



Full wwPDB EM Validation Report ⓘ

Sep 22, 2024 – 08:35 PM EDT

PDB ID : 8W0F
EMDB ID : EMD-43708
Title : Cryo-EM structure of a human MCM2-7 double hexamer on dsDNA
Authors : Hunker, O.; Yang, R.; Bleichert, F.
Deposited on : 2024-02-13
Resolution : 2.80 Å (reported)

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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.dev112
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.38.3

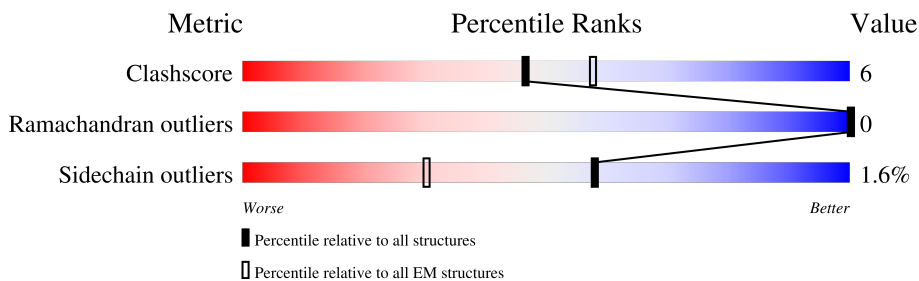
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.






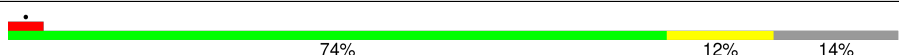
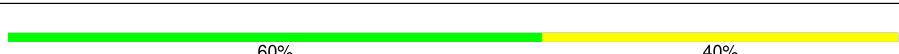
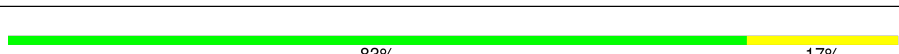
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	2	904	
1	A	904	
2	3	810	
2	B	810	
3	4	866	
3	C	866	
4	5	734	
4	D	734	

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Mol	Chain	Length	Quality of chain
5	6	821	 <p>66% 12% 22%</p>
5	E	821	 <p>9% 72% 13% 15%</p>
6	7	719	 <p>72% 13% 15%</p>
6	F	719	 <p>74% 12% 14%</p>
7	O	47	 <p>60% 40%</p>
8	S	47	 <p>83% 17%</p>

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 126041 atoms, of which 62720 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 DNA replication licensing factor MCM2.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	2	649	10277	3228	5143	917	959	30	0	0
1	A	669	10605	3336	5302	948	989	30	0	0

- Molecule 2 is a protein called DNA replication licensing factor MCM3.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	3	638	10019	3126	5018	879	970	26	0	0
2	B	651	10230	3189	5130	896	989	26	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	-1	SER	-	expression tag	UNP P25205
3	0	ASN	-	expression tag	UNP P25205
3	1	ALA	-	expression tag	UNP P25205
B	-1	SER	-	expression tag	UNP P25205
B	0	ASN	-	expression tag	UNP P25205
B	1	ALA	-	expression tag	UNP P25205

- Molecule 3 is a protein called DNA replication licensing factor MCM4.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	4	648	10367	3246	5206	921	967	27	0	0
3	C	646	10337	3237	5190	919	964	27	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	-2	SER	-	expression tag	UNP P33991
4	-1	ASN	-	expression tag	UNP P33991
4	0	ALA	-	expression tag	UNP P33991
4	650	MET	LEU	variant	UNP P33991
C	-2	SER	-	expression tag	UNP P33991
C	-1	ASN	-	expression tag	UNP P33991
C	0	ALA	-	expression tag	UNP P33991
C	650	MET	LEU	variant	UNP P33991

- Molecule 4 is a protein called DNA replication licensing factor MCM5.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	5	627	Total 9855	C 3073	H 4950	N 873	O 924	S 35	0	0
4	D	625	Total 9814	C 3061	H 4932	N 868	O 918	S 35	0	0

- Molecule 5 is a protein called DNA replication licensing factor MCM6.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	6	637	Total 10175	C 3187	H 5099	N 903	O 960	S 26	0	0
5	E	696	Total 11209	C 3510	H 5631	N 986	O 1055	S 27	0	0

- Molecule 6 is a protein called DNA replication licensing factor MCM7.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	7	614	Total 9804	C 3057	H 4928	N 865	O 922	S 32	0	0
6	F	621	Total 9921	C 3091	H 4988	N 878	O 932	S 32	0	0

- Molecule 7 is a DNA chain called DNA (47-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
7	O	47	Total 1505	C 470	H 542	N 163	O 283	P 47	0	0

- Molecule 8 is a DNA chain called DNA (47-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
8	S	47	1505	470	541	166	281	47	0	0

- Molecule 9 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
9	2	1	Total	Zn	0
			1	1	
9	4	1	Total	Zn	0
			1	1	
9	5	1	Total	Zn	0
			1	1	
9	6	1	Total	Zn	0
			1	1	
9	7	1	Total	Zn	0
			1	1	
9	A	1	Total	Zn	0
			1	1	
9	C	1	Total	Zn	0
			1	1	
9	D	1	Total	Zn	0
			1	1	
9	E	1	Total	Zn	0
			1	1	
9	F	1	Total	Zn	0
			1	1	

- Molecule 10 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

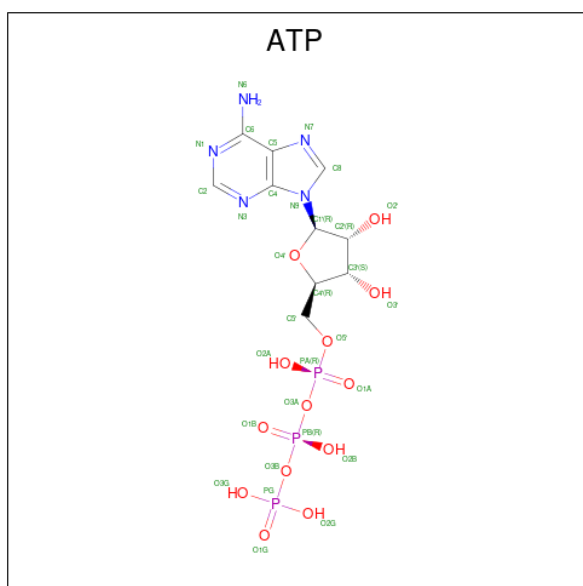
Mol	Chain	Residues	Atoms		AltConf
10	2	1	Total	Mg	0
			1	1	
10	3	1	Total	Mg	0
			1	1	
10	5	1	Total	Mg	0
			1	1	
10	6	1	Total	Mg	0
			1	1	
10	7	1	Total	Mg	0
			1	1	
10	A	1	Total	Mg	0
			1	1	
10	B	1	Total	Mg	0
			1	1	

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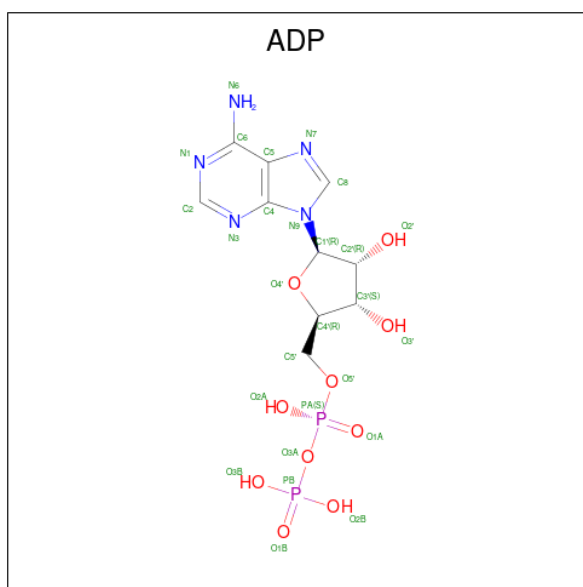
Mol	Chain	Residues	Atoms		AltConf
10	D	1	Total	Mg	0
			1	1	
10	E	1	Total	Mg	0
			1	1	
10	F	1	Total	Mg	0
			1	1	

- Molecule 11 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).

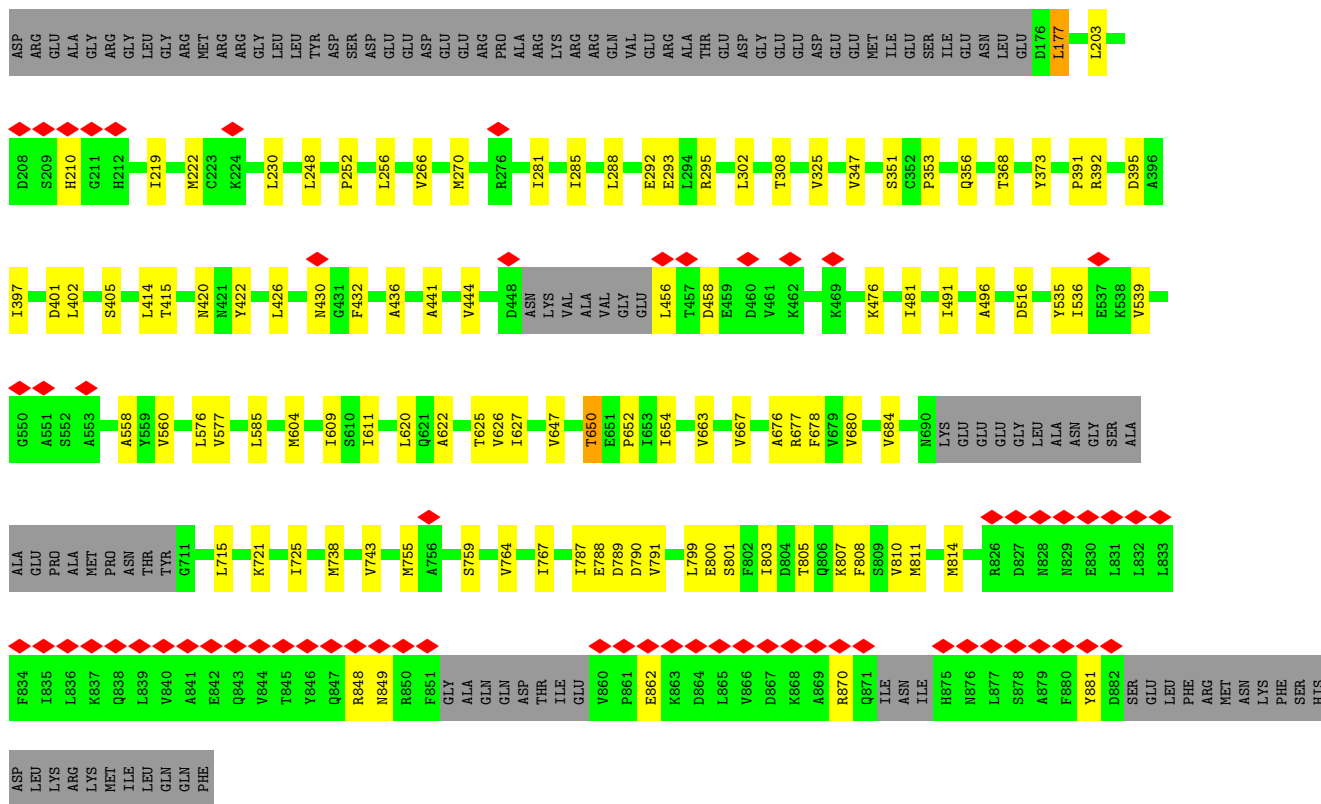


Mol	Chain	Residues	Atoms					AltConf	
11	2	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
11	A	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	

- Molecule 12 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

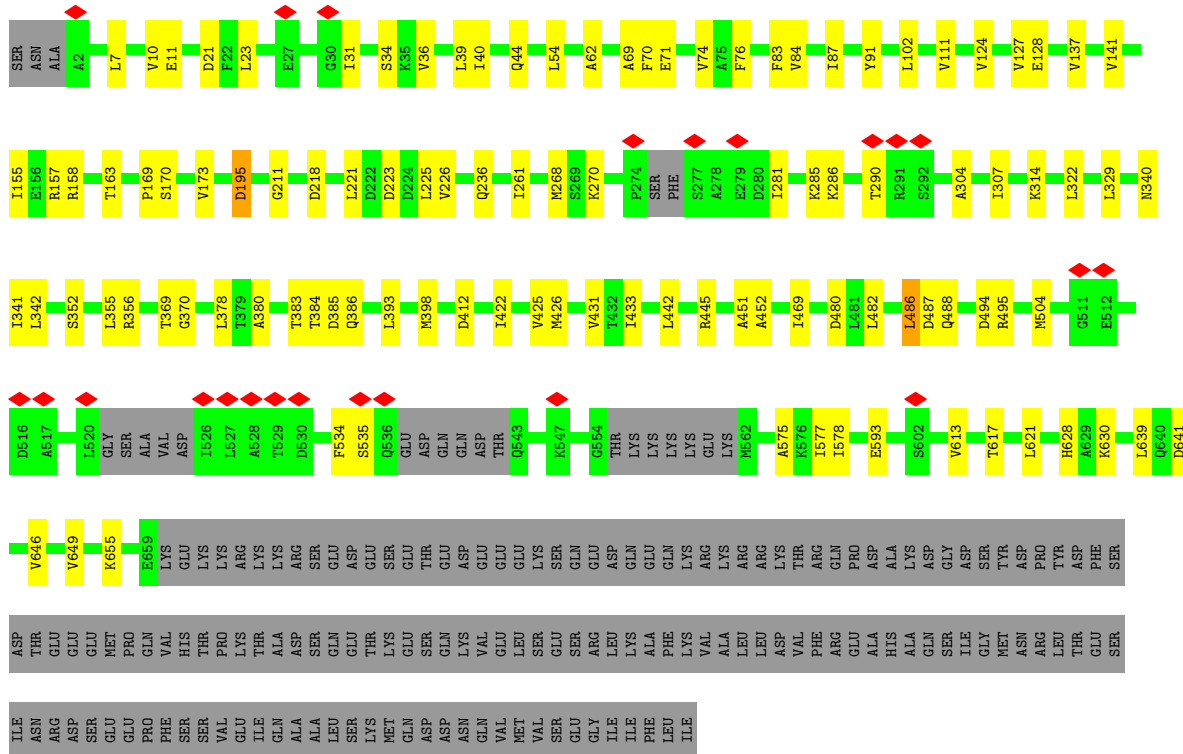


Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
12	3	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
12	5	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
12	6	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
12	7	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
12	B	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
12	D	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
12	E	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
12	F	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	



• Molecule 2: DNA replication licensing factor MCM3

Chain 3:



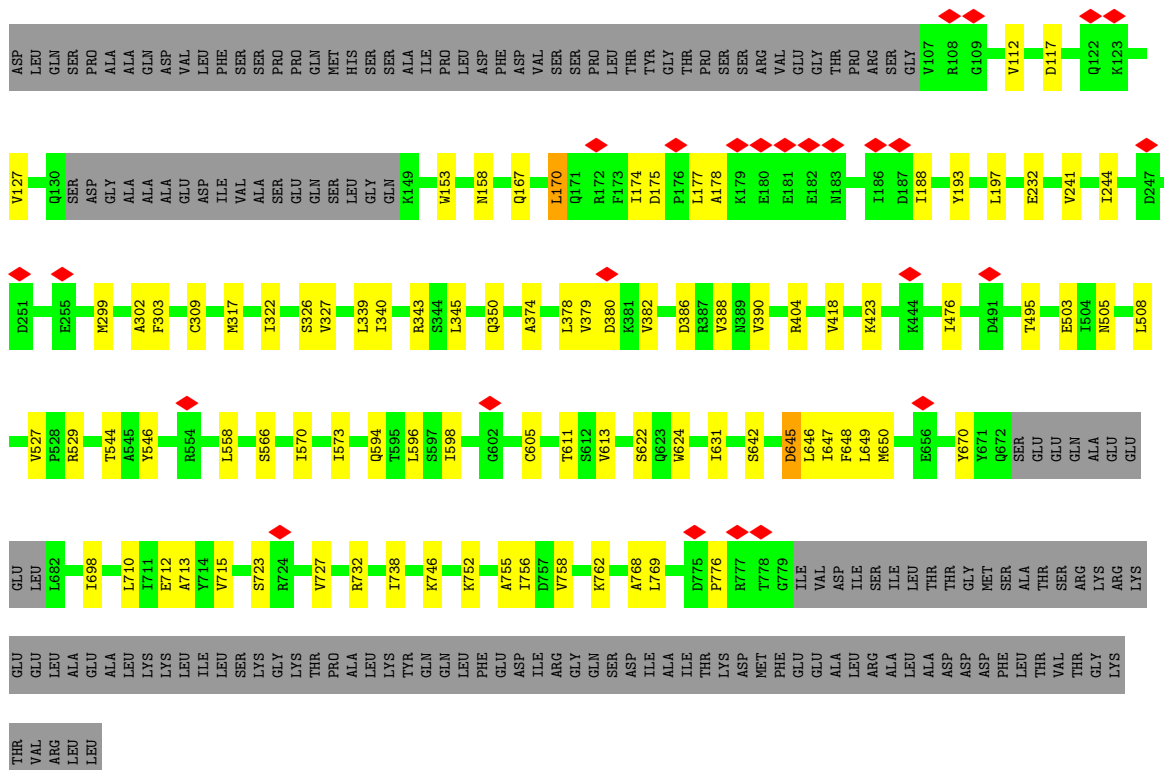
ALA
LEU
ARG
ALA
LEU
ALA
ASP
ASP
PHE
LEU
THR
THR
THR
GLY
LYS
THR
VAL
ARG
LEU
LEU

• Molecule 3: DNA replication licensing factor MCM4

Chain C:



SER
ASN
MET
SER
PRO
PRO
ALA
SER
THR
SER
ARG
ARG
GLY
SER
GLN
ARG
ARG
GLY
ARG
ALA
THR
PRO
ALA
GLN
THR
PRO
ARG
GLU
SER
ASP
ALA
ARG
SER
SER
PRO
GLN
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LEU
GLN
PRO
MET
PRO
THR
SER
PRO
GLY
VAL

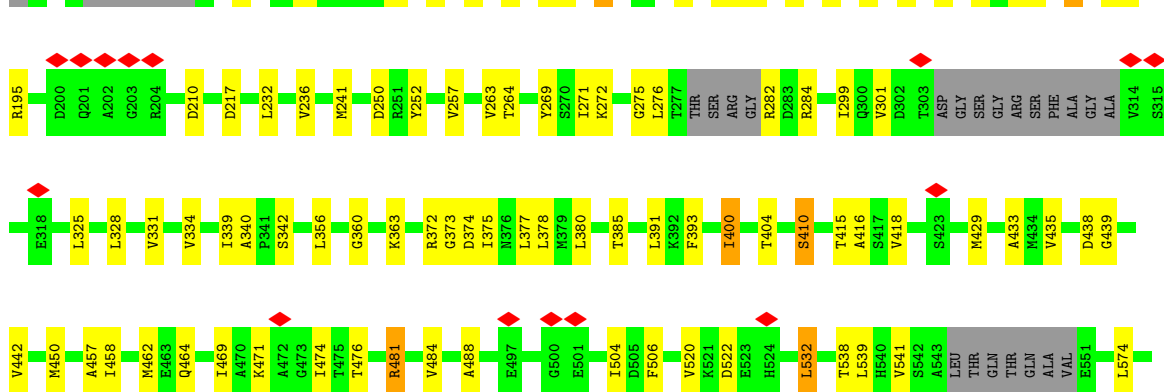


• Molecule 4: DNA replication licensing factor MCM5

Chain 5:

