wwPDB EM Validation Summary Report (i)

Aug 27, 2026 – 12:22 am BST

PDB ID	:	8R1A / pdb_00008r1a
EMDB ID	:	EMD-18806
Title	:	Model of the membrane-bound GBP1 oligomer
Authors	:	Weismehl, M.; Chu, X.; Kutsch, M.; Lauterjung, P.; Herrmann, C.; Kudryashev, M.; Daumke, O.
Deposited on	:	2023-11-01
Resolution	:	26.80 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:

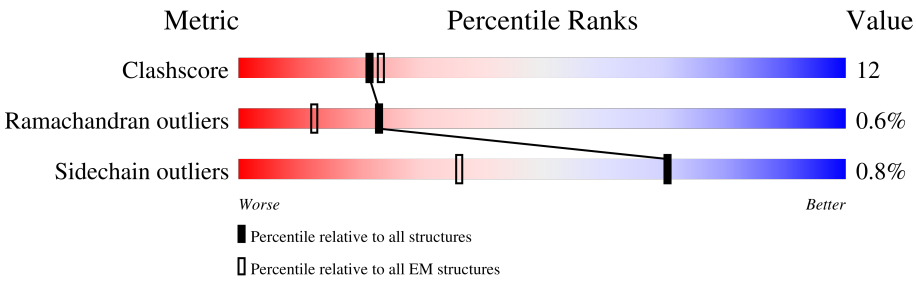
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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)	:	2.50

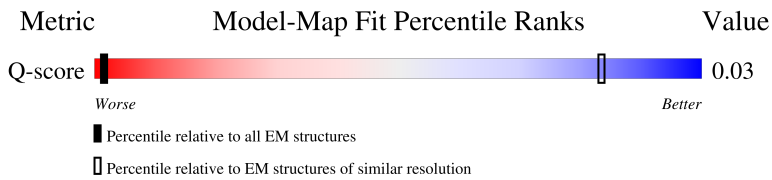
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 26.80 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	6 (26.50 - 27.20)

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	603	25% 85% 11% • •
1	B	603	28% 86% 10% • •
1	C	603	32% 85% 11% • •
1	D	603	47% 86% 10% • •

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Mol	Chain	Length	Quality of chain
1	E	603	48% 85% 11%
1	F	603	30% 86% 10%

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
4	GDP	A	602	-	-	X	-
4	GDP	B	602	-	-	X	-
4	GDP	C	602	-	-	X	-
4	GDP	D	602	-	-	X	-
4	GDP	E	602	-	-	X	-
4	GDP	F	602	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 28566 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 Guanylate binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	587	4728	2978	812	912	26	0	0
1	B	587	4728	2978	812	912	26	0	0
1	C	587	4728	2978	812	912	26	0	0
1	D	587	4728	2978	812	912	26	0	0
1	E	587	4728	2978	812	912	26	0	0
1	F	587	4728	2978	812	912	26	0	0

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	initiating methionine	UNP Q5D1D5
A	-9	ARG	-	expression tag	UNP Q5D1D5
A	-8	GLY	-	expression tag	UNP Q5D1D5
A	-7	SER	-	expression tag	UNP Q5D1D5
A	-6	HIS	-	expression tag	UNP Q5D1D5
A	-5	HIS	-	expression tag	UNP Q5D1D5
A	-4	HIS	-	expression tag	UNP Q5D1D5
A	-3	HIS	-	expression tag	UNP Q5D1D5
A	-2	HIS	-	expression tag	UNP Q5D1D5
A	-1	HIS	-	expression tag	UNP Q5D1D5
A	0	GLY	-	expression tag	UNP Q5D1D5
A	1	SER	-	expression tag	UNP Q5D1D5
A	409	GLY	ALA	variant	UNP Q5D1D5
B	-10	MET	-	initiating methionine	UNP Q5D1D5
B	-9	ARG	-	expression tag	UNP Q5D1D5
B	-8	GLY	-	expression tag	UNP Q5D1D5
B	-7	SER	-	expression tag	UNP Q5D1D5
B	-6	HIS	-	expression tag	UNP Q5D1D5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	HIS	-	expression tag	UNP Q5D1D5
B	-4	HIS	-	expression tag	UNP Q5D1D5
B	-3	HIS	-	expression tag	UNP Q5D1D5
B	-2	HIS	-	expression tag	UNP Q5D1D5
B	-1	HIS	-	expression tag	UNP Q5D1D5
B	0	GLY	-	expression tag	UNP Q5D1D5
B	1	SER	-	expression tag	UNP Q5D1D5
B	409	GLY	ALA	variant	UNP Q5D1D5
C	-10	MET	-	initiating methionine	UNP Q5D1D5
C	-9	ARG	-	expression tag	UNP Q5D1D5
C	-8	GLY	-	expression tag	UNP Q5D1D5
C	-7	SER	-	expression tag	UNP Q5D1D5
C	-6	HIS	-	expression tag	UNP Q5D1D5
C	-5	HIS	-	expression tag	UNP Q5D1D5
C	-4	HIS	-	expression tag	UNP Q5D1D5
C	-3	HIS	-	expression tag	UNP Q5D1D5
C	-2	HIS	-	expression tag	UNP Q5D1D5
C	-1	HIS	-	expression tag	UNP Q5D1D5
C	0	GLY	-	expression tag	UNP Q5D1D5
C	1	SER	-	expression tag	UNP Q5D1D5
C	409	GLY	ALA	variant	UNP Q5D1D5
D	-10	MET	-	initiating methionine	UNP Q5D1D5
D	-9	ARG	-	expression tag	UNP Q5D1D5
D	-8	GLY	-	expression tag	UNP Q5D1D5
D	-7	SER	-	expression tag	UNP Q5D1D5
D	-6	HIS	-	expression tag	UNP Q5D1D5
D	-5	HIS	-	expression tag	UNP Q5D1D5
D	-4	HIS	-	expression tag	UNP Q5D1D5
D	-3	HIS	-	expression tag	UNP Q5D1D5
D	-2	HIS	-	expression tag	UNP Q5D1D5
D	-1	HIS	-	expression tag	UNP Q5D1D5
D	0	GLY	-	expression tag	UNP Q5D1D5
D	1	SER	-	expression tag	UNP Q5D1D5
D	409	GLY	ALA	variant	UNP Q5D1D5
E	-10	MET	-	initiating methionine	UNP Q5D1D5
E	-9	ARG	-	expression tag	UNP Q5D1D5
E	-8	GLY	-	expression tag	UNP Q5D1D5
E	-7	SER	-	expression tag	UNP Q5D1D5
E	-6	HIS	-	expression tag	UNP Q5D1D5
E	-5	HIS	-	expression tag	UNP Q5D1D5
E	-4	HIS	-	expression tag	UNP Q5D1D5
E	-3	HIS	-	expression tag	UNP Q5D1D5

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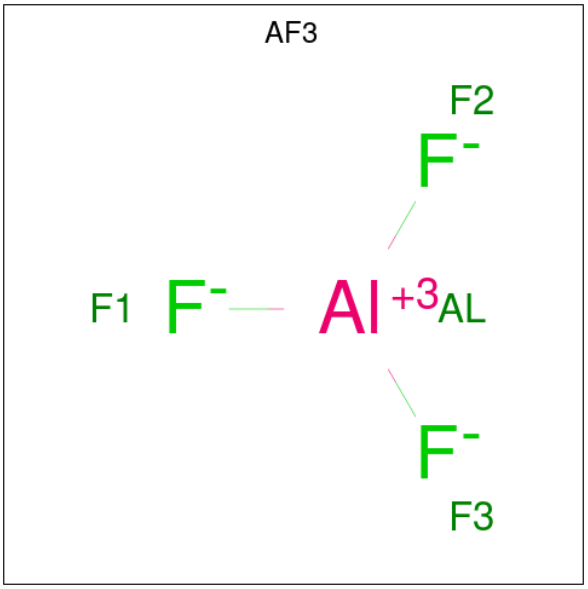
Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	HIS	-	expression tag	UNP Q5D1D5
E	-1	HIS	-	expression tag	UNP Q5D1D5
E	0	GLY	-	expression tag	UNP Q5D1D5
E	1	SER	-	expression tag	UNP Q5D1D5
E	409	GLY	ALA	variant	UNP Q5D1D5
F	-10	MET	-	initiating methionine	UNP Q5D1D5
F	-9	ARG	-	expression tag	UNP Q5D1D5
F	-8	GLY	-	expression tag	UNP Q5D1D5
F	-7	SER	-	expression tag	UNP Q5D1D5
F	-6	HIS	-	expression tag	UNP Q5D1D5
F	-5	HIS	-	expression tag	UNP Q5D1D5
F	-4	HIS	-	expression tag	UNP Q5D1D5
F	-3	HIS	-	expression tag	UNP Q5D1D5
F	-2	HIS	-	expression tag	UNP Q5D1D5
F	-1	HIS	-	expression tag	UNP Q5D1D5
F	0	GLY	-	expression tag	UNP Q5D1D5
F	1	SER	-	expression tag	UNP Q5D1D5
F	409	GLY	ALA	variant	UNP Q5D1D5

- Molecule 2 is ALUMINUM FLUORIDE (CCD ID: AF3) (formula: AlF_3).



Mol	Chain	Residues	Atoms			AltConf
			Total	Al	F	
2	A	1	4	1	3	0
2	B	1	4	1	3	0

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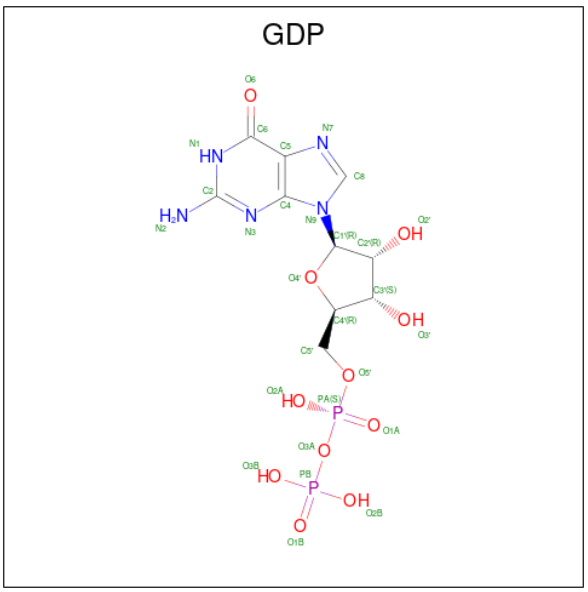
Mol	Chain	Residues	Atoms			AltConf
2	C	1	Total 4	Al 1	F 3	0
2	D	1	Total 4	Al 1	F 3	0
2	E	1	Total 4	Al 1	F 3	0
2	F	1	Total 4	Al 1	F 3	0

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total 1	Mg 1	0
3	B	1	Total 1	Mg 1	0
3	C	1	Total 1	Mg 1	0
3	D	1	Total 1	Mg 1	0
3	E	1	Total 1	Mg 1	0
3	F	1	Total 1	Mg 1	0

