



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 09:59 PM UTC

PDB ID : 8Y82 / pdb_00008y82
EMDB ID : EMD-39030
Title : Cryo-EM structure of the tetrameric SPARSA gRNA-ssDNA-NAD⁺ complex
Authors : Zhang, J.T.; Cui, N.; Wei, X.Y.; Jia, N.
Deposited on : 2024-02-05
Resolution : 3.40 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

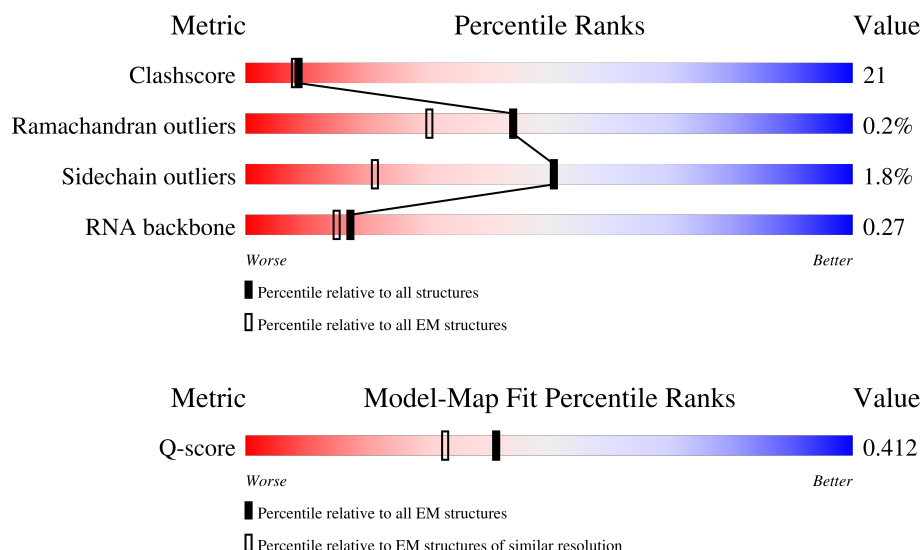
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	A	587	19% 54% 25% 21%
1	E	587	17% 63% 35% •
1	I	587	42% 50% 27% • 21%

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Mol	Chain	Length	Quality of chain
1	M	587	
2	B	473	
2	F	473	
2	J	473	
2	N	473	
3	C	21	
3	G	21	
3	K	21	
3	O	21	
4	D	25	
4	H	25	
4	L	25	
4	P	25	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	AMP	M	601	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 34526 atoms, of which 12 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 Sir2 superfamily protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	463	Total	C	N	O	S	0	0
			3659	2350	633	664	12		
1	E	576	Total	C	N	O	S	0	0
			4609	2953	797	845	14		
1	I	463	Total	C	N	O	S	0	0
			3659	2350	633	664	12		
1	M	576	Total	C	N	O	S	0	0
			4609	2953	797	845	14		

- Molecule 2 is a protein called Piwi domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	456	Total	C	N	O	S	0	0
			3629	2327	613	671	18		
2	F	456	Total	C	N	O	S	0	0
			3629	2327	613	671	18		
2	J	456	Total	C	N	O	S	0	0
			3629	2327	613	671	18		
2	N	456	Total	C	N	O	S	0	0
			3629	2327	613	671	18		

- Molecule 3 is a RNA chain called RNA (21-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	21	Total	C	N	O	P	0	0
			442	198	73	150	21		
3	G	21	Total	C	N	O	P	0	0
			442	198	73	150	21		
3	K	21	Total	C	N	O	P	0	0
			442	198	73	150	21		
3	O	21	Total	C	N	O	P	0	0
			442	198	73	150	21		

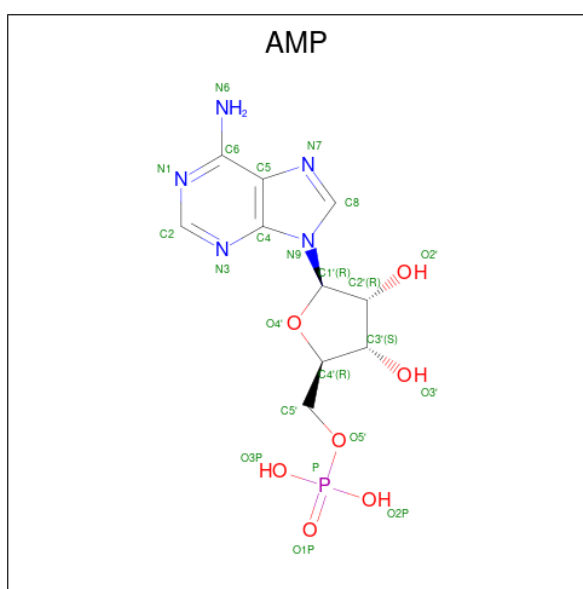
- Molecule 4 is a DNA chain called DNA (25-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	20	Total	C	N	O	P	0	0
			411	196	80	115	20		
4	H	20	Total	C	N	O	P	0	0
			411	196	80	115	20		
4	L	20	Total	C	N	O	P	0	0
			411	196	80	115	20		
4	P	20	Total	C	N	O	P	0	0
			411	196	80	115	20		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	C	1	Total	Mg	0
			1	1	
5	F	1	Total	Mg	0
			1	1	
5	K	1	Total	Mg	0
			1	1	
5	N	1	Total	Mg	0
			1	1	

- Molecule 6 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: C₁₀H₁₄N₅O₇P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
6	E	1	Total	C	H	N	O	P
			35	10	12	5	7	1
								0

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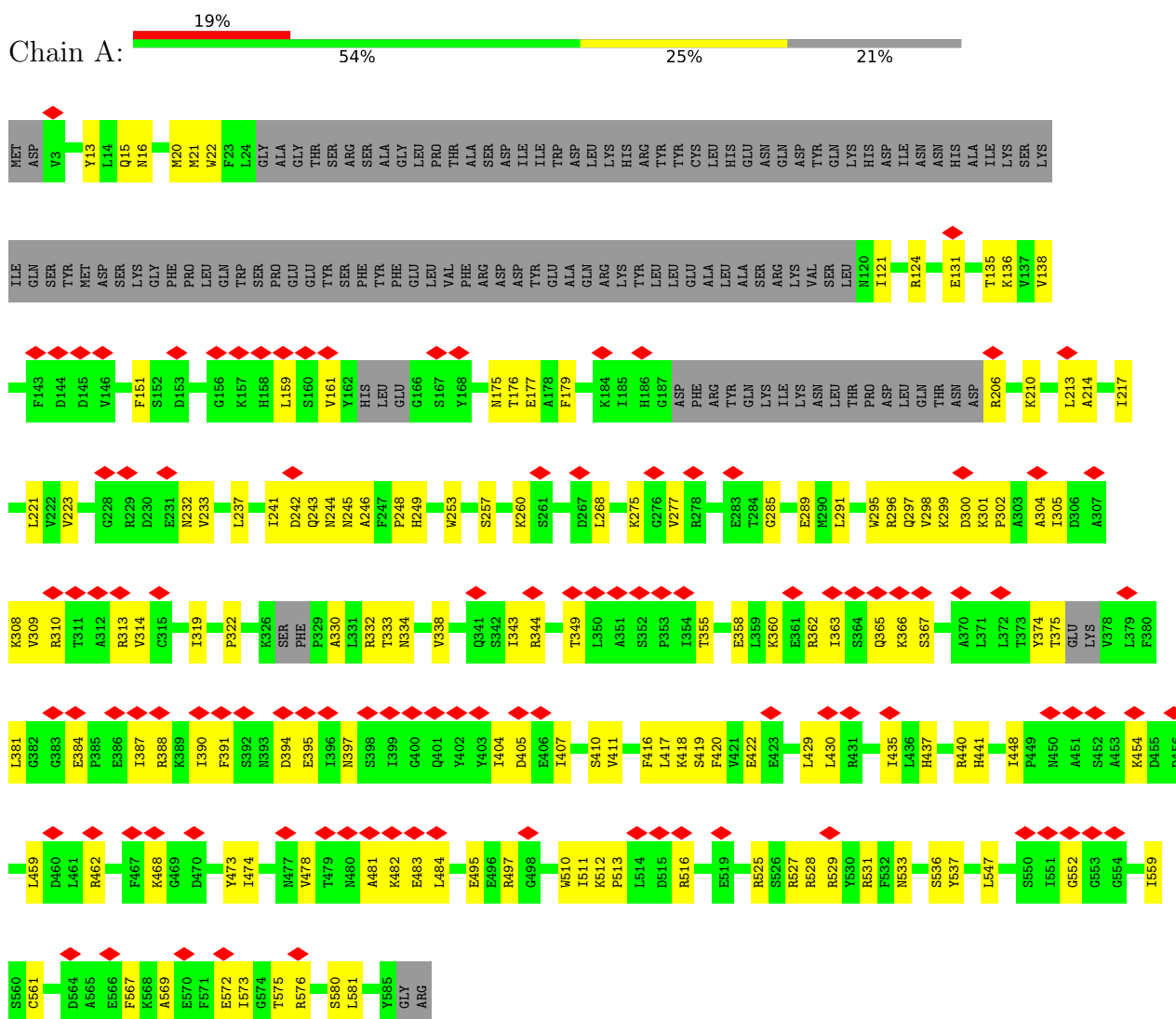
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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
6	M	1	23	10	5	7	1	0

3 Residue-property plots

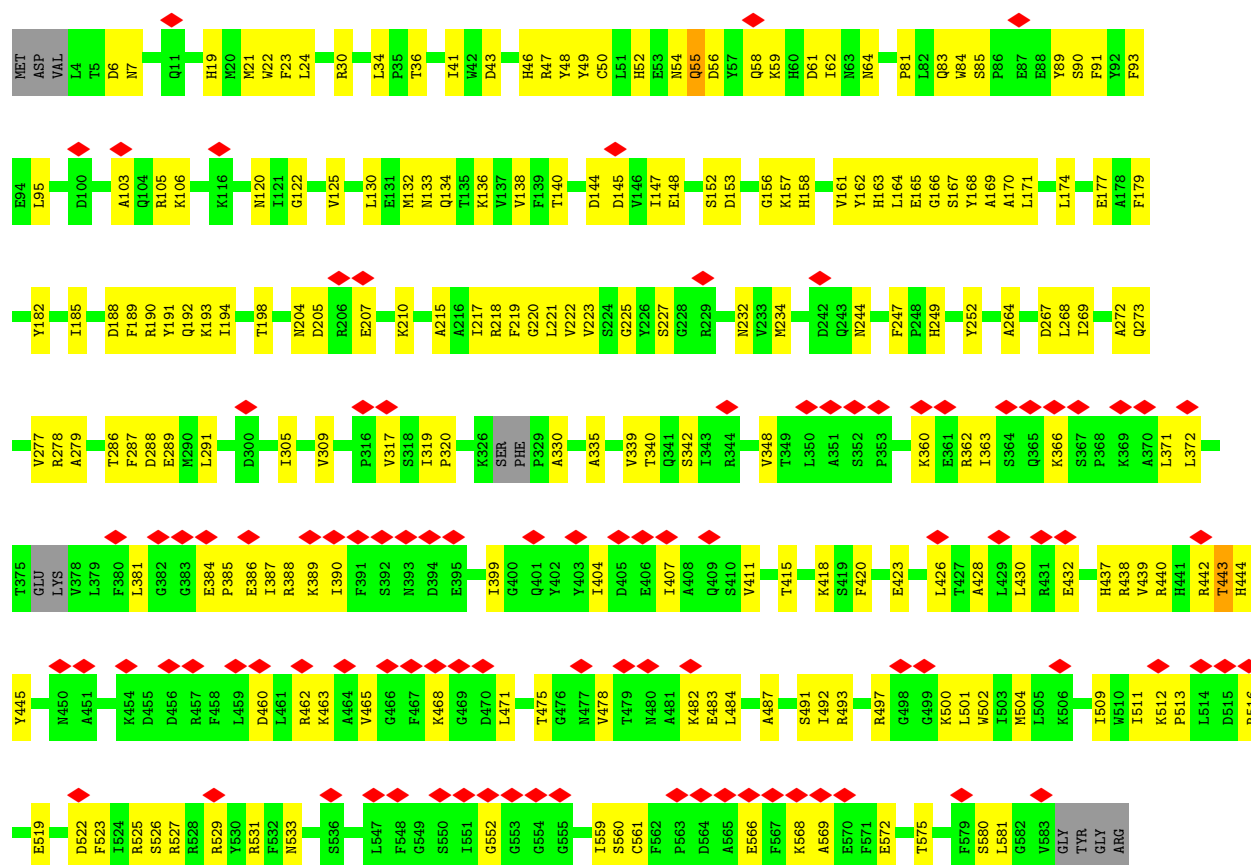
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Sir2 superfamily protein

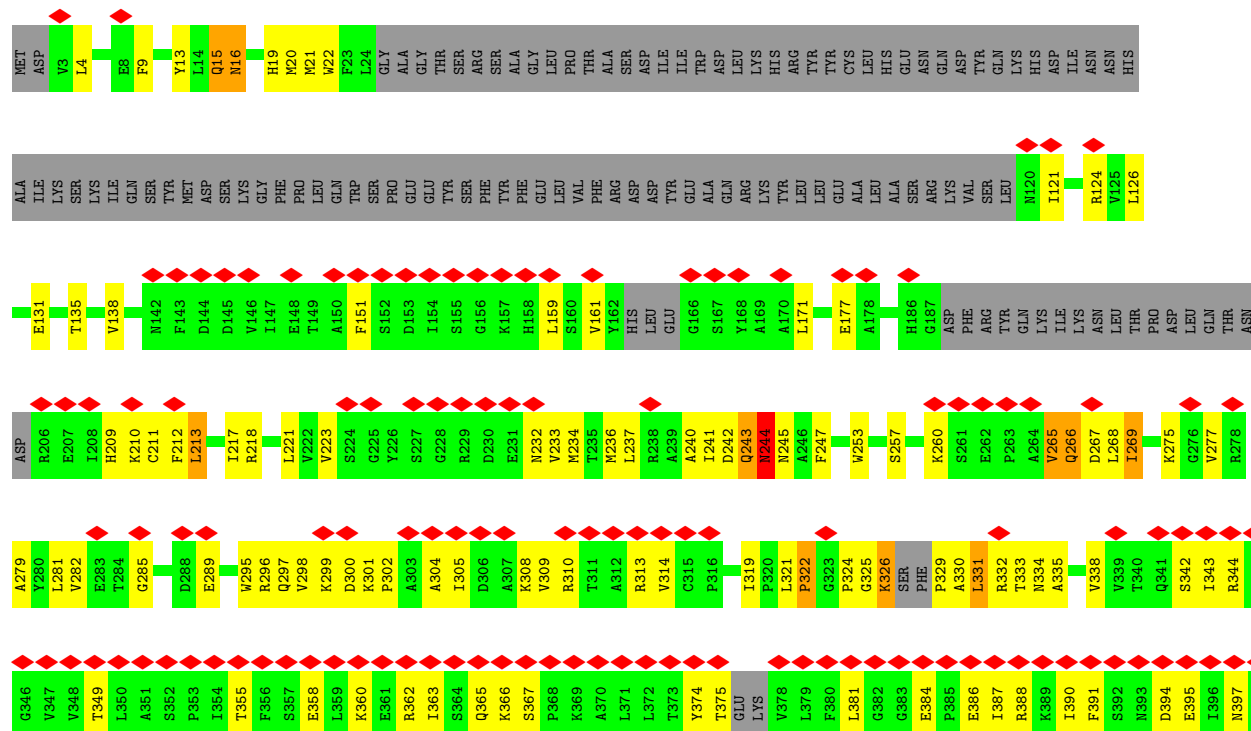
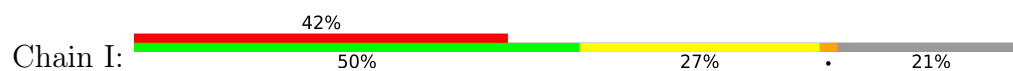


- Molecule 1: Sir2 superfamily protein

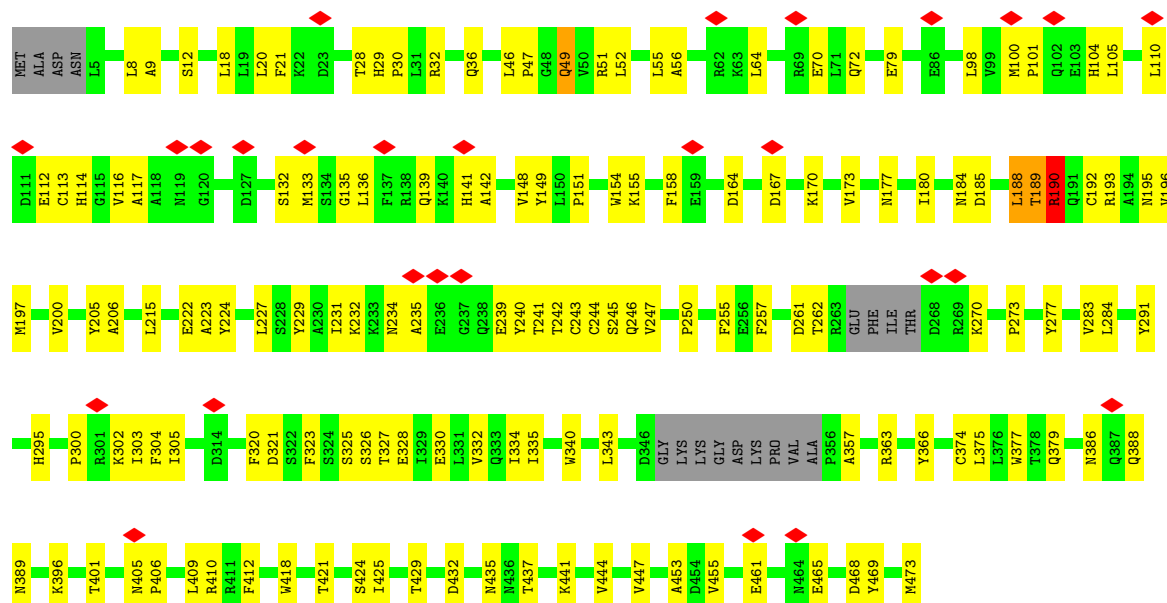




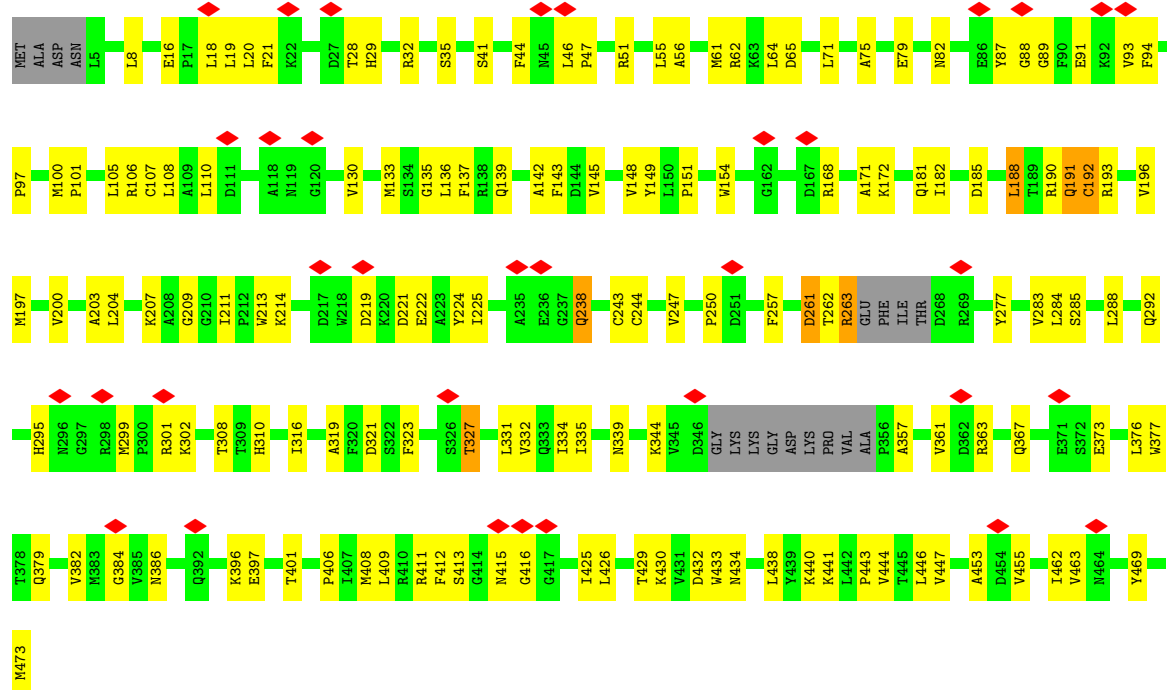
• Molecule 1: Sir2 superfamily protein



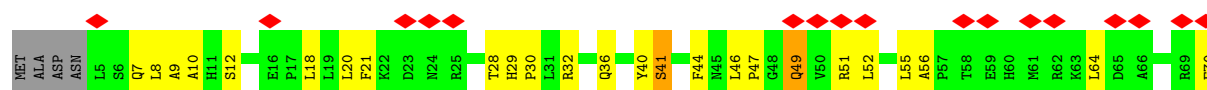


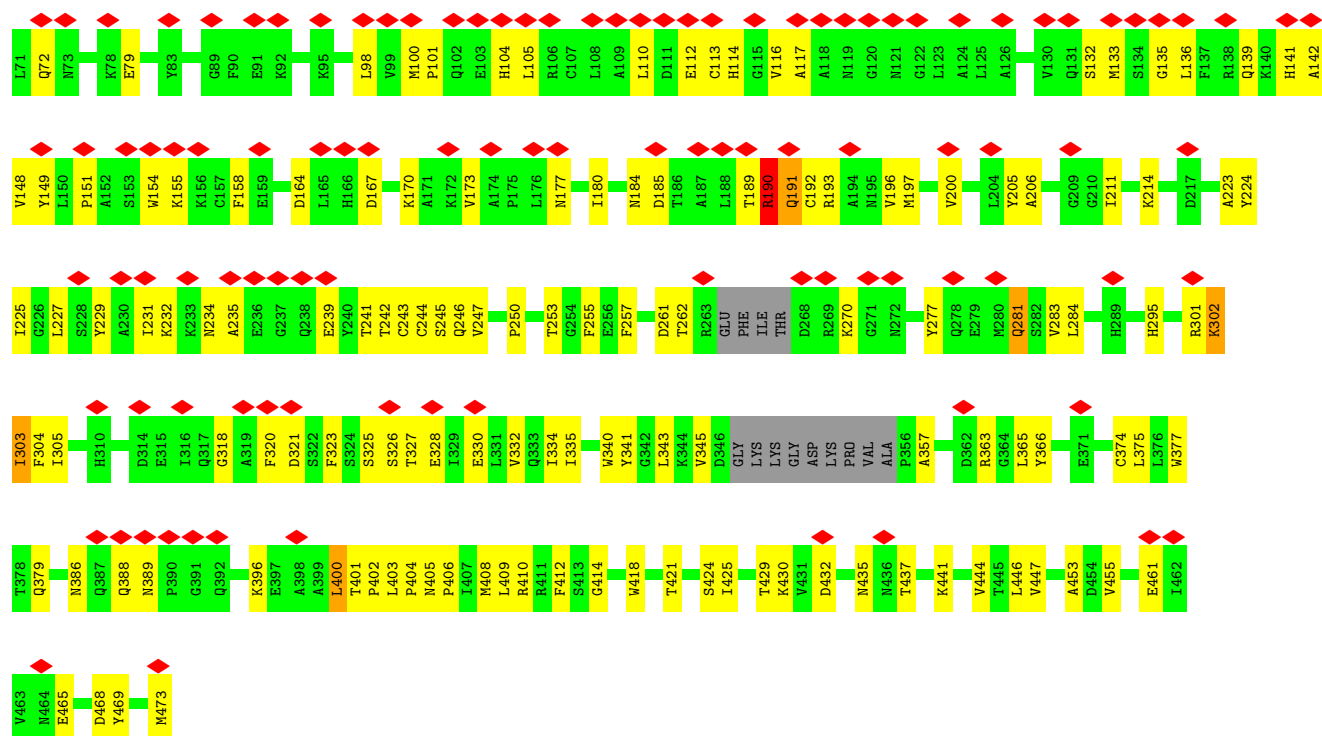


• Molecule 2: Piwi domain protein

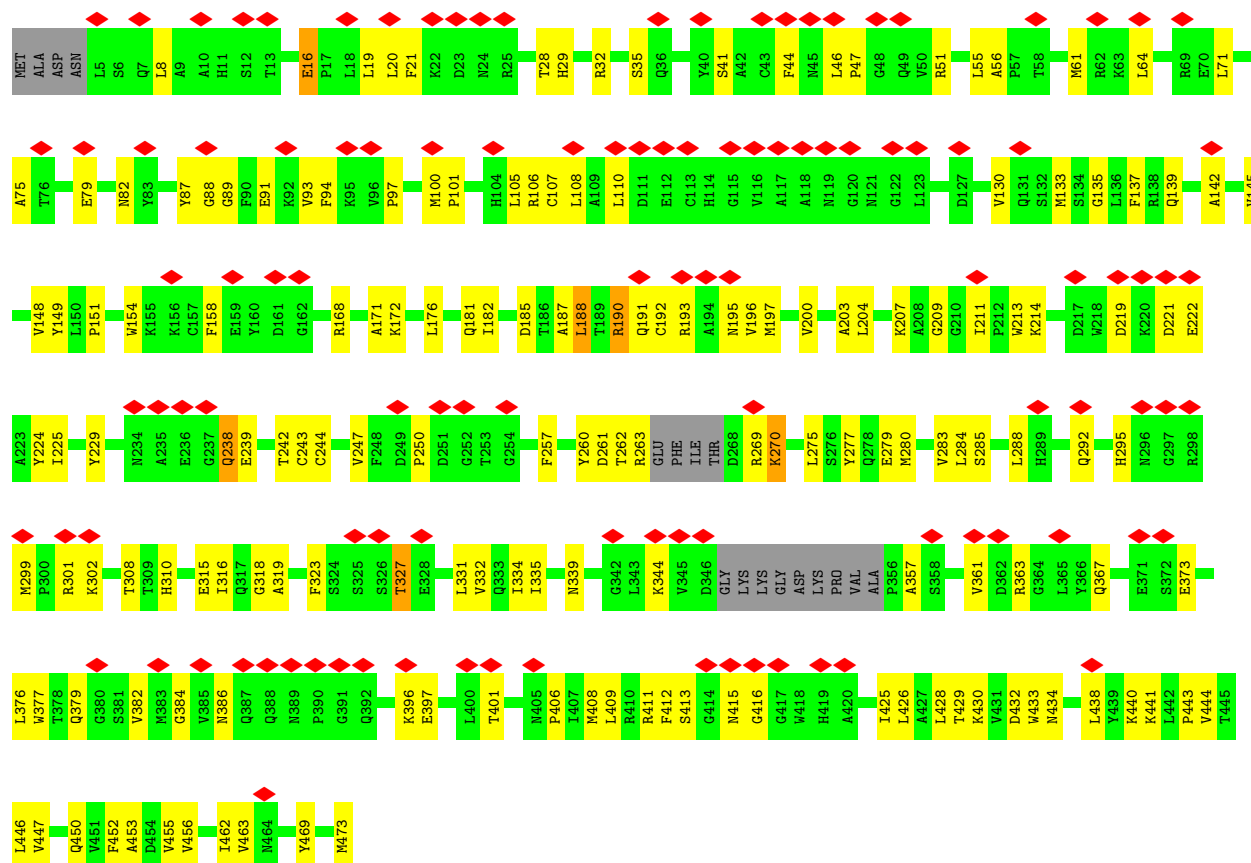


• Molecule 2: Piwi domain protein

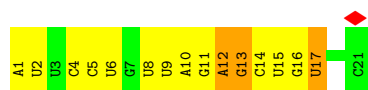




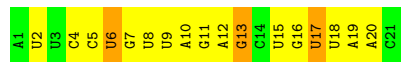
• Molecule 2: Piwi domain protein



- Molecule 3: RNA (21-mer)