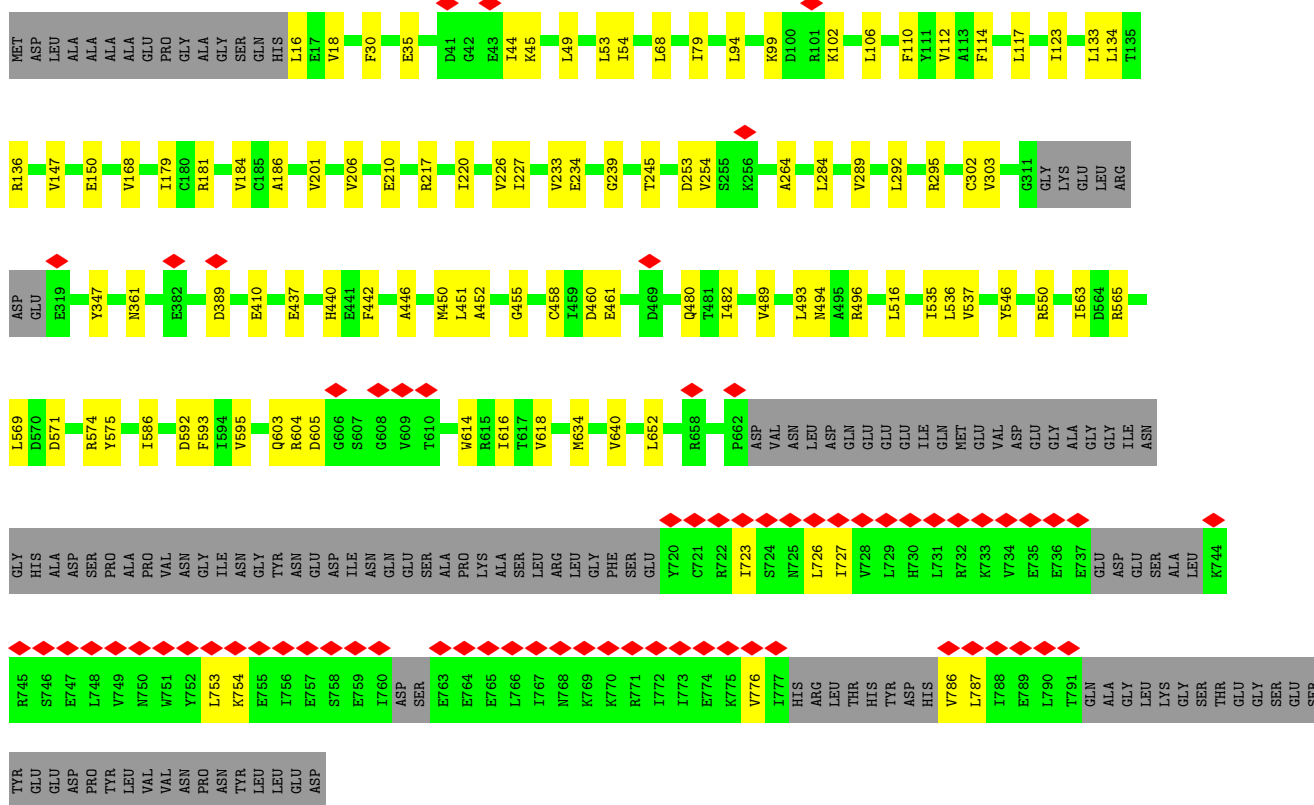


THR
VAL
ARG
LEU
LEU

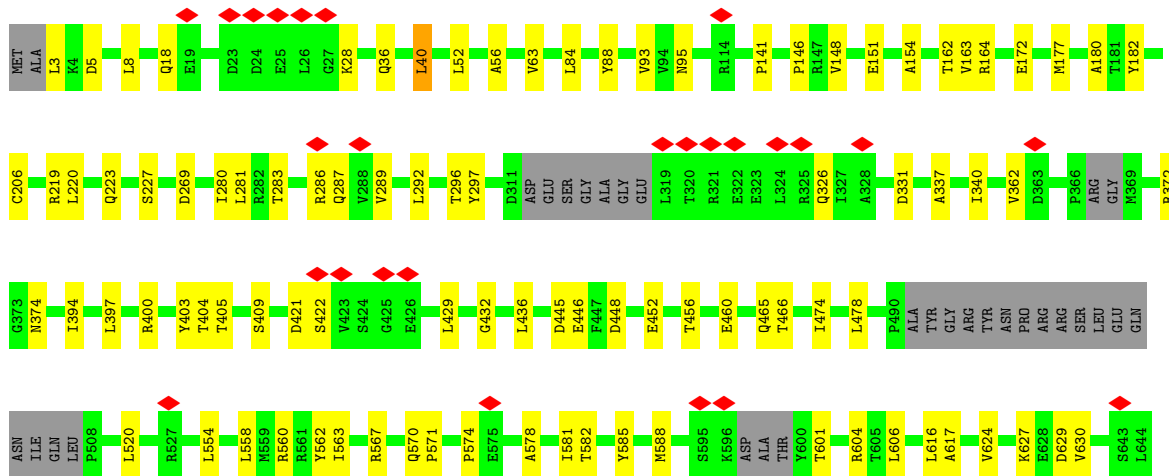


ASP
PRO
TYR
LEU
VAL
VAL
ASN
PRO
ASN
LEU
LEU
GLU
ASP

• Molecule 5: DNA replication licensing factor MCM6



• Molecule 6: DNA replication licensing factor MCM7



L646	GLY
	ASP
	LYS
	GLN
	GLN
	THR
	ALA
	ALA
	SER
	ARG
	THR
	GLN
	ARG
	PRO
	ALA
	ASP
	VAL
	ILE
	PHE
	ALA
	THR
	VAL
	GLU
	GLU
	LEU
	VAL
	SER
	GLY
	GLY
	ARG
	SER
	VAL
	ARG
	PHE
	SER
	SER
	GLU
	ALA
	ALA
	GLN
	ARG
	CYS
	VAL
	VAL
	SER
	ARG
	GLY
	PHE
	THR
	PRO
	PRO
	ALA
	ALA
	GLN
	PHE
	GLN
	ALA
	ALA
	LEU
	LEU
	ASP
	GLU
	TYR
	GLU
	LEU

• Molecule 6: DNA replication licensing factor MCM7

Chain F:



MET	ALA	L3	L17	D24	E25	L26	G27	A56	E57	D58	V63	F77	V81	V93	V94	M108	R114	V119	E135	L136	Y137	R164	Y182	T183	C184	D185	Q186	C187	G188	Q193	C206	P207	S208	R215	R219	L220	T224	F229	E234	T254	V255	L256	L276	G284	F285	R286	Q287	Y297	L298	E299	A300	H301	D311	ASP	GLU	SER	GLY	ALA	GLY	L319	T320	R321	E322	E323	L324	R325	Q326	I327	A328	E329	E330	A337	I340	E343	I344	K351	K352	L355	L356	V362	D363	Q364	R367	G368	M369	K370	L371	R372	G373	N374	G384	K387	D395	R396	L397	S401	T405	G406	R407	T415	A416	A417	R420	D421	S422	V423	S424	L429	L434	V435	F447	M450	D454	I458	V461	Q465	T466	I467	S468	I469	I474	L478	F490	ALA	TYR	GLY	ARG	TYR
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• Molecule 7: DNA (47-MER)

Chain O:



A2	A12	A18	A19	T31	T32	T33	T34	T35	T36	T37	T38	T39	T40	T41	T42	T43	T44	T45	T46	T47	T48
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• Molecule 8: DNA (47-MER)

Chain S:



A-38	A-38	T-14	T-13	T-10	T-9	T-5	T-4	T-3	T-2
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	100748	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 ($e^-/\text{\AA}^2$)	50.96, 49.86	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k), GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.603	Depositor
Minimum map value	-0.274	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	416.0, 416.0, 416.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	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: ZN, MG, 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	2	0.25	0/5229	0.49	0/7065
1	A	0.26	0/5401	0.49	0/7295
2	3	0.25	0/5076	0.50	0/6854
2	B	0.26	0/5179	0.50	0/6993
3	4	0.25	0/5252	0.50	0/7098
3	C	0.25	0/5238	0.49	0/7079
4	5	0.26	0/4982	0.52	0/6699
4	D	0.26	0/4959	0.51	0/6669
5	6	0.26	0/5159	0.51	0/6961
5	E	0.26	0/5663	0.51	0/7634
6	7	0.25	0/4950	0.51	0/6677
6	F	0.25	0/5008	0.51	0/6757
7	O	0.51	0/1079	1.02	0/1663
8	S	0.51	0/1081	1.02	0/1666
All	All	0.27	0/64256	0.53	0/87110

