



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 08:19 AM UTC

PDB ID : 9WBZ / pdb_00009wbz
EMDB ID : EMD-65851
Title : The structure of NCP-motor-ARP module of ncBAF-nucleosome complex
Authors : Chen, K.J.; Chen, Z.C.
Deposited on : 2025-08-15
Resolution : 2.90 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
MolProbity : 4-5-2 with Phenix2.0
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

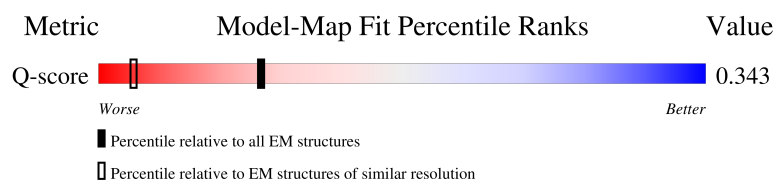
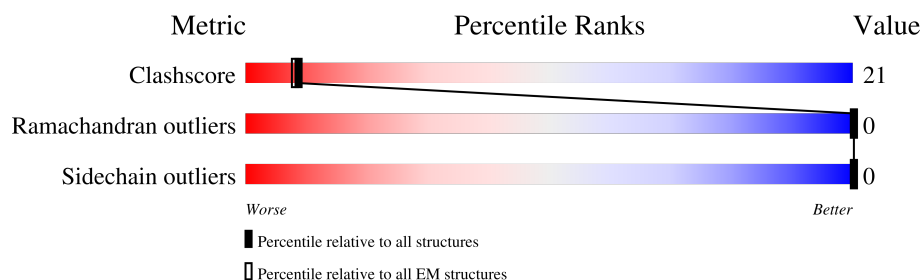
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 Å.

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




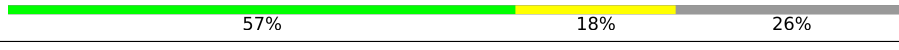
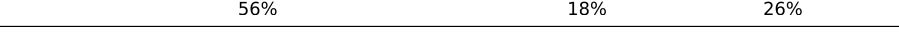

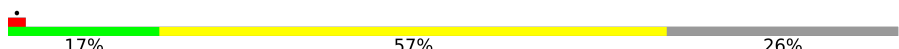
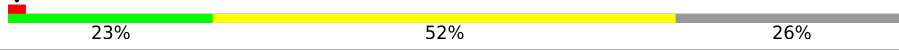

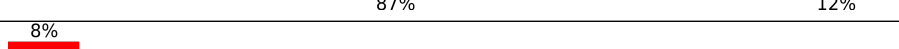


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	1614	
2	B	102	
2	F	102	
3	C	129	

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Mol	Chain	Length	Quality of chain
3	G	129	
4	D	125	
4	H	125	
5	E	135	
5	K	135	
6	I	207	
7	J	207	
8	L	375	
9	N	429	
10	O	210	

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 31470 atoms, of which 6897 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 Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	681	Total	C	H	N	O	S	0	0
			6178	3567	569	999	1016	27		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	F	86	Total	C	N	O	S	0	0
			672	424	130	117	1		

- Molecule 3 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	107	Total	C	N	O	0	0
			811	510	158	143		
3	G	108	Total	C	N	O	0	0
			828	522	162	144		

- Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	93	Total	C	N	O	S	0	0
			717	450	128	137	2		
4	H	93	Total	C	N	O	S	0	0
			725	456	130	137	2		

- Molecule 5 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	95	Total	C	N	O	S	0	0
			779	492	148	136	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	98	Total	C	N	O	S	0	0
			801	506	153	139	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	102	ALA	GLY	conflict	UNP P84233
K	102	ALA	GLY	conflict	UNP P84233

- Molecule 6 is a DNA chain called DNA (207-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	154	Total	C	N	O	P	0	0
			3139	1489	572	924	154		

- Molecule 7 is a DNA chain called DNA (207-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	154	Total	C	N	O	P	0	0
			3175	1501	596	924	154		

- Molecule 8 is a protein called Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
8	L	375	Total	C	H	N	O	S	0	0
			5816	1850	2891	491	561	23		

- Molecule 9 is a protein called Actin-like protein 6A.