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



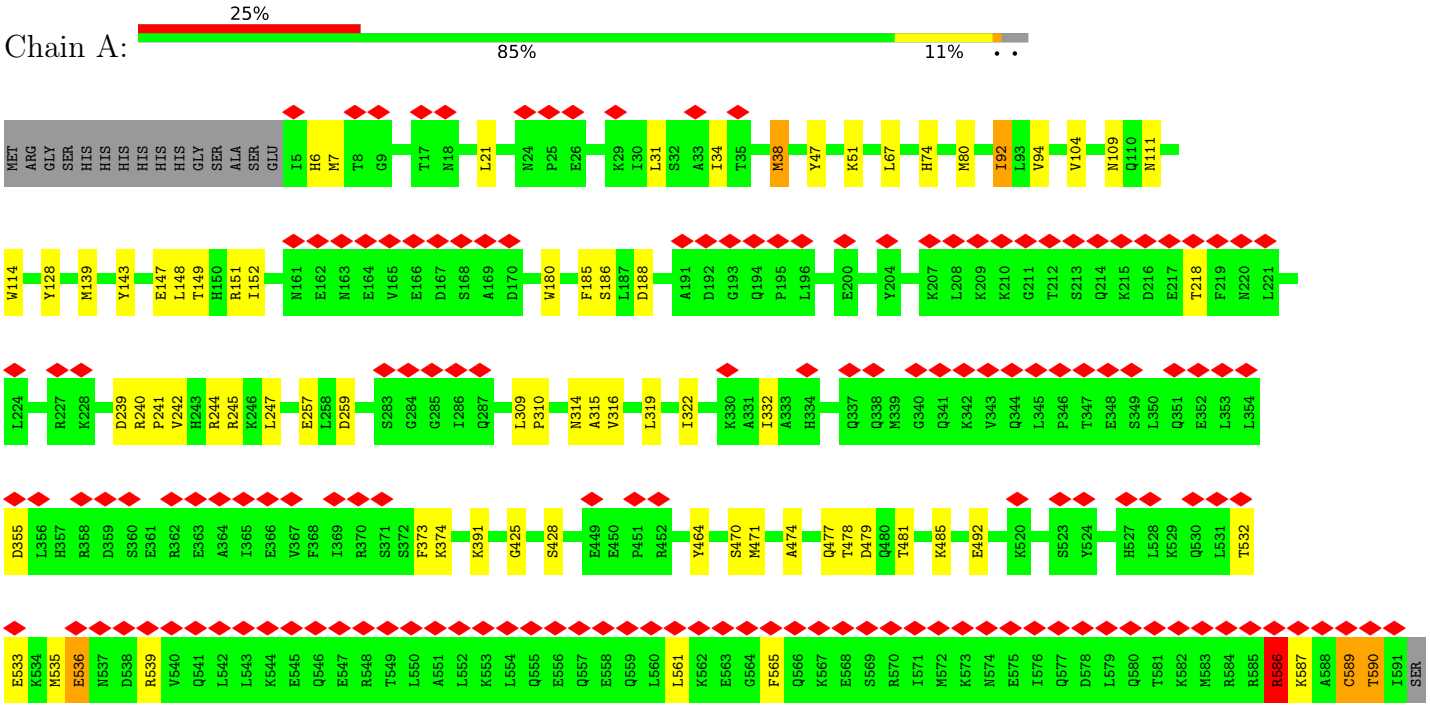
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
4	A	1	28	10	5	11	2	0
4	B	1	28	10	5	11	2	0
4	C	1	28	10	5	11	2	0
4	D	1	28	10	5	11	2	0
4	E	1	28	10	5	11	2	0
4	F	1	28	10	5	11	2	0

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.

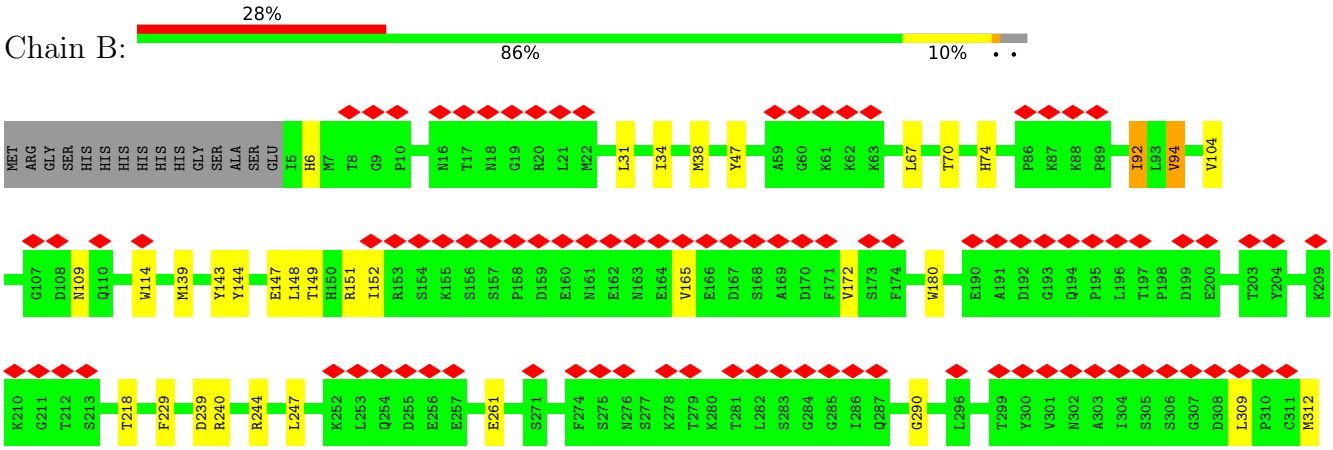
- Molecule 1: Guanylate binding protein 1

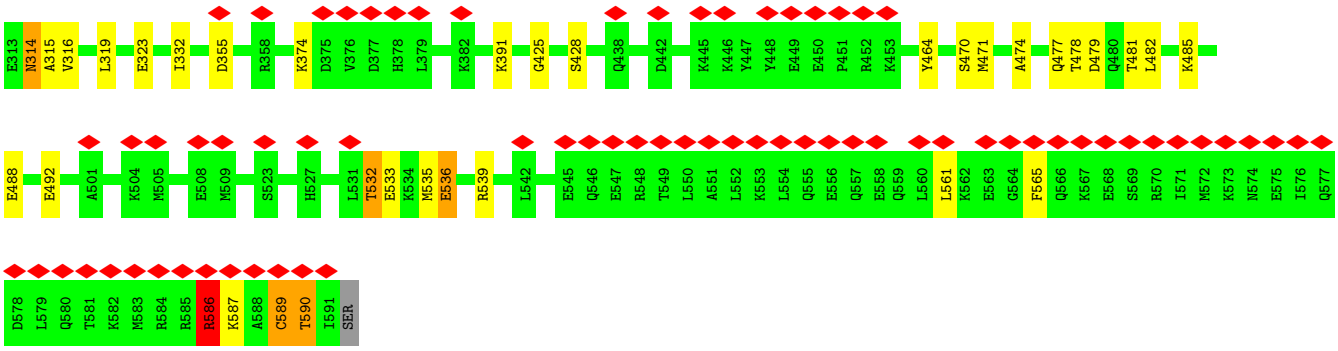
Chain A:



- Molecule 1: Guanylate binding protein 1

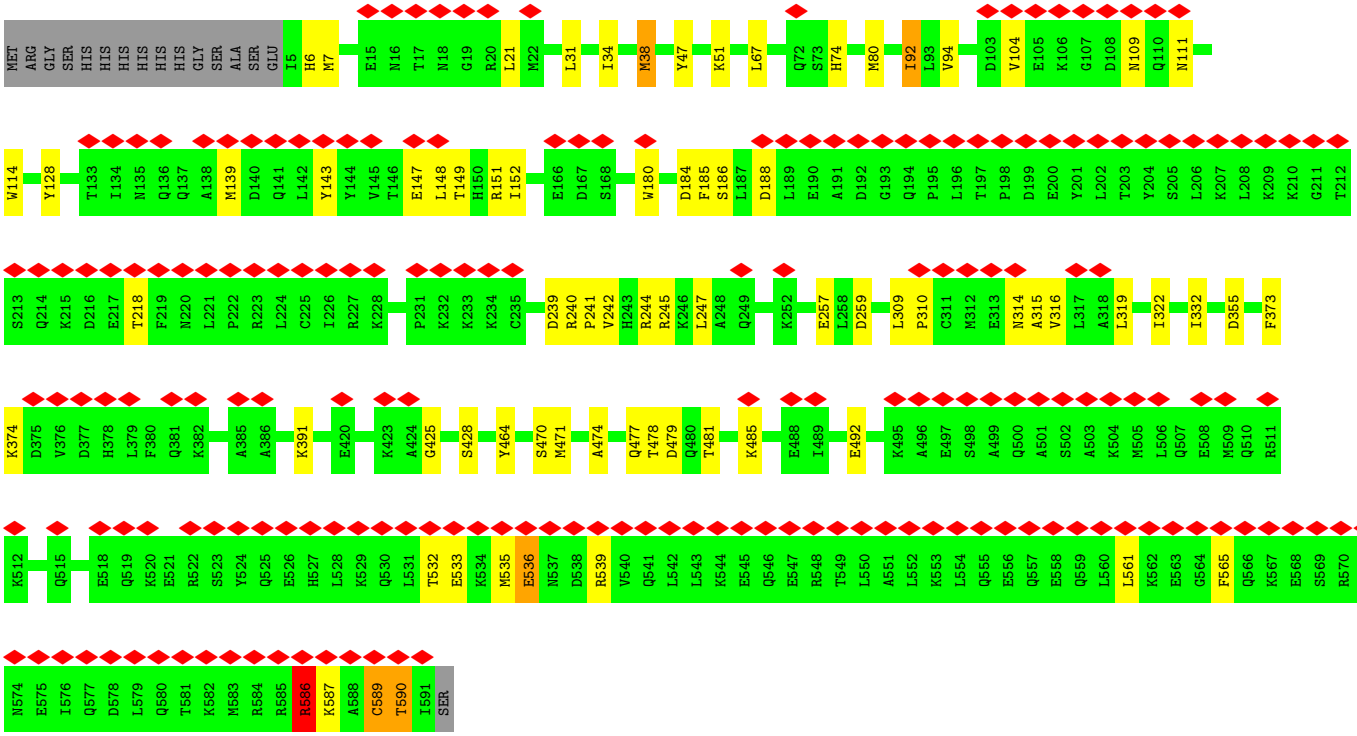
Chain B:





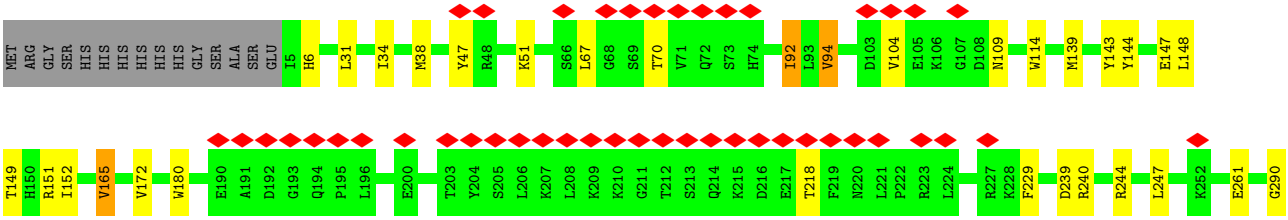
- Molecule 1: Guanylate binding protein 1

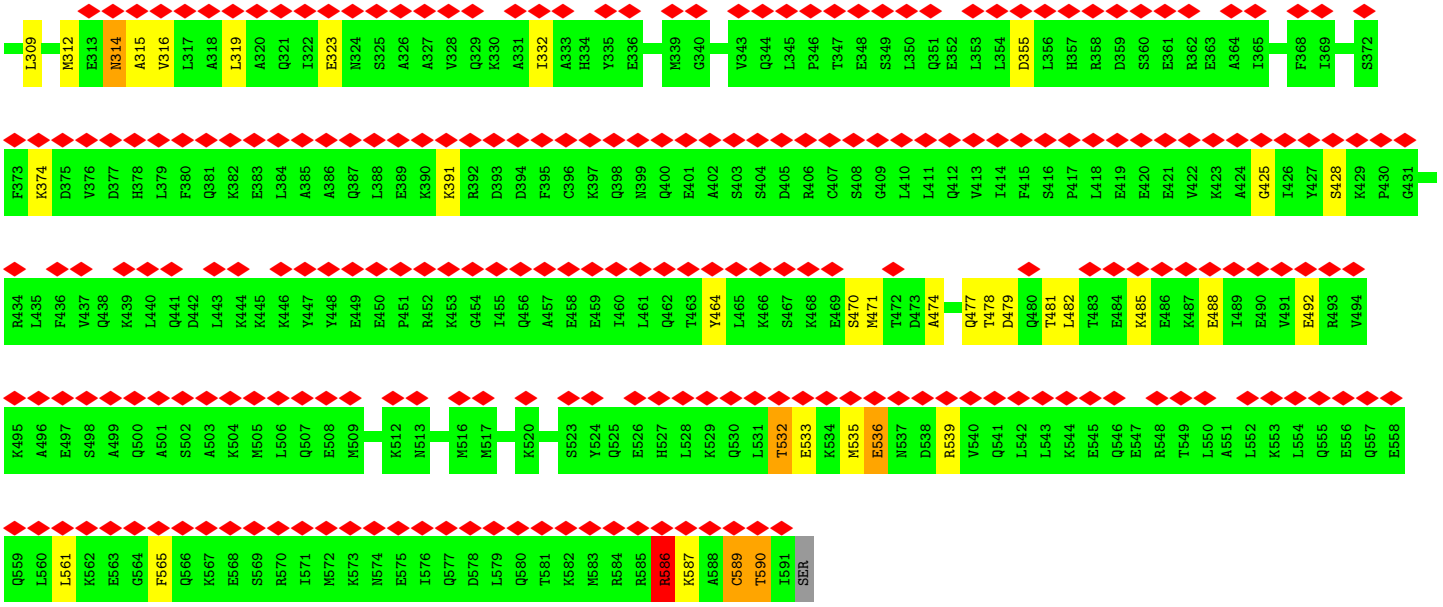
Chain C:



