Full wwPDB EM Validation Report ⓘ

Nov 23, 2022 – 08:04 PM EST

PDB ID	:	8DAS
EMDB ID	:	EMD-27274
Title	:	Saccharomyces cerevisiae Ufd1/Npl4/Cdc48 complex bound to two ubiquitin moieties in presence of SUMO-ubiquitin(K48polyUb)-mEOS and ATP, state 1 (intA)
Authors	:	Lee, H.G.; Lima, C.D.
Deposited on	:	2022-06-14
Resolution	:	3.50 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

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

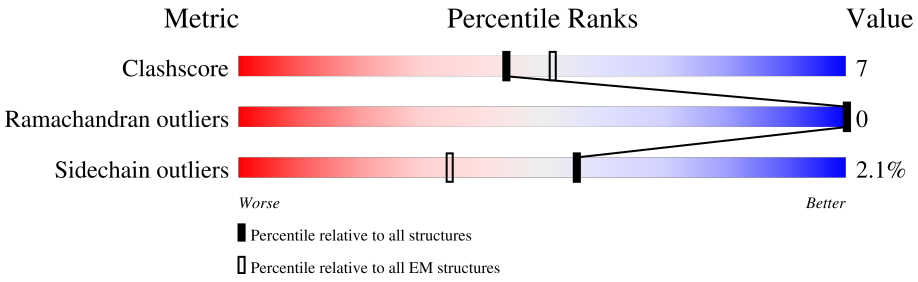
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 3.50 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	838	24% 72% 13% 15%
1	B	838	8% 56% 11% 33%
1	C	838	24% 70% 15% 15%
1	D	838	8% 56% 11% 33%
1	E	838	6% 54% 10% 36%
1	F	838	5% 55% 9% 35%
2	G	583	62% 19% 19%
3	H	363	15% 84%

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Mol	Chain	Length	Quality of chain
4	J	76	
4	K	76	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 34059 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 Cell division control protein 48.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	712	Total	C	N	O	S	0	0
			5560	3497	966	1072	25		
1	B	564	Total	C	N	O	S	0	0
			4385	2750	778	837	20		
1	C	716	Total	C	N	O	S	0	0
			5590	3513	974	1078	25		
1	D	561	Total	C	N	O	S	0	0
			4365	2734	769	842	20		
1	E	539	Total	C	N	O	S	0	0
			4174	2623	725	806	20		
1	F	541	Total	C	N	O	S	0	0
			4190	2632	730	808	20		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P25694
A	-1	SER	-	expression tag	UNP P25694
A	0	HIS	-	expression tag	UNP P25694
B	-2	GLY	-	expression tag	UNP P25694
B	-1	SER	-	expression tag	UNP P25694
B	0	HIS	-	expression tag	UNP P25694
C	-2	GLY	-	expression tag	UNP P25694
C	-1	SER	-	expression tag	UNP P25694
C	0	HIS	-	expression tag	UNP P25694
D	-2	GLY	-	expression tag	UNP P25694
D	-1	SER	-	expression tag	UNP P25694
D	0	HIS	-	expression tag	UNP P25694
E	-2	GLY	-	expression tag	UNP P25694
E	-1	SER	-	expression tag	UNP P25694
E	0	HIS	-	expression tag	UNP P25694
F	-2	GLY	-	expression tag	UNP P25694
F	-1	SER	-	expression tag	UNP P25694
F	0	HIS	-	expression tag	UNP P25694

- Molecule 2 is a protein called Nuclear protein localization protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	474	Total	C	N	O	S	0	0
			3815	2415	640	739	21		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-2	GLY	-	expression tag	UNP P33755
G	-1	SER	-	expression tag	UNP P33755
G	0	HIS	-	expression tag	UNP P33755

- Molecule 3 is a protein called Ubiquitin fusion degradation protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	59	Total	C	N	O	S	0	0
			453	292	74	84	3		

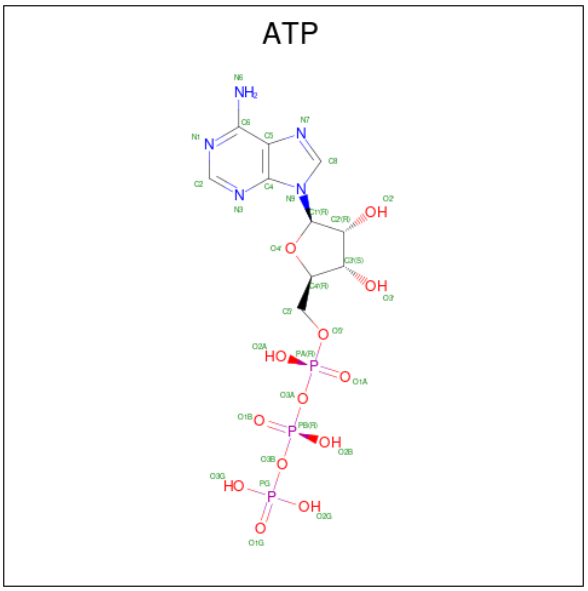
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-1	GLY	-	expression tag	UNP P53044
H	0	SER	-	expression tag	UNP P53044

- Molecule 4 is a protein called Ubiquitin.

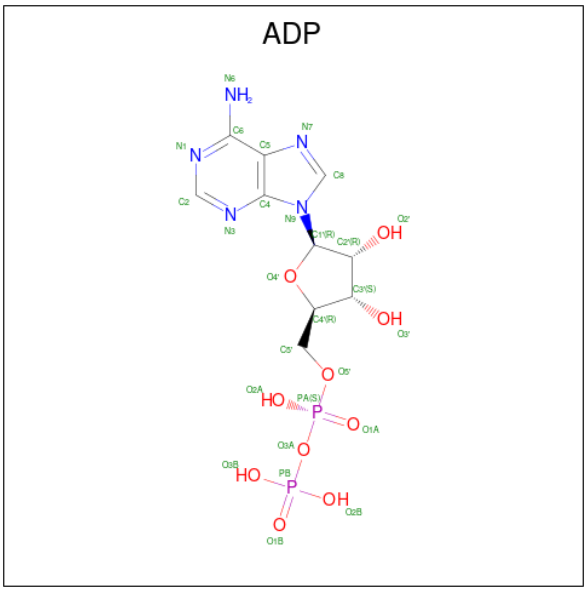
Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	73	Total	C	N	O	S	0	0
			581	365	99	116	1		
4	K	76	Total	C	N	O	S	0	0
			600	375	105	119	1		

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	E	1	Total	C	N	O	P	0
			31	10	5	13	3	
5	F	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	C	1	Total	C	N	O	P	0
			54	20	10	20	4	
6	C	1	Total	C	N	O	P	0
			54	20	10	20	4	
6	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	F	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

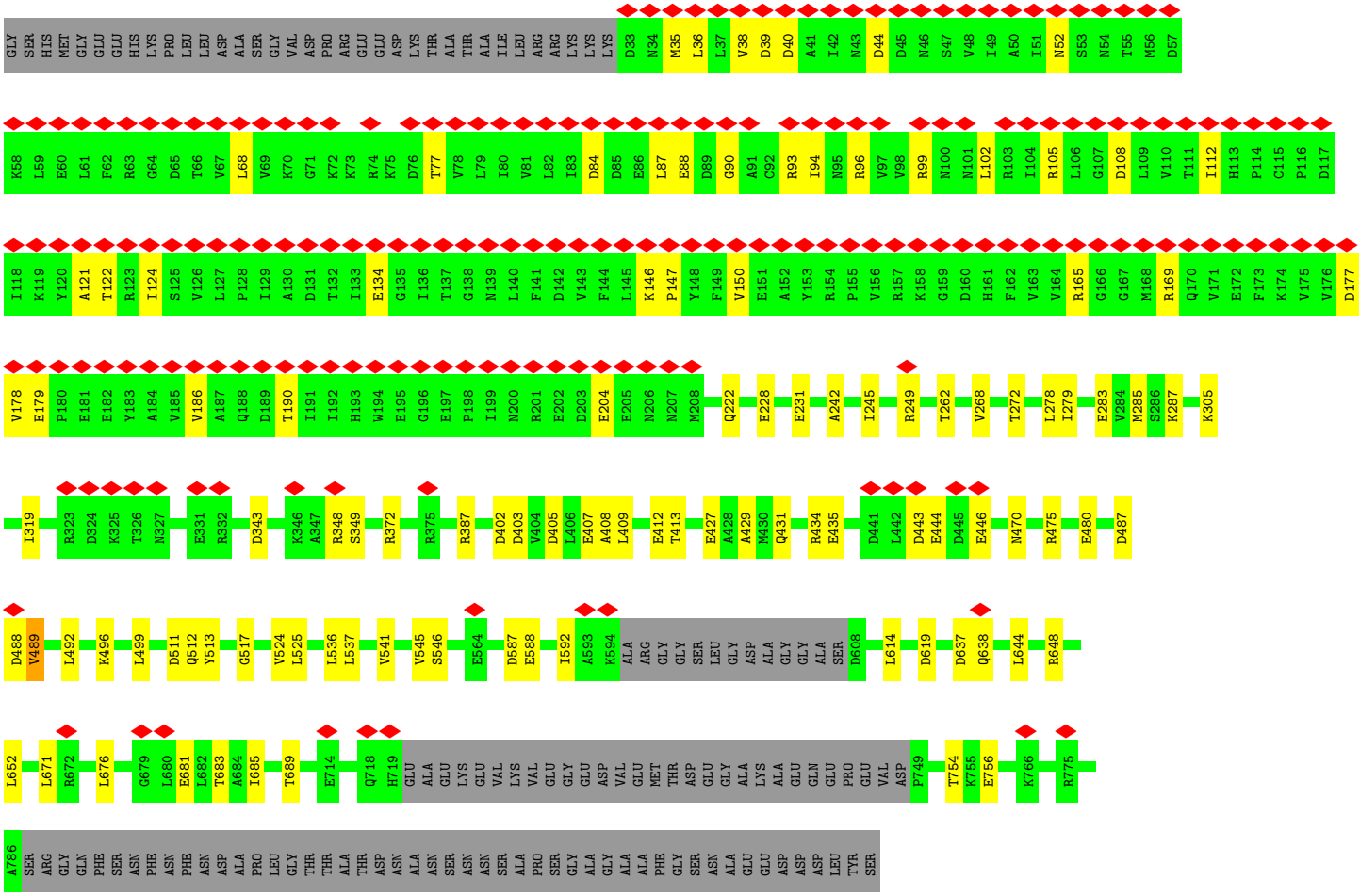
Mol	Chain	Residues	Atoms		AltConf
7	G	2	Total	Zn	0
			2	2	

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.

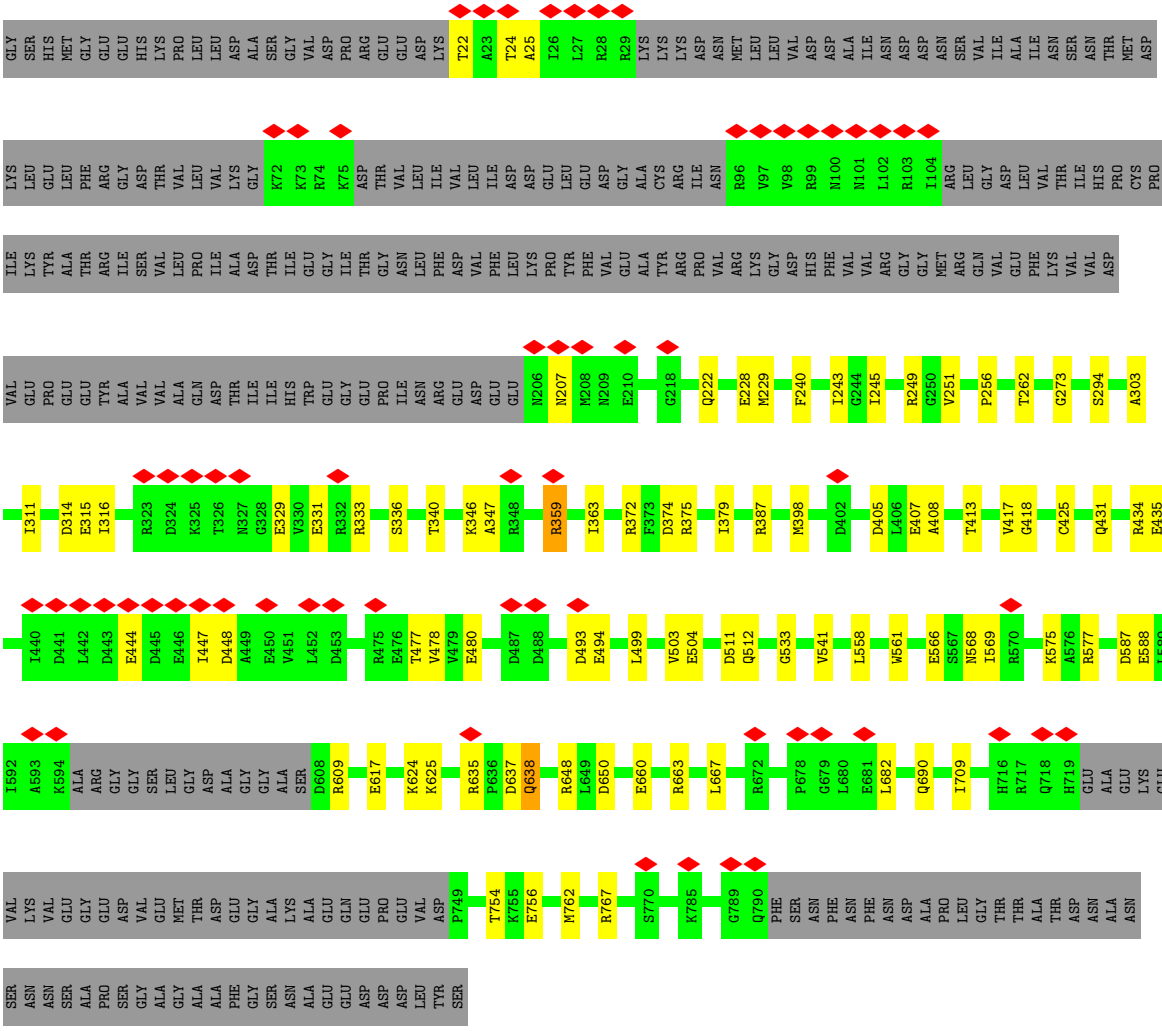
• Molecule 1: Cell division control protein 48

Chain A:



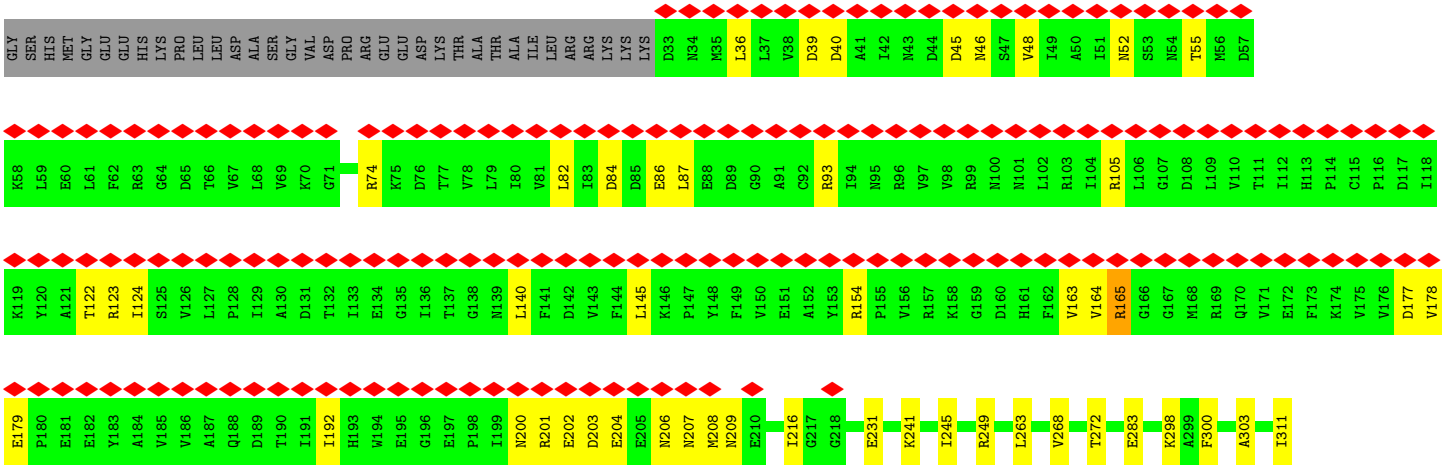
• Molecule 1: Cell division control protein 48

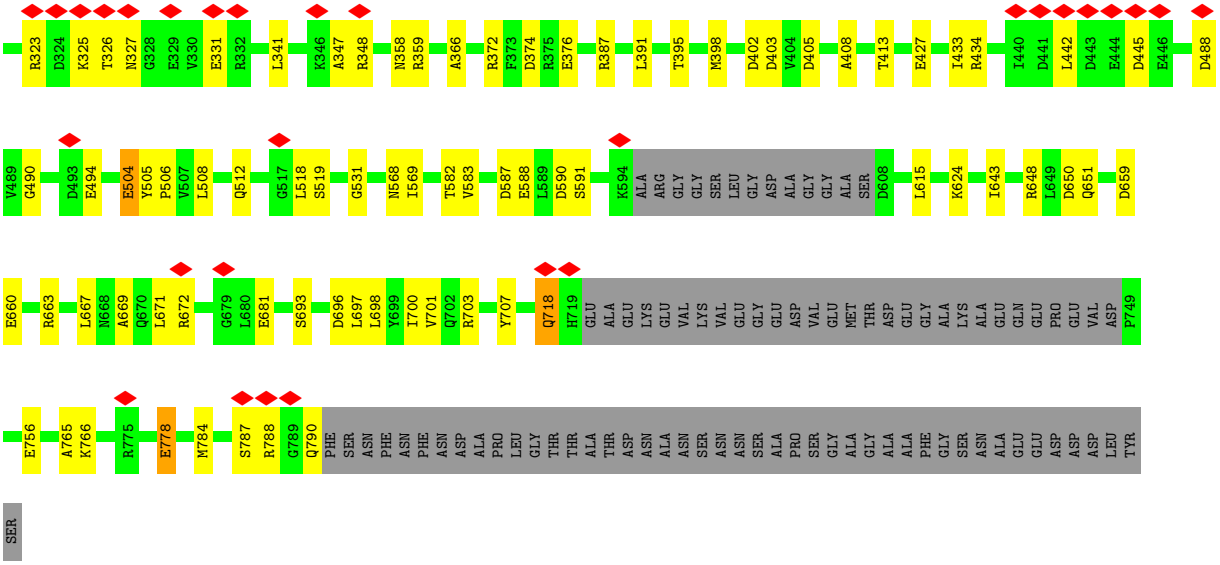
Chain B:



• Molecule 1: Cell division control protein 48

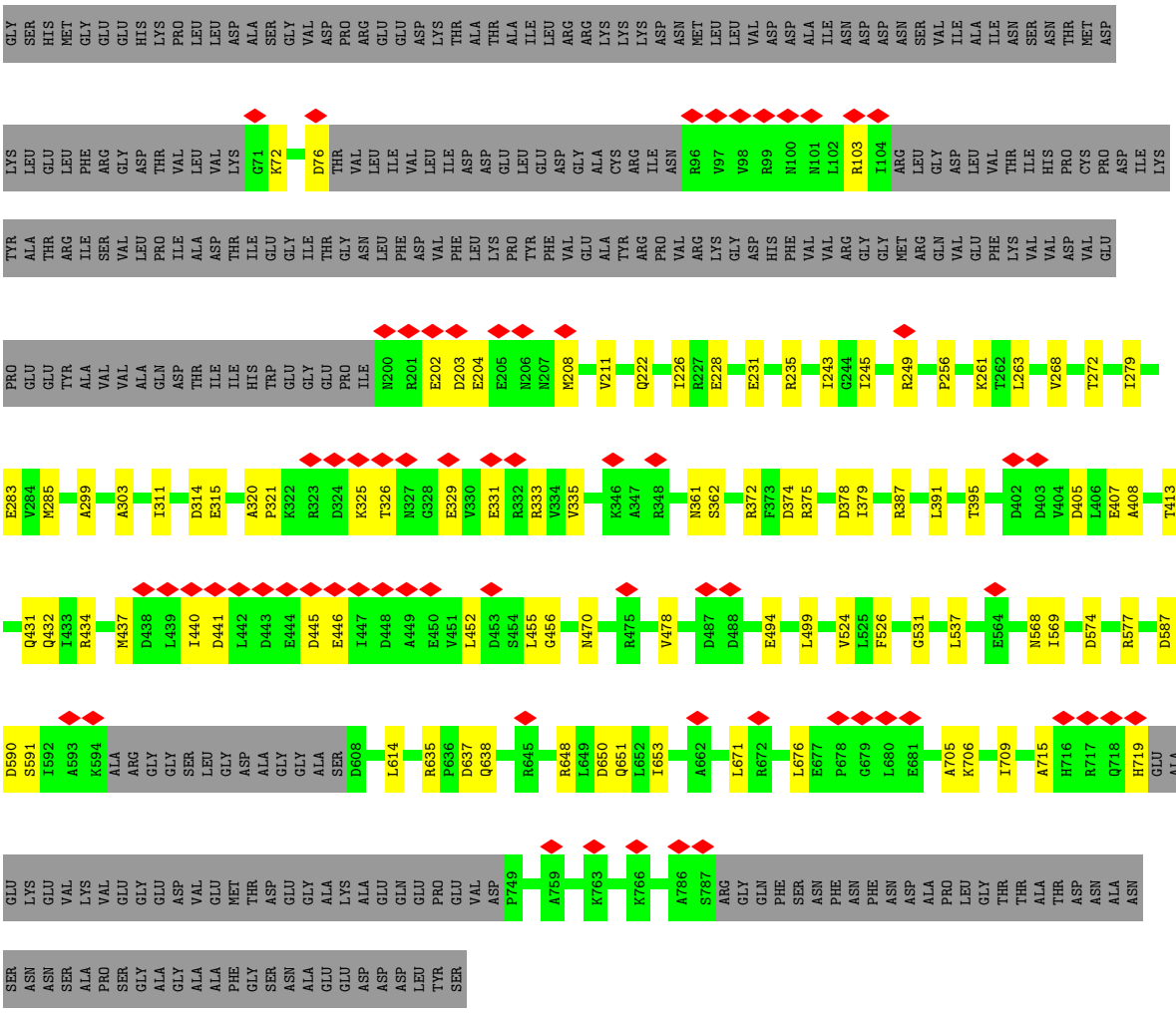
Chain C:





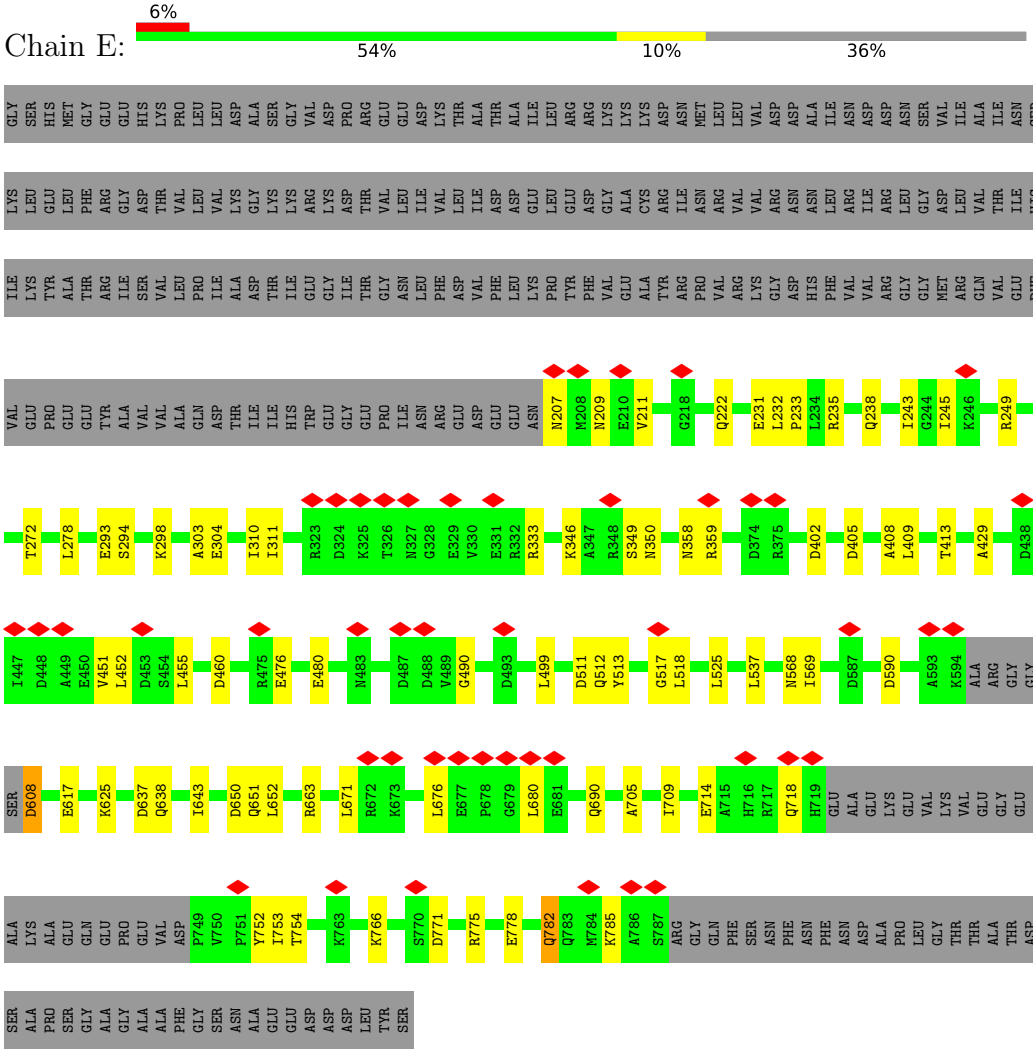
• Molecule 1: Cell division control protein 48

Chain D:



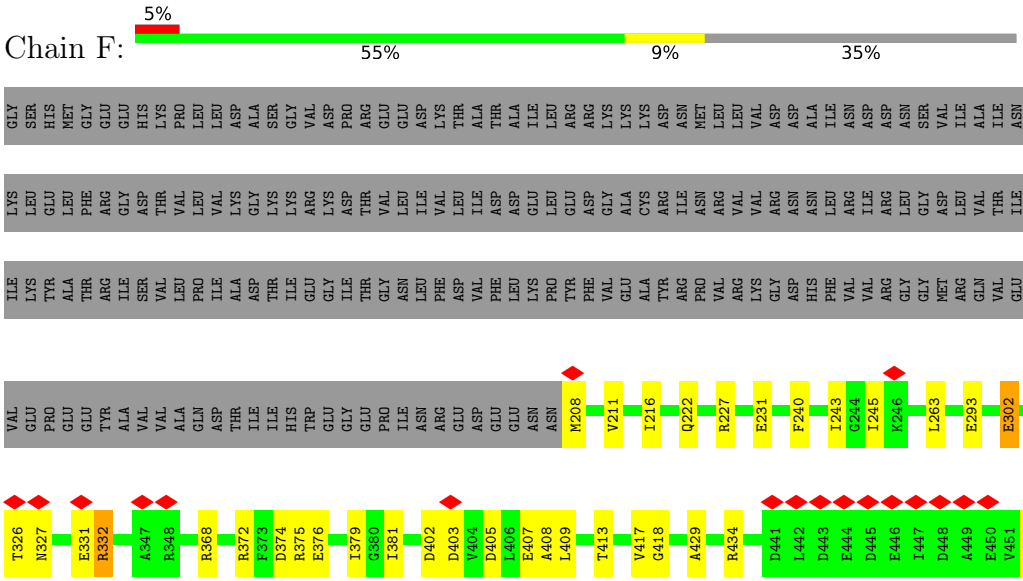
• Molecule 1: Cell division control protein 48

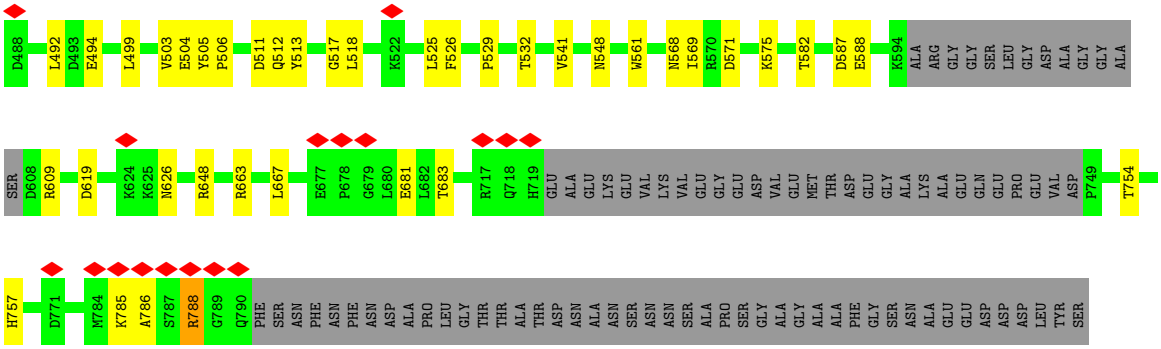
Chain E:



• Molecule 1: Cell division control protein 48

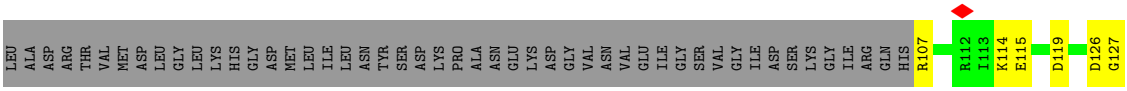
Chain F:

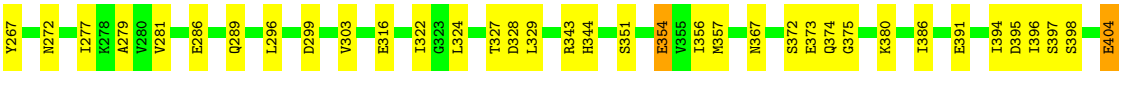


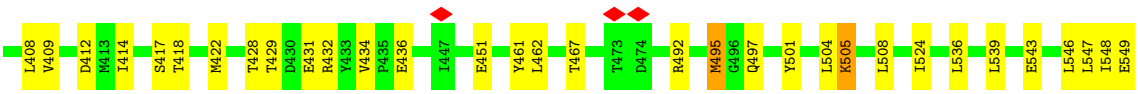


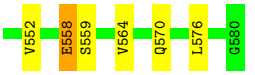
• Molecule 2: Nuclear protein localization protein 4

Chain G:



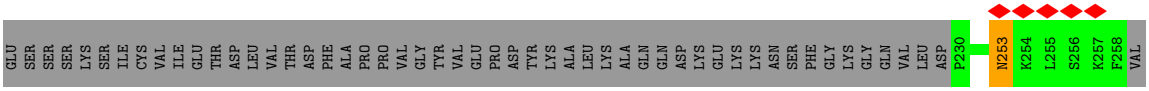


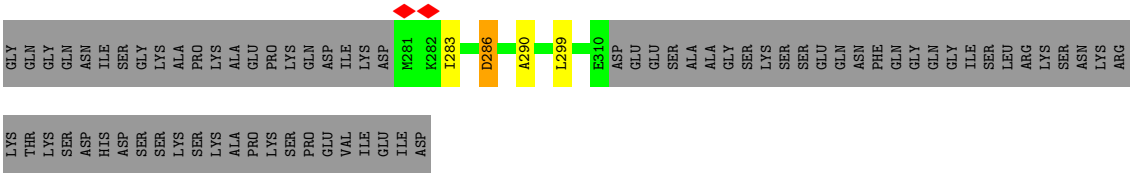




• Molecule 3: Ubiquitin fusion degradation protein 1

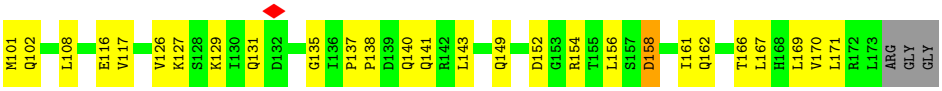
Chain H:





• Molecule 4: Ubiquitin

Chain J:



• Molecule 4: Ubiquitin

Chain K:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29595	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 ($e^-/Å^2$)	70.577	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	68.013	Depositor
Minimum map value	-27.384	Depositor
Average map value	-0.016	Depositor
Map value standard deviation	1.079	Depositor
Recommended contour level	9.0	Depositor
Map size (Å)	408.576, 408.576, 408.576	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.064, 1.064, 1.064	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, ATP, ADP

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	0.25	0/5650	0.48	0/7645
1	B	0.26	0/4450	0.48	0/6004
1	C	0.25	0/5680	0.48	0/7684
1	D	0.25	0/4431	0.48	0/5980
1	E	0.25	0/4242	0.46	0/5734
1	F	0.25	0/4258	0.47	0/5754
2	G	0.28	0/3906	0.46	0/5275
3	H	0.27	0/462	0.47	0/617
4	J	0.25	0/586	0.49	0/788
4	K	0.24	0/605	0.49	0/812
All	All	0.25	0/34270	0.47	0/46293