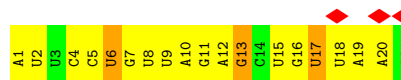
- Molecule 3: RNA (21-mer)



- Molecule 3: RNA (21-mer)



- Molecule 3: RNA (21-mer)



- Molecule 4: DNA (25-mer)



- Molecule 4: DNA (25-mer)



- Molecule 4: DNA (25-mer)





• Molecule 4: DNA (25-mer)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31412	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.238	Depositor
Minimum map value	-1.381	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.058	Depositor
Recommended contour level	0.375	Depositor
Map size ($\text{\AA}$)	380.42, 380.42, 380.42	wwPDB
Map dimensions	460, 460, 460	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.827, 0.827, 0.827	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.14	0/3737	0.31	0/5054
1	E	0.20	0/4716	0.37	0/6382
1	I	0.30	0/3737	0.53	4/5054 (0.1%)
1	M	0.26	0/4716	0.52	1/6382 (0.0%)
2	B	0.16	0/3724	0.34	0/5060
2	F	0.17	0/3724	0.38	1/5060 (0.0%)
2	J	0.25	0/3724	0.45	0/5060
2	N	0.23	0/3724	0.47	2/5060 (0.0%)
3	C	0.15	0/492	0.34	0/763
3	G	0.16	0/492	0.36	0/763
3	K	0.15	0/492	0.34	0/763
3	O	0.16	0/492	0.36	0/763
4	D	0.19	0/462	0.39	0/710
4	H	0.19	0/462	0.37	0/710
4	L	0.19	0/462	0.39	0/710
4	P	0.19	0/462	0.37	0/710
All	All	0.21	0/35618	0.42	8/49004 (0.0%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	191	GLN	N-CA-C	5.33	122.16	110.80
2	N	462	ILE	N-CA-C	-5.32	108.09	113.20
2	F	462	ILE	N-CA-C	-5.30	108.11	113.20
1	I	15	GLN	CA-C-N	-5.18	116.09	123.03
1	I	15	GLN	C-N-CA	-5.18	116.09	123.03
1	M	14	LEU	N-CA-C	-5.15	105.67	111.28
1	I	244	ASN	CA-C-N	-5.01	116.31	123.03
1	I	244	ASN	C-N-CA	-5.01	116.31	123.03

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	3659	0	3682	158	0
1	E	4609	0	4590	244	0
1	I	3659	0	3680	185	0
1	M	4609	0	4591	314	0
2	B	3629	0	3564	115	0
2	F	3629	0	3564	126	0
2	J	3629	0	3564	188	0
2	N	3629	0	3564	192	0
3	C	442	0	224	16	0
3	G	442	0	224	15	0
3	K	442	0	224	12	0
3	O	442	0	224	23	0
4	D	411	0	225	14	0
4	H	411	0	225	19	0
4	L	411	0	225	14	0
4	P	411	0	225	15	0
5	C	1	0	0	0	0
5	F	1	0	0	0	0
5	K	1	0	0	0	0
5	N	1	0	0	0	0
6	E	23	12	12	4	0
6	M	23	0	12	11	0
All	All	34514	12	32619	1411	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 21.