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	5134	5143	5143	67	0
1	A	5303	5302	5302	74	0
2	3	5001	5018	5018	78	0
2	B	5100	5130	5130	46	0
3	4	5161	5206	5206	70	0
3	C	5147	5190	5190	62	0
4	5	4905	4950	4950	78	0
4	D	4882	4932	4932	58	0
5	6	5076	5099	5099	64	0
5	E	5578	5631	5631	73	0
6	7	4876	4928	4928	56	0
6	F	4933	4988	4988	63	0
7	O	963	542	542	17	0
8	S	964	541	541	6	0
9	2	1	0	0	0	0
9	4	1	0	0	0	0
9	5	1	0	0	0	0
9	6	1	0	0	0	0
9	7	1	0	0	0	0
9	A	1	0	0	0	0
9	C	1	0	0	0	0
9	D	1	0	0	0	0
9	E	1	0	0	0	0
9	F	1	0	0	0	0
10	2	1	0	0	0	0
10	3	1	0	0	0	0
10	5	1	0	0	0	0
10	6	1	0	0	0	0
10	7	1	0	0	0	0
10	A	1	0	0	0	0
10	B	1	0	0	0	0
10	D	1	0	0	0	0
10	E	1	0	0	0	0
10	F	1	0	0	0	0
11	2	31	12	12	3	0
11	A	31	12	12	1	0
12	3	27	12	12	1	0
12	5	27	12	12	2	0
12	6	27	12	12	1	0
12	7	27	12	12	0	0
12	B	27	12	12	1	0
12	D	27	12	12	0	0
12	E	27	12	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	F	27	12	12	1	0
All	All	63321	62720	62720	746	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (746) 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)
2:3:378:LEU:HD21	2:3:422:ILE:HD11	1.47	0.94
6:7:340:ILE:HD11	6:7:394:ILE:HD11	1.50	0.93
3:C:170:LEU:HD21	3:C:241:VAL:HG12	1.56	0.87
6:F:588:MET:HE1	6:F:609:ILE:HD11	1.61	0.82
12:3:1002:ADP:O3A	4:5:611:ARG:NH2	2.17	0.77
1:2:573:ALA:HB1	1:2:577:VAL:HG21	1.66	0.75
5:E:575:TYR:OH	5:E:634:MET:O	2.04	0.75
6:F:588:MET:CE	6:F:609:ILE:HD11	2.17	0.75
3:4:302:ALA:HB2	3:4:322:ILE:HD13	1.69	0.74
1:A:203:LEU:HD12	1:A:266:VAL:HG11	1.69	0.74
3:C:642:SER:OG	3:C:732:ARG:NH1	2.21	0.74
1:2:502:GLY:O	1:2:779:ARG:NH1	2.20	0.74
1:A:302:LEU:HD22	1:A:420:ASN:HB2	1.71	0.73
3:4:238:ASP:OD1	3:4:260:VAL:HG12	1.88	0.72
3:C:232:GLU:OE1	3:C:232:GLU:N	2.22	0.71
4:5:609:THR:N	4:5:612:GLN:OE1	2.23	0.71
3:C:127:VAL:HG21	3:C:153:TRP:HE3	1.55	0.71
4:5:145:MET:O	4:5:146:SER:OG	2.07	0.71
3:C:503:GLU:OE1	3:C:594:GLN:NE2	2.24	0.71
6:7:585:TYR:HB2	6:7:606:LEU:HD23	1.73	0.70
3:4:187:ASP:N	3:4:195:GLN:OE1	2.23	0.70
3:4:545:ALA:HB1	3:4:558:LEU:HD21	1.73	0.70
4:D:335:ILE:O	4:D:339:ILE:HG23	1.90	0.70
1:A:801:SER:O	1:A:805:THR:HG23	1.92	0.69
2:B:40:ILE:HD11	2:B:84:VAL:HG13	1.74	0.69
4:5:46:THR:O	4:5:50:GLY:N	2.25	0.69
6:F:356:LEU:HD13	6:F:612:LEU:HD22	1.75	0.69
4:5:415:THR:HG21	4:5:457:ALA:HB3	1.74	0.68
1:A:456:LEU:O	1:A:456:LEU:HD23	1.94	0.68
3:4:241:VAL:HG11	3:4:258:ILE:HG21	1.77	0.67
1:A:248:LEU:HD21	1:A:285:ILE:HG13	1.76	0.67
3:C:174:ILE:HD12	3:C:174:ILE:O	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:675:LEU:HD11	11:2:1002:ATP:C6	2.30	0.67
3:4:387:ARG:NH2	3:4:530:GLY:O	2.27	0.67
4:5:504:ILE:HD12	4:5:504:ILE:O	1.95	0.67
2:B:287:PHE:CE2	2:B:295:ILE:HD11	2.30	0.66
2:3:281:ILE:HG22	2:3:285:LYS:NZ	2.11	0.66
3:4:271:MET:SD	3:4:370:VAL:HG11	2.36	0.66
5:E:54:ILE:HD13	5:E:102:LYS:HZ3	1.60	0.66
1:2:723:TYR:OH	1:2:780:ILE:O	2.10	0.66
6:7:581:ILE:HG22	6:7:606:LEU:HD21	1.79	0.65
6:7:36:GLN:O	6:7:40:LEU:HD12	1.97	0.65
4:D:612:GLN:N	4:D:612:GLN:OE1	2.30	0.65
4:D:46:THR:O	4:D:50:GLY:N	2.30	0.65
2:3:575:ALA:O	2:3:578:ILE:HG22	1.97	0.65
5:6:68:LEU:HD21	5:6:79:ILE:HD12	1.79	0.65
4:5:385:THR:HG21	4:5:520:VAL:HG12	1.78	0.65
2:3:69:ALA:HB2	2:3:124:VAL:HG23	1.78	0.64
3:4:706:ALA:HB2	3:4:754:GLU:HA	1.79	0.64
5:6:16:LEU:O	5:6:16:LEU:HD13	1.98	0.64
6:F:343:GLU:O	6:F:536:HIS:NE2	2.31	0.64
4:5:439:GLY:N	4:5:481:ARG:O	2.31	0.64
7:O:40:DT:H2'	7:O:41:DT:H72	1.80	0.64
3:4:470:ILE:HD13	3:4:519:LEU:HD22	1.79	0.64
5:E:147:VAL:HG13	5:E:233:VAL:HG21	1.79	0.64
6:F:56:ALA:HB2	6:F:63:VAL:HG21	1.80	0.64
7:O:31:DT:H2''	7:O:32:DT:H72	1.78	0.64
6:F:276:ILE:HD13	6:F:299:GLU:OE2	1.98	0.63
1:2:620:LEU:HD23	1:2:620:LEU:H	1.63	0.63
5:6:54:ILE:HG21	5:6:102:LYS:HG2	1.81	0.63
4:D:77:LEU:CD2	4:D:88:LEU:HD12	2.28	0.63
6:F:256:LEU:HD12	6:F:297:TYR:CD2	2.32	0.63
2:3:304:ALA:O	2:3:314:LYS:NZ	2.27	0.63
4:5:385:THR:HG21	4:5:520:VAL:CG1	2.28	0.63
4:5:415:THR:HG21	4:5:457:ALA:CB	2.28	0.63
5:6:114:PHE:O	5:6:245:THR:HG21	1.99	0.62
4:D:128:LEU:HD12	4:D:128:LEU:O	1.99	0.62
2:3:380:ALA:HB2	2:3:442:LEU:HD12	1.81	0.62
3:C:302:ALA:HB2	3:C:322:ILE:HD13	1.80	0.62
3:C:527:VAL:HG11	3:C:570:ILE:HD12	1.80	0.62
6:F:416:ALA:HB2	6:F:478:LEU:HD21	1.79	0.62
6:F:415:THR:HG23	6:F:467:ILE:HG21	1.80	0.62
1:A:177:LEU:O	1:A:177:LEU:HD12	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:7:337:ALA:O	6:7:340:ILE:HG22	2.00	0.62
3:4:580:ASN:OD1	3:4:583:THR:HG22	1.98	0.62
3:C:386:ASP:OD1	3:C:529:ARG:NH1	2.33	0.61
2:3:102:LEU:HD12	2:3:124:VAL:HG11	1.82	0.61
4:5:462:MET:SD	4:5:484:VAL:HG21	2.40	0.61
12:B:1002:ADP:O1B	4:D:611:ARG:NH2	2.33	0.61
2:3:340:ASN:N	2:3:480:ASP:OD2	2.28	0.61
3:C:546:TYR:O	3:C:558:LEU:HD12	1.99	0.60
6:7:581:ILE:CG2	6:7:606:LEU:HD21	2.31	0.60
1:A:288:LEU:HD12	1:A:415:THR:HG23	1.84	0.60
1:A:516:ASP:HB3	1:A:625:THR:HG22	1.84	0.60
2:B:384:THR:OG1	8:S:-38:DA:OP1	2.13	0.60
3:4:560:THR:CG2	5:6:220:ILE:HD11	2.31	0.60
4:5:377:LEU:HD23	4:5:378:LEU:N	2.17	0.60
6:7:146:PRO:HA	6:7:162:THR:HG23	1.84	0.59
3:4:280:ASP:N	3:4:394:TYR:O	2.32	0.59
5:6:591:GLU:O	5:6:595:VAL:HG13	2.01	0.59
2:3:195:ASP:HB3	2:3:226:VAL:HG11	1.83	0.59
3:4:388:VAL:HG12	3:4:423:LYS:HD2	1.84	0.59
3:C:544:THR:HA	3:C:596:LEU:HD21	1.83	0.59
1:2:582:GLY:O	1:2:625:THR:HG22	2.03	0.59
2:B:25:ASP:OD1	2:B:31:ILE:N	2.35	0.59
2:3:342:LEU:HD23	2:3:482:LEU:HD13	1.83	0.59
1:A:325:VAL:HA	1:A:368:THR:HG23	1.85	0.59
6:F:256:LEU:HD12	6:F:297:TYR:CE2	2.37	0.59
8:S:-14:DT:H2'	8:S:-13:DT:H72	1.85	0.59
3:4:558:LEU:HD23	3:4:559:GLN:N	2.18	0.59
1:A:222:MET:CE	1:A:281:ILE:HD12	2.32	0.59
6:7:374:ASN:OD1	6:7:465:GLN:NE2	2.34	0.58
6:F:362:VAL:HG22	6:F:614:THR:HG21	1.84	0.58
2:3:378:LEU:CD2	2:3:422:ILE:HD11	2.26	0.58
4:5:404:THR:HG21	4:5:433:ALA:HB2	1.85	0.58
1:2:633:ILE:HG22	1:2:646:ASN:O	2.03	0.58
2:3:398:MET:SD	2:3:425:VAL:HG11	2.43	0.58
2:3:221:LEU:HD13	2:3:225:LEU:O	2.04	0.58
6:7:452:GLU:O	6:7:456:THR:HG23	2.04	0.58
6:F:395:ASP:O	6:F:401:SER:OG	2.14	0.57
2:3:383:THR:HG22	2:3:384:THR:H	1.69	0.57
3:C:756:ILE:HD12	3:C:756:ILE:H	1.69	0.57
3:4:563:LEU:HD13	3:4:590:VAL:HG21	1.87	0.57
2:3:137:VAL:HG23	2:3:137:VAL:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:170:LEU:CD1	3:4:241:VAL:HG22	2.33	0.57
1:A:667:VAL:HG13	1:A:667:VAL:O	2.04	0.57
3:C:505:ASN:N	3:C:645:ASP:OD1	2.33	0.57
3:4:604:ILE:HD11	5:6:451:LEU:HD12	1.87	0.57
5:6:587:SER:O	5:6:590:SER:OG	2.20	0.57
1:A:476:LYS:HE3	1:A:715:LEU:HD21	1.86	0.57
1:2:684:VAL:HG21	5:6:591:GLU:OE2	2.04	0.57
4:D:589:MET:CE	4:D:648:THR:HG21	2.35	0.57
5:E:726:LEU:HD11	5:E:776:VAL:HG21	1.87	0.57
1:2:232:VAL:HG13	1:2:285:ILE:HD13	1.87	0.57
1:2:573:ALA:HB1	1:2:577:VAL:CG2	2.34	0.57
4:5:188:LEU:HD13	4:5:272:LYS:HE2	1.87	0.57
1:A:481:ILE:HD12	1:A:496:ALA:HB2	1.85	0.56
1:A:432:PHE:CZ	5:E:227:ILE:HD11	2.39	0.56
5:6:30:PHE:O	5:6:34:LEU:HD12	2.06	0.56
3:C:350:GLN:OE1	3:C:380:ASP:N	2.35	0.56
3:C:167:GLN:CG	3:C:244:ILE:HD11	2.36	0.56
3:C:647:ILE:O	3:C:768:ALA:HB1	2.05	0.56
5:E:117:LEU:HD11	5:E:134:LEU:HG	1.87	0.56
5:6:364:VAL:HG21	5:6:536:LEU:HD21	1.86	0.56
6:F:417:ALA:O	6:F:429:LEU:HD12	2.06	0.56
8:S:-10:DT:H2'	8:S:-9:DT:H72	1.87	0.56
2:3:163:THR:HG23	6:7:289:VAL:HG23	1.87	0.56
4:5:380:LEU:HD21	4:5:506:PHE:HE2	1.70	0.56
6:F:182:TYR:OH	6:F:193:GLN:OE1	2.17	0.56
2:3:378:LEU:HD21	2:3:422:ILE:CD1	2.31	0.55
1:A:222:MET:HE3	1:A:281:ILE:HD12	1.88	0.55
1:A:426:LEU:HD23	1:A:432:PHE:O	2.06	0.55
4:D:265:ILE:HD13	4:D:294:ILE:HG21	1.88	0.55
5:E:239:GLY:HA3	5:E:451:LEU:HD12	1.87	0.55
6:F:135:GLU:OE2	6:F:137:TYR:OH	2.23	0.55
5:6:602:ARG:NH2	5:6:616:ILE:O	2.39	0.55
1:A:849:ASN:CB	5:E:727:ILE:HD11	2.36	0.55
1:2:325:VAL:HA	1:2:368:THR:HG23	1.86	0.55
3:4:187:ASP:O	3:4:195:GLN:NE2	2.38	0.55
1:A:577:VAL:HG21	1:A:620:LEU:CD1	2.36	0.55
5:6:186:ALA:O	1:A:356:GLN:NE2	2.37	0.55
2:3:355:LEU:HD11	2:3:451:ALA:HB2	1.88	0.55
1:A:650:THR:HG22	1:A:652:PRO:HD2	1.88	0.55
4:D:452:GLU:O	4:D:456:VAL:HG23	2.05	0.55
2:3:7:LEU:HD12	2:B:154:THR:HG22	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:731:VAL:HG21	1:2:782:LEU:HG	1.89	0.55
2:3:307:ILE:O	2:3:314:LYS:NZ	2.31	0.55
2:B:128:GLU:OE2	2:B:236:GLN:NE2	2.40	0.55
4:D:268:ILE:O	4:D:270:SER:OG	2.20	0.55
3:4:527:VAL:HG11	3:4:570:ILE:HD12	1.87	0.55
4:5:257:VAL:HG11	4:5:299:ILE:HG21	1.89	0.54
3:4:727:VAL:HB	3:4:769:LEU:HD21	1.88	0.54
4:D:170:ILE:HD11	4:D:179:LEU:HD23	1.88	0.54
5:E:605:ASP:HB2	5:E:616:ILE:HD13	1.90	0.54
4:D:385:THR:HG21	4:D:520:VAL:HG11	1.90	0.54
2:3:83:PHE:O	2:3:87:ILE:HD12	2.07	0.54
6:7:617:ALA:N	6:7:629:ASP:OD2	2.41	0.54
1:A:203:LEU:CD1	1:A:266:VAL:HG11	2.37	0.54
1:A:764:VAL:HG13	4:D:536:VAL:HG21	1.90	0.54
5:E:284:LEU:HD22	5:E:289:VAL:HG21	1.90	0.54
2:3:355:LEU:HD11	2:3:451:ALA:CB	2.38	0.54
5:E:254:VAL:O	5:E:254:VAL:HG13	2.06	0.54
1:A:759:SER:HB3	1:A:810:VAL:HG11	1.90	0.54
2:3:628:HIS:ND1	2:3:641:ASP:OD1	2.40	0.54
3:4:501:ARG:O	3:4:739:ARG:NE	2.36	0.54
5:6:30:PHE:CE2	5:6:34:LEU:HD11	2.43	0.54
5:6:278:THR:HG23	5:6:278:THR:O	2.07	0.54
1:A:803:ILE:HD12	1:A:814:MET:HB3	1.89	0.54
2:B:614:THR:O	2:B:617:THR:N	2.41	0.54
4:D:380:LEU:HD13	4:D:504:ILE:HG22	1.90	0.54
3:C:388:VAL:HG12	3:C:423:LYS:HD2	1.90	0.53
6:F:356:LEU:HD21	6:F:616:LEU:HG	1.90	0.53
2:3:322:LEU:O	2:3:630:LYS:NZ	2.38	0.53
4:5:342:SER:O	4:5:539:LEU:HD11	2.07	0.53
2:B:336:ARG:NH2	2:B:480:ASP:OD1	2.41	0.53
2:3:128:GLU:N	2:3:128:GLU:OE1	2.39	0.53
2:3:495:ARG:HA	4:5:587:ILE:HD11	1.90	0.53
6:F:421:ASP:OD1	6:F:422:SER:N	2.40	0.53
1:2:587:ASP:OD1	1:2:588:GLU:N	2.41	0.53
2:3:431:VAL:HG12	2:3:433:ILE:HG23	1.89	0.53
4:5:145:MET:CE	4:5:271:ILE:HG23	2.38	0.53
4:5:257:VAL:CG1	4:5:299:ILE:HG21	2.38	0.53
4:D:339:ILE:O	4:D:393:PHE:CZ	2.62	0.53
4:D:339:ILE:HD12	4:D:340:ALA:CB	2.39	0.53
6:F:387:LYS:NZ	12:F:1002:ADP:O2B	2.42	0.53
6:F:206:CYS:SG	6:F:208:SER:OG	2.62	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:414:LEU:HD11	1:A:441:ALA:CB	2.39	0.53
1:A:764:VAL:CG1	4:D:536:VAL:HG21	2.39	0.53
4:D:148:LEU:HD13	4:D:297:LEU:HD12	1.91	0.53
1:A:347:VAL:O	1:A:347:VAL:HG13	2.08	0.52
2:B:614:THR:HG22	2:B:615:ALA:N	2.23	0.52
5:E:565:ARG:NH2	5:E:569:LEU:HD13	2.24	0.52
1:2:801:SER:O	1:2:805:THR:HG23	2.09	0.52
1:2:751:ARG:NH2	4:5:522:ASP:O	2.39	0.52
4:D:416:ALA:HB2	4:D:435:VAL:HG11	1.90	0.52
3:4:237:PHE:CB	3:4:260:VAL:HG11	2.38	0.52
3:4:693:TYR:HE1	3:4:697:THR:HG21	1.74	0.52
5:E:494:ASN:OD1	5:E:496:ARG:NH2	2.42	0.52
5:6:184:VAL:O	5:6:184:VAL:HG13	2.08	0.52
3:C:326:SER:O	3:C:327:VAL:HG23	2.10	0.52
4:D:170:ILE:HD12	4:D:212:TYR:CG	2.45	0.52
1:A:288:LEU:HD12	1:A:415:THR:CG2	2.39	0.52
3:C:566:SER:O	3:C:611:THR:HG22	2.10	0.52
2:3:155:ILE:HG23	2:B:4:THR:HG23	1.92	0.52
6:7:574:PRO:HG3	6:7:624:VAL:HG13	1.91	0.52
4:D:265:ILE:HD12	4:D:265:ILE:O	2.10	0.52
3:4:152:ILE:HD12	3:4:157:VAL:HG21	1.92	0.52
2:B:526:ILE:HD12	2:B:526:ILE:H	1.75	0.52
3:C:112:VAL:O	3:C:112:VAL:HG13	2.10	0.52
6:F:187:CYS:SG	6:F:188:GLY:N	2.83	0.52
1:2:751:ARG:NH2	4:5:522:ASP:OD1	2.43	0.52
2:B:380:ALA:HB3	2:B:433:ILE:HD13	1.92	0.52
3:C:476:ILE:HD13	3:C:650:MET:CE	2.39	0.52
3:C:768:ALA:O	3:C:769:LEU:HD12	2.10	0.52
4:D:578:ALA:HB1	4:D:637:VAL:HG21	1.92	0.52
4:5:275:GLY:C	4:5:276:LEU:HD23	2.30	0.51
4:5:418:VAL:HG12	4:5:429:MET:HG2	1.92	0.51
4:5:380:LEU:HD21	4:5:506:PHE:CE2	2.45	0.51
1:A:422:TYR:OH	1:A:436:ALA:O	2.16	0.51
3:4:237:PHE:HB2	3:4:260:VAL:HG11	1.92	0.51
4:5:372:ARG:NH1	4:5:374:ASP:O	2.41	0.51
5:6:604:ARG:NH2	5:6:656:ILE:O	2.43	0.51
6:7:281:LEU:HG	6:7:283:THR:HG23	1.92	0.51
6:7:400:ARG:NH2	6:7:436:LEU:O	2.43	0.51
1:A:585:LEU:HD23	1:A:627:ILE:HB	1.92	0.51
3:C:558:LEU:HD23	5:E:220:ILE:HD13	1.92	0.51
5:E:726:LEU:HD11	5:E:776:VAL:CG2	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:495:LEU:HD12	1:2:536:ILE:HG13	1.93	0.51
3:4:211:ASN:OD1	3:4:213:GLU:N	2.40	0.51
5:E:168:VAL:HG23	5:E:168:VAL:O	2.11	0.51
5:6:134:LEU:HD12	5:6:246:GLY:O	2.10	0.51
5:E:586:ILE:HA	5:E:640:VAL:HG12	1.93	0.51
3:C:170:LEU:HD21	3:C:241:VAL:CG1	2.35	0.51
3:4:212:CYS:HA	3:4:215:ILE:HD12	1.93	0.51
3:4:706:ALA:HB2	3:4:754:GLU:CA	2.41	0.51
4:5:649:LEU:HD12	4:5:649:LEU:O	2.11	0.51
5:E:68:LEU:HD21	5:E:79:ILE:CD1	2.40	0.51
5:E:616:ILE:HD12	5:E:616:ILE:N	2.26	0.51
6:F:234:GLU:OE2	6:F:254:THR:HG23	2.11	0.51
4:5:325:LEU:HD12	4:5:328:LEU:HD12	1.93	0.50
2:3:195:ASP:OD1	6:7:154:ALA:N	2.38	0.50
3:4:367:PRO:CD	6:7:478:LEU:HD13	2.41	0.50
4:D:645:GLN:HA	4:D:648:THR:HG22	1.93	0.50
2:3:173:VAL:HG22	4:D:204:ARG:CZ	2.42	0.50
1:2:464:ILE:HG23	1:2:723:TYR:CD2	2.46	0.50
1:2:495:LEU:HD13	1:2:627:ILE:HD13	1.91	0.50
4:5:110:VAL:HG23	4:5:111:THR:HG23	1.92	0.50
3:C:386:ASP:OD2	5:E:217:ARG:NH2	2.44	0.50
3:C:193:TYR:O	3:C:197:LEU:HD22	2.12	0.50
4:D:265:ILE:HG22	4:D:299:ILE:HD13	1.94	0.50
5:E:68:LEU:HD21	5:E:79:ILE:HD12	1.94	0.50
6:F:374:ASN:OD1	6:F:465:GLN:NE2	2.44	0.50
2:3:157:ARG:NH1	2:3:158:ARG:O	2.45	0.50
6:7:18:GLN:OE1	6:7:84:LEU:HD21	2.12	0.50
1:2:779:ARG:O	1:2:782:LEU:HD12	2.12	0.50
2:3:286:LYS:O	2:3:290:THR:HG23	2.11	0.50
7:O:32:DT:C2'	7:O:33:DT:H71	2.41	0.50
7:O:44:DT:H2'	7:O:45:DT:H72	1.94	0.50
3:C:598:ILE:O	3:C:598:ILE:HD12	2.11	0.50
3:4:560:THR:HG23	5:6:220:ILE:HD11	1.94	0.50
1:A:203:LEU:HD11	1:A:219:ILE:HD11	1.93	0.50
6:F:276:ILE:HD12	6:F:276:ILE:N	2.26	0.50
5:6:104:ILE:HD12	5:6:105:PRO:O	2.12	0.49
5:6:188:ARG:NH1	1:A:353:PRO:O	2.41	0.49
4:D:339:ILE:HD12	4:D:340:ALA:N	2.27	0.49
7:O:36:DT:H2'	7:O:37:DT:H72	1.94	0.49
5:6:225:GLU:OE2	5:6:295:ARG:NH1	2.44	0.49
6:7:280:ILE:HD11	6:7:297:TYR:CD2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:7:403:TYR:HE1	6:7:405:THR:HG1	1.59	0.49
1:A:862:GLU:OE1	1:A:881:TYR:OH	2.19	0.49
2:B:497:ILE:O	2:B:501:VAL:HG23	2.12	0.49
1:2:502:GLY:N	1:2:515:GLY:O	2.41	0.49
2:B:336:ARG:NH1	2:B:338:ASP:O	2.44	0.49
3:C:727:VAL:HG21	3:C:769:LEU:CD2	2.42	0.49
2:3:422:ILE:O	2:3:422:ILE:HG22	2.11	0.49
2:B:223:ASP:N	2:B:223:ASP:OD1	2.45	0.49
2:B:585:GLU:OE1	2:B:585:GLU:N	2.41	0.49
4:D:597:GLU:OE1	4:D:603:ARG:NH1	2.45	0.49
7:O:45:DT:H2'	7:O:46:DT:H72	1.94	0.49
3:4:282:LEU:CD1	3:4:419:ILE:HD12	2.42	0.49
4:5:360:GLY:N	4:5:373:GLY:O	2.45	0.49
6:7:93:VAL:HG12	6:7:95:ASN:H	1.76	0.49
6:F:405:THR:HG22	6:F:406:GLY:H	1.78	0.49
4:5:138:ARG:NH2	4:5:241:MET:O	2.45	0.49
1:A:676:ALA:HB3	5:E:595:VAL:HG23	1.95	0.49
6:F:344:ILE:O	6:F:351:LYS:NZ	2.40	0.49
1:2:787:ILE:HG22	1:2:788:GLU:N	2.28	0.49
6:7:362:VAL:HG11	6:7:571:PRO:HD2	1.94	0.49
1:2:481:ILE:HD12	1:2:496:ALA:HB2	1.94	0.49
2:3:40:ILE:HD11	2:3:84:VAL:HG13	1.95	0.49
4:D:197:CYS:SG	4:D:199:THR:HG22	2.53	0.49
7:O:46:DT:H2'	7:O:47:DT:H72	1.95	0.49
1:2:467:LEU:HD11	1:2:723:TYR:CD2	2.47	0.48
4:5:39:LEU:HD23	4:5:103:ALA:HA	1.95	0.48
4:5:418:VAL:HG23	4:5:471:LYS:HG3	1.95	0.48
2:B:375:GLY:O	2:B:378:LEU:N	2.45	0.48
3:C:167:GLN:HG2	3:C:244:ILE:HD11	1.95	0.48
7:O:43:DT:H2'	7:O:44:DT:H72	1.95	0.48
2:B:51:VAL:HG22	2:B:103:GLU:O	2.13	0.48
2:B:513:GLN:N	2:B:513:GLN:OE1	2.46	0.48
3:C:309:CYS:O	5:E:18:VAL:HG22	2.12	0.48
1:2:675:LEU:HD11	11:2:1002:ATP:N6	2.27	0.48
6:F:429:LEU:HD11	6:F:474:ILE:CD1	2.43	0.48
6:F:516:ASP:OD2	6:F:611:ARG:NH1	2.44	0.48
6:7:18:GLN:CD	6:7:84:LEU:HD21	2.34	0.48
1:A:516:ASP:CB	1:A:625:THR:HG22	2.44	0.48
1:A:577:VAL:HG22	1:A:622:ALA:HB2	1.94	0.48
5:E:450:MET:HE3	5:E:493:LEU:HD22	1.94	0.48
6:F:434:LEU:HD12	6:F:467:ILE:HD11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:639:LEU:HD23	2:3:639:LEU:O	2.13	0.48
3:4:470:ILE:CD1	3:4:519:LEU:HD22	2.44	0.48
1:A:576:LEU:O	1:A:622:ALA:HB1	2.14	0.48
5:E:117:LEU:HD12	5:E:136:ARG:HB2	1.95	0.48
2:3:486:LEU:HD11	2:3:655:LYS:HE2	1.96	0.48
6:7:588:MET:SD	6:7:601:THR:OG1	2.64	0.48
1:2:617:VAL:HG21	2:3:211:GLY:HA2	1.94	0.48
4:5:339:ILE:O	4:5:393:PHE:CZ	2.67	0.48
2:3:44:GLN:O	2:3:91:TYR:OH	2.27	0.48
2:3:422:ILE:HG22	2:3:426:MET:HG3	1.95	0.48
6:7:56:ALA:HB2	6:7:63:VAL:HG21	1.95	0.48
2:B:387:GLU:HG3	2:B:388:THR:HG23	1.96	0.48
7:O:32:DT:H2''	7:O:33:DT:H71	1.95	0.48
4:D:59:LEU:HD21	4:D:70:ILE:HD13	1.95	0.48
5:E:446:ALA:HB1	5:E:450:MET:HB2	1.96	0.48
2:3:384:THR:HG23	7:O:12:DA:OP1	2.14	0.47
4:5:173:ARG:O	4:5:176:ARG:NH1	2.47	0.47
6:7:52:LEU:HD12	6:7:141:PRO:HD3	1.96	0.47
6:7:372:ARG:NH2	6:7:374:ASN:O	2.46	0.47
2:B:84:VAL:HG11	2:B:98:PHE:CZ	2.49	0.47
3:C:573:ILE:CD1	3:C:613:VAL:HG13	2.44	0.47
2:3:380:ALA:CB	2:3:433:ILE:HD13	2.44	0.47
2:3:393:LEU:HD12	2:3:433:ILE:HD11	1.95	0.47
5:E:535:ILE:HG22	5:E:537:VAL:HG23	1.96	0.47
1:2:731:VAL:HG13	1:2:784:ASP:OD1	2.13	0.47
4:5:464:GLN:OE1	4:5:464:GLN:N	2.47	0.47
3:C:723:SER:OG	3:C:776:PRO:O	2.19	0.47
1:2:524:ASP:OD2	1:2:665:ASP:N	2.39	0.47
1:2:546:THR:HG21	1:2:556:LEU:HD11	1.95	0.47
3:4:760:GLU:OE2	3:4:763:ARG:NH2	2.48	0.47
6:7:223:GLN:O	6:7:227:SER:OG	2.17	0.47
3:C:732:ARG:NH2	12:E:1002:ADP:O2B	2.44	0.47
1:2:308:THR:HG22	1:2:309:SER:N	2.29	0.47
5:6:228:LEU:HD13	5:6:232:ALA:O	2.15	0.47
2:3:31:ILE:O	2:3:34:SER:OG	2.26	0.47
2:3:71:GLU:OE1	2:3:71:GLU:N	2.43	0.47
3:4:512:PRO:O	6:7:604:ARG:NE	2.37	0.47
4:5:416:ALA:HB2	4:5:435:VAL:HG21	1.95	0.47
4:5:504:ILE:HD11	4:5:605:SER:HB2	1.95	0.47
5:6:244:PHE:HD2	5:6:303:VAL:HG22	1.79	0.47
2:B:436:ALA:CB	6:F:417:ALA:HB3	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:303:PHE:O	3:C:339:LEU:HD12	2.14	0.47
4:D:589:MET:HE1	4:D:648:THR:HG21	1.97	0.47
5:E:206:VAL:HG22	5:E:226:VAL:HG13	1.95	0.47
6:7:84:LEU:HD22	6:7:88:TYR:HE2	1.80	0.47
6:7:220:LEU:HD23	6:7:220:LEU:H	1.78	0.47
1:A:604:MET:CE	1:A:626:VAL:HG11	2.45	0.47
4:D:175:CYS:SG	4:D:177:ASN:ND2	2.88	0.47
2:3:613:VAL:HA	2:3:617:THR:HG21	1.97	0.47
5:E:652:LEU:HD13	5:E:652:LEU:O	2.14	0.47
2:3:383:THR:HG22	2:3:384:THR:N	2.29	0.47
1:A:759:SER:CB	1:A:810:VAL:HG11	2.45	0.47
4:D:62:HIS:ND1	4:D:69:TRP:O	2.48	0.47
11:2:1002:ATP:O3'	5:6:622:GLU:OE2	2.31	0.46
2:B:5:VAL:HG23	2:B:5:VAL:O	2.15	0.46
4:D:340:ALA:O	4:D:350:LYS:NZ	2.47	0.46