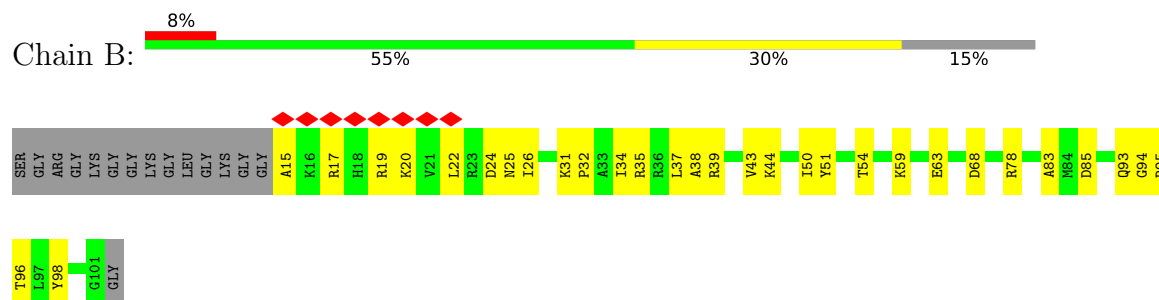
Mol	Chain	Residues	Atoms					AltConf	Trace	
9	N	427	Total	C	H	N	O	S	0	0
			6555	2086	3242	565	637	25		

- Molecule 10 is a protein called B-cell CLL/lymphoma 7 protein family member A.

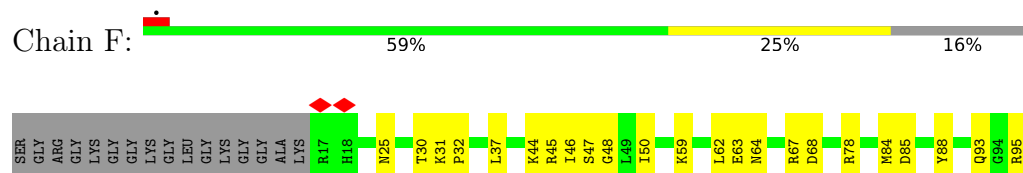
Mol	Chain	Residues	Atoms					AltConf	Trace	
10	O	44	Total	C	H	N	O	S	0	0
			571	240	195	72	63	1		