All (1411) 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:F:185:ASP:HA	2:F:188:LEU:CD1	1.16	1.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:185:ASP:CA	2:F:188:LEU:CD1	1.91	1.48
1:A:217:ILE:CG2	1:M:217:ILE:HD13	1.45	1.43
2:F:185:ASP:CA	2:F:188:LEU:HD11	1.44	1.41
2:N:187:ALA:CB	3:O:2:U:H5	1.31	1.41
2:N:187:ALA:CB	3:O:2:U:C5	2.08	1.35
2:N:187:ALA:HB1	3:O:2:U:C5	1.59	1.35
2:F:185:ASP:C	2:F:188:LEU:HD12	1.49	1.35
1:A:217:ILE:HG21	1:M:217:ILE:CD1	1.61	1.30
2:F:185:ASP:O	2:F:188:LEU:HD12	1.18	1.30
1:M:227:SER:CB	6:M:601:AMP:O3'	1.78	1.29
1:E:192:GLN:HB2	1:M:168:TYR:CZ	1.67	1.28
1:M:144:ASP:OD1	1:M:189:PHE:HE2	1.11	1.27
1:E:148:GLU:OE2	1:E:161:VAL:HG11	1.21	1.27
1:M:112:LEU:HB3	1:M:144:ASP:OD2	1.28	1.26
1:M:112:LEU:HB3	1:M:144:ASP:CG	1.60	1.26
2:J:330:GLU:OE1	2:J:414:GLY:CA	1.82	1.25
2:N:239:GLU:OE2	2:N:269:ARG:HG2	1.33	1.25
2:J:302:LYS:NZ	2:J:330:GLU:CG	1.98	1.25
2:N:262:THR:CG2	2:N:283:VAL:CG2	2.14	1.25
1:M:126:LEU:HD23	1:M:147:ILE:CD1	1.67	1.24
2:N:262:THR:CG2	2:N:283:VAL:HG21	1.67	1.23
2:J:302:LYS:HZ3	2:J:330:GLU:HG3	1.05	1.21
2:J:330:GLU:OE1	2:J:414:GLY:HA3	1.03	1.21
1:E:148:GLU:HB3	1:M:158:HIS:CD2	1.73	1.20
2:N:239:GLU:CD	2:N:269:ARG:HG2	1.66	1.20
2:F:261:ASP:OD2	2:F:463:VAL:CG1	1.88	1.19
1:E:192:GLN:CB	1:M:168:TYR:OH	1.90	1.19
2:F:261:ASP:OD2	2:F:463:VAL:HG12	1.04	1.19
1:A:217:ILE:CG1	1:M:217:ILE:HD13	1.73	1.18
1:E:148:GLU:CD	1:E:161:VAL:HG11	1.66	1.18
2:N:190:ARG:HH22	2:N:195:ASN:CB	1.59	1.16
2:N:280:MET:CE	2:N:315:GLU:HG2	1.76	1.13
1:M:144:ASP:OD1	1:M:189:PHE:CE2	2.01	1.13
1:M:227:SER:CB	6:M:601:AMP:HO3'	1.57	1.13
1:E:169:ALA:HB2	1:M:191:TYR:CE1	1.82	1.13
1:M:227:SER:HB3	6:M:601:AMP:O3'	0.97	1.12
2:J:223:ALA:CB	2:J:303:ILE:HD11	1.80	1.11
2:N:187:ALA:HB2	3:O:2:U:H5	1.12	1.11
1:E:217:ILE:HD13	1:I:217:ILE:HG21	1.32	1.11
2:N:190:ARG:NH2	2:N:195:ASN:HB3	1.65	1.11
2:N:262:THR:HG22	2:N:283:VAL:HG22	1.22	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:ILE:CG2	1:M:217:ILE:CD1	2.21	1.10
1:E:217:ILE:CD1	1:I:217:ILE:HD13	1.81	1.10
2:J:223:ALA:O	2:J:303:ILE:CD1	1.99	1.09
2:N:262:THR:HG22	2:N:283:VAL:CG2	1.80	1.09
2:N:277:TYR:CE1	2:N:318:GLY:HA2	1.88	1.09
1:E:148:GLU:OE2	1:E:161:VAL:CG1	2.01	1.08
1:I:330:ALA:HB2	1:I:581:LEU:HA	1.24	1.08
2:J:302:LYS:CE	2:J:330:GLU:HG2	1.83	1.07
1:M:126:LEU:CD2	1:M:147:ILE:CD1	2.33	1.07
1:E:169:ALA:CB	1:M:191:TYR:CE1	2.37	1.06
1:A:244:ASN:HD21	1:M:213:LEU:HB2	1.18	1.06
1:M:228:GLY:O	1:M:229:ARG:HB3	1.48	1.06
2:N:261:ASP:OD2	2:N:463:VAL:HA	1.53	1.06
1:E:217:ILE:HD13	1:I:217:ILE:HD13	1.38	1.06
1:A:217:ILE:HG21	1:M:217:ILE:HB	1.32	1.05
2:J:223:ALA:O	2:J:303:ILE:HD12	1.54	1.05
1:A:217:ILE:HG21	1:M:217:ILE:CB	1.86	1.05
1:A:217:ILE:CB	1:M:217:ILE:HD13	1.84	1.05
1:A:175:ASN:CG	1:M:248:PRO:HB3	1.82	1.05
1:M:126:LEU:HD23	1:M:147:ILE:HD13	1.35	1.04
2:N:262:THR:HB	2:N:283:VAL:CG2	1.86	1.04
1:E:177:GLU:OE2	1:I:19:HIS:CD2	2.10	1.04
1:E:192:GLN:HB2	1:M:168:TYR:OH	1.51	1.04
2:J:223:ALA:HB3	2:J:303:ILE:CD1	1.88	1.04
2:J:302:LYS:HE2	2:J:330:GLU:HG2	1.38	1.04
2:J:40:TYR:HE2	2:J:214:LYS:HD3	1.22	1.03
1:A:244:ASN:ND2	1:M:213:LEU:HB2	1.74	1.03
1:E:188:ASP:OD2	1:E:190:ARG:NH2	1.91	1.03
2:N:261:ASP:CG	2:N:463:VAL:HA	1.86	1.01
2:N:262:THR:HG21	2:N:283:VAL:HG21	1.36	1.01
1:E:158:HIS:CD2	1:M:148:GLU:HB3	1.96	1.01
2:J:190:ARG:CZ	2:J:190:ARG:HA	1.91	1.01
2:J:302:LYS:NZ	2:J:330:GLU:HG2	1.73	1.01
2:J:401:THR:OG1	2:J:402:PRO:HD2	1.57	1.01
2:N:262:THR:CB	2:N:283:VAL:CG2	2.40	1.00
1:E:192:GLN:N	1:M:168:TYR:OH	1.94	1.00
1:A:217:ILE:CG1	1:M:217:ILE:CD1	2.41	0.99
2:N:277:TYR:HE1	2:N:318:GLY:HA2	1.24	0.99
2:F:185:ASP:C	2:F:188:LEU:CD1	2.28	0.98
2:J:190:ARG:O	2:J:192:CYS:N	1.97	0.97
2:J:302:LYS:HZ1	2:J:330:GLU:CG	1.73	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:280:MET:HE3	2:N:315:GLU:CG	1.95	0.97
2:J:302:LYS:HZ1	2:J:330:GLU:CD	1.73	0.97
1:E:177:GLU:OE2	1:I:19:HIS:HD2	1.43	0.96
1:A:217:ILE:HG21	1:M:217:ILE:CG1	1.95	0.96
1:I:330:ALA:CB	1:I:581:LEU:HA	1.95	0.96
2:N:190:ARG:HH22	2:N:195:ASN:CG	1.72	0.96
2:N:280:MET:CE	2:N:315:GLU:CG	2.42	0.96
2:F:185:ASP:CA	2:F:188:LEU:HD12	1.77	0.96
2:N:262:THR:CG2	2:N:283:VAL:HG22	1.86	0.95
1:E:148:GLU:CG	1:E:161:VAL:HG11	1.96	0.95
2:J:401:THR:OG1	2:J:402:PRO:CD	2.13	0.95
1:M:112:LEU:CB	1:M:144:ASP:OD2	2.14	0.95
1:M:148:GLU:CD	1:M:161:VAL:HG11	1.91	0.94
1:A:217:ILE:HD12	1:M:217:ILE:CD1	1.97	0.94
2:J:190:ARG:HH12	2:J:191:GLN:HG3	1.33	0.94
2:N:261:ASP:OD2	2:N:463:VAL:CA	2.14	0.94
2:N:280:MET:HE2	2:N:315:GLU:HG2	1.46	0.94
1:E:210:LYS:HG3	1:I:244:ASN:ND2	1.82	0.94
2:J:223:ALA:HB3	2:J:303:ILE:HD11	0.94	0.93
1:A:217:ILE:HG13	1:M:217:ILE:CD1	1.98	0.93
1:M:112:LEU:HB3	1:M:144:ASP:OD1	1.68	0.93
2:J:302:LYS:NZ	2:J:330:GLU:HG3	1.70	0.93
1:E:169:ALA:CB	1:M:191:TYR:HE1	1.77	0.93
2:F:79:GLU:OE1	2:F:190:ARG:NH2	2.02	0.92
2:F:185:ASP:O	2:F:188:LEU:CD1	2.14	0.92
1:E:148:GLU:HB3	1:M:158:HIS:CG	2.05	0.91
1:E:169:ALA:HB2	1:M:191:TYR:CD1	2.04	0.91
1:M:27:GLY:O	1:M:30:ARG:HB3	1.70	0.91
2:J:341:TYR:CD2	2:J:403:LEU:HD23	2.05	0.91
1:M:139:PHE:HZ	1:M:211:CYS:SG	1.94	0.91
2:B:100:MET:HE3	2:B:101:PRO:HD2	1.51	0.90
2:N:190:ARG:NH2	2:N:195:ASN:CB	2.25	0.90
2:J:190:ARG:HA	2:J:190:ARG:NE	1.83	0.90
1:I:448:ILE:HD13	1:I:474:ILE:HD12	1.54	0.90
2:J:100:MET:HE3	2:J:101:PRO:HD2	1.51	0.90
2:N:263:ARG:NH1	2:N:463:VAL:HB	1.87	0.88
2:N:262:THR:CB	2:N:283:VAL:HG21	2.00	0.88
1:A:214:ALA:HB2	1:M:245:ASN:ND2	1.88	0.88
1:E:148:GLU:CB	1:M:158:HIS:CD2	2.56	0.88
1:E:30:ARG:HE	1:E:36:THR:HG21	1.37	0.88
1:M:119:LEU:HD21	1:M:149:THR:CG2	2.04	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:448:ILE:HD13	1:A:474:ILE:HD12	1.54	0.88
2:B:190:ARG:HB3	2:B:190:ARG:CZ	2.01	0.87
1:M:16:ASN:O	1:M:16:ASN:ND2	2.08	0.87
2:N:239:GLU:OE2	2:N:269:ARG:CG	2.20	0.87
1:A:217:ILE:CD1	1:M:217:ILE:CD1	2.52	0.87
1:A:175:ASN:OD1	1:M:248:PRO:HB3	1.74	0.87
1:A:217:ILE:CG2	1:M:217:ILE:HB	2.05	0.86
1:A:217:ILE:CD1	1:M:217:ILE:HD13	2.05	0.86
1:I:16:ASN:O	1:I:16:ASN:ND2	2.07	0.86
1:M:148:GLU:HG2	1:M:161:VAL:HG11	1.53	0.86
1:A:175:ASN:CG	1:M:248:PRO:CB	2.46	0.86
2:B:185:ASP:HA	2:B:188:LEU:HD12	1.54	0.86
2:N:277:TYR:CE1	2:N:318:GLY:CA	2.58	0.86
1:I:330:ALA:HB1	1:I:580:SER:O	1.74	0.86
1:M:119:LEU:HD21	1:M:149:THR:HG21	1.58	0.85
2:F:221:ASP:HB3	2:F:301:ARG:HG2	1.58	0.85
2:J:302:LYS:HZ3	2:J:330:GLU:CG	1.68	0.85
1:M:226:TYR:OH	1:M:230:ASP:HB2	1.76	0.85
1:E:210:LYS:HD3	1:I:244:ASN:HD22	1.41	0.85
1:M:148:GLU:CG	1:M:161:VAL:HG11	2.06	0.85
1:M:14:LEU:O	1:M:14:LEU:HD12	1.77	0.85
2:N:280:MET:HE3	2:N:315:GLU:HG2	1.53	0.84
2:N:188:LEU:O	2:N:193:ARG:NH2	2.10	0.84
1:A:217:ILE:HG23	1:M:217:ILE:HD13	1.59	0.84
2:N:263:ARG:HH11	2:N:463:VAL:HB	1.42	0.84
1:M:148:GLU:OE2	1:M:161:VAL:HG11	1.77	0.83
1:I:330:ALA:HB2	1:I:581:LEU:CA	2.07	0.83
2:J:41:SER:OG	2:J:211:ILE:N	2.10	0.83
1:E:192:GLN:CB	1:M:168:TYR:CZ	2.55	0.82
2:J:330:GLU:CD	2:J:414:GLY:CA	2.52	0.82
2:N:221:ASP:HB3	2:N:301:ARG:HG2	1.58	0.82
2:J:44:PHE:CZ	2:J:253:THR:OG1	2.31	0.82
1:M:27:GLY:C	6:M:601:AMP:C2	2.58	0.82
2:N:187:ALA:CB	3:O:2:U:C6	2.62	0.81
2:J:304:PHE:CE1	2:J:421:THR:HG22	2.14	0.81
2:N:277:TYR:HE1	2:N:318:GLY:CA	1.93	0.81
1:M:27:GLY:HA3	6:M:601:AMP:N3	1.95	0.81
2:J:250:PRO:HD2	2:J:255:PHE:HA	1.62	0.81
1:M:148:GLU:HG2	1:M:161:VAL:CG1	2.11	0.81
1:E:217:ILE:CD1	1:I:217:ILE:HG21	2.11	0.80
1:M:24:LEU:HD11	1:M:126:LEU:HD22	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:250:PRO:HD2	2:B:255:PHE:HA	1.62	0.79
1:E:439:VAL:HG23	1:E:443:THR:O	1.82	0.79
1:E:210:LYS:CG	1:I:244:ASN:ND2	2.45	0.79
1:E:440:ARG:HB3	1:E:445:TYR:HE2	1.44	0.79
4:H:8:DC:H2'	4:H:9:DA:H8	1.48	0.79
2:J:301:ARG:NH1	1:M:59:LYS:O	2.16	0.79
1:E:148:GLU:HG2	1:E:161:VAL:CG1	2.13	0.79
1:M:212:PHE:CD2	1:M:236:MET:SD	2.77	0.78
4:P:8:DC:H2'	4:P:9:DA:H8	1.48	0.78
1:A:237:LEU:HD22	1:A:268:LEU:HD11	1.63	0.78
1:E:217:ILE:HD11	1:I:217:ILE:HD13	1.65	0.78
1:I:326:LYS:HA	1:I:581:LEU:CB	2.13	0.78
2:N:239:GLU:OE1	2:N:269:ARG:HG2	1.83	0.78
1:I:266:GLN:HA	1:I:266:GLN:NE2	1.97	0.78
1:E:217:ILE:HD13	1:I:217:ILE:CD1	2.12	0.78
2:J:40:TYR:CE2	2:J:214:LYS:HD3	2.13	0.77
1:M:126:LEU:CD2	1:M:147:ILE:HD12	2.14	0.77
1:M:145:ASP:HB2	1:M:148:GLU:HB2	1.64	0.77
1:I:331:LEU:O	1:I:331:LEU:HD23	1.85	0.77
2:J:341:TYR:CE2	2:J:403:LEU:CD2	2.68	0.77
1:A:210:LYS:HE2	1:M:244:ASN:OD1	1.84	0.77
2:N:280:MET:CE	2:N:315:GLU:CD	2.57	0.77
1:E:106:LYS:HE3	1:M:176:THR:CG2	2.15	0.76
1:A:381:LEU:HD11	1:A:569:ALA:HB2	1.68	0.76
2:N:187:ALA:O	2:N:196:VAL:HG21	1.86	0.76
1:I:212:PHE:CD2	1:I:236:MET:HG2	2.21	0.76
2:J:330:GLU:CD	2:J:414:GLY:HA2	2.10	0.76
2:J:51:ARG:NH2	2:J:141:HIS:O	2.19	0.76
2:N:93:VAL:HG13	2:N:94:PHE:HD1	1.50	0.76
2:N:261:ASP:OD1	2:N:463:VAL:HA	1.84	0.76
1:A:214:ALA:HB2	1:M:245:ASN:CG	2.10	0.76
2:J:40:TYR:HE2	2:J:214:LYS:CD	1.99	0.75
2:B:51:ARG:NH2	2:B:141:HIS:O	2.19	0.75
2:F:93:VAL:HG13	2:F:94:PHE:HD1	1.51	0.75
1:M:213:LEU:N	1:M:213:LEU:HD23	2.01	0.75
1:A:214:ALA:CB	1:M:245:ASN:HD21	2.00	0.75
2:N:187:ALA:HB2	3:O:2:U:C5	2.01	0.75
2:N:396:LYS:HD3	2:N:397:GLU:HG3	1.69	0.75
1:E:192:GLN:HB3	1:M:168:TYR:OH	1.83	0.74
1:I:212:PHE:HD2	1:I:236:MET:CG	2.00	0.74
1:I:381:LEU:HD11	1:I:569:ALA:HB2	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:190:ARG:NH1	2:J:191:GLN:HG3	2.02	0.74
1:A:297:GLN:NE2	1:E:50:CYS:O	2.19	0.74
1:M:112:LEU:CB	1:M:144:ASP:OD1	2.34	0.74
1:E:210:LYS:CD	1:I:244:ASN:HD22	2.00	0.74
1:A:410:SER:HB2	1:A:417:LEU:HD23	1.70	0.74
2:B:164:ASP:OD1	3:C:1:A:N6	2.21	0.74
2:J:164:ASP:OD1	3:K:1:A:N6	2.21	0.74
1:I:212:PHE:CE2	1:I:236:MET:HG2	2.23	0.73
2:J:40:TYR:CD2	2:J:214:LYS:HB2	2.23	0.73
2:F:396:LYS:HD3	2:F:397:GLU:HG3	1.69	0.73
1:I:410:SER:HB2	1:I:417:LEU:HD23	1.70	0.73
1:M:126:LEU:HD23	1:M:147:ILE:HD12	1.68	0.73
1:E:165:GLU:OE2	1:E:193:LYS:HG2	1.88	0.73
1:E:443:THR:OG1	1:E:493:ARG:NH1	2.22	0.73
1:I:344:ARG:HH21	1:I:567:PHE:HA	1.53	0.73
1:A:344:ARG:HH21	1:A:567:PHE:HA	1.53	0.73
2:N:188:LEU:C	2:N:188:LEU:HD12	2.13	0.73
1:I:330:ALA:HB2	1:I:581:LEU:HG	1.71	0.73
2:J:304:PHE:CE1	2:J:330:GLU:HB2	2.23	0.73
1:E:192:GLN:CA	1:M:168:TYR:OH	2.37	0.73
1:E:210:LYS:HG3	1:I:244:ASN:HD21	1.53	0.72
1:M:56:ASP:HB3	1:M:59:LYS:HB2	1.72	0.72
1:M:123:HIS:CE1	1:M:146:VAL:HG11	2.23	0.72
4:P:8:DC:H2'	4:P:9:DA:C8	2.25	0.72
1:E:509:ILE:HD11	1:E:531:ARG:HH22	1.55	0.72
2:J:341:TYR:HE2	2:J:403:LEU:HD21	1.55	0.72
2:N:41:SER:HB3	2:N:211:ILE:HB	1.71	0.72
2:F:41:SER:HB3	2:F:211:ILE:HB	1.71	0.72
2:N:261:ASP:OD2	2:N:463:VAL:CB	2.37	0.72
2:B:363:ARG:NH2	2:B:429:THR:OG1	2.23	0.72
2:N:190:ARG:NH2	2:N:195:ASN:CG	2.45	0.72
1:E:30:ARG:NE	1:E:36:THR:HG21	2.04	0.72
2:J:363:ARG:NH2	2:J:429:THR:OG1	2.23	0.71
2:J:104:HIS:NE2	2:J:139:GLN:OE1	2.23	0.71
4:L:8:DC:H2'	4:L:9:DA:H8	1.55	0.71
1:M:21:MET:HG3	1:M:219:PHE:HB2	1.71	0.71
1:A:214:ALA:CB	1:M:245:ASN:ND2	2.53	0.71
1:A:430:LEU:HD23	1:A:435:ILE:HG13	1.72	0.71
4:H:8:DC:H2'	4:H:9:DA:C8	2.25	0.71
1:M:164:LEU:CD1	1:M:208:ILE:HD12	2.20	0.71
1:I:330:ALA:CB	1:I:581:LEU:HG	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:297:GLN:NE2	1:M:50:CYS:O	2.19	0.71
1:E:56:ASP:HB3	1:E:59:LYS:HB2	1.72	0.71
1:I:326:LYS:C	1:I:581:LEU:HB3	2.14	0.71
4:L:8:DC:H2'	4:L:9:DA:C8	2.25	0.71
1:I:269:ILE:HD13	1:I:279:ALA:HB1	1.72	0.71
2:B:104:HIS:NE2	2:B:139:GLN:OE1	2.24	0.71
2:B:242:THR:OG1	2:B:270:LYS:NZ	2.23	0.70
4:D:8:DC:H2'	4:D:9:DA:C8	2.25	0.70
1:I:430:LEU:HD23	1:I:435:ILE:HG13	1.71	0.70
2:J:242:THR:OG1	2:J:270:LYS:NZ	2.23	0.70
4:D:8:DC:H2'	4:D:9:DA:H8	1.55	0.70
1:E:21:MET:HG3	1:E:219:PHE:HB2	1.71	0.70
1:I:212:PHE:CD2	1:I:236:MET:CG	2.74	0.70
1:A:511:ILE:HG22	1:A:513:PRO:HD2	1.74	0.70
2:J:341:TYR:CE2	2:J:403:LEU:HD21	2.26	0.70
1:M:509:ILE:HD11	1:M:531:ARG:HH22	1.55	0.70
2:N:190:ARG:HH21	2:N:195:ASN:HB3	1.53	0.70
1:E:148:GLU:CG	1:E:161:VAL:CG1	2.68	0.70
2:J:189:THR:O	2:J:191:GLN:N	2.25	0.70
1:A:217:ILE:CD1	1:M:217:ILE:HD11	2.22	0.70
2:N:280:MET:HE1	2:N:315:GLU:CD	2.17	0.70
1:M:139:PHE:HZ	1:M:211:CYS:HG	1.37	0.70
2:F:149:TYR:HE2	2:F:188:LEU:HD21	1.57	0.69
2:F:82:ASN:OD1	2:F:386:ASN:ND2	2.24	0.69
2:J:223:ALA:O	2:J:303:ILE:HD13	1.89	0.69
3:K:11:G:H2'	3:K:12:A:C8	2.28	0.69
2:N:262:THR:HB	2:N:283:VAL:HG21	1.63	0.69
2:F:261:ASP:OD2	2:F:463:VAL:CB	2.39	0.69
2:F:192:CYS:SG	2:F:193:ARG:N	2.65	0.69
2:F:425:ILE:HG23	2:F:443:PRO:HG3	1.74	0.69
2:N:239:GLU:OE2	2:N:269:ARG:HA	1.93	0.69
1:E:148:GLU:OE2	1:E:161:VAL:CB	2.40	0.68
2:N:82:ASN:OD1	2:N:386:ASN:ND2	2.24	0.68
2:N:425:ILE:HG23	2:N:443:PRO:HG3	1.74	0.68
1:E:148:GLU:HG2	1:E:161:VAL:HG11	1.71	0.68
1:E:165:GLU:HG3	1:E:191:TYR:CG	2.27	0.68
2:J:44:PHE:HZ	2:J:253:THR:CB	2.06	0.68
1:I:511:ILE:HG22	1:I:513:PRO:HD2	1.74	0.68
3:C:11:G:H2'	3:C:12:A:C8	2.28	0.68
1:E:23:PHE:HB2	1:E:221:LEU:HD11	1.76	0.68
1:E:319:ILE:HD12	1:E:320:PRO:HD2	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:106:LYS:HE3	1:M:176:THR:HG22	1.74	0.68
1:E:210:LYS:CD	1:I:244:ASN:ND2	2.56	0.68
1:M:126:LEU:CD2	1:M:147:ILE:HD11	2.21	0.68
2:N:91:GLU:HG3	2:N:97:PRO:HA	1.76	0.68
1:A:124:ARG:HG2	1:A:309:VAL:HG12	1.76	0.68
2:N:434:ASN:HB2	2:N:473:MET:HB2	1.76	0.68
1:I:124:ARG:HG2	1:I:309:VAL:HG12	1.76	0.67
1:E:497:ARG:NH1	2:F:373:GLU:OE2	2.27	0.67
2:F:434:ASN:HB2	2:F:473:MET:HB2	1.76	0.67
1:M:139:PHE:CZ	1:M:211:CYS:SG	2.81	0.67
2:B:190:ARG:HB3	2:B:190:ARG:NH1	2.10	0.67
2:F:91:GLU:HG3	2:F:97:PRO:HA	1.76	0.67
1:M:497:ARG:NH1	2:N:373:GLU:OE2	2.27	0.67
2:N:262:THR:CB	2:N:283:VAL:HG22	2.20	0.67
1:I:326:LYS:HA	1:I:581:LEU:HB2	1.77	0.67
1:M:319:ILE:HD12	1:M:320:PRO:HD2	1.75	0.67
1:A:330:ALA:HB2	1:A:581:LEU:HG	1.77	0.66
2:B:196:VAL:O	2:B:200:VAL:HG23	1.95	0.66
2:F:301:ARG:HH12	2:F:302:LYS:HD2	1.60	0.66
1:M:126:LEU:HD22	1:M:147:ILE:CD1	2.24	0.66
1:E:348:VAL:HG12	1:E:399:ILE:HG12	1.77	0.66
1:E:440:ARG:HB3	1:E:445:TYR:CE2	2.29	0.66
1:I:241:ILE:HG12	1:I:247:PHE:HE2	1.58	0.66
1:E:504:MET:HE3	1:E:504:MET:HA	1.77	0.66
1:I:268:LEU:HD23	1:I:268:LEU:O	1.95	0.66
1:I:326:LYS:HA	1:I:581:LEU:HB3	1.77	0.66
2:J:196:VAL:O	2:J:200:VAL:HG23	1.95	0.66
1:E:192:GLN:HB2	1:M:168:TYR:CE1	2.29	0.66
2:N:301:ARG:HH12	2:N:302:LYS:HD2	1.60	0.66
1:M:119:LEU:HD21	1:M:149:THR:HG22	1.78	0.66
2:N:16:GLU:OE2	2:N:363:ARG:NH1	2.29	0.65
1:M:14:LEU:HD22	1:M:297:GLN:HB3	1.78	0.65
1:A:243:GLN:HG2	1:A:246:ALA:HB2	1.79	0.65
1:I:296:ARG:NH2	2:J:328:GLU:OE2	2.27	0.65
2:J:190:ARG:HH22	2:J:191:GLN:HG3	1.62	0.65
1:M:348:VAL:HG12	1:M:399:ILE:HG12	1.77	0.65
1:M:511:ILE:HG22	1:M:513:PRO:HD2	1.79	0.65
2:J:432:ASP:OD1	2:J:469:TYR:OH	2.12	0.65
2:N:261:ASP:H	2:N:452:PHE:HE2	1.42	0.65
1:E:225:GLY:HA2	6:E:601:AMP:N3	2.11	0.65
1:E:348:VAL:HG11	1:E:387:ILE:HG21	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:528:ARG:HA	1:I:531:ARG:HG3	1.78	0.65
2:J:326:SER:O	1:M:59:LYS:NZ	2.24	0.65
1:E:165:GLU:HG3	1:E:191:TYR:CD2	2.31	0.65
1:M:504:MET:HE3	1:M:504:MET:HA	1.77	0.65
2:B:326:SER:O	1:E:59:LYS:NZ	2.24	0.65
1:E:148:GLU:HB3	1:M:158:HIS:HD2	1.56	0.64
1:M:34:LEU:HD13	1:M:144:ASP:OD2	1.97	0.64
2:F:16:GLU:OE2	2:F:363:ARG:NH1	2.29	0.64
1:I:326:LYS:CA	1:I:581:LEU:HB3	2.27	0.64
2:J:190:ARG:HH12	2:J:191:GLN:CG	2.05	0.64
1:A:296:ARG:NH1	1:E:54:ASN:OD1	2.31	0.64
2:J:223:ALA:C	2:J:303:ILE:CD1	2.71	0.64
2:J:304:PHE:HE1	2:J:421:THR:HG22	1.59	0.64
1:A:528:ARG:HA	1:A:531:ARG:HG3	1.78	0.64
2:B:304:PHE:HE1	2:B:421:THR:HG22	1.63	0.64
1:M:348:VAL:HG11	1:M:387:ILE:HG21	1.79	0.64
1:E:171:LEU:O	1:E:171:LEU:HD12	1.98	0.64
1:A:296:ARG:NH2	2:B:328:GLU:OE2	2.27	0.64
4:P:9:DA:H2'	4:P:10:DG:C8	2.33	0.64
2:F:145:VAL:HG11	2:F:204:LEU:HD22	1.80	0.63
2:N:443:PRO:HD2	2:N:446:LEU:HD12	1.79	0.63
4:H:9:DA:H2'	4:H:10:DG:C8	2.33	0.63
1:M:31:SER:O	1:M:33:GLY:N	2.30	0.63
1:E:210:LYS:HD3	1:I:244:ASN:ND2	2.12	0.63
1:E:366:LYS:NZ	1:E:389:LYS:O	2.32	0.63
2:F:443:PRO:HD2	2:F:446:LEU:HD12	1.80	0.63
1:M:132:MET:O	1:M:134:GLN:NE2	2.29	0.63
2:B:425:ILE:O	2:B:429:THR:HG23	1.99	0.63
1:E:153:ASP:HA	1:M:156:GLY:CA	2.29	0.63
2:F:20:LEU:N	2:F:214:LYS:O	2.30	0.63
2:J:341:TYR:CE2	2:J:403:LEU:HD23	2.33	0.63
2:J:396:LYS:HD2	2:J:437:THR:HB	1.80	0.63
1:M:387:ILE:HA	1:M:390:ILE:HD12	1.80	0.63
1:A:533:ASN:ND2	2:B:357:ALA:O	2.32	0.63
2:J:425:ILE:O	2:J:429:THR:HG23	1.99	0.63
2:N:280:MET:HE3	2:N:315:GLU:CB	2.28	0.63
1:E:511:ILE:HG22	1:E:513:PRO:HD2	1.79	0.63
2:J:341:TYR:CD2	2:J:403:LEU:CD2	2.82	0.63
1:E:210:LYS:HA	1:I:244:ASN:ND2	2.14	0.62
1:E:132:MET:O	1:E:134:GLN:NE2	2.29	0.62
1:M:428:ALA:HB2	1:M:561:CYS:HB3	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:166:GLY:HA2	1:M:165:GLU:HG3	1.80	0.62
2:B:396:LYS:HD2	2:B:437:THR:HB	1.80	0.62
1:M:11:GLN:O	1:M:15:GLN:HB2	1.99	0.62
2:N:145:VAL:HG11	2:N:204:LEU:HD22	1.80	0.62
1:A:214:ALA:HB1	1:M:245:ASN:HD21	1.65	0.62
1:A:513:PRO:HB2	1:A:516:ARG:HB2	1.81	0.62
2:F:185:ASP:CB	2:F:188:LEU:CD1	2.76	0.62
3:C:12:A:H2'	3:C:13:G:C8	2.34	0.62
2:F:224:TYR:HB2	2:F:247:VAL:HG22	1.81	0.62
2:J:304:PHE:CE1	2:J:330:GLU:CB	2.82	0.62
1:M:16:ASN:ND2	1:M:20:MET:HE2	2.15	0.62
1:E:428:ALA:HB2	1:E:561:CYS:HB3	1.80	0.62
2:F:277:TYR:OH	2:F:321:ASP:OD2	2.18	0.62
1:I:296:ARG:NH1	1:M:54:ASN:OD1	2.31	0.62
2:J:79:GLU:HB2	2:J:192:CYS:HB2	1.82	0.62
2:N:20:LEU:N	2:N:214:LYS:O	2.30	0.62
1:I:513:PRO:HB2	1:I:516:ARG:HB2	1.81	0.62
3:K:12:A:H2'	3:K:13:G:C8	2.34	0.62
1:I:326:LYS:C	1:I:582:GLY:O	2.43	0.62
2:J:64:LEU:HD11	2:J:149:TYR:HB2	1.81	0.62
2:J:302:LYS:HB2	2:J:328:GLU:HB2	1.80	0.62
1:A:217:ILE:HD12	1:M:217:ILE:HD13	1.67	0.61
1:E:169:ALA:HB2	1:M:191:TYR:HE1	1.36	0.61
1:M:30:ARG:HE	1:M:36:THR:HG21	1.65	0.61
2:N:224:TYR:HB2	2:N:247:VAL:HG22	1.81	0.61
2:F:82:ASN:ND2	4:H:23:DT:OP2	2.33	0.61
2:F:107:CYS:SG	2:F:108:LEU:N	2.74	0.61
2:B:250:PRO:HA	2:B:295:HIS:CE1	2.35	0.61
1:E:217:ILE:CD1	1:I:217:ILE:CD1	2.68	0.61
1:I:533:ASN:ND2	2:J:357:ALA:O	2.32	0.61
1:I:268:LEU:HD23	1:I:268:LEU:C	2.26	0.61
1:M:366:LYS:NZ	1:M:389:LYS:O	2.32	0.61
2:N:242:THR:HG22	2:N:270:LYS:HZ2	1.64	0.61
2:J:304:PHE:CD1	2:J:330:GLU:HB2	2.35	0.61
1:M:126:LEU:HD22	1:M:147:ILE:HD11	1.81	0.61
2:B:79:GLU:HB2	2:B:192:CYS:HB2	1.82	0.61
2:J:184:ASN:ND2	3:K:1:A:N3	2.42	0.61
1:M:28:THR:N	6:M:601:AMP:H2	1.98	0.61
1:M:28:THR:N	6:M:601:AMP:C2	2.68	0.61
2:N:82:ASN:ND2	4:P:23:DT:OP2	2.33	0.61
2:B:432:ASP:OD1	2:B:469:TYR:OH	2.13	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:148:GLU:OE2	1:E:161:VAL:HG21	2.00	0.61
1:E:192:GLN:OE1	1:E:192:GLN:HA	2.00	0.61
1:E:387:ILE:HA	1:E:390:ILE:HD12	1.80	0.61
2:F:71:LEU:HD21	2:F:200:VAL:HG12	1.82	0.61
1:E:161:VAL:HG12	1:E:182:TYR:HD2	1.66	0.61
1:M:212:PHE:HD2	1:M:236:MET:SD	2.23	0.61
2:B:64:LEU:HD11	2:B:149:TYR:HB2	1.82	0.61
1:E:157:LYS:C	1:M:152:SER:OG	2.43	0.61
1:A:454:LYS:HZ2	1:A:462:ARG:HH12	1.49	0.60
1:I:213:LEU:HD23	1:I:213:LEU:N	2.15	0.60
4:L:9:DA:H2'	4:L:10:DG:C8	2.36	0.60
1:M:188:ASP:HB3	1:M:190:ARG:HD3	1.81	0.60
2:N:263:ARG:C	2:N:463:VAL:HG21	2.26	0.60
2:N:269:ARG:CZ	2:N:269:ARG:HB3	2.31	0.60
2:J:250:PRO:HA	2:J:295:HIS:CE1	2.35	0.60
1:M:228:GLY:O	1:M:229:ARG:CB	2.32	0.60
2:N:71:LEU:HD21	2:N:200:VAL:HG12	1.82	0.60
2:F:190:ARG:NH1	2:F:191:GLN:HB2	2.16	0.60
1:I:171:LEU:CD1	1:I:211:CYS:HA	2.30	0.60
1:I:454:LYS:HZ2	1:I:462:ARG:HH12	1.48	0.60
2:B:149:TYR:HE2	2:B:188:LEU:HD11	1.65	0.60
1:E:41:ILE:HD11	1:E:89:TYR:HB2	1.83	0.60
2:J:281:GLN:OE1	2:J:321:ASP:CB	2.50	0.60
1:M:362:ARG:NH2	1:M:390:ILE:O	2.33	0.60
1:A:405:ASP:OD1	1:A:405:ASP:N	2.35	0.60
2:B:190:ARG:NE	3:C:2:U:O4	2.30	0.60
2:F:250:PRO:HA	2:F:295:HIS:CE1	2.37	0.60
2:N:107:CYS:SG	2:N:108:LEU:N	2.73	0.60
2:J:44:PHE:HZ	2:J:253:THR:HB	1.65	0.60
2:J:281:GLN:OE1	2:J:321:ASP:HB3	2.01	0.60
2:N:335:ILE:HB	2:N:408:MET:HB3	1.84	0.60
1:E:169:ALA:HB3	1:M:191:TYR:HE1	1.63	0.59
2:J:261:ASP:OD1	2:J:262:THR:N	2.35	0.59
1:M:23:PHE:HB2	1:M:221:LEU:HD11	1.84	0.59
1:M:161:VAL:HG12	1:M:182:TYR:HD2	1.66	0.59
1:M:204:ASN:OD1	1:M:232:ASN:ND2	2.35	0.59
1:E:30:ARG:O	1:E:30:ARG:HD3	2.02	0.59
1:E:106:LYS:HE3	1:M:176:THR:HG21	1.84	0.59
2:J:400:LEU:HD23	2:J:400:LEU:N	2.16	0.59
1:M:41:ILE:HD11	1:M:89:TYR:HB2	1.83	0.59
1:E:144:ASP:OD1	1:E:144:ASP:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:10:A:H2'	3:K:11:G:C8	2.38	0.59
4:D:9:DA:H2'	4:D:10:DG:C8	2.36	0.59
1:E:217:ILE:HD13	1:I:217:ILE:CG2	2.21	0.59
1:M:148:GLU:OE2	1:M:161:VAL:CG1	2.49	0.59
2:B:261:ASP:OD1	2:B:262:THR:N	2.35	0.59
1:E:204:ASN:OD1	1:E:232:ASN:ND2	2.35	0.59
2:F:262:THR:HG22	2:F:262:THR:O	2.02	0.59
2:F:335:ILE:HB	2:F:408:MET:HB3	1.84	0.59
4:L:9:DA:H2'	4:L:10:DG:H8	1.67	0.59
1:E:362:ARG:NH2	1:E:390:ILE:O	2.33	0.59
2:N:250:PRO:HA	2:N:295:HIS:CE1	2.37	0.59
1:M:552:GLY:HA2	1:M:575:THR:HG23	1.84	0.59
1:E:152:SER:OG	1:M:157:LYS:C	2.46	0.59
1:A:151:PHE:HD2	1:A:159:LEU:HB2	1.67	0.59
1:A:338:VAL:HG22	1:A:573:ILE:HG13	1.85	0.59
3:C:10:A:H2'	3:C:11:G:C8	2.38	0.59
1:I:330:ALA:HB1	1:I:580:SER:C	2.27	0.59
2:B:184:ASN:ND2	3:C:1:A:N3	2.42	0.59