1:2:723:TYR:OH	1:2:782:LEU:HD13	2.15	0.46
2:B:287:PHE:CZ	2:B:295:ILE:HD11	2.49	0.46
3:C:350:GLN:HB2	3:C:379:VAL:HG13	1.98	0.46
4:D:40:ARG:NH1	4:D:109:GLU:OE1	2.48	0.46
1:2:497:LEU:O	1:2:517:ILE:HD12	2.15	0.46
1:2:667:VAL:O	1:2:667:VAL:HG23	2.16	0.46
3:C:158:ASN:OD1	3:C:158:ASN:N	2.43	0.46
5:E:264:ALA:HB2	5:E:292:LEU:HD11	1.97	0.46
5:E:361:ASN:OD1	5:E:536:LEU:HD22	2.15	0.46
8:S:-5:DT:H2'	8:S:-4:DT:H72	1.97	0.46
6:7:5:ASP:OD2	6:7:8:LEU:HD23	2.15	0.46
2:B:393:LEU:HD22	2:B:433:ILE:HD11	1.98	0.46
5:E:184:VAL:O	5:E:184:VAL:HG22	2.15	0.46
2:3:329:LEU:N	2:3:329:LEU:HD12	2.30	0.46
2:3:369:THR:HG22	2:3:370:GLY:N	2.31	0.46
4:5:282:ARG:NH2	5:6:440:HIS:O	2.48	0.46
6:7:570:GLN:OE1	6:7:570:GLN:N	2.41	0.46
3:C:175:ASP:HB3	3:C:178:ALA:HB2	1.98	0.46
5:E:302:CYS:SG	5:E:303:VAL:N	2.88	0.46
1:2:268:LEU:HD11	1:2:275:ASP:HB2	1.98	0.46
2:3:70:PHE:O	2:3:74:VAL:HG23	2.15	0.46
3:4:159:VAL:HG13	3:4:236:THR:HG22	1.96	0.46
5:6:434:VAL:HG12	5:6:435:ARG:N	2.30	0.46
2:B:621:LEU:HD21	2:B:649:VAL:HG11	1.98	0.46
6:F:119:VAL:HG13	6:F:119:VAL:O	2.16	0.46
2:3:261:ILE:N	2:3:261:ILE:HD12	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:257:VAL:HG12	4:5:301:VAL:CG2	2.46	0.46
1:A:414:LEU:HD11	1:A:441:ALA:HB1	1.98	0.46
1:2:278:THR:O	1:2:278:THR:HG22	2.16	0.46
4:5:442:VAL:O	4:5:442:VAL:HG23	2.15	0.46
5:6:402:LYS:NZ	12:6:1002:ADP:O3B	2.44	0.46
3:C:624:TRP:CZ3	3:C:649:LEU:HD22	2.51	0.46
6:F:435:VAL:CG2	6:F:478:LEU:HD23	2.46	0.46
3:4:112:VAL:HG22	3:4:257:GLN:HG3	1.98	0.46
1:A:392:ARG:NH2	5:E:234:GLU:OE2	2.43	0.46
3:C:755:ALA:HA	3:C:758:VAL:HG22	1.97	0.46
5:E:753:LEU:HD23	5:E:754:LYS:HD2	1.98	0.46
1:2:193:LEU:HD23	1:2:193:LEU:C	2.36	0.46
3:4:710:LEU:HD23	3:4:758:VAL:HG13	1.98	0.46
5:6:82:GLU:O	5:6:86:VAL:HG22	2.15	0.46
5:6:391:ASN:OD1	5:6:499:ILE:N	2.47	0.46
3:C:404:ARG:HE	7:O:31:DT:P	2.39	0.46
6:F:77:PHE:O	6:F:81:VAL:HG23	2.15	0.46
6:F:362:VAL:HG23	6:F:364:GLN:OE1	2.16	0.46
2:3:281:ILE:HG22	2:3:285:LYS:HZ2	1.78	0.45
2:3:380:ALA:CB	2:3:442:LEU:HD12	2.44	0.45
2:3:494:ASP:OD1	4:5:587:ILE:HD13	2.15	0.45
3:4:663:ALA:O	3:4:667:VAL:HG23	2.16	0.45
3:4:514:THR:HG22	3:4:515:SER:H	1.81	0.45
4:5:538:THR:O	4:5:541:VAL:HG22	2.15	0.45
6:7:574:PRO:CG	6:7:624:VAL:HG13	2.46	0.45
1:A:491:ILE:HD11	1:A:663:VAL:HG22	1.98	0.45
5:E:53:LEU:HD21	5:E:110:PHE:CD1	2.52	0.45
4:5:634:GLU:HA	4:5:637:VAL:HG12	1.97	0.45
4:D:637:VAL:O	4:D:641:LEU:HD23	2.16	0.45
4:5:257:VAL:HG12	4:5:301:VAL:HG22	1.99	0.45
5:6:465:MET:SD	5:6:473:ILE:HD12	2.56	0.45
5:E:571:ASP:OD1	5:E:574:ARG:NH2	2.45	0.45
7:O:34:DT:H2'	7:O:35:DT:H71	1.99	0.45
2:3:141:VAL:HG12	6:7:292:LEU:HB2	1.97	0.45
5:6:378:LYS:O	5:6:386:LEU:N	2.50	0.45
2:B:288:SER:O	2:B:292:SER:OG	2.33	0.45
3:C:340:ILE:HG21	3:C:343:ARG:HG3	1.98	0.45
6:F:415:THR:HG22	6:F:416:ALA:N	2.31	0.45
6:F:563:ILE:O	6:F:567:ARG:HG3	2.17	0.45
1:2:783:ARG:O	1:2:784:ASP:HB2	2.16	0.45
2:B:291:ARG:HB2	2:B:295:ILE:HD13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:179:ILE:O	5:E:181:ARG:NH2	2.43	0.45
1:2:456:LEU:N	1:2:456:LEU:HD22	2.31	0.45
1:2:783:ARG:HD3	1:2:787:ILE:HD12	1.99	0.45
2:3:621:LEU:HD23	2:3:649:VAL:HG21	1.97	0.45
4:5:232:LEU:O	4:5:236:VAL:HG23	2.17	0.45
6:7:429:LEU:HD11	6:7:474:ILE:HD12	1.99	0.45
2:B:291:ARG:O	2:B:295:ILE:HD13	2.16	0.45
3:C:476:ILE:HD13	3:C:650:MET:HE3	1.98	0.45
6:F:416:ALA:CB	6:F:478:LEU:HD21	2.46	0.45
4:5:363:LYS:NZ	4:5:621:GLU:OE2	2.44	0.45
4:5:574:LEU:HD23	4:5:632:ALA:HB3	1.99	0.45
1:A:373:TYR:CE1	1:A:397:ILE:HG23	2.51	0.45
2:B:244:LEU:HD21	2:B:259:VAL:HG11	1.99	0.45
3:C:508:LEU:HD13	3:C:650:MET:HE1	1.99	0.45
4:D:232:LEU:O	4:D:236:VAL:HG23	2.15	0.45
5:E:389:ASP:OD2	5:E:480:GLN:NE2	2.47	0.45
5:E:516:LEU:HD12	5:E:614:TRP:CE3	2.51	0.45
5:6:154:GLY:O	5:6:168:VAL:HG12	2.17	0.45
1:A:684:VAL:HG22	5:E:586:ILE:HB	1.98	0.45
1:A:721:LYS:O	1:A:725:ILE:HG12	2.17	0.45
6:F:523:ASP:OD1	6:F:523:ASP:N	2.49	0.45
1:2:420:ASN:OD1	1:2:435:PHE:HB3	2.17	0.45
3:4:682:LEU:CD2	3:4:686:VAL:HG13	2.46	0.45
12:5:1002:ADP:O1A	12:5:1002:ADP:O1B	2.35	0.45
1:2:227:ARG:O	1:2:228:GLU:HG2	2.17	0.44
3:4:367:PRO:HD2	6:7:478:LEU:HD13	1.98	0.44
3:4:560:THR:HG22	5:6:220:ILE:HD11	1.98	0.44
5:6:325:ILE:O	5:6:329:MET:HG3	2.17	0.44
1:A:680:VAL:O	1:A:684:VAL:HG23	2.17	0.44
3:C:127:VAL:HG21	3:C:153:TRP:CE3	2.43	0.44
1:2:513:VAL:O	1:2:513:VAL:HG23	2.16	0.44
3:4:187:ASP:OD1	3:4:189:THR:HG22	2.17	0.44
3:4:302:ALA:HB1	3:4:339:LEU:HD13	1.99	0.44
4:5:418:VAL:HG22	4:5:469:ILE:HG21	1.99	0.44
1:A:203:LEU:C	1:A:203:LEU:HD13	2.38	0.44
2:B:303:LEU:O	2:B:357:TYR:OH	2.34	0.44
2:B:417:MET:SD	6:F:407:ARG:NE	2.90	0.44
2:B:495:ARG:HG2	4:D:587:ILE:HD13	1.99	0.44
4:D:275:GLY:C	4:D:276:LEU:HD23	2.38	0.44
5:E:35:GLU:O	5:E:44:ILE:HD13	2.17	0.44
6:F:17:LEU:HD21	6:F:81:VAL:HG22	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:190:GLU:O	3:4:195:GLN:NE2	2.50	0.44
3:4:295:LEU:HD11	3:4:379:VAL:CG1	2.47	0.44
3:4:402:ASN:HB2	3:4:405:VAL:HG22	1.98	0.44
6:7:182:TYR:HB2	6:7:220:LEU:HD12	1.99	0.44
1:A:647:VAL:HG11	1:A:654:ILE:HD11	1.98	0.44
1:A:848:ARG:NH1	5:E:603:GLN:O	2.50	0.44
2:3:593:GLU:HG2	2:3:646:VAL:HG22	1.99	0.44
4:5:150:LYS:HE2	4:5:264:THR:HG21	1.98	0.44
4:5:178:THR:HG22	4:5:179:LEU:N	2.33	0.44
6:7:148:VAL:O	6:7:151:GLU:N	2.50	0.44
6:F:184:CYS:SG	6:F:185:ASP:N	2.91	0.44
7:O:38:DT:H2''	7:O:39:DT:C7	2.48	0.44
8:S:-4:DT:H2'	8:S:-3:DT:H72	1.99	0.44
5:6:604:ARG:HH21	5:6:656:ILE:HG22	1.83	0.44
1:A:402:LEU:O	1:A:405:SER:OG	2.16	0.44
2:B:6:VAL:HG11	2:B:9:ASP:HB2	1.99	0.44
2:B:614:THR:HG21	6:F:384:GLY:HA3	1.99	0.44
3:C:374:ALA:HB1	3:C:378:LEU:HB2	1.99	0.44
6:F:434:LEU:CD1	6:F:467:ILE:HD11	2.46	0.44
7:O:18:DA:H2''	7:O:19:DA:C8	2.53	0.44
1:2:827:ASP:OD1	1:2:830:GLU:N	2.39	0.44
6:7:616:LEU:O	6:7:616:LEU:HD13	2.18	0.44
1:A:738:MET:HG3	1:A:791:VAL:HG21	2.00	0.44
2:B:408:ILE:HG21	2:B:414:MET:HE3	1.99	0.44
1:2:356:GLN:NE2	5:E:186:ALA:O	2.48	0.44
4:5:474:ILE:HD12	4:5:476:THR:CG2	2.47	0.44
5:6:573:ARG:O	5:6:577:LEU:HD23	2.16	0.44
2:B:25:ASP:O	2:B:30:GLY:N	2.49	0.44
2:B:223:ASP:O	2:B:224:ASP:OD1	2.35	0.44
3:C:698:ILE:HG21	3:C:746:LYS:HA	2.00	0.44
5:E:123:ILE:HD12	5:E:210:GLU:HA	2.00	0.44
6:F:224:THR:HG22	6:F:229:PHE:HZ	1.81	0.44
1:2:215:PHE:CE1	1:2:230:LEU:HD21	2.53	0.44
6:7:404:THR:HG23	6:7:409:SER:HG	1.82	0.44
3:C:188:ILE:O	3:C:188:ILE:HG22	2.17	0.44
6:F:215:ARG:HE	6:F:215:ARG:HA	1.83	0.44
1:2:430:ASN:HB2	5:6:254:VAL:HG12	1.99	0.44
2:3:593:GLU:HG2	2:3:646:VAL:HG13	1.99	0.44
4:5:450:MET:SD	4:5:458:ILE:HD12	2.58	0.44
5:6:224:LEU:C	5:6:224:LEU:HD12	2.39	0.44
1:A:807:LYS:O	1:A:811:MET:N	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:614:THR:HG22	2:B:615:ALA:H	1.82	0.44
5:E:30:PHE:HZ	5:E:112:VAL:HG11	1.82	0.44
5:E:99:LYS:NZ	5:E:106:LEU:HD13	2.33	0.44
7:O:31:DT:H2''	7:O:32:DT:C7	2.47	0.44
1:2:207:VAL:O	1:2:213:ASN:N	2.51	0.43
6:F:340:ILE:HD12	6:F:355:LEU:HB2	2.00	0.43
1:2:336:LEU:HD21	1:2:361:PHE:CE1	2.53	0.43
3:4:473:HIS:ND1	3:4:476:ILE:HD12	2.33	0.43
1:A:203:LEU:HD13	1:A:203:LEU:O	2.18	0.43
5:E:16:LEU:N	5:E:16:LEU:HD23	2.32	0.43
1:2:414:LEU:HD12	1:2:444:VAL:HG22	2.00	0.43
1:2:495:LEU:HD11	1:2:627:ILE:HG21	2.01	0.43
3:4:263:PHE:HA	3:4:391:THR:HG21	2.01	0.43
3:4:624:TRP:CD1	3:4:651:LEU:HD11	2.54	0.43
4:5:380:LEU:HD23	4:5:488:ALA:HB3	2.00	0.43
3:C:622:SER:OG	6:F:510:ALA:N	2.51	0.43
5:E:450:MET:CE	5:E:493:LEU:HD22	2.48	0.43
1:2:735:LEU:CD2	1:2:771:ILE:HG23	2.49	0.43
1:A:849:ASN:HB2	5:E:727:ILE:HD11	1.99	0.43
2:B:502:LEU:HD21	4:D:613:LEU:HD21	1.99	0.43
5:E:450:MET:SD	5:E:482:ILE:HD12	2.58	0.43
2:3:369:THR:HG22	2:3:370:GLY:H	1.83	0.43
4:5:356:LEU:HD12	4:5:375:ILE:HB	2.01	0.43
6:7:563:ILE:O	6:7:567:ARG:HG2	2.18	0.43
4:D:339:ILE:HD12	4:D:340:ALA:HB2	2.01	0.43
6:F:319:LEU:HD22	6:F:319:LEU:N	2.34	0.43
1:2:657:PHE:HB2	1:2:660:LEU:HD11	1.99	0.43
4:5:146:SER:N	4:5:269:TYR:O	2.36	0.43
8:S:-5:DT:C2'	8:S:-4:DT:H72	2.48	0.43
3:4:604:ILE:HD11	5:6:451:LEU:CD1	2.49	0.43
4:5:650:ASP:OD1	4:5:651:ALA:N	2.51	0.43
1:A:536:ILE:HG21	1:A:627:ILE:HD12	2.01	0.43
2:B:597:LEU:CD1	2:B:613:VAL:HG11	2.48	0.43
3:C:598:ILE:HD11	3:C:605:CYS:SG	2.59	0.43
6:F:415:THR:CG2	6:F:469:ILE:HD11	2.47	0.43
5:6:358:ILE:O	5:6:365:LYS:NZ	2.42	0.43
6:7:421:ASP:OD1	6:7:422:SER:N	2.46	0.43
6:7:578:ALA:O	6:7:582:THR:HG23	2.19	0.43
6:7:177:MET:SD	6:7:180:ALA:HB2	2.58	0.43
1:A:787:ILE:HG22	1:A:788:GLU:N	2.34	0.43
3:C:117:ASP:N	3:C:117:ASP:OD1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:308:THR:HG22	1:2:309:SER:H	1.83	0.43
2:3:340:ASN:C	2:3:341:ILE:HD12	2.39	0.43
4:5:400:ILE:HD13	4:5:438:ASP:O	2.19	0.43
5:6:225:GLU:OE1	5:6:225:GLU:N	2.43	0.43
1:A:292:GLU:O	1:A:308:THR:HG22	2.19	0.43
1:A:458:ASP:OD1	1:A:458:ASP:N	2.50	0.43
3:C:713:ALA:HB2	3:C:762:LYS:HD2	2.00	0.43
5:E:442:PHE:HB2	5:E:489:VAL:HG11	2.01	0.43
6:F:58:ASP:OD1	6:F:58:ASP:N	2.52	0.43
7:O:38:DT:H2"	7:O:39:DT:H72	2.00	0.43
5:6:162:GLN:N	5:6:162:GLN:OE1	2.51	0.42
4:D:325:LEU:HD12	4:D:328:LEU:HD12	2.00	0.42
1:2:425:SER:HG	1:2:435:PHE:HE1	1.65	0.42
2:3:469:ILE:HD13	2:3:482:LEU:HD21	2.01	0.42
3:4:717:MET:HA	3:4:720:ILE:HG22	2.00	0.42
4:5:339:ILE:HG13	4:5:340:ALA:H	1.84	0.42
5:6:561:GLU:O	5:6:562:SER:OG	2.36	0.42
2:B:195:ASP:OD1	2:B:195:ASP:N	2.45	0.42
4:D:524:HIS:CG	4:D:524:HIS:O	2.71	0.42
2:3:169:PRO:O	2:3:173:VAL:HG23	2.19	0.42
4:5:128:LEU:HD23	4:5:128:LEU:N	2.33	0.42
5:6:147:VAL:HG13	5:6:233:VAL:HG21	2.01	0.42
5:6:206:VAL:HG22	5:6:226:VAL:HG22	2.01	0.42
6:7:326:GLN:OE1	6:7:562:TYR:OH	2.25	0.42
6:7:404:THR:HG23	6:7:409:SER:OG	2.20	0.42
4:D:582:LEU:HD13	4:D:582:LEU:C	2.39	0.42
1:2:546:THR:HG21	1:2:556:LEU:CD1	2.48	0.42
5:6:68:LEU:HD21	5:6:79:ILE:CD1	2.48	0.42
5:6:117:LEU:HD22	5:6:119:THR:O	2.20	0.42
5:6:277:GLU:OE1	4:D:198:ASN:ND2	2.52	0.42
5:6:343:ASP:OD2	5:6:567:TYR:OH	2.36	0.42
3:C:390:VAL:HG23	3:C:418:VAL:HG13	2.00	0.42
4:D:321:GLU:OE2	4:D:558:LYS:NZ	2.44	0.42
2:3:157:ARG:NH2	2:3:170:SER:O	2.53	0.42
3:4:515:SER:O	3:4:519:LEU:HD23	2.18	0.42
4:5:331:VAL:HA	4:5:334:VAL:HG12	2.01	0.42
6:7:163:VAL:HG12	6:7:164:ARG:N	2.35	0.42
1:A:430:ASN:ND2	5:E:437:GLU:O	2.53	0.42
5:E:452:ALA:O	5:E:455:GLY:N	2.49	0.42
1:2:599:SER:HA	4:5:410:SER:HB2	2.02	0.42
3:4:241:VAL:CG1	3:4:258:ILE:HG21	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:6:387:ARG:NH1	5:6:529:ARG:O	2.45	0.42
5:6:605:ASP:HB2	5:6:616:ILE:HD13	2.02	0.42
1:A:799:LEU:O	1:A:800:GLU:C	2.58	0.42
3:C:170:LEU:CD2	3:C:241:VAL:HG12	2.38	0.42
3:C:715:VAL:HG21	5:E:546:TYR:CE2	2.55	0.42
4:D:608:ILE:HD12	4:D:608:ILE:N	2.35	0.42
5:E:786:VAL:HG22	5:E:787:LEU:H	1.85	0.42
1:A:230:LEU:HD23	1:A:230:LEU:C	2.39	0.42
6:F:458:ILE:O	6:F:461:VAL:HG12	2.19	0.42
4:5:217:ASP:OD1	4:5:217:ASP:N	2.52	0.42
5:6:148:HIS:NE2	5:6:436:ASP:OD2	2.51	0.42
5:6:179:ILE:HD12	5:6:188:ARG:CG	2.50	0.42
2:B:524:VAL:HG13	2:B:525:ASP:N	2.35	0.42
3:4:117:ASP:OD1	3:4:117:ASP:N	2.50	0.42
3:4:386:ASP:OD1	3:4:529:ARG:NH1	2.53	0.42
3:4:723:SER:OG	3:4:724:ARG:N	2.53	0.42
4:D:269:TYR:HA	4:D:294:ILE:HD13	2.01	0.42
6:F:397:LEU:C	6:F:397:LEU:HD23	2.40	0.42
6:F:507:LEU:HG	6:F:512:LEU:HD11	2.02	0.42
1:2:735:LEU:HD21	1:2:771:ILE:HG23	2.02	0.42
3:4:237:PHE:HB3	3:4:260:VAL:HG11	2.02	0.42
3:4:608:ASN:OD1	5:6:212:GLN:NE2	2.53	0.42
4:5:155:ILE:HD11	4:5:263:VAL:HG21	2.02	0.41
5:E:460:ASP:OD1	5:E:461:GLU:N	2.51	0.41
6:F:362:VAL:HG13	6:F:614:THR:CG2	2.50	0.41
6:F:420:ARG:NH1	6:F:421:ASP:O	2.53	0.41
1:2:230:LEU:C	1:2:230:LEU:HD23	2.40	0.41
1:2:421:ASN:HB3	5:6:195:THR:HG21	2.01	0.41
2:3:236:GLN:HB2	2:3:534:PHE:CD2	2.55	0.41
2:3:385:ASP:O	2:3:386:GLN:HB3	2.20	0.41
3:4:330:ARG:NH1	5:6:18:VAL:HG22	2.35	0.41
3:4:775:ASP:N	3:4:775:ASP:OD1	2.53	0.41
4:5:380:LEU:HD13	4:5:504:ILE:HG22	2.01	0.41
4:5:585:ARG:HG3	4:5:641:LEU:HD13	2.02	0.41
4:5:649:LEU:HD12	4:5:649:LEU:C	2.41	0.41
5:6:570:ASP:OD1	5:6:573:ARG:NH1	2.53	0.41
6:7:3:LEU:N	6:7:3:LEU:HD22	2.35	0.41
6:7:627:LYS:HA	6:7:630:VAL:HG12	2.02	0.41
1:A:293:GLU:OE2	1:A:295:ARG:NH2	2.53	0.41
4:D:339:ILE:HD11	4:D:350:LYS:HG2	2.02	0.41
1:2:590:ASP:N	1:2:590:ASP:OD1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:223:ASP:N	2:3:223:ASP:OD1	2.53	0.41
4:5:67:GLU:O	4:5:252:TYR:CZ	2.73	0.41
6:7:397:LEU:O	6:7:560:ARG:NE	2.53	0.41
3:C:299:MET:HE3	5:E:292:LEU:HD13	2.02	0.41
4:D:361:SER:N	4:D:621:GLU:OE1	2.47	0.41
6:F:447:PHE:HE1	6:F:458:ILE:HG21	1.86	0.41
2:3:393:LEU:N	2:3:393:LEU:HD22	2.35	0.41
3:4:348:ASP:OD1	5:6:128:SER:OG	2.35	0.41
3:4:388:VAL:HG12	3:4:423:LYS:CD	2.49	0.41
4:5:145:MET:HE1	4:5:271:ILE:HG23	2.00	0.41
5:6:126:LEU:HD11	5:6:137:ILE:HG21	2.02	0.41
5:6:400:THR:HG21	5:6:536:LEU:HB3	2.02	0.41
6:7:460:GLU:HG2	6:7:466:THR:O	2.20	0.41
1:A:558:ALA:HB3	1:A:611:ILE:HD11	2.02	0.41
3:C:382:VAL:O	3:C:382:VAL:HG23	2.19	0.41
3:C:495:THR:HG22	5:E:563:ILE:HG13	2.02	0.41
3:C:710:LEU:HD13	3:C:738:ILE:HG12	2.02	0.41
6:F:606:LEU:C	6:F:606:LEU:HD23	2.40	0.41
1:2:414:LEU:HD11	1:2:441:ALA:CB	2.50	0.41
1:2:464:ILE:HG21	1:2:726:TYR:CD2	2.55	0.41
4:5:532:LEU:HD21	12:5:1002:ADP:C6	2.56	0.41
1:A:391:PRO:CD	5:E:493:LEU:HD23	2.51	0.41
2:B:424:GLU:OE1	6:F:405:THR:HG21	2.20	0.41
3:C:712:GLU:HA	3:C:715:VAL:HG12	2.03	0.41
5:E:54:ILE:HG21	5:E:102:LYS:HZ3	1.86	0.41
5:E:68:LEU:HD22	5:E:114:PHE:CE1	2.56	0.41
1:2:414:LEU:HD11	1:2:441:ALA:HB2	2.01	0.41
3:4:167:GLN:HG3	3:4:240:ALA:HB1	2.02	0.41
1:A:414:LEU:CD1	1:A:444:VAL:HG12	2.51	0.41
1:A:560:VAL:O	1:A:560:VAL:HG13	2.20	0.41
3:C:167:GLN:HG3	3:C:244:ILE:HD11	2.03	0.41
6:F:512:LEU:HD12	6:F:518:LEU:HD13	2.01	0.41
2:3:10:VAL:HG13	2:3:11:GLU:N	2.36	0.41
2:3:412:ASP:HB2	2:3:452:ALA:HB1	2.03	0.41
2:3:577:ILE:HD12	2:3:577:ILE:N	2.35	0.41
3:4:288:MET:HE2	3:4:290:ILE:HD13	2.03	0.41
5:6:587:SER:N	5:6:590:SER:OG	2.54	0.41
6:7:172:GLU:OE1	6:7:172:GLU:N	2.43	0.41
1:A:535:TYR:CZ	1:A:539:VAL:HG21	2.56	0.41
1:A:789:ASP:OD1	1:A:790:ASP:N	2.54	0.41
3:C:631:ILE:HD11	3:C:727:VAL:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:376:ASN:O	4:D:515:ASP:N	2.54	0.41
4:D:582:LEU:HD13	4:D:582:LEU:O	2.21	0.41
1:2:254:GLU:OE1	1:2:254:GLU:N	2.43	0.41
1:2:787:ILE:CG2	1:2:788:GLU:N	2.84	0.41
2:3:36:VAL:O	2:3:40:ILE:HD13	2.20	0.41
4:5:168:ILE:HD13	4:5:184:MET:HE1	2.02	0.41
1:A:609:ILE:HG23	4:D:410:SER:HB3	2.03	0.41
5:E:546:TYR:O	5:E:550:ARG:HG3	2.20	0.41
2:3:54:LEU:HD12	2:3:62:ALA:HA	2.03	0.41
3:4:453:SER:CB	3:4:749:LEU:HD12	2.51	0.41
4:5:538:THR:O	4:5:539:LEU:C	2.59	0.41
5:6:186:ALA:HB3	1:A:351:SER:O	2.20	0.41
6:7:432:GLY:O	6:7:436:LEU:HG	2.21	0.41
11:A:1002:ATP:C8	5:E:618:VAL:HG11	2.56	0.41
2:B:482:LEU:HD23	2:B:482:LEU:C	2.42	0.41
4:D:145:MET:O	4:D:146:SER:OG	2.23	0.41
4:D:337:LYS:O	4:D:337:LYS:HD3	2.21	0.41
5:E:94:LEU:HD23	5:E:110:PHE:HB3	2.02	0.41
5:E:253:ASP:HB2	5:E:295:ARG:HG3	2.03	0.41
6:F:603:ALA:O	6:F:607:LEU:HD23	2.20	0.41
7:O:33:DT:H2'	7:O:34:DT:H72	2.02	0.41
1:2:373:TYR:OH	4:5:284:ARG:NH2	2.54	0.41
2:3:111:VAL:O	2:3:127:VAL:HA	2.20	0.41
2:3:352:SER:O	2:3:356:ARG:HG2	2.21	0.41
3:4:533:THR:HG22	3:4:534:SER:N	2.36	0.41
6:7:445:ASP:OD1	6:7:446:GLU:N	2.54	0.41
2:B:497:ILE:HG21	4:D:610:VAL:HG21	2.03	0.41
5:E:150:GLU:O	5:E:201:VAL:N	2.51	0.41
6:F:337:ALA:HB1	6:F:352:LYS:HG3	2.03	0.41
6:F:395:ASP:HA	6:F:401:SER:HB2	2.02	0.41
6:F:450:MET:HG2	6:F:454:ASP:HB2	2.03	0.41
2:3:268:MET:HA	2:3:534:PHE:CE2	2.55	0.40
2:3:270:LYS:HG2	2:3:535:SER:O	2.21	0.40
3:4:640:LEU:HD13	3:4:640:LEU:O	2.20	0.40
6:7:554:LEU:HD22	6:7:558:LEU:HD23	2.04	0.40
1:A:252:PRO:O	1:A:256:LEU:HD13	2.21	0.40
3:C:646:LEU:HD23	3:C:648:PHE:CE2	2.56	0.40
1:2:610:SER:O	4:5:410:SER:O	2.39	0.40
2:3:54:LEU:O	2:3:54:LEU:HD13	2.21	0.40
3:4:573:ILE:HD13	3:4:587:LEU:HD21	2.02	0.40
6:7:448:ASP:OD1	6:7:448:ASP:N	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:301:VAL:O	4:D:301:VAL:HG13	2.22	0.40
5:E:450:MET:HE1	5:E:493:LEU:HD13	2.02	0.40
5:E:786:VAL:HG22	5:E:787:LEU:N	2.36	0.40
2:3:488:GLN:O	4:5:590:ARG:NH2	2.54	0.40
4:5:164:LYS:NZ	4:5:187:GLY:O	2.48	0.40
1:A:743:VAL:HG21	4:D:537:ILE:HD13	2.03	0.40
1:A:764:VAL:O	1:A:767:ILE:HG12	2.21	0.40
3:4:107:VAL:HG22	3:4:109:GLY:H	1.86	0.40
4:5:195:ARG:NE	4:5:210:ASP:OD1	2.49	0.40
5:6:515:SER:O	5:6:519:ASN:ND2	2.48	0.40
5:E:45:LYS:O	5:E:49:LEU:HD23	2.21	0.40
6:F:93:VAL:HG12	6:F:94:VAL:N	2.36	0.40
2:3:487:ASP:OD1	4:5:590:ARG:NH2	2.43	0.40
1:A:677:ARG:NH2	5:E:592:ASP:OD1	2.50	0.40
4:D:586:TYR:CE2	4:D:613:LEU:HD12	2.57	0.40
5:E:410:GLU:OE2	5:E:458:CYS:HB2	2.22	0.40
5:E:723:ILE:O	5:E:727:ILE:HG23	2.21	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	2	643/904 (71%)	598 (93%)	45 (7%)	0	100	100
1	A	659/904 (73%)	628 (95%)	31 (5%)	0	100	100
2	3	628/810 (78%)	599 (95%)	29 (5%)	0	100	100
2	B	647/810 (80%)	622 (96%)	25 (4%)	0	100	100
3	4	642/866 (74%)	608 (95%)	34 (5%)	0	100	100
3	C	640/866 (74%)	604 (94%)	36 (6%)	0	100	100
4	5	617/734 (84%)	579 (94%)	38 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	615/734 (84%)	585 (95%)	30 (5%)	0	100	100
5	6	631/821 (77%)	609 (96%)	22 (4%)	0	100	100
5	E	684/821 (83%)	659 (96%)	25 (4%)	0	100	100
6	7	604/719 (84%)	575 (95%)	29 (5%)	0	100	100
6	F	613/719 (85%)	577 (94%)	36 (6%)	0	100	100
All	All	7623/9708 (78%)	7243 (95%)	380 (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	2	568/781 (73%)	558 (98%)	10 (2%)	54	83
1	A	586/781 (75%)	576 (98%)	10 (2%)	56	84
2	3	550/708 (78%)	541 (98%)	9 (2%)	58	85
2	B	561/708 (79%)	552 (98%)	9 (2%)	58	85
3	4	572/755 (76%)	562 (98%)	10 (2%)	56	84
3	C	570/755 (76%)	563 (99%)	7 (1%)	67	89
4	5	533/625 (85%)	523 (98%)	10 (2%)	52	82
4	D	530/625 (85%)	526 (99%)	4 (1%)	79	93
5	6	565/724 (78%)	554 (98%)	11 (2%)	52	82
5	E	624/724 (86%)	618 (99%)	6 (1%)	73	91
6	7	535/619 (86%)	525 (98%)	10 (2%)	52	82
6	F	541/619 (87%)	531 (98%)	10 (2%)	54	83
All	All	6735/8424 (80%)	6629 (98%)	106 (2%)	58	85