VAL	LYS	GLN	CYS	LYS	ARG	ASP	D1257	I1193	L1126	L1063	I996	K934	L370	R801	A735	GLN
LYS	ASP	ASP	GLN	ASP	LYS	ASP	E1258	Q1196	D1127	G1064	K997	S935	A871	I902	H736	ALA
SER	SER	ALA	ASP	ARG	ARG	GLU	E1259	N1197	G1128	F1065	C998	C936	K372	N903	A737	ALA
SER	SER	VAL	VAL	GLY	ASP	GLU	E1260	E1198	T1129	T1066	S937	S937	I873	P905	V739	PRO
GLY	ARG	ALA	ASP	ARG	ALA	ARG	D1261	R1199	D1134	G1067	V1006	T938	M875	R874	E740	THR
LEU	GLY	LEU	LEU	GLY	GLY	THR	V1263	V1201	R1135	I1069	V1009	F939	K376	L807	R741	LEU
THR	THR	THR	THR	CYS	GLY	CYS	F1264	M1137	G1136	Q1071	R1009	Q941	Y877	I809	V742	VAL
GLY	SER	SER	GLY	GLY	GLY	GLY	F1265	L1138	L1138	L1073	H1010	V942	M878	V810	D743	VAL
GLY	SER	THR	GLY	GLY	GLY	GLY	E1267	L1139	K1140	D1074	V1016	F943	I879	V880	K744	GLY
GLY	THR	THR	GLY	THR	THR	GLY	T1268	T1141	L1075	L1076	G1015	N944	V881	L815	A747	GLY
GLY	THR	THR	GLY	THR	THR	GLY	V1269	F1142	R1077	R1077	V1016	A945	M886	A819	Q745	GLY
GLY	THR	THR	GLY	THR	THR	GLY	N1270	N1143	A1078	A1078	L1017	P946	K887	Y820	K746	GLY
GLY	THR	THR	GLY	THR	THR	GLY	I1211	G1146	S1079	S1079	L1017	F947	N888	Y820	S746	LYS
GLY	THR	THR	GLY	THR	THR	GLY	E1212	E1147	A1080	A1080	L1018	A948	E821	M749	A748	LYS
GLY	THR	THR	GLY	THR	THR	GLY	K1213	E1148	G1081	G1081	L1019	T950	H889	F822	L748	LYS
GLY	THR	THR	GLY	THR	THR	GLY	I1214	E1149	K1082	K1082	L1020	T950	H890	D823	V750	PRO
GLY	THR	THR	GLY	THR	THR	GLY	A1218	E1150	E1083	E1083	S1022	G951	C891	A826	Q755	SER
GLY	THR	THR	GLY	THR	THR	GLY	K1219	F1151	L1084	L1084	GLY	E952	K892	A826	Q756	ASP
GLY	THR	THR	GLY	THR	THR	GLY	I1220	E1152	L1085	L1085	GLY	K953	L893	P827	Y757	ASP
GLY	THR	THR	GLY	THR	THR	GLY	K1221	L1153	D1086	D1086	GLY	T954	T894	Q758	VAL	VAL
GLY	THR	THR	GLY	THR	THR	GLY	L1222	L1154	R1087	R1087	GLY	D955	Q895	V829	K760	GLY
GLY	THR	THR	GLY	THR	THR	GLY	M1223	S1155	L1088	L1088	GLY	L956	V954	V830	G761	VAL
GLY	THR	THR	GLY	THR	THR	GLY	V1224	L1156	L1089	L1089	GLY	N957	K831	V831	L762	ASP
GLY	THR	THR	GLY	THR	THR	GLY	F1225	R1157	F1090	F1090	GLY	E958	Y834	Y834	L764	ALA
GLY	THR	THR	GLY	THR	THR	GLY	Q1226	A1158	K1091	K1091	GLY	E959	K835	K835	L765	ARG
GLY	THR	THR	GLY	THR	THR	GLY	M1227	G1159	L1094	L1094	GLY	V902	G836	G836	V766	HIS
GLY	THR	THR	GLY	THR	THR	GLY	G1160	T1095	T1095	T1095	GLY	A903	S837	S837	S767	ILE
GLY	THR	THR	GLY	THR	THR	GLY	L1161	N1096	N1096	N1096	GLY	R906	P838	P838	L768	GLY