- Molecule 1: Guanylate binding protein 1

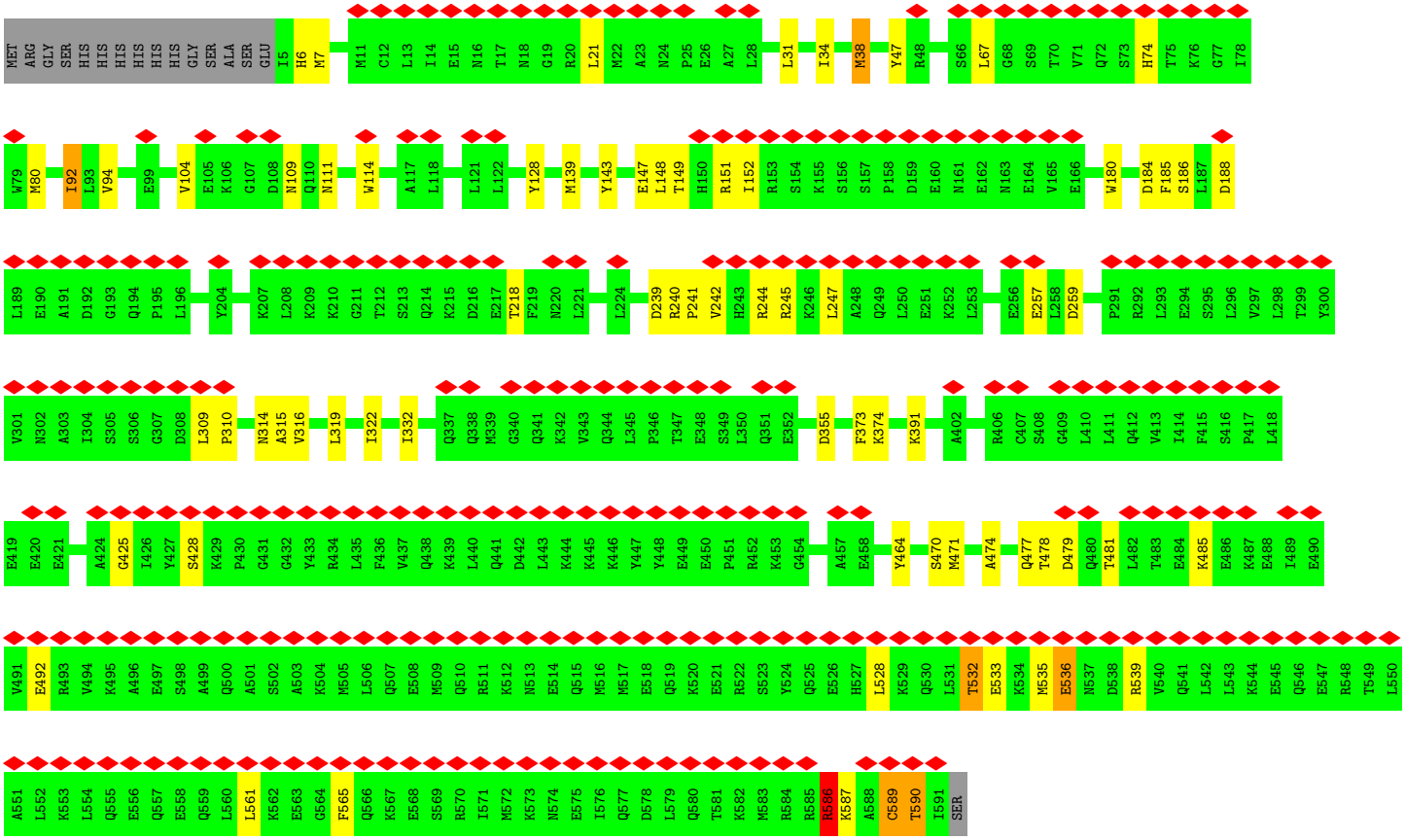
Chain D:





- Molecule 1: Guanylate binding protein 1

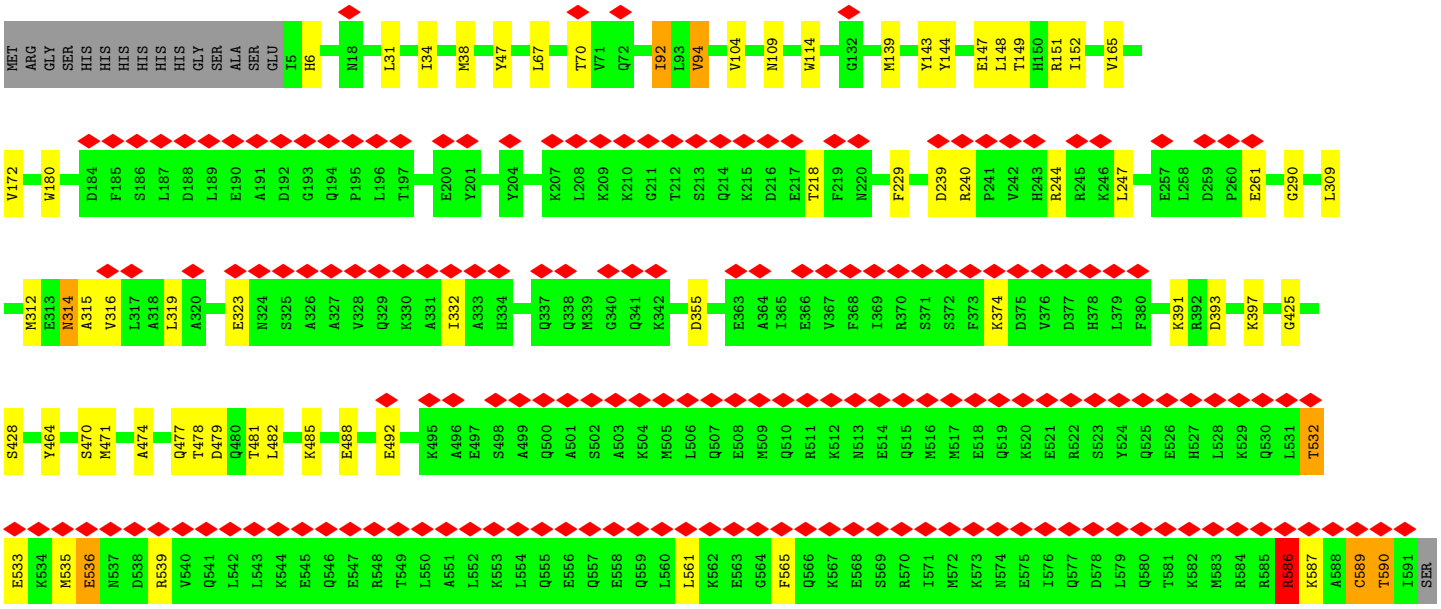
Chain E:



- Molecule 1: Guanylate binding protein 1

Chain F:

30%
86%
10%


MET ARG GLY SER HIS HIS HIS HIS HIS HIS GLY SER ALA SER GLU I5 H6 N18 L31 I34 M38 Y47 L67 T70 V71 Q72 I92 L93 V94 V104 N109 W114 G132 M139 Y143 Y144 E147 L148 T149 H150 R151 I152 V165
V172 W180 D184 F185 S186 L187 D188 L189 E190 A191 D192 G193 Q194 P195 L196 T197 E200 Y201 Y204 K207 L208 K209 K210 G211 T212 S213 Q214 K215 D216 E217 T218 F219 N220 F229 D239 R240 P241 V242 H243 R244 R245 K246 L247 E257 L258 D259 P260 E261 G290 L309
M312 E313 N314 A315 V316 L317 A318 L319 A320 E323 N324 S325 A326 A327 V328 Q329 K330 A331 I332 A333 H334 Q337 Q338 M339 G340 Q341 K342 D355 E363 A364 I365 E366 V367 F368 I369 R370 S371 S372 F373 K374 D375 V376 D377 H378 L379 F380 K391 R392 D393 K397 G425
S428 Y464 S470 M471 A474 Q477 T478 D479 Q480 T481 L482 K485 E488 E492 K495 A496 E497 S498 A499 Q500 A501 S502 A503 K504 M505 L506 Q507 E508 M509 Q510 R511 K512 N513 E514 Q515 M516 M517 E518 Q519 K520 E521 R522 S523 Y524 Q525 E526 H527 L528 K529 Q530 L531 T532
E533 K534 M535 E536 N537 D538 R539 V540 Q541 L542 L543 K544 E545 Q546 E547 R548 T549 L550 A551 L552 K553 L554 Q555 E556 Q557 E558 Q559 L560 L561 K562 E563 G564 F565 Q566 K567 E568 S569 R570 I571 M572 K573 N574 E575 I576 Q577 D578 L579 Q580 T581 K582 M583 R584 R585 R586 K587 A588 C589 T590 I591 SER

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	6146	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	130	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	42000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.933	Depositor
Minimum map value	-3.356	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.321	Depositor
Recommended contour level	0.75	Depositor
Map size (Å)	563.2, 563.2, 563.2	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	4.4, 4.4, 4.4	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: MG, AF3, GDP

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	0.89	1/4804 (0.0%)	1.52	15/6459 (0.2%)
1	B	0.89	1/4804 (0.0%)	1.44	15/6459 (0.2%)
1	C	0.89	1/4804 (0.0%)	1.52	15/6459 (0.2%)
1	D	0.89	1/4804 (0.0%)	1.44	14/6459 (0.2%)
1	E	0.89	1/4804 (0.0%)	1.52	15/6459 (0.2%)
1	F	0.89	1/4804 (0.0%)	1.44	14/6459 (0.2%)
All	All	0.89	6/28824 (0.0%)	1.48	88/38754 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	4
1	C	0	5
1	D	0	4
1	E	0	5
1	F	0	4
All	All	0	27

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	532	THR	C-O	-6.96	1.15	1.24
1	D	532	THR	C-O	-6.94	1.15	1.24
1	B	532	THR	C-O	-6.86	1.15	1.24
1	C	92	ILE	CA-C	-6.05	1.45	1.52
1	A	92	ILE	CA-C	-6.03	1.45	1.52

The worst 5 of 88 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	532	THR	CB-CA-C	-11.32	91.72	110.29
1	F	532	THR	CB-CA-C	-11.32	91.73	110.29
1	D	532	THR	CB-CA-C	-11.31	91.75	110.29
1	E	532	THR	N-CA-C	10.24	124.92	109.25
1	C	532	THR	CB-CA-C	-10.23	93.51	110.29

There are no chirality outliers.

5 of 27 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	128	TYR	Sidechain
1	A	464	TYR	Sidechain
1	A	586	ARG	Peptide
1	A	589	CYS	Peptide
1	A	590	THR	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	4728	0	4762	190	0
1	B	4728	0	4759	196	0
1	C	4728	0	4762	186	0
1	D	4728	0	4759	192	0
1	E	4728	0	4762	192	0
1	F	4728	0	4759	196	0
2	A	4	0	0	1	0
2	B	4	0	0	0	0
2	C	4	0	0	1	0
2	D	4	0	0	1	0
2	E	4	0	0	0	0
2	F	4	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	28	0	12	10	0
4	B	28	0	12	15	0
4	C	28	0	12	11	0
4	D	28	0	12	14	0
4	E	28	0	12	11	0
4	F	28	0	12	15	0
All	All	28566	0	28635	669	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 12.

The worst 5 of 669 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:474:ALA:CB	1:B:474:ALA:HB1	1.37	1.54
1:C:474:ALA:CB	1:D:474:ALA:HB1	1.37	1.53
1:E:474:ALA:CB	1:F:474:ALA:HB1	1.37	1.50
1:E:143:TYR:OH	1:F:316:VAL:CG2	1.76	1.34
1:E:474:ALA:CB	1:F:474:ALA:CB	2.06	1.34

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	585/603 (97%)	568 (97%)	14 (2%)	3 (0%)	24 63
1	B	585/603 (97%)	566 (97%)	15 (3%)	4 (1%)	18 56
1	C	585/603 (97%)	568 (97%)	14 (2%)	3 (0%)	24 63

Continued on next page...