All (106) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	2	228	GLU
1	2	268	LEU
1	2	276	ARG
1	2	369	ILE
1	2	469	LYS
1	2	512	LYS
1	2	663	VAL
1	2	726	TYR
1	2	735	LEU
1	2	785	TYR
2	3	21	ASP
2	3	23	LEU
2	3	39	LEU
2	3	76	PHE
2	3	195	ASP
2	3	218	ASP
2	3	445	ARG
2	3	486	LEU
2	3	504	MET
3	4	150	LEU
3	4	247	ASP
3	4	317	MET
3	4	354	LEU
3	4	475	ASP
3	4	489	ARG
3	4	640	LEU
3	4	643	ARG
3	4	658	TYR
3	4	751	ASN
4	5	90	LYS
4	5	128	LEU
4	5	147	HIS
4	5	184	MET
4	5	250	ASP
4	5	391	LEU
4	5	400	ILE
4	5	410	SER
4	5	481	ARG
4	5	532	LEU
5	6	34	LEU
5	6	200	PHE
5	6	247	THR
5	6	326	LYS

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Mol	Chain	Res	Type
5	6	332	LYS
5	6	347	TYR
5	6	422	LYS
5	6	469	ASP
5	6	492	THR
5	6	533	PHE
5	6	551	ARG
6	7	28	LYS
6	7	40	LEU
6	7	206	CYS
6	7	219	ARG
6	7	269	ASP
6	7	286	ARG
6	7	287	GLN
6	7	296	THR
6	7	331	ASP
6	7	520	LEU
1	A	177	LEU
1	A	210	HIS
1	A	270	MET
1	A	395	ASP
1	A	401	ASP
1	A	650	THR
1	A	678	PHE
1	A	755	MET
1	A	808	PHE
1	A	870	ARG
2	B	4	THR
2	B	33	GLN
2	B	70	PHE
2	B	76	PHE
2	B	224	ASP
2	B	293	LYS
2	B	478	ARG
2	B	603	MET
2	B	609	ARG
3	C	170	LEU
3	C	177	LEU
3	C	317	MET
3	C	345	LEU
3	C	645	ASP
3	C	670	TYR

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Mol	Chain	Res	Type
3	C	752	LYS
4	D	224	PHE
4	D	276	LEU
4	D	290	ARG
4	D	364	ARG
5	E	133	LEU
5	E	245	THR
5	E	347	TYR
5	E	440	HIS
5	E	593	PHE
5	E	604	ARG
6	F	108	MET
6	F	164	ARG
6	F	206	CYS
6	F	219	ARG
6	F	220	LEU
6	F	301	HIS
6	F	372	ARG
6	F	405	THR
6	F	461	VAL
6	F	524	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	2	563	HIS
1	2	806	GLN

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

Of 30 ligands modelled in this entry, 20 are monoatomic - leaving 10 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
11	ATP	2	1002	10	28,33,33	0.76	0	34,52,52	0.96	1 (2%)
12	ADP	6	1002	10	24,29,29	0.88	0	29,45,45	1.22	2 (6%)
12	ADP	5	1002	10	24,29,29	0.92	0	29,45,45	1.19	2 (6%)
11	ATP	A	1002	10	28,33,33	1.34	2 (7%)	34,52,52	1.07	3 (8%)
12	ADP	F	1002	10	24,29,29	0.88	0	29,45,45	1.23	2 (6%)
12	ADP	7	1002	10	24,29,29	0.86	0	29,45,45	1.25	2 (6%)
12	ADP	E	1002	10	24,29,29	0.88	0	29,45,45	1.24	2 (6%)
12	ADP	B	1002	10	24,29,29	0.89	0	29,45,45	1.36	3 (10%)
12	ADP	3	1002	-	24,29,29	0.87	0	29,45,45	1.26	2 (6%)
12	ADP	D	1002	10	24,29,29	0.90	0	29,45,45	1.24	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
11	ATP	2	1002	10	-	7/18/38/38	0/3/3/3
12	ADP	6	1002	10	-	2/12/32/32	0/3/3/3
12	ADP	5	1002	10	-	10/12/32/32	0/3/3/3
11	ATP	A	1002	10	-	2/18/38/38	0/3/3/3
12	ADP	F	1002	10	-	3/12/32/32	0/3/3/3
12	ADP	7	1002	10	-	1/12/32/32	0/3/3/3
12	ADP	E	1002	10	-	2/12/32/32	0/3/3/3
12	ADP	B	1002	10	-	6/12/32/32	0/3/3/3
12	ADP	3	1002	-	-	2/12/32/32	0/3/3/3
12	ADP	D	1002	10	-	2/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	1002	ATP	PB-O3B	-5.45	1.53	1.59
11	A	1002	ATP	PA-O3A	-2.20	1.57	1.59

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	F	1002	ADP	N3-C2-N1	-4.29	122.85	128.67
12	B	1002	ADP	N3-C2-N1	-4.27	122.88	128.67
12	E	1002	ADP	N3-C2-N1	-4.26	122.90	128.67
12	3	1002	ADP	N3-C2-N1	-4.18	122.99	128.67
12	D	1002	ADP	N3-C2-N1	-4.18	123.00	128.67
12	5	1002	ADP	N3-C2-N1	-4.15	123.04	128.67
12	7	1002	ADP	N3-C2-N1	-4.08	123.14	128.67
12	6	1002	ADP	N3-C2-N1	-3.92	123.36	128.67
12	B	1002	ADP	O4'-C1'-N9	2.77	112.41	108.75
12	6	1002	ADP	C4-C5-N7	-2.70	106.48	109.34
12	B	1002	ADP	C4-C5-N7	-2.54	106.65	109.34
12	D	1002	ADP	C4-C5-N7	-2.54	106.65	109.34
12	7	1002	ADP	C4-C5-N7	-2.52	106.67	109.34
12	3	1002	ADP	C4-C5-N7	-2.51	106.69	109.34
12	F	1002	ADP	C4-C5-N7	-2.34	106.86	109.34
12	E	1002	ADP	C4-C5-N7	-2.29	106.91	109.34
12	5	1002	ADP	C4-C5-N7	-2.27	106.94	109.34
11	A	1002	ATP	O3A-PA-O1A	-2.27	103.89	110.70
11	A	1002	ATP	C5-C6-N6	2.23	123.70	120.31
11	A	1002	ATP	O4'-C1'-N9	-2.17	105.87	108.75
11	2	1002	ATP	C5-C6-N6	2.09	123.50	120.31

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	2	1002	ATP	C5'-O5'-PA-O1A
12	5	1002	ADP	C5'-O5'-PA-O2A
12	5	1002	ADP	C5'-O5'-PA-O3A
12	B	1002	ADP	C5'-O5'-PA-O3A
12	D	1002	ADP	C5'-O5'-PA-O2A
12	D	1002	ADP	C5'-O5'-PA-O3A
12	E	1002	ADP	C5'-O5'-PA-O3A
12	F	1002	ADP	C5'-O5'-PA-O2A
12	F	1002	ADP	C5'-O5'-PA-O3A

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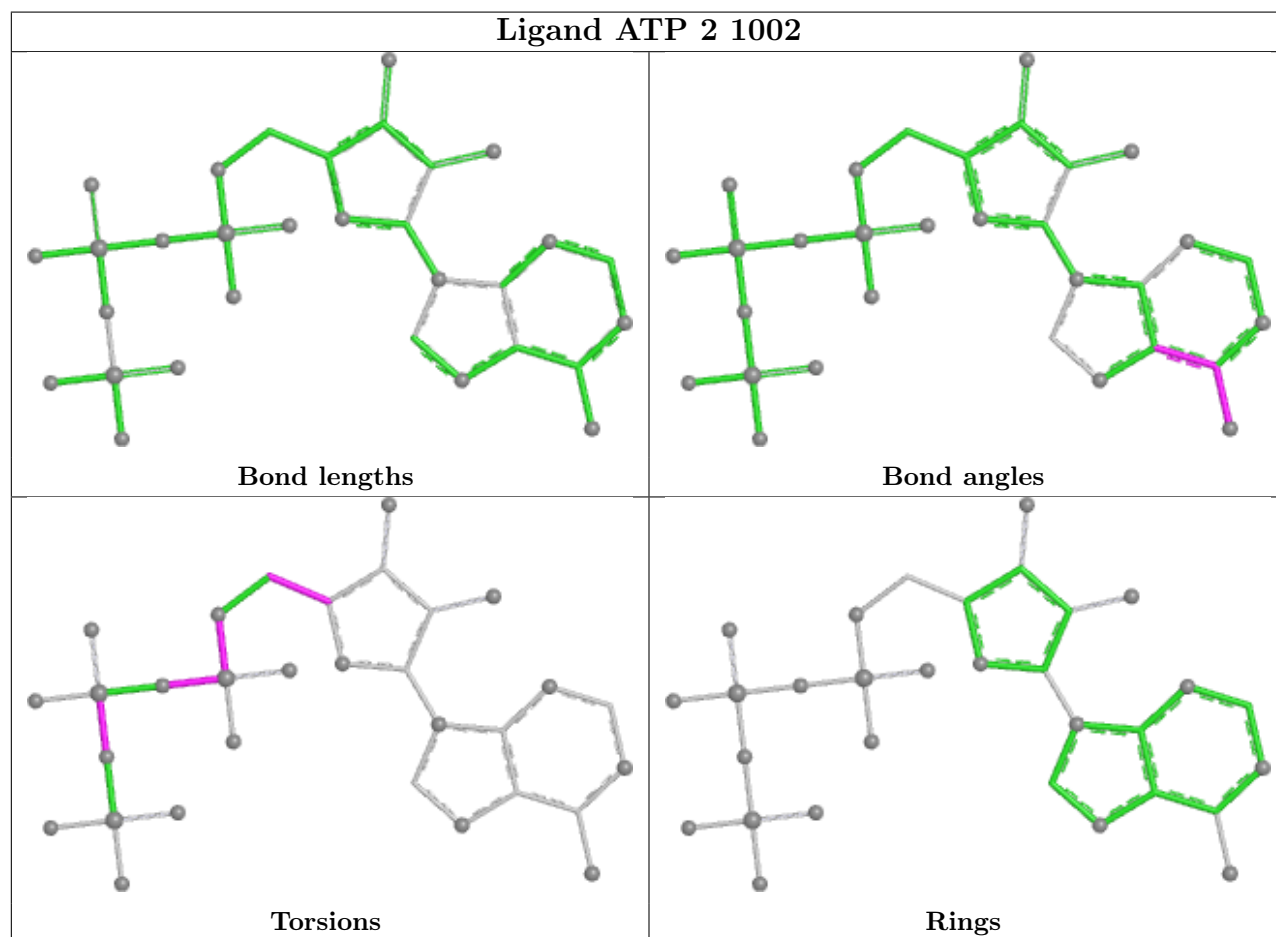
Mol	Chain	Res	Type	Atoms
11	2	1002	ATP	O4'-C4'-C5'-O5'
11	2	1002	ATP	C3'-C4'-C5'-O5'
12	6	1002	ADP	O4'-C4'-C5'-O5'
12	6	1002	ADP	C3'-C4'-C5'-O5'
12	5	1002	ADP	O4'-C4'-C5'-O5'
11	A	1002	ATP	C3'-C4'-C5'-O5'
12	5	1002	ADP	C3'-C4'-C5'-O5'
12	B	1002	ADP	O4'-C4'-C5'-O5'
12	5	1002	ADP	PA-O3A-PB-O1B
11	2	1002	ATP	PG-O3B-PB-O2B
12	3	1002	ADP	PB-O3A-PA-O2A
12	5	1002	ADP	PB-O3A-PA-O1A
11	A	1002	ATP	O4'-C4'-C5'-O5'
12	B	1002	ADP	C5'-O5'-PA-O1A
12	E	1002	ADP	C5'-O5'-PA-O1A
12	F	1002	ADP	C5'-O5'-PA-O1A
12	5	1002	ADP	C4'-C5'-O5'-PA
12	5	1002	ADP	PA-O3A-PB-O2B
12	5	1002	ADP	PA-O3A-PB-O3B
12	B	1002	ADP	C3'-C4'-C5'-O5'
11	2	1002	ATP	PG-O3B-PB-O1B
11	2	1002	ATP	PB-O3A-PA-O1A
11	2	1002	ATP	PB-O3A-PA-O2A
12	3	1002	ADP	PB-O3A-PA-O1A
12	B	1002	ADP	PB-O3A-PA-O1A
12	7	1002	ADP	O4'-C4'-C5'-O5'
12	5	1002	ADP	PB-O3A-PA-O2A
12	B	1002	ADP	PB-O3A-PA-O2A