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

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	5560	0	5587	74	0
1	B	4385	0	4439	62	0
1	C	5590	0	5616	82	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	4365	0	4392	69	0
1	E	4174	0	4197	60	0
1	F	4190	0	4215	51	0
2	G	3815	0	3688	70	0
3	H	453	0	458	9	0
4	J	581	0	601	18	0
4	K	600	0	622	15	0
5	A	31	0	12	1	0
5	B	31	0	12	1	0
5	D	31	0	12	1	0
5	E	31	0	12	1	0
5	F	31	0	12	0	0
6	A	27	0	12	1	0
6	B	27	0	12	1	0
6	C	54	0	24	2	0
6	D	27	0	12	1	0
6	E	27	0	12	2	0
6	F	27	0	12	0	0
7	G	2	0	0	0	0
All	All	34059	0	33959	468	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (468) 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:C:36:LEU:HD11	1:C:55:THR:HG21	1.48	0.94
1:B:249:ARG:NH2	1:B:347:ALA:O	2.09	0.85
2:G:167:ILE:O	2:G:171:SER:OG	1.95	0.84
1:E:262:THR:OG1	5:E:901:ATP:O3G	1.94	0.84
2:G:259:ARG:NH2	2:G:286:GLU:OE1	2.10	0.84
1:C:249:ARG:NH2	1:C:347:ALA:O	2.13	0.82
4:K:262:GLN:O	4:K:265:SER:OG	1.95	0.81
1:A:287:LYS:O	1:B:333:ARG:NH1	2.13	0.81
2:G:243:GLU:OE1	2:G:243:GLU:N	2.14	0.81
1:B:480:GLU:N	1:B:480:GLU:OE1	2.14	0.80
1:B:262:THR:OG1	5:B:901:ATP:O3G	2.00	0.80
4:K:231:GLN:O	4:K:235:GLY:N	2.14	0.80
1:B:660:GLU:OE1	1:B:663:ARG:NH2	2.15	0.80
1:F:458:THR:OG1	1:F:460:ASP:OD1	1.99	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:431:GLN:OE1	1:D:434:ARG:NH2	2.14	0.79
1:B:503:VAL:HG21	1:B:541:VAL:HG13	1.65	0.79
2:G:417:SER:OG	2:G:422:MET:O	2.01	0.78
1:C:494:GLU:N	1:C:494:GLU:OE1	2.16	0.78
1:A:262:THR:OG1	5:A:901:ATP:O3G	2.02	0.78
1:E:676:LEU:HD11	1:E:680:LEU:HD23	1.66	0.77
1:D:329:GLU:OE2	1:D:333:ARG:NH2	2.17	0.77
1:D:470:ASN:OD1	1:E:625:LYS:NZ	2.16	0.77
1:A:431:GLN:OE1	1:A:434:ARG:NH1	2.18	0.76
2:G:412:ASP:OD2	2:G:432:ARG:NH1	2.18	0.76
1:A:44:ASP:OD2	1:A:165:ARG:NH1	2.17	0.76
1:D:715:ALA:O	1:D:719:HIS:ND1	2.18	0.76
4:J:137:PRO:O	4:J:140:GLN:NE2	2.19	0.76
4:J:101:MET:N	4:J:117:VAL:O	2.19	0.76
1:D:407:GLU:OE1	1:D:407:GLU:N	2.18	0.76
2:G:391:GLU:N	2:G:391:GLU:OE1	2.19	0.75
1:A:222:GLN:N	1:A:222:GLN:OE1	2.20	0.75
1:A:480:GLU:N	1:A:480:GLU:OE1	2.20	0.74
1:E:480:GLU:N	1:E:480:GLU:OE1	2.19	0.74
1:E:771:ASP:OD1	1:E:775:ARG:NH1	2.20	0.74
4:J:102:GLN:NE2	4:J:116:GLU:OE1	2.20	0.74
1:E:766:LYS:NZ	1:F:786:ALA:O	2.17	0.73
2:G:357:MET:SD	3:H:299:LEU:HD11	2.28	0.73
2:G:497:GLN:OE1	2:G:497:GLN:N	2.21	0.73
1:D:494:GLU:N	1:D:494:GLU:OE1	2.19	0.73
1:C:163:VAL:O	1:C:165:ARG:NH1	2.22	0.73
1:B:273:GLY:O	2:G:213:ARG:NH2	2.22	0.73
1:A:475:ARG:NH2	1:B:617:GLU:OE1	2.21	0.73
1:B:762:MET:O	1:C:790:GLN:NE2	2.22	0.72
1:C:434:ARG:NH1	1:D:228:GLU:OE1	2.22	0.72
1:D:331:GLU:OE1	1:D:331:GLU:N	2.21	0.72
4:K:251:GLU:N	4:K:251:GLU:OE1	2.23	0.71
1:A:407:GLU:N	1:A:407:GLU:OE1	2.23	0.71
1:F:302:GLU:N	1:F:302:GLU:OE1	2.23	0.71
1:A:146:LYS:O	1:A:150:VAL:HG23	1.91	0.71
1:B:359:ARG:NH2	1:B:566:GLU:OE1	2.24	0.71
2:G:451:GLU:N	2:G:451:GLU:OE1	2.24	0.71
1:D:231:GLU:HG2	1:D:272:THR:HG22	1.72	0.71
1:C:202:GLU:OE1	1:C:206:ASN:ND2	2.23	0.71
1:D:531:GLY:N	6:D:902:ADP:O1B	2.18	0.70
1:A:409:LEU:O	1:A:413:THR:HG22	1.89	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:705:ALA:HB3	1:E:518:LEU:HD11	1.73	0.70
1:F:409:LEU:O	1:F:413:THR:HG22	1.91	0.70
1:C:331:GLU:N	1:C:331:GLU:OE1	2.24	0.70
1:F:494:GLU:N	1:F:494:GLU:OE1	2.23	0.70
1:D:387:ARG:NE	1:D:413:THR:O	2.24	0.70
1:C:387:ARG:NE	1:C:413:THR:O	2.24	0.70
4:J:149:GLN:OE1	4:J:149:GLN:N	2.23	0.69
1:A:231:GLU:HG2	1:A:272:THR:HG22	1.75	0.69
4:K:219:SER:O	4:K:255:THR:OG1	2.11	0.69
1:C:122:THR:N	1:C:179:GLU:O	2.26	0.68
2:G:354:GLU:OE1	3:H:299:LEU:HD12	1.92	0.68
4:K:217:VAL:HG11	4:K:226:VAL:CG2	2.24	0.68
1:C:86:GLU:OE1	1:C:86:GLU:N	2.26	0.68
1:E:249:ARG:NH1	1:E:349:SER:O	2.27	0.68
1:E:608:ASP:N	1:E:608:ASP:OD1	2.26	0.67
2:G:558:GLU:OE1	2:G:559:SER:N	2.27	0.67
1:D:222:GLN:N	1:D:222:GLN:OE1	2.27	0.67
1:E:766:LYS:O	1:F:788:ARG:NH2	2.27	0.67
2:G:570:GLN:OE1	2:G:570:GLN:N	2.26	0.67
1:E:303:ALA:CB	1:E:311:ILE:HD11	2.25	0.67
2:G:296:LEU:HD11	3:H:299:LEU:HD23	1.75	0.67
1:B:767:ARG:O	1:C:788:ARG:NH2	2.28	0.66
1:D:72:LYS:NZ	1:D:103:ARG:O	2.23	0.66
1:A:536:LEU:HD12	1:A:537:LEU:N	2.11	0.66
2:G:247:GLU:OE2	2:G:492:ARG:NH1	2.28	0.66
2:G:236:HIS:ND1	2:G:467:THR:O	2.28	0.66
1:C:358:ASN:OD1	1:C:359:ARG:N	2.29	0.65
2:G:251:ALA:O	2:G:255:THR:HG22	1.96	0.65
1:A:387:ARG:NE	1:A:413:THR:O	2.29	0.65
1:A:36:LEU:HD12	1:A:112:ILE:HD12	1.78	0.65
1:A:443:ASP:OD1	1:A:444:GLU:N	2.30	0.65
1:A:587:ASP:OD1	1:A:588:GLU:N	2.30	0.65
1:A:84:ASP:OD2	1:A:93:ARG:NH1	2.30	0.64
1:B:387:ARG:NE	1:B:413:THR:O	2.29	0.64
1:C:74:ARG:O	1:C:74:ARG:HG2	1.96	0.64
1:C:231:GLU:HG2	1:C:272:THR:HG22	1.79	0.64
1:E:231:GLU:HG2	1:E:272:THR:HG22	1.78	0.64
1:F:331:GLU:N	1:F:331:GLU:OE1	2.31	0.64
1:A:228:GLU:OE2	1:F:434:ARG:NH2	2.31	0.64
1:C:531:GLY:N	6:C:902:ADP:O1B	2.31	0.64
1:A:470:ASN:OD1	1:B:625:LYS:NZ	2.26	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:754:THR:OG1	1:B:756:GLU:OE2	2.16	0.64
4:J:117:VAL:HG21	4:J:126:VAL:HG22	1.79	0.63
1:D:202:GLU:OE1	1:D:202:GLU:N	2.31	0.63
1:E:409:LEU:O	1:E:413:THR:HG22	1.98	0.63
1:E:714:GLU:OE2	1:E:718:GLN:NE2	2.30	0.63
1:D:705:ALA:CB	1:E:518:LEU:HD11	2.28	0.63
1:A:435:GLU:HA	1:B:22:THR:HG21	1.81	0.63
1:B:568:ASN:OD1	1:B:569:ILE:N	2.32	0.63
1:E:222:GLN:OE1	1:E:222:GLN:N	2.30	0.62
4:K:201:MET:N	4:K:217:VAL:O	2.32	0.62
1:E:294:SER:OG	1:E:298:LYS:NZ	2.32	0.62
1:B:690:GLN:N	1:B:690:GLN:OE1	2.32	0.62
2:G:495:MET:SD	2:G:495:MET:N	2.70	0.62
2:G:115:GLU:N	2:G:115:GLU:OE1	2.33	0.61
1:A:87:LEU:HD21	1:A:93:ARG:HG3	1.82	0.61
1:E:490:GLY:H	6:E:902:ADP:HN61	1.47	0.61
2:G:548:ILE:O	2:G:552:VAL:HG12	2.01	0.61
3:H:286:ASP:OD1	3:H:286:ASP:N	2.33	0.61
1:A:446:GLU:N	1:A:446:GLU:OE1	2.33	0.61
1:C:659:ASP:OD1	1:C:660:GLU:N	2.33	0.61
2:G:119:ASP:OD1	2:G:170:HIS:NE2	2.34	0.60
2:G:357:MET:CE	3:H:299:LEU:HD21	2.30	0.60
1:F:327:ASN:O	1:F:332:ARG:NH2	2.34	0.60
2:G:260:PHE:CE2	2:G:324:LEU:HD12	2.36	0.60
1:A:405:ASP:O	1:A:408:ALA:N	2.33	0.60
1:A:637:ASP:OD1	1:A:638:GLN:N	2.34	0.60
1:B:207:ASN:O	1:B:207:ASN:ND2	2.35	0.60
1:C:405:ASP:O	1:C:408:ALA:N	2.35	0.60
1:D:499:LEU:CD1	1:D:537:LEU:HD21	2.32	0.60
1:C:681:GLU:N	1:C:681:GLU:OE1	2.33	0.60
1:A:343:ASP:OD2	1:A:372:ARG:NH2	2.35	0.59
1:F:211:VAL:HG23	1:F:211:VAL:O	2.02	0.59
4:J:162:GLN:N	4:J:162:GLN:OE1	2.35	0.59
2:G:546:LEU:HD12	2:G:547:LEU:N	2.17	0.59
1:E:303:ALA:HB3	1:E:311:ILE:HD11	1.85	0.59
1:F:561:TRP:O	1:F:609:ARG:NH2	2.35	0.59
4:K:217:VAL:HG11	4:K:226:VAL:HG21	1.85	0.59
1:D:635:ARG:NE	1:D:638:GLN:OE1	2.35	0.59
1:B:511:ASP:OD1	1:B:512:GLN:N	2.35	0.59
1:B:444:GLU:OE1	1:B:444:GLU:N	2.35	0.59
1:B:331:GLU:OE1	1:B:331:GLU:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:395:ASP:OD1	2:G:396:ILE:N	2.36	0.59
4:J:166:THR:O	4:J:167:LEU:HD23	2.02	0.59
1:A:94:ILE:O	1:A:99:ARG:NH1	2.36	0.59
1:E:778:GLU:O	1:E:782:GLN:NE2	2.33	0.59
1:D:568:ASN:OD1	1:D:569:ILE:N	2.35	0.58
1:B:294:SER:OG	2:G:436:GLU:OE1	2.20	0.58
1:E:617:GLU:N	1:E:617:GLU:OE1	2.36	0.58
1:B:407:GLU:OE1	1:B:407:GLU:N	2.35	0.58
1:C:39:ASP:OD1	1:C:40:ASP:N	2.34	0.58
1:E:405:ASP:O	1:E:408:ALA:N	2.36	0.58
1:A:499:LEU:HD23	1:A:541:VAL:CG2	2.34	0.58
1:B:303:ALA:CB	1:B:311:ILE:HD11	2.34	0.57
1:C:784:MET:O	1:C:787:SER:OG	2.18	0.57
2:G:434:VAL:HG23	2:G:434:VAL:O	2.03	0.57
1:F:405:ASP:O	1:F:408:ALA:N	2.37	0.57
2:G:281:VAL:HG12	2:G:322:ILE:HD11	1.86	0.57
1:E:207:ASN:OD1	1:E:209:ASN:ND2	2.38	0.57
1:C:323:ARG:NH1	1:C:327:ASN:OD1	2.38	0.57
2:G:404:GLU:O	2:G:408:LEU:N	2.38	0.57
1:A:402:ASP:OD1	1:A:403:ASP:N	2.38	0.56
1:C:298:LYS:NZ	2:G:373:GLU:OE2	2.37	0.56
1:D:211:VAL:HG23	1:D:211:VAL:O	2.05	0.56
1:A:52:ASN:ND2	1:A:87:LEU:O	2.36	0.56
1:A:88:GLU:N	1:A:88:GLU:OE1	2.39	0.56
1:B:494:GLU:OE1	1:B:494:GLU:N	2.34	0.56
1:D:203:ASP:OD1	1:D:204:GLU:N	2.37	0.56
1:A:413:THR:O	1:A:413:THR:HG23	2.05	0.56
4:K:217:VAL:HG11	4:K:226:VAL:HG22	1.87	0.56
1:C:669:ALA:O	1:C:672:ARG:NH1	2.39	0.56
1:E:568:ASN:OD1	1:E:569:ILE:N	2.38	0.56
2:G:230:GLU:OE1	2:G:230:GLU:N	2.39	0.56
1:C:52:ASN:ND2	1:C:87:LEU:O	2.39	0.56
1:F:326:THR:O	1:F:332:ARG:NE	2.39	0.56
1:A:283:GLU:HA	1:B:340:THR:HG21	1.87	0.55
1:B:499:LEU:O	1:B:503:VAL:HG22	2.06	0.55
1:C:391:LEU:O	1:C:395:THR:OG1	2.13	0.55
1:C:700:ILE:HD11	1:C:765:ALA:HB2	1.89	0.55
1:A:545:VAL:O	1:A:546:SER:OG	2.22	0.55
1:B:222:GLN:N	1:B:222:GLN:OE1	2.38	0.55
1:D:283:GLU:OE2	2:G:147:TYR:OH	2.14	0.55
1:F:525:LEU:HD23	1:F:526:PHE:N	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:445:ASP:OD1	1:D:446:GLU:N	2.40	0.54
1:D:648:ARG:O	1:D:650:ASP:N	2.40	0.54
1:E:413:THR:HG23	1:E:413:THR:O	2.07	0.54
1:C:703:ARG:NH2	1:C:707:TYR:OH	2.41	0.54
1:F:499:LEU:O	1:F:503:VAL:HG22	2.08	0.54
1:F:587:ASP:OD1	1:F:588:GLU:N	2.40	0.54
4:K:201:MET:HE2	4:K:256:LEU:HD13	1.89	0.54
1:B:431:GLN:NE2	1:B:435:GLU:OE2	2.41	0.54
1:C:203:ASP:OD1	1:C:204:GLU:N	2.41	0.54
1:F:511:ASP:OD1	1:F:512:GLN:N	2.40	0.54
2:G:356:ILE:HD11	2:G:414:ILE:HG22	1.90	0.54
1:C:587:ASP:OD1	1:C:588:GLU:N	2.41	0.54
4:J:131:GLN:O	4:J:135:GLY:N	2.39	0.54
1:A:671:LEU:HD12	1:A:676:LEU:HD21	1.88	0.54
1:D:321:PRO:HG3	1:D:326:THR:HG21	1.90	0.53
1:A:268:VAL:O	1:A:272:THR:HG23	2.09	0.53
1:C:568:ASN:OD1	1:C:569:ILE:N	2.41	0.53
1:A:412:GLU:OE1	1:B:624:LYS:NZ	2.42	0.53
1:D:590:ASP:OD1	1:D:591:SER:N	2.41	0.53
1:A:39:ASP:OD1	1:A:40:ASP:N	2.41	0.53
2:G:351:SER:OG	2:G:354:GLU:OE2	2.26	0.53
1:A:489:VAL:HA	6:A:902:ADP:HN61	1.74	0.53
1:B:316:ILE:HG23	1:B:363:ILE:HD12	1.91	0.53
1:A:134:GLU:O	1:A:169:ARG:NH1	2.43	0.52
1:F:372:ARG:O	1:F:374:ASP:N	2.41	0.52
2:G:356:ILE:HD11	2:G:414:ILE:CG2	2.39	0.52
1:E:511:ASP:OD1	1:E:512:GLN:N	2.41	0.52
2:G:168:SER:OG	2:G:171:SER:OG	2.26	0.52
2:G:229:GLN:NE2	2:G:231:PHE:O	2.43	0.52
2:G:505:LYS:CA	2:G:576:LEU:HD11	2.39	0.52
1:C:427:GLU:OE1	1:D:375:ARG:NH2	2.41	0.52
1:E:476:GLU:N	1:E:476:GLU:OE1	2.43	0.52
1:C:693:SER:N	1:C:696:ASP:OD2	2.42	0.52
1:A:245:ILE:HD13	1:F:429:ALA:CB	2.39	0.52
1:C:718:GLN:OE1	1:C:718:GLN:N	2.42	0.52
1:B:374:ASP:OD1	1:B:375:ARG:N	2.43	0.52
1:A:278:LEU:HD23	1:A:279:ILE:N	2.25	0.51
1:D:499:LEU:HD11	1:D:537:LEU:HD21	1.92	0.51
2:G:260:PHE:HE2	2:G:324:LEU:HD12	1.74	0.51
1:C:45:ASP:OD2	1:C:154:ARG:NH1	2.43	0.51
1:C:123:ARG:NH2	1:C:179:GLU:OE2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:293:GLU:OE1	1:E:293:GLU:N	2.37	0.51
1:A:754:THR:OG1	1:A:756:GLU:OE2	2.29	0.51
4:J:161:ILE:HG23	4:J:161:ILE:O	2.10	0.51
1:A:525:LEU:HD23	1:A:652:LEU:HD22	1.90	0.51
1:D:499:LEU:HD13	1:D:537:LEU:HD21	1.93	0.51
2:G:374:GLN:OE1	2:G:374:GLN:N	2.40	0.51
1:A:285:MET:HG2	1:A:319:ILE:HG22	1.92	0.51
1:B:477:THR:O	1:B:575:LYS:NZ	2.43	0.51
1:C:372:ARG:O	1:C:374:ASP:N	2.44	0.51
1:C:433:ILE:HD11	1:D:243:ILE:HD12	1.91	0.51
1:E:293:GLU:OE2	1:E:333:ARG:NH1	2.44	0.51
1:D:432:GLN:NE2	1:D:456:GLY:O	2.44	0.51
1:A:204:GLU:OE1	1:A:204:GLU:N	2.39	0.51
1:C:615:LEU:HD21	1:C:643:ILE:HD13	1.92	0.51
1:D:405:ASP:O	1:D:408:ALA:N	2.43	0.50
2:G:126:ASP:OD1	2:G:127:GLY:N	2.44	0.50
2:G:249:ILE:HD13	2:G:394:ILE:HD12	1.91	0.50
2:G:552:VAL:HG13	2:G:552:VAL:O	2.11	0.50
4:J:117:VAL:HG23	4:J:129:LYS:HE3	1.93	0.50
1:A:177:ASP:OD1	1:A:178:VAL:N	2.45	0.50
1:B:587:ASP:OD1	1:B:588:GLU:N	2.44	0.50
1:C:376:GLU:N	1:C:376:GLU:OE1	2.45	0.50
1:F:374:ASP:OD1	1:F:375:ARG:N	2.42	0.50
1:A:619:ASP:OD2	1:A:648:ARG:NH2	2.44	0.50
1:C:671:LEU:HD21	1:C:701:VAL:HG13	1.94	0.50
1:D:378:ASP:OD1	1:D:379:ILE:N	2.45	0.50
1:B:229:MET:SD	1:B:251:VAL:HG22	2.51	0.50
1:C:445:ASP:OD2	1:D:235:ARG:NH2	2.45	0.50
2:G:267:TYR:OH	2:G:380:LYS:O	2.28	0.50
1:F:402:ASP:OD1	1:F:403:ASP:N	2.45	0.50
1:F:568:ASN:OD1	1:F:569:ILE:N	2.43	0.49
1:C:698:LEU:HD23	1:C:698:LEU:O	2.12	0.49
1:D:331:GLU:O	1:D:335:VAL:HG23	2.11	0.49
1:C:207:ASN:O	1:C:209:ASN:N	2.44	0.49
4:J:166:THR:C	4:J:167:LEU:HD23	2.32	0.49
1:C:140:LEU:C	1:C:140:LEU:HD23	2.33	0.49
1:E:513:TYR:O	1:E:517:GLY:N	2.44	0.49
2:G:564:VAL:O	2:G:570:GLN:NE2	2.43	0.49
1:C:660:GLU:OE1	1:C:663:ARG:NH2	2.39	0.49
1:C:667:LEU:CD2	1:C:697:LEU:HD13	2.42	0.49
1:E:709:ILE:HD11	1:F:512:GLN:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:ARG:NH2	1:A:349:SER:OG	2.46	0.49
2:G:505:LYS:HA	2:G:576:LEU:HD11	1.95	0.49
2:G:357:MET:HE1	3:H:299:LEU:HD21	1.94	0.49
1:C:650:ASP:OD1	1:C:651:GLN:N	2.42	0.48
1:D:226:ILE:HG21	1:D:268:VAL:HG21	1.94	0.48
1:E:358:ASN:OD1	1:E:359:ARG:N	2.46	0.48
2:G:539:LEU:HD23	2:G:543:GLU:OE1	2.13	0.48
1:F:681:GLU:OE1	1:F:683:THR:N	2.46	0.48
1:A:536:LEU:HD12	1:A:537:LEU:H	1.79	0.48
1:B:336:SER:O	1:B:340:THR:HG23	2.14	0.48
1:D:709:ILE:HD11	1:E:512:GLN:HB2	1.96	0.48
1:F:413:THR:O	1:F:413:THR:HG23	2.13	0.48
1:B:590:ASP:OD1	1:B:591:SER:N	2.46	0.48
1:C:402:ASP:OD1	1:C:403:ASP:N	2.46	0.48
1:D:314:ASP:OD1	1:D:315:GLU:N	2.46	0.48
2:G:279:ALA:HB1	2:G:322:ILE:HD12	1.95	0.48
1:A:487:ASP:OD1	1:A:488:ASP:N	2.47	0.47
1:C:84:ASP:OD2	1:C:93:ARG:NH2	2.47	0.47
1:D:391:LEU:O	1:D:395:THR:OG1	2.21	0.47
1:A:35:MET:SD	1:A:35:MET:N	2.86	0.47
1:B:561:TRP:O	1:B:609:ARG:NH2	2.46	0.47
1:C:268:VAL:O	1:C:272:THR:HG23	2.14	0.47
1:D:303:ALA:HB3	1:D:311:ILE:HD11	1.96	0.47
1:A:511:ASP:OD1	1:A:512:GLN:N	2.48	0.47
1:E:490:GLY:H	6:E:902:ADP:N6	2.10	0.47
4:J:141:GLN:HB3	4:J:169:LEU:HD11	1.95	0.47
1:C:36:LEU:CD1	1:C:55:THR:HG21	2.33	0.47
2:G:397:SER:OG	2:G:398:SER:N	2.46	0.47
1:A:429:ALA:CB	1:B:245:ILE:HD13	2.44	0.47
4:K:267:LEU:N	4:K:267:LEU:HD22	2.29	0.47
1:B:577:ARG:HB3	1:B:625:LYS:HZ3	1.80	0.47
1:B:709:ILE:HD11	1:C:512:GLN:HB2	1.96	0.47
1:E:238:GLN:OE1	1:E:238:GLN:N	2.45	0.47
1:F:492:LEU:N	1:F:492:LEU:HD12	2.29	0.47
2:G:255:THR:HG23	2:G:257:MET:H	1.79	0.47
2:G:505:LYS:N	2:G:576:LEU:HD11	2.29	0.47
1:D:320:ALA:HA	1:D:335:VAL:HG22	1.95	0.47
1:E:429:ALA:CB	1:F:245:ILE:HD13	2.45	0.47
1:F:754:THR:HG1	1:F:757:HIS:CG	2.33	0.47
2:G:501:TYR:HE1	2:G:536:LEU:HD21	1.80	0.47
4:K:221:ASP:OD1	4:K:222:THR:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:434:ARG:NE	1:B:228:GLU:OE2	2.48	0.47
1:F:513:TYR:O	1:F:517:GLY:N	2.47	0.47
1:F:240:PHE:HA	1:F:243:ILE:HG22	1.97	0.47
1:A:644:LEU:HD22	1:A:652:LEU:HD21	1.97	0.46
1:D:279:ILE:HD11	1:D:299:ALA:CB	2.45	0.46
1:E:429:ALA:HB1	1:F:245:ILE:HD13	1.97	0.46
1:B:240:PHE:HA	1:B:243:ILE:HG22	1.96	0.46
1:C:263:LEU:O	1:C:263:LEU:HD23	2.15	0.46
1:D:321:PRO:CG	1:D:326:THR:HG21	2.45	0.46
1:F:381:ILE:HG23	1:F:478:VAL:HG11	1.97	0.46
1:F:407:GLU:OE1	1:F:407:GLU:N	2.42	0.46
1:E:637:ASP:OD1	1:E:638:GLN:N	2.48	0.46
1:E:671:LEU:HD21	1:E:676:LEU:HD13	1.97	0.46
1:A:231:GLU:CG	1:A:272:THR:HG22	2.43	0.46
1:B:405:ASP:O	1:B:408:ALA:N	2.48	0.46
1:D:650:ASP:OD1	1:D:651:GLN:N	2.48	0.46
2:G:461:TYR:C	2:G:462:LEU:HD12	2.35	0.46
1:C:145:LEU:HD23	1:C:164:VAL:HG21	1.98	0.46
1:B:372:ARG:O	1:B:374:ASP:N	2.48	0.46
1:D:524:VAL:HG21	1:D:653:ILE:HD12	1.96	0.46
2:G:327:THR:HG22	2:G:386:ILE:HD12	1.97	0.46
1:D:372:ARG:O	1:D:374:ASP:N	2.49	0.45
1:F:368:ARG:NH2	1:F:376:GLU:OE2	2.49	0.45
3:H:283:ILE:N	3:H:283:ILE:HD12	2.31	0.45
1:C:74:ARG:O	1:C:74:ARG:CG	2.62	0.45
1:F:263:LEU:O	1:F:263:LEU:HD23	2.17	0.45
1:A:513:TYR:O	1:A:517:GLY:N	2.49	0.45
1:D:263:LEU:HD23	1:D:263:LEU:C	2.36	0.45
1:E:440:ILE:HG12	1:E:451:VAL:HG11	1.99	0.45
1:B:222:GLN:HG2	1:B:379:ILE:HD13	1.99	0.45
1:C:648:ARG:O	1:C:650:ASP:N	2.49	0.45
4:J:170:VAL:HG22	4:J:171:LEU:N	2.30	0.45
1:B:398:MET:HE3	1:B:425:CYS:HB3	1.98	0.45
1:F:417:VAL:HG12	1:F:418:GLY:N	2.32	0.45
2:G:324:LEU:HD23	2:G:324:LEU:H	1.81	0.45
2:G:418:THR:HG22	3:H:290:ALA:H	1.80	0.45
1:A:122:THR:HG22	1:A:179:GLU:O	2.16	0.45
1:C:504:GLU:CD	1:C:508:LEU:HD12	2.36	0.45
1:A:38:VAL:HG23	1:A:108:ASP:O	2.17	0.45
1:C:303:ALA:HB3	1:C:311:ILE:HD11	1.98	0.45
1:D:279:ILE:HD11	1:D:299:ALA:HB1	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:503:VAL:HG21	1:F:541:VAL:HG13	1.97	0.45
2:G:187:SER:OG	2:G:188:SER:N	2.50	0.45
1:F:503:VAL:HG23	1:F:504:GLU:N	2.32	0.45
1:E:663:ARG:NH2	1:E:690:GLN:OE1	2.50	0.44
1:A:36:LEU:HD22	1:A:90:GLY:HA2	1.99	0.44
1:D:325:LYS:HG3	1:D:326:THR:HG23	1.99	0.44
1:E:671:LEU:CD2	1:E:676:LEU:HD13	2.46	0.44
1:F:216:ILE:HG12	1:F:263:LEU:HD22	1.99	0.44
1:B:417:VAL:HG12	1:B:418:GLY:N	2.32	0.44
1:C:177:ASP:OD1	1:C:178:VAL:N	2.51	0.44
4:J:127:LYS:NZ	4:J:138:PRO:O	2.36	0.44
1:E:650:ASP:OD1	1:E:651:GLN:N	2.51	0.44
1:F:477:THR:O	1:F:575:LYS:NZ	2.48	0.44
1:D:537:LEU:C	1:D:537:LEU:HD23	2.37	0.44
1:D:587:ASP:OD1	1:D:588:GLU:N	2.50	0.44
1:E:310:ILE:HG23	1:E:310:ILE:O	2.18	0.44
1:E:643:ILE:O	1:E:643:ILE:HG22	2.18	0.44
2:G:328:ASP:OD2	2:G:343:ARG:NE	2.45	0.44
4:J:108:LEU:HD21	4:J:170:VAL:HA	1.99	0.44
1:D:268:VAL:O	1:D:272:THR:HG23	2.18	0.44
1:E:304:GLU:OE2	1:E:349:SER:OG	2.21	0.44
1:F:222:GLN:HG2	1:F:379:ILE:HD13	2.00	0.44
1:B:503:VAL:HG23	1:B:504:GLU:N	2.33	0.44
1:C:778:GLU:N	1:C:778:GLU:OE1	2.51	0.44
1:D:614:LEU:O	1:D:614:LEU:HD23	2.18	0.44
1:A:592:ILE:O	1:A:592:ILE:HG22	2.18	0.44
1:F:619:ASP:OD2	1:F:648:ARG:NH2	2.45	0.44
1:D:574:ASP:OD1	1:D:577:ARG:NH1	2.51	0.44
1:C:442:LEU:H	1:C:442:LEU:HD22	1.83	0.43
2:G:372:SER:OG	2:G:375:GLY:N	2.52	0.43
4:K:215:LEU:HG	4:K:230:ILE:HD11	1.99	0.43
4:K:239:ASP:OD1	4:K:239:ASP:N	2.50	0.43
1:C:582:THR:HG22	1:C:583:VAL:H	1.83	0.43
1:D:452:LEU:HA	1:D:455:LEU:HD23	2.01	0.43
1:C:398:MET:CE	1:D:245:ILE:HG22	2.48	0.43
1:C:490:GLY:H	6:C:902:ADP:N6	2.17	0.43
1:D:261:LYS:N	5:D:901:ATP:O2B	2.51	0.43
2:G:252:TRP:O	2:G:256:GLY:N	2.49	0.43
3:H:253:ASN:OD1	3:H:253:ASN:N	2.51	0.43
4:K:258:ASP:OD1	4:K:258:ASP:N	2.49	0.43
1:B:667:LEU:HD23	1:B:682:LEU:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:366:ALA:O	1:C:372:ARG:NH1	2.46	0.43
1:C:488:ASP:N	1:C:488:ASP:OD1	2.51	0.43
1:D:671:LEU:HD12	1:D:676:LEU:HD21	2.00	0.43
1:A:245:ILE:HD13	1:F:429:ALA:HB1	2.00	0.43
1:C:303:ALA:CB	1:C:311:ILE:HD11	2.48	0.43
1:E:705:ALA:HB3	1:F:518:LEU:HD21	2.00	0.43
1:A:343:ASP:OD1	1:A:372:ARG:NE	2.46	0.43
1:C:700:ILE:HD11	1:C:765:ALA:CB	2.49	0.43
1:F:227:ARG:NE	1:F:231:GLU:OE2	2.48	0.43
4:J:154:ARG:HH21	4:J:158:ASP:HB2	1.83	0.43
1:B:637:ASP:OD1	1:B:638:GLN:N	2.52	0.42
1:C:216:ILE:N	1:C:216:ILE:HD12	2.34	0.42
1:D:614:LEU:HD23	1:D:614:LEU:C	2.38	0.42
1:B:493:ASP:N	1:B:493:ASP:OD1	2.52	0.42
1:D:226:ILE:CG2	1:D:268:VAL:HG21	2.49	0.42
1:E:211:VAL:HG23	1:E:211:VAL:O	2.17	0.42
4:J:143:LEU:N	4:J:143:LEU:HD22	2.35	0.42
1:A:524:VAL:HG12	1:A:525:LEU:N	2.35	0.42
1:B:431:GLN:OE1	1:B:434:ARG:NH1	2.52	0.42
1:F:293:GLU:OE1	1:F:293:GLU:N	2.47	0.42
2:G:428:THR:HG22	2:G:429:THR:N	2.35	0.42
1:C:48:VAL:CG1	1:C:82:LEU:HD12	2.50	0.42
1:E:499:LEU:HD11	1:E:537:LEU:HD21	2.00	0.42
1:E:753:ILE:HG22	1:E:754:THR:N	2.35	0.42
1:F:663:ARG:O	1:F:667:LEU:HD23	2.19	0.42
2:G:235:ASP:OD2	2:G:277:ILE:N	2.43	0.42
1:B:24:THR:O	1:B:25:ALA:HB3	2.19	0.42
1:B:398:MET:HE2	1:C:245:ILE:HG22	2.02	0.42
1:A:121:ALA:O	1:A:190:THR:OG1	2.17	0.42
1:A:434:ARG:HG2	1:B:22:THR:HG22	2.02	0.42
1:E:268:VAL:O	1:E:272:THR:HG23	2.20	0.42
1:A:685:ILE:O	1:A:689:THR:HG23	2.20	0.42
1:B:256:PRO:HG3	1:B:478:VAL:HG12	2.01	0.42
1:C:200:ASN:OD1	1:C:201:ARG:N	2.53	0.42
1:C:582:THR:HG22	1:C:583:VAL:N	2.34	0.42
1:D:637:ASP:OD1	1:D:637:ASP:N	2.53	0.42
1:D:706:LYS:HA	1:D:709:ILE:HG22	2.02	0.42
2:G:131:ARG:NH2	2:G:147:TYR:O	2.53	0.42
1:C:590:ASP:OD1	1:C:591:SER:N	2.53	0.42
1:E:590:ASP:OD1	1:E:590:ASP:N	2.53	0.41
1:A:242:ALA:CB	1:F:452:LEU:HD21	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:231:GLU:O	1:E:235:ARG:N	2.38	0.41
1:B:314:ASP:OD1	1:B:315:GLU:N	2.53	0.41
1:B:648:ARG:O	1:B:650:ASP:N	2.53	0.41
1:F:529:PRO:O	1:F:532:THR:HG23	2.20	0.41
1:C:505:TYR:HB2	1:C:506:PRO:HD3	2.02	0.41
1:D:231:GLU:CG	1:D:272:THR:HG22	2.48	0.41
1:E:232:LEU:HB2	1:E:233:PRO:HD3	2.02	0.41
4:K:201:MET:CE	4:K:256:LEU:HD13	2.50	0.41
1:D:263:LEU:HD23	1:D:263:LEU:O	2.21	0.41
2:G:524:ILE:O	2:G:524:ILE:CG2	2.67	0.41
1:A:146:LYS:HB3	1:A:147:PRO:HD3	2.01	0.41
1:C:300:PHE:CD1	1:C:341:LEU:HD13	2.55	0.41
4:J:156:LEU:HB3	4:J:161:ILE:HG22	2.03	0.41
1:A:77:THR:HG22	1:A:102:LEU:HD21	2.03	0.41
1:C:325:LYS:O	1:C:326:THR:C	2.59	0.41
2:G:168:SER:O	2:G:170:HIS:N	2.54	0.41
1:A:489:VAL:O	1:A:496:LYS:NZ	2.36	0.41
1:A:681:GLU:OE2	1:A:683:THR:OG1	2.35	0.41
1:D:526:PHE:CZ	1:D:537:LEU:HD22	2.56	0.41
1:E:452:LEU:HA	1:E:455:LEU:HD23	2.03	0.41
1:F:548:ASN:HB2	1:F:582:THR:HG22	2.03	0.41
2:G:329:LEU:HD11	2:G:386:ILE:HG22	2.03	0.41
1:A:614:LEU:C	1:A:614:LEU:HD23	2.41	0.41
1:C:45:ASP:OD1	1:C:46:ASN:N	2.53	0.41
1:D:76:ASP:OD1	1:D:76:ASP:N	2.54	0.41
1:D:361:ASN:OD1	1:D:362:SER:N	2.54	0.41
2:G:409:VAL:O	2:G:409:VAL:HG22	2.20	0.41
1:B:447:ILE:HG22	1:B:448:ASP:N	2.37	0.40
1:C:518:LEU:HD23	1:C:519:SER:N	2.35	0.40
1:D:440:ILE:HG22	1:D:441:ASP:N	2.36	0.40
1:E:263:LEU:HD23	1:E:263:LEU:O	2.19	0.40
1:E:525:LEU:HD23	1:E:652:LEU:HD11	2.02	0.40
1:B:533:GLY:N	6:B:902:ADP:O1A	2.48	0.40
1:B:558:LEU:HD11	1:B:591:SER:HB2	2.03	0.40
1:D:256:PRO:HG3	1:D:478:VAL:HG12	2.02	0.40
1:E:243:ILE:HG23	1:E:245:ILE:HG22	2.02	0.40
1:F:505:TYR:HB2	1:F:506:PRO:HD3	2.04	0.40
2:G:281:VAL:O	2:G:281:VAL:HG23	2.21	0.40
2:G:299:ASP:O	2:G:303:VAL:HG23	2.21	0.40
1:A:124:ILE:HD13	1:A:186:VAL:HG22	2.04	0.40
1:C:124:ILE:HD11	1:C:192:ILE:HG12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:615:LEU:CD2	1:C:643:ILE:HD13	2.52	0.40
1:E:350:ASN:N	1:E:350:ASN:OD1	2.54	0.40
1:E:402:ASP:N	1:E:402:ASP:OD1	2.54	0.40

