wwPDB EM Validation Summary Report (i)

Nov 19, 2022 – 10:13 pm GMT

PDB ID	:	6F0X
EMDB ID	:	EMD-4166
Title	:	Cryo-EM structure of TRIP13 in complex with ATP gamma S, p31comet, C-Mad2 and Cdc20
Authors	:	Alfieri, C.; Chang, L.; Barford, D.
Deposited on	:	2017-11-20
Resolution	:	4.60 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 (1)) were used in the production of this report:

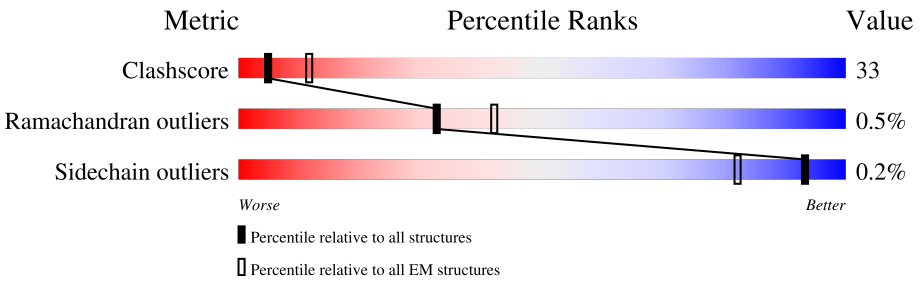
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 4.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	432	15%, 34%, 37%, ·, 29%
1	B	432	27%, 42%, 50%, 8%
1	C	432	25%, 45%, 46%, ·, 8%
1	D	432	12%, 38%, 52%, ·, 8%
1	E	432	36%, 50%, 41%, 8%
1	F	432	33%, 26%, 39%, 35%
2	P	274	14%, 34%, 37%, 29%
3	Q	499	·, ··, 98%

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Mol	Chain	Length	Quality of chain
4	Z	205	43% 41% 59%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	AGS	A	901	-	-	X	-
5	AGS	B	901	-	-	X	-
5	AGS	C	901	-	-	X	-
5	AGS	D	901	-	-	X	-
5	AGS	E	901	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 20450 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 Pachytene checkpoint protein 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	308	2410	1549	410	444	7	0	0
1	B	398	3097	1977	536	576	8	0	0
1	C	398	3077	1964	534	570	9	0	0
1	D	398	3118	1991	539	580	8	0	0
1	E	398	3071	1962	530	571	8	0	0
1	F	282	2241	1441	382	411	7	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	253	GLN	GLU	conflict	UNP Q15645
B	253	GLN	GLU	conflict	UNP Q15645
C	253	GLN	GLU	conflict	UNP Q15645
D	253	GLN	GLU	conflict	UNP Q15645
E	253	GLN	GLU	conflict	UNP Q15645
F	253	GLN	GLU	conflict	UNP Q15645

- Molecule 2 is a protein called MAD2L1-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	P	194	1563	1009	271	270	13	0	0

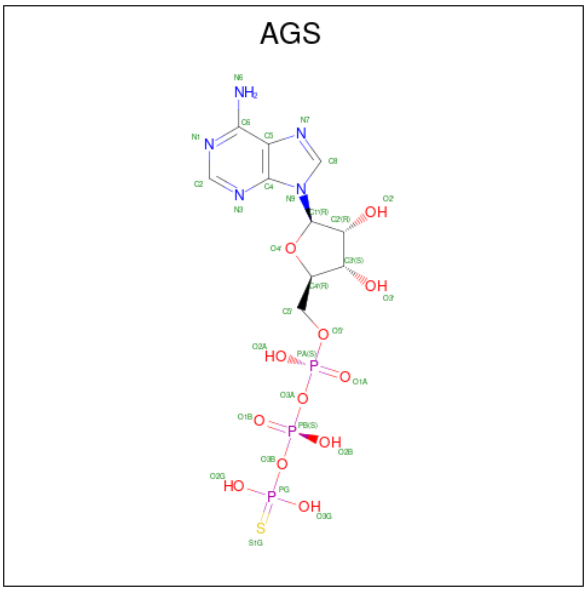
- Molecule 3 is a protein called Cell division cycle protein 20 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	Q	9	70	46	14	10	0	0

- Molecule 4 is a protein called Mitotic spindle assembly checkpoint protein MAD2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	Z	204	1648	1054	270	320	4	0	0

- Molecule 5 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$).



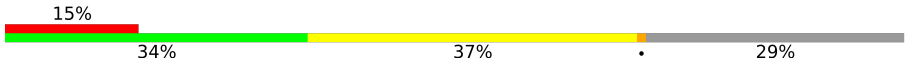
Mol	Chain	Residues	Atoms						AltConf
			Total	C	N	O	P	S	
5	A	1	31	10	5	12	3	1	0
5	B	1	31	10	5	12	3	1	0
5	C	1	31	10	5	12	3	1	0
5	D	1	31	10	5	12	3	1	0
5	E	1	31	10	5	12	3	1	0

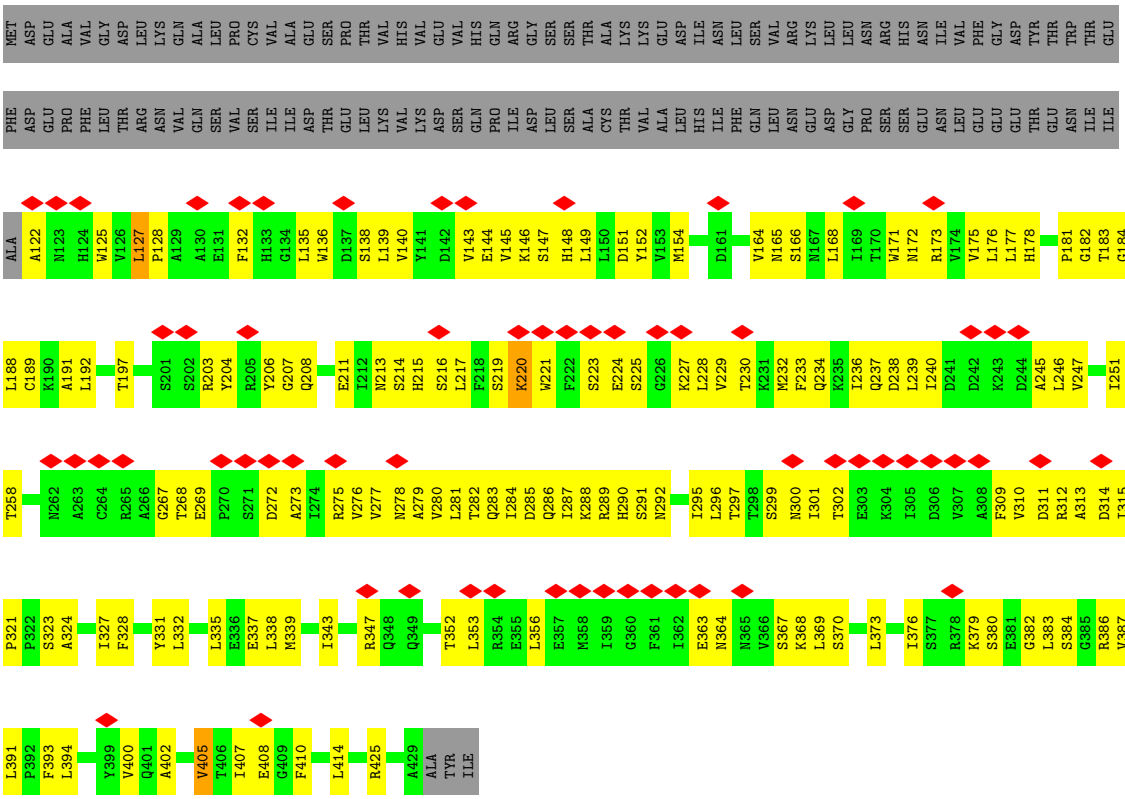
3 Residue-property plots (i)

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: Pachytene checkpoint protein 2 homolog

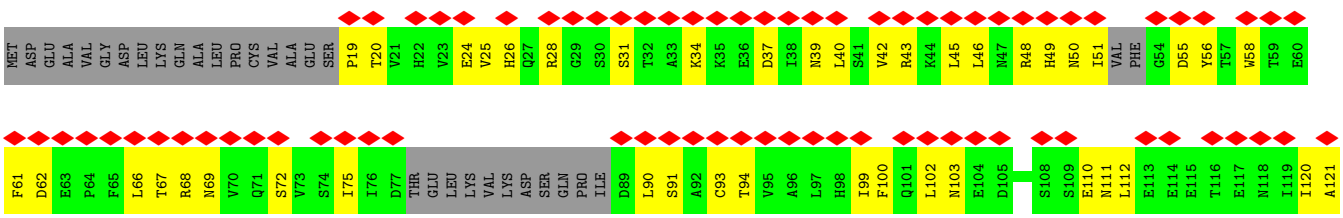
Chain A:

