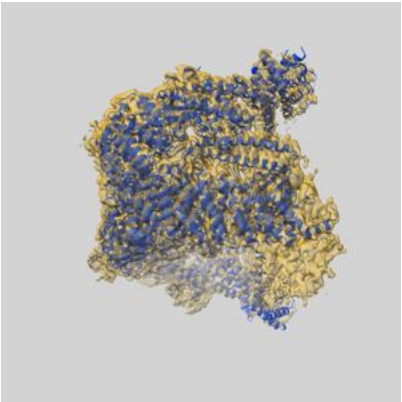
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-15653 and PDB model 8ATM. Per-residue inclusion information can be found in section 3 on page 4.

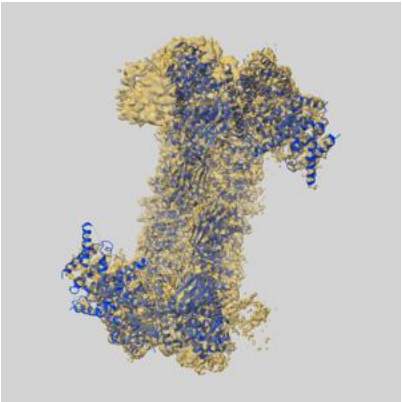
9.1 Map-model overlay (i)



X



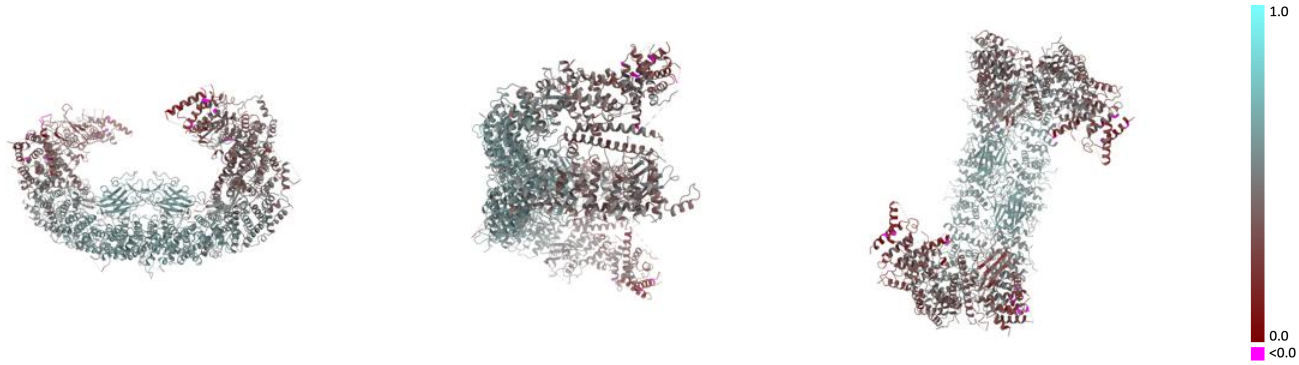
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.5 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.

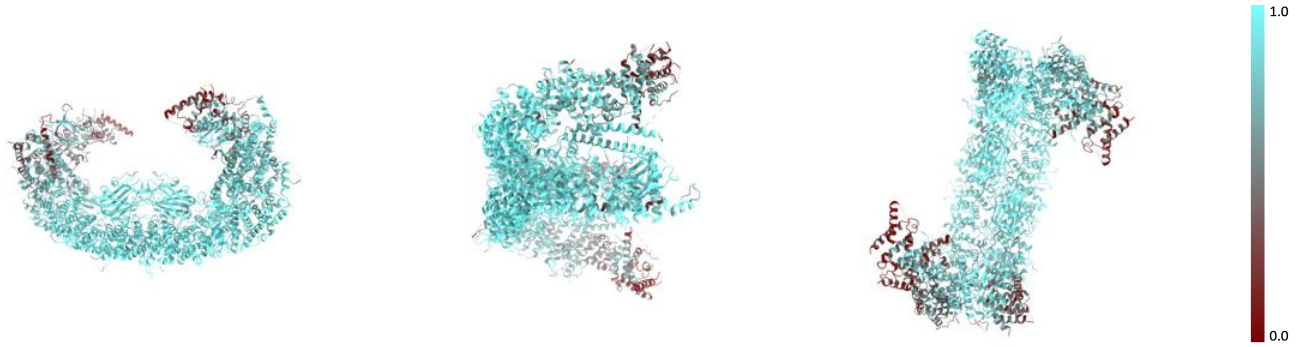
9.2 Q-score mapped to coordinate model (i)



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.