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	706/838 (84%)	684 (97%)	22 (3%)	0	100	100
1	B	552/838 (66%)	531 (96%)	21 (4%)	0	100	100
1	C	710/838 (85%)	684 (96%)	26 (4%)	0	100	100
1	D	551/838 (66%)	530 (96%)	21 (4%)	0	100	100
1	E	533/838 (64%)	509 (96%)	24 (4%)	0	100	100
1	F	535/838 (64%)	515 (96%)	20 (4%)	0	100	100
2	G	472/583 (81%)	415 (88%)	57 (12%)	0	100	100
3	H	55/363 (15%)	46 (84%)	9 (16%)	0	100	100
4	J	71/76 (93%)	68 (96%)	3 (4%)	0	100	100
4	K	74/76 (97%)	67 (90%)	7 (10%)	0	100	100
All	All	4259/6126 (70%)	4049 (95%)	210 (5%)	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	603/697 (86%)	595 (99%)	8 (1%)	69	86
1	B	470/697 (67%)	465 (99%)	5 (1%)	73	88
1	C	606/697 (87%)	594 (98%)	12 (2%)	55	79
1	D	469/697 (67%)	465 (99%)	4 (1%)	78	90
1	E	448/697 (64%)	440 (98%)	8 (2%)	59	81
1	F	449/697 (64%)	442 (98%)	7 (2%)	62	83
2	G	425/518 (82%)	400 (94%)	25 (6%)	19	53
3	H	50/315 (16%)	48 (96%)	2 (4%)	31	64
4	J	68/69 (99%)	66 (97%)	2 (3%)	42	71
4	K	69/69 (100%)	66 (96%)	3 (4%)	29	62
All	All	3657/5153 (71%)	3581 (98%)	76 (2%)	56	79

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	LEU
1	A	96	ARG
1	A	105	ARG
1	A	305	LYS
1	A	348	ARG
1	A	427	GLU
1	A	489	VAL
1	A	492	LEU
1	B	329	GLU
1	B	346	LYS
1	B	359	ARG
1	B	635	ARG
1	B	638	GLN
1	C	105	ARG
1	C	165	ARG
1	C	208	MET
1	C	241	LYS
1	C	283	GLU
1	C	348	ARG
1	C	504	GLU
1	C	624	LYS
1	C	718	GLN

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Mol	Chain	Res	Type
1	C	756	GLU
1	C	766	LYS
1	C	778	GLU
1	D	208	MET
1	D	249	ARG
1	D	285	MET
1	D	437	MET
1	E	254	TYR
1	E	278	LEU
1	E	346	LYS
1	E	460	ASP
1	E	608	ASP
1	E	752	TYR
1	E	782	GLN
1	E	785	LYS
1	F	208	MET
1	F	302	GLU
1	F	332	ARG
1	F	571	ASP
1	F	626	ASN
1	F	785	LYS
1	F	788	ARG
2	G	107	ARG
2	G	114	LYS
2	G	136	LEU
2	G	142	ARG
2	G	144	MET
2	G	148	CYS
2	G	160	GLU
2	G	175	LYS
2	G	205	HIS
2	G	211	TRP
2	G	215	ILE
2	G	272	ASN
2	G	289	GLN
2	G	316	GLU
2	G	344	HIS
2	G	354	GLU
2	G	367	ASN
2	G	404	GLU
2	G	431	GLU
2	G	495	MET

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Mol	Chain	Res	Type
2	G	504	LEU
2	G	505	LYS
2	G	508	LEU
2	G	549	GLU
2	G	558	GLU
3	H	253	ASN
3	H	286	ASP
4	J	152	ASP
4	J	158	ASP
4	K	254	ARG
4	K	267	LEU
4	K	272	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	207	ASN
1	E	209	ASN
2	G	344	HIS
2	G	361	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)

Of 14 ligands modelled in this entry, 2 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	$\#\|Z\| > 2$
6	ADP	B	902	-	24,29,29	0.91	1 (4%)	29,45,45	1.52	4 (13%)
6	ADP	C	901	-	24,29,29	0.69	0	29,45,45	0.84	2 (6%)
5	ATP	D	901	-	26,33,33	0.63	0	31,52,52	1.08	2 (6%)
6	ADP	A	902	-	24,29,29	0.67	0	29,45,45	0.86	2 (6%)
5	ATP	B	901	-	26,33,33	0.63	0	31,52,52	1.09	2 (6%)
5	ATP	A	901	-	26,33,33	0.63	0	31,52,52	1.09	2 (6%)
5	ATP	F	901	-	26,33,33	0.63	0	31,52,52	1.10	2 (6%)
6	ADP	C	902	-	24,29,29	0.92	1 (4%)	29,45,45	1.51	4 (13%)
6	ADP	D	902	-	24,29,29	0.91	1 (4%)	29,45,45	1.51	4 (13%)
5	ATP	E	901	-	26,33,33	0.63	0	31,52,52	1.09	2 (6%)
6	ADP	E	902	-	24,29,29	0.69	0	29,45,45	0.81	1 (3%)
6	ADP	F	902	-	24,29,29	0.68	0	29,45,45	0.83	2 (6%)