GLY	THR	THR	GLY	THR	THR	GLY	G1162	H1097	H1097	H1097	GLY	T961	A839	A839	N771	ASN
GLY	THR	THR	GLY	THR	THR	GLY	M1164	K1098	K1098	K1098	GLY	I962	A840	A840	N772	ALA
GLY	THR	THR	GLY	THR	THR	GLY	L1165	L1099	L1099	L1099	GLY	L963	R841	R841	L773	LYS
GLY	THR	THR	GLY	THR	THR	GLY	Q1166	V1099	V1099	V1099	GLY	I964	R842	R842	N774	GLN
GLY	THR	THR	GLY	THR	THR	GLY	S1167	L1100	L1100	L1100	GLY	L965	A843	A843	G775	ASP
GLY	THR	THR	GLY	THR	THR	GLY	A1168	F1102	F1102	F1102	GLY	R966	A943	A943	V776	VAL
GLY	THR	THR	GLY	THR	THR	GLY	D1169	C1103	C1103	C1103	GLY	R967	P846	P846	I777	ASP
GLY	THR	THR	GLY	THR	THR	GLY	V1170	Q1104	Q1104	Q1104	GLY	L968	Q847	Q847	L777	ASP
GLY	THR	THR	GLY	THR	THR	GLY	V1171	M1105	M1105	M1105	GLY	H969	L848	L848	A778	TYR
GLY	THR	THR	GLY	THR	THR	GLY	I1172	L1106	L1106	L1106	GLY	K370	N916	N916	D779	GLY
GLY	THR	THR	GLY	THR	THR	GLY	F1173	S1107	S1107	S1107	GLY	V971	K917	K917	E780	VAL
GLY	THR	THR	GLY	THR	THR	GLY	F1174	L1108	L1108	L1108	GLY	L972	N854	N854	M781	VAL
GLY	THR	THR	GLY	THR	THR	GLY	D1177	M1109	M1109	M1109	GLY	R973	V855	V855	G782	SER
GLY	THR	THR	GLY	THR	THR	GLY	W1178	T1110	T1110	T1110	GLY	P974	L856	L856	L783	GLN
GLY	THR	THR	GLY	THR	THR	GLY	M1179	I1111	I1111	I1111	GLY	F975	L857	L857	G784	ALA
GLY	THR	THR	GLY	THR	THR	GLY	P1180	M1112	M1112	M1112	GLY	L976	T858	T858	K785	LEU
GLY	THR	THR	GLY	THR	THR	GLY	Q1185	E1113	E1113	E1113	GLY	V922	T859	T859	T786	ARG
GLY	THR	THR	GLY	THR	THR	GLY	A1188	F1114	F1114	F1114	GLY	L977	Y860	Y860	Q788	GLY
GLY	THR	THR	GLY	THR	THR	GLY	Q1187	D1115	D1115	D1115	GLY	R979	E861	E861	T789	LEU
GLY	THR	THR	GLY	THR	THR	GLY	D1188	F1116	F1116	F1116	GLY	L980	Y862	Y862	I790	GLN
GLY	THR	THR	GLY	THR	THR	GLY	R1189	E1117	E1117	E1117	GLY	K981	I863	I863	T791	SER
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GLY	THR	THR	GLY	THR	THR	GLY	H1191	K1122	K1122	K1122	GLY	E985	L929	L929	A793	VAL
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GLY	THR	THR	GLY	THR	THR	GLY	E1255	L1251	L1251	L1251	GLY	K990	D866	D866	M797	LYS
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GLY	THR	THR	GLY	THR	THR	GLY	E1256	L1254	L1254	L1254	GLY	E993	P933	P933	K800	VAL
GLY	THR	THR	GLY	THR	THR	GLY	E1256	R1125	R1125	R1125	GLY	Y994	I932	I932	V734	VAL
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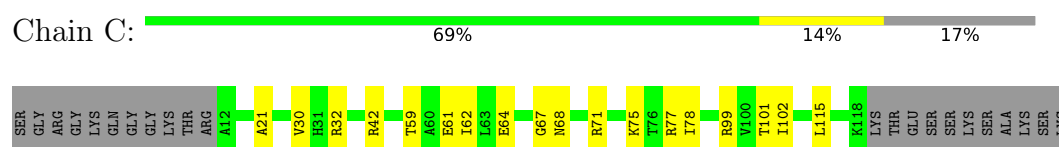
- Molecule 2: Histone H4