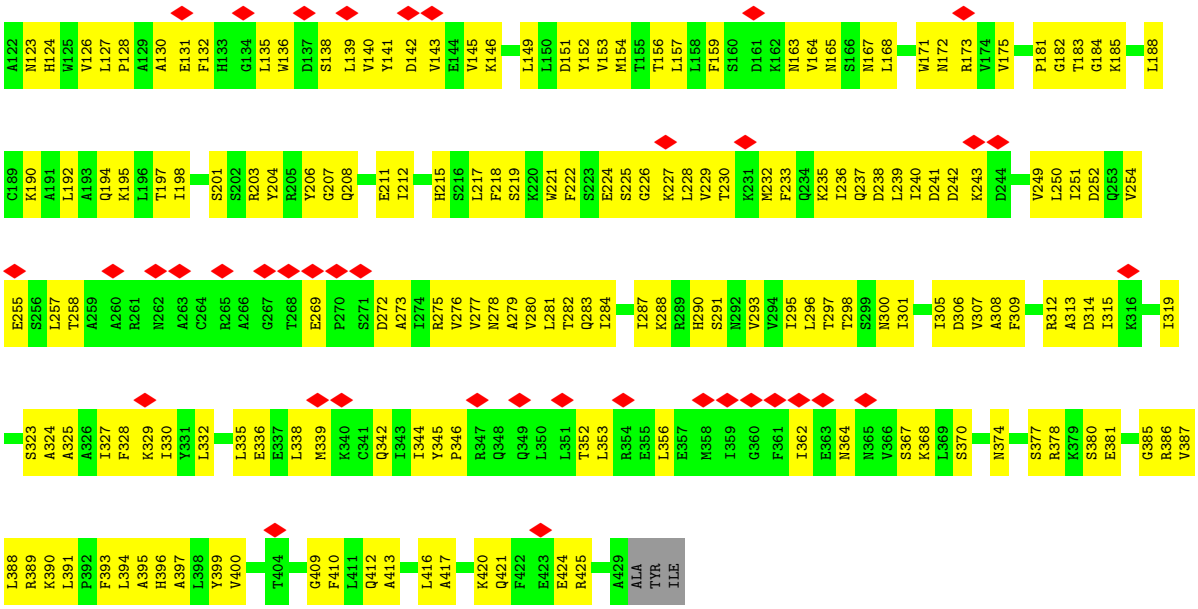




• Molecule 1: Pachytene checkpoint protein 2 homolog

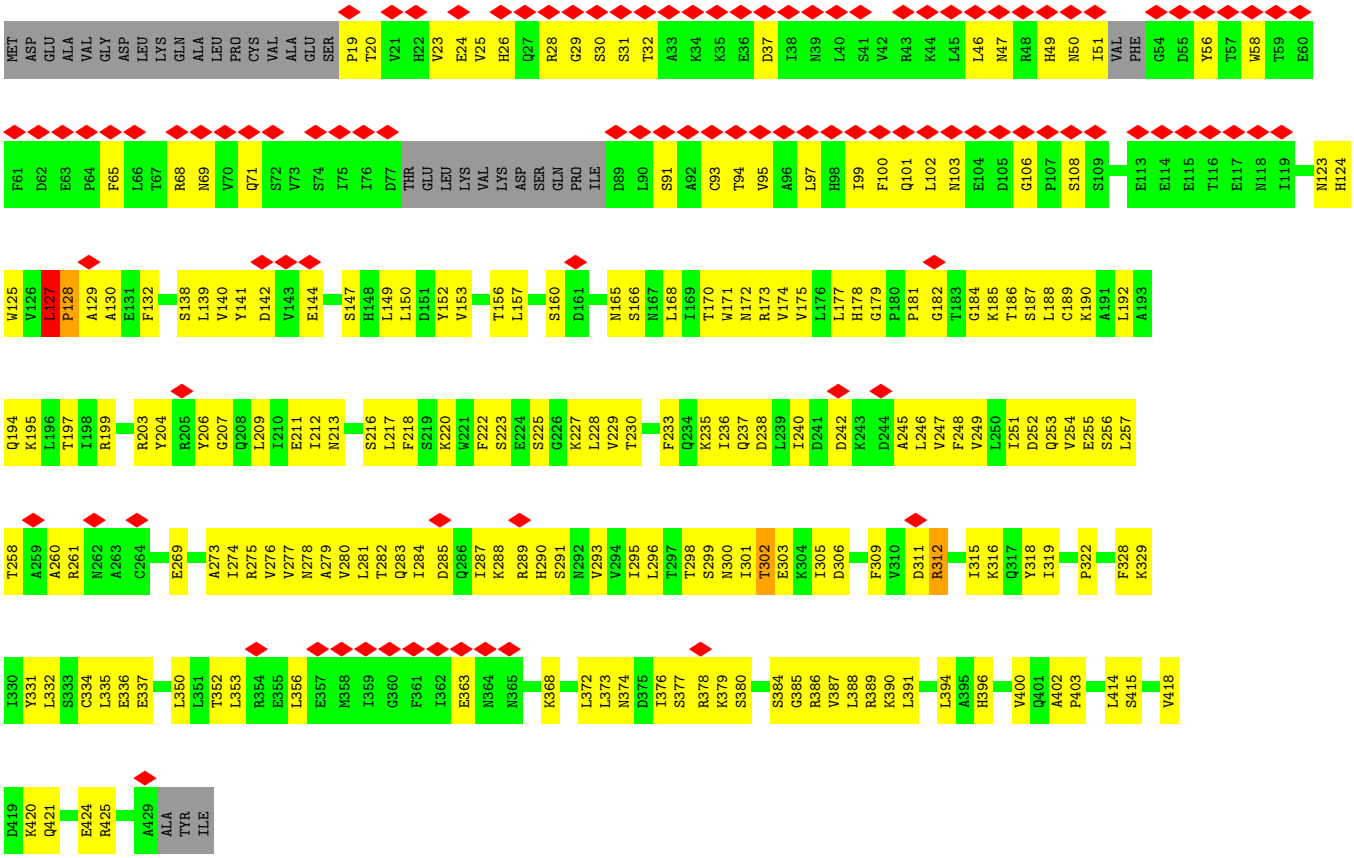
Chain B:





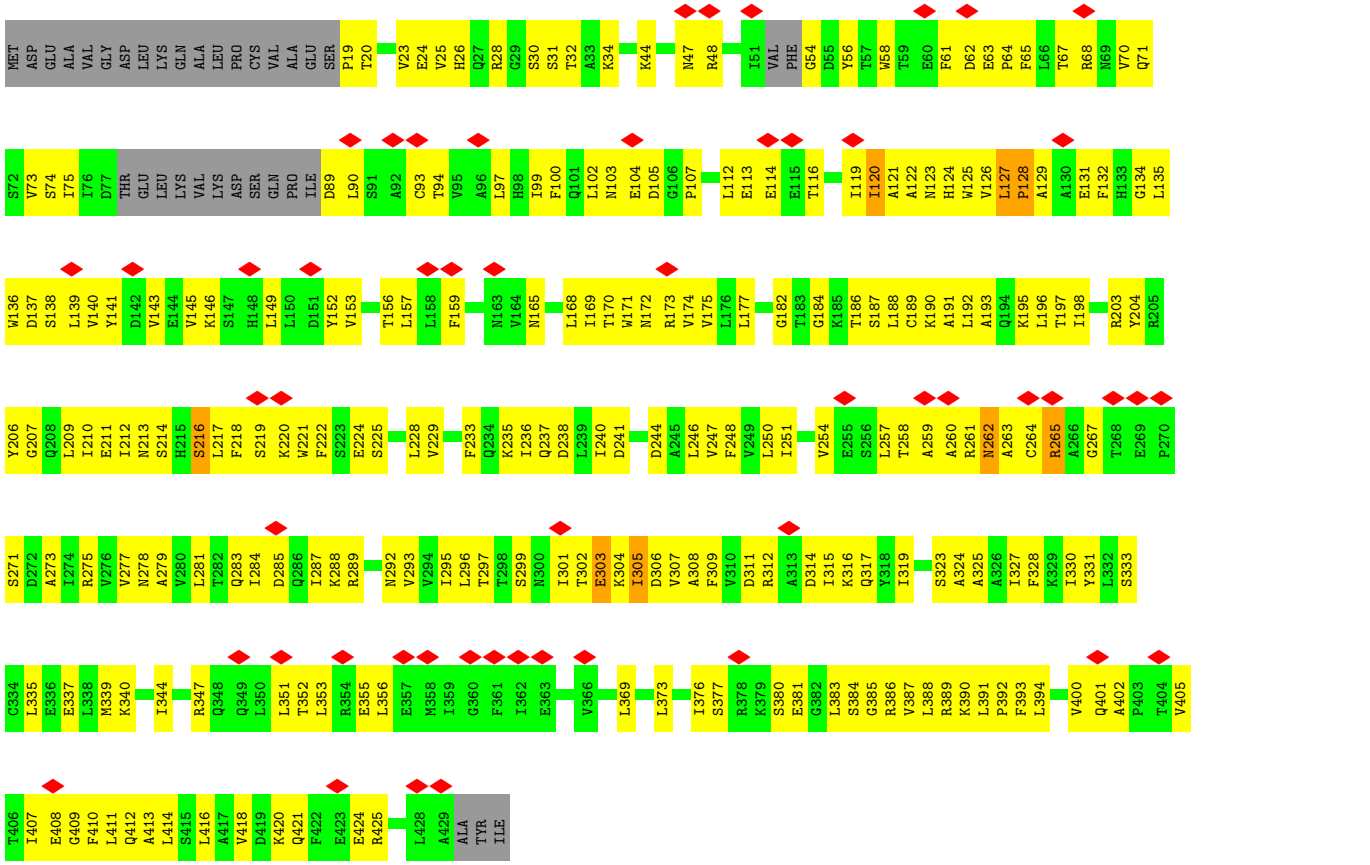
- Molecule 1: Pachytene checkpoint protein 2 homolog

Chain C:



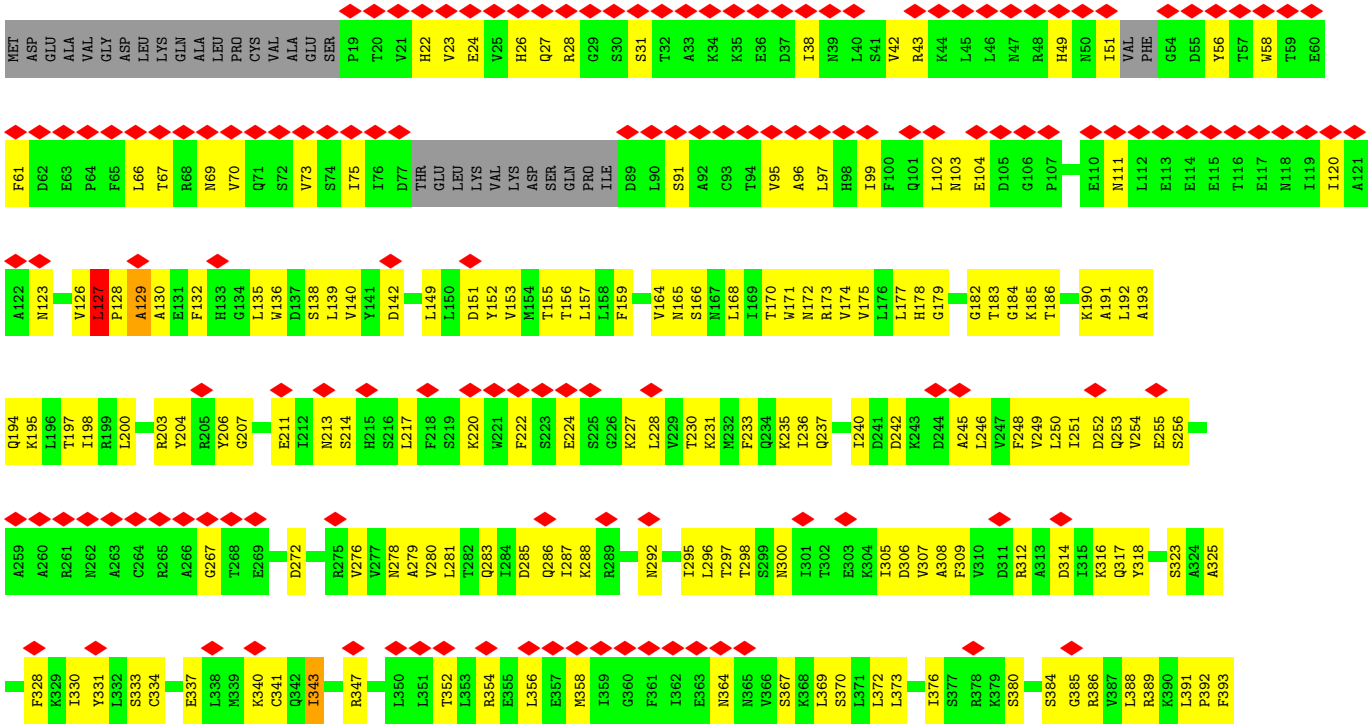
- Molecule 1: Pachytene checkpoint protein 2 homolog