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
6	ADP	B	902	-	-	3/12/32/32	0/3/3/3
6	ADP	C	901	-	-	4/12/32/32	0/3/3/3
5	ATP	D	901	-	-	4/18/38/38	0/3/3/3
6	ADP	A	902	-	-	5/12/32/32	0/3/3/3
5	ATP	B	901	-	-	5/18/38/38	0/3/3/3
5	ATP	A	901	-	-	3/18/38/38	0/3/3/3
5	ATP	F	901	-	-	4/18/38/38	0/3/3/3
6	ADP	C	902	-	-	3/12/32/32	0/3/3/3
6	ADP	D	902	-	-	3/12/32/32	0/3/3/3
5	ATP	E	901	-	-	3/18/38/38	0/3/3/3
6	ADP	E	902	-	-	3/12/32/32	0/3/3/3
6	ADP	F	902	-	-	5/12/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	902	ADP	C5-C4	2.29	1.47	1.40
6	C	902	ADP	C5-C4	2.29	1.47	1.40
6	D	902	ADP	C5-C4	2.26	1.46	1.40

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	C	902	ADP	PA-O3A-PB	-3.89	119.48	132.83
6	B	902	ADP	PA-O3A-PB	-3.85	119.61	132.83
6	C	902	ADP	N3-C2-N1	-3.66	122.96	128.68
6	D	902	ADP	N3-C2-N1	-3.63	123.01	128.68
6	B	902	ADP	N3-C2-N1	-3.57	123.10	128.68
6	D	902	ADP	PA-O3A-PB	-3.50	120.82	132.83
6	D	902	ADP	C3'-C2'-C1'	3.00	105.50	100.98
6	C	902	ADP	C3'-C2'-C1'	2.91	105.36	100.98
6	B	902	ADP	C4-C5-N7	-2.86	106.42	109.40
6	D	902	ADP	C4-C5-N7	-2.73	106.55	109.40
6	B	902	ADP	C3'-C2'-C1'	2.66	104.98	100.98
6	C	902	ADP	C4-C5-N7	-2.64	106.65	109.40
6	A	902	ADP	C3'-C2'-C1'	2.40	104.60	100.98
5	E	901	ATP	C5-C6-N6	2.29	123.84	120.35
5	B	901	ATP	C5-C6-N6	2.29	123.83	120.35
5	D	901	ATP	C5-C6-N6	2.29	123.83	120.35
5	A	901	ATP	C5-C6-N6	2.28	123.82	120.35
5	F	901	ATP	C5-C6-N6	2.27	123.80	120.35
6	A	902	ADP	C5-C6-N6	2.26	123.79	120.35
6	F	902	ADP	C5-C6-N6	2.25	123.77	120.35
6	C	901	ADP	C5-C6-N6	2.21	123.71	120.35
6	E	902	ADP	C5-C6-N6	2.18	123.67	120.35
6	C	901	ADP	PA-O3A-PB	-2.18	125.35	132.83
6	F	902	ADP	PA-O3A-PB	-2.16	125.41	132.83
5	E	901	ATP	PB-O3B-PG	2.07	139.92	132.83
5	D	901	ATP	PB-O3B-PG	2.06	139.90	132.83
5	A	901	ATP	PB-O3B-PG	2.06	139.89	132.83
5	B	901	ATP	PB-O3B-PG	2.06	139.88	132.83
5	F	901	ATP	PB-O3B-PG	2.05	139.86	132.83

There are no chirality outliers.

All (45) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	901	ATP	PB-O3B-PG-O2G
6	A	902	ADP	PA-O3A-PB-O2B
6	B	902	ADP	C5'-O5'-PA-O3A
6	C	901	ADP	PA-O3A-PB-O2B
6	C	901	ADP	PA-O3A-PB-O3B
6	E	902	ADP	C5'-O5'-PA-O1A
6	E	902	ADP	C5'-O5'-PA-O3A
6	E	902	ADP	C4'-C5'-O5'-PA
6	F	902	ADP	C3'-C4'-C5'-O5'
6	A	902	ADP	O4'-C4'-C5'-O5'
6	A	902	ADP	C3'-C4'-C5'-O5'
6	F	902	ADP	O4'-C4'-C5'-O5'
6	F	902	ADP	C4'-C5'-O5'-PA
5	D	901	ATP	PA-O3A-PB-O1B
6	C	902	ADP	PB-O3A-PA-O1A
6	B	902	ADP	C3'-C4'-C5'-O5'
5	B	901	ATP	PB-O3B-PG-O1G
6	A	902	ADP	PA-O3A-PB-O1B
5	A	901	ATP	PB-O3B-PG-O2G
5	E	901	ATP	PB-O3B-PG-O2G
6	D	902	ADP	PB-O3A-PA-O1A
6	B	902	ADP	C5'-O5'-PA-O1A
6	A	902	ADP	C4'-C5'-O5'-PA
6	C	902	ADP	PB-O3A-PA-O2A
6	D	902	ADP	PB-O3A-PA-O2A
5	D	901	ATP	O4'-C4'-C5'-O5'
5	B	901	ATP	PA-O3A-PB-O1B
5	F	901	ATP	PA-O3A-PB-O1B
5	D	901	ATP	PB-O3B-PG-O1G
5	A	901	ATP	PB-O3B-PG-O3G
5	B	901	ATP	PB-O3B-PG-O2G
5	B	901	ATP	PB-O3B-PG-O3G
5	E	901	ATP	PB-O3B-PG-O3G
5	F	901	ATP	PB-O3B-PG-O3G
6	F	902	ADP	C5'-O5'-PA-O3A
6	D	902	ADP	O4'-C4'-C5'-O5'
5	F	901	ATP	PA-O3A-PB-O3B
6	C	901	ADP	C5'-O5'-PA-O1A
6	F	902	ADP	C5'-O5'-PA-O2A
5	A	901	ATP	O4'-C4'-C5'-O5'
5	B	901	ATP	O4'-C4'-C5'-O5'
5	E	901	ATP	O4'-C4'-C5'-O5'
5	F	901	ATP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
6	C	901	ADP	O4'-C4'-C5'-O5'
6	C	902	ADP	O4'-C4'-C5'-O5'

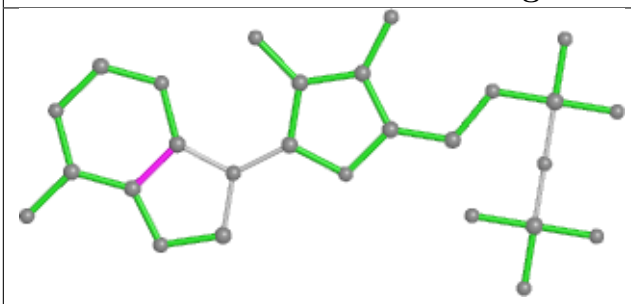
There are no ring outliers.

9 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	902	ADP	1	0
5	D	901	ATP	1	0
6	A	902	ADP	1	0
5	B	901	ATP	1	0
5	A	901	ATP	1	0
6	C	902	ADP	2	0
6	D	902	ADP	1	0
5	E	901	ATP	1	0
6	E	902	ADP	2	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 ADP B 902



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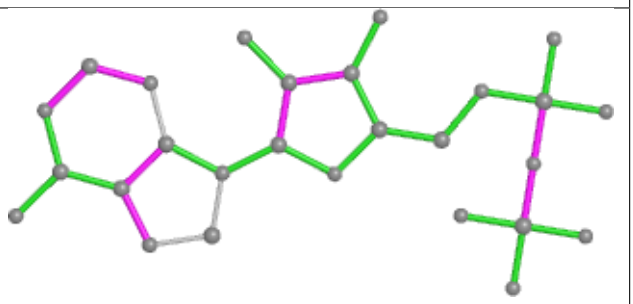
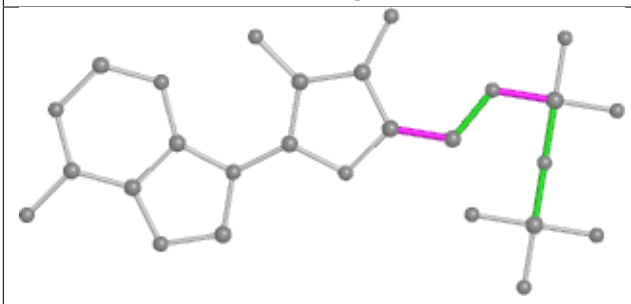
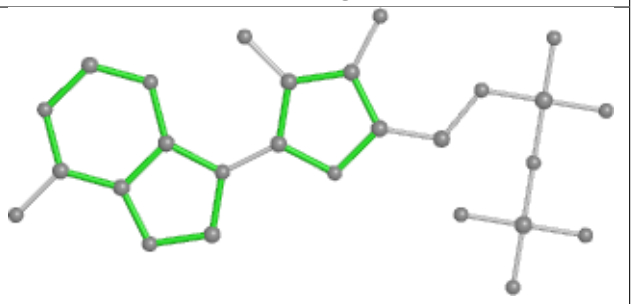


Bond angles

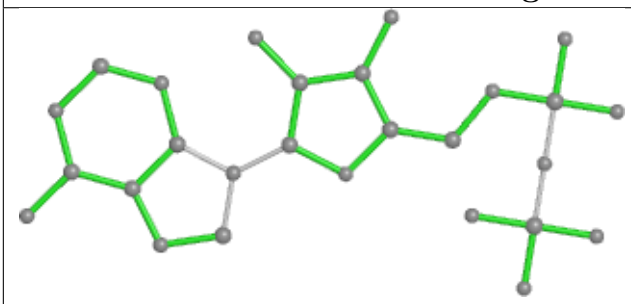


Torsions



Rings

Ligand ADP C 901



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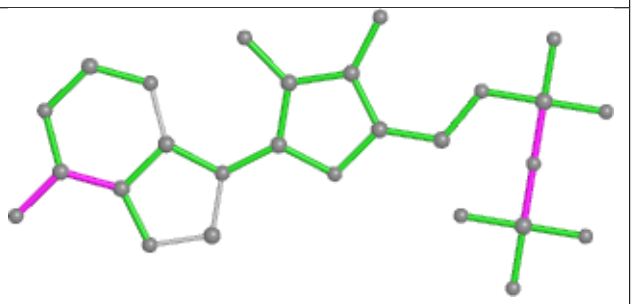

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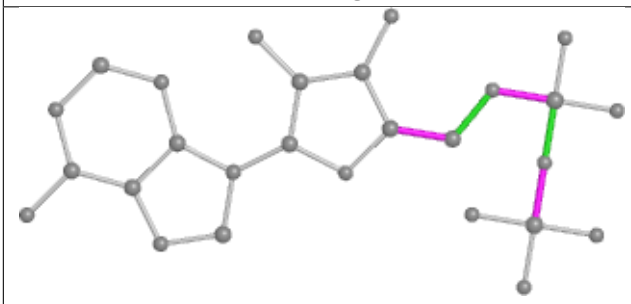

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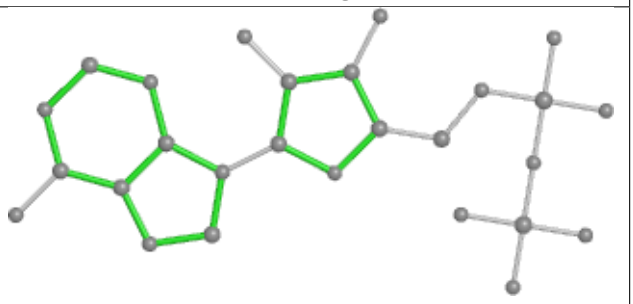
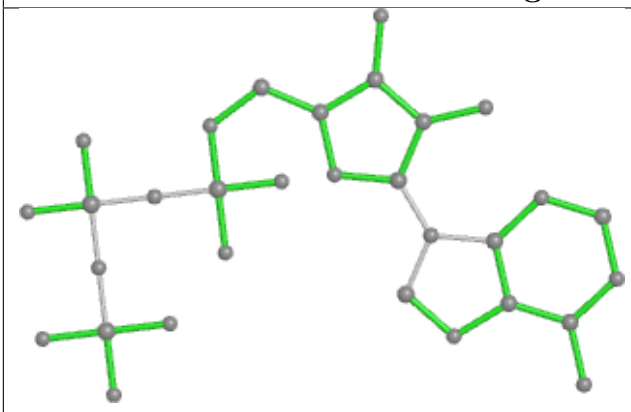


Rings

Ligand ATP D 901



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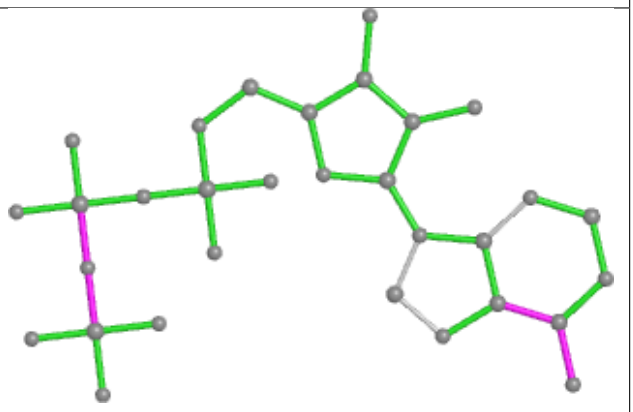

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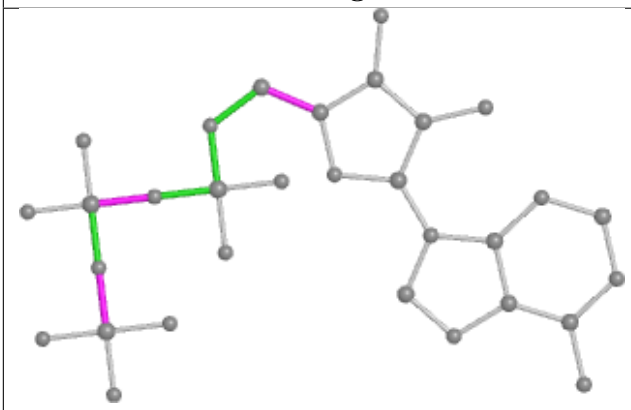

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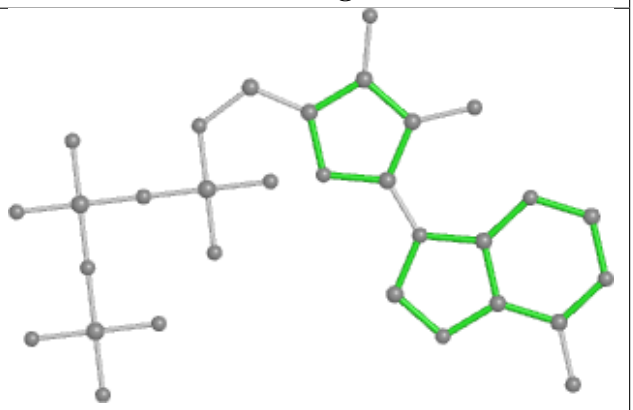
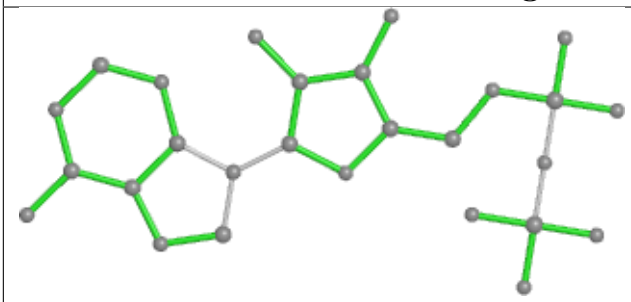


Rings

Ligand ADP A 902



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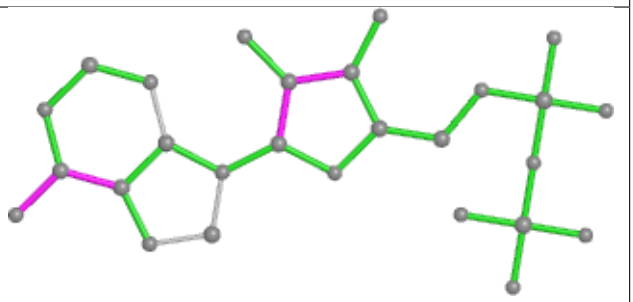

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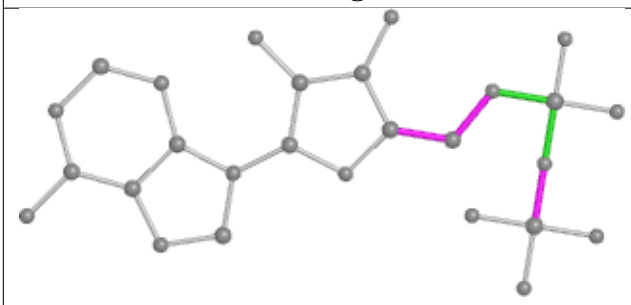

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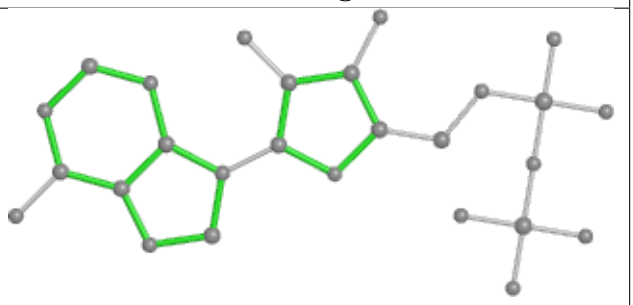
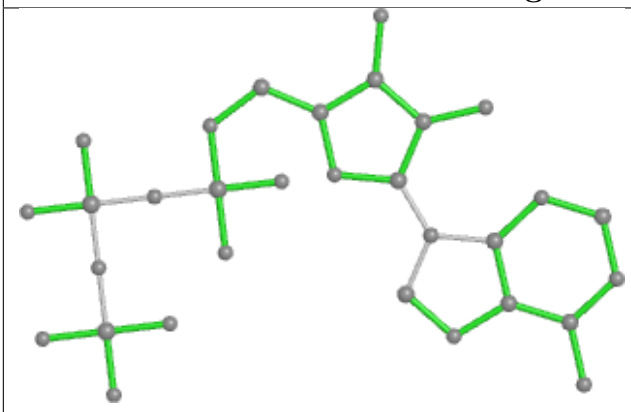


Rings

Ligand ATP B 901



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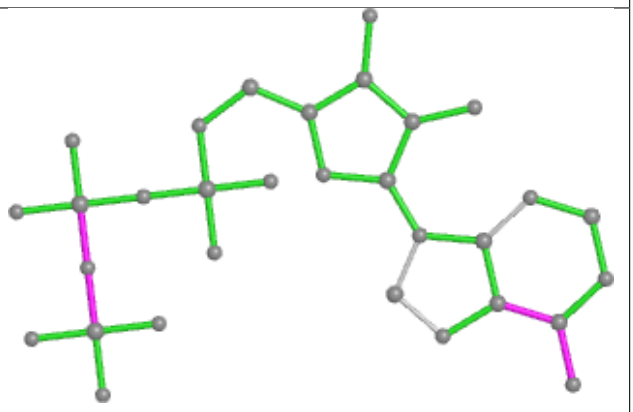