1:E:157:LYS:C	1:M:152:SER:HG	2.10	0.59
1:I:319:ILE:HD11	2:J:418:TRP:CE2	2.38	0.59
2:B:231:ILE:HB	4:D:15:DA:H5''	1.85	0.58
2:N:51:ARG:NH1	2:N:142:ALA:O	2.35	0.58
1:A:245:ASN:HB3	1:M:214:ALA:HB2	1.85	0.58
1:A:300:ASP:OD1	1:E:58:GLN:NE2	2.37	0.58
1:E:152:SER:HG	1:M:157:LYS:C	2.10	0.58
2:F:51:ARG:NH1	2:F:142:ALA:O	2.35	0.58
2:N:75:ALA:H	2:N:87:TYR:HB3	1.68	0.58
1:E:552:GLY:HA2	1:E:575:THR:HG23	1.83	0.58
3:O:11:G:H2'	3:O:12:A:C8	2.39	0.58
1:E:210:LYS:HA	1:I:244:ASN:HD21	1.68	0.58
1:E:167:SER:OG	1:E:207:GLU:OE1	2.22	0.58
1:I:257:SER:HB3	1:I:260:LYS:HG2	1.86	0.58
1:M:222:VAL:HG22	1:M:252:TYR:HB2	1.85	0.58
4:D:9:DA:H2'	4:D:10:DG:H8	1.66	0.58
2:F:75:ALA:H	2:F:87:TYR:HB3	1.68	0.58
1:M:566:GLU:H	1:M:566:GLU:CD	2.12	0.58
1:A:244:ASN:HD22	1:M:210:LYS:HA	1.68	0.58
1:I:171:LEU:HD21	1:I:210:LYS:NZ	2.19	0.58
1:I:338:VAL:HG22	1:I:573:ILE:HG13	1.85	0.58
1:M:247:PHE:O	1:M:278:ARG:NH1	2.37	0.58
1:E:407:ILE:O	1:E:411:VAL:HG22	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:330:ALA:O	2:J:345:VAL:HG22	2.03	0.58
1:A:333:THR:HG21	2:B:340:TRP:HE3	1.69	0.58
1:I:151:PHE:HD2	1:I:159:LEU:HB2	1.67	0.58
1:M:273:GLN:NE2	1:M:279:ALA:O	2.37	0.58
1:M:430:LEU:HD22	1:M:437:HIS:HB2	1.85	0.58
1:E:566:GLU:CD	1:E:566:GLU:H	2.12	0.58
1:I:333:THR:HG21	2:J:340:TRP:HE3	1.69	0.58
2:J:386:ASN:ND2	2:J:389:ASN:O	2.32	0.58
1:E:22:TRP:HE3	1:E:24:LEU:HD21	1.67	0.57
3:G:11:G:H2'	3:G:12:A:C8	2.39	0.57
1:M:14:LEU:HD12	1:M:14:LEU:C	2.25	0.57
2:B:262:THR:HG22	2:B:283:VAL:HG21	1.86	0.57
1:E:273:GLN:NE2	1:E:279:ALA:O	2.37	0.57
1:M:162:TYR:CD2	1:M:169:ALA:HB3	2.39	0.57
1:A:214:ALA:HA	1:M:217:ILE:HG21	1.87	0.57
2:J:301:ARG:O	2:J:327:THR:HA	2.03	0.57
1:A:355:THR:HG23	1:A:358:GLU:H	1.70	0.57
1:A:217:ILE:HD12	1:M:217:ILE:HD11	1.78	0.57
4:H:9:DA:H2'	4:H:10:DG:H8	1.69	0.57
2:J:40:TYR:OH	2:J:214:LYS:HE2	2.05	0.57
1:M:407:ILE:O	1:M:411:VAL:HG22	2.04	0.57
1:M:533:ASN:ND2	2:N:357:ALA:O	2.36	0.57
1:A:257:SER:HB3	1:A:260:LYS:HG2	1.86	0.57
1:A:319:ILE:HD11	2:B:418:TRP:CE2	2.38	0.57
2:B:55:LEU:HD23	2:B:148:VAL:HG22	1.87	0.57
1:E:430:LEU:HD22	1:E:437:HIS:HB2	1.85	0.57
1:I:360:LYS:HA	1:I:363:ILE:HD12	1.87	0.57
1:E:222:VAL:HG22	1:E:252:TYR:HB2	1.85	0.57
2:J:40:TYR:CE2	2:J:214:LYS:CD	2.82	0.57
2:B:386:ASN:ND2	2:B:389:ASN:O	2.32	0.57
2:J:231:ILE:HB	4:L:15:DA:H5''	1.85	0.57
2:N:261:ASP:OD2	2:N:463:VAL:HB	2.04	0.57
2:N:261:ASP:HB3	2:N:456:VAL:HG21	1.85	0.57
1:M:188:ASP:HB3	1:M:190:ARG:CD	2.34	0.57
1:A:248:PRO:HB2	1:M:175:ASN:ND2	2.20	0.56
1:M:209:HIS:C	1:M:209:HIS:HD1	2.12	0.56
1:A:175:ASN:ND2	1:M:248:PRO:HB3	2.20	0.56
1:I:405:ASP:N	1:I:405:ASP:OD1	2.35	0.56
2:J:40:TYR:HB3	2:J:211:ILE:O	2.04	0.56
2:N:239:GLU:OE1	2:N:269:ARG:CG	2.53	0.56
2:N:262:THR:HB	2:N:283:VAL:HG23	1.80	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:300:ASP:OD1	1:M:58:GLN:NE2	2.37	0.56
1:A:429:LEU:HG	1:A:547:LEU:HD12	1.87	0.56
1:E:513:PRO:HB2	1:E:516:ARG:HB2	1.88	0.56
1:E:533:ASN:ND2	2:F:357:ALA:O	2.36	0.56
2:F:334:ILE:HG13	2:F:446:LEU:HD11	1.87	0.56
1:I:330:ALA:CB	1:I:580:SER:O	2.50	0.56
1:A:15:GLN:HE22	1:E:103:ALA:HB1	1.69	0.56
1:E:30:ARG:NE	1:E:36:THR:CG2	2.68	0.56
1:E:156:GLY:CA	1:M:153:ASP:HA	2.35	0.56
1:E:439:VAL:CG2	1:E:443:THR:O	2.52	0.56
1:A:175:ASN:CG	1:M:248:PRO:HB2	2.30	0.56
1:I:171:LEU:CD2	1:I:210:LYS:NZ	2.69	0.56
2:B:435:ASN:OD1	2:B:437:THR:OG1	2.18	0.56
2:J:262:THR:HG22	2:J:283:VAL:HG21	1.86	0.56
2:N:334:ILE:HG13	2:N:446:LEU:HD11	1.87	0.56
1:A:360:LYS:HA	1:A:363:ILE:HD12	1.87	0.56
2:F:440:LYS:HD2	2:F:447:VAL:HG11	1.88	0.56
1:I:367:SER:O	1:I:367:SER:OG	2.21	0.56
2:B:468:ASP:OD1	2:B:469:TYR:N	2.39	0.56
2:F:19:LEU:HB3	2:F:21:PHE:HE1	1.71	0.56
2:J:468:ASP:OD1	2:J:469:TYR:N	2.39	0.56
1:E:120:ASN:ND2	1:E:288:ASP:OD2	2.40	0.55
1:E:153:ASP:HA	1:M:156:GLY:HA2	1.88	0.55
1:I:429:LEU:HG	1:I:547:LEU:HD12	1.87	0.55
2:J:55:LEU:HD23	2:J:148:VAL:HG22	1.87	0.55
1:E:174:LEU:HD11	1:E:215:ALA:HB2	1.87	0.55
1:I:22:TRP:HB2	1:I:138:VAL:HG22	1.88	0.55
1:I:234:MET:SD	1:I:268:LEU:HD12	2.46	0.55
1:I:355:THR:HG23	1:I:358:GLU:H	1.70	0.55
1:M:18:GLN:O	1:M:134:GLN:O	2.25	0.55
1:M:27:GLY:CA	6:M:601:AMP:N3	2.68	0.55
2:N:440:LYS:HD2	2:N:447:VAL:HG11	1.88	0.55
2:J:244:CYS:SG	2:J:245:SER:N	2.80	0.55
1:E:247:PHE:O	1:E:278:ARG:NH1	2.37	0.55
1:M:174:LEU:HD11	1:M:215:ALA:HB2	1.87	0.55
1:A:302:PRO:HD2	1:A:305:ILE:HD12	1.88	0.55
1:E:153:ASP:HB2	1:M:156:GLY:O	2.07	0.55
2:N:188:LEU:O	2:N:193:ARG:CZ	2.55	0.55
1:A:22:TRP:HB2	1:A:138:VAL:HG22	1.88	0.55
2:B:244:CYS:SG	2:B:245:SER:N	2.80	0.55
1:I:253:TRP:CE2	1:I:265:VAL:HG22	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:328:GLU:HG3	1:M:59:LYS:HE3	1.89	0.55
1:M:475:THR:HG23	1:M:487:ALA:HB2	1.89	0.55
2:N:187:ALA:HB1	3:O:2:U:C6	2.29	0.55
1:E:133:ASN:OD1	1:E:136:LYS:NZ	2.27	0.55
2:J:170:LYS:HA	2:J:173:VAL:HG12	1.89	0.55
2:N:32:ARG:NH2	2:N:384:GLY:O	2.40	0.55
4:P:9:DA:H2'	4:P:10:DG:H8	1.69	0.55
2:J:190:ARG:NH2	2:J:191:GLN:HG3	2.22	0.55
4:L:15:DA:H8	4:L:15:DA:H5'	1.72	0.55
2:B:170:LYS:HA	2:B:173:VAL:HG12	1.89	0.55
1:E:105:ARG:HB2	1:E:194:ILE:HD11	1.88	0.55
1:E:483:GLU:OE2	1:E:516:ARG:NE	2.40	0.55
2:F:79:GLU:OE1	2:F:190:ARG:CZ	2.54	0.55
1:I:429:LEU:HD13	1:I:559:ILE:HD13	1.89	0.55
3:K:11:G:H2'	3:K:12:A:H8	1.72	0.55
1:M:317:VAL:HG21	2:N:411:ARG:HB3	1.89	0.55
1:E:580:SER:OG	2:F:367:GLN:NE2	2.40	0.54
2:F:32:ARG:NH2	2:F:384:GLY:O	2.40	0.54
1:I:302:PRO:HD2	1:I:305:ILE:HD12	1.89	0.54
2:B:149:TYR:OH	2:B:185:ASP:OD1	2.25	0.54
2:N:263:ARG:HH11	2:N:463:VAL:CB	2.18	0.54
2:N:263:ARG:C	2:N:463:VAL:CG2	2.80	0.54
1:E:475:THR:HG23	1:E:487:ALA:HB2	1.89	0.54
1:M:162:TYR:CE2	1:M:169:ALA:HB1	2.43	0.54
4:H:14:DT:H2''	4:H:15:DA:H8	1.73	0.54
1:I:16:ASN:HD22	1:I:16:ASN:C	2.06	0.54
1:M:23:PHE:HD1	1:M:23:PHE:O	1.91	0.54
1:M:105:ARG:HB2	1:M:194:ILE:HD11	1.88	0.54
1:M:120:ASN:ND2	1:M:288:ASP:OD2	2.40	0.54
1:A:552:GLY:HA2	1:A:575:THR:HG22	1.90	0.54
4:D:15:DA:H5'	4:D:15:DA:H8	1.72	0.54
1:E:168:TYR:C	1:E:168:TYR:CD2	2.85	0.54
2:J:401:THR:HG1	2:J:402:PRO:HD2	1.69	0.54
2:N:187:ALA:HB3	3:O:2:U:C6	2.39	0.54
1:A:175:ASN:HB3	1:M:248:PRO:HB2	1.89	0.54
2:B:377:TRP:CE2	2:B:406:PRO:HB3	2.43	0.54
1:E:106:LYS:CE	1:M:176:THR:HG22	2.37	0.54
1:E:165:GLU:CG	1:E:191:TYR:CD2	2.90	0.54
1:M:164:LEU:CD1	1:M:208:ILE:CD1	2.86	0.54
1:M:168:TYR:CD1	1:M:168:TYR:C	2.86	0.54
1:I:552:GLY:HA2	1:I:575:THR:HG22	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:93:VAL:HG13	2:N:94:PHE:CD1	2.38	0.54
2:N:275:LEU:HB2	2:N:280:MET:HE2	1.89	0.54
1:E:317:VAL:HG21	2:F:411:ARG:HB3	1.89	0.54
1:A:429:LEU:HD13	1:A:559:ILE:HD13	1.89	0.54
2:B:229:TYR:HA	2:B:241:THR:O	2.08	0.54
2:F:61:MET:HE1	2:F:106:ARG:HG3	1.90	0.54
2:F:203:ALA:O	2:F:207:LYS:HG3	2.08	0.54
1:M:513:PRO:HB2	1:M:516:ARG:HB2	1.88	0.54
1:M:580:SER:OG	2:N:367:GLN:NE2	2.40	0.54
2:N:19:LEU:HB3	2:N:21:PHE:HE1	1.71	0.54
1:E:158:HIS:CG	1:M:148:GLU:HB3	2.42	0.54
2:N:61:MET:HE1	2:N:106:ARG:HG3	1.90	0.53
1:I:171:LEU:CD2	1:I:210:LYS:HE3	2.39	0.53
1:I:213:LEU:HD13	1:I:240:ALA:HA	1.90	0.53
2:J:229:TYR:HA	2:J:241:THR:O	2.08	0.53
2:N:261:ASP:N	2:N:452:PHE:HE2	2.06	0.53
2:B:135:GLY:O	2:B:139:GLN:NE2	2.41	0.53
2:B:328:GLU:HG3	1:E:59:LYS:HE3	1.89	0.53
1:M:30:ARG:NE	1:M:36:THR:HG21	2.23	0.53
1:M:164:LEU:HA	1:M:167:SER:HB2	1.89	0.53
2:N:47:PRO:HG3	2:N:209:GLY:HA3	1.90	0.53
1:I:269:ILE:HD13	1:I:279:ALA:CB	2.38	0.53
1:I:324:PRO:HB3	2:J:7:GLN:HG2	1.90	0.53
2:N:308:THR:HG23	2:N:446:LEU:HD22	1.90	0.53
2:J:135:GLY:O	2:J:139:GLN:NE2	2.41	0.53
2:J:190:ARG:O	2:J:191:GLN:C	2.50	0.53
1:A:572:GLU:N	1:A:572:GLU:OE1	2.42	0.53
1:E:335:ALA:HB2	1:E:504:MET:HE1	1.90	0.53
1:I:462:ARG:HD3	1:I:474:ILE:HG23	1.91	0.53
4:P:14:DT:H2''	4:P:15:DA:H8	1.73	0.53
1:A:349:THR:HB	1:A:397:ASN:HB2	1.91	0.53
1:I:572:GLU:OE1	1:I:572:GLU:N	2.42	0.53
2:J:277:TYR:OH	2:J:321:ASP:OD2	2.27	0.53
2:J:377:TRP:CE2	2:J:406:PRO:HB3	2.43	0.53
2:B:136:LEU:HA	2:B:139:GLN:HE21	1.73	0.53
3:C:11:G:H2'	3:C:12:A:H8	1.72	0.53
1:I:349:THR:HB	1:I:397:ASN:HB2	1.91	0.53
2:B:284:LEU:HD11	2:B:305:ILE:HD11	1.91	0.53
3:C:13:G:H2'	3:C:14:C:C6	2.44	0.53
2:F:47:PRO:HG3	2:F:209:GLY:HA3	1.90	0.53
2:J:40:TYR:CE2	2:J:214:LYS:CE	2.92	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:213:LEU:HB3	1:I:243:GLN:OE1	2.09	0.53
2:J:136:LEU:HA	2:J:139:GLN:HE21	1.73	0.53
2:J:435:ASN:OD1	2:J:437:THR:OG1	2.18	0.53
1:M:162:TYR:HD2	1:M:169:ALA:HB3	1.74	0.53
1:M:483:GLU:OE2	1:M:516:ARG:NE	2.40	0.53
2:N:203:ALA:O	2:N:207:LYS:HG3	2.08	0.53
2:N:277:TYR:CD1	2:N:318:GLY:CA	2.92	0.53
1:E:210:LYS:CG	1:I:244:ASN:HD21	2.15	0.52
2:F:308:THR:HG23	2:F:446:LEU:HD22	1.90	0.52
1:E:227:SER:HB3	6:E:601:AMP:H4'	1.90	0.52
2:B:444:VAL:HA	2:B:447:VAL:HG12	1.91	0.52
3:G:12:A:H2'	3:G:13:G:C8	2.44	0.52
1:I:213:LEU:N	1:I:213:LEU:CD2	2.73	0.52
2:J:190:ARG:C	2:J:192:CYS:N	2.67	0.52
2:B:334:ILE:HD11	2:B:425:ILE:HD13	1.91	0.52
2:J:193:ARG:O	2:J:197:MET:HG2	2.09	0.52
2:B:277:TYR:OH	2:B:321:ASP:OD2	2.27	0.52
1:E:148:GLU:OE2	1:E:161:VAL:CG2	2.58	0.52
2:F:93:VAL:HG13	2:F:94:PHE:CD1	2.38	0.52
1:A:217:ILE:HG13	1:M:217:ILE:CG1	2.39	0.52
2:B:196:VAL:HG12	3:C:2:U:C4	2.44	0.52
1:E:156:GLY:HA2	1:M:153:ASP:HA	1.92	0.52
1:E:244:ASN:HD22	1:I:213:LEU:HD12	1.74	0.52
1:M:123:HIS:CE1	1:M:146:VAL:CG1	2.93	0.52
3:O:12:A:H2'	3:O:13:G:C8	2.44	0.52
3:K:13:G:H2'	3:K:14:C:C6	2.44	0.52
1:M:133:ASN:OD1	1:M:136:LYS:NZ	2.27	0.52
2:J:223:ALA:CB	2:J:303:ILE:CD1	2.67	0.52
2:J:374:CYS:SG	2:J:375:LEU:N	2.82	0.52
1:M:335:ALA:HB2	1:M:504:MET:HE1	1.90	0.52
2:N:188:LEU:O	2:N:188:LEU:HD12	2.09	0.52
2:F:284:LEU:HD13	2:F:323:PHE:HE1	1.75	0.52
1:I:299:LYS:NZ	1:M:47:ARG:HH22	2.08	0.52
2:B:374:CYS:SG	2:B:375:LEU:N	2.82	0.52
2:F:28:THR:O	2:F:430:LYS:NZ	2.42	0.52
2:F:262:THR:HG23	2:F:283:VAL:CG2	2.40	0.52
1:I:171:LEU:HD21	1:I:210:LYS:HZ2	1.75	0.52
1:I:459:LEU:O	1:I:462:ARG:HB2	2.10	0.52
2:J:196:VAL:HG12	3:K:2:U:C4	2.44	0.52
1:A:512:LYS:HB3	1:A:513:PRO:HD3	1.92	0.51
1:E:442:ARG:HG2	4:H:10:DG:OP2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:48:TYR:HE1	1:M:52:HIS:NE2	2.08	0.51
2:N:269:ARG:NH1	2:N:269:ARG:CB	2.73	0.51
1:A:299:LYS:NZ	1:E:47:ARG:HH22	2.08	0.51
2:J:149:TYR:OH	2:J:185:ASP:OD1	2.25	0.51
2:J:284:LEU:HD11	2:J:305:ILE:HD11	1.91	0.51
2:J:444:VAL:HA	2:J:447:VAL:HG12	1.91	0.51
2:B:190:ARG:NH1	2:B:190:ARG:CB	2.73	0.51
1:E:580:SER:HB3	2:F:8:LEU:HB2	1.92	0.51
1:M:440:ARG:HB3	1:M:445:TYR:HE2	1.76	0.51
2:N:28:THR:O	2:N:430:LYS:NZ	2.42	0.51
2:N:284:LEU:HD13	2:N:323:PHE:HE1	1.75	0.51
2:N:426:LEU:O	2:N:429:THR:OG1	2.29	0.51
2:N:89:GLY:O	2:N:93:VAL:HG12	2.11	0.51
1:A:462:ARG:HD3	1:A:474:ILE:HG23	1.91	0.51
1:I:237:LEU:HD22	1:I:268:LEU:HD11	1.93	0.51
2:N:46:LEU:HB2	2:N:47:PRO:HD3	1.91	0.51
2:N:261:ASP:OD1	2:N:261:ASP:O	2.28	0.51
2:N:277:TYR:CE1	2:N:318:GLY:N	2.77	0.51
1:E:191:TYR:CE1	1:M:169:ALA:HB2	2.46	0.51
2:F:46:LEU:HB2	2:F:47:PRO:HD3	1.91	0.51
1:I:237:LEU:HD22	1:I:268:LEU:HD21	1.92	0.51
1:A:459:LEU:O	1:A:462:ARG:HB2	2.10	0.51
2:B:185:ASP:O	2:B:189:THR:OG1	2.27	0.51
2:B:193:ARG:O	2:B:197:MET:HG2	2.09	0.51
1:E:244:ASN:O	1:E:244:ASN:OD1	2.28	0.51
1:E:560:SER:HB2	1:E:568:LYS:HD3	1.93	0.51
1:I:268:LEU:C	1:I:268:LEU:CD2	2.84	0.51
2:N:242:THR:HG22	2:N:270:LYS:NZ	2.26	0.51
2:B:243:CYS:SG	2:B:453:ALA:HA	2.51	0.51
1:E:244:ASN:ND2	1:I:213:LEU:HB3	2.25	0.51
2:B:105:LEU:HD21	2:B:142:ALA:HB3	1.93	0.51
1:I:481:ALA:HB1	1:I:484:LEU:HD13	1.92	0.51
2:J:44:PHE:HZ	2:J:253:THR:HG1	1.36	0.51
1:A:213:LEU:HD13	1:A:243:GLN:HE22	1.75	0.50
1:A:481:ALA:HB1	1:A:484:LEU:HD13	1.92	0.50
2:B:114:HIS:O	2:B:117:ALA:HB3	2.11	0.50
1:E:48:TYR:HE1	1:E:52:HIS:NE2	2.08	0.50
2:N:269:ARG:HB3	2:N:269:ARG:NH1	2.26	0.50
2:N:432:ASP:OD1	2:N:469:TYR:OH	2.23	0.50
2:B:55:LEU:HD11	2:B:132:SER:HB3	1.93	0.50
2:J:55:LEU:HD22	2:J:133:MET:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:105:LEU:HD21	2:J:142:ALA:HB3	1.92	0.50
2:J:334:ILE:HD11	2:J:425:ILE:HD13	1.91	0.50
2:J:379:GLN:NE2	2:J:405:ASN:O	2.44	0.50
2:F:292:GLN:NE2	2:F:299:MET:SD	2.85	0.50
2:N:261:ASP:CG	2:N:463:VAL:HG23	2.37	0.50
2:N:292:GLN:NE2	2:N:299:MET:SD	2.85	0.50
2:F:426:LEU:O	2:F:429:THR:OG1	2.29	0.50
2:J:196:VAL:HG12	3:K:2:U:C5	2.47	0.50
1:M:31:SER:C	1:M:33:GLY:N	2.69	0.50
1:M:580:SER:HB3	2:N:8:LEU:HB2	1.92	0.50
1:I:21:MET:SD	1:I:221:LEU:HD12	2.52	0.50
1:I:313:ARG:HB2	2:J:320:PHE:CE2	2.46	0.50
1:M:500:LYS:HE2	1:M:502:TRP:HZ2	1.77	0.50
1:E:156:GLY:O	1:M:153:ASP:HB2	2.11	0.50
1:I:232:ASN:ND2	1:I:233:VAL:HG13	2.27	0.50
1:A:176:THR:O	1:M:19:HIS:CE1	2.65	0.50
1:A:313:ARG:HB2	2:B:320:PHE:CE2	2.46	0.50
1:E:148:GLU:CG	1:M:158:HIS:CD2	2.95	0.50
1:E:500:LYS:HE2	1:E:502:TRP:HZ2	1.77	0.50
1:I:525:ARG:HH12	1:I:529:ARG:HH11	1.60	0.50
2:N:242:THR:CG2	2:N:270:LYS:HZ2	2.24	0.50
1:A:416:PHE:HE2	3:C:17:U:H1'	1.77	0.50
2:J:243:CYS:SG	2:J:453:ALA:HA	2.51	0.50
1:A:232:ASN:ND2	1:A:233:VAL:HG13	2.27	0.50
2:B:323:PHE:CD2	2:B:327:THR:HG21	2.47	0.50
1:I:324:PRO:HB3	2:J:7:GLN:CG	2.42	0.50
1:A:244:ASN:CG	1:M:213:LEU:HB2	2.36	0.49
2:B:222:GLU:HG2	2:B:302:LYS:HB3	1.94	0.49
1:E:46:HIS:HB2	1:E:62:ILE:HD13	1.93	0.49
1:E:478:VAL:HG13	1:E:523:PHE:CD2	2.47	0.49
2:F:89:GLY:O	2:F:93:VAL:HG12	2.11	0.49
1:I:416:PHE:HE2	3:K:17:U:H1'	1.77	0.49
2:N:56:ALA:HB2	2:N:149:TYR:HB3	1.94	0.49
3:G:11:G:H2'	3:G:12:A:H8	1.77	0.49
2:J:190:ARG:NH1	2:J:191:GLN:N	2.61	0.49
2:J:323:PHE:CD2	2:J:327:THR:HG21	2.47	0.49
1:M:423:GLU:OE1	1:M:444:HIS:NE2	2.33	0.49
2:N:415:ASN:OD1	2:N:416:GLY:N	2.45	0.49
3:O:11:G:H2'	3:O:12:A:H8	1.77	0.49
1:A:244:ASN:ND2	1:M:210:LYS:O	2.45	0.49
2:B:196:VAL:HG12	3:C:2:U:C5	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:423:GLU:OE1	1:E:444:HIS:NE2	2.33	0.49
1:I:253:TRP:CZ3	1:I:268:LEU:HD13	2.46	0.49
2:J:167:ASP:OD2	2:J:455:VAL:HA	2.13	0.49
2:N:181:GLN:NE2	2:N:182:ILE:O	2.45	0.49
2:N:335:ILE:HD12	4:P:12:DT:H5''	1.94	0.49
2:B:167:ASP:OD2	2:B:455:VAL:HA	2.13	0.49
1:E:210:LYS:CA	1:I:244:ASN:HD21	2.25	0.49
1:E:384:GLU:O	1:E:388:ARG:HG2	2.12	0.49
1:I:512:LYS:HB3	1:I:513:PRO:HD3	1.92	0.49
2:F:415:ASN:OD1	2:F:416:GLY:N	2.45	0.49
1:M:478:VAL:HG13	1:M:523:PHE:CD2	2.47	0.49
2:B:55:LEU:HD22	2:B:133:MET:HB3	1.94	0.49
1:I:536:SER:HB3	2:J:343:LEU:HD21	1.94	0.49
1:M:46:HIS:HB2	1:M:62:ILE:HD13	1.93	0.49
1:M:440:ARG:HB3	1:M:445:TYR:CE2	2.47	0.49
1:A:21:MET:SD	1:A:221:LEU:HD12	2.52	0.49
1:I:212:PHE:HD2	1:I:236:MET:HG3	1.77	0.49
1:M:428:ALA:HB1	1:M:559:ILE:HG13	1.94	0.49
1:M:560:SER:HB2	1:M:568:LYS:HD3	1.93	0.49
3:O:10:A:H2'	3:O:11:G:C8	2.48	0.49
1:A:525:ARG:HH12	1:A:529:ARG:HH11	1.60	0.49
1:I:209:HIS:O	1:I:213:LEU:HD23	2.12	0.49
1:I:322:PRO:HD2	2:J:9:ALA:HB1	1.94	0.49
2:J:55:LEU:HD11	2:J:132:SER:HB3	1.92	0.49
1:A:561:CYS:SG	1:A:569:ALA:HB3	2.53	0.49
2:F:56:ALA:HB2	2:F:149:TYR:HB3	1.94	0.49
2:J:114:HIS:O	2:J:117:ALA:HB3	2.11	0.49
1:M:43:ASP:O	1:M:47:ARG:HG3	2.13	0.49
1:M:509:ILE:HD11	1:M:531:ARG:NH2	2.27	0.49
2:N:284:LEU:HD13	2:N:323:PHE:CE1	2.48	0.49
4:P:7:DA:H2'	4:P:8:DC:C6	2.48	0.49
1:I:331:LEU:HD13	2:J:365:LEU:HD21	1.93	0.48
4:H:6:DA:H2'	4:H:7:DA:C8	2.49	0.48
2:N:280:MET:HE3	2:N:315:GLU:CD	2.33	0.48
1:A:536:SER:HB3	2:B:343:LEU:HD21	1.94	0.48
1:E:43:ASP:O	1:E:47:ARG:HG3	2.13	0.48
1:E:152:SER:OG	1:M:157:LYS:N	2.46	0.48
1:E:191:TYR:CD1	1:M:169:ALA:HB2	2.48	0.48
1:E:244:ASN:ND2	1:I:213:LEU:HD12	2.29	0.48
2:F:181:GLN:NE2	2:F:182:ILE:O	2.45	0.48
2:F:335:ILE:HD12	4:H:12:DT:H5''	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:212:PHE:HE2	1:I:236:MET:HG2	1.78	0.48
1:M:23:PHE:CD1	1:M:23:PHE:C	2.92	0.48
1:M:463:LYS:HD2	1:M:463:LYS:O	2.14	0.48
2:N:344:LYS:HB2	2:N:361:VAL:HA	1.94	0.48
2:J:49:GLN:H	2:J:49:GLN:NE2	2.11	0.48
1:M:19:HIS:HB2	1:M:249:HIS:CD2	2.49	0.48
1:M:256:PRO:HG3	6:M:601:AMP:C8	2.48	0.48
1:M:522:ASP:O	1:M:526:SER:N	2.38	0.48
2:N:285:SER:HA	2:N:288:LEU:CD2	2.44	0.48
1:E:19:HIS:HB2	1:E:249:HIS:CD2	2.49	0.48
1:E:162:TYR:CD2	1:E:170:ALA:HA	2.48	0.48
2:F:100:MET:HG2	2:F:101:PRO:HD2	1.96	0.48
4:H:7:DA:H2'	4:H:8:DC:C6	2.48	0.48
2:J:70:GLU:HB3	2:J:197:MET:HE1	1.96	0.48
2:J:206:ALA:HB3	2:J:473:MET:HE1	1.96	0.48
1:M:112:LEU:HD13	1:M:144:ASP:OD2	2.13	0.48
4:P:6:DA:H2'	4:P:7:DA:H8	1.79	0.48
1:A:245:ASN:HD22	1:M:214:ALA:HB1	1.77	0.48
2:B:29:HIS:HD2	2:B:30:PRO:HD2	1.79	0.48
2:B:49:GLN:H	2:B:49:GLN:NE2	2.11	0.48
2:B:70:GLU:HB3	2:B:197:MET:HE1	1.96	0.48
1:E:428:ALA:HB1	1:E:559:ILE:HG13	1.94	0.48
1:I:309:VAL:HG23	1:I:310:ARG:H	1.79	0.48
1:I:407:ILE:O	1:I:411:VAL:HG13	2.13	0.48
1:M:164:LEU:CD2	1:M:186:HIS:C	2.87	0.48
1:M:384:GLU:O	1:M:388:ARG:HG2	2.12	0.48
2:N:280:MET:HE3	2:N:315:GLU:HB3	1.95	0.48
4:P:6:DA:H2'	4:P:7:DA:C8	2.49	0.48
4:D:16:DA:H2''	4:D:17:DC:H5''	1.96	0.48
2:F:327:THR:O	2:F:327:THR:OG1	2.31	0.48
1:M:460:ASP:N	1:M:460:ASP:OD1	2.47	0.48
1:E:463:LYS:HD2	1:E:463:LYS:O	2.13	0.48
2:F:285:SER:HA	2:F:288:LEU:CD2	2.44	0.48
1:I:561:CYS:SG	1:I:569:ALA:HB3	2.53	0.48
1:M:484:LEU:HD21	1:M:519:GLU:HB2	1.96	0.48
1:A:245:ASN:HD22	1:M:214:ALA:CB	2.27	0.48
2:B:190:ARG:HH11	2:B:190:ARG:HA	1.78	0.48
1:E:145:ASP:HB2	1:E:148:GLU:HB2	1.94	0.48
1:I:419:SER:HA	1:I:422:GLU:HG2	1.96	0.48
2:J:386:ASN:ND2	2:J:388:GLN:O	2.47	0.48
2:B:206:ALA:HB3	2:B:473:MET:HE1	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:332:VAL:HG11	2:B:409:LEU:HD23	1.96	0.47
2:B:401:THR:HB	3:C:6:U:H4'	1.95	0.47
4:H:18:DA:H2''	4:H:19:DG:O5'	2.14	0.47
1:I:241:ILE:HG23	1:I:277:VAL:HG21	1.95	0.47
1:A:374:TYR:HD1	1:A:375:THR:N	2.13	0.47
1:A:407:ILE:O	1:A:411:VAL:HG13	2.13	0.47
1:A:419:SER:HA	1:A:422:GLU:HG2	1.96	0.47
2:B:409:LEU:HD21	2:B:425:ILE:HD12	1.97	0.47
1:E:247:PHE:HB2	1:E:277:VAL:HG21	1.95	0.47
2:F:190:ARG:NH2	4:H:21:DA:C5	2.82	0.47
2:F:284:LEU:HD13	2:F:323:PHE:CE1	2.48	0.47
2:F:344:LYS:HB2	2:F:361:VAL:HA	1.94	0.47
3:G:10:A:H2'	3:G:11:G:C8	2.48	0.47
4:H:23:DT:H2''	4:H:24:DA:OP2	2.15	0.47
1:I:295:TRP:O	1:I:298:VAL:HG12	2.15	0.47
2:N:242:THR:CG2	2:N:270:LYS:NZ	2.77	0.47
1:A:309:VAL:HG23	1:A:310:ARG:H	1.79	0.47
1:I:171:LEU:HD21	1:I:210:LYS:CE	2.44	0.47
1:I:269:ILE:CD1	1:I:279:ALA:HB1	2.39	0.47
2:J:56:ALA:HB2	2:J:149:TYR:HB3	1.96	0.47
1:M:81:PRO:HD2	1:M:91:PHE:CE2	2.49	0.47
2:N:401:THR:HB	3:O:6:U:H5''	1.96	0.47
2:B:465:GLU:OE1	2:B:465:GLU:N	2.47	0.47
1:I:13:TYR:OH	1:I:22:TRP:NE1	2.42	0.47
2:J:29:HIS:HD2	2:J:30:PRO:HD2	1.79	0.47
4:L:16:DA:H2''	4:L:17:DC:H5''	1.96	0.47
4:P:18:DA:H2''	4:P:19:DG:O5'	2.14	0.47
1:A:381:LEU:HB2	1:A:420:PHE:HZ	1.80	0.47
4:D:18:DA:H4'	4:D:19:DG:OP1	2.14	0.47
4:H:6:DA:H2'	4:H:7:DA:H8	1.79	0.47
1:I:374:TYR:HD1	1:I:375:THR:N	2.13	0.47
1:M:31:SER:C	1:M:33:GLY:H	2.22	0.47
1:A:483:GLU:OE2	1:A:516:ARG:NE	2.47	0.47
2:B:386:ASN:ND2	2:B:388:GLN:O	2.47	0.47
1:M:31:SER:O	1:M:32:ALA:C	2.56	0.47
2:N:87:TYR:CE2	2:N:197:MET:HB3	2.49	0.47
2:N:277:TYR:HE1	2:N:318:GLY:N	2.12	0.47
1:E:484:LEU:HD21	1:E:519:GLU:HB2	1.96	0.47
2:F:87:TYR:CE2	2:F:197:MET:HB3	2.49	0.47
2:F:401:THR:HB	3:G:6:U:H5''	1.96	0.47
1:I:171:LEU:HD21	1:I:210:LYS:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:253:TRP:HZ3	1:I:268:LEU:HD13	1.79	0.47
1:I:483:GLU:OE2	1:I:516:ARG:NE	2.47	0.47
2:J:190:ARG:CZ	2:J:191:GLN:HG3	2.44	0.47
1:M:61:ASP:OD1	1:M:64:ASN:N	2.46	0.47
1:M:445:TYR:CE1	1:M:491:SER:HB3	2.49	0.47
1:A:214:ALA:HB2	1:M:245:ASN:OD1	2.14	0.47
1:E:163:HIS:NE2	1:E:191:TYR:HE2	2.13	0.47
1:E:445:TYR:CE1	1:E:491:SER:HB3	2.49	0.47
1:I:305:ILE:O	1:I:309:VAL:HG22	2.15	0.47
1:A:295:TRP:O	1:A:298:VAL:HG12	2.14	0.47
1:A:580:SER:HB3	2:B:8:LEU:HB2	1.97	0.47
2:B:190:ARG:CZ	2:B:190:ARG:CB	2.85	0.47
2:F:79:GLU:OE1	2:F:190:ARG:NH1	2.48	0.47
2:F:171:ALA:HB2	2:F:455:VAL:HG13	1.97	0.47
1:I:121:ILE:HD12	1:I:121:ILE:H	1.80	0.47
1:M:502:TRP:HH2	2:N:8:LEU:HD21	1.80	0.47
1:A:440:ARG:HG2	1:A:441:HIS:ND1	2.30	0.47
2:B:379:GLN:NE2	2:B:405:ASN:O	2.48	0.47
1:E:81:PRO:HD2	1:E:91:PHE:CE2	2.49	0.47
1:I:325:GLY:HA3	2:J:10:ALA:HB2	1.95	0.47
1:I:508:GLU:OE2	1:I:517:ARG:NH1	2.43	0.47
2:N:444:VAL:HA	2:N:447:VAL:HG22	1.96	0.47
1:A:291:LEU:HD23	1:A:291:LEU:HA	1.79	0.46
1:E:83:GLN:O	1:E:85:SER:N	2.48	0.46
1:E:162:TYR:CD2	1:E:170:ALA:CA	2.98	0.46
1:M:83:GLN:O	1:M:85:SER:N	2.48	0.46
1:M:247:PHE:HB2	1:M:277:VAL:HG21	1.95	0.46
1:A:175:ASN:CB	1:M:248:PRO:HB2	2.45	0.46
1:A:305:ILE:O	1:A:309:VAL:HG22	2.15	0.46
2:B:56:ALA:HB2	2:B:149:TYR:HB3	1.96	0.46
1:E:162:TYR:CE2	1:E:170:ALA:HA	2.50	0.46
2:F:44:PHE:HD2	2:F:46:LEU:HG	1.79	0.46
2:F:185:ASP:HA	2:F:188:LEU:HD11	0.49	0.46
2:F:219:ASP:HB3	2:F:222:GLU:HG3	1.97	0.46
1:I:237:LEU:HD13	1:I:268:LEU:HD11	1.97	0.46
1:I:580:SER:HB3	2:J:8:LEU:HB2	1.97	0.46
2:N:219:ASP:HB3	2:N:222:GLU:HG3	1.97	0.46
2:B:12:SER:HB2	2:B:366:TYR:CE2	2.50	0.46
2:F:444:VAL:HA	2:F:447:VAL:HG22	1.96	0.46
2:J:155:LYS:HA	2:J:158:PHE:CG	2.50	0.46
3:K:8:U:H2'	3:K:9:U:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:326:LYS:CA	1:I:581:LEU:CB	2.87	0.46
2:J:224:TYR:HB2	2:J:247:VAL:HG12	1.97	0.46