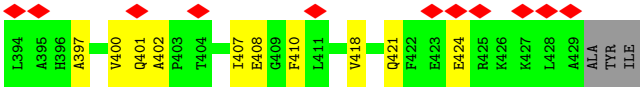
Chain D:



- Molecule 1: Pachytene checkpoint protein 2 homolog

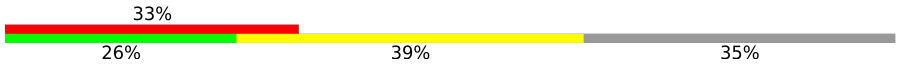
Chain E:

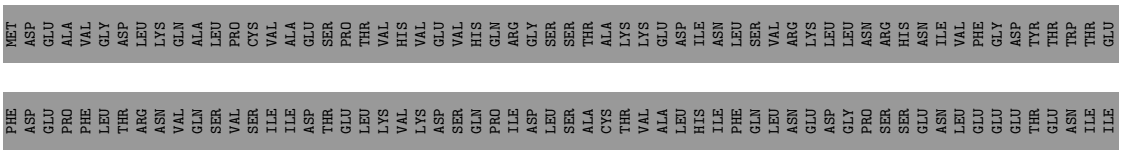


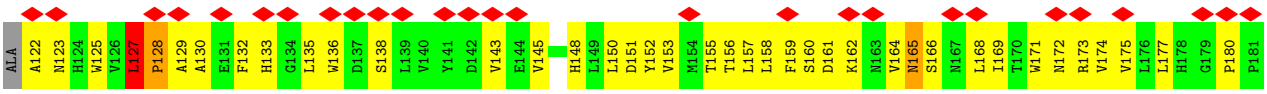


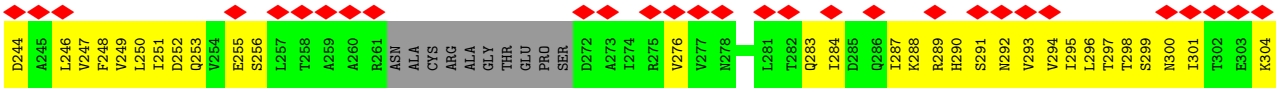
- Molecule 1: Pachytene checkpoint protein 2 homolog

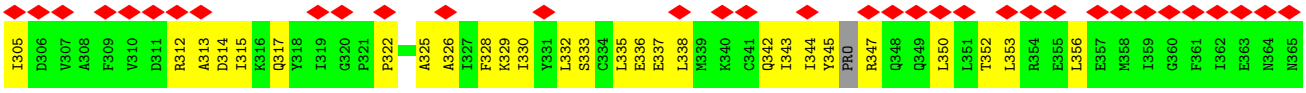
Chain F:

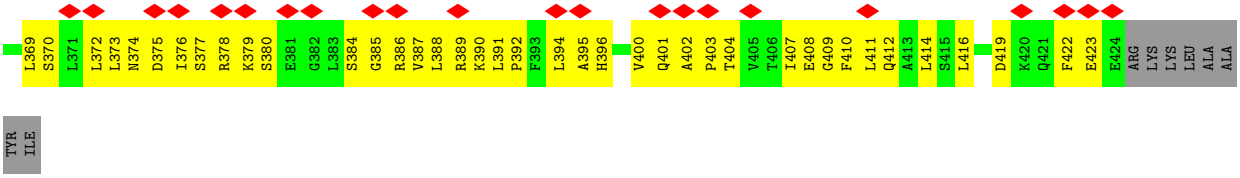






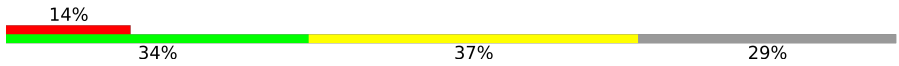


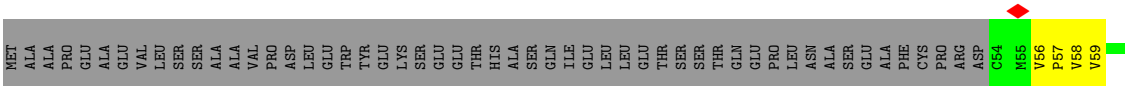


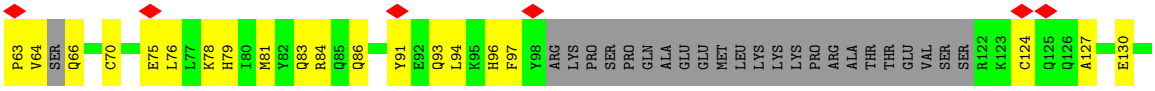


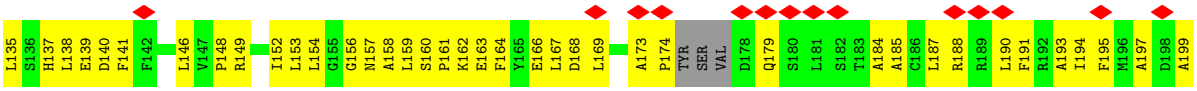
- Molecule 2: MAD2L1-binding protein

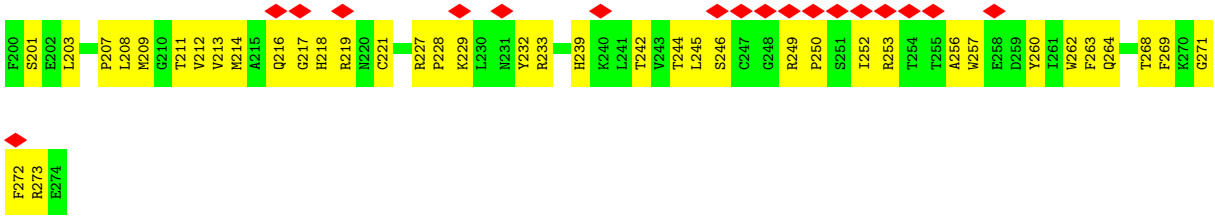
Chain P:





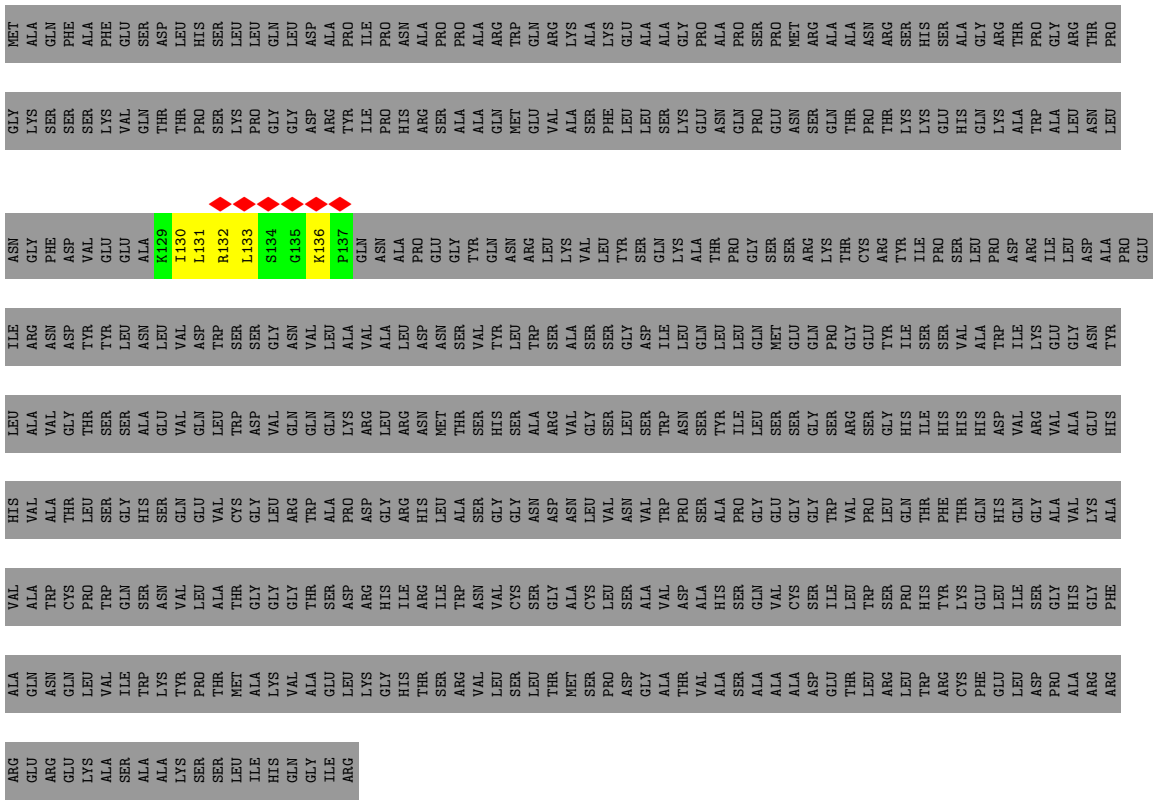






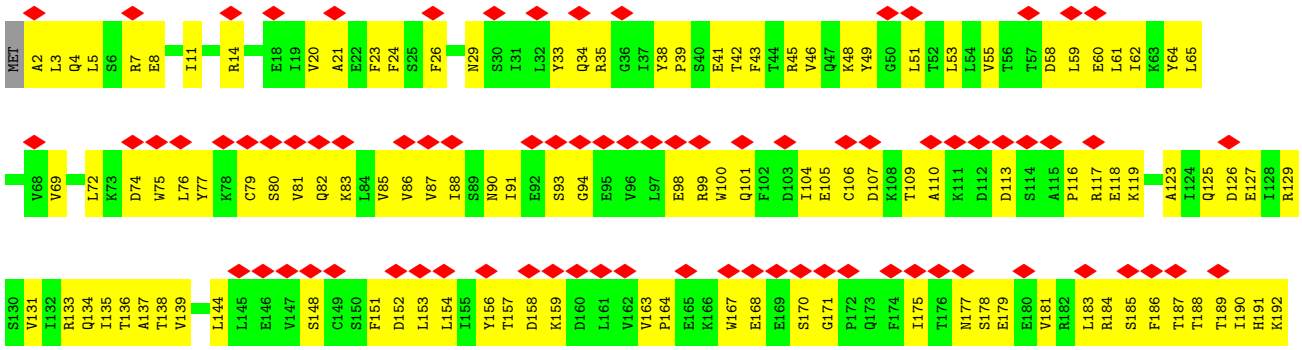
• Molecule 3: Cell division cycle protein 20 homolog