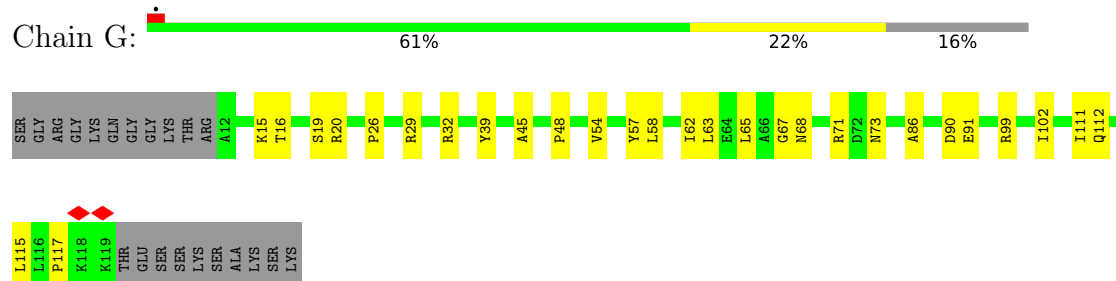
- Molecule 2: Histone H4



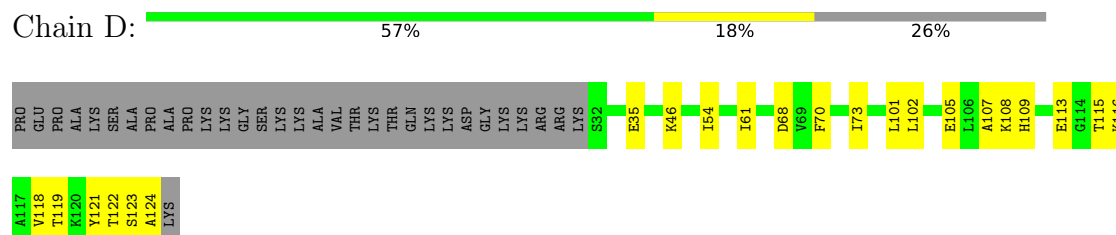
- Molecule 3: Histone H2A



- Molecule 3: Histone H2A

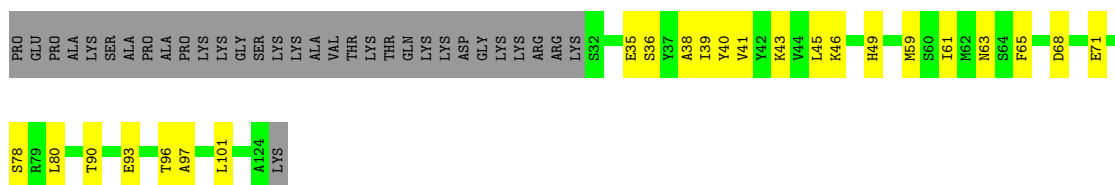


- Molecule 4: Histone H2B 1.1



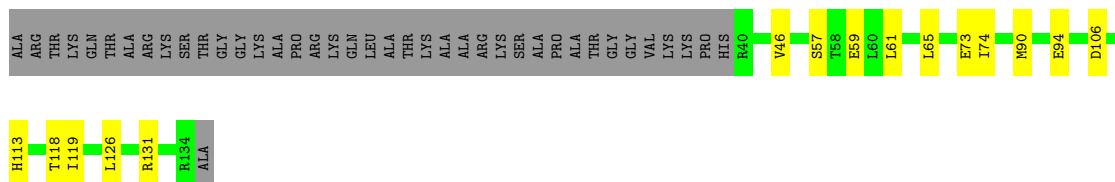
- Molecule 4: Histone H2B 1.1





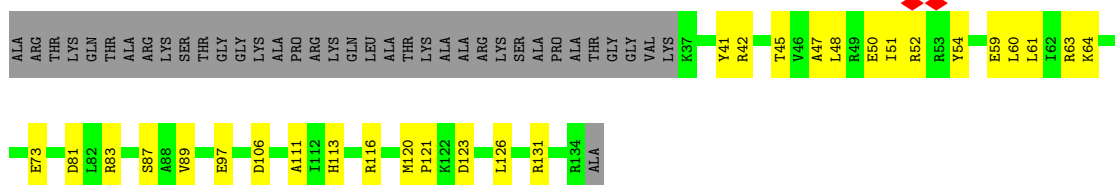