2:J:281:GLN:OE1	2:J:321:ASP:HB2	2.14	0.46
2:J:332:VAL:HG11	2:J:409:LEU:HD23	1.96	0.46
1:M:125:VAL:HG12	1:M:291:LEU:HD12	1.98	0.46
2:N:100:MET:HG2	2:N:101:PRO:HD2	1.96	0.46
2:B:330:GLU:N	2:B:330:GLU:OE1	2.48	0.46
1:E:144:ASP:HA	1:E:189:PHE:CE2	2.51	0.46
1:E:502:TRP:HH2	2:F:8:LEU:HD21	1.80	0.46
1:E:509:ILE:HD11	1:E:531:ARG:NH2	2.27	0.46
2:J:12:SER:HB2	2:J:366:TYR:CE2	2.50	0.46
1:M:162:TYR:CD2	1:M:169:ALA:CB	2.98	0.46
3:O:18:U:H2'	3:O:19:A:C8	2.51	0.46
1:A:367:SER:O	1:A:367:SER:OG	2.21	0.46
3:C:11:G:N2	4:D:14:DT:O2	2.49	0.46
1:E:169:ALA:HB3	1:M:191:TYR:CE1	2.42	0.46
2:F:432:ASP:OD1	2:F:469:TYR:OH	2.23	0.46
1:I:384:GLU:O	1:I:388:ARG:HG2	2.16	0.46
2:J:246:GLN:O	2:J:257:PHE:HA	2.16	0.46
4:L:18:DA:H4'	4:L:19:DG:OP1	2.14	0.46
1:M:286:THR:HG23	1:M:289:GLU:H	1.80	0.46
1:M:339:VAL:HG12	1:M:572:GLU:HG3	1.97	0.46
1:A:121:ILE:HD12	1:A:121:ILE:H	1.81	0.46
2:B:379:GLN:NE2	2:B:441:LYS:HD2	2.31	0.46
3:C:8:U:H2'	3:C:9:U:C6	2.51	0.46
1:E:23:PHE:HB3	1:E:223:VAL:HG23	1.98	0.46
1:E:460:ASP:OD1	1:E:460:ASP:N	2.47	0.46
2:F:225:ILE:HG23	2:F:244:CYS:SG	2.56	0.46
1:I:381:LEU:HB2	1:I:420:PHE:HZ	1.80	0.46
2:N:44:PHE:HD2	2:N:46:LEU:HG	1.80	0.46
4:P:23:DT:H2''	4:P:24:DA:OP2	2.14	0.46
1:E:244:ASN:HD21	1:I:213:LEU:HB3	1.81	0.46
4:H:16:DA:H2''	4:H:17:DC:H5''	1.97	0.46
2:N:225:ILE:HG23	2:N:244:CYS:SG	2.56	0.46
1:A:384:GLU:O	1:A:388:ARG:HG2	2.16	0.46
1:E:83:GLN:HG3	1:E:84:TRP:H	1.81	0.46
2:F:316:ILE:HD11	2:F:412:PHE:HD2	1.81	0.46
1:I:440:ARG:HG2	1:I:441:HIS:ND1	2.30	0.46
2:J:277:TYR:CE1	2:J:281:GLN:HG3	2.50	0.46
2:J:409:LEU:HD21	2:J:425:ILE:HD12	1.97	0.46
4:L:15:DA:H5'	4:L:15:DA:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:83:GLN:HG3	1:M:84:TRP:H	1.81	0.46
1:M:91:PHE:CZ	1:M:95:LEU:HD12	2.51	0.46
1:M:492:ILE:HA	1:M:504:MET:O	2.16	0.46
2:B:155:LYS:HA	2:B:158:PHE:CG	2.50	0.46
2:B:173:VAL:HG21	2:B:180:ILE:HD11	1.97	0.46
2:J:408:MET:HE3	2:J:408:MET:HB2	1.82	0.46
1:A:217:ILE:CG2	1:M:217:ILE:CB	2.73	0.45
1:E:286:THR:HG23	1:E:289:GLU:H	1.80	0.45
2:J:173:VAL:HG21	2:J:180:ILE:HD11	1.97	0.45
2:N:270:LYS:HE3	2:N:279:GLU:OE1	2.15	0.45
2:B:224:TYR:HB2	2:B:247:VAL:HG12	1.97	0.45
1:E:91:PHE:CZ	1:E:95:LEU:HD12	2.51	0.45
1:E:360:LYS:HD3	1:E:360:LYS:HA	1.77	0.45
1:E:468:LYS:HA	1:E:468:LYS:HD2	1.73	0.45
1:I:171:LEU:CD2	1:I:210:LYS:CE	2.94	0.45
2:J:113:CYS:O	2:J:116:VAL:HG12	2.16	0.45
2:J:379:GLN:NE2	2:J:441:LYS:HD2	2.31	0.45
4:P:16:DA:H2"	4:P:17:DC:H5"	1.97	0.45
1:E:339:VAL:HG12	1:E:572:GLU:HG3	1.97	0.45
2:J:302:LYS:HE3	2:J:328:GLU:HB3	1.97	0.45
1:M:227:SER:HB2	6:M:601:AMP:O3'	2.00	0.45
2:N:239:GLU:OE1	2:N:269:ARG:CD	2.64	0.45
1:A:298:VAL:HG13	1:A:301:LYS:HD3	1.99	0.45
1:E:30:ARG:HD3	1:E:30:ARG:C	2.41	0.45
3:K:11:G:N2	4:L:14:DT:O2	2.49	0.45
2:N:239:GLU:CD	2:N:269:ARG:CG	2.60	0.45
2:N:316:ILE:HD11	2:N:412:PHE:HD2	1.81	0.45
1:E:125:VAL:HG12	1:E:291:LEU:HD12	1.98	0.45
1:E:385:PRO:O	1:E:389:LYS:HG3	2.17	0.45
1:E:386:GLU:H	1:E:386:GLU:HG2	1.58	0.45
2:F:247:VAL:HG12	2:F:257:PHE:CD1	2.51	0.45
1:I:495:GLU:OE2	2:J:340:TRP:NE1	2.32	0.45
1:I:531:ARG:O	2:J:402:PRO:HB3	2.16	0.45
1:E:134:GLN:CD	1:E:134:GLN:N	2.75	0.45
1:E:174:LEU:HD21	1:E:218:ARG:HD3	1.99	0.45
2:N:190:ARG:HE	2:N:190:ARG:HB3	1.49	0.45
1:A:333:THR:HG22	1:A:334:ASN:H	1.81	0.45
1:A:387:ILE:HA	1:A:390:ILE:HG22	1.99	0.45
1:E:171:LEU:HD12	1:E:171:LEU:C	2.41	0.45
2:F:262:THR:HG23	2:F:283:VAL:HG23	1.98	0.45
1:M:6:ASP:OD1	1:M:7:ASN:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:171:ALA:HB2	2:N:455:VAL:HG13	1.97	0.45
2:N:229:TYR:O	2:N:450:GLN:NE2	2.40	0.45
1:A:217:ILE:HG13	1:M:217:ILE:HG12	1.99	0.45
2:B:52:LEU:O	2:B:101:PRO:HB3	2.17	0.45
2:B:113:CYS:O	2:B:116:VAL:HG12	2.16	0.45
2:B:246:GLN:O	2:B:257:PHE:HA	2.16	0.45
3:G:18:U:H2'	3:G:19:A:C8	2.51	0.45
2:J:40:TYR:O	2:J:40:TYR:CD1	2.70	0.45
1:M:134:GLN:N	1:M:134:GLN:CD	2.75	0.45
1:M:174:LEU:HD21	1:M:218:ARG:HD3	1.99	0.45
1:E:61:ASP:OD2	1:E:64:ASN:HB2	2.17	0.45
1:E:106:LYS:NZ	1:M:176:THR:HG22	2.32	0.45
2:J:277:TYR:CD1	2:J:281:GLN:HG3	2.52	0.45
1:M:61:ASP:OD2	1:M:64:ASN:HB2	2.17	0.45
1:A:175:ASN:ND2	1:M:248:PRO:CB	2.80	0.45
1:E:165:GLU:CG	1:E:191:TYR:HB3	2.47	0.45
1:E:305:ILE:O	1:E:309:VAL:HG23	2.17	0.45
2:F:310:HIS:HB2	2:F:412:PHE:CZ	2.51	0.45
1:M:165:GLU:HG2	1:M:191:TYR:HB3	1.98	0.45
1:M:385:PRO:O	1:M:389:LYS:HG3	2.17	0.45
2:N:247:VAL:HG12	2:N:257:PHE:CD1	2.51	0.45
1:A:418:LYS:NZ	4:D:11:DC:OP1	2.50	0.44
1:E:342:SER:HA	1:E:404:ILE:O	2.17	0.44
2:J:52:LEU:O	2:J:101:PRO:HB3	2.17	0.44
2:J:330:GLU:OE2	2:J:414:GLY:HA2	2.16	0.44
2:J:465:GLU:N	2:J:465:GLU:OE1	2.47	0.44
1:M:23:PHE:O	1:M:23:PHE:CD1	2.70	0.44
2:N:310:HIS:HB2	2:N:412:PHE:CZ	2.51	0.44
1:A:248:PRO:HB2	1:M:175:ASN:CG	2.42	0.44
2:B:234:ASN:OD1	2:B:235:ALA:N	2.50	0.44
1:E:381:LEU:HB2	1:E:420:PHE:HZ	1.82	0.44
1:E:492:ILE:HA	1:E:504:MET:O	2.16	0.44
1:I:342:SER:OG	1:I:404:ILE:O	2.32	0.44
1:I:387:ILE:HA	1:I:390:ILE:HG22	1.99	0.44
1:I:418:LYS:NZ	4:L:11:DC:OP1	2.50	0.44
2:J:281:GLN:HG2	2:J:318:GLY:O	2.17	0.44
2:J:377:TRP:CD2	2:J:406:PRO:HB3	2.53	0.44
1:M:226:TYR:HH	1:M:230:ASP:HB2	1.81	0.44
1:M:305:ILE:O	1:M:309:VAL:HG23	2.17	0.44
1:M:360:LYS:HD3	1:M:360:LYS:HA	1.77	0.44
2:N:19:LEU:HB3	2:N:21:PHE:CE1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:260:TYR:O	2:N:260:TYR:CD1	2.70	0.44
2:F:35:SER:HA	2:F:93:VAL:HG23	1.98	0.44
1:I:330:ALA:HB2	1:I:581:LEU:CG	2.44	0.44
2:J:232:LYS:HB3	2:J:239:GLU:HB3	1.99	0.44
1:A:131:GLU:HB2	1:A:151:PHE:HE1	1.83	0.44
1:E:227:SER:HB3	6:E:601:AMP:O3'	2.17	0.44
2:F:29:HIS:CG	2:F:32:ARG:HB3	2.53	0.44
2:F:301:ARG:NH1	2:F:302:LYS:HD2	2.29	0.44
2:F:376:LEU:HD22	2:F:409:LEU:HD11	1.99	0.44
1:I:331:LEU:HD13	2:J:365:LEU:CD2	2.47	0.44
1:M:371:LEU:HD21	1:M:423:GLU:HG2	2.00	0.44
2:N:29:HIS:CG	2:N:32:ARG:HB3	2.53	0.44
2:B:377:TRP:CD2	2:B:406:PRO:HB3	2.53	0.44
1:E:482:LYS:HB3	1:E:482:LYS:HE2	1.77	0.44
2:F:44:PHE:CD2	2:F:46:LEU:HG	2.52	0.44
2:F:55:LEU:HB3	2:F:148:VAL:HG22	2.00	0.44
2:N:158:PHE:O	3:O:1:A:N6	2.35	0.44
2:N:188:LEU:C	2:N:193:ARG:NH2	2.73	0.44
2:N:275:LEU:HB2	2:N:280:MET:CE	2.48	0.44
1:A:213:LEU:HG	1:M:244:ASN:ND2	2.32	0.44
2:B:232:LYS:HB3	2:B:239:GLU:HB3	1.99	0.44
4:D:6:DA:H2'	4:D:7:DA:H8	1.83	0.44
1:E:6:ASP:OD1	1:E:7:ASN:N	2.50	0.44
2:J:225:ILE:N	2:J:304:PHE:O	2.48	0.44
2:J:234:ASN:OD1	2:J:235:ALA:N	2.50	0.44
1:M:342:SER:HA	1:M:404:ILE:O	2.17	0.44
2:N:284:LEU:HD12	2:N:319:ALA:HA	2.00	0.44
2:N:376:LEU:HD22	2:N:409:LEU:HD11	1.99	0.44
4:P:18:DA:H4'	4:P:19:DG:OP1	2.18	0.44
1:E:130:LEU:HD21	1:E:138:VAL:HG23	2.00	0.44
1:E:136:LYS:HB3	1:E:179:PHE:CG	2.53	0.44
1:E:165:GLU:CD	1:E:191:TYR:HB3	2.42	0.44
1:E:371:LEU:HD21	1:E:423:GLU:HG2	2.00	0.44
1:E:512:LYS:HB3	1:E:513:PRO:HD3	1.99	0.44
2:F:379:GLN:HE21	2:F:441:LYS:HG3	1.83	0.44
1:M:502:TRP:CH2	2:N:8:LEU:HD21	2.53	0.44
2:N:87:TYR:HD1	2:N:88:GLY:N	2.16	0.44
2:N:188:LEU:C	2:N:188:LEU:CD1	2.85	0.44
1:A:394:ASP:OD1	1:A:395:GLU:N	2.51	0.44
2:B:46:LEU:HD11	2:F:137:PHE:CD2	2.53	0.44
4:D:15:DA:H5'	4:D:15:DA:C8	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:24:LEU:HD12	1:E:147:ILE:HD11	1.98	0.44
3:G:11:G:N2	4:H:14:DT:O2	2.51	0.44
1:I:468:LYS:HB3	1:I:468:LYS:HE3	1.74	0.44
2:J:223:ALA:CA	2:J:303:ILE:CD1	2.96	0.44
1:M:381:LEU:HB2	1:M:420:PHE:HZ	1.82	0.44
1:A:217:ILE:HG23	1:M:217:ILE:CD1	2.26	0.44
1:E:153:ASP:N	1:M:156:GLY:O	2.51	0.44
2:F:55:LEU:HD23	2:F:148:VAL:HG22	1.99	0.44
2:J:20:LEU:HD12	2:J:20:LEU:HA	1.83	0.44
2:J:410:ARG:HG2	2:J:412:PHE:CE2	2.53	0.44
1:A:210:LYS:CG	1:M:245:ASN:HB3	2.48	0.43
2:B:18:LEU:HD23	2:B:28:THR:HG22	1.99	0.43
2:B:410:ARG:HG2	2:B:412:PHE:CE2	2.53	0.43
1:E:148:GLU:HB3	1:M:158:HIS:CB	2.46	0.43
1:I:333:THR:HG22	1:I:334:ASN:H	1.81	0.43
1:M:227:SER:HB3	6:M:601:AMP:HO3'	0.61	0.43
1:M:497:ARG:HA	1:M:497:ARG:HD3	1.70	0.43
2:N:44:PHE:CD2	2:N:46:LEU:HG	2.52	0.43
1:E:522:ASP:O	1:E:526:SER:N	2.38	0.43
2:F:87:TYR:HD1	2:F:88:GLY:N	2.16	0.43
2:F:331:LEU:HB2	2:F:413:SER:HB3	2.00	0.43
1:I:131:GLU:HB2	1:I:151:PHE:HE1	1.83	0.43
1:I:309:VAL:HG23	1:I:310:ARG:N	2.33	0.43
1:I:310:ARG:HB2	2:J:325:SER:HB2	2.00	0.43
1:M:136:LYS:HB3	1:M:179:PHE:CG	2.53	0.43
1:M:330:ALA:HB2	1:M:581:LEU:HA	2.01	0.43
1:M:426:LEU:HG	1:M:444:HIS:CD2	2.53	0.43
1:M:437:HIS:C	1:M:438:ARG:HD2	2.44	0.43
2:N:327:THR:O	2:N:327:THR:OG1	2.31	0.43
3:O:17:U:H2'	3:O:18:U:C6	2.54	0.43
1:A:309:VAL:HG23	1:A:310:ARG:N	2.33	0.43
1:E:169:ALA:CB	1:M:191:TYR:CD1	2.85	0.43
3:G:7:G:H2'	3:G:8:U:C6	2.54	0.43
4:H:18:DA:H4'	4:H:19:DG:OP1	2.18	0.43
1:I:285:GLY:HA3	1:I:289:GLU:OE1	2.18	0.43
1:I:298:VAL:HG13	1:I:301:LYS:HD3	1.99	0.43
2:J:341:TYR:HD2	2:J:403:LEU:HD23	1.69	0.43
1:M:130:LEU:HD21	1:M:138:VAL:HG23	2.00	0.43
1:M:234:MET:SD	1:M:268:LEU:HD13	2.58	0.43
1:M:512:LYS:HB3	1:M:513:PRO:HD3	1.99	0.43
2:N:35:SER:HA	2:N:93:VAL:HG23	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:79:GLU:HG3	2:N:192:CYS:HB2	1.99	0.43
1:E:234:MET:SD	1:E:268:LEU:HD13	2.58	0.43
1:E:502:TRP:CH2	2:F:8:LEU:HD21	2.53	0.43
2:F:135:GLY:O	2:F:139:GLN:NE2	2.52	0.43
2:F:262:THR:OG1	2:F:283:VAL:HG21	2.17	0.43
2:J:40:TYR:CE2	2:J:214:LYS:HB2	2.52	0.43
4:L:6:DA:H2'	4:L:7:DA:H8	1.82	0.43
2:N:379:GLN:HE21	2:N:441:LYS:HG3	1.83	0.43
1:E:272:ALA:O	1:E:277:VAL:HG12	2.19	0.43
1:E:426:LEU:HG	1:E:444:HIS:CD2	2.53	0.43
3:G:17:U:H2'	3:G:18:U:C6	2.54	0.43
2:J:304:PHE:CZ	2:J:421:THR:HG22	2.54	0.43
1:A:249:HIS:CE1	1:M:175:ASN:O	2.71	0.43
1:A:310:ARG:HB2	2:B:325:SER:HB2	2.00	0.43
1:A:362:ARG:HD2	1:A:391:PHE:HE1	1.83	0.43
2:J:18:LEU:HD23	2:J:28:THR:HG22	2.00	0.43
2:J:46:LEU:HD11	2:N:137:PHE:CD2	2.53	0.43
1:M:209:HIS:HE1	1:M:213:LEU:HD11	1.84	0.43
1:M:218:ARG:HE	1:M:218:ARG:HB3	1.57	0.43
3:O:11:G:N2	4:P:14:DT:O2	2.51	0.43
1:A:468:LYS:HB3	1:A:468:LYS:HE3	1.74	0.43
1:E:437:HIS:C	1:E:438:ARG:HD2	2.43	0.43
1:I:463:LYS:HD2	1:I:463:LYS:HA	1.73	0.43
1:M:112:LEU:CB	1:M:144:ASP:CG	2.55	0.43
1:M:291:LEU:HD13	1:M:291:LEU:HA	1.81	0.43
2:N:135:GLY:O	2:N:139:GLN:NE2	2.52	0.43
1:A:16:ASN:O	1:A:16:ASN:ND2	2.50	0.43
2:B:195:ASN:OD1	3:C:2:U:N3	2.48	0.43
1:E:153:ASP:CA	1:M:156:GLY:O	2.66	0.43
1:M:22:TRP:HE3	1:M:24:LEU:HD21	1.83	0.43
1:M:272:ALA:O	1:M:277:VAL:HG12	2.19	0.43
2:N:238:GLN:OE1	3:O:12:A:H4'	2.19	0.43
2:N:269:ARG:HH11	2:N:269:ARG:HB2	1.84	0.43
1:E:61:ASP:OD1	1:E:64:ASN:N	2.46	0.43
2:F:105:LEU:HD23	2:F:105:LEU:HA	1.82	0.43
1:M:220:GLY:HA3	1:M:249:HIS:HB2	2.01	0.43
1:M:468:LYS:HD2	1:M:468:LYS:HA	1.73	0.43
2:N:280:MET:CE	2:N:315:GLU:OE1	2.66	0.43
1:A:176:THR:O	1:M:19:HIS:HE1	2.02	0.43
1:A:322:PRO:HD2	2:B:9:ALA:HB1	2.01	0.43
2:B:229:TYR:HB3	2:B:242:THR:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:377:TRP:CD2	2:F:406:PRO:HB3	2.54	0.43
1:I:394:ASP:OD1	1:I:395:GLU:N	2.51	0.43
1:M:465:VAL:HG11	1:M:527:ARG:NH2	2.34	0.43
1:A:285:GLY:HA3	1:A:289:GLU:OE1	2.18	0.42
2:B:177:ASN:O	2:B:177:ASN:ND2	2.52	0.42
1:E:525:ARG:O	1:E:529:ARG:HG3	2.19	0.42
2:J:21:PHE:HZ	2:J:30:PRO:HA	1.84	0.42
2:J:229:TYR:HB3	2:J:242:THR:HG22	2.01	0.42
1:M:22:TRP:CE3	1:M:24:LEU:HD21	2.54	0.42
2:N:55:LEU:HB3	2:N:148:VAL:HG22	2.00	0.42
2:N:55:LEU:HD23	2:N:148:VAL:HG22	1.99	0.42
3:O:7:G:H2'	3:O:8:U:C6	2.54	0.42
1:E:157:LYS:N	1:M:152:SER:OG	2.52	0.42
2:F:284:LEU:HD12	2:F:319:ALA:HA	2.00	0.42
1:I:321:LEU:O	1:I:322:PRO:O	2.36	0.42
1:M:432:GLU:OE1	1:M:432:GLU:N	2.52	0.42
1:M:525:ARG:O	1:M:529:ARG:HG3	2.19	0.42
2:N:280:MET:HE1	2:N:315:GLU:OE1	2.18	0.42
3:O:8:U:H2'	3:O:9:U:C6	2.54	0.42
1:A:237:LEU:O	1:A:241:ILE:HG13	2.20	0.42
1:A:242:ASP:OD2	1:A:275:LYS:NZ	2.51	0.42
1:E:291:LEU:HD13	1:E:291:LEU:HA	1.81	0.42
1:E:330:ALA:HB2	1:E:581:LEU:HA	2.00	0.42
1:E:465:VAL:HG11	1:E:527:ARG:NH2	2.34	0.42
2:F:382:VAL:HG11	2:F:438:LEU:HD21	2.01	0.42
3:G:8:U:H2'	3:G:9:U:C6	2.54	0.42
2:J:446:LEU:HD23	2:J:446:LEU:HA	1.84	0.42
1:M:395:GLU:H	1:M:395:GLU:HG2	1.66	0.42
2:N:168:ARG:HE	2:N:172:LYS:HE2	1.85	0.42
2:N:284:LEU:HD23	2:N:284:LEU:HA	1.74	0.42
2:N:377:TRP:CD2	2:N:406:PRO:HB3	2.54	0.42
1:A:366:LYS:HA	1:A:366:LYS:HD2	1.86	0.42
1:A:497:ARG:HD3	1:A:497:ARG:HA	1.62	0.42
1:E:220:GLY:HA3	1:E:249:HIS:HB2	2.01	0.42
1:M:165:GLU:OE1	1:M:165:GLU:HA	2.11	0.42
2:N:262:THR:HG21	2:N:283:VAL:CG2	2.12	0.42
2:N:301:ARG:NH1	2:N:302:LYS:HD2	2.29	0.42
2:N:382:VAL:HG11	2:N:438:LEU:HD21	2.01	0.42
1:A:13:TYR:OH	1:A:22:TRP:NE1	2.44	0.42
1:A:223:VAL:HG13	1:A:253:TRP:HA	2.02	0.42
1:E:287:PHE:N	6:E:601:AMP:N1	2.64	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:265:VAL:CG1	1:I:281:LEU:CD1	2.97	0.42
2:B:72:GLN:HG3	2:B:98:LEU:HD23	2.01	0.42
1:I:223:VAL:HG13	1:I:253:TRP:HA	2.02	0.42
1:I:362:ARG:HD2	1:I:391:PHE:HE1	1.83	0.42
2:J:72:GLN:HG3	2:J:98:LEU:HD23	2.01	0.42
2:J:301:ARG:O	2:J:328:GLU:N	2.49	0.42
2:J:461:GLU:O	2:J:461:GLU:HG2	2.19	0.42
2:N:105:LEU:HD23	2:N:105:LEU:HA	1.82	0.42
2:N:331:LEU:HB2	2:N:413:SER:HB3	2.00	0.42
1:A:241:ILE:HG23	1:A:277:VAL:HG21	2.02	0.42
1:A:343:ILE:HD12	1:A:343:ILE:HA	1.86	0.42
1:I:386:GLU:H	1:I:386:GLU:HG2	1.61	0.42
2:N:213:TRP:CE2	2:N:433:TRP:HD1	2.38	0.42
1:A:495:GLU:OE2	2:B:340:TRP:NE1	2.32	0.42
1:A:576:ARG:HA	1:A:576:ARG:HD3	1.92	0.42
2:F:168:ARG:HE	2:F:172:LYS:HE2	1.85	0.42
2:F:196:VAL:HG22	3:G:2:U:C4	2.55	0.42
2:N:61:MET:HB3	2:N:61:MET:HE2	1.79	0.42
2:N:196:VAL:HG22	3:O:2:U:C5	2.55	0.42
1:A:332:ARG:HD3	1:A:537:TYR:HE1	1.85	0.42
2:F:238:GLN:OE1	3:G:12:A:H4'	2.19	0.42
1:I:22:TRP:HD1	1:I:135:THR:OG1	2.03	0.42
1:A:484:LEU:HD23	1:A:511:ILE:HG21	2.02	0.42
2:B:151:PRO:HD2	2:B:154:TRP:CE3	2.55	0.42
1:E:122:GLY:N	1:E:288:ASP:OD1	2.53	0.42
1:E:164:LEU:HD21	1:E:185:ILE:O	2.19	0.42
1:E:167:SER:OG	1:E:205:ASP:OD2	2.18	0.42
1:I:366:LYS:HA	1:I:366:LYS:HD2	1.86	0.42
2:J:363:ARG:HH22	2:J:429:THR:HG1	1.68	0.42
1:M:122:GLY:N	1:M:288:ASP:OD1	2.53	0.42
1:M:268:LEU:HD23	1:M:269:ILE:HD13	2.02	0.42
1:M:411:VAL:HG21	1:M:501:LEU:HD21	2.01	0.42
1:A:304:ALA:O	1:A:308:LYS:HG2	2.20	0.41
2:B:21:PHE:HZ	2:B:30:PRO:HA	1.84	0.41
2:B:47:PRO:HG3	2:B:205:TYR:CZ	2.55	0.41
1:E:148:GLU:C	1:M:158:HIS:HB2	2.45	0.41
2:F:19:LEU:HB3	2:F:21:PHE:CE1	2.52	0.41
2:F:130:VAL:O	2:F:133:MET:HB2	2.20	0.41
1:I:4:LEU:HD12	1:I:4:LEU:HA	1.93	0.41
2:J:224:TYR:CE2	2:J:424:SER:HB2	2.55	0.41
2:J:430:LYS:HE2	2:J:430:LYS:HB3	1.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:162:TYR:CE2	1:M:169:ALA:CB	3.02	0.41
1:M:310:ARG:HE	1:M:310:ARG:HB2	1.67	0.41
2:N:110:LEU:HD12	2:N:110:LEU:H	1.85	0.41
2:N:151:PRO:HD2	2:N:154:TRP:CE3	2.55	0.41
2:N:285:SER:O	2:N:288:LEU:HD23	2.20	0.41
1:I:552:GLY:O	1:I:576:ARG:NE	2.53	0.41
2:J:177:ASN:O	2:J:177:ASN:ND2	2.52	0.41
1:M:132:MET:HE2	1:M:134:GLN:OE1	2.20	0.41
1:M:264:ALA:HA	1:M:267:ASP:OD2	2.20	0.41
2:B:110:LEU:HD12	2:B:112:GLU:H	1.85	0.41
2:B:461:GLU:HG2	2:B:461:GLU:O	2.19	0.41
1:E:493:ARG:NH2	2:F:339:ASN:OD1	2.51	0.41
1:E:561:CYS:SG	1:E:569:ALA:HB3	2.60	0.41
2:F:213:TRP:CE2	2:F:433:TRP:HD1	2.38	0.41
1:I:478:VAL:HG13	1:I:481:ALA:HB3	2.02	0.41
1:I:484:LEU:HD23	1:I:511:ILE:HG21	2.02	0.41
2:J:44:PHE:CD2	2:N:176:LEU:HD21	2.56	0.41
2:J:151:PRO:HD2	2:J:154:TRP:CE3	2.55	0.41
2:B:303:ILE:HG13	2:B:323:PHE:CE2	2.56	0.41
4:D:20:DG:H2"	4:D:21:DA:H8	1.85	0.41
1:E:22:TRP:CE3	1:E:24:LEU:HD21	2.53	0.41
1:E:24:LEU:O	1:E:140:THR:OG1	2.29	0.41
1:E:165:GLU:OE2	1:E:191:TYR:HB3	2.20	0.41
2:F:151:PRO:HD2	2:F:154:TRP:CE3	2.55	0.41
2:F:261:ASP:HB2	2:F:463:VAL:HA	2.02	0.41
1:I:177:GLU:OE2	1:I:218:ARG:NH2	2.53	0.41
1:I:440:ARG:HD3	1:I:510:TRP:CZ3	2.56	0.41
2:J:64:LEU:HD11	2:J:149:TYR:CB	2.48	0.41
1:M:23:PHE:O	1:M:223:VAL:HG23	2.21	0.41
1:A:241:ILE:HG22	1:A:275:LYS:HD2	2.01	0.41
1:E:340:THR:OG1	1:E:572:GLU:HG2	2.20	0.41
1:E:411:VAL:HG21	1:E:501:LEU:HD21	2.01	0.41
1:E:497:ARG:HD3	1:E:497:ARG:HA	1.70	0.41
2:F:61:MET:HE2	2:F:61:MET:HB3	1.79	0.41
2:F:243:CYS:SG	2:F:453:ALA:HA	2.61	0.41
2:F:332:VAL:HG22	2:F:411:ARG:HG2	2.02	0.41
2:J:47:PRO:HG3	2:J:205:TYR:CZ	2.55	0.41
4:L:20:DG:H2"	4:L:21:DA:H8	1.85	0.41
2:N:269:ARG:CB	2:N:269:ARG:HH11	2.33	0.41
1:A:478:VAL:HG13	1:A:481:ALA:HB3	2.02	0.41
1:A:482:LYS:HA	1:A:482:LYS:HD3	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:224:TYR:CE2	2:B:424:SER:HB2	2.55	0.41
2:B:227:LEU:HD23	2:B:244:CYS:HB2	2.02	0.41
1:E:192:GLN:HB3	1:M:168:TYR:HH	1.82	0.41
1:E:526:SER:HA	1:E:529:ARG:HG3	2.03	0.41
2:F:196:VAL:HG22	3:G:2:U:C5	2.55	0.41
1:I:171:LEU:HD13	1:I:211:CYS:CA	2.50	0.41
1:I:217:ILE:HA	1:I:245:ASN:O	2.20	0.41
1:M:340:THR:OG1	1:M:572:GLU:HG2	2.20	0.41
2:N:130:VAL:O	2:N:133:MET:HB2	2.20	0.41
1:A:22:TRP:HD1	1:A:135:THR:OG1	2.03	0.41
1:A:362:ARG:O	1:A:365:GLN:HG2	2.21	0.41
1:E:190:ARG:NH1	1:E:191:TYR:CZ	2.89	0.41
1:E:415:THR:OG1	4:H:9:DA:N3	2.44	0.41
2:F:64:LEU:HD21	2:F:149:TYR:HB2	2.03	0.41
3:G:7:G:H2'	3:G:8:U:H6	1.86	0.41
1:I:430:LEU:HD22	1:I:437:HIS:HB2	2.01	0.41
1:M:164:LEU:HD21	1:M:186:HIS:HA	2.01	0.41
1:M:209:HIS:C	1:M:209:HIS:ND1	2.72	0.41
1:M:568:LYS:HE3	1:M:568:LYS:HB3	1.93	0.41
2:N:196:VAL:HG22	3:O:2:U:C4	2.55	0.41
1:A:343:ILE:HG22	1:A:404:ILE:HD11	2.03	0.41
1:A:552:GLY:O	1:A:576:ARG:NE	2.53	0.41
2:B:223:ALA:HB3	2:B:303:ILE:HD13	2.02	0.41
1:E:166:GLY:CA	1:M:165:GLU:HG3	2.49	0.41
2:F:285:SER:O	2:F:288:LEU:HD23	2.20	0.41
1:I:126:LEU:HD12	1:I:126:LEU:HA	1.88	0.41
1:I:135:THR:HG23	1:I:135:THR:O	2.21	0.41
1:I:241:ILE:HG12	1:I:247:PHE:CE2	2.47	0.41
2:J:335:ILE:HA	4:L:13:DC:OP1	2.21	0.41
1:M:90:SER:CB	1:M:198:THR:H	2.34	0.41
1:M:561:CYS:SG	1:M:569:ALA:HB3	2.60	0.41
2:N:64:LEU:HD21	2:N:149:TYR:HB2	2.03	0.41
1:A:206:ARG:HD2	1:A:206:ARG:O	2.21	0.41
1:A:217:ILE:HG13	1:M:217:ILE:HD11	1.91	0.41
1:A:333:THR:HG21	2:B:340:TRP:CE3	2.54	0.41
1:A:440:ARG:HD3	1:A:510:TRP:CZ3	2.56	0.41
1:E:268:LEU:HD23	1:E:269:ILE:HD13	2.02	0.41
1:E:418:LYS:NZ	4:H:11:DC:OP1	2.54	0.41
1:E:432:GLU:OE1	1:E:432:GLU:N	2.52	0.41
2:F:261:ASP:CG	2:F:263:ARG:HD3	2.46	0.41
1:I:362:ARG:O	1:I:365:GLN:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:425:ILE:HG21	1:I:503:ILE:HD11	2.03	0.41
2:J:32:ARG:O	2:J:36:GLN:HG2	2.21	0.41
2:J:110:LEU:HD12	2:J:112:GLU:H	1.85	0.41
1:M:16:ASN:HD21	1:M:20:MET:HE2	1.85	0.41
1:M:363:ILE:HD11	1:M:372:LEU:HD13	2.03	0.41
1:M:462:ARG:HG2	1:M:471:LEU:HG	2.03	0.41
2:B:335:ILE:HA	4:D:13:DC:OP1	2.21	0.41
3:C:13:G:H2'	3:C:14:C:H6	1.84	0.41
1:E:132:MET:HE2	1:E:134:GLN:OE1	2.20	0.41
1:E:363:ILE:HD11	1:E:372:LEU:HD13	2.03	0.41
2:F:62:ARG:HA	2:F:65:ASP:OD2	2.21	0.41
2:F:110:LEU:HD12	2:F:110:LEU:H	1.85	0.41
3:G:19:A:H2'	3:G:20:A:O4'	2.21	0.41
1:I:343:ILE:HG22	1:I:404:ILE:HD11	2.03	0.41
1:M:62:ILE:O	1:M:68:LYS:HG3	2.21	0.41
3:O:19:A:H2'	3:O:20:A:O4'	2.21	0.41
1:A:430:LEU:HD22	1:A:437:HIS:HB2	2.01	0.40
2:B:32:ARG:O	2:B:36:GLN:HG2	2.20	0.40
1:E:34:LEU:HD12	1:E:144:ASP:OD2	2.20	0.40
1:E:49:TYR:CZ	1:E:55:GLN:HG3	2.56	0.40
1:I:9:PHE:HB2	1:I:282:VAL:HG11	2.03	0.40
2:J:44:PHE:CZ	2:J:253:THR:CB	2.90	0.40
2:J:227:LEU:HD23	2:J:244:CYS:HB2	2.02	0.40
1:M:35:PRO:HG2	1:M:112:LEU:HD21	2.02	0.40
2:N:243:CYS:SG	2:N:453:ALA:HA	2.61	0.40
1:A:135:THR:HG23	1:A:135:THR:O	2.21	0.40
1:A:177:GLU:HB2	1:M:19:HIS:NE2	2.36	0.40
1:A:217:ILE:HD13	1:A:245:ASN:O	2.22	0.40
1:A:473:TYR:O	1:A:527:ARG:NH2	2.54	0.40
1:A:478:VAL:HG12	1:A:484:LEU:O	2.22	0.40
1:E:90:SER:CB	1:E:198:THR:H	2.34	0.40
1:E:462:ARG:HG2	1:E:471:LEU:HG	2.03	0.40
2:F:18:LEU:HD12	2:F:18:LEU:H	1.87	0.40
2:F:136:LEU:HB3	2:F:143:PHE:CE2	2.57	0.40
1:I:237:LEU:O	1:I:241:ILE:HG13	2.21	0.40
1:I:304:ALA:O	1:I:308:LYS:HG2	2.19	0.40
1:I:332:ARG:HD3	1:I:537:TYR:HE1	1.85	0.40
1:I:335:ALA:HB1	1:I:502:TRP:HB3	2.03	0.40
1:I:437:HIS:O	1:I:438:ARG:HD2	2.22	0.40
1:M:493:ARG:NH2	2:N:339:ASN:OD1	2.51	0.40
2:N:239:GLU:OE1	2:N:269:ARG:HD2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:64:LEU:HD11	2:B:149:TYR:CB	2.48	0.40
2:B:291:TYR:CD2	2:B:300:PRO:HG3	2.56	0.40
2:F:379:GLN:NE2	2:F:441:LYS:HG3	2.37	0.40
1:M:49:TYR:CZ	1:M:55:GLN:HG3	2.56	0.40
1:A:136:LYS:HB3	1:A:179:PHE:CG	2.57	0.40
2:B:20:LEU:HD12	2:B:20:LEU:HA	1.82	0.40
2:B:190:ARG:NH1	2:B:190:ARG:CA	2.85	0.40
2:B:215:LEU:HD23	2:B:215:LEU:HA	1.95	0.40
2:B:240:TYR:CE2	2:B:273:PRO:HD3	2.57	0.40
1:E:152:SER:O	1:M:156:GLY:HA2	2.21	0.40
1:E:264:ALA:HA	1:E:267:ASP:OD2	2.20	0.40
2:F:20:LEU:HA	2:F:20:LEU:HD12	1.85	0.40
2:J:223:ALA:CA	2:J:303:ILE:HD11	2.47	0.40
1:M:35:PRO:HG2	1:M:112:LEU:CD2	2.51	0.40
2:N:332:VAL:HG22	2:N:411:ARG:HG2	2.02	0.40
2:N:428:LEU:HD23	2:N:428:LEU:HA	1.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	451/587 (77%)	433 (96%)	18 (4%)	0	100	100
1	E	570/587 (97%)	539 (95%)	31 (5%)	0	100	100
1	I	451/587 (77%)	431 (96%)	19 (4%)	1 (0%)	43	71
1	M	570/587 (97%)	537 (94%)	33 (6%)	0	100	100
2	B	450/473 (95%)	426 (95%)	23 (5%)	1 (0%)	43	71
2	F	450/473 (95%)	434 (96%)	15 (3%)	1 (0%)	43	71
2	J	450/473 (95%)	424 (94%)	23 (5%)	3 (1%)	18	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	N	450/473 (95%)	434 (96%)	16 (4%)	0	100	100
All	All	3842/4240 (91%)	3658 (95%)	178 (5%)	6 (0%)	44	71