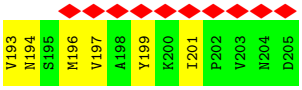
Chain Q: 98%



• Molecule 4: Mitotic spindle assembly checkpoint protein MAD2A

Chain Z: 43% 41% 59%




V193
N194
S195
M196
V197
A198
Y199
K200
I201
P202
V203
N204
D205

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	354157	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 ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.334	Depositor
Minimum map value	-0.185	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.0765	Depositor
Map size (Å)	200.2, 200.2, 200.2	wwPDB
Map dimensions	140, 140, 140	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.43, 1.43, 1.43	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.36	0/2453	0.55	0/3328
1	B	0.38	0/3149	0.52	0/4272
1	C	0.41	0/3128	0.54	0/4244
1	D	0.41	0/3170	0.56	0/4296
1	E	0.36	0/3121	0.51	0/4235
1	F	0.33	0/2274	0.52	0/3076
2	P	0.40	0/1603	0.52	0/2169
3	Q	0.25	0/70	0.55	0/91
4	Z	0.34	0/1676	0.50	0/2271
All	All	0.38	0/20644	0.53	0/27982

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	C	0	2
1	D	0	3
1	E	0	2
1	F	0	1
All	All	0	10

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	127	LEU	Peptide
1	A	405	VAL	Peptide
1	C	127	LEU	Peptide
1	C	312	ARG	Peptide
1	D	120	ILE	Peptide

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	2410	0	2453	178	0
1	B	3097	0	3089	216	0
1	C	3077	0	3063	236	0
1	D	3118	0	3146	272	0
1	E	3071	0	3050	178	0
1	F	2241	0	2319	178	0
2	P	1563	0	1560	83	0
3	Q	70	0	86	13	0
4	Z	1648	0	1665	136	0
5	A	31	0	12	11	0
5	B	31	0	12	11	0
5	C	31	0	12	12	0
5	D	31	0	12	9	0
5	E	31	0	12	10	0
All	All	20450	0	20491	1358	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 33.

The worst 5 of 1358 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:A:390:LYS:HZ1	1:A:394:LEU:HG	1.10	1.12
1:E:173:ARG:NH1	1:E:288:LYS:O	1.88	1.06
1:B:24:GLU:OE2	1:B:195:LYS:NZ	1.90	1.04
1:C:390:LYS:HZ2	1:D:172:ASN:N	1.56	1.03
1:D:103:ASN:OD1	2:P:229:LYS:NZ	1.95	0.99

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	306/432 (71%)	251 (82%)	55 (18%)	0	100	100
1	B	392/432 (91%)	326 (83%)	66 (17%)	0	100	100
1	C	392/432 (91%)	315 (80%)	74 (19%)	3 (1%)	19	60
1	D	392/432 (91%)	314 (80%)	75 (19%)	3 (1%)	19	60
1	E	392/432 (91%)	316 (81%)	73 (19%)	3 (1%)	19	60
1	F	272/432 (63%)	219 (80%)	50 (18%)	3 (1%)	14	52
2	P	186/274 (68%)	161 (87%)	24 (13%)	1 (0%)	29	68
3	Q	7/499 (1%)	6 (86%)	1 (14%)	0	100	100
4	Z	202/205 (98%)	174 (86%)	28 (14%)	0	100	100
All	All	2541/3570 (71%)	2082 (82%)	446 (18%)	13 (0%)	32	68

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	128	PRO
1	E	128	PRO
1	F	128	PRO
1	E	127	LEU
1	C	127	LEU

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	263/385 (68%)	262 (100%)	1 (0%)	91	94
1	B	334/385 (87%)	334 (100%)	0	100	100
1	C	329/385 (86%)	329 (100%)	0	100	100
1	D	341/385 (89%)	338 (99%)	3 (1%)	78	87
1	E	327/385 (85%)	327 (100%)	0	100	100
1	F	251/385 (65%)	251 (100%)	0	100	100
2	P	170/240 (71%)	170 (100%)	0	100	100
3	Q	8/411 (2%)	8 (100%)	0	100	100
4	Z	189/190 (100%)	188 (100%)	1 (0%)	88	93
All	All	2212/3151 (70%)	2207 (100%)	5 (0%)	93	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	220	LYS
1	D	68	ARG
1	D	262	ASN
1	D	265	ARG
4	Z	45	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
2	P	79	HIS
4	Z	125	GLN
2	P	83	GLN
4	Z	34	GLN
1	C	396	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

5 ligands are modelled in this entry.

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	$\#\|Z\| > 2$
5	AGS	E	901	1	26,33,33	0.79	0	26,52,52	1.38	2 (7%)
5	AGS	B	901	1	26,33,33	0.74	0	26,52,52	1.33	2 (7%)
5	AGS	A	901	1	26,33,33	0.80	0	26,52,52	1.35	2 (7%)
5	AGS	D	901	1	26,33,33	0.74	0	26,52,52	1.11	2 (7%)
5	AGS	C	901	1	26,33,33	0.69	0	26,52,52	1.20	3 (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
5	AGS	E	901	1	-	3/17/38/38	0/3/3/3
5	AGS	B	901	1	-	5/17/38/38	0/3/3/3
5	AGS	A	901	1	-	6/17/38/38	0/3/3/3
5	AGS	D	901	1	-	4/17/38/38	0/3/3/3
5	AGS	C	901	1	-	5/17/38/38	0/3/3/3

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	901	AGS	PA-O3A-PB	-5.83	112.82	132.83
5	E	901	AGS	PA-O3A-PB	-5.63	113.49	132.83

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	901	AGS	PA-O3A-PB	-5.29	114.66	132.83
5	C	901	AGS	PA-O3A-PB	-4.43	117.63	132.83
5	D	901	AGS	PA-O3A-PB	-3.57	120.58	132.83

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	901	AGS	C5'-O5'-PA-O2A
5	A	901	AGS	C5'-O5'-PA-O3A
5	B	901	AGS	C5'-O5'-PA-O1A
5	B	901	AGS	C5'-O5'-PA-O2A
5	B	901	AGS	C5'-O5'-PA-O3A

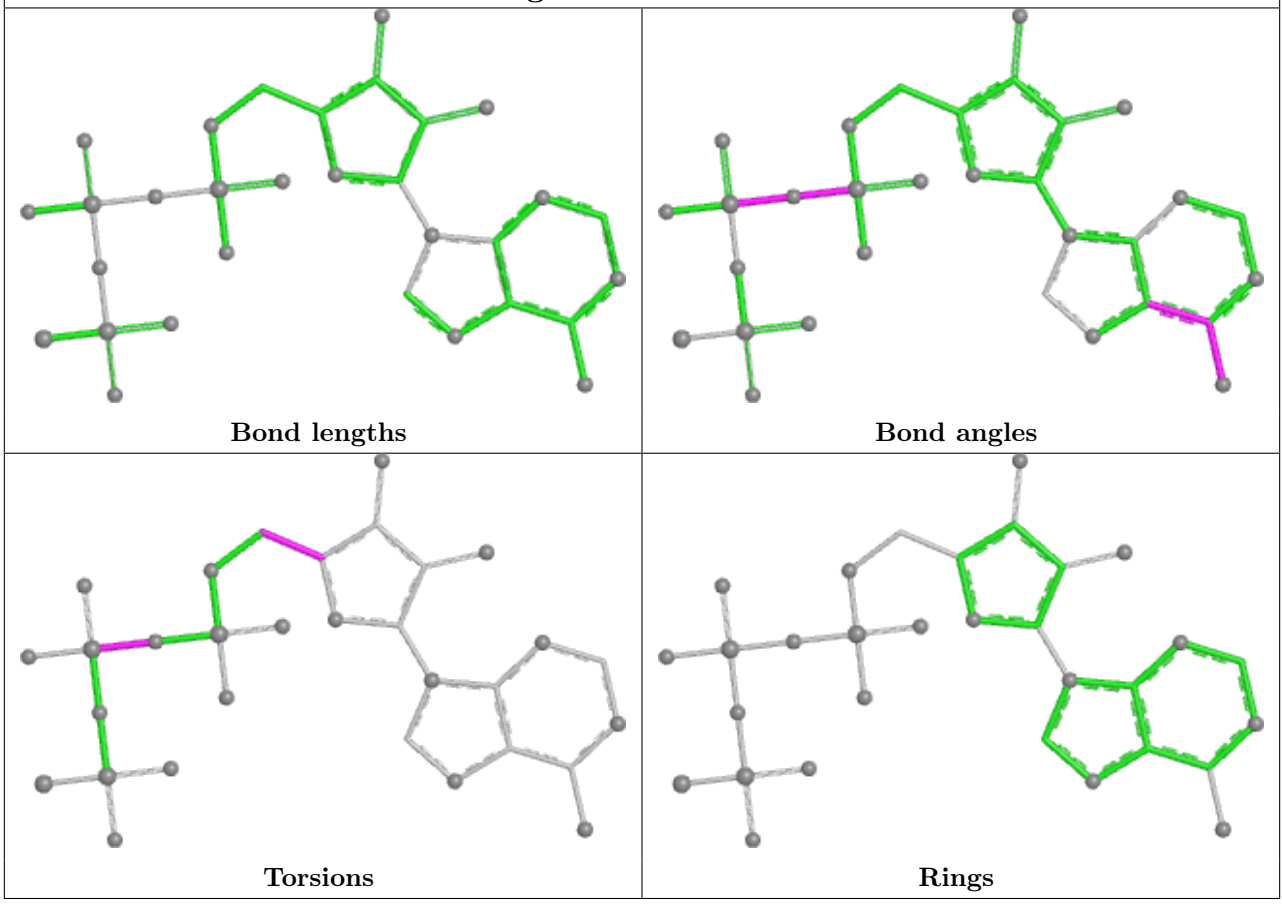
There are no ring outliers.