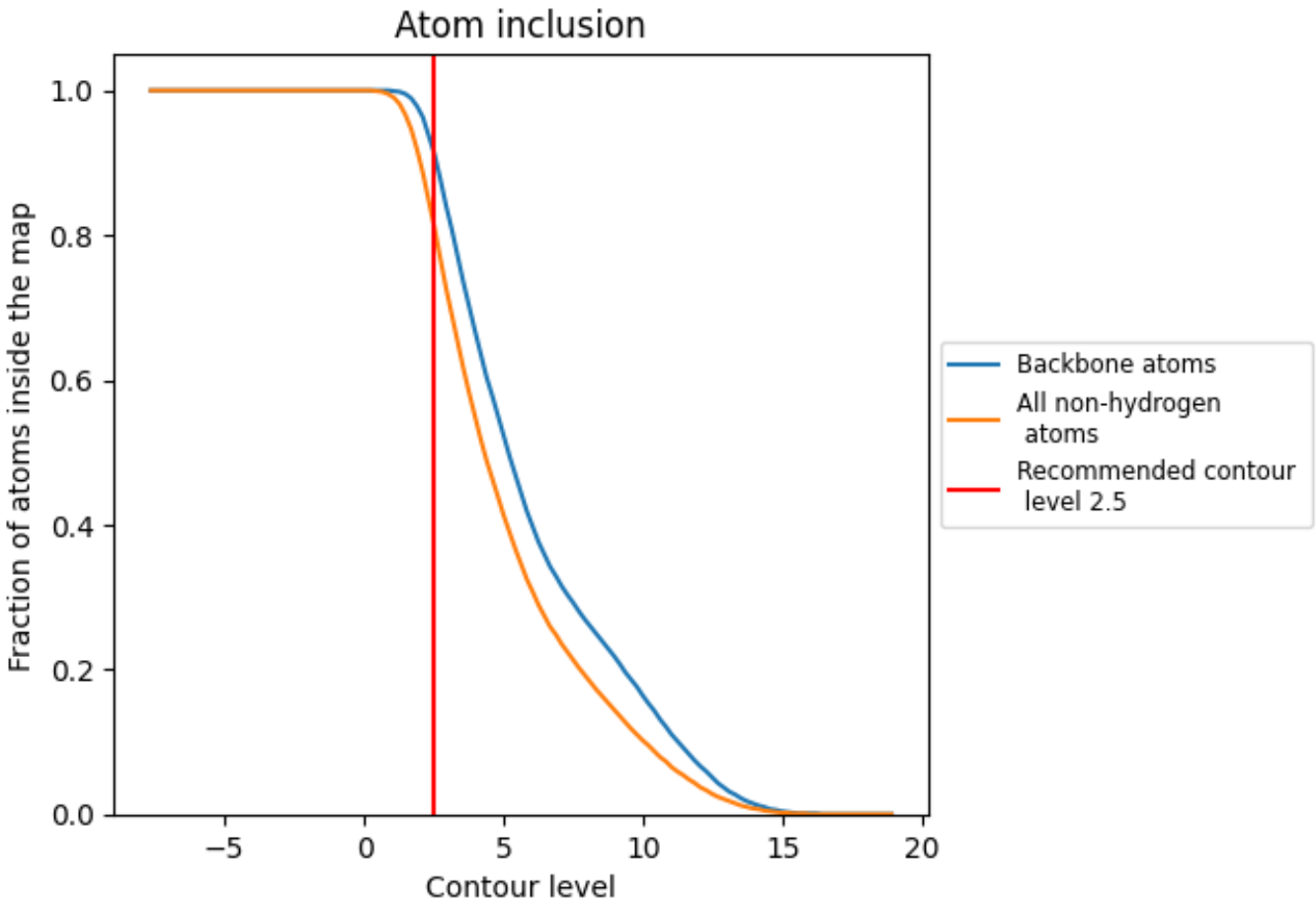
9.3 Atom inclusion mapped to coordinate model (i)



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 (2.5).

9.4 Atom inclusion (i)



At the recommended contour level, 92% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8130	0.4680
A	0.8100	0.4680
B	0.8170	0.4670