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	J	190	ARG
2	J	191	GLN
1	I	322	PRO
2	B	190	ARG
2	F	261	ASP
2	J	404	PRO

5.3.2 Protein sidechains ⓘ

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	389/502 (78%)	386 (99%)	3 (1%)	73	77
1	E	492/502 (98%)	489 (99%)	3 (1%)	78	80
1	I	389/502 (78%)	372 (96%)	17 (4%)	25	51
1	M	492/502 (98%)	478 (97%)	14 (3%)	38	60
2	B	394/407 (97%)	390 (99%)	4 (1%)	68	75
2	F	394/407 (97%)	388 (98%)	6 (2%)	57	69
2	J	394/407 (97%)	387 (98%)	7 (2%)	51	67
2	N	394/407 (97%)	387 (98%)	7 (2%)	51	67
All	All	3338/3636 (92%)	3277 (98%)	61 (2%)	51	67

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	MET
1	A	161	VAL

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Mol	Chain	Res	Type
1	A	314	VAL
2	B	49	GLN
2	B	188	LEU
2	B	189	THR
2	B	190	ARG
1	E	55	GLN
1	E	93	PHE
1	E	443	THR
2	F	188	LEU
2	F	191	GLN
2	F	192	CYS
2	F	238	GLN
2	F	263	ARG
2	F	327	THR
1	I	15	GLN
1	I	16	ASN
1	I	20	MET
1	I	161	VAL
1	I	213	LEU
1	I	242	ASP
1	I	243	GLN
1	I	244	ASN
1	I	265	VAL
1	I	266	GLN
1	I	267	ASP
1	I	269	ILE
1	I	275	LYS
1	I	314	VAL
1	I	326	LYS
1	I	329	PRO
1	I	331	LEU
2	J	41	SER
2	J	49	GLN
2	J	190	ARG
2	J	281	GLN
2	J	302	LYS
2	J	303	ILE
2	J	400	LEU
1	M	14	LEU
1	M	30	ARG
1	M	55	GLN
1	M	93	PHE

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Mol	Chain	Res	Type
1	M	147	ILE
1	M	149	THR
1	M	164	LEU
1	M	165	GLU
1	M	189	PHE
1	M	190	ARG
1	M	209	HIS
1	M	211	CYS
1	M	213	LEU
1	M	350	LEU
2	N	16	GLU
2	N	185	ASP
2	N	188	LEU
2	N	190	ARG
2	N	238	GLN
2	N	270	LYS
2	N	327	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	15	GLN
1	A	244	ASN
2	B	45	ASN
2	B	114	HIS
2	B	379	GLN
1	E	16	ASN
1	E	55	GLN
1	E	83	GLN
1	E	244	ASN
1	E	538	GLN
2	F	72	GLN
2	F	114	HIS
2	F	139	GLN
2	F	272	ASN
2	F	333	GLN
2	F	379	GLN
2	F	386	ASN
2	F	434	ASN
1	I	7	ASN
1	I	19	HIS