5 monomers are involved in 53 short contacts:

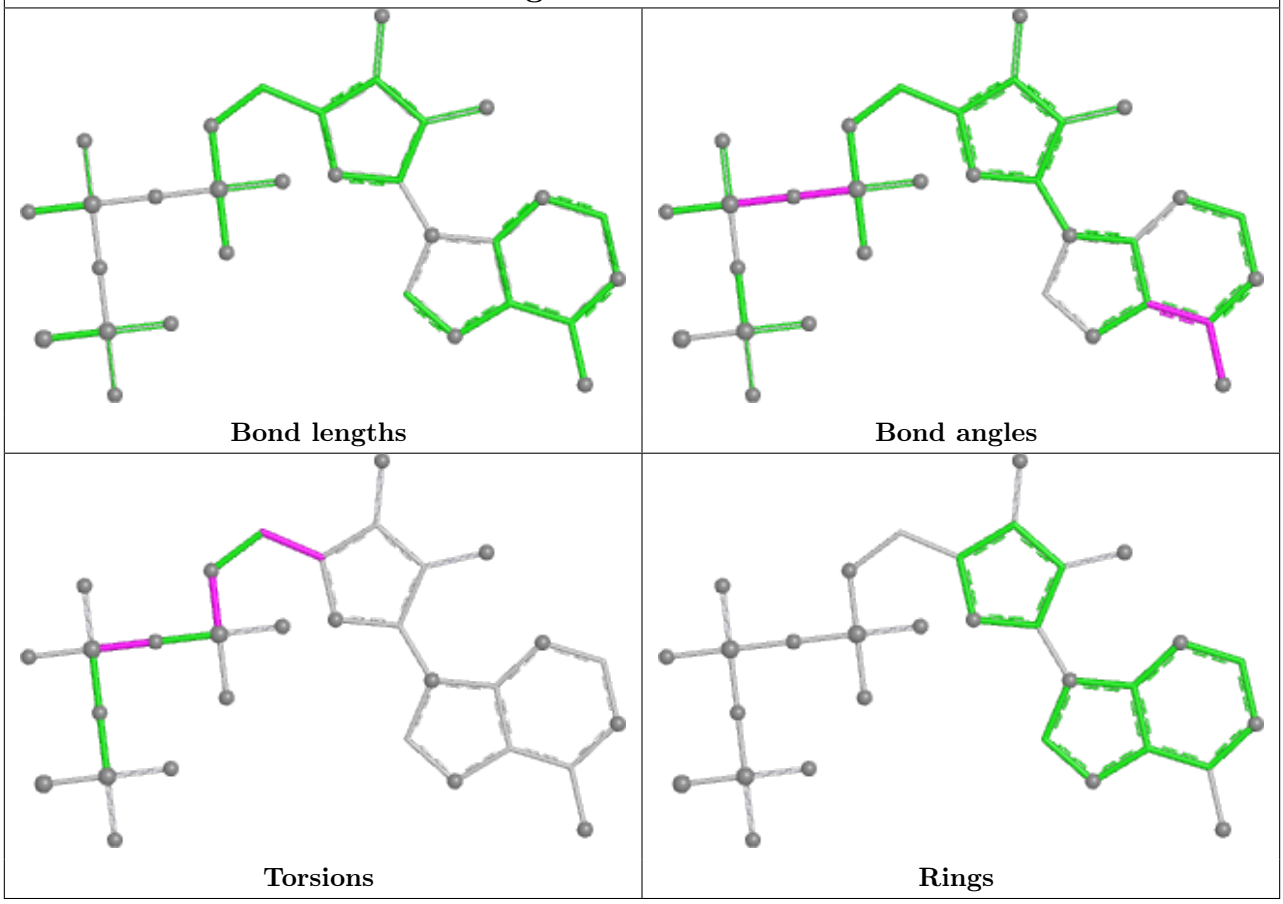
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	901	AGS	10	0
5	B	901	AGS	11	0
5	A	901	AGS	11	0
5	D	901	AGS	9	0
5	C	901	AGS	12	0

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.

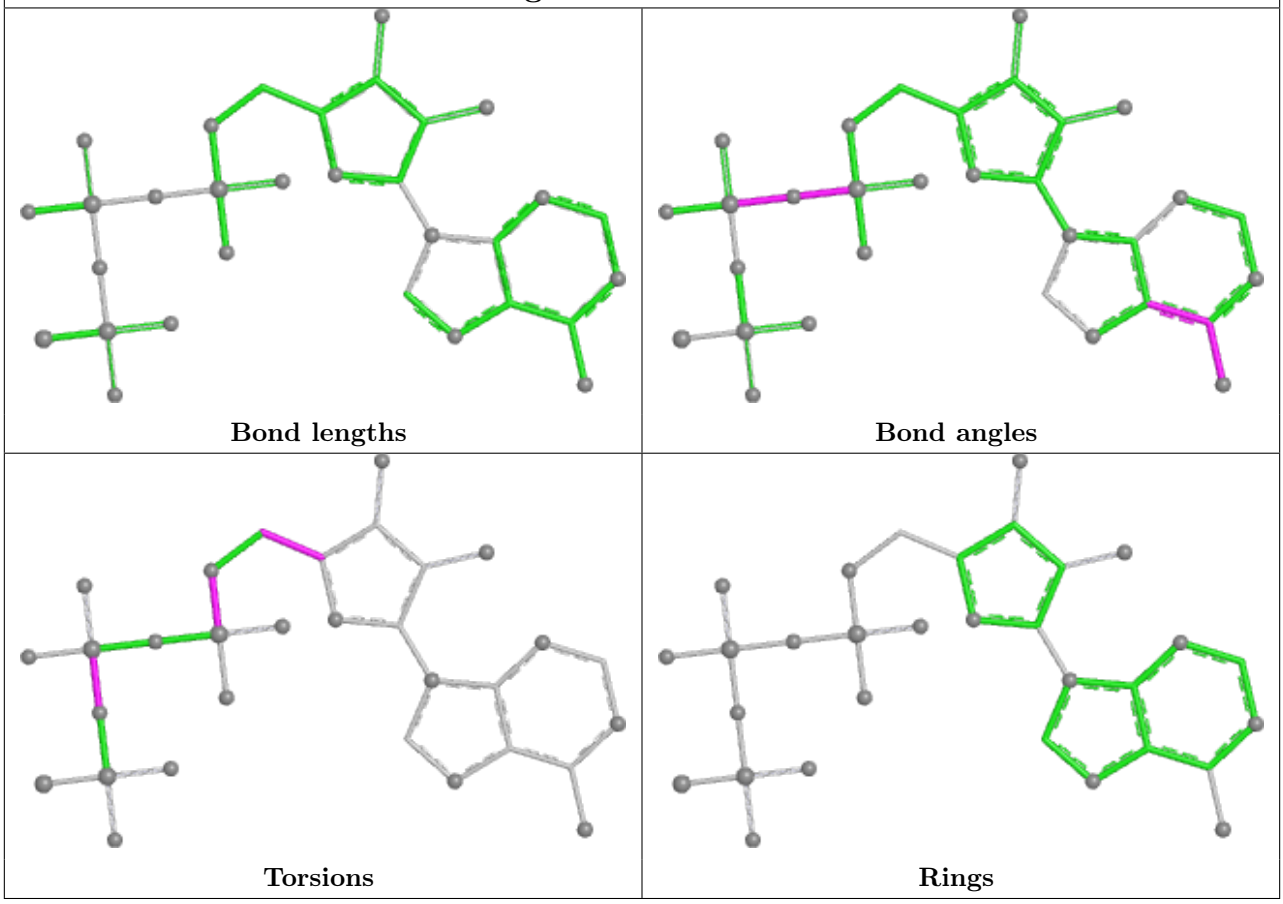
Ligand AGS E 901

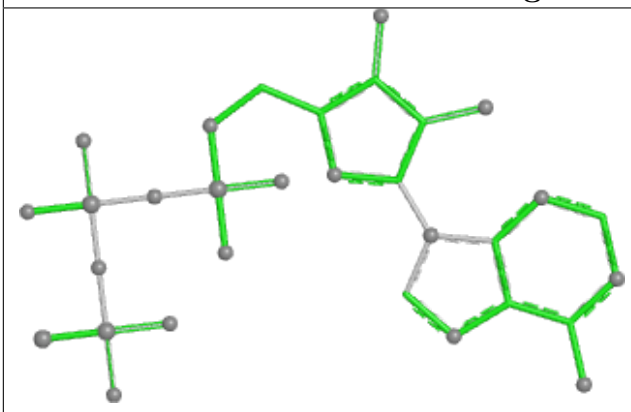
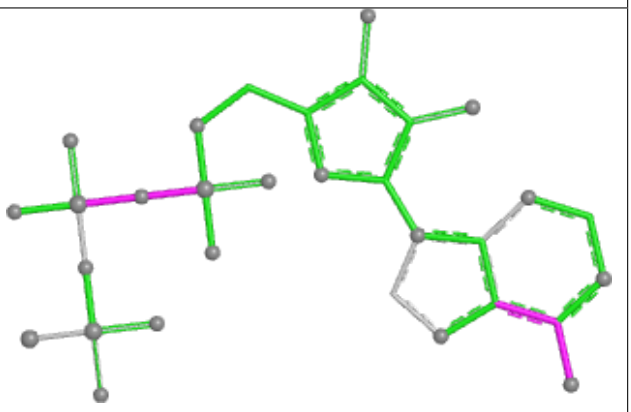
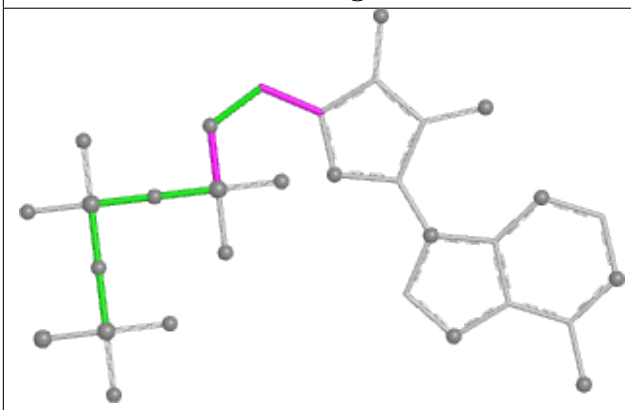
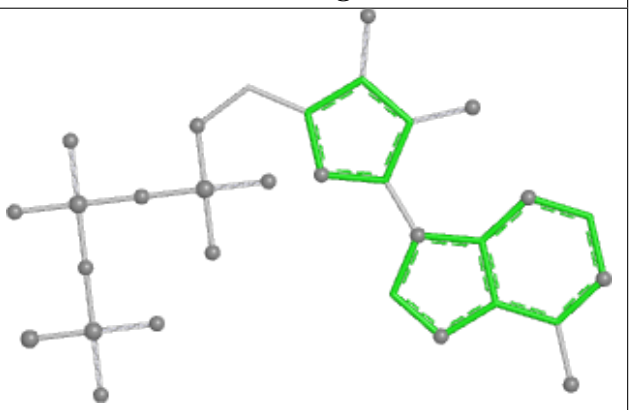