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	585/603 (97%)	566 (97%)	15 (3%)	4 (1%)	18	56
1	E	585/603 (97%)	568 (97%)	14 (2%)	3 (0%)	24	63
1	F	585/603 (97%)	566 (97%)	15 (3%)	4 (1%)	18	56
All	All	3510/3618 (97%)	3402 (97%)	87 (2%)	21 (1%)	23	59

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	314	ASN
1	D	314	ASN
1	F	314	ASN
1	A	587	LYS
1	B	587	LYS

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	528/541 (98%)	524 (99%)	4 (1%)	73	80
1	B	528/541 (98%)	524 (99%)	4 (1%)	73	80
1	C	528/541 (98%)	524 (99%)	4 (1%)	73	80
1	D	528/541 (98%)	524 (99%)	4 (1%)	73	80
1	E	528/541 (98%)	524 (99%)	4 (1%)	73	80
1	F	528/541 (98%)	524 (99%)	4 (1%)	73	80
All	All	3168/3246 (98%)	3144 (99%)	24 (1%)	70	80

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	565	PHE
1	E	561	LEU
1	E	47	TYR
1	E	565	PHE

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Mol	Chain	Res	Type
1	B	565	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	36	GLN
1	E	500	GLN
1	E	91	HIS
1	E	287	GLN
1	F	109	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)

Of 18 ligands modelled in this entry, 6 are monoatomic - leaving 12 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	GDP	C	602	3,2	28,30,30	1.10	2 (7%)	44,47,47	1.76	7 (15%)
4	GDP	A	602	3,2	28,30,30	1.10	2 (7%)	44,47,47	1.75	7 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	GDP	E	602	3,2	28,30,30	1.10	2 (7%)	44,47,47	1.75	7 (15%)
4	GDP	F	602	3,2	28,30,30	1.13	2 (7%)	44,47,47	1.78	7 (15%)
2	AF3	F	600	4	0,3,3	-	-	-		
4	GDP	B	602	3,2	28,30,30	1.12	2 (7%)	44,47,47	1.78	7 (15%)
2	AF3	D	600	4	0,3,3	-	-	-		
2	AF3	A	600	4	0,3,3	-	-	-		
4	GDP	D	602	3,2	28,30,30	1.13	2 (7%)	44,47,47	1.78	7 (15%)
2	AF3	E	600	4	0,3,3	-	-	-		
2	AF3	B	600	4	0,3,3	-	-	-		
2	AF3	C	600	4	0,3,3	-	-	-		

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
4	GDP	E	602	3,2	-	0/16/32/32	0/3/3/3
4	GDP	C	602	3,2	-	0/16/32/32	0/3/3/3
4	GDP	A	602	3,2	-	0/16/32/32	0/3/3/3
4	GDP	F	602	3,2	-	0/16/32/32	0/3/3/3
4	GDP	B	602	3,2	-	0/16/32/32	0/3/3/3
4	GDP	D	602	3,2	-	0/16/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	602	GDP	C5-C4	3.06	1.47	1.38
4	B	602	GDP	C5-C4	3.05	1.47	1.38
4	F	602	GDP	C5-C4	3.03	1.47	1.38
4	C	602	GDP	C5-C4	2.99	1.47	1.38
4	A	602	GDP	C5-C4	2.97	1.47	1.38

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	602	GDP	C5-C4-N3	-5.60	119.38	128.46
4	D	602	GDP	C5-C4-N3	-5.59	119.39	128.46
4	F	602	GDP	C5-C4-N3	-5.59	119.40	128.46
4	A	602	GDP	C5-C4-N3	-5.53	119.48	128.46
4	C	602	GDP	C5-C4-N3	-5.52	119.51	128.46

There are no chirality outliers.

There are no torsion outliers.

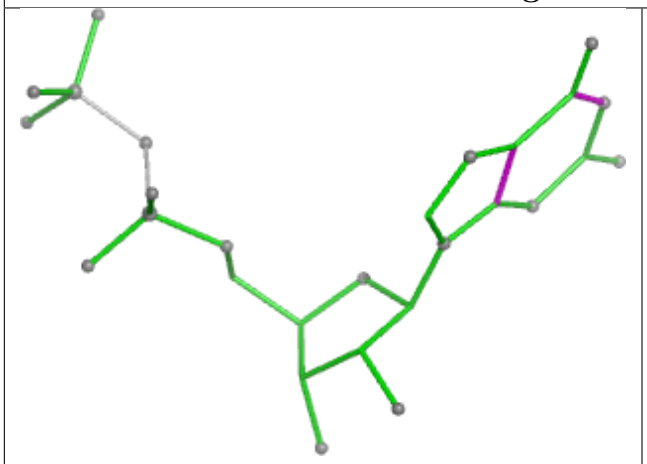
There are no ring outliers.

9 monomers are involved in 79 short contacts:

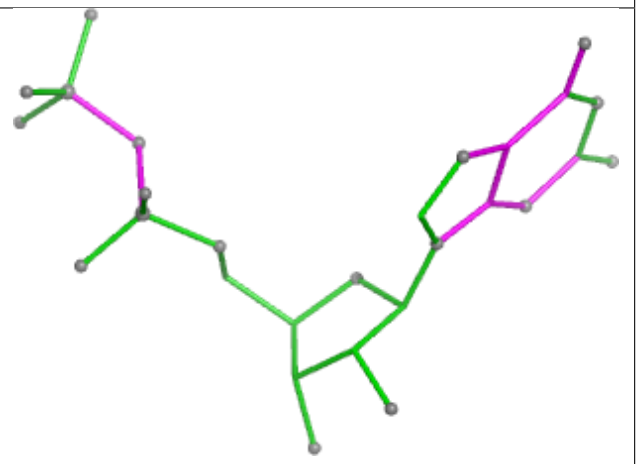
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	602	GDP	11	0
4	A	602	GDP	10	0
4	E	602	GDP	11	0
4	F	602	GDP	15	0
4	B	602	GDP	15	0
2	D	600	AF3	1	0
2	A	600	AF3	1	0
4	D	602	GDP	14	0
2	C	600	AF3	1	0

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.