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Mol	Chain	Res	Type
1	I	244	ASN
2	J	45	ASN
2	J	379	GLN
1	M	55	GLN
1	M	83	GLN
1	M	123	HIS
1	M	163	HIS
1	M	538	GLN
2	N	72	GLN
2	N	114	HIS
2	N	139	GLN
2	N	272	ASN
2	N	281	GLN
2	N	333	GLN
2	N	379	GLN
2	N	386	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C	20/21 (95%)	7 (35%)	0
3	G	20/21 (95%)	7 (35%)	0
3	K	20/21 (95%)	7 (35%)	0
3	O	20/21 (95%)	7 (35%)	0
All	All	80/84 (95%)	28 (35%)	0

All (28) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	C	4	C
3	C	5	C
3	C	12	A
3	C	13	G
3	C	15	U
3	C	16	G
3	C	17	U
3	G	4	C
3	G	5	C
3	G	6	U
3	G	13	G
3	G	15	U

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Mol	Chain	Res	Type
3	G	16	G
3	G	17	U
3	K	4	C
3	K	5	C
3	K	12	A
3	K	13	G
3	K	15	U
3	K	16	G
3	K	17	U
3	O	4	C
3	O	5	C
3	O	6	U
3	O	13	G
3	O	15	U
3	O	16	G
3	O	17	U

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	AMP	M	601	-	25,25,25	1.41	4 (16%)	37,38,38	2.05	12 (32%)
6	AMP	E	601	-	25,25,25	1.39	5 (20%)	37,38,38	2.01	11 (29%)

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	AMP	M	601	-	-	5/10/26/26	0/3/3/3
6	AMP	E	601	-	-	3/10/26/26	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	M	601	AMP	C5-C4	4.30	1.46	1.39
6	E	601	AMP	C5-C4	4.18	1.46	1.39
6	E	601	AMP	C5-N7	-2.61	1.34	1.39
6	M	601	AMP	C5-N7	-2.53	1.34	1.39
6	M	601	AMP	C5-C6	2.51	1.48	1.41
6	E	601	AMP	C5-C6	2.44	1.47	1.41
6	E	601	AMP	C8-N7	2.26	1.36	1.31
6	M	601	AMP	C8-N7	2.25	1.36	1.31
6	E	601	AMP	C4-N9	-2.01	1.33	1.37

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	601	AMP	C5-C4-N3	-5.94	118.54	126.72
6	M	601	AMP	C5-C4-N3	-5.74	118.81	126.72
6	E	601	AMP	N3-C4-N9	4.60	134.99	127.17
6	M	601	AMP	N3-C4-N9	4.49	134.81	127.17
6	M	601	AMP	N3-C2-N1	-4.03	122.48	128.58
6	E	601	AMP	C2-N3-C4	3.98	121.55	111.83
6	M	601	AMP	C2-N3-C4	3.97	121.53	111.83
6	E	601	AMP	N3-C2-N1	-3.81	122.82	128.58
6	E	601	AMP	C4-C5-N7	-3.53	106.55	110.58
6	M	601	AMP	C4-C5-N7	-3.49	106.59	110.58
6	M	601	AMP	O4'-C1'-N9	2.94	113.74	108.09
6	E	601	AMP	C5-N7-C8	2.71	107.71	103.45
6	E	601	AMP	C4-N9-C8	2.70	108.57	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	M	601	AMP	C4-N9-C8	2.69	108.56	105.74
6	M	601	AMP	C5-N7-C8	2.63	107.58	103.45
6	M	601	AMP	C2-N1-C6	2.33	122.55	118.73
6	E	601	AMP	N9-C8-N7	-2.28	110.70	113.94
6	M	601	AMP	C6-C5-N7	2.27	136.46	132.09
6	M	601	AMP	N9-C8-N7	-2.15	110.89	113.94
6	E	601	AMP	C6-C5-N7	2.15	136.23	132.09
6	E	601	AMP	C2-N1-C6	2.10	122.18	118.73
6	E	601	AMP	C3'-C2'-C1'	2.01	105.27	101.46
6	M	601	AMP	O3P-P-O2P	2.01	115.33	107.80

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	E	601	AMP	C5'-O5'-P-O1P
6	E	601	AMP	C5'-O5'-P-O2P
6	E	601	AMP	C5'-O5'-P-O3P
6	M	601	AMP	C3'-C4'-C5'-O5'
6	M	601	AMP	O4'-C4'-C5'-O5'
6	M	601	AMP	C2'-C1'-N9-C8
6	M	601	AMP	C2'-C1'-N9-C4
6	M	601	AMP	O4'-C1'-N9-C8

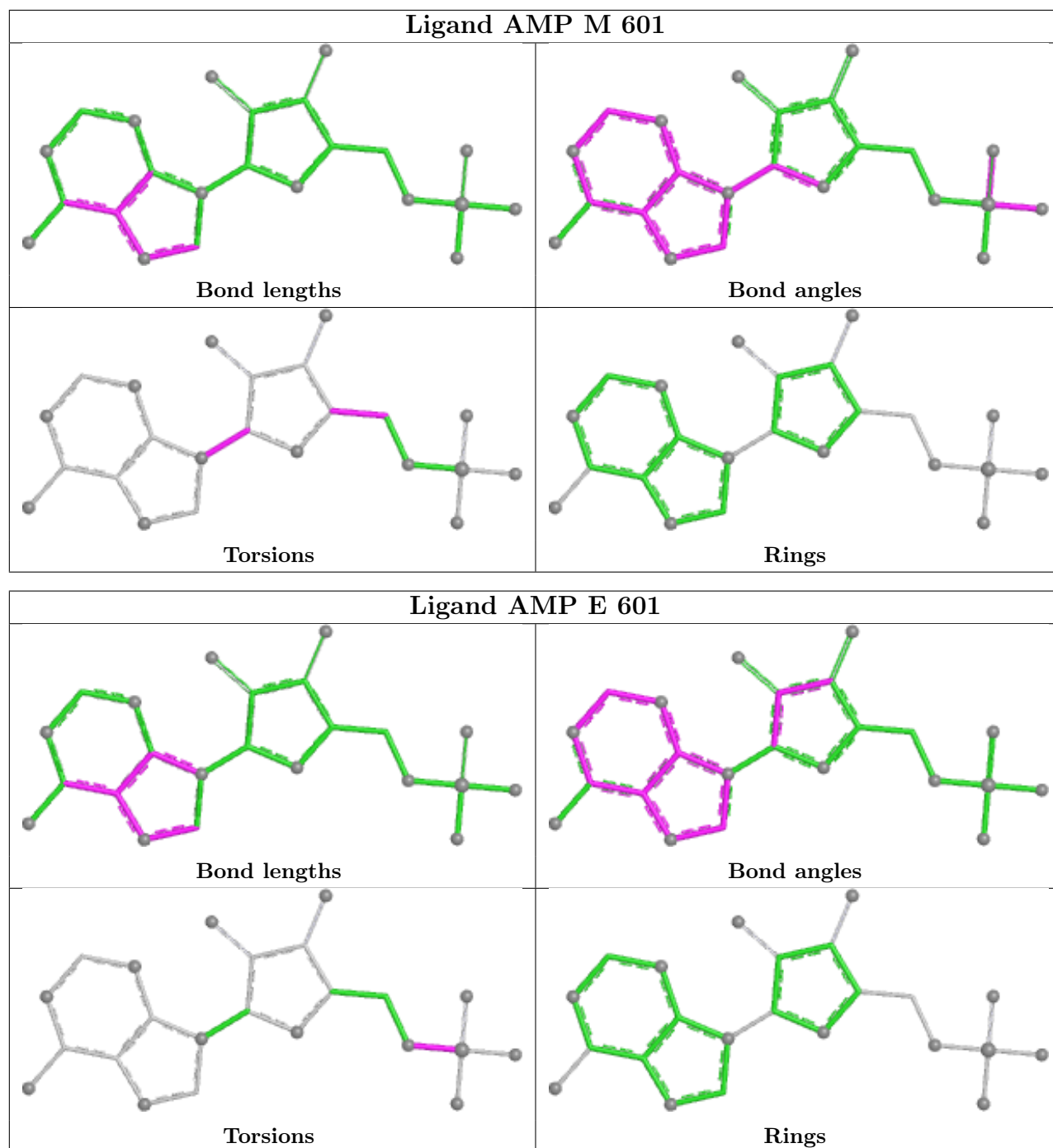
There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	M	601	AMP	11	0
6	E	601	AMP	4	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

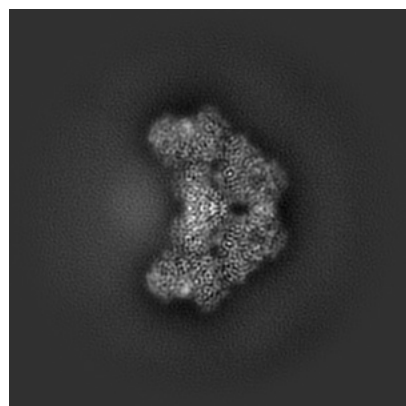
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39030. These allow visual inspection of the internal detail of the map and identification of artifacts.

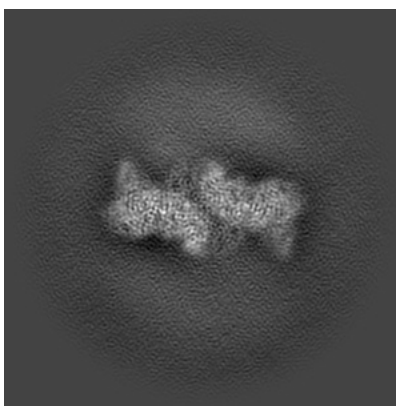
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

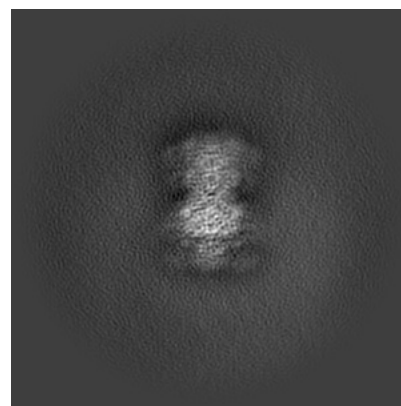
6.1.1 Primary map



X

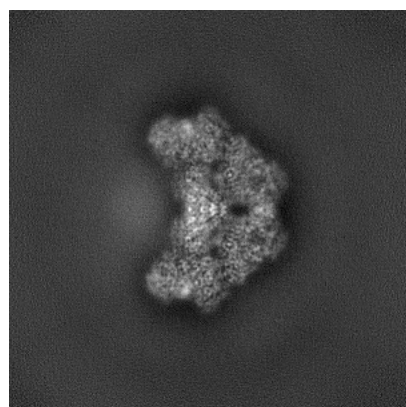


Y

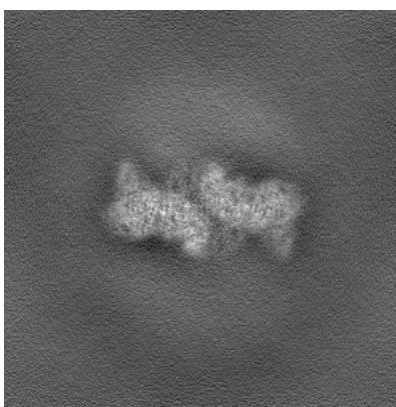


Z

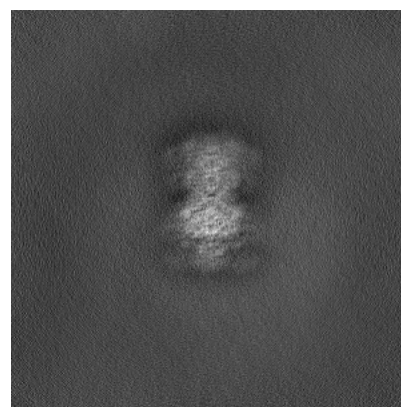
6.1.2 Raw map



X



Y

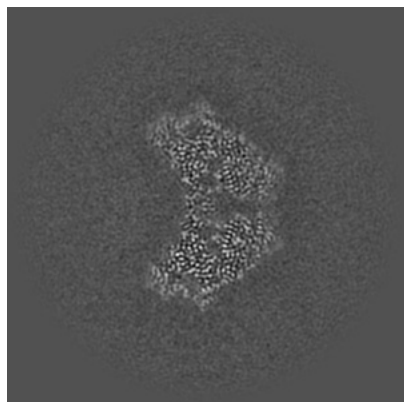


Z

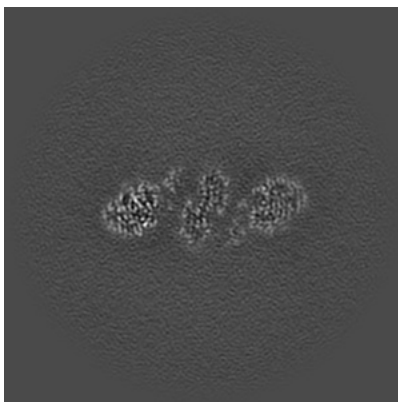
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 230

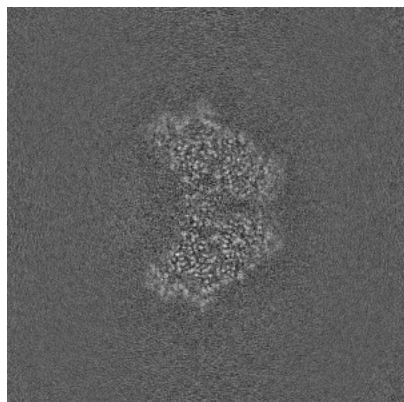


Y Index: 230

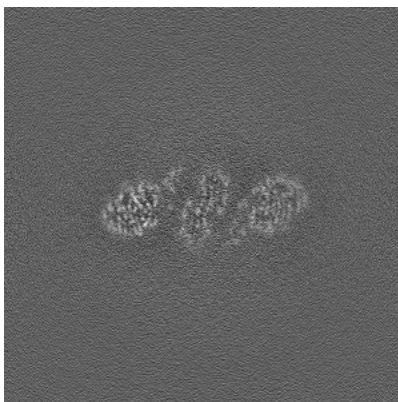


Z Index: 230

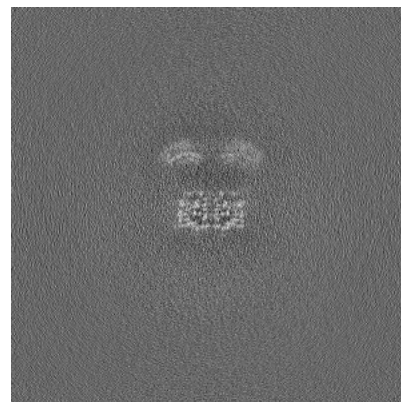
6.2.2 Raw map



X Index: 230



Y Index: 230

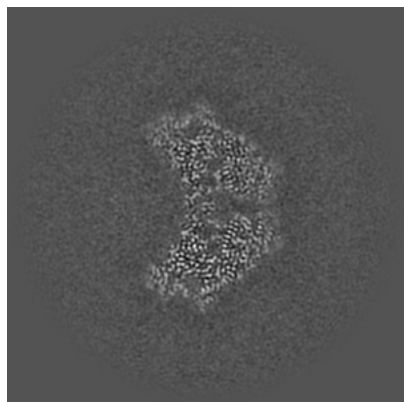


Z Index: 230

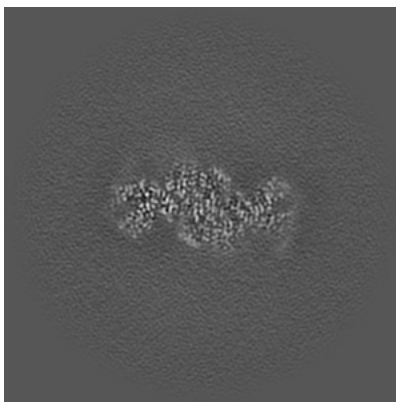
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 229

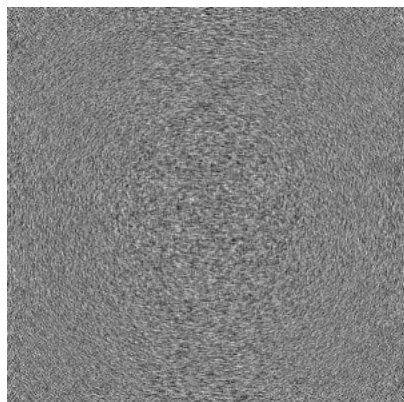


Y Index: 213

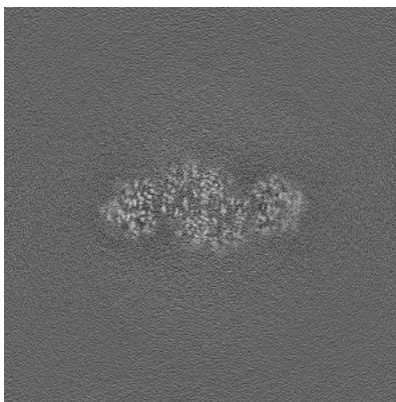


Z Index: 167

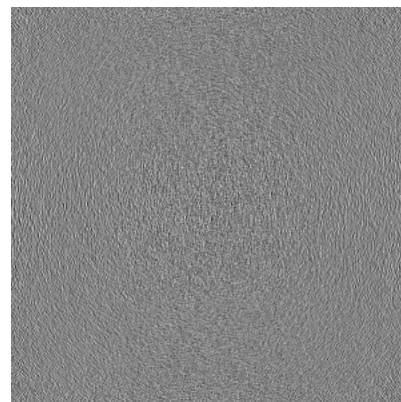
6.3.2 Raw map



X Index: 0



Y Index: 221

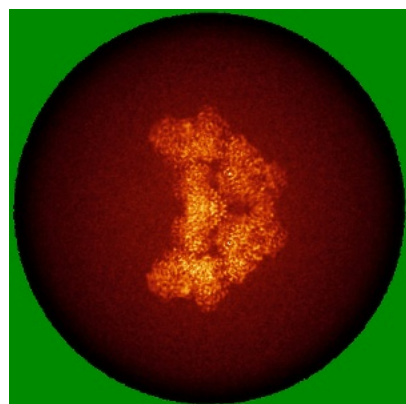


Z Index: 0

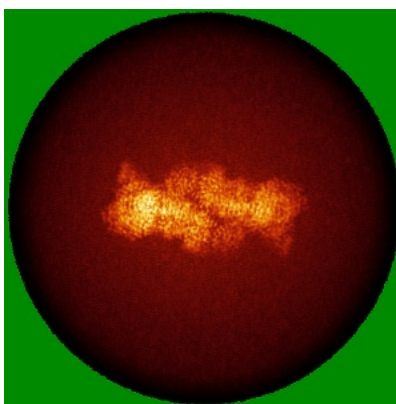
The images above show the largest variance slices of the map in three orthogonal directions.

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

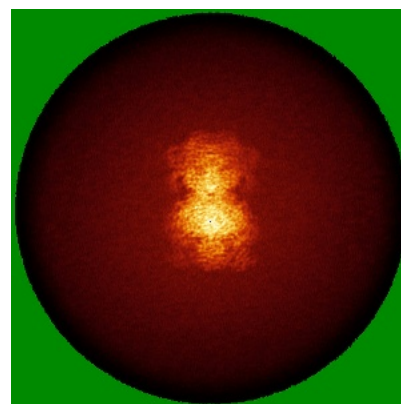
6.4.1 Primary map



X

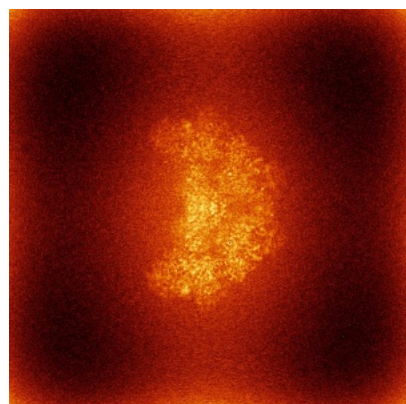


Y

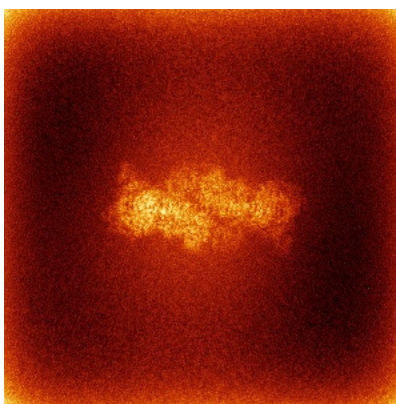


Z

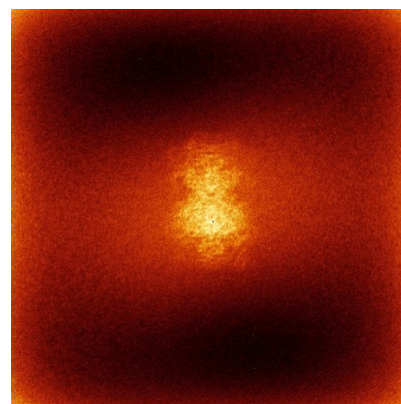
6.4.2 Raw map



X



Y

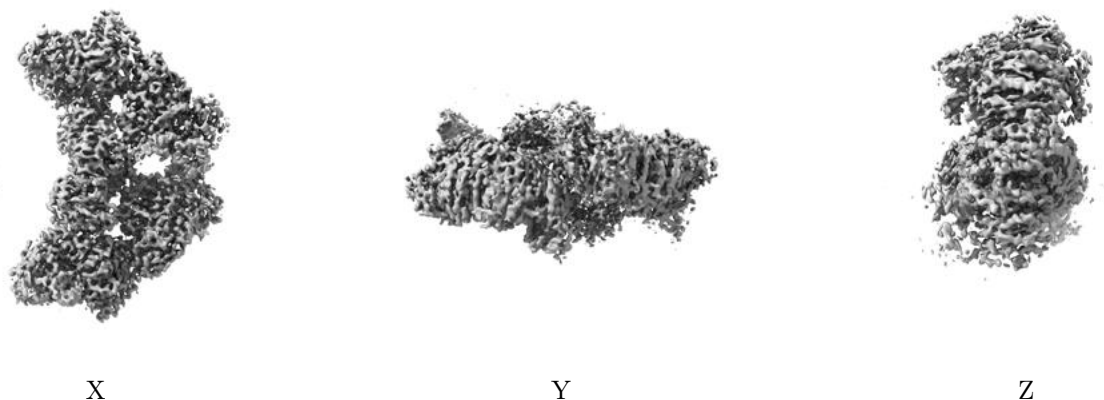


Z

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

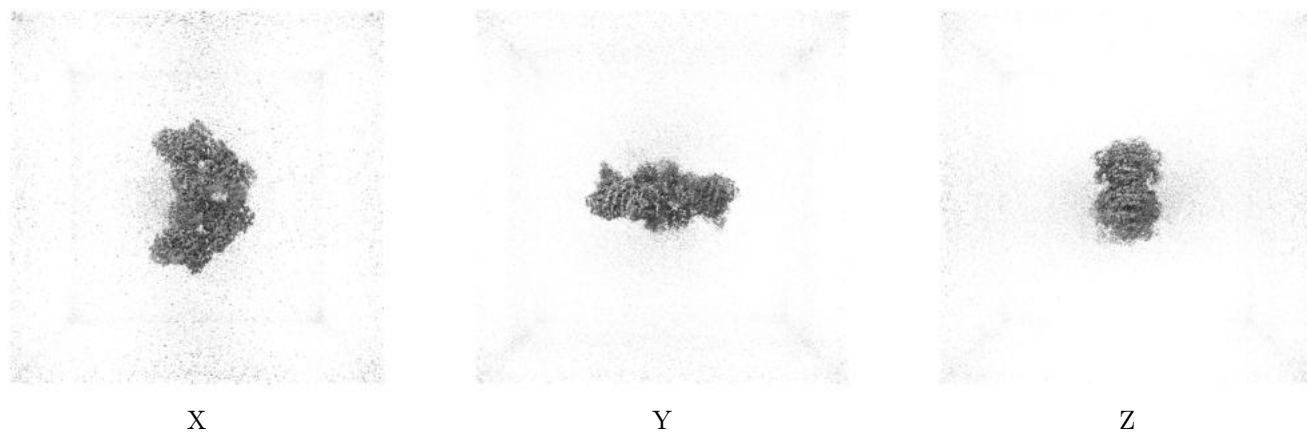
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.375. 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.