• Molecule 5: Histone H3.2

Chain E: 59% 11% 30%



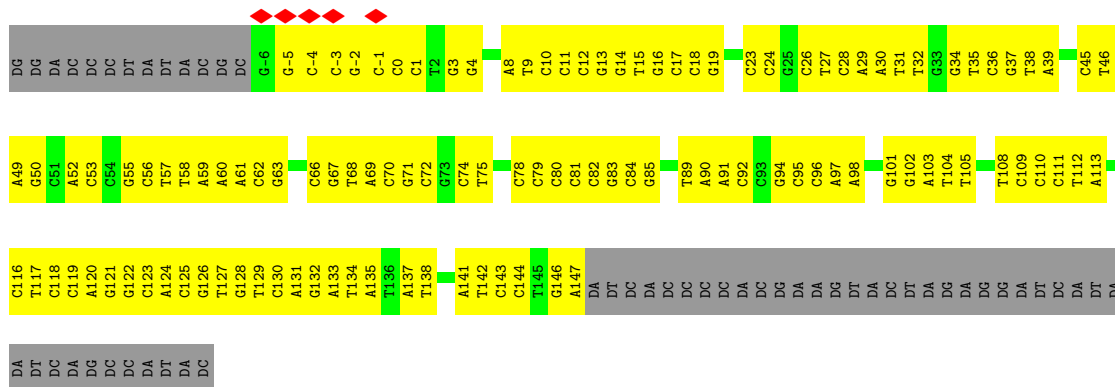
• Molecule 5: Histone H3.2

Chain K: 50% 22% 27%



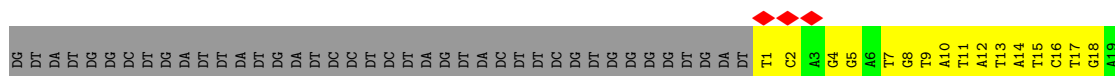
• Molecule 6: DNA (207-MER)

Chain I: 17% 57% 26%

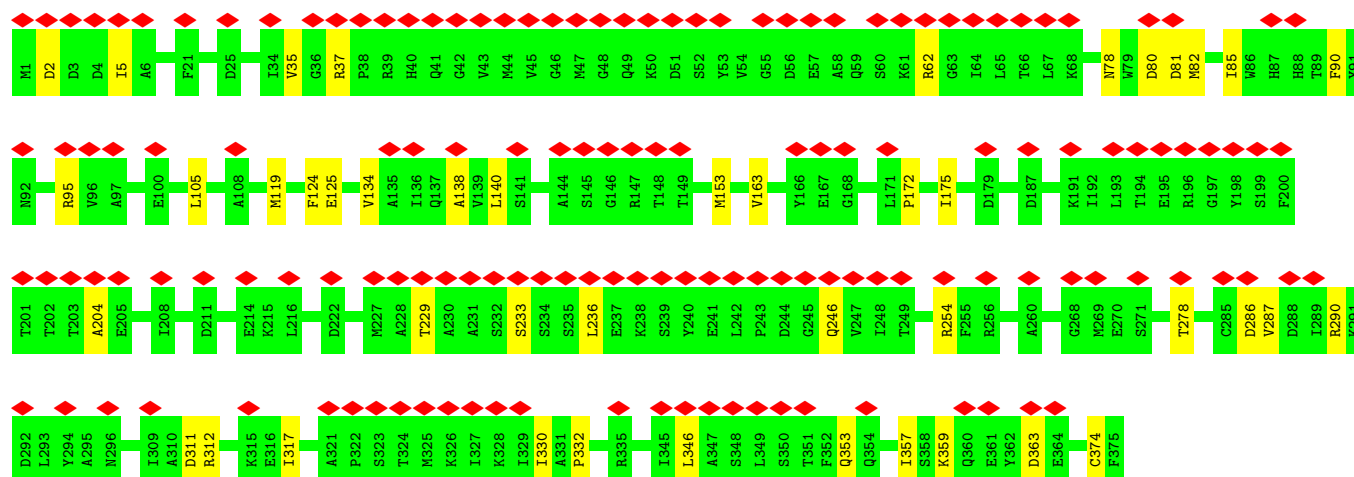
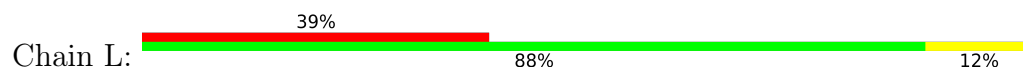