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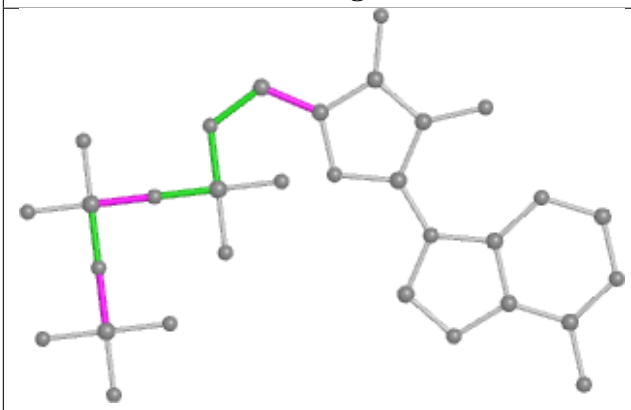

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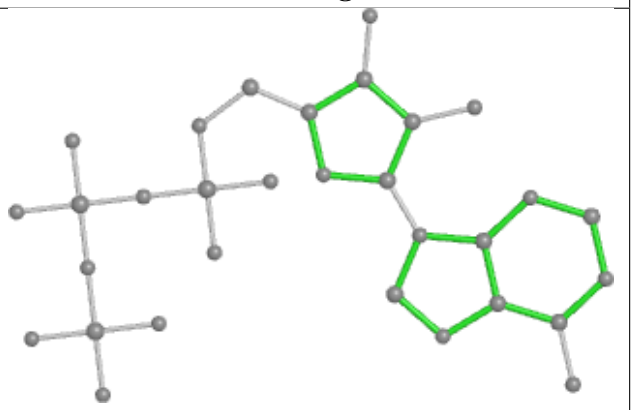

Rings

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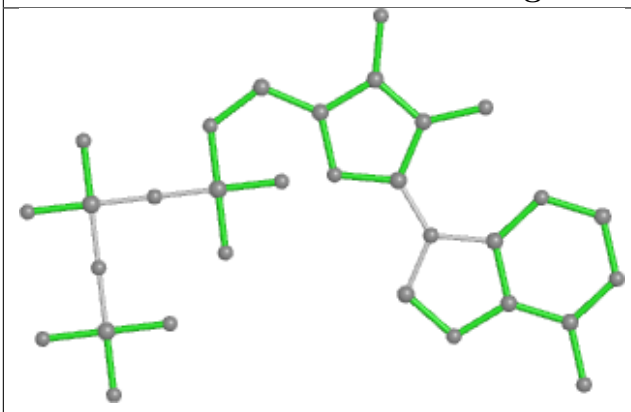

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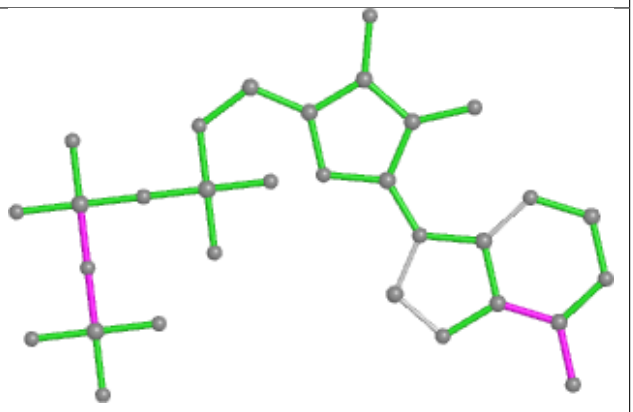

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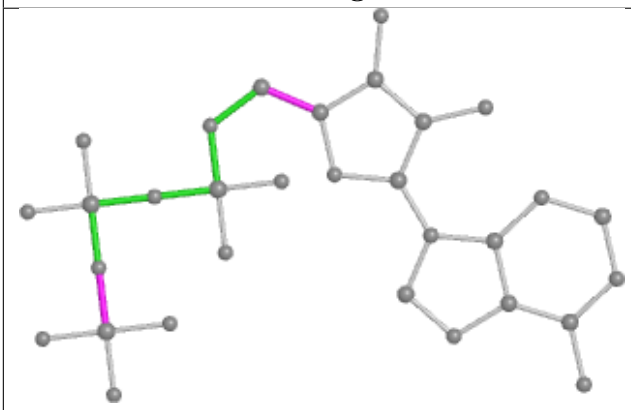

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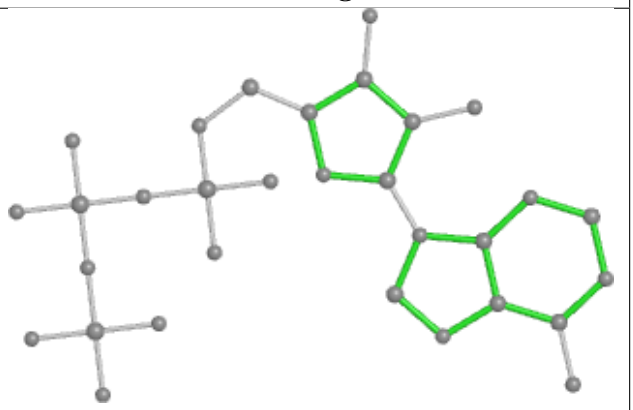
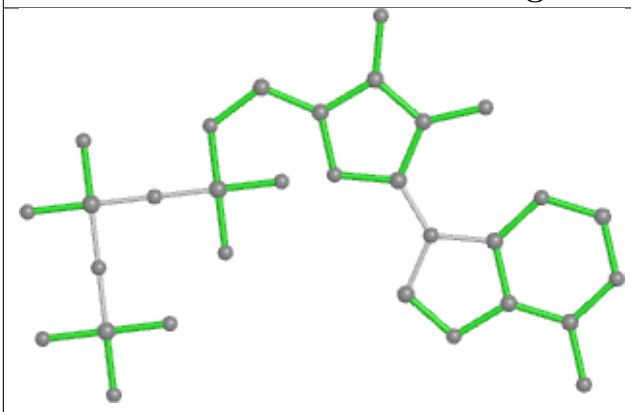


Rings

Ligand ATP F 901



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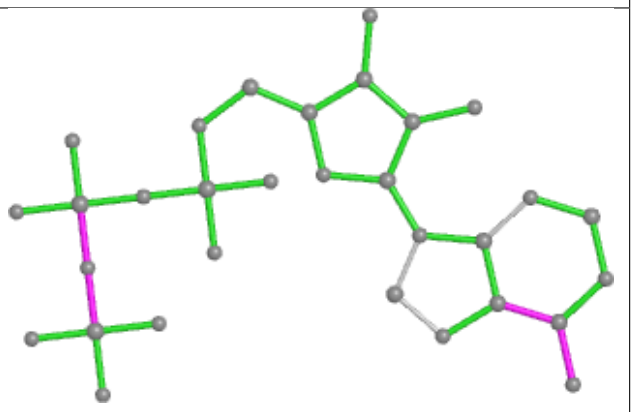

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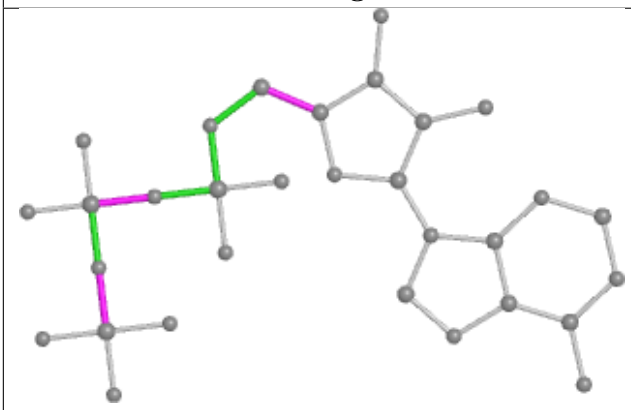

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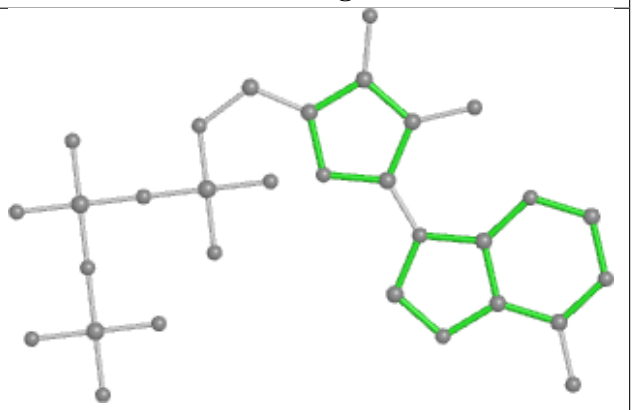
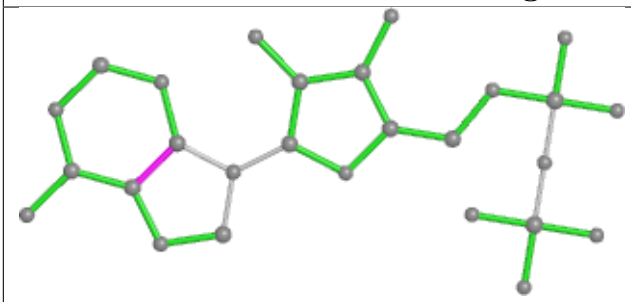


Rings

Ligand ADP C 902



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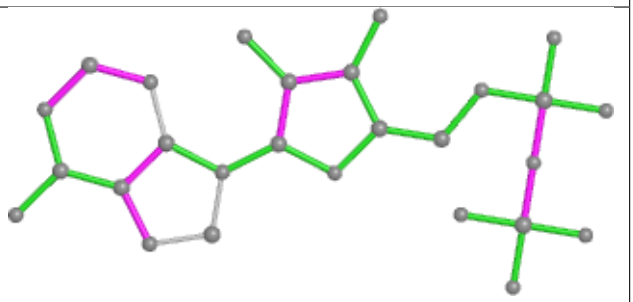
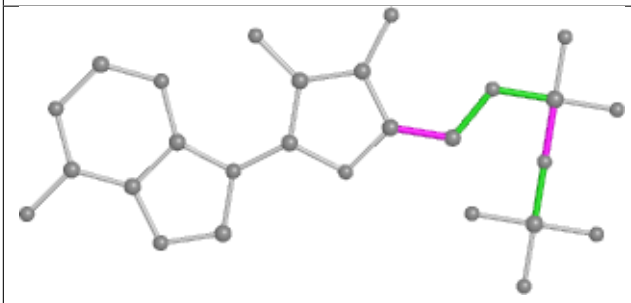
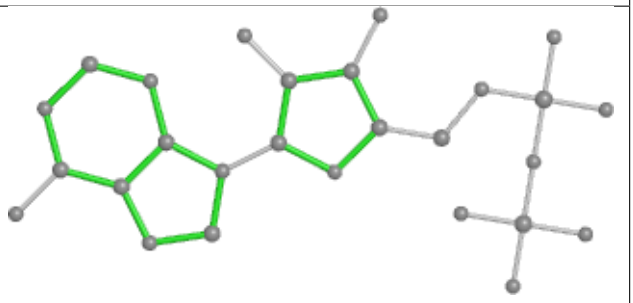