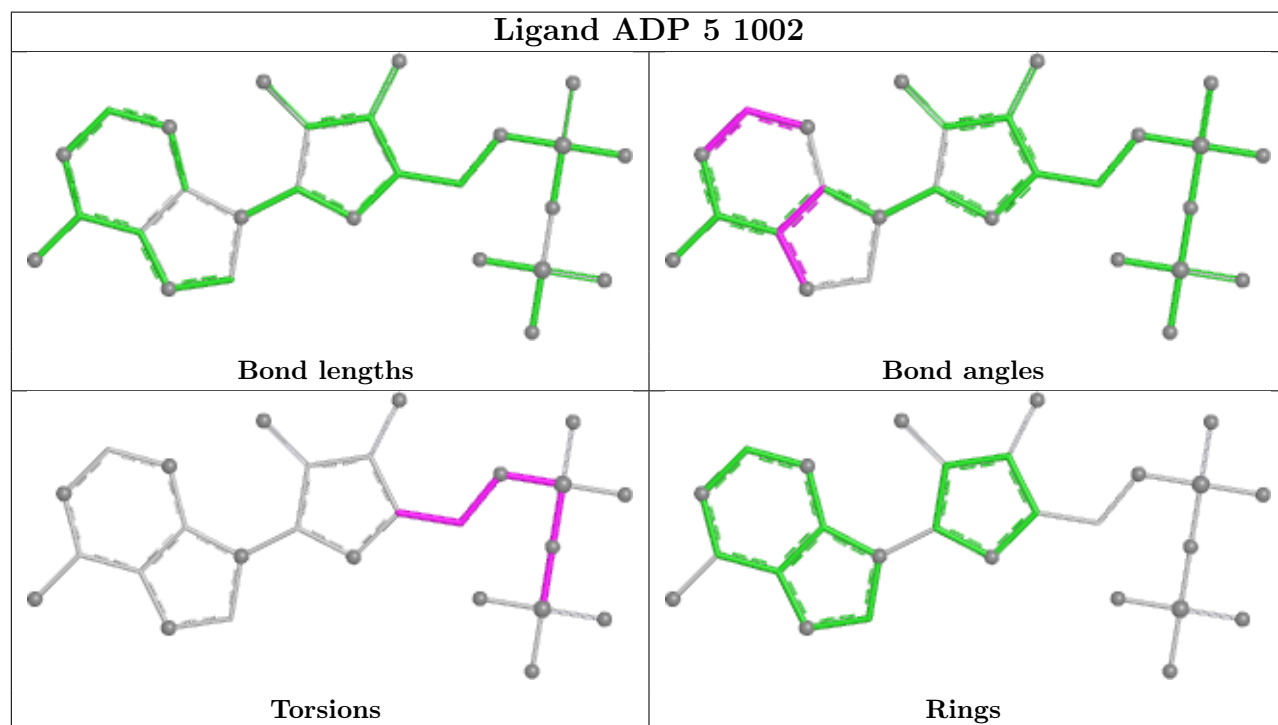
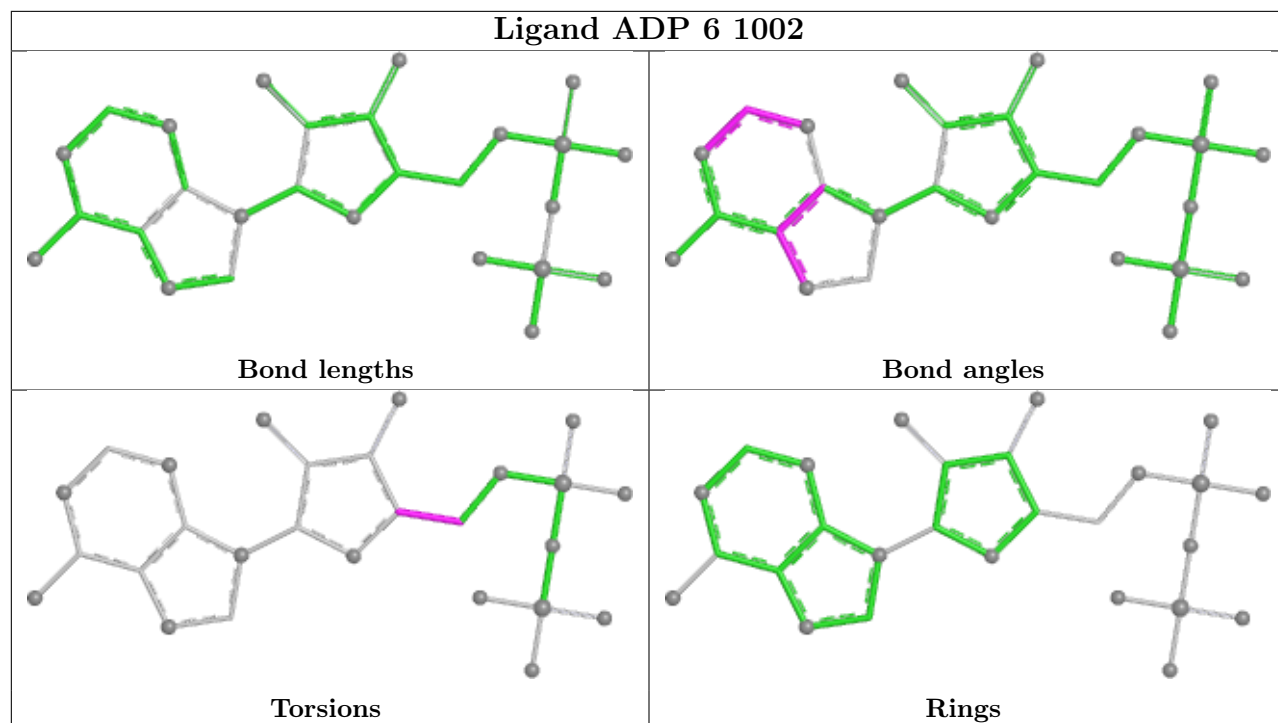
There are no ring outliers.

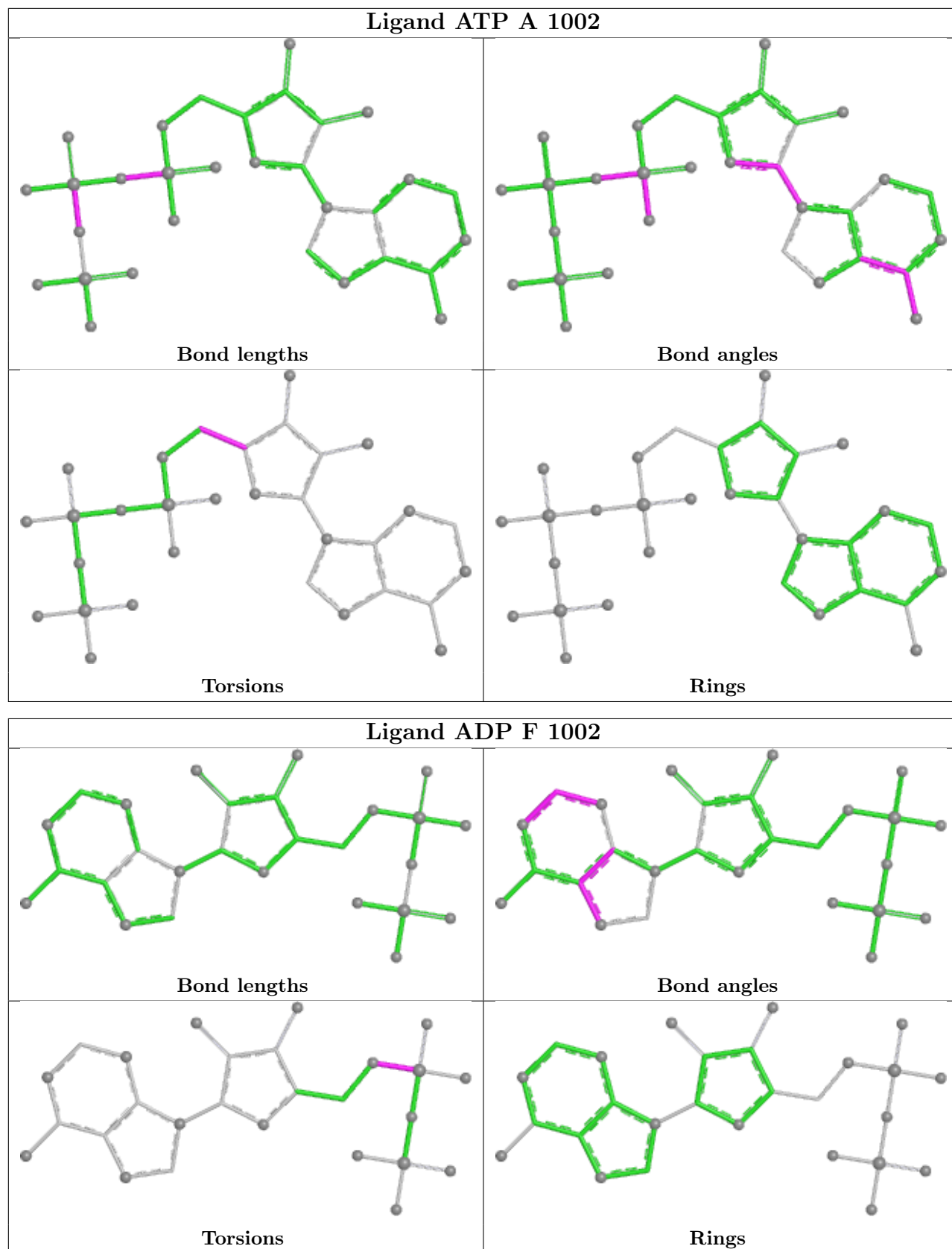
8 monomers are involved in 11 short contacts:

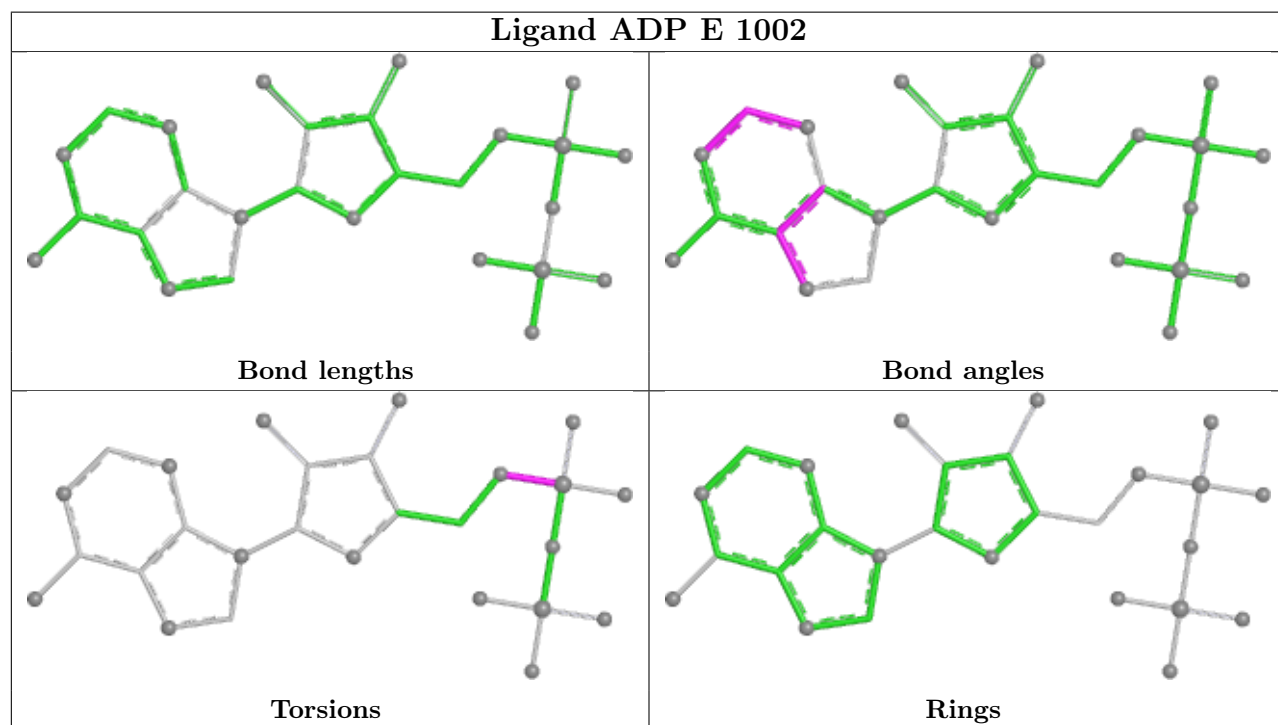
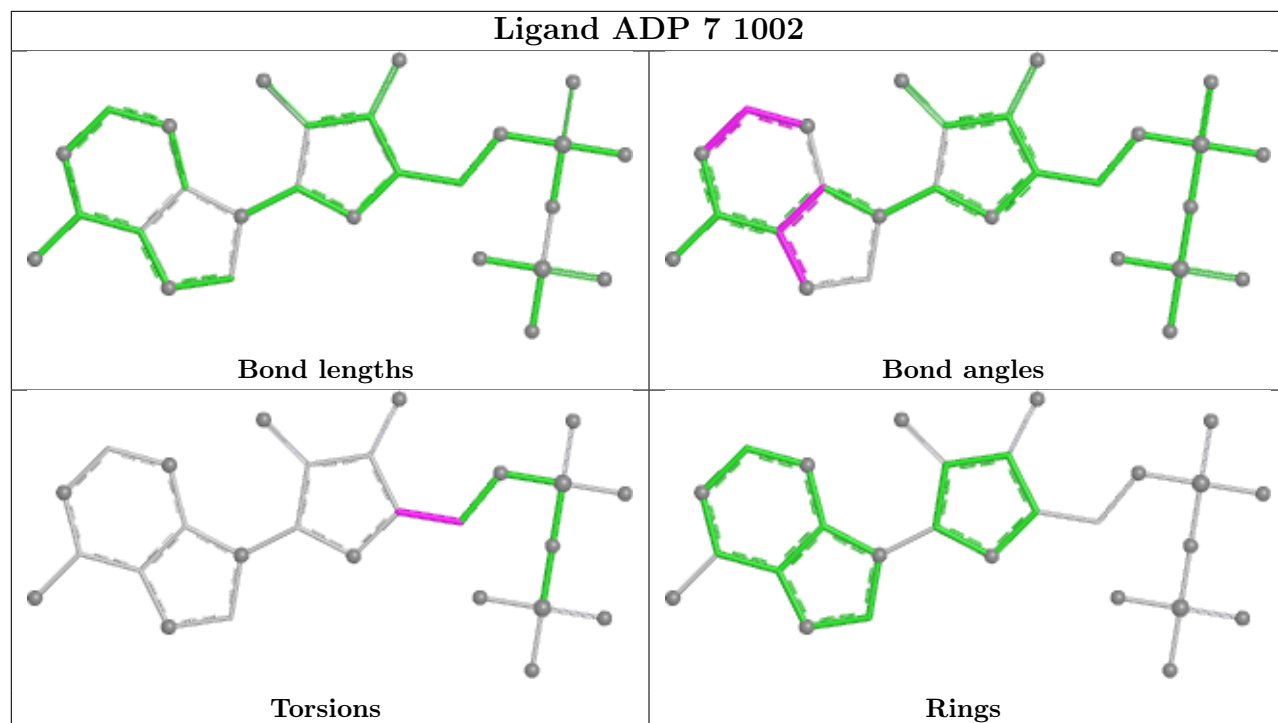
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	2	1002	ATP	3	0
12	6	1002	ADP	1	0
12	5	1002	ADP	2	0
11	A	1002	ATP	1	0
12	F	1002	ADP	1	0
12	E	1002	ADP	1	0
12	B	1002	ADP	1	0
12	3	1002	ADP	1	0

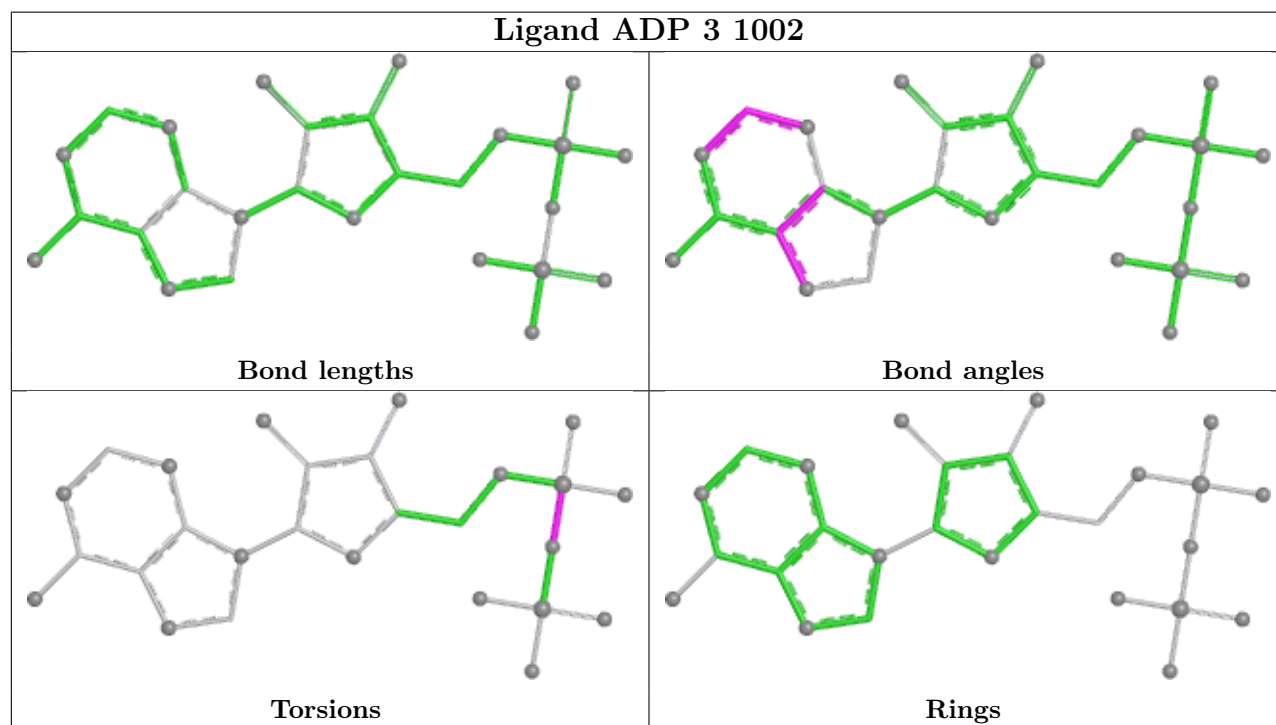
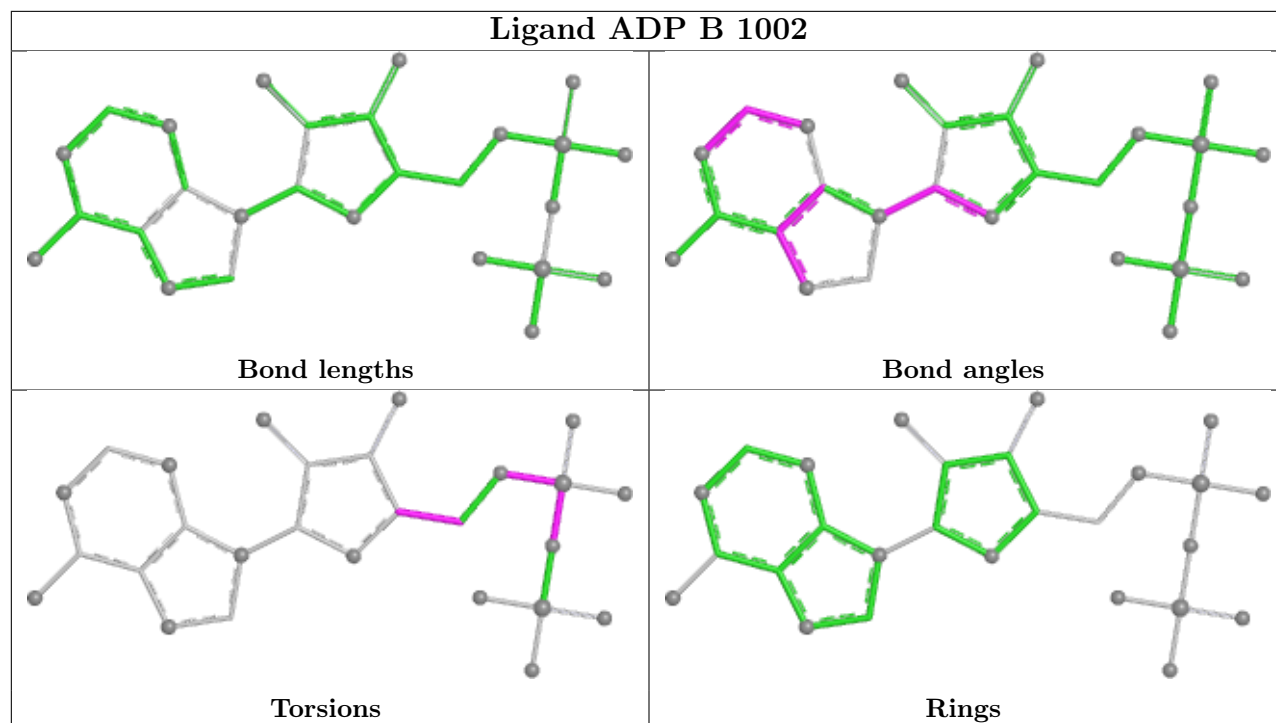
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 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.