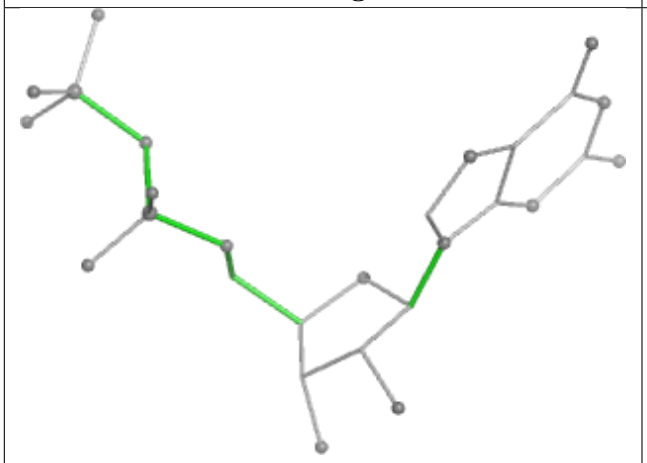
Ligand GDP C 602



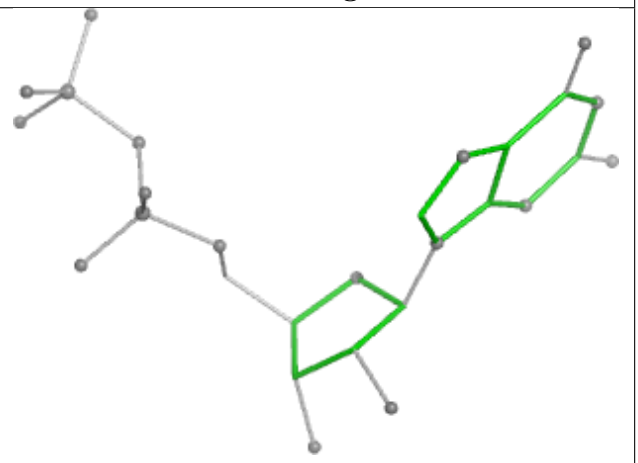
Bond lengths



Bond angles

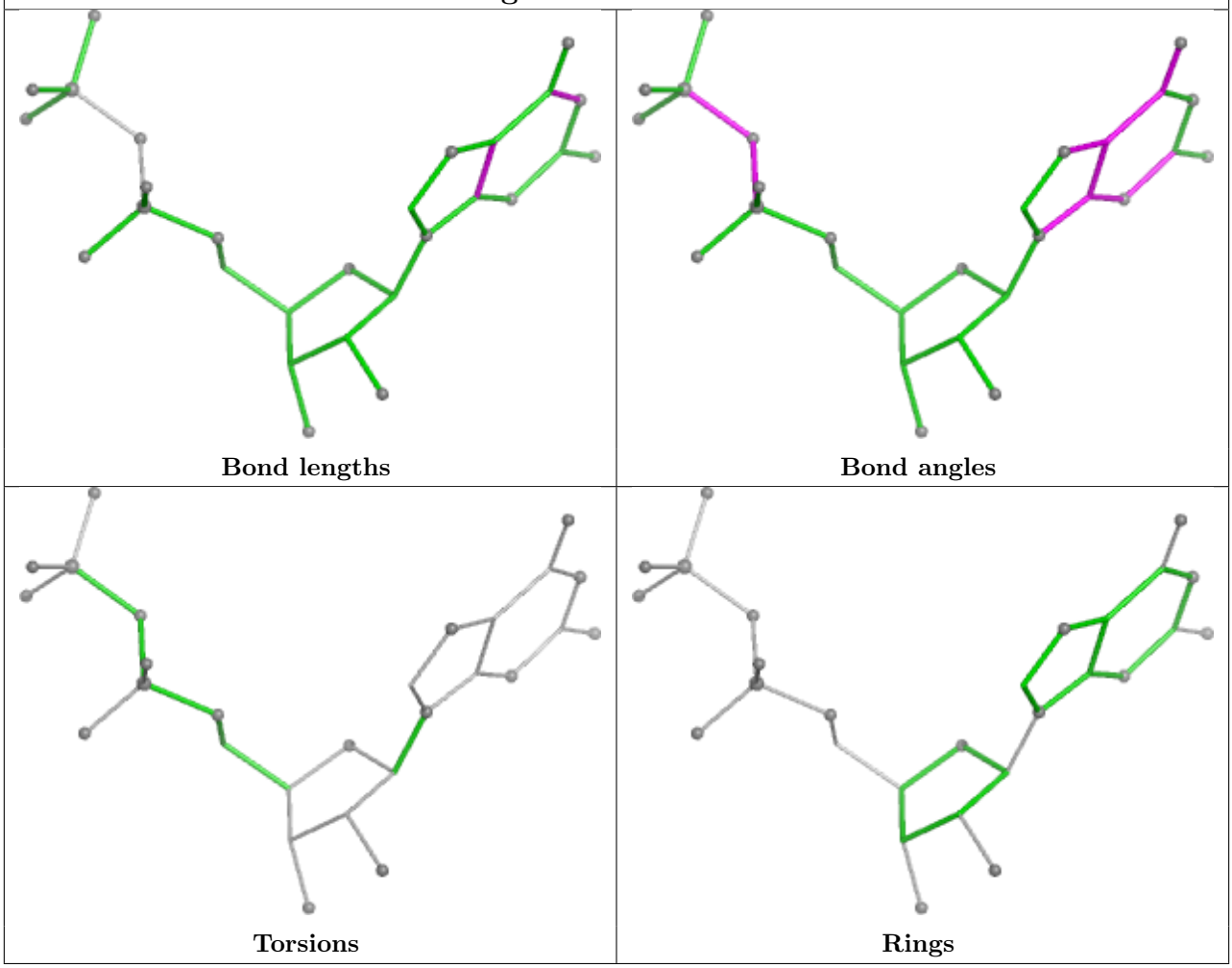


Torsions

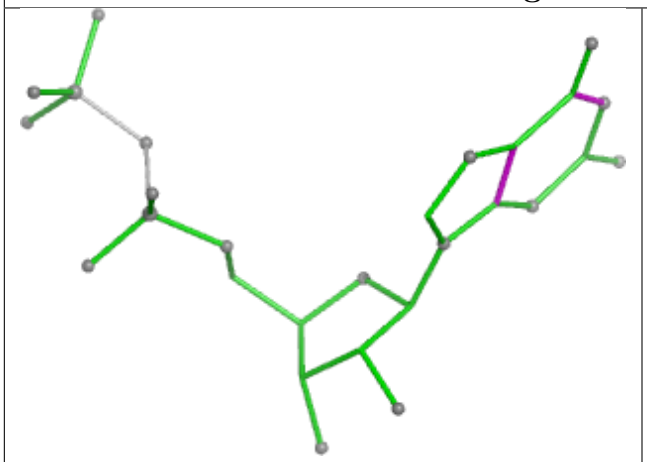


Rings

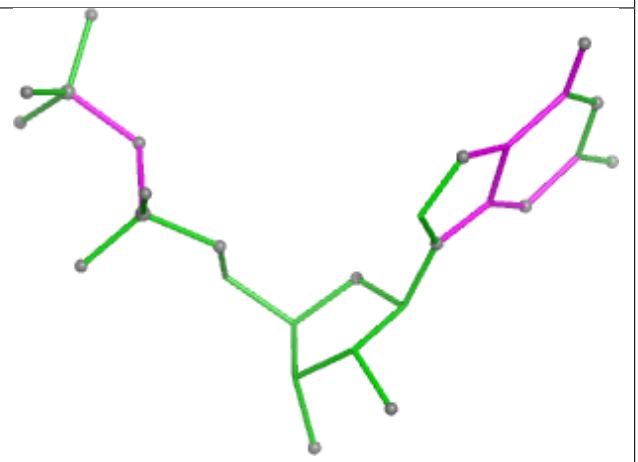
Ligand GDP A 602



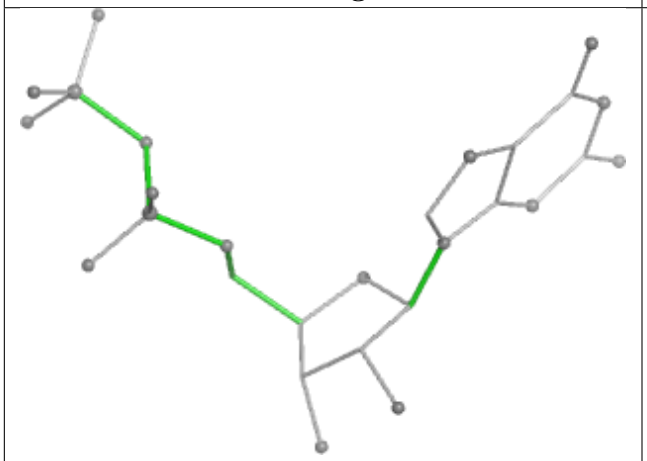
Ligand GDP E 602



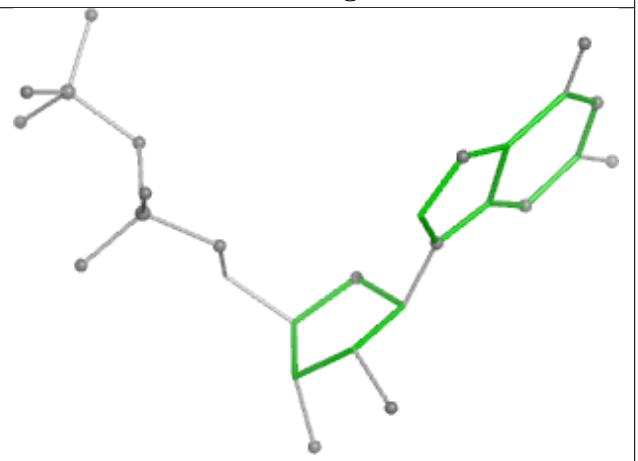
Bond lengths



Bond angles

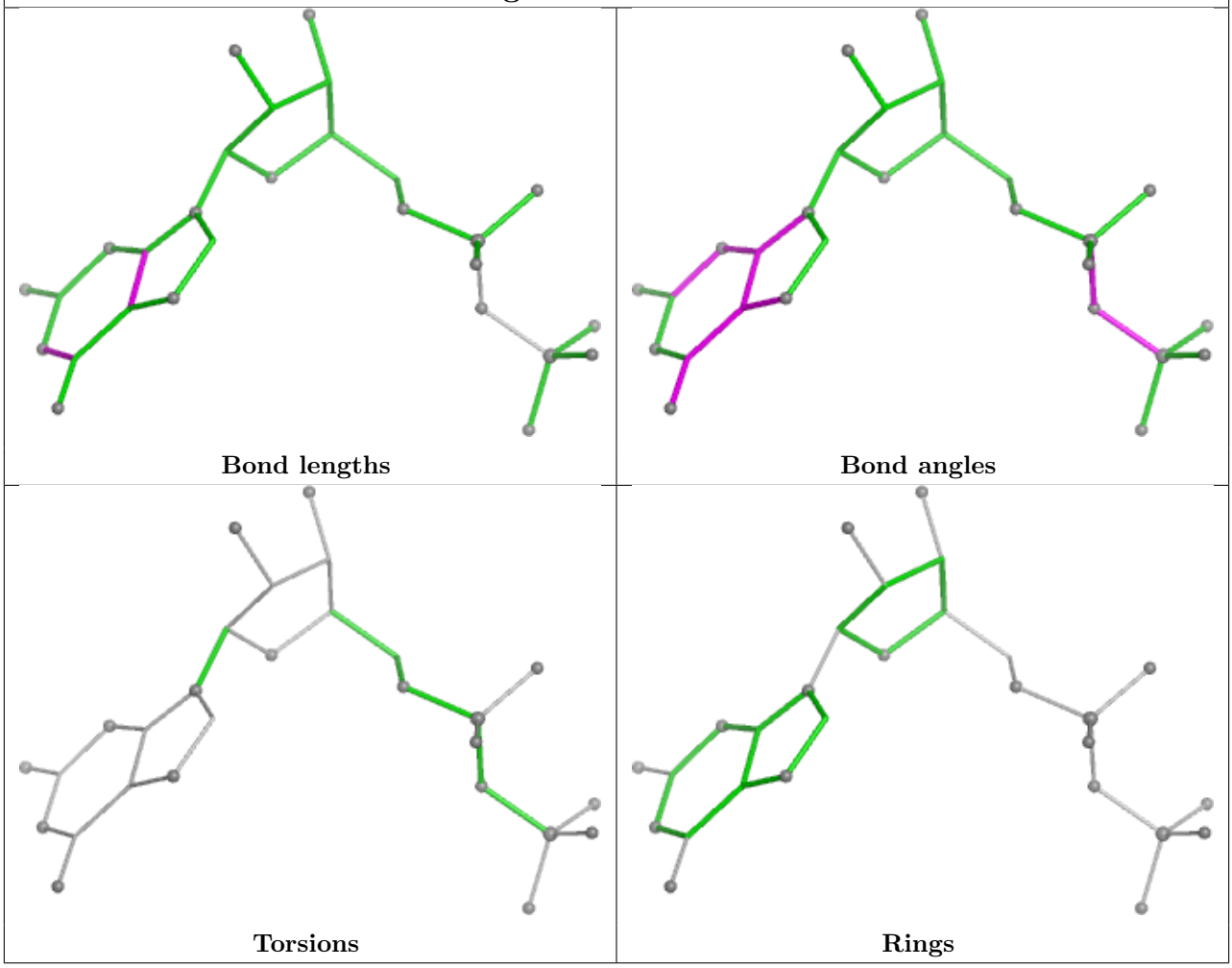


Torsions

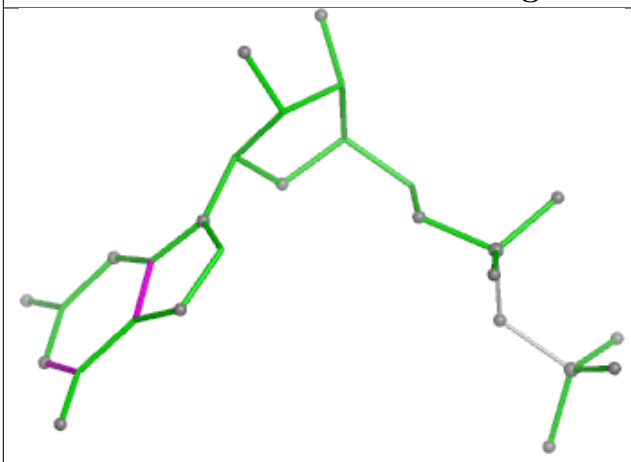


Rings

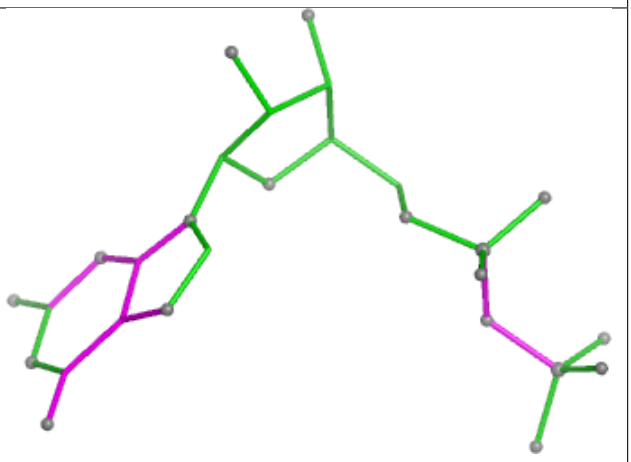
Ligand GDP F 602



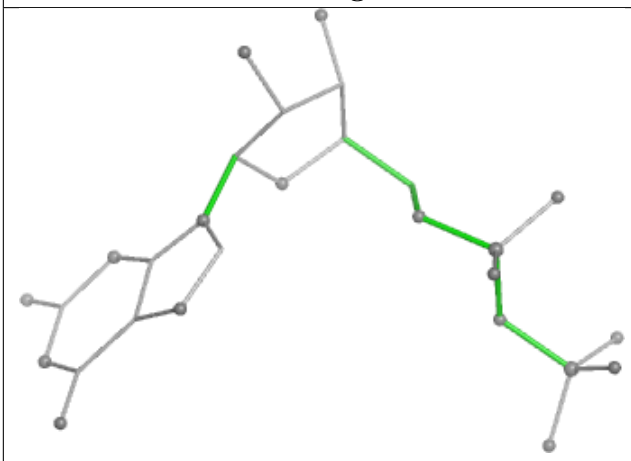
Ligand GDP B 602



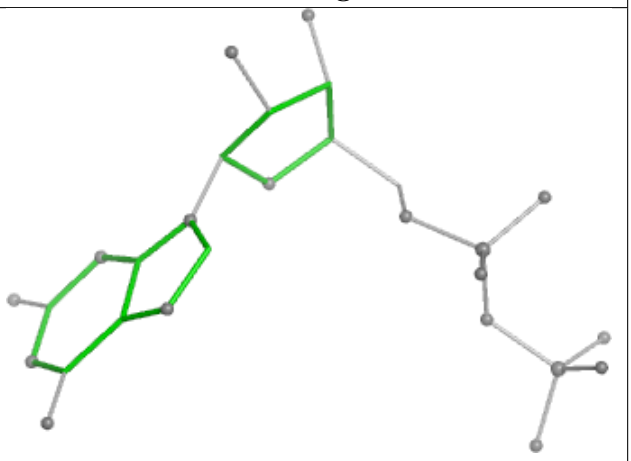
Bond lengths



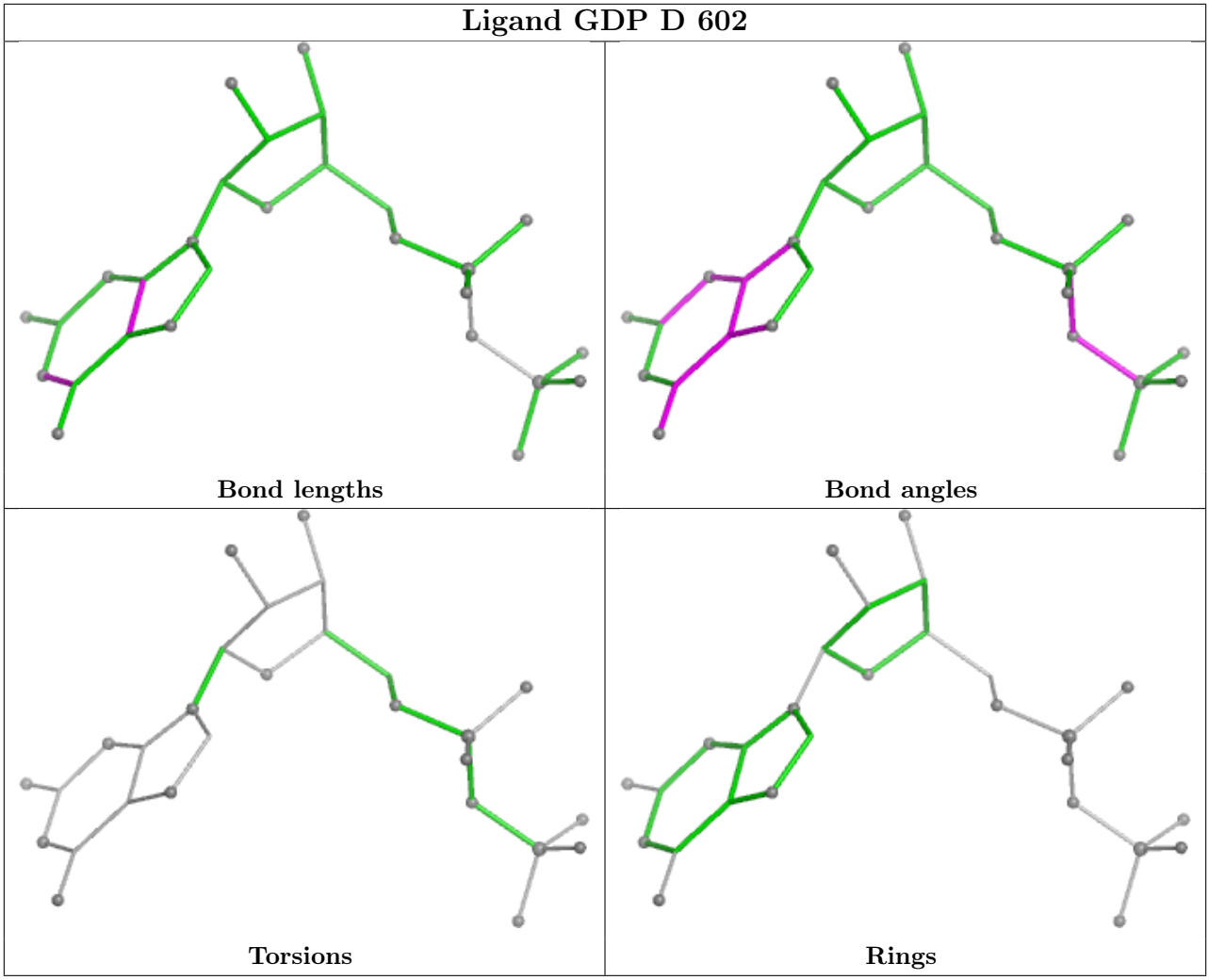
Bond angles



Torsions



Rings



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

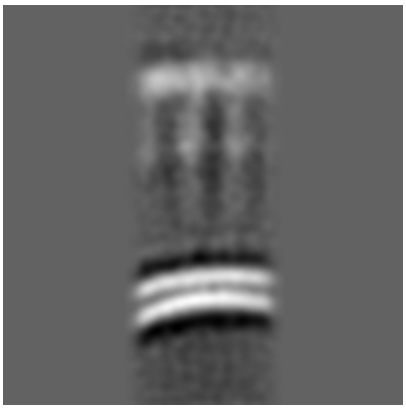
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-18806. These allow visual inspection of the internal detail of the map and identification of artifacts.

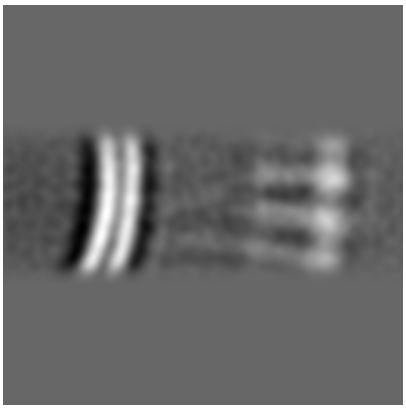
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

6.1.1 Primary map



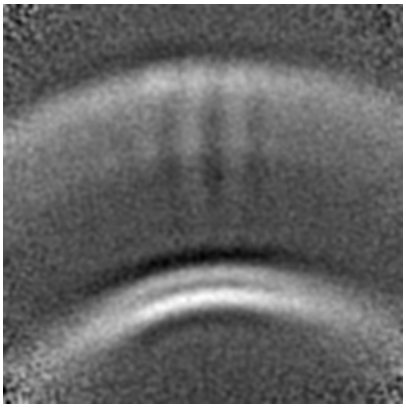
X



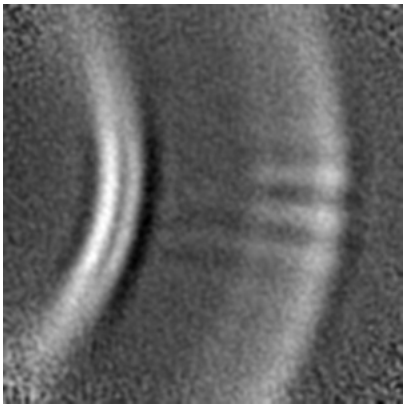
Y

Z

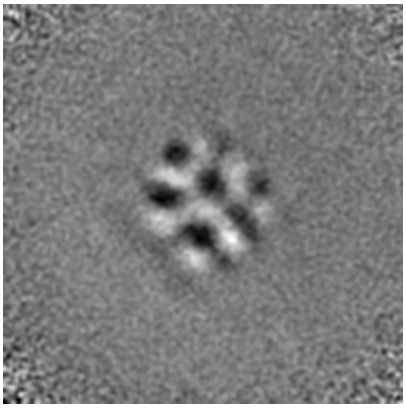