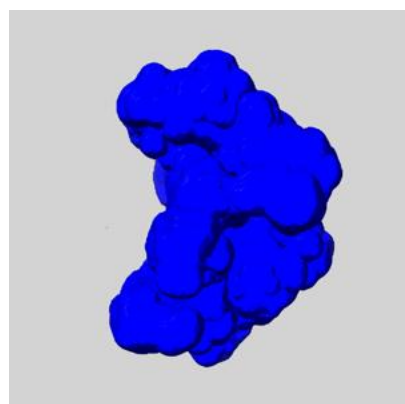
6.6 Mask visualisation [i](#)

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

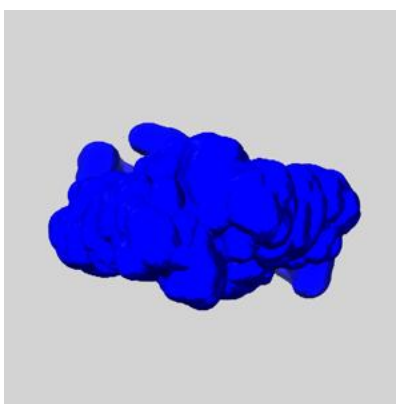
A mask typically either:

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

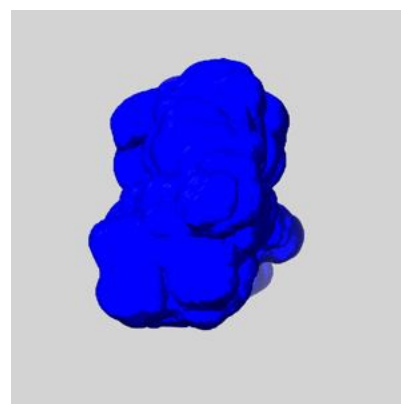
6.6.1 emd_39030_msk_1.map [i](#)



X



Y

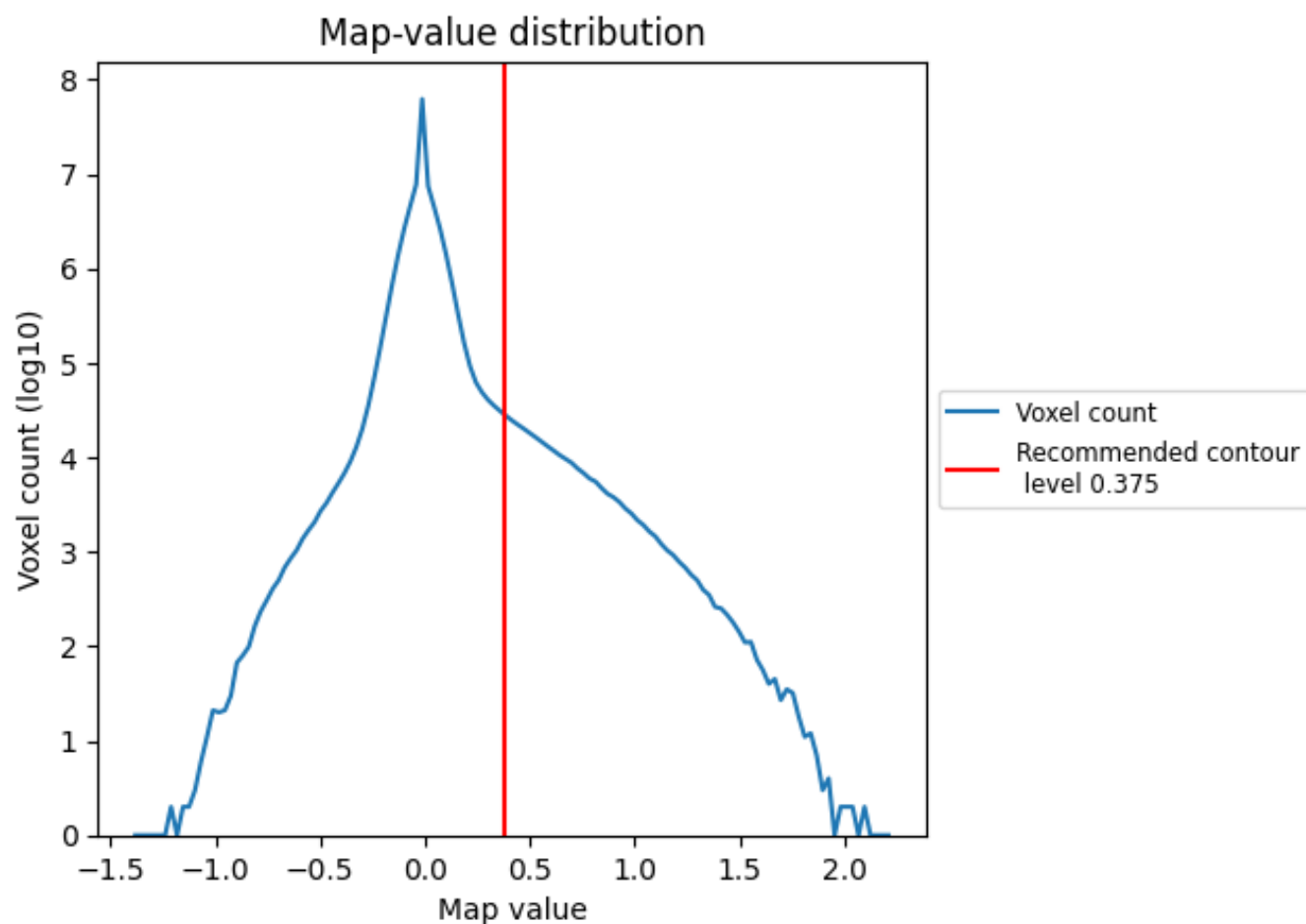


Z

7 Map analysis [i](#)

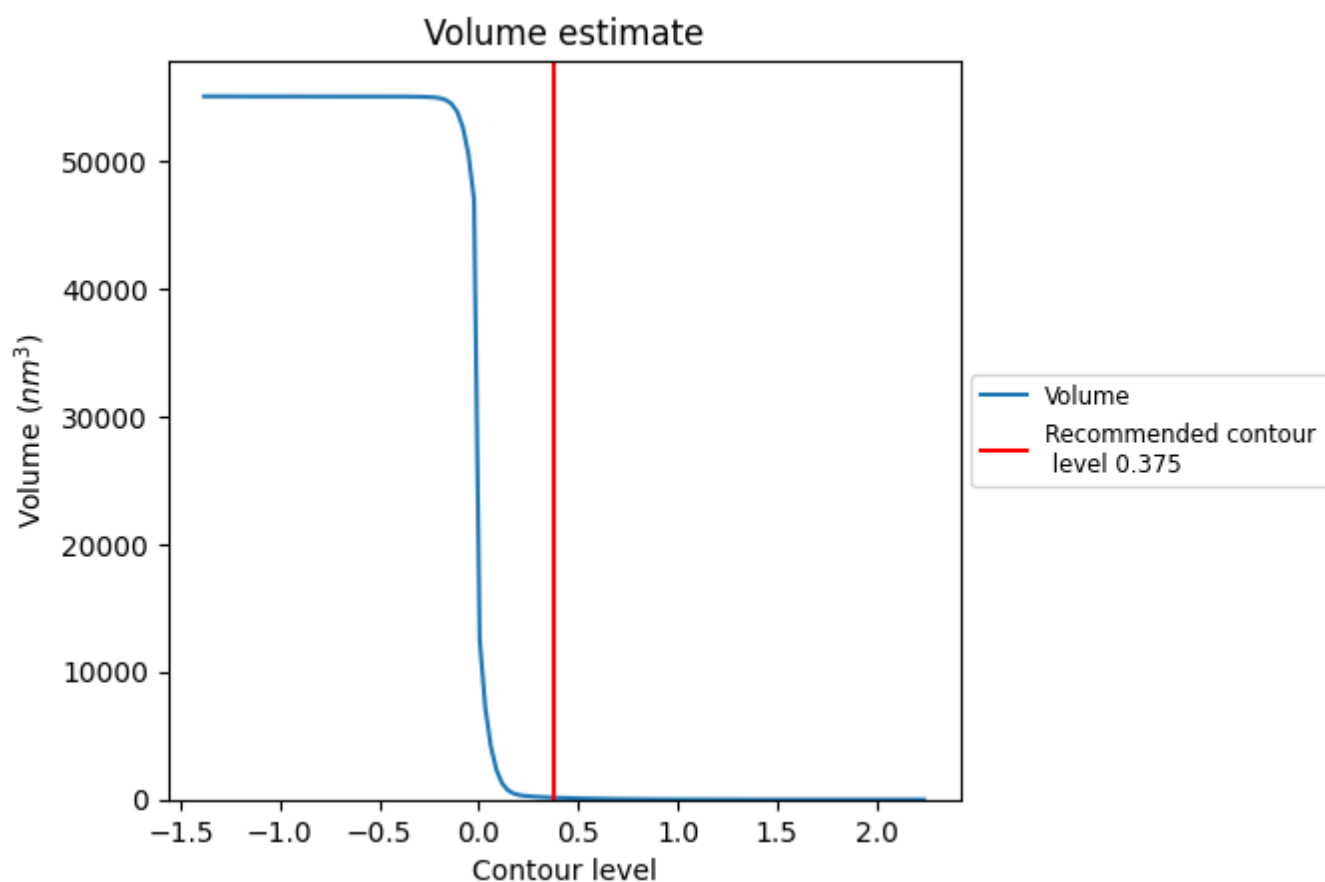
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

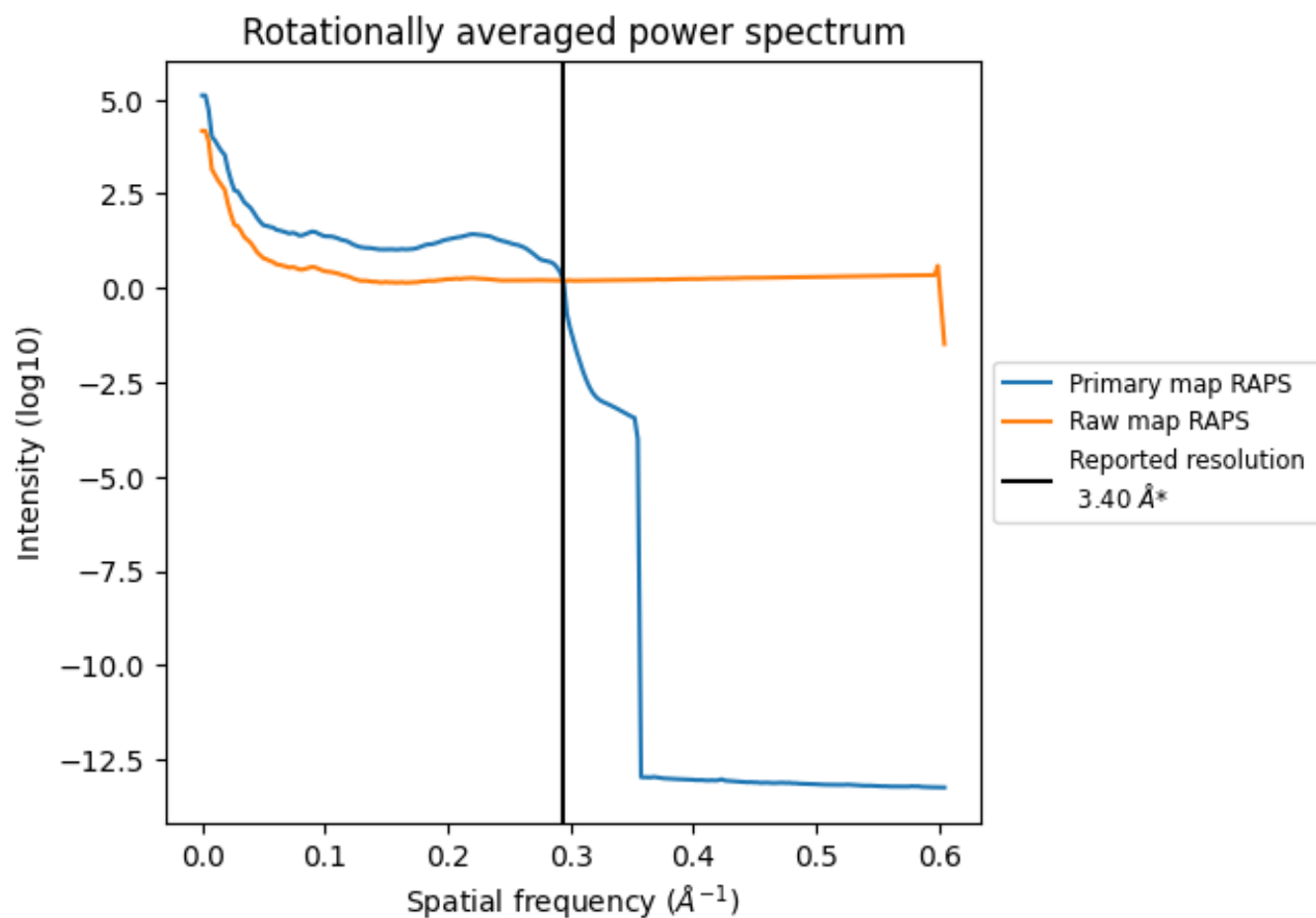
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 153 nm³; this corresponds to an approximate mass of 139 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 ⓘ

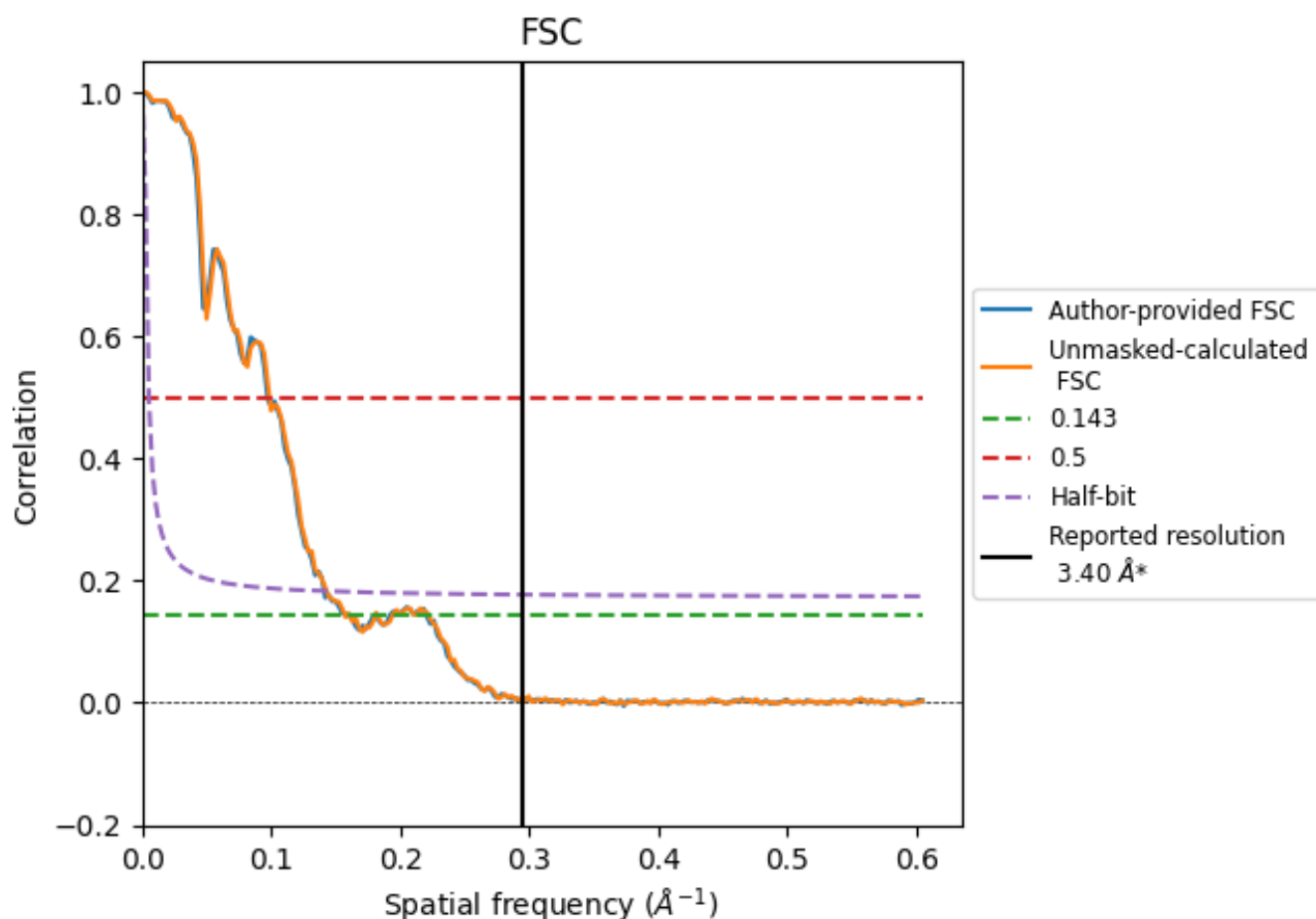


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 $0.294 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	6.23	10.30	7.09
Unmasked-calculated*	6.36	10.14	6.99

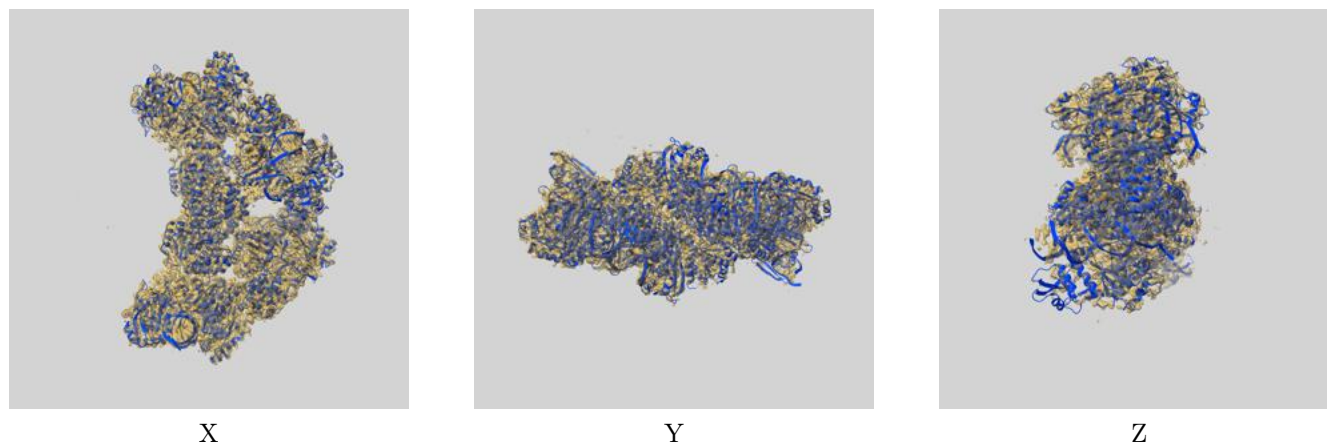
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 6.23 differs from the reported value 3.4 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.36 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

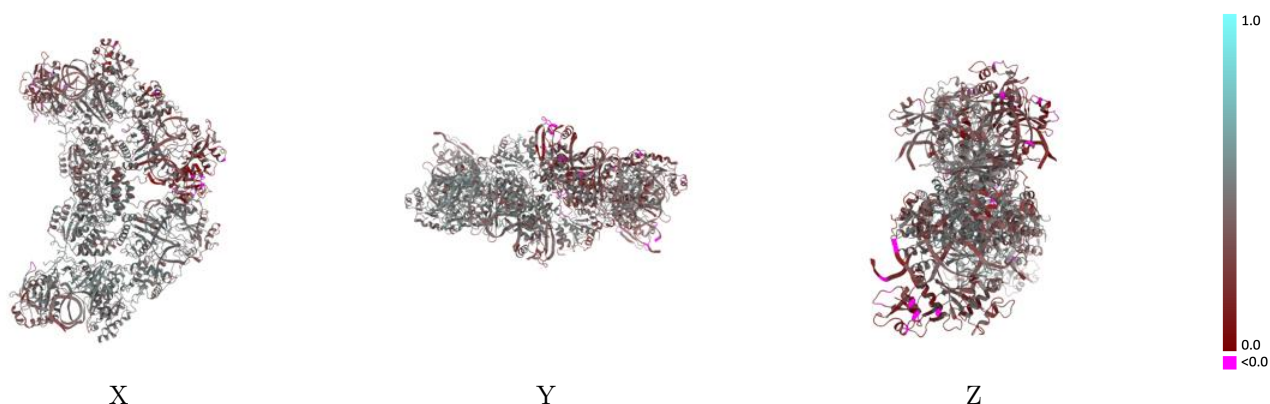
This section contains information regarding the fit between EMDB map EMD-39030 and PDB model 8Y82. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



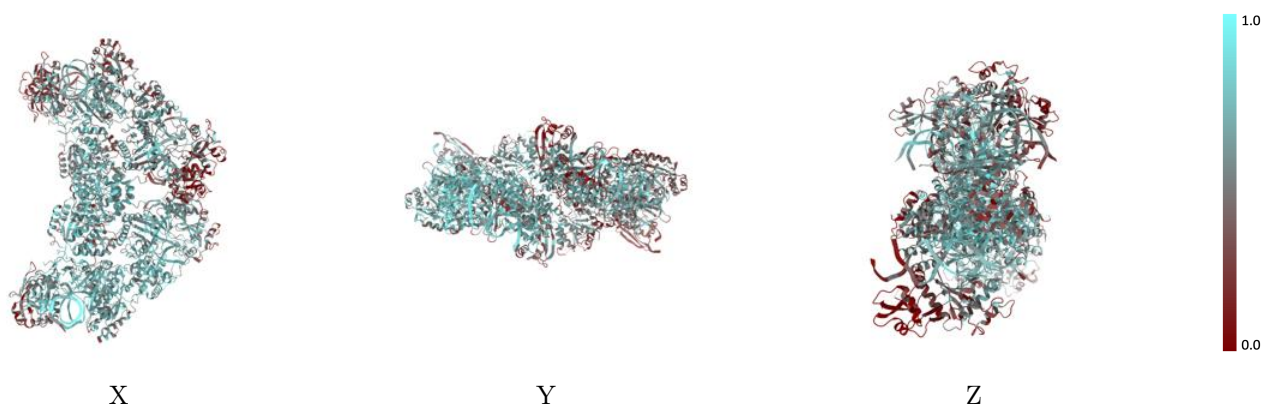
The images above show the 3D surface view of the map at the recommended contour level 0.375 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



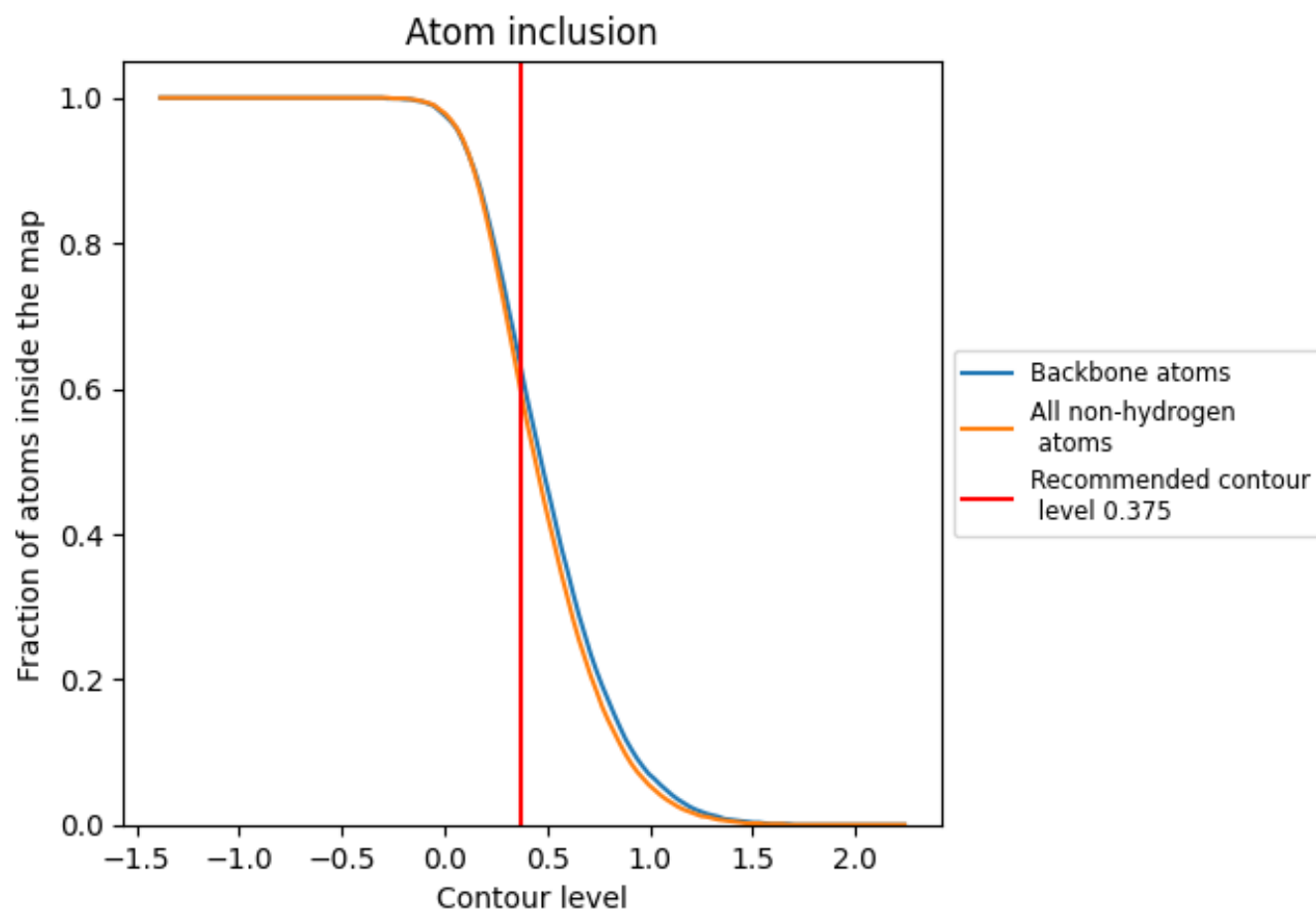
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.375).

9.4 Atom inclusion ⓘ



At the recommended contour level, 62% of all backbone atoms, 59% 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 (0.375) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5910	0.4120
A	0.5890	0.4460
B	0.7180	0.4940
C	0.7970	0.4130
D	0.8080	0.4270
E	0.6400	0.4540
F	0.7060	0.4860
G	0.8010	0.4130
H	0.8130	0.4120
I	0.3850	0.3320
J	0.5690	0.4080
K	0.5850	0.2950
L	0.5520	0.3180
M	0.5200	0.3460
N	0.5580	0.3840
O	0.6130	0.3050
P	0.6010	0.3200