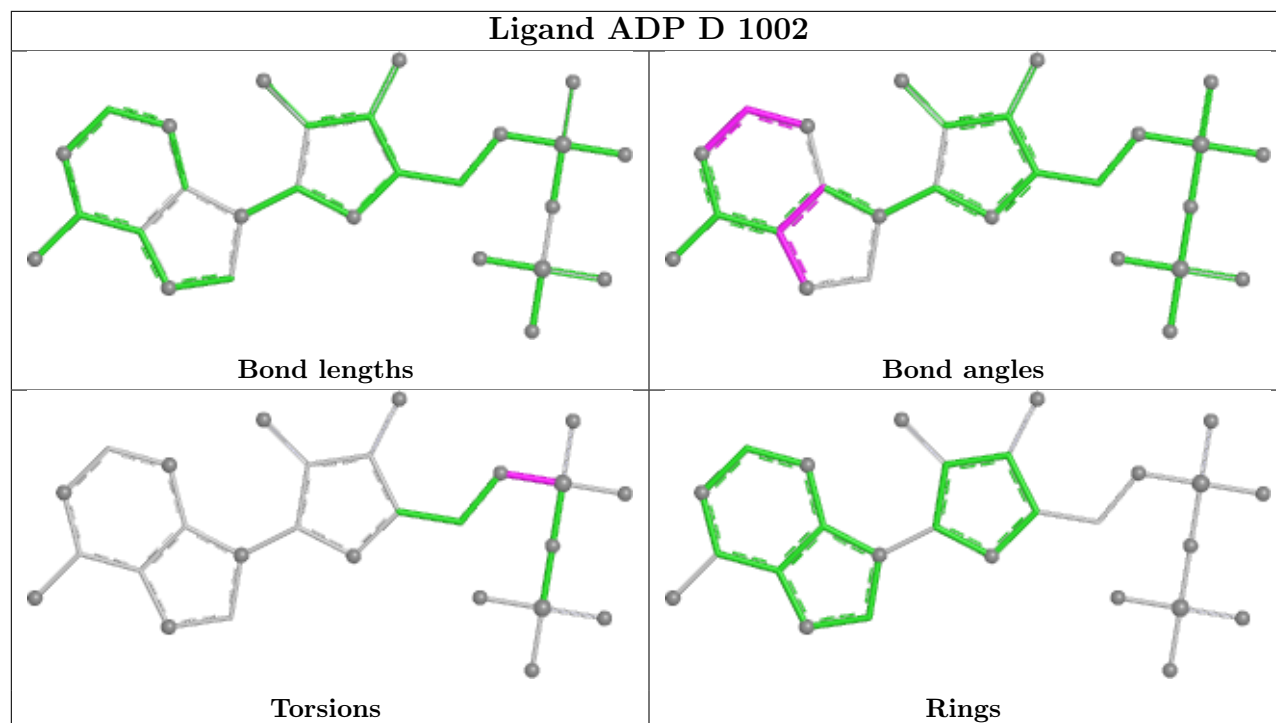












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

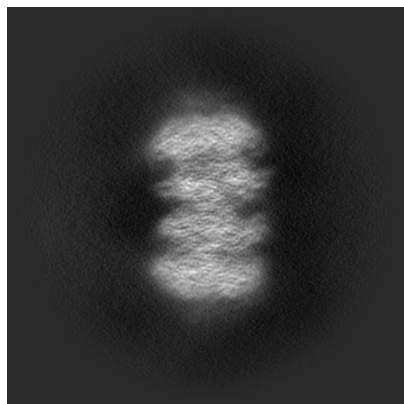
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43708. These allow visual inspection of the internal detail of the map and identification of artifacts.

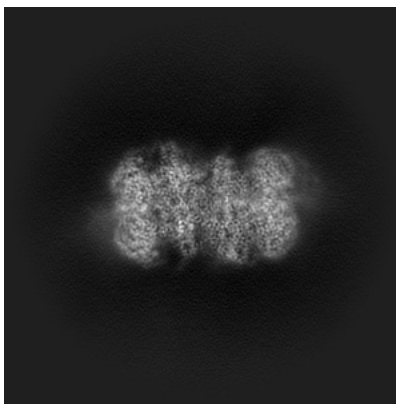
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

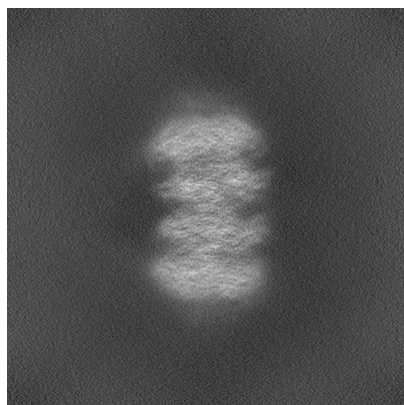


Y

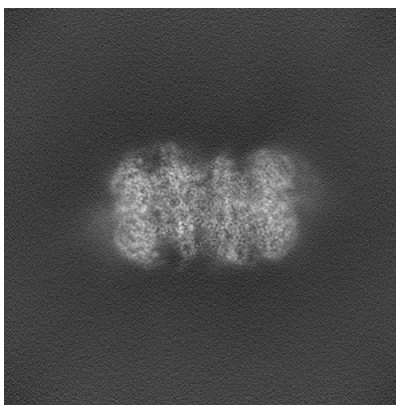


Z

6.1.2 Raw map



X



Y

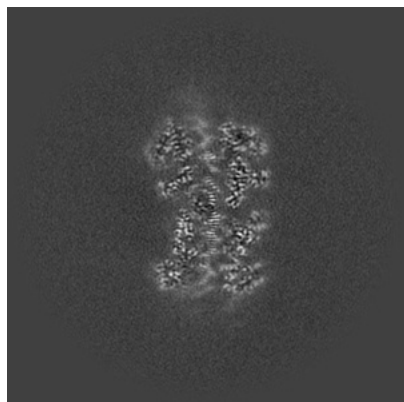


Z

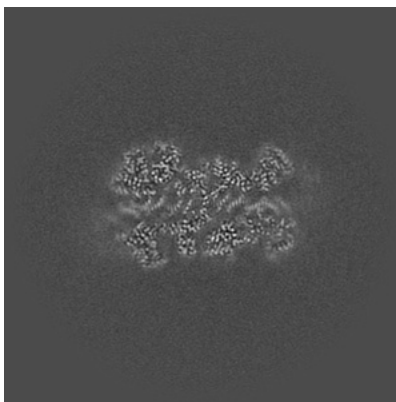
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

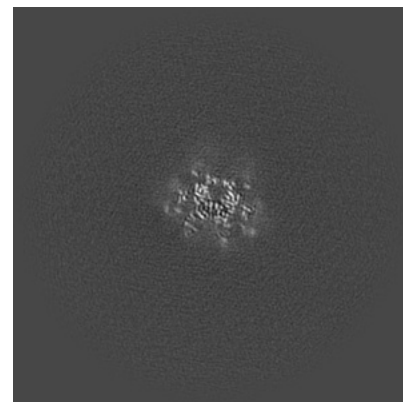
6.2.1 Primary map



X Index: 250

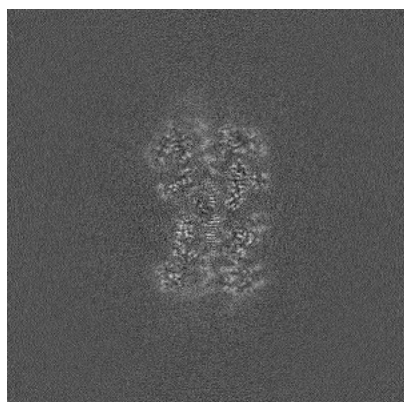


Y Index: 250

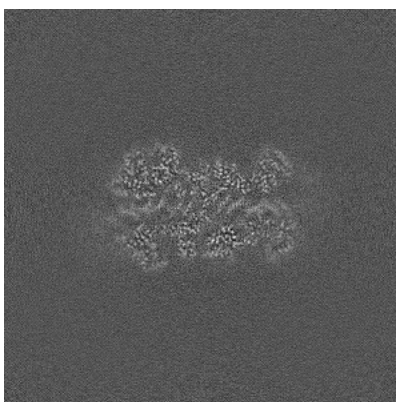


Z Index: 250

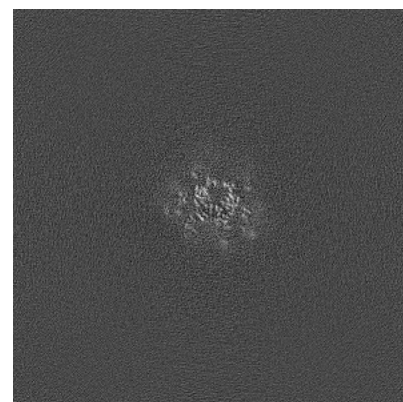
6.2.2 Raw map



X Index: 250



Y Index: 250

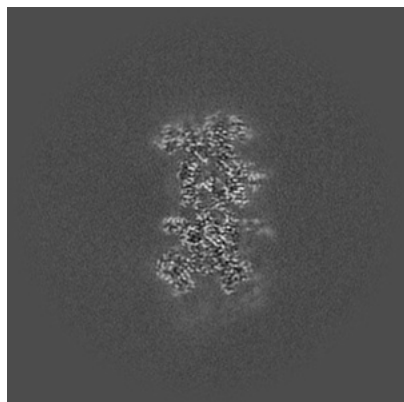


Z Index: 250

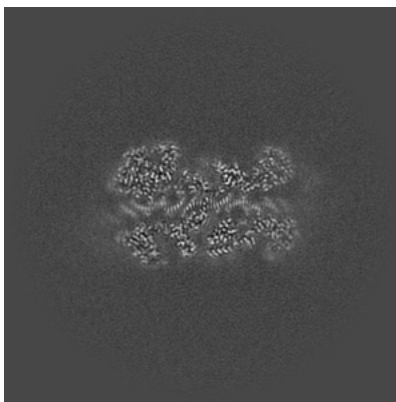
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

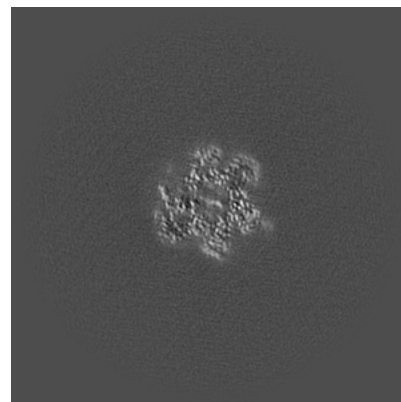
6.3.1 Primary map



X Index: 226

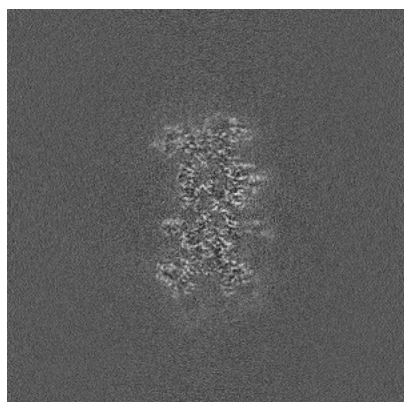


Y Index: 253

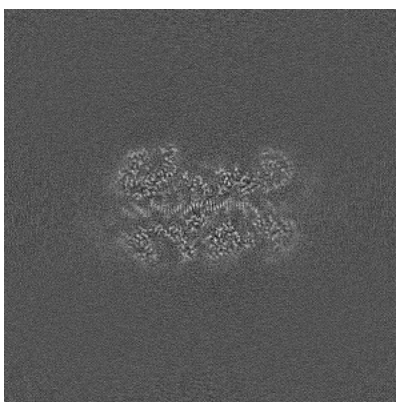


Z Index: 278

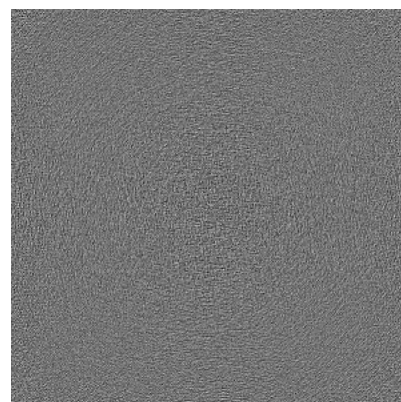
6.3.2 Raw map



X Index: 227



Y Index: 255

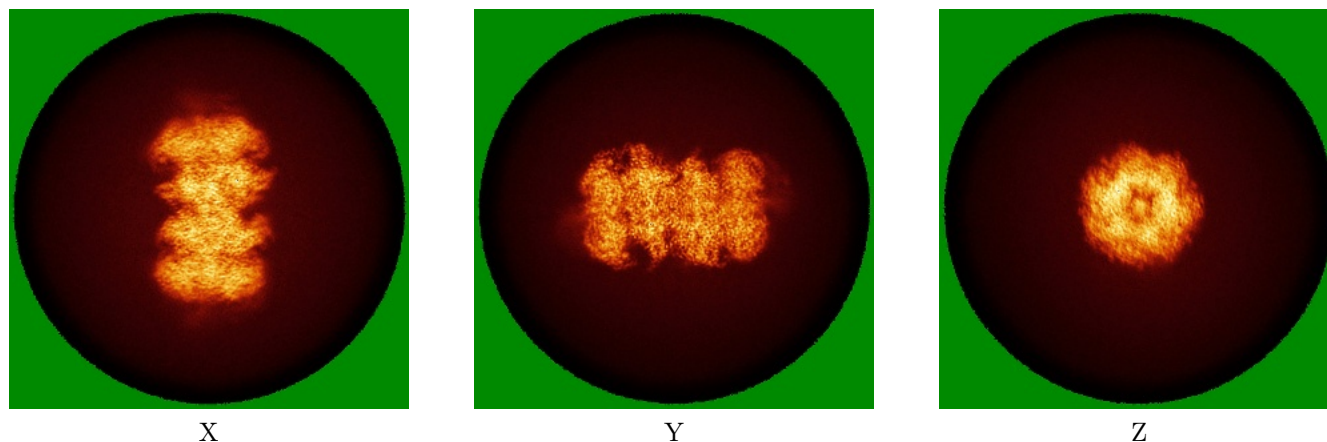


Z Index: 0

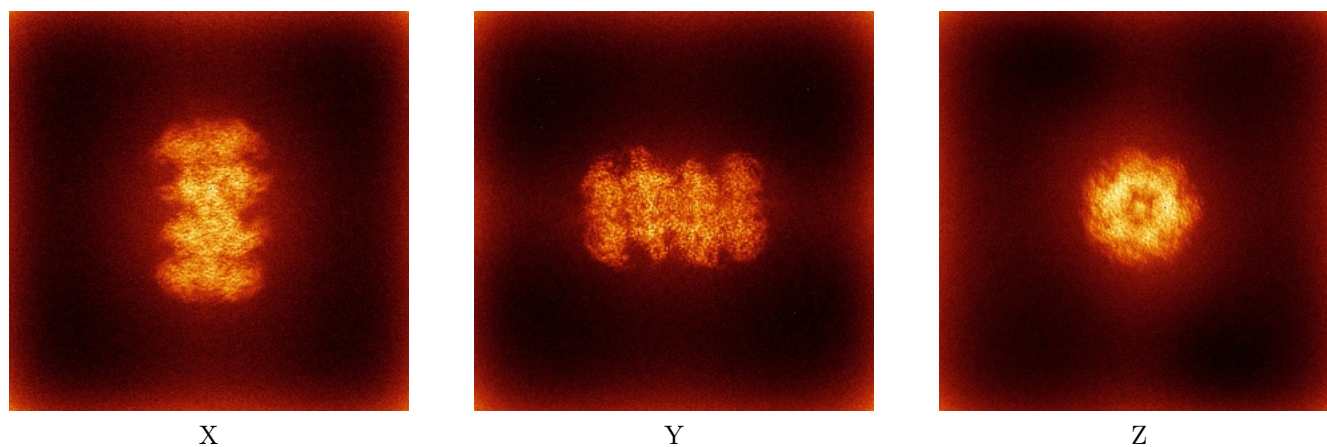
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



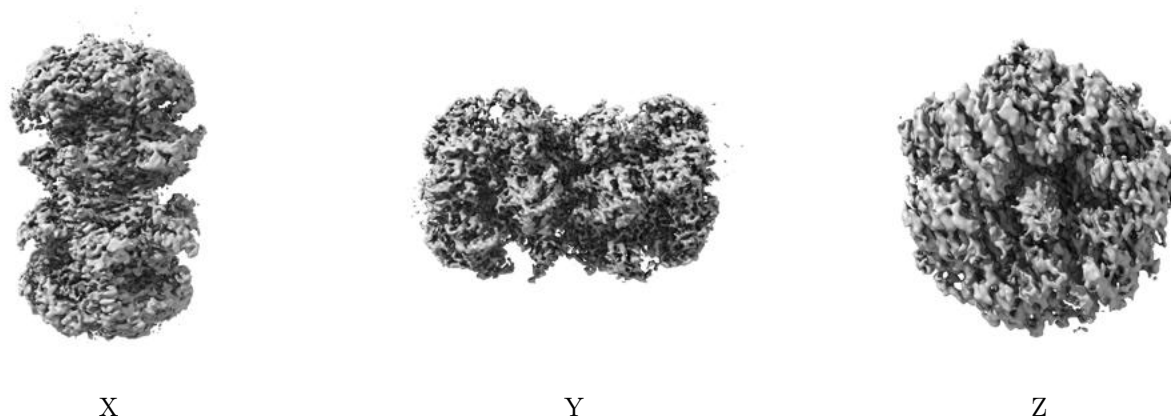
6.4.2 Raw map



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

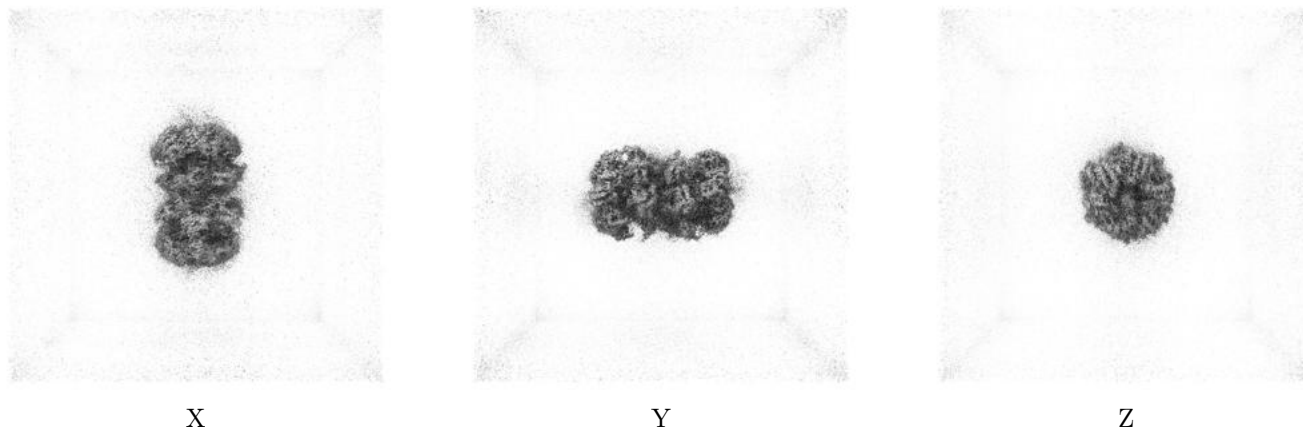
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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



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.

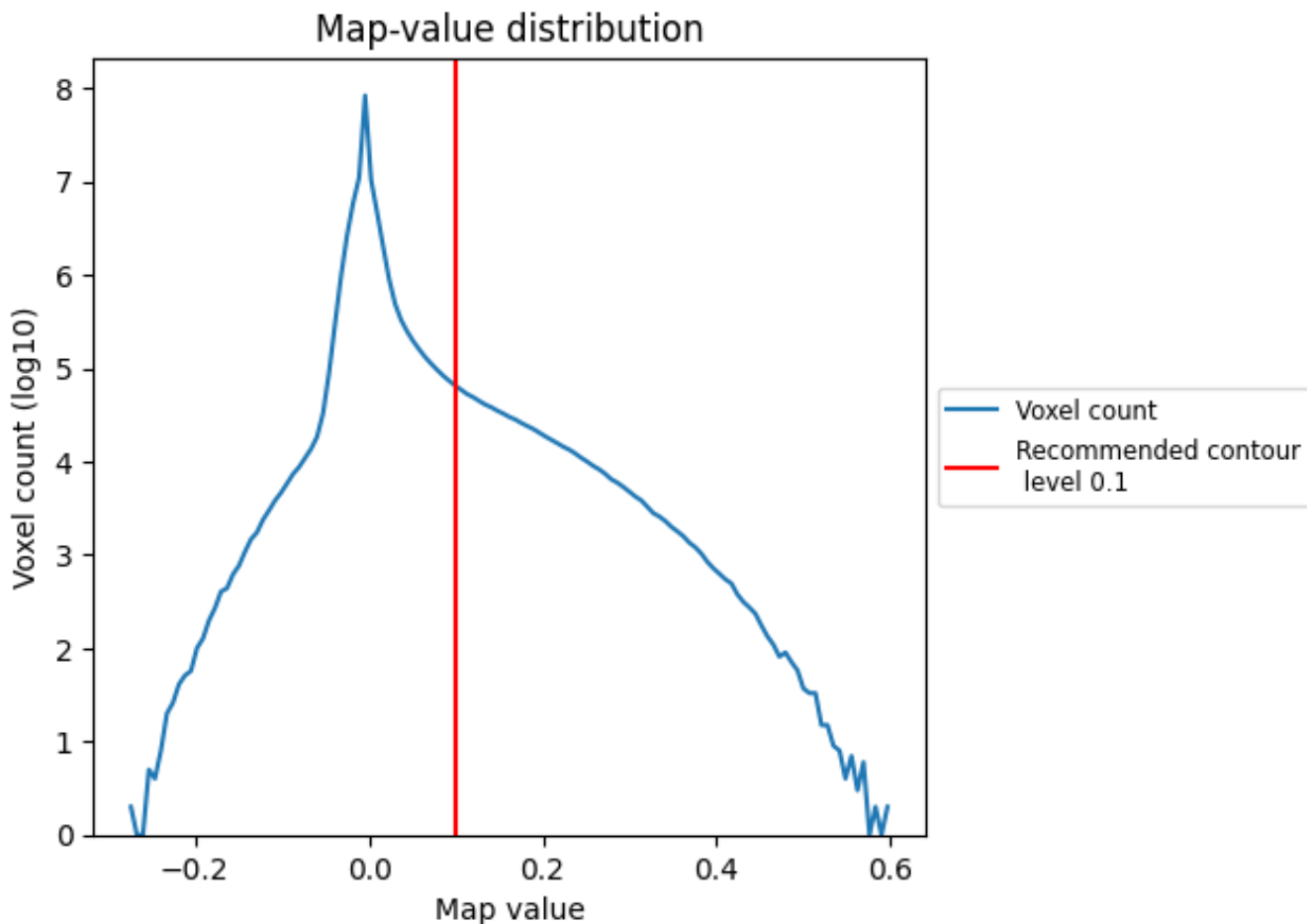
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