Bond angles

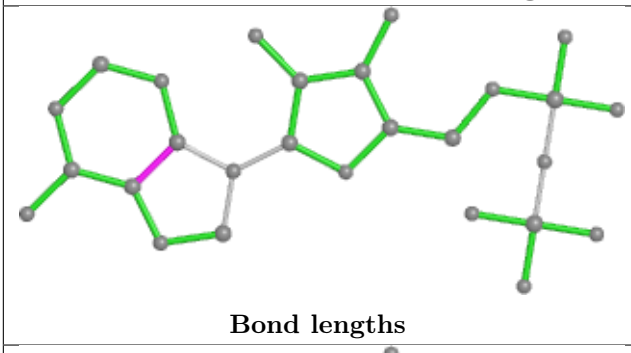


Torsions

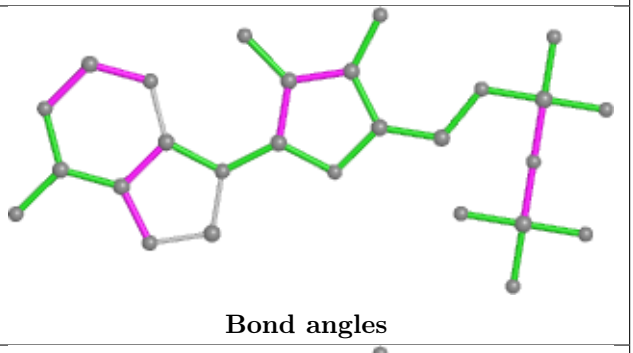


Rings

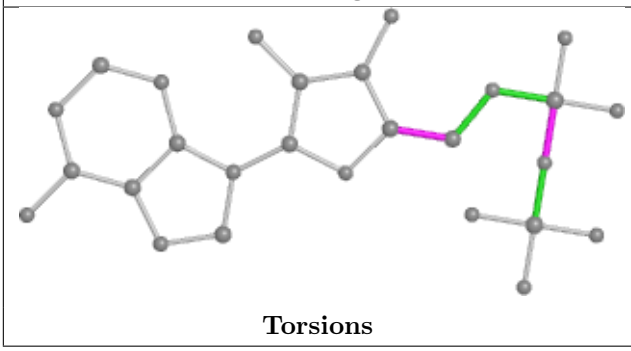
Ligand ADP D 902



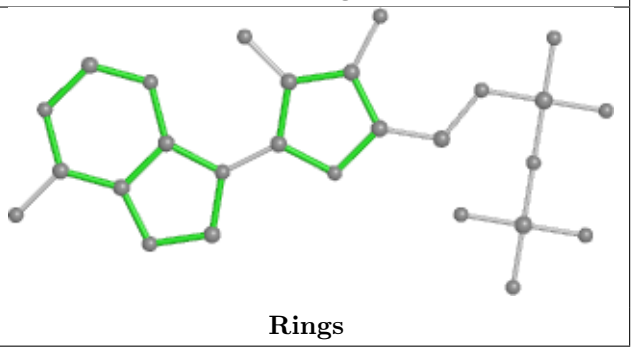
Bond lengths



Bond angles

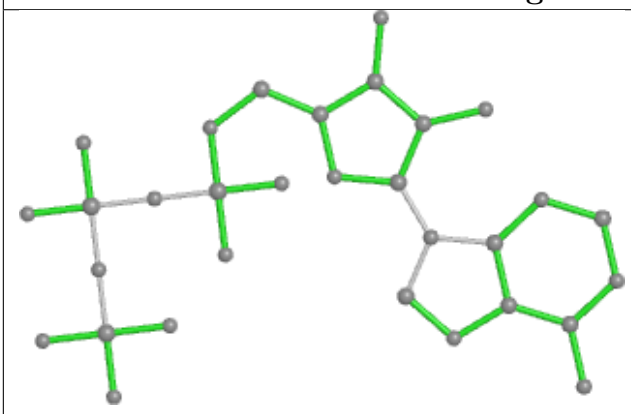


Torsions

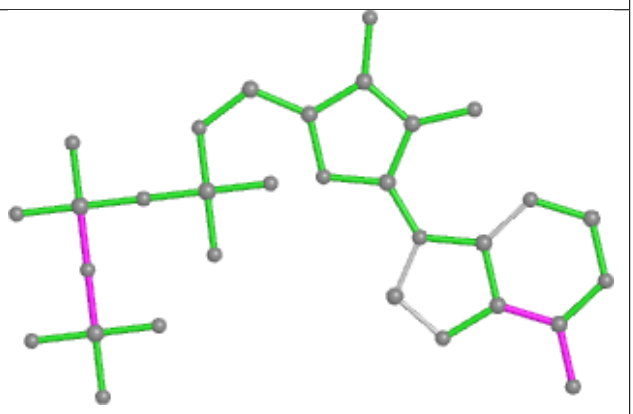


Rings

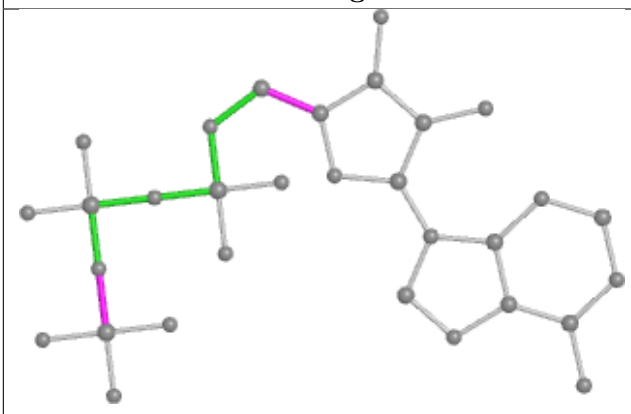
Ligand ATP E 901



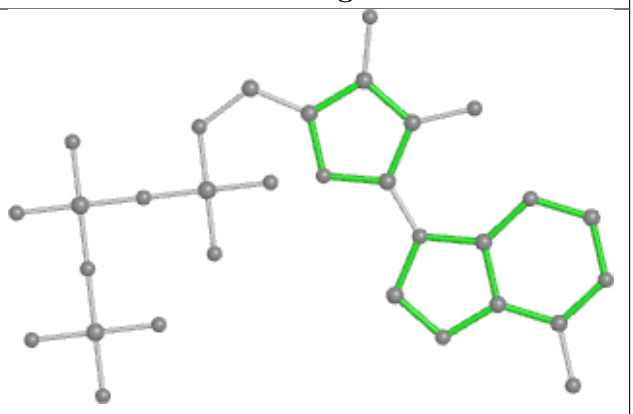
Bond lengths



Bond angles

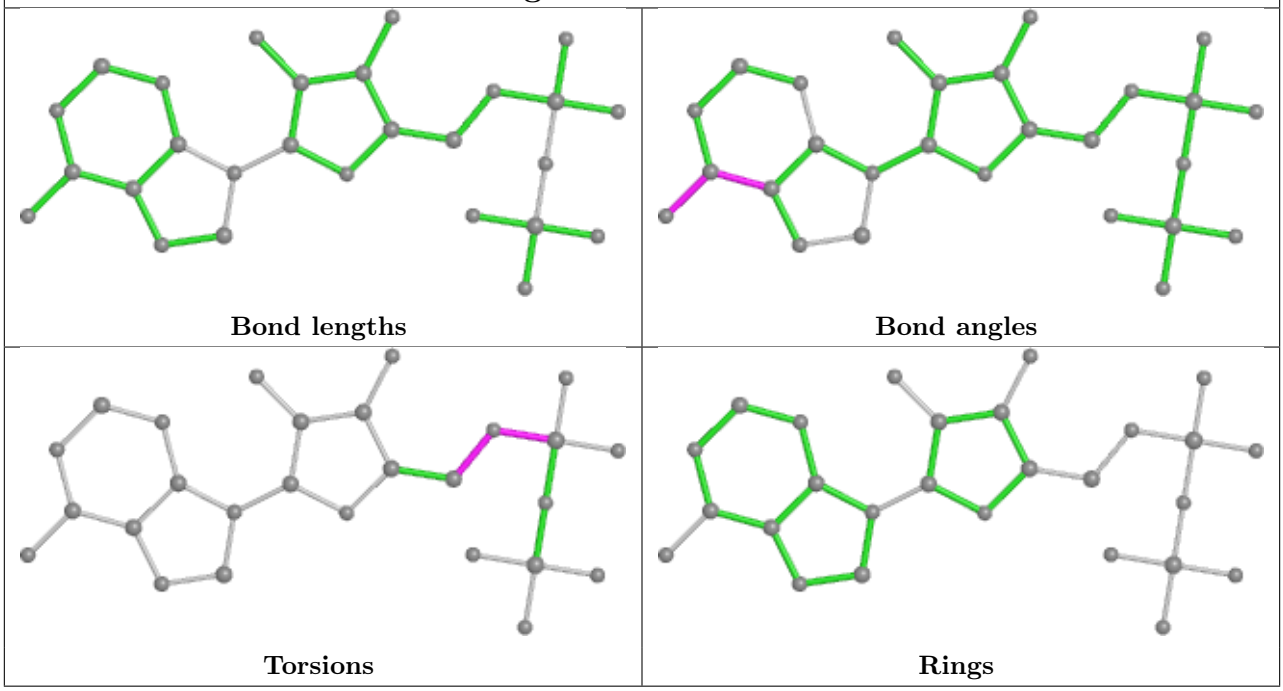


Torsions

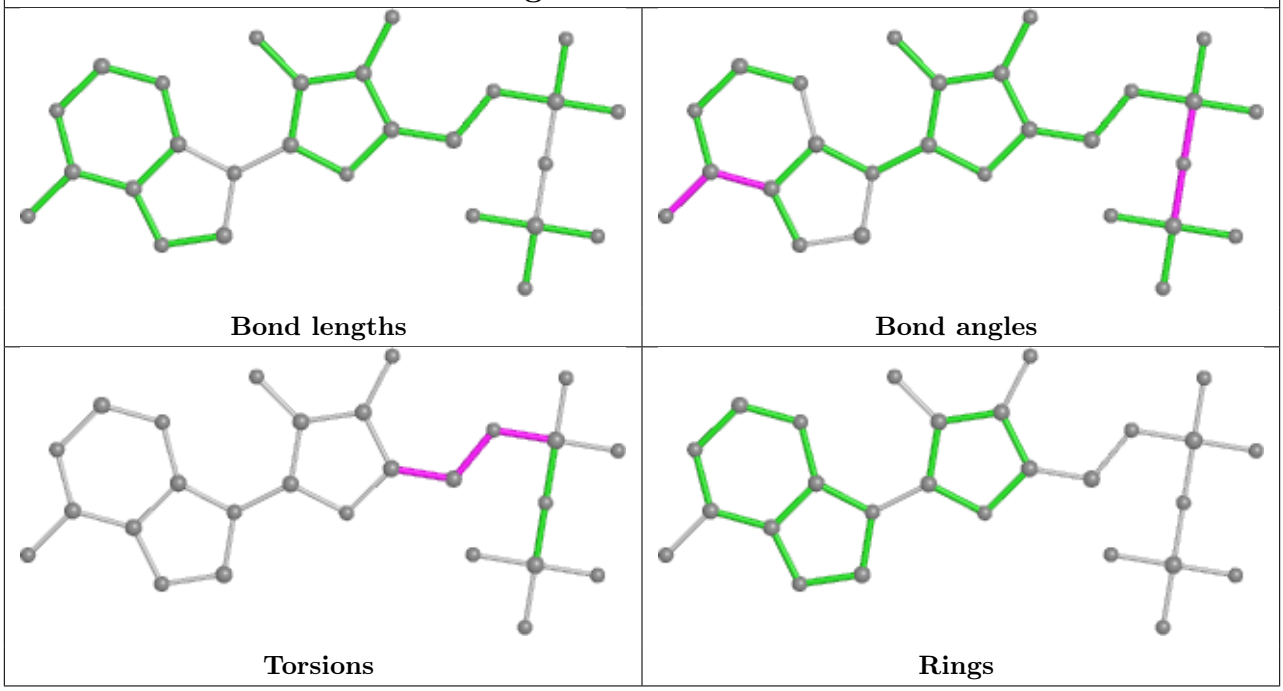


Rings

Ligand ADP E 902



Ligand ADP F 902



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.

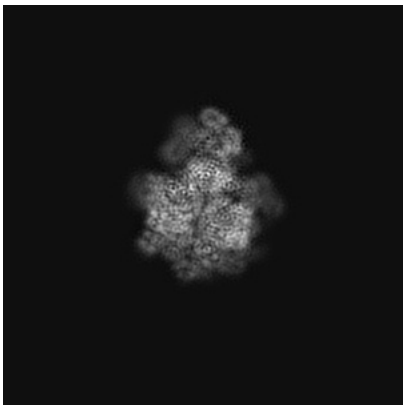
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-27274. These allow visual inspection of the internal detail of the map and identification of artifacts.

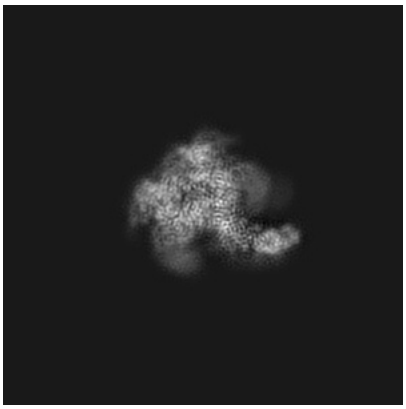
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

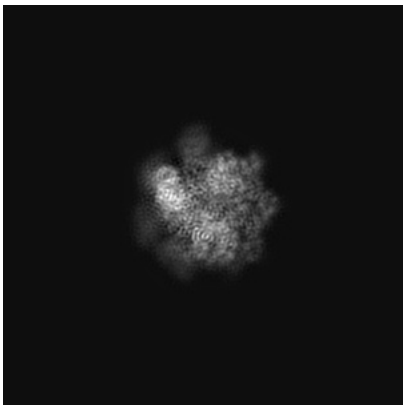
6.1.1 Primary map



X

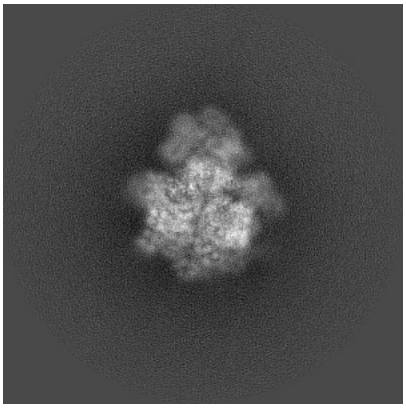


Y

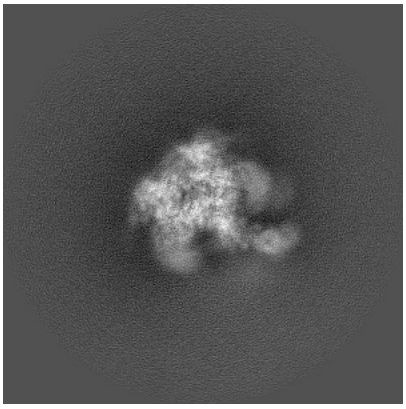


Z

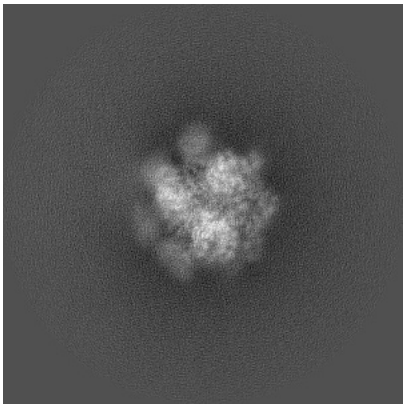
6.1.2 Raw map



X



Y



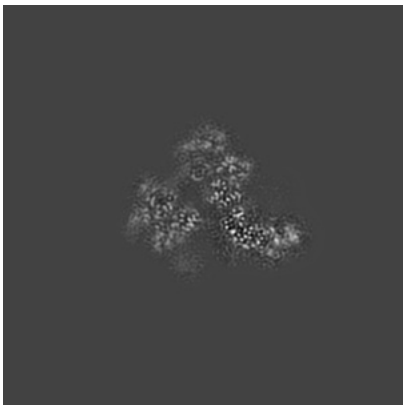
Z

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

6.2 Central slices (i)

6.2.1 Primary map

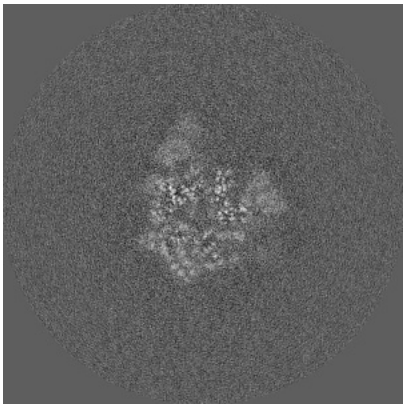
X Index: 192



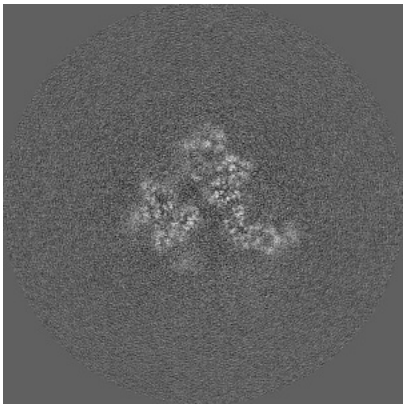
Y Index: 192

Z Index: 192

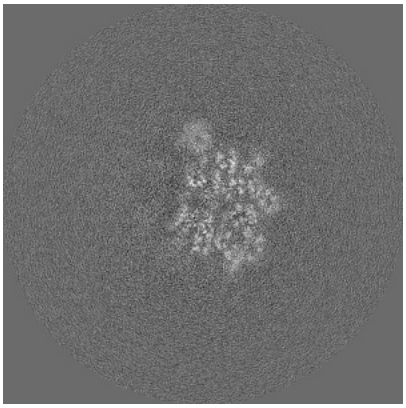
6.2.2 Raw map



X Index: 192



Y Index: 192

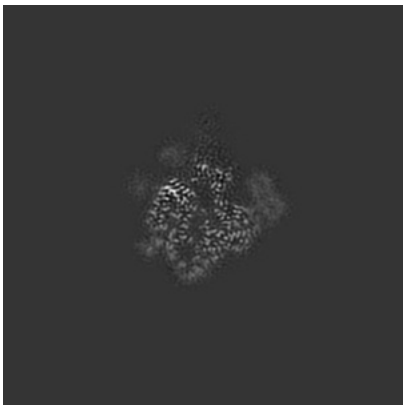


Z Index: 192

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

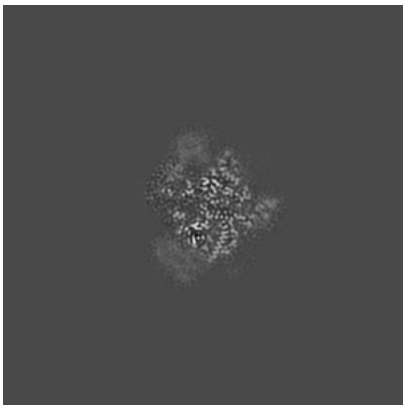
6.3 Largest variance slices (i)

6.3.1 Primary map



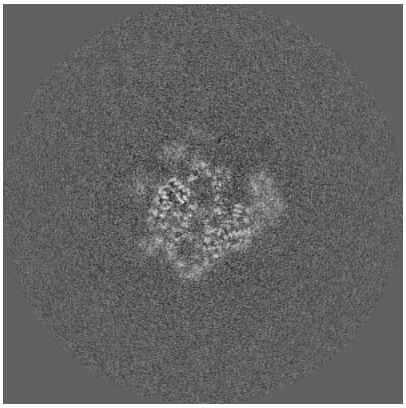
X Index: 183

Y Index: 206

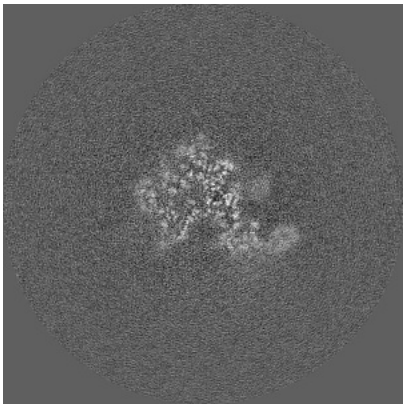


Z Index: 208

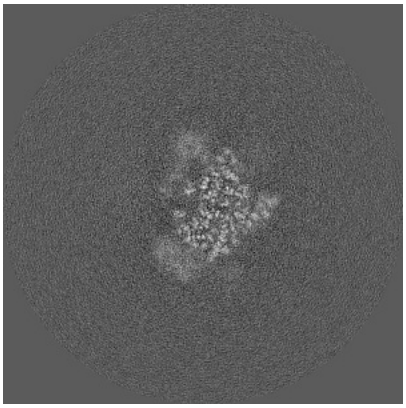
6.3.2 Raw map



X Index: 184



Y Index: 206



Z Index: 207

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

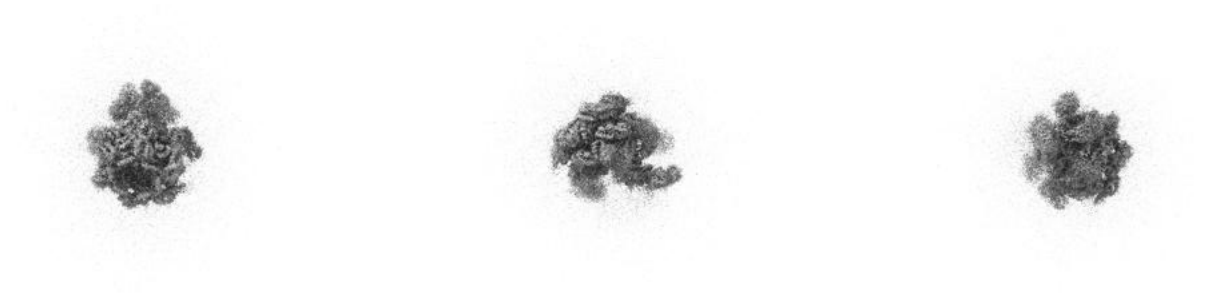
6.4 Orthogonal surface views (i)

6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 9.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

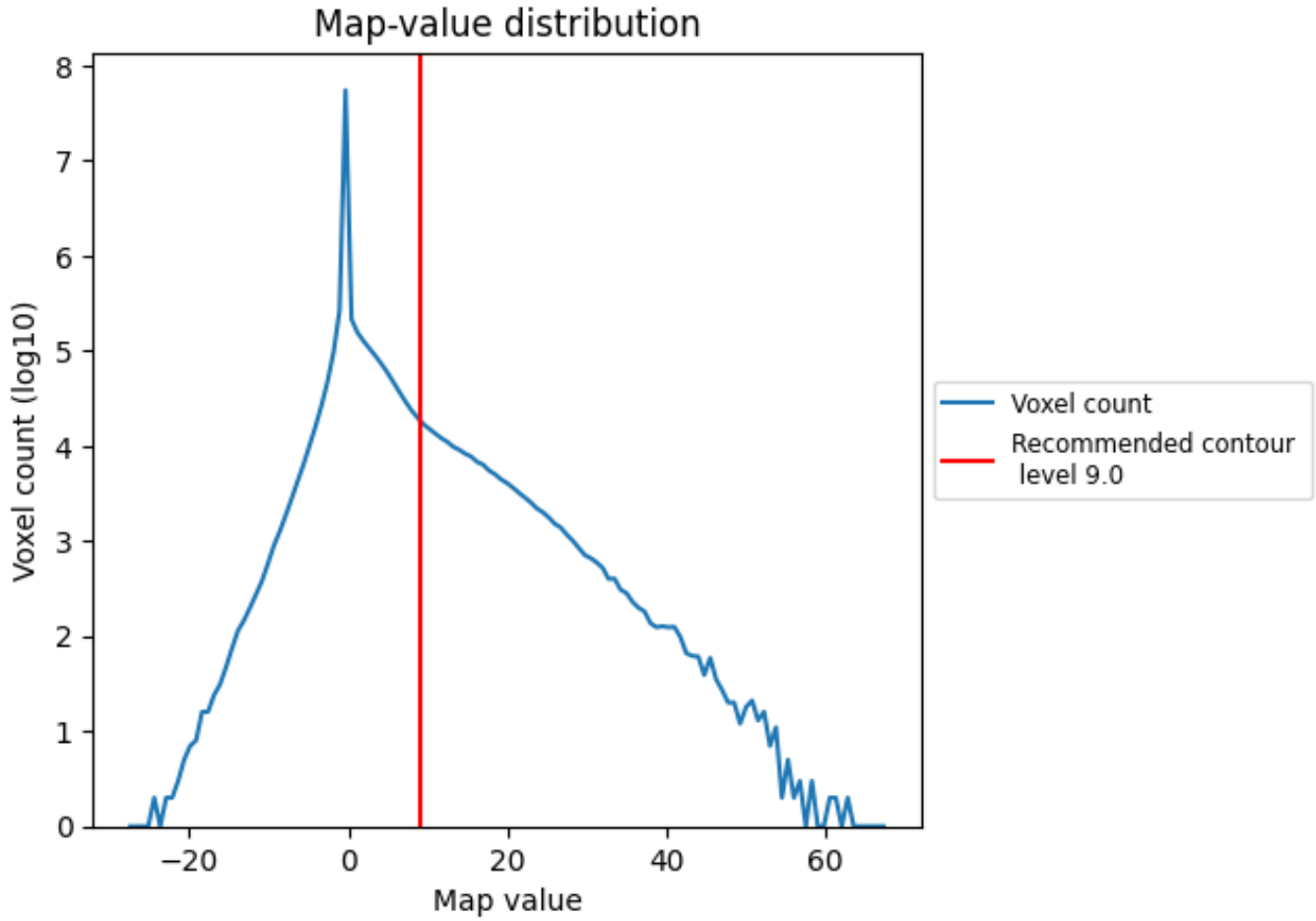
6.5 Mask visualisation (i)