• Molecule 7: DNA (207-MER)

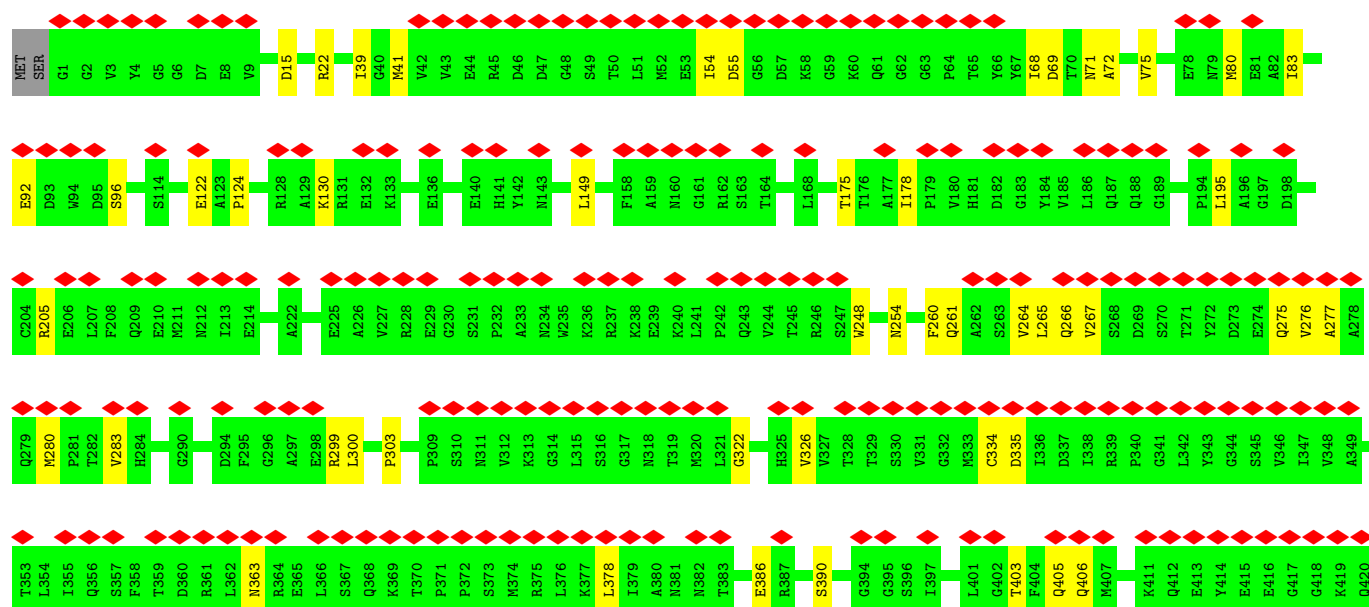
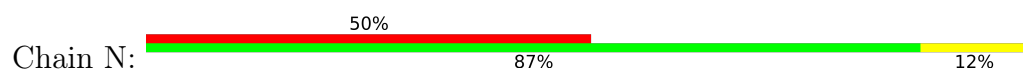
Chain J: 23% 52% 26%