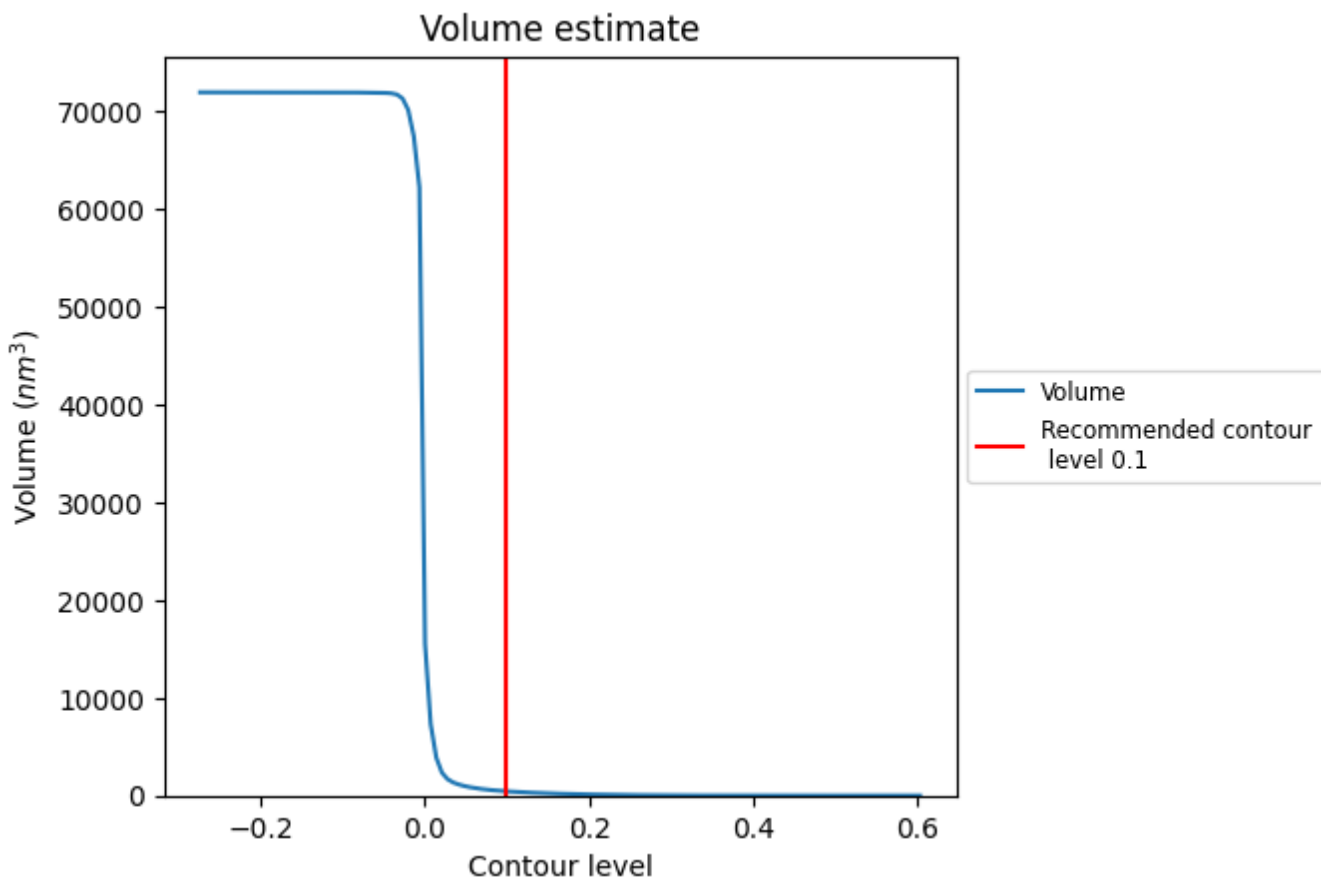
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

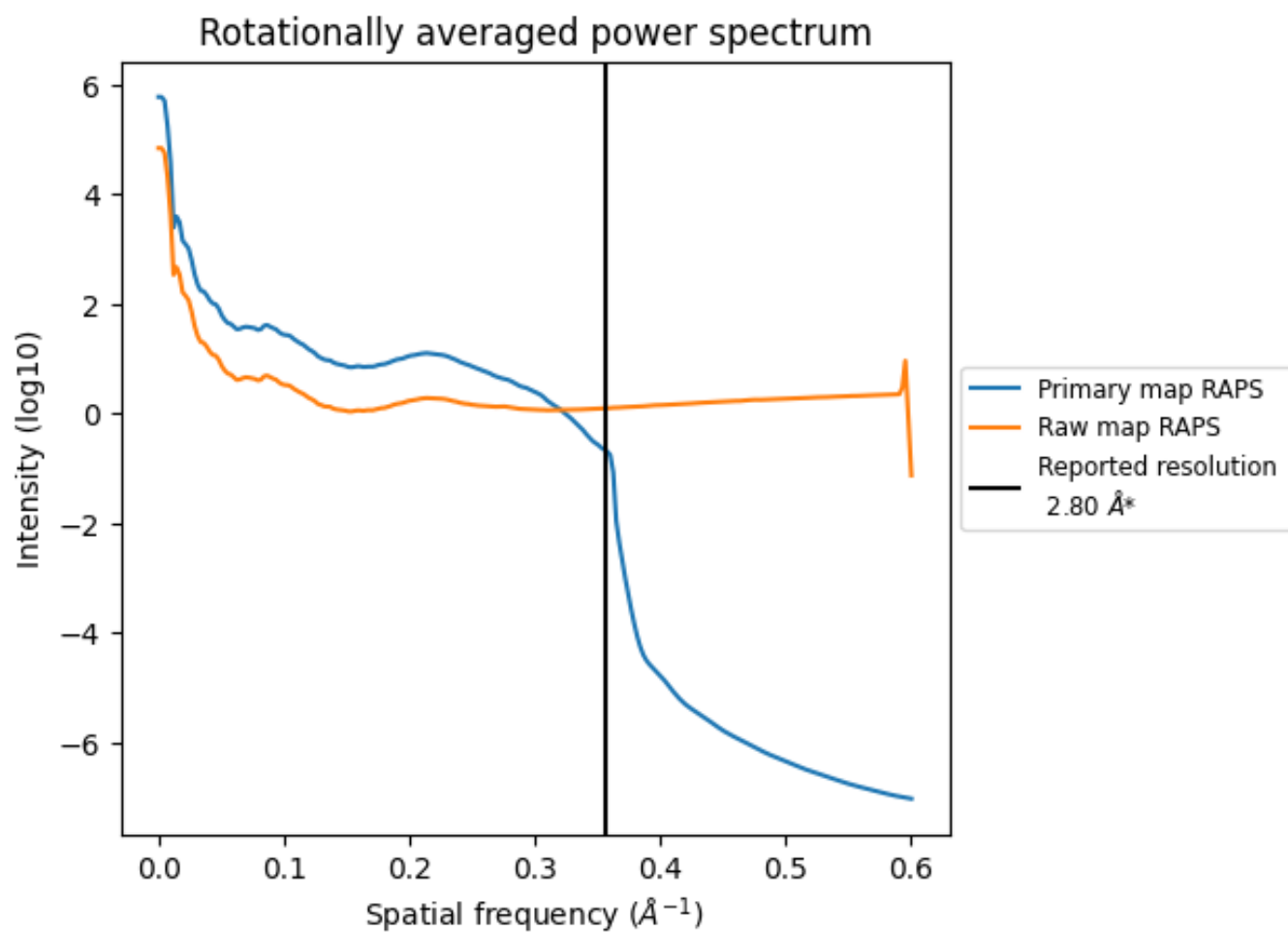
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 434 nm^3 ; this corresponds to an approximate mass of 392 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

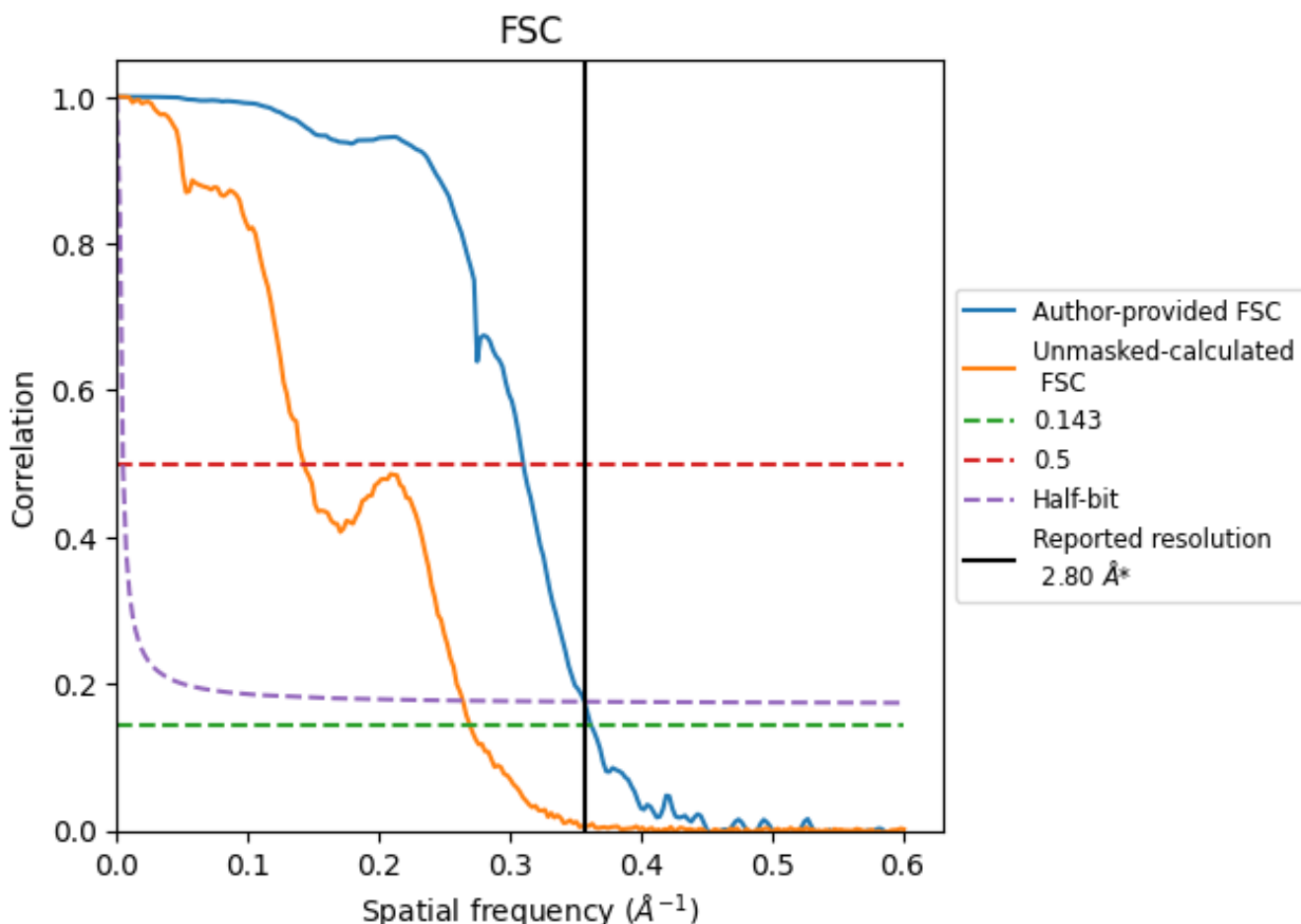


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357\AA^{-1}

8.2 Resolution estimates [i](#)

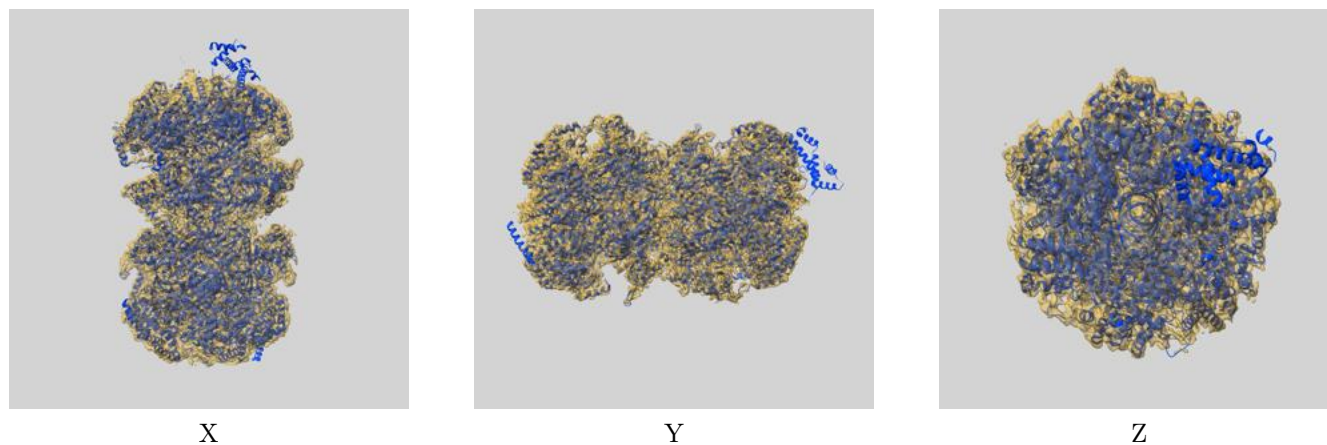
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.76	3.22	2.80
Unmasked-calculated*	3.71	7.00	3.78

*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 3.71 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

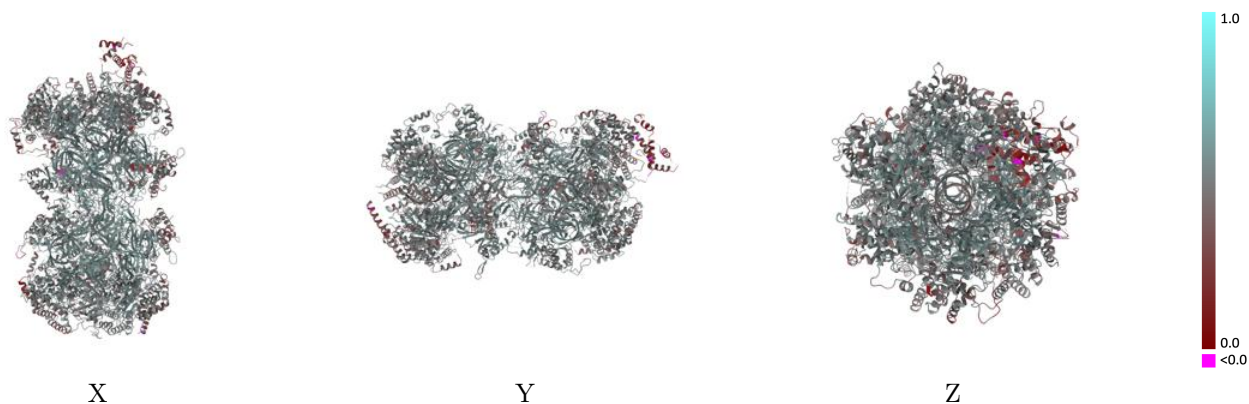
This section contains information regarding the fit between EMDB map EMD-43708 and PDB model 8W0F. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



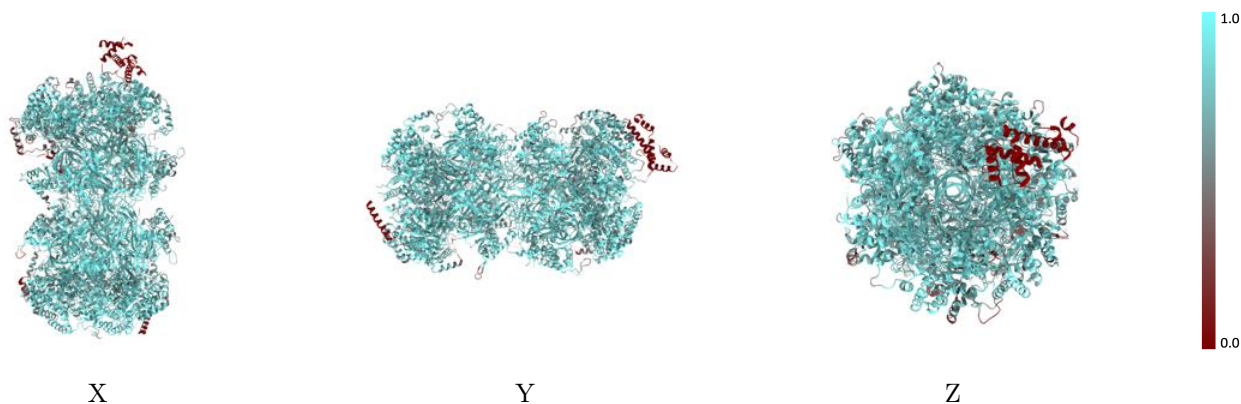
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



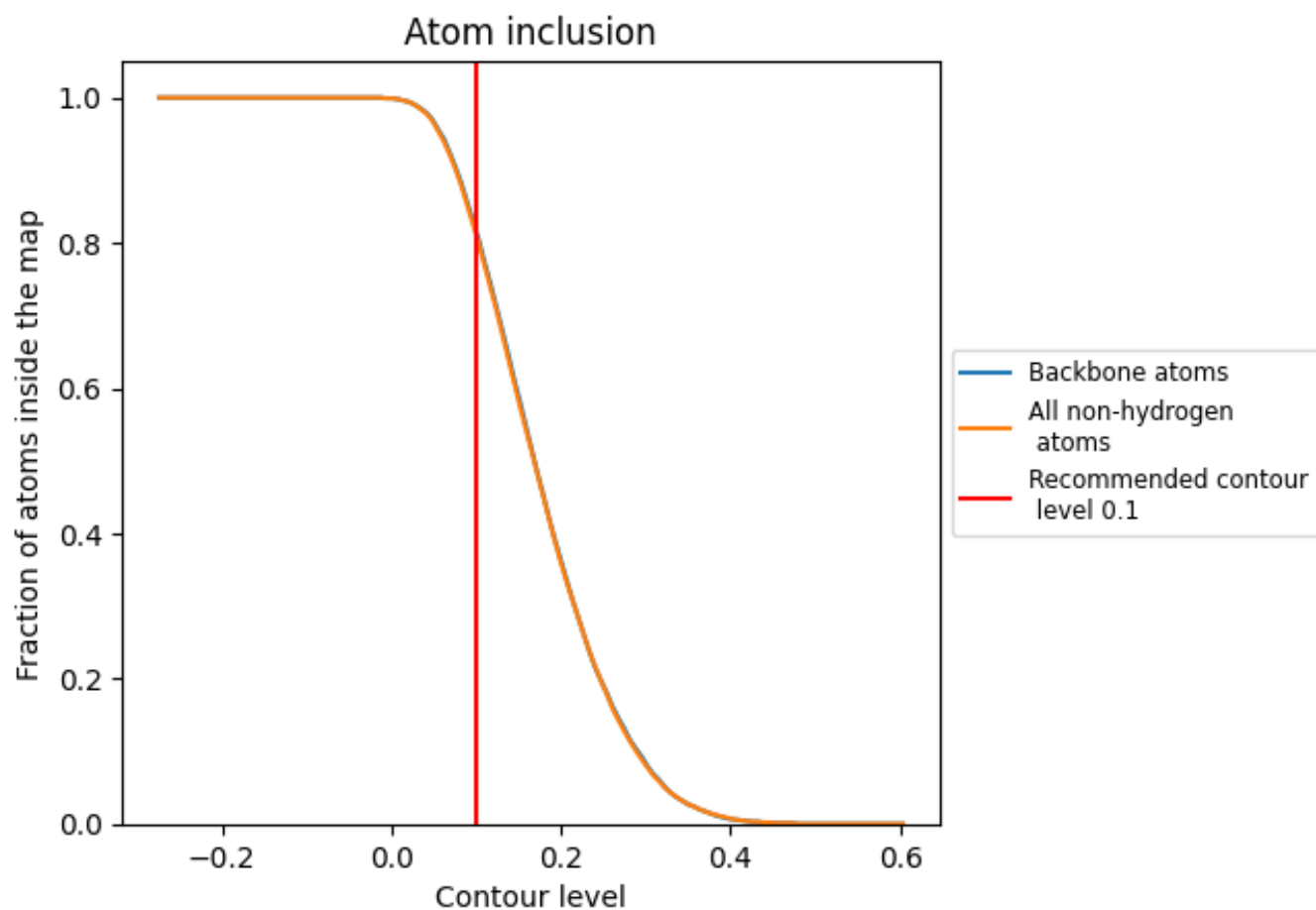
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8120	 0.5010
2	 0.7980	 0.4760
3	 0.8210	 0.5010
4	 0.8500	 0.5210
5	 0.8440	 0.5070
6	 0.8510	 0.5130
7	 0.8410	 0.5030
A	 0.7610	 0.4850
B	 0.7810	 0.4910
C	 0.8380	 0.5090
D	 0.8310	 0.5150
E	 0.7580	 0.4840
F	 0.8320	 0.5080
O	 0.9010	 0.4930
S	 0.9100	 0.4990