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices (i)

6.2.1 Primary map

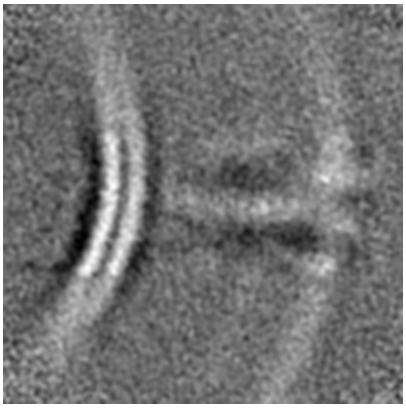
X Index: 64

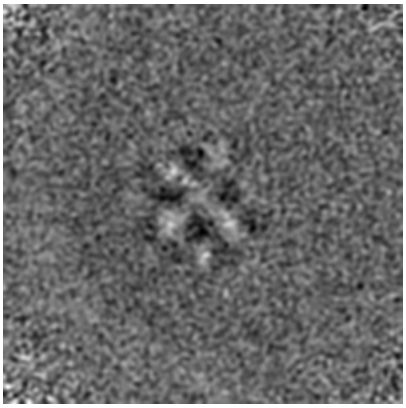
Y Index: 64

Z Index: 64

6.2.2 Raw map

X Index: 64


Y Index: 64

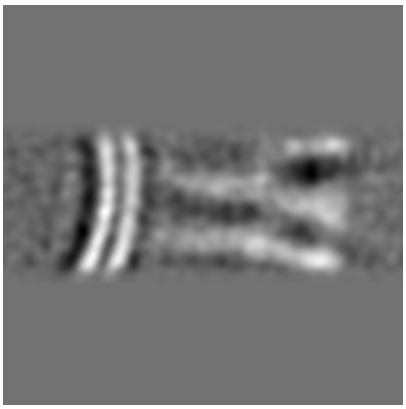

Z Index: 64

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

6.3 Largest variance slices (i)

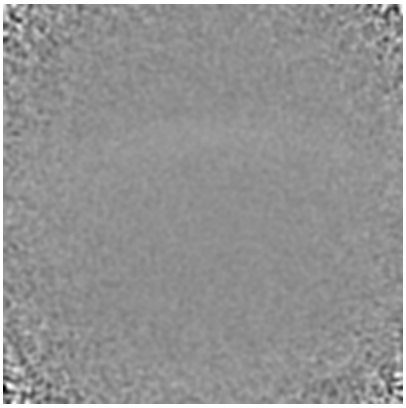
6.3.1 Primary map

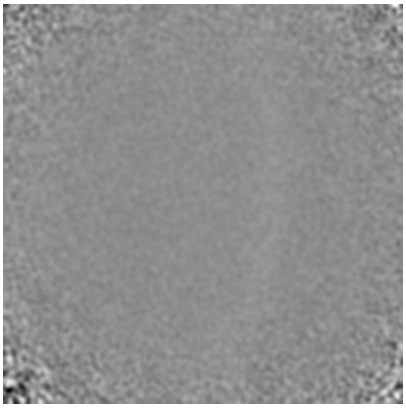
X Index: 72

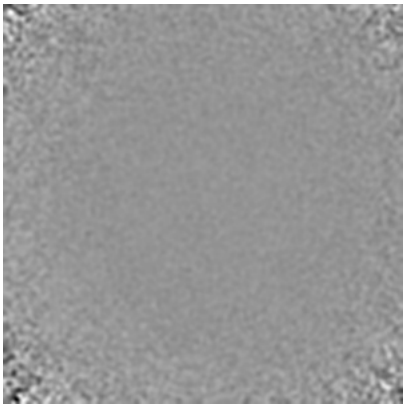

Y Index: 58

Z Index: 28

6.3.2 Raw map


X Index: 1

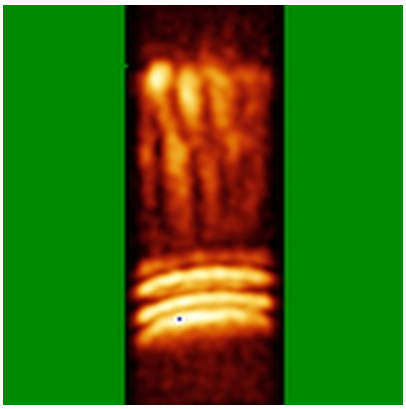

Y Index: 1

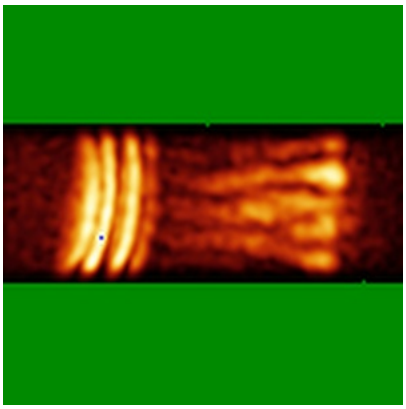

Z Index: 1

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

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

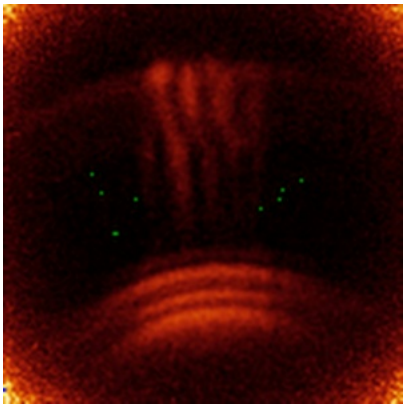
6.4.1 Primary map

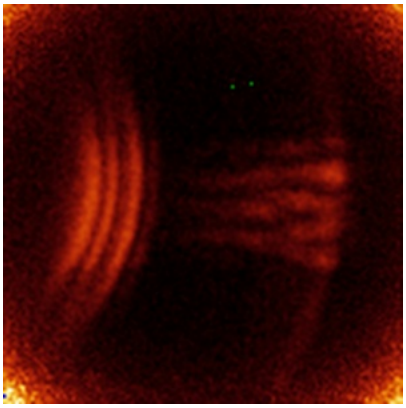

X

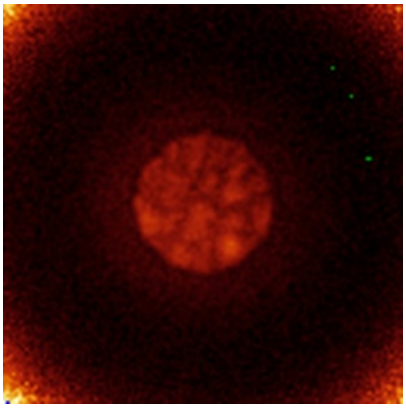

Y

Z

6.4.2 Raw map


X

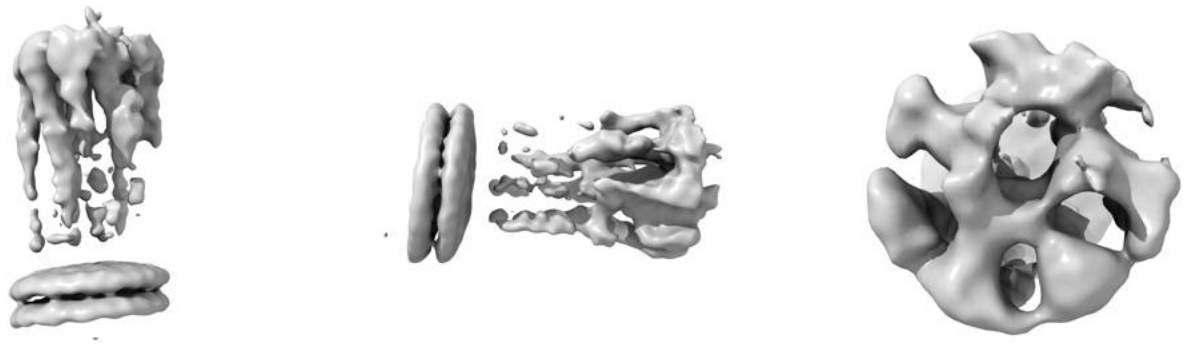

Y


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

6.5.2 Raw map

X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

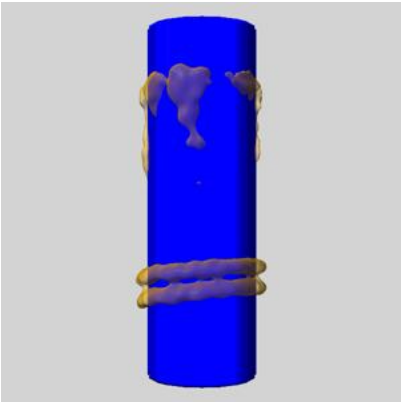
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