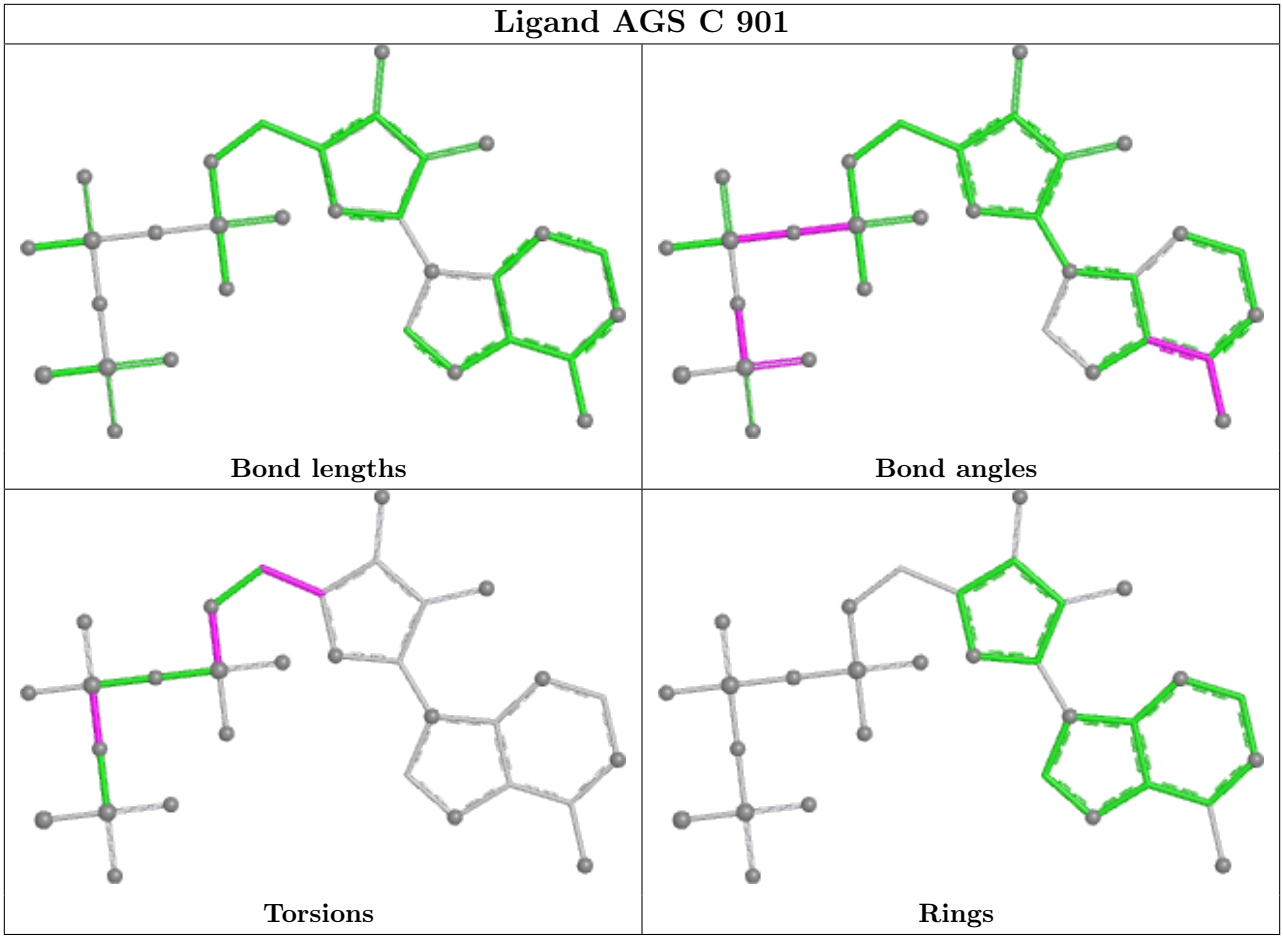
Ligand AGS B 901



Ligand AGS A 901



Ligand AGS D 901	
 Bond lengths	 Bond angles
 Torsions	 Rings



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F	143:VAL	C	144:GLU	N	3.76

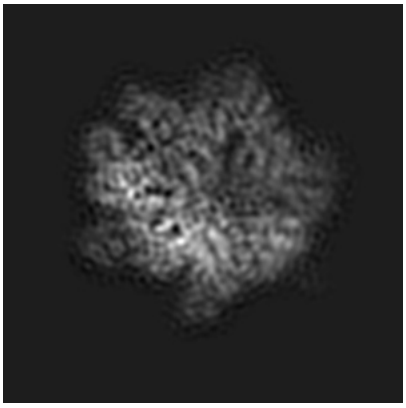
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-4166. These allow visual inspection of the internal detail of the map and identification of artifacts.

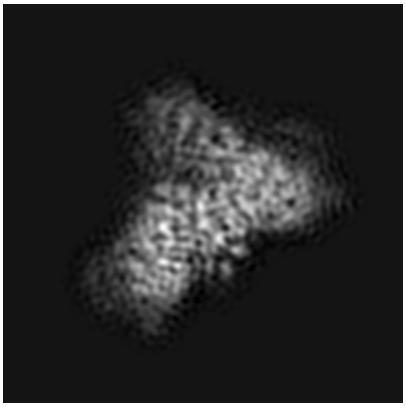
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

6.1.1 Primary map



X



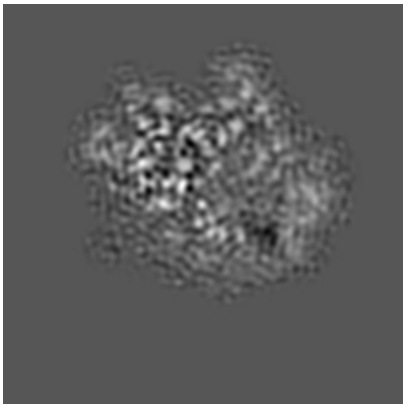
Y

Z

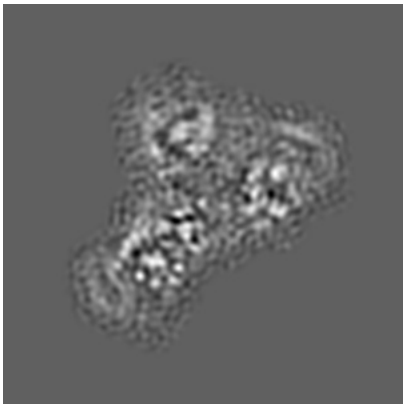
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map



X Index: 70



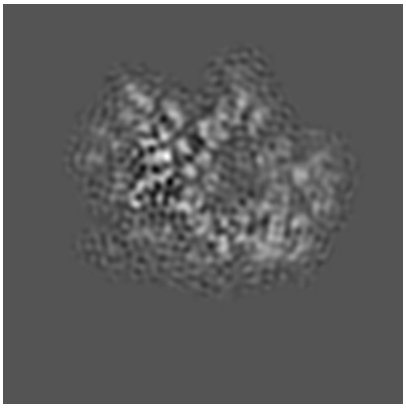
Y Index: 70

Z Index: 70

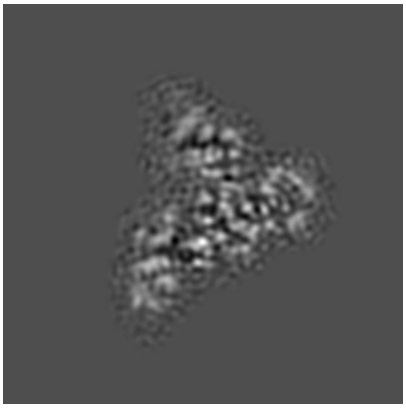
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

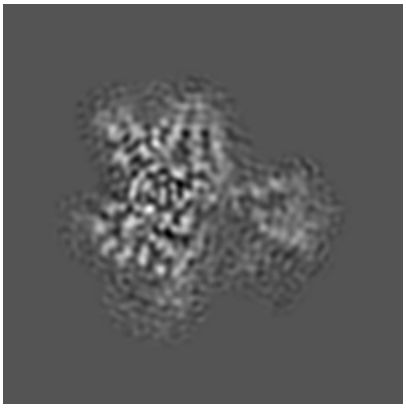
6.3.1 Primary map



X Index: 67



Y Index: 52



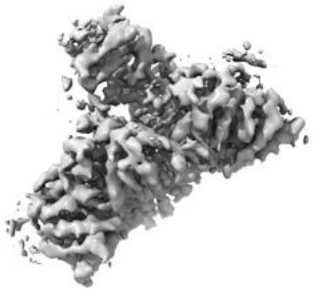
Z Index: 57

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 0.0765. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