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

7 Map analysis

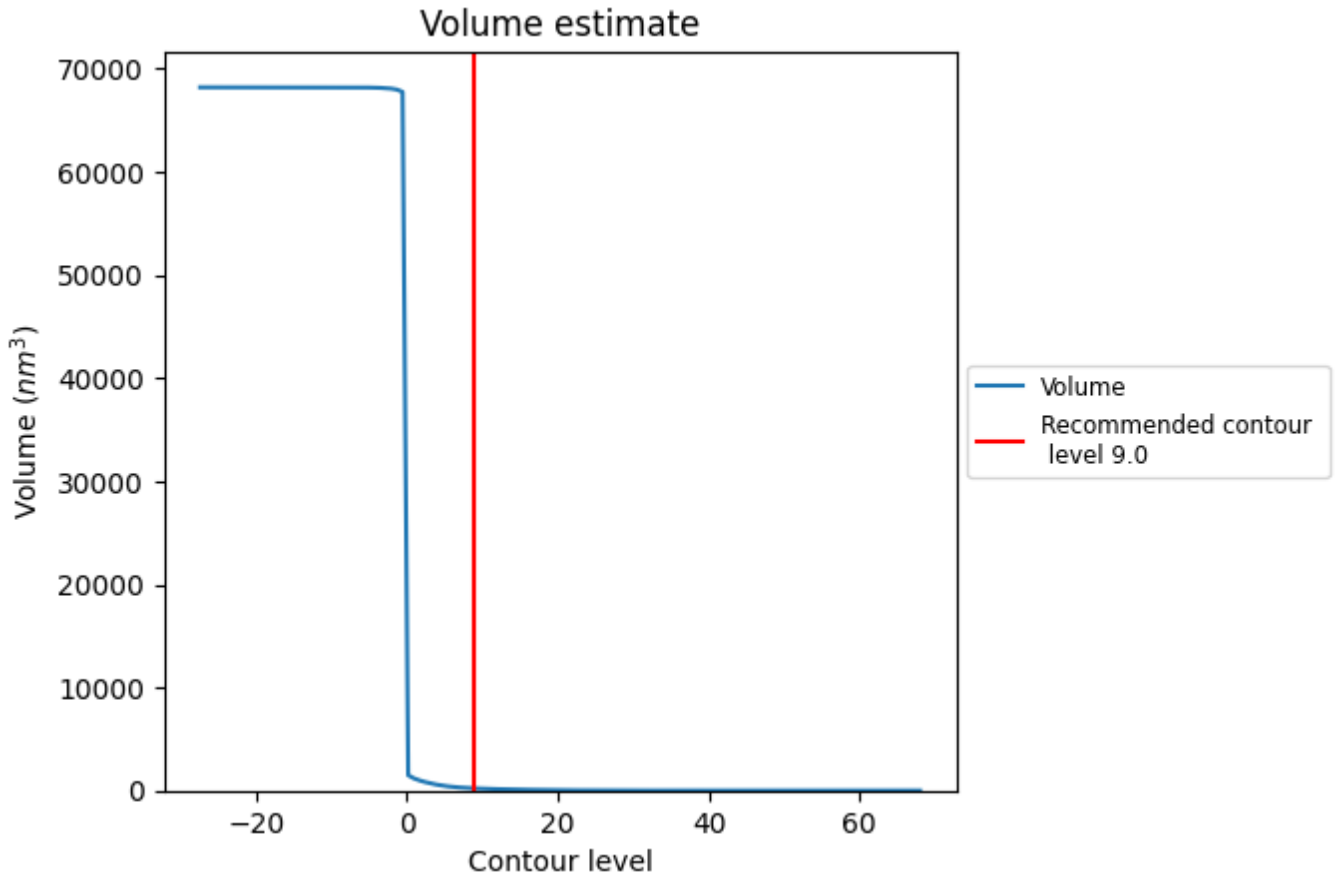
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

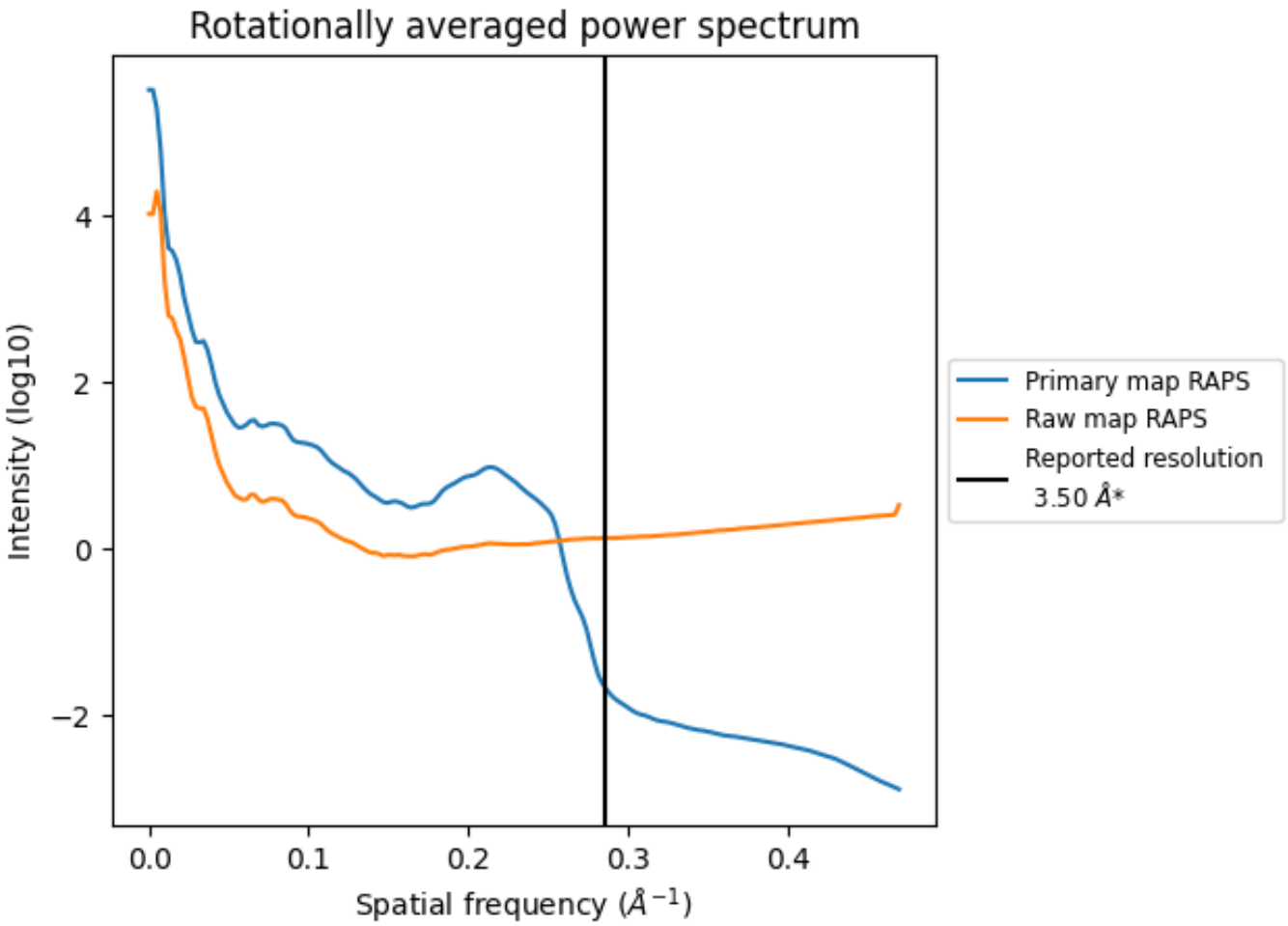
7.2 Volume estimate



The volume at the recommended contour level is 213 nm^3; this corresponds to an approximate mass of 193 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)

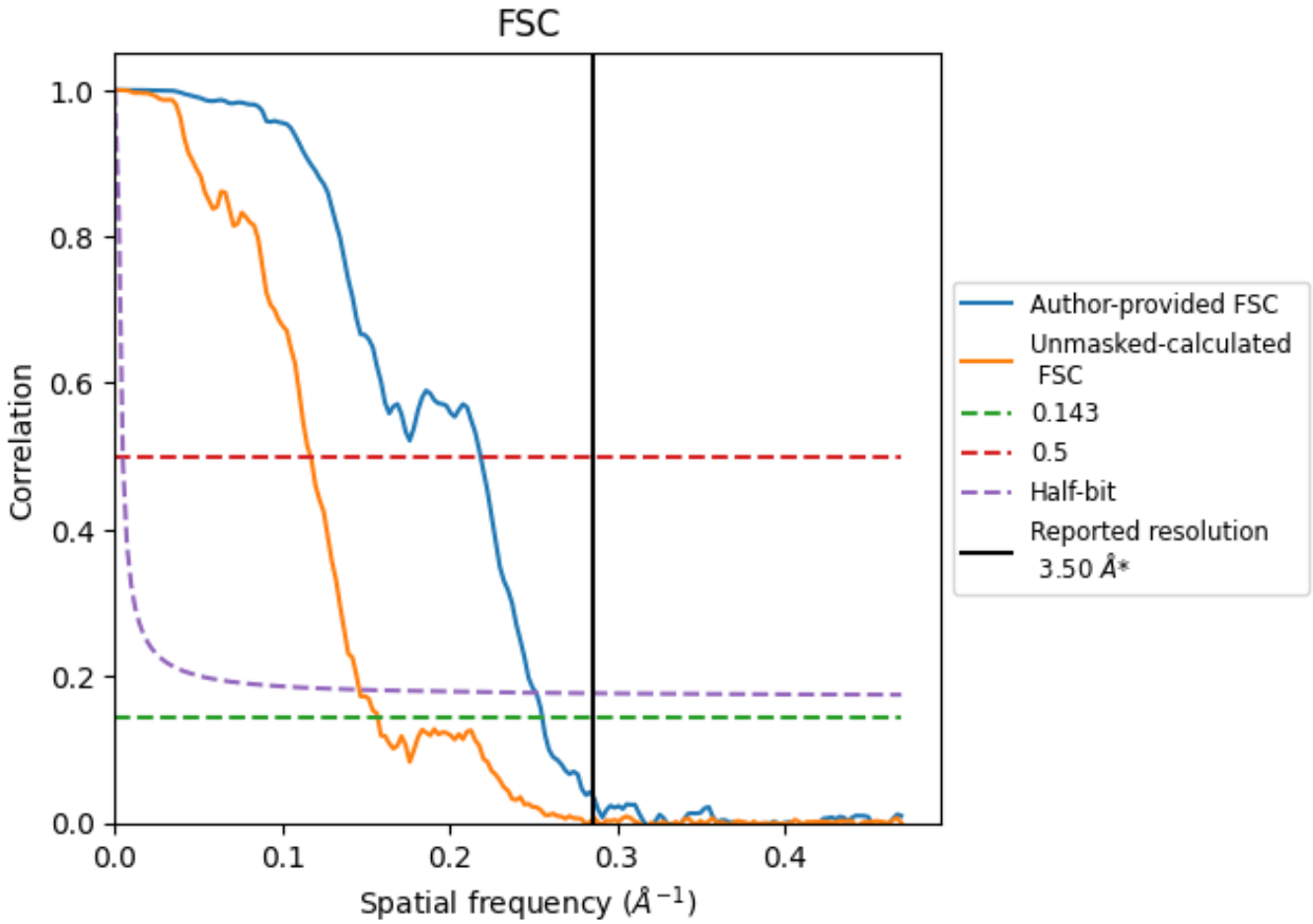


*Reported resolution corresponds to spatial frequency of 0.286 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.286 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.92	4.58	3.97
Unmasked-calculated*	6.37	8.55	6.84

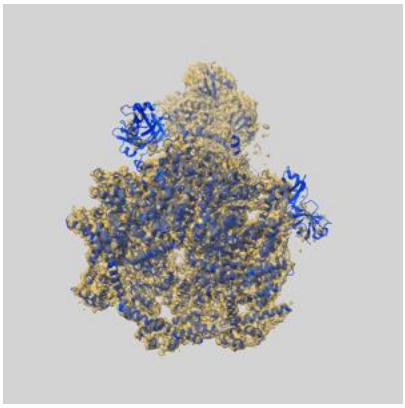
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.92 differs from the reported value 3.5 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.37 differs from the reported value 3.5 by more than 10 %

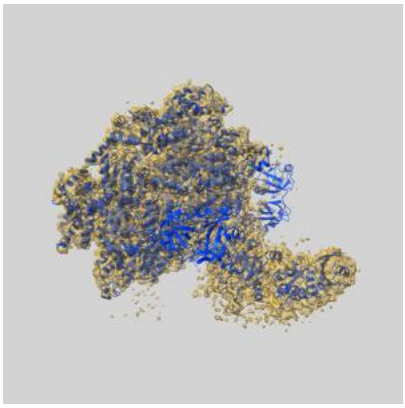
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-27274 and PDB model 8DAS. Per-residue inclusion information can be found in section 3 on page 8.

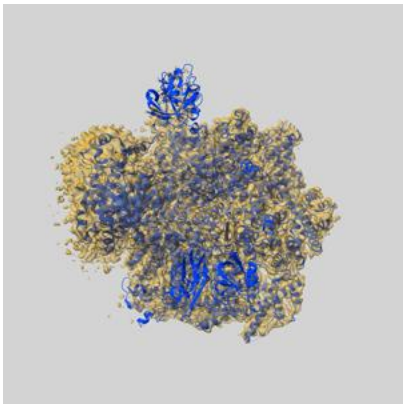
9.1 Map-model overlay



X



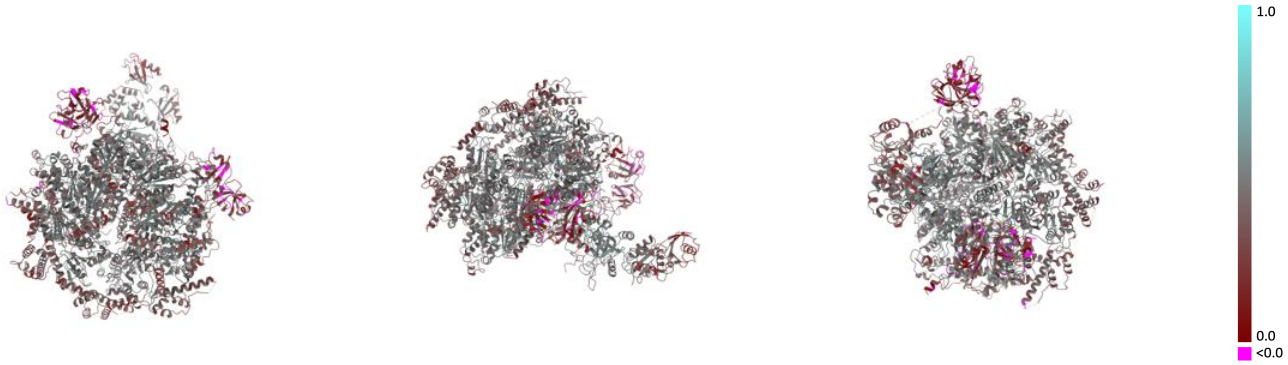
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 9.0 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.

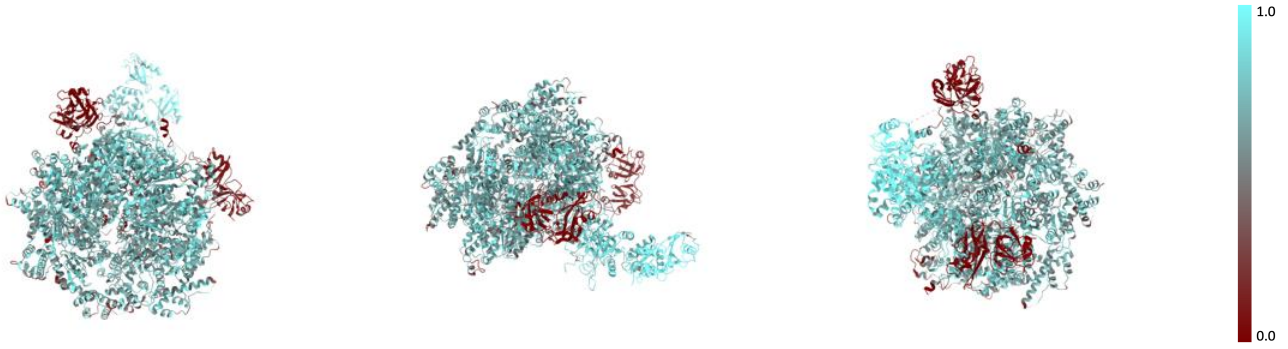
9.2 Q-score mapped to coordinate model (i)



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.

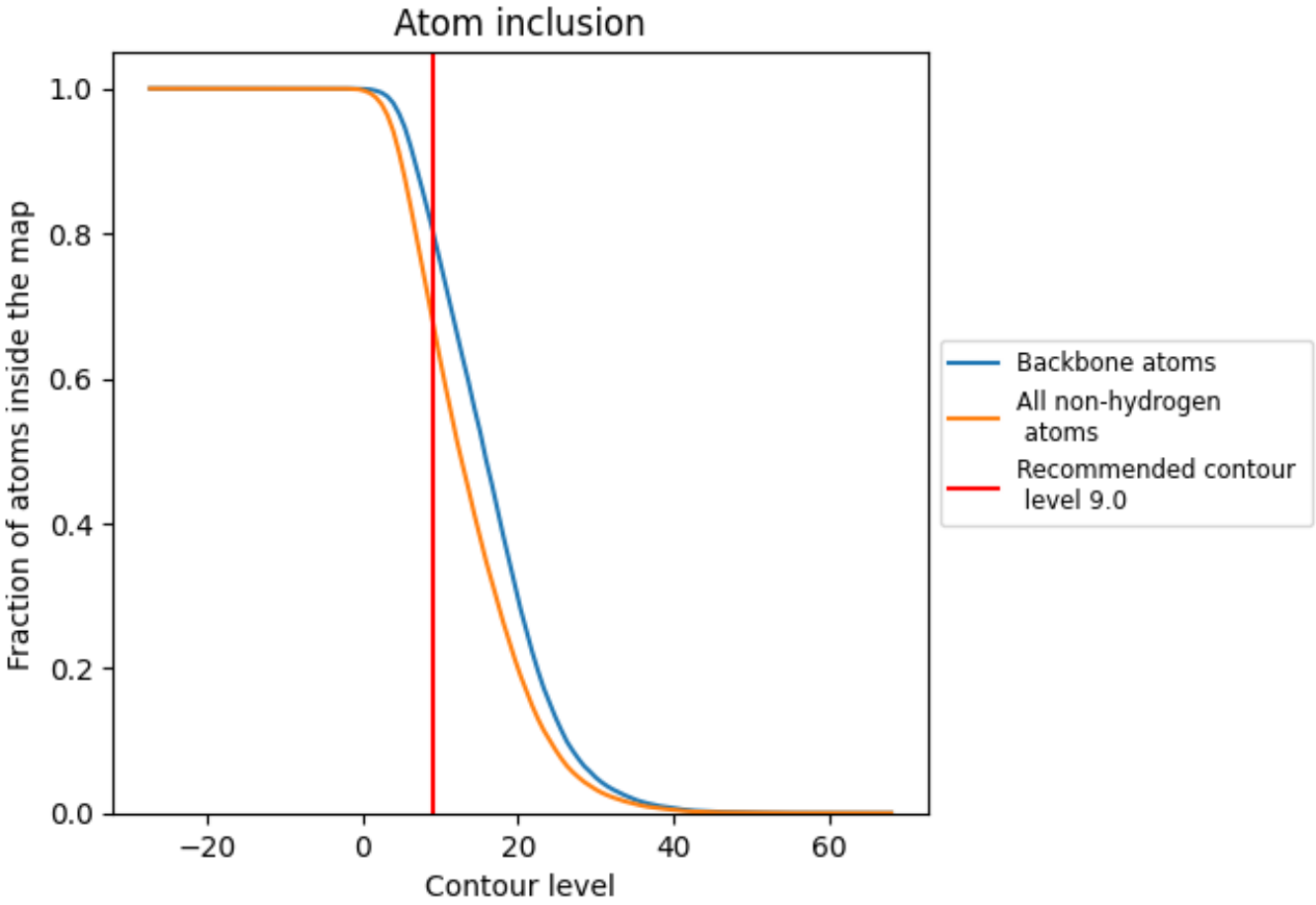
9.3 Atom inclusion mapped to coordinate model (i)



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 (9.0).

9.4 Atom inclusion (i)



At the recommended contour level, 80% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (9.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6785	0.4110
A	0.5585	0.3710
B	0.7072	0.4310
C	0.5608	0.3760
D	0.6928	0.4260
E	0.6926	0.4270
F	0.7011	0.4320
G	0.8541	0.4730
H	0.7321	0.4090
J	0.9408	0.3570
K	0.9120	0.2770