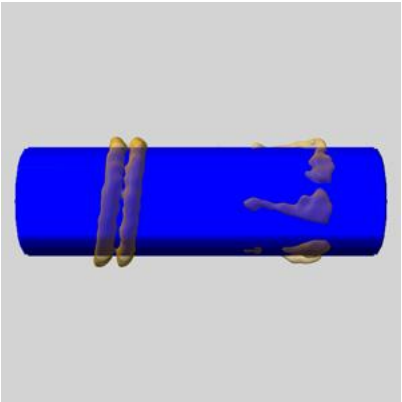
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

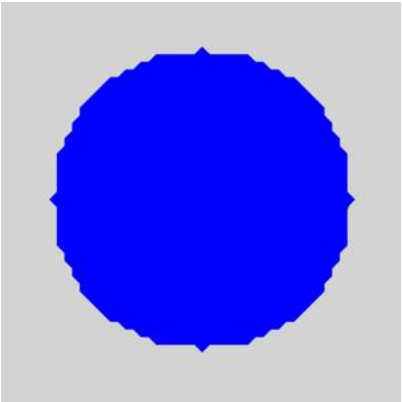
6.6.1 emd_18806_msk_1.map (i)



X



Y

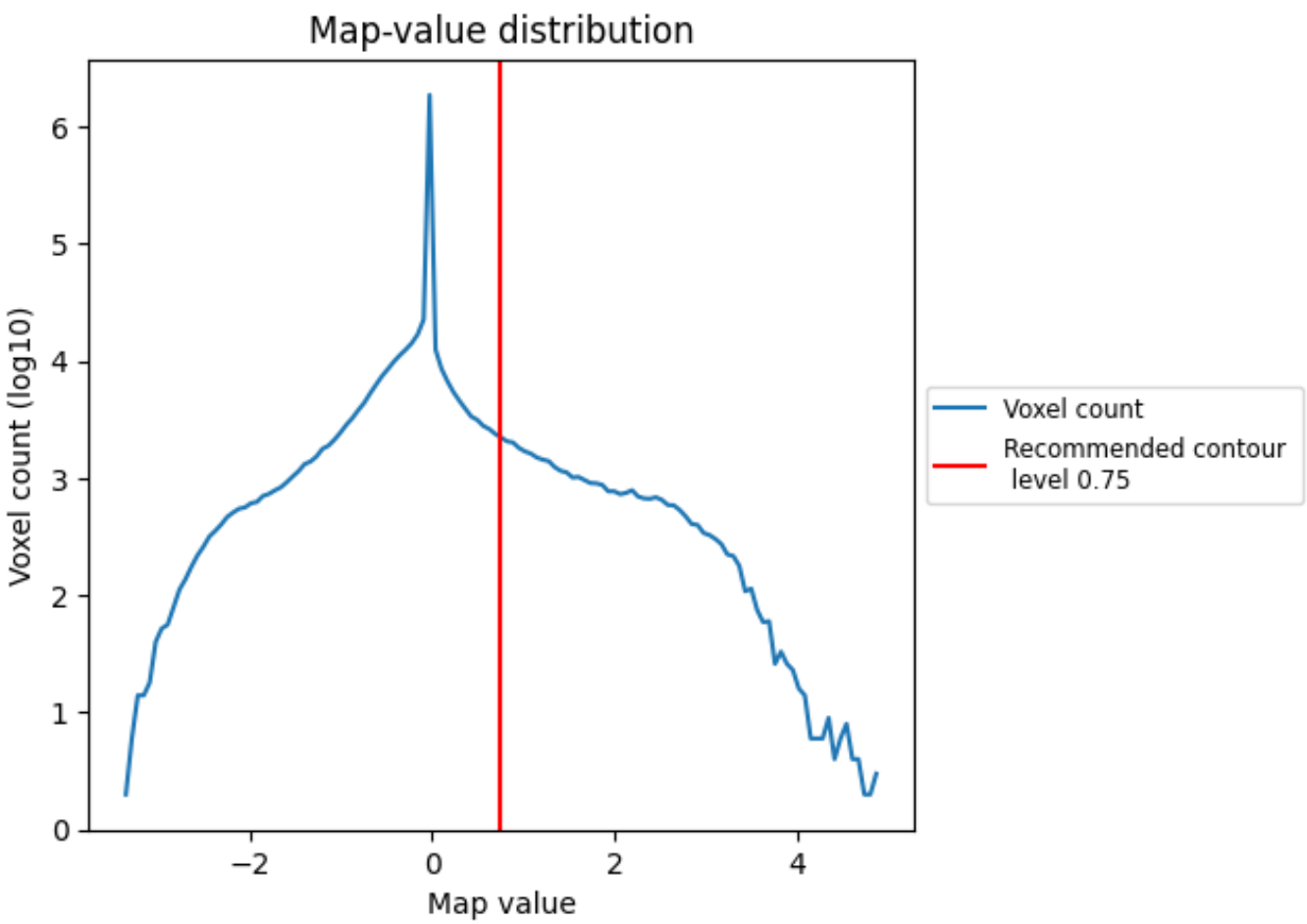


Z

7 Map analysis (i)

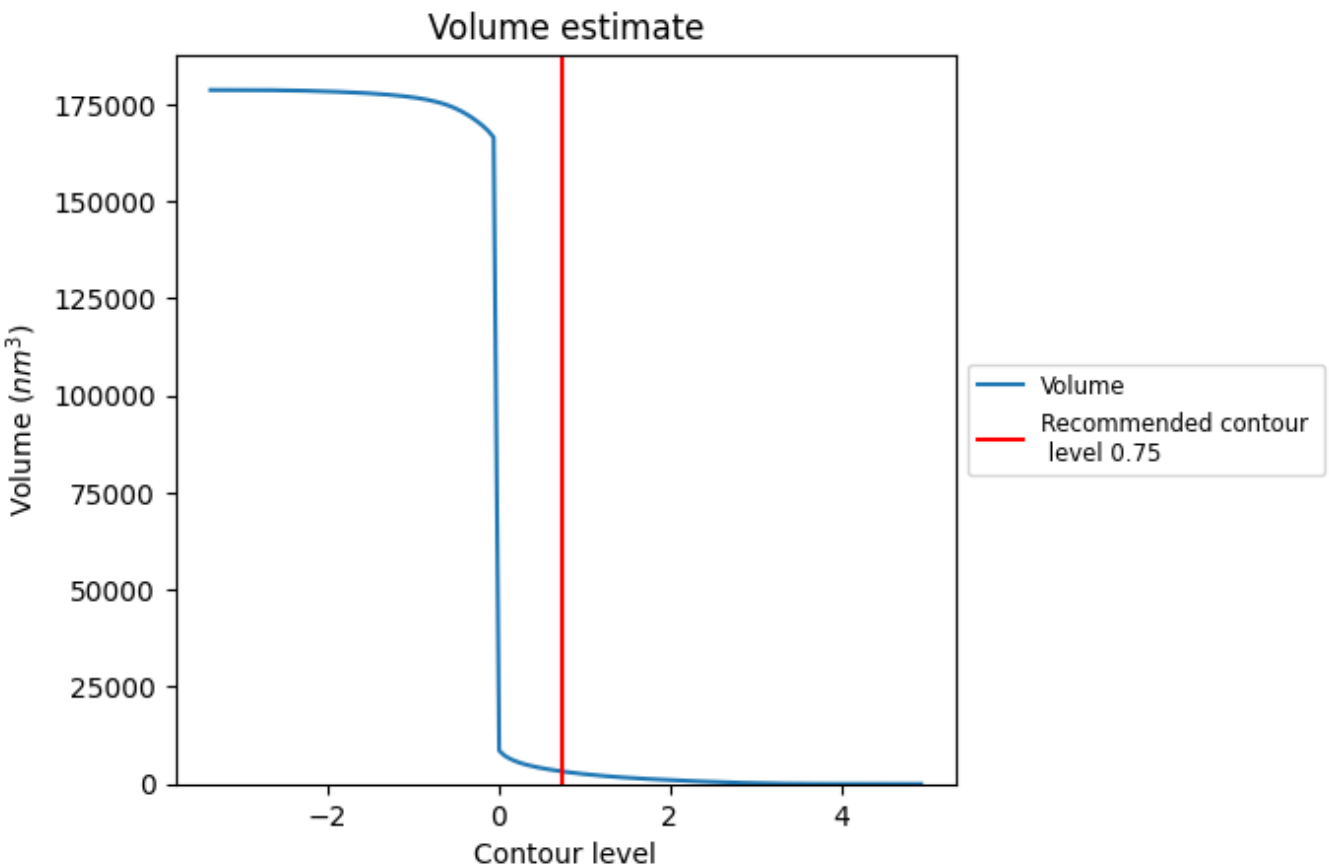
This section contains the results of statistical analysis of the map.

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.

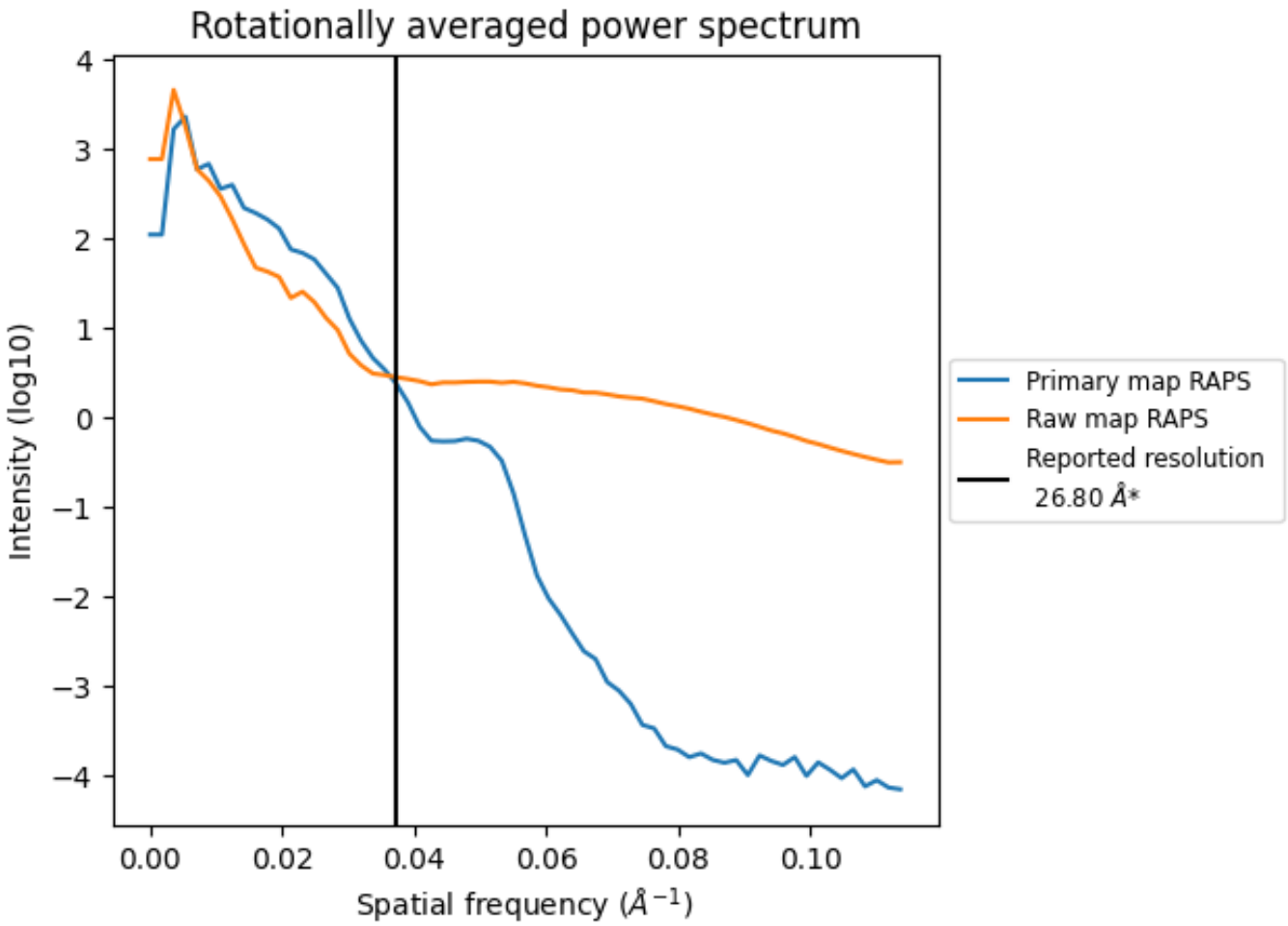
7.2 Volume estimate (i)