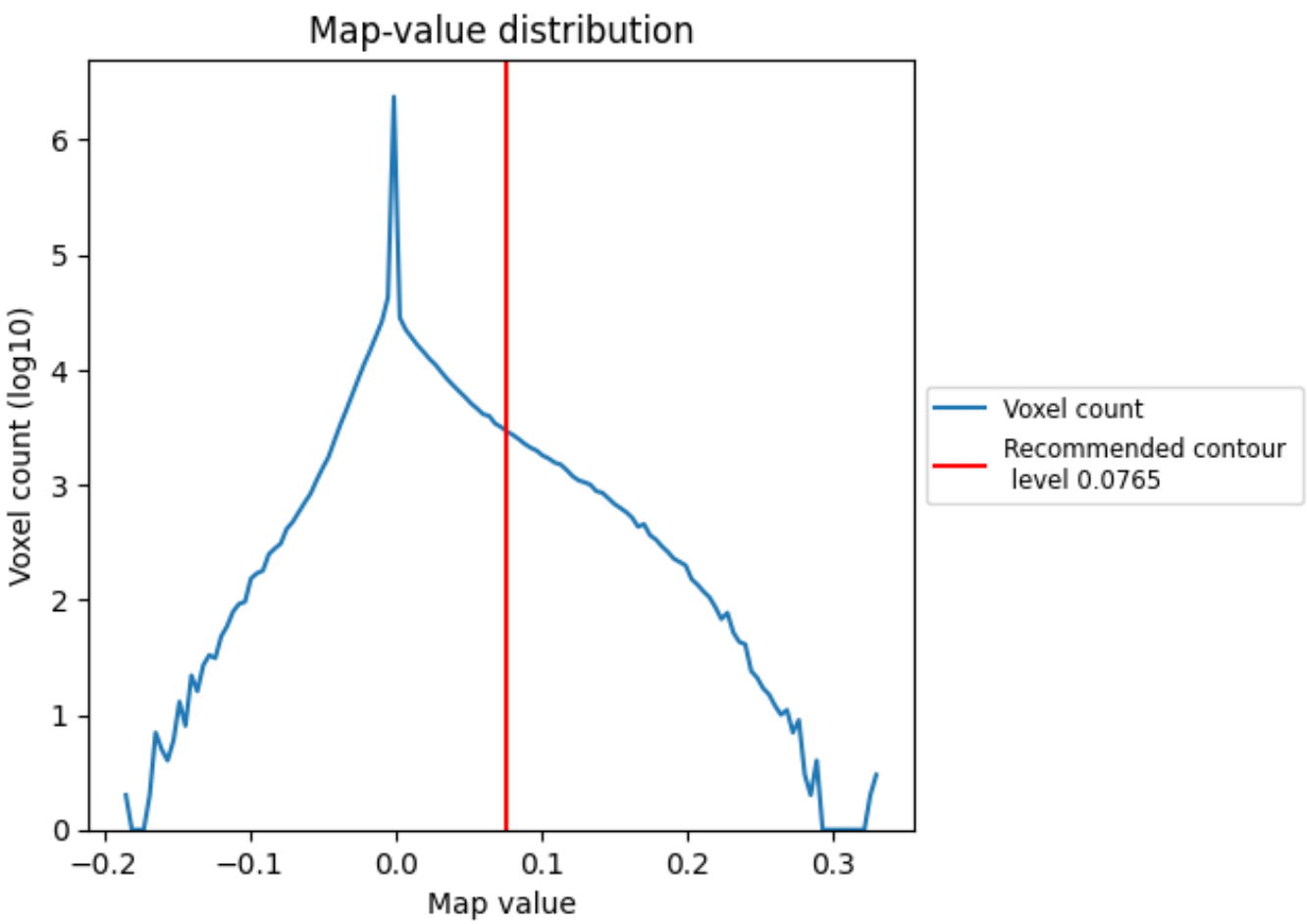
6.5 Mask visualisation (i)

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

7 Map analysis (i)

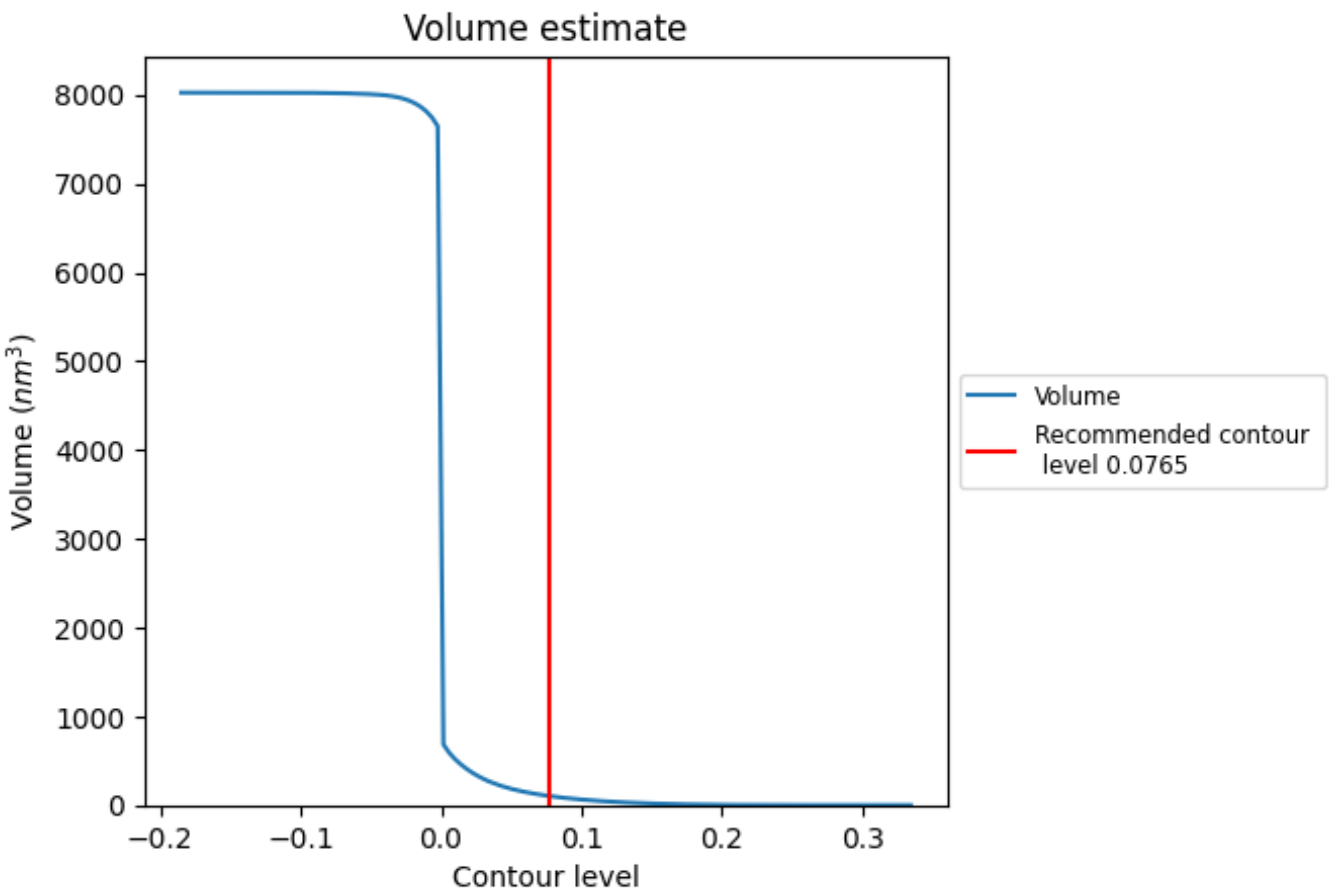
This section contains the results of statistical analysis of the map.

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.

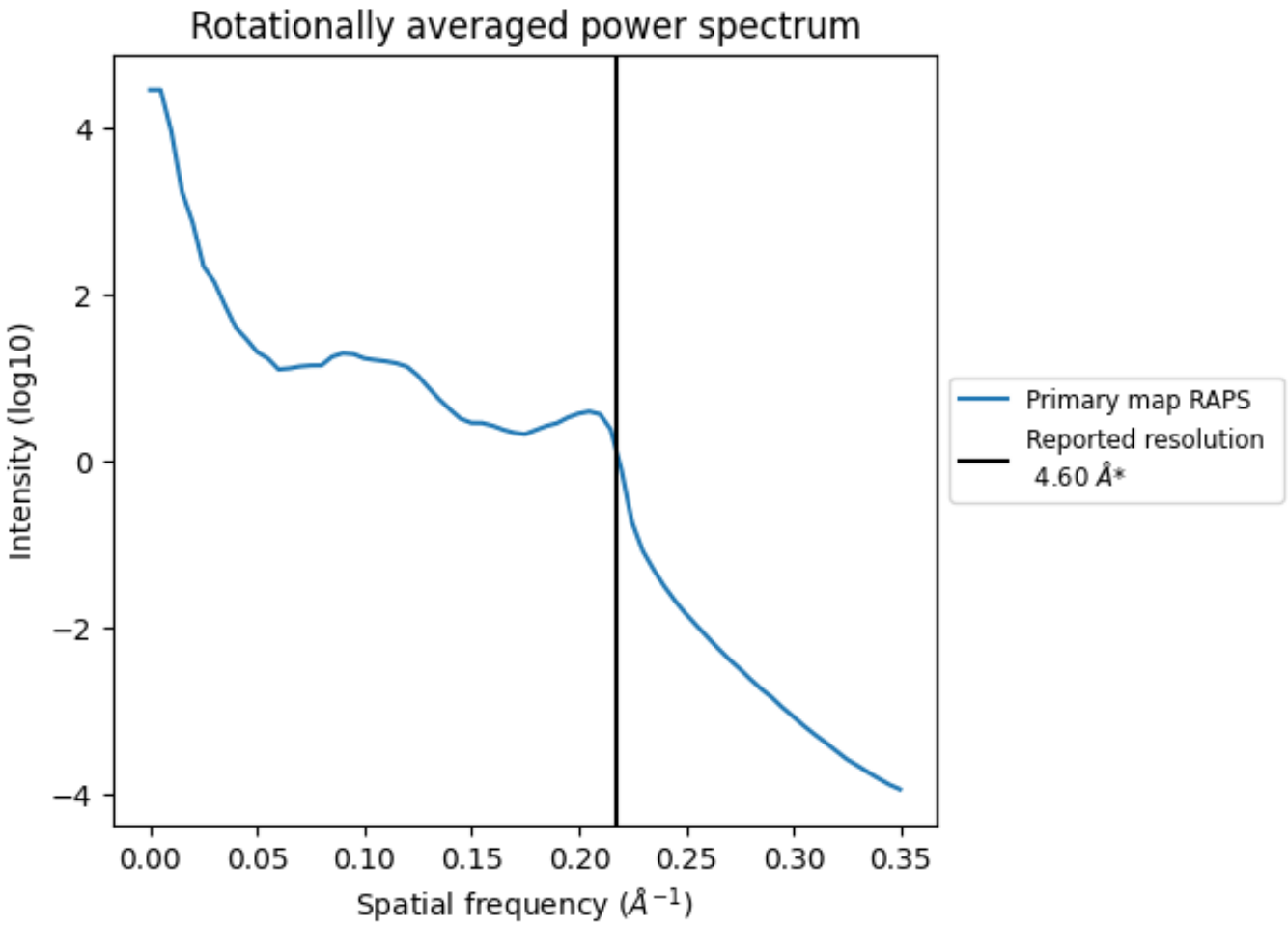
7.2 Volume estimate (i)