The volume at the recommended contour level is 3214 nm^3; this corresponds to an approximate mass of 2903 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)

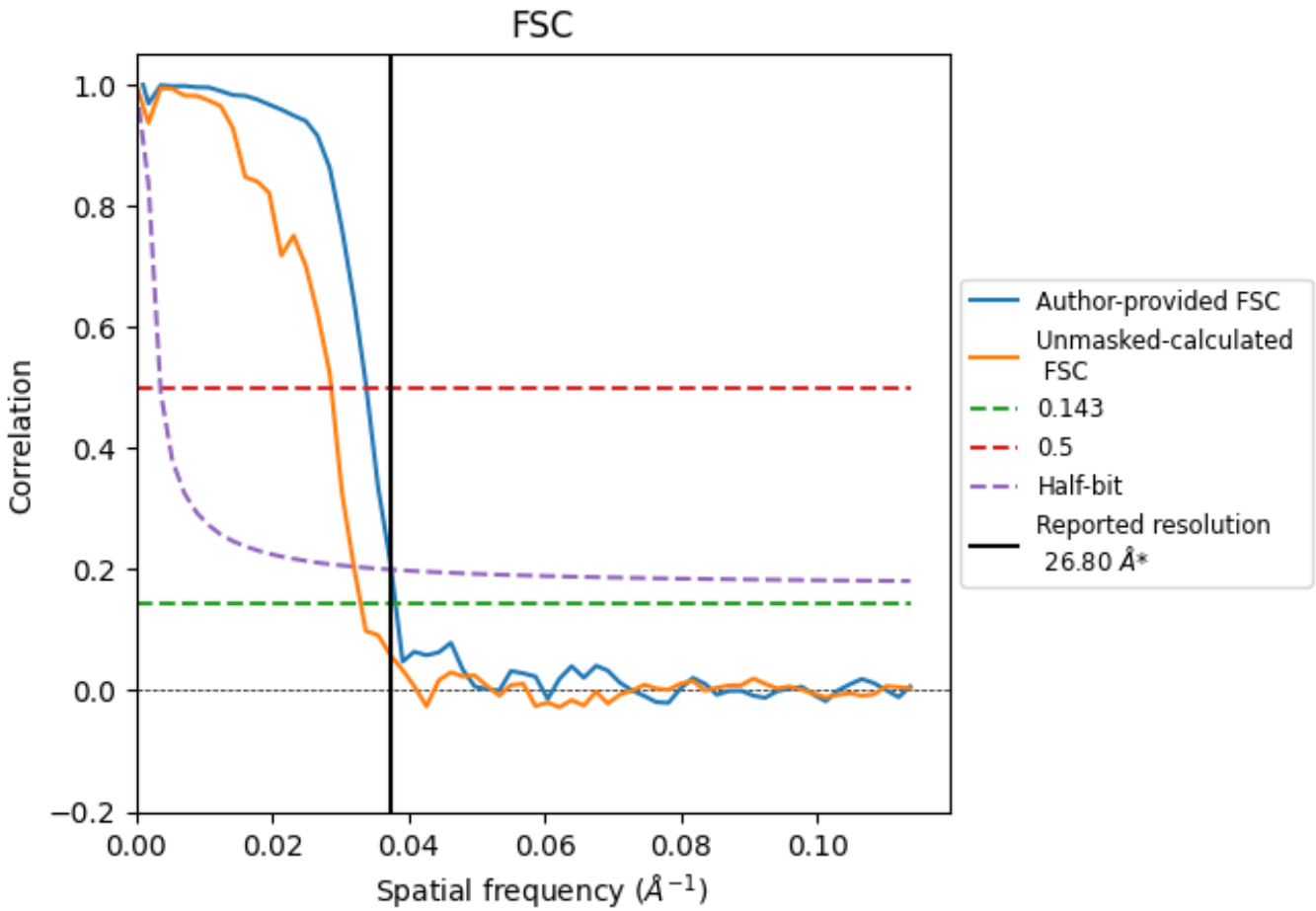


*Reported resolution corresponds to spatial frequency of 0.037 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.037 Å^{-1}

8.2 Resolution estimates (i)

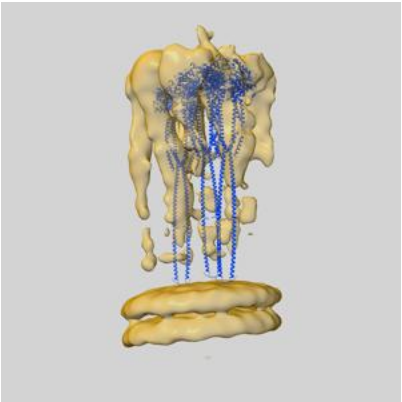
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	26.80	-	-
Author-provided FSC curve	26.32	29.59	26.74
Unmasked-calculated*	30.30	34.97	31.35

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 30.30 differs from the reported value 26.8 by more than 10 %

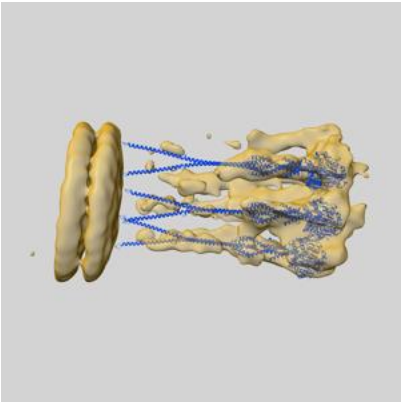
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-18806 and PDB model 8R1A. Per-residue inclusion information can be found in section 3 on page 9.

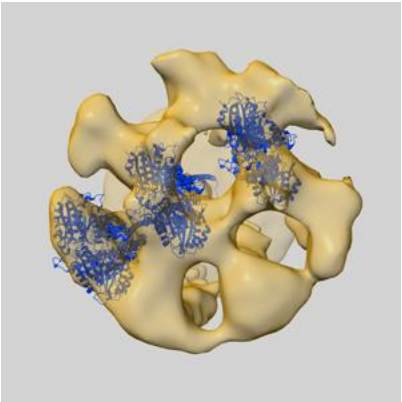
9.1 Map-model overlay (i)



X



Y



Z

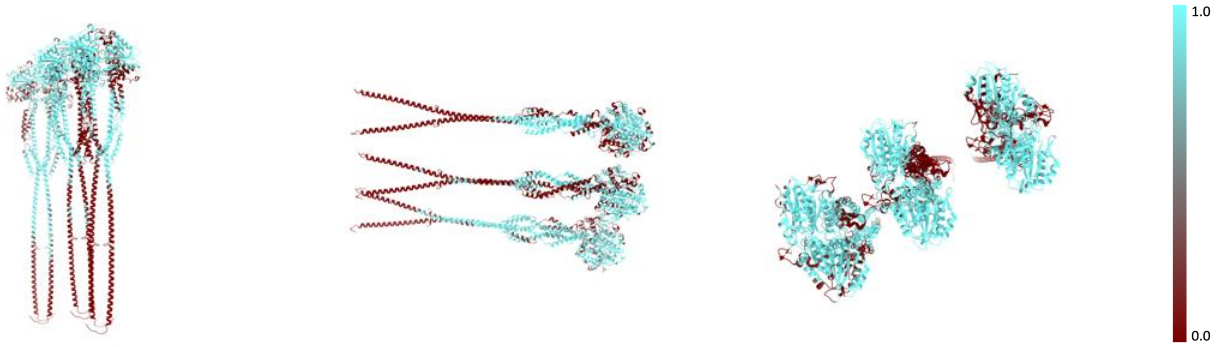
The images above show the 3D surface view of the map at the recommended contour level 0.75 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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.

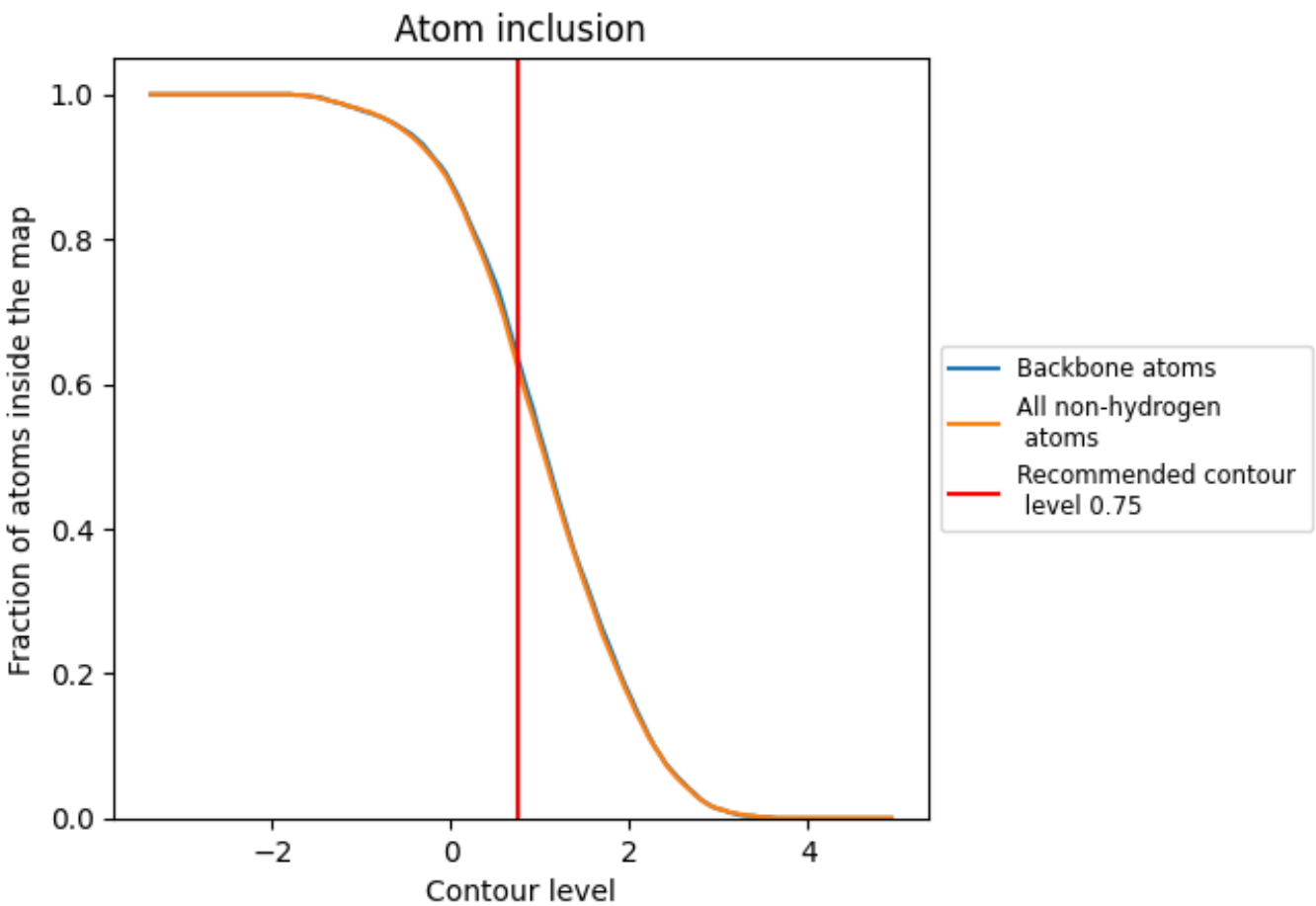
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.75).

9.4 Atom inclusion (i)



At the recommended contour level, 64% of all backbone atoms, 62% 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 (0.75) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6220	0.0300
A	0.7260	0.0370
B	0.6900	0.0280
C	0.6490	0.0310
D	0.5020	0.0260
E	0.4880	0.0210
F	0.6750	0.0380