The volume at the recommended contour level is 104 nm^3; this corresponds to an approximate mass of 94 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 0.217 Å^{-1}

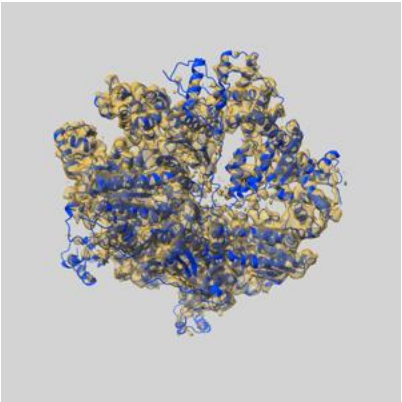
8 Fourier-Shell correlation (i)

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

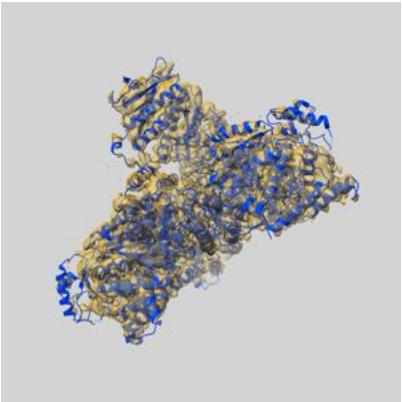
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-4166 and PDB model 6F0X. Per-residue inclusion information can be found in section 3 on page 6.

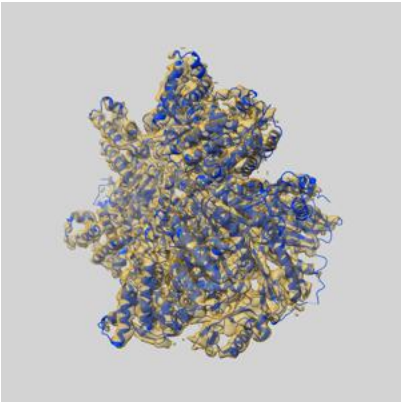
9.1 Map-model overlay (i)



X



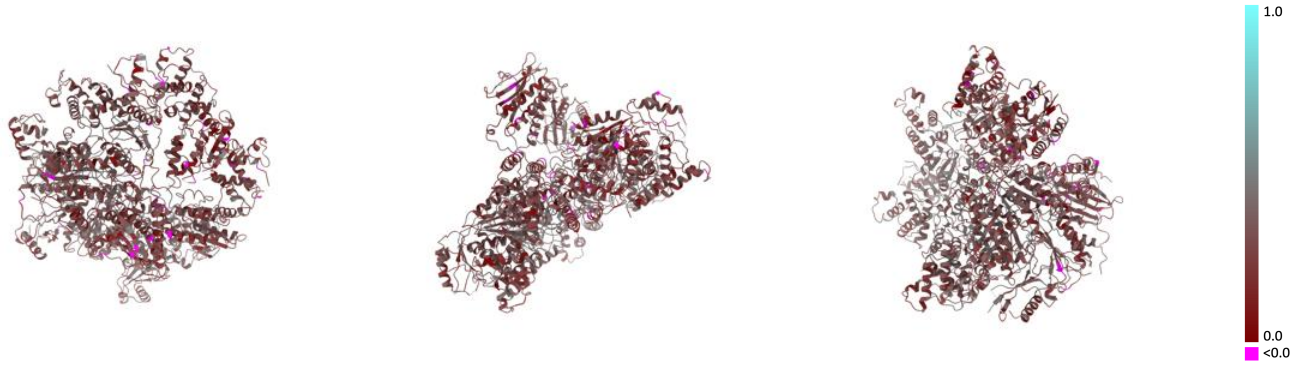
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0765 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.

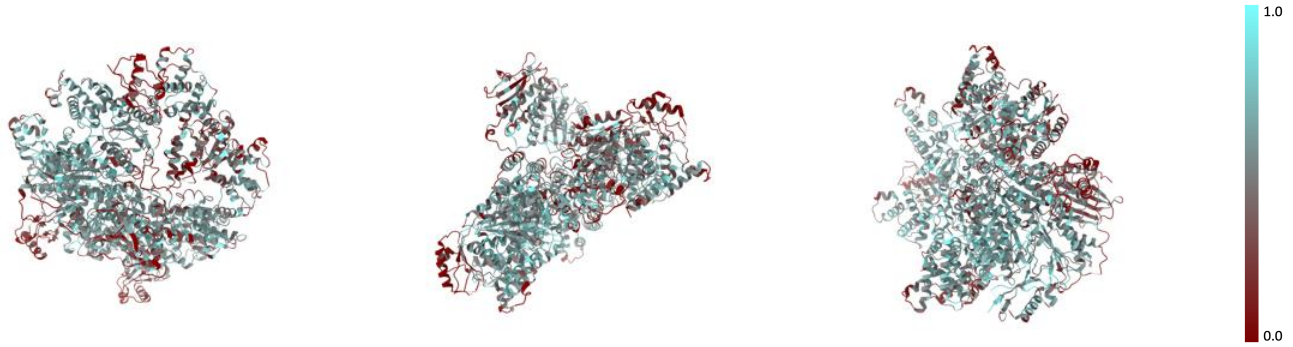
9.2 Q-score mapped to coordinate model (i)



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.

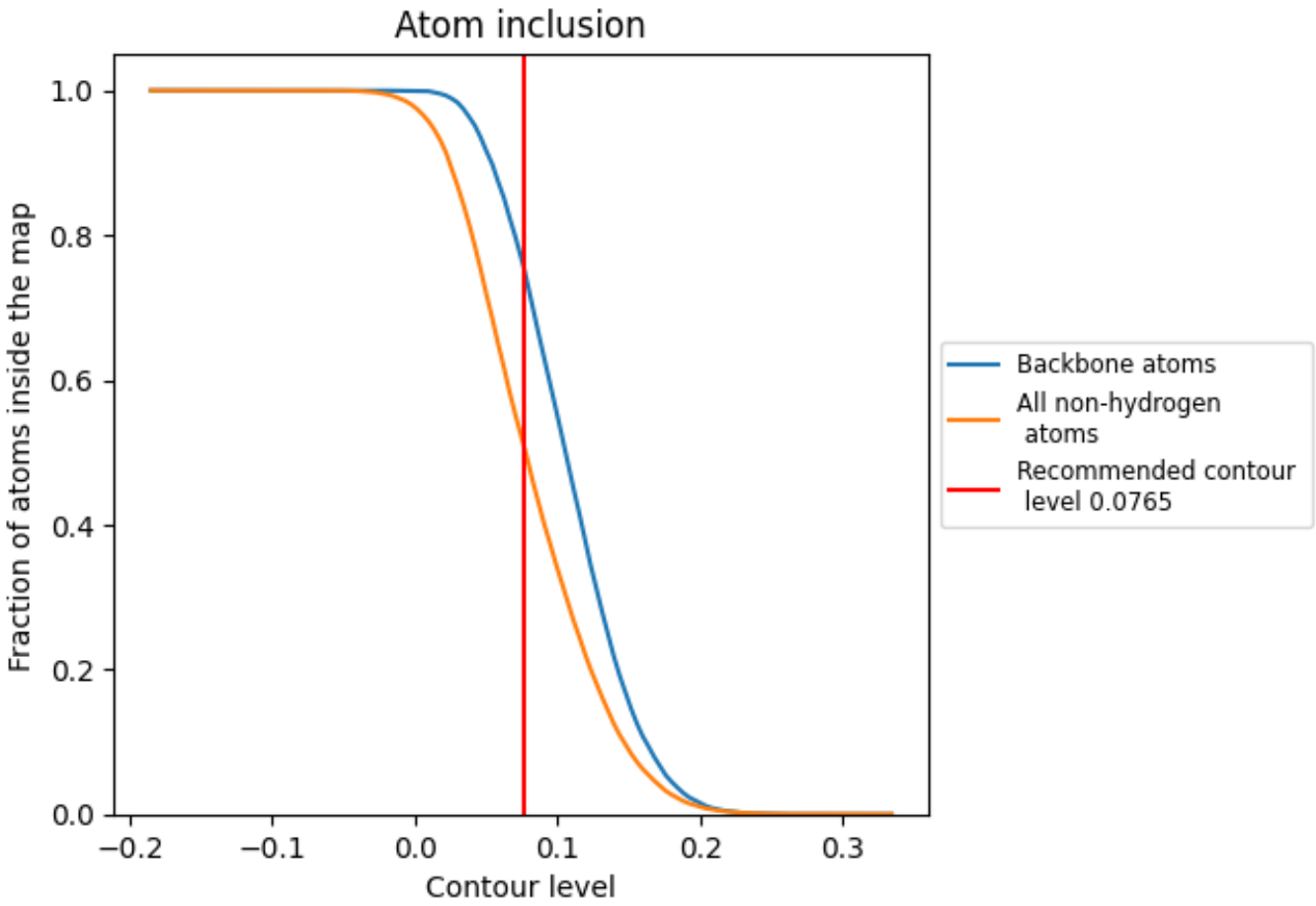
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.0765).

9.4 Atom inclusion (i)



At the recommended contour level, 76% of all backbone atoms, 51% 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 (0.0765) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5094	0.3060
A	0.5439	0.2900
B	0.5312	0.3260
C	0.5301	0.3280
D	0.6174	0.3420
E	0.4473	0.2980
F	0.3938	0.2460
P	0.5524	0.3090
Q	0.2941	0.3500
Z	0.4147	0.2650