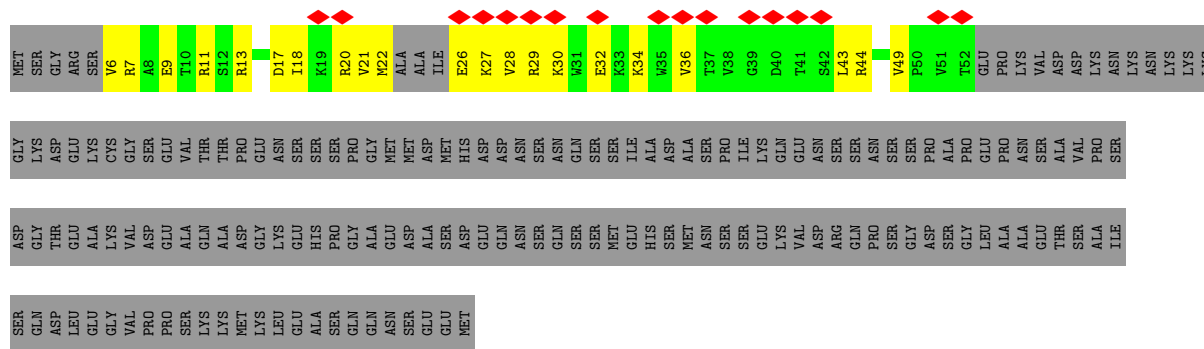


- Molecule 8: Actin, cytoplasmic 1



- Molecule 9: Actin-like protein 6A





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	175820	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.664	Depositor
Minimum map value	-0.242	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	389.69998, 389.69998, 389.69998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.0825, 1.0825, 1.0825	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.09	0/5715	0.26	0/7683
2	B	0.17	0/711	0.27	0/950
2	F	0.17	0/680	0.28	0/912
3	C	0.14	0/821	0.23	0/1112
3	G	0.14	0/838	0.27	0/1131
4	D	0.15	0/728	0.28	0/983
4	H	0.15	0/736	0.24	0/991
5	E	0.15	0/789	0.24	0/1059
5	K	0.15	0/813	0.27	0/1093
6	I	0.20	0/3517	0.36	0/5421
7	J	0.20	0/3565	0.33	0/5505
8	L	0.09	0/2988	0.23	0/4045
9	N	0.10	0/3386	0.26	0/4587
10	O	0.11	0/382	0.36	0/511
All	All	0.14	0/25669	0.29	0/35983

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5609	569	5687	481	0
2	B	703	0	757	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	672	0	698	20	0
3	C	811	0	849	25	0
3	G	828	0	884	31	0
4	D	717	0	723	24	0
4	H	725	0	745	22	0
5	E	779	0	815	14	0
5	K	801	0	831	34	0
6	I	3139	0	1727	165	0
7	J	3175	0	1727	150	0
8	L	2925	2891	2891	36	0
9	N	3313	3242	3244	31	0
10	O	376	195	399	23	0
All	All	24573	6897	21977	984	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 (984) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:780:GLU:HB2	1:A:783:LEU:HD13	1.31	1.09
1:A:994:TYR:HB2	1:A:1272:MET:HE3	1.26	1.09
1:A:1088:ILE:HD12	1:A:1273:ILE:HD11	1.33	1.08
7:J:49:DC:H2''	7:J:50:DT:H71	1.39	1.04
6:I:13:DG:H2''	6:I:14:DG:H5''	1.40	1.03
2:B:44:LYS:HB2	3:G:115:LEU:HD23	1.40	1.01
1:A:1265:ASP:HB3	1:A:1268:THR:HB	1.44	0.99
6:I:47:DC:H2''	6:I:48:DT:H71	1.44	0.98
3:G:111:ILE:HD11	5:K:51:ILE:HG21	1.43	0.97
1:A:1310:LEU:HD23	1:A:1312:SER:H	1.30	0.94
7:J:95:DG:H2''	7:J:96:DT:H5'	1.49	0.94
1:A:756:GLN:HE22	1:A:760:LYS:HE2	1.33	0.94
1:A:921:LEU:HD11	1:A:1229:ILE:HD11	1.49	0.94
1:A:966:ARG:HD2	1:A:1244:ARG:HG2	1.47	0.94
1:A:914:LEU:HD11	1:A:918:LEU:HA	1.50	0.93
7:J:117:DA:H1'	7:J:118:DT:H5'	1.50	0.93
1:A:1088:ILE:HG23	1:A:1273:ILE:HD13	1.50	0.92
6:I:95:DC:O2	7:J:53:DG:N2	2.02	0.91
6:I:14:DG:H2''	6:I:15:DT:H5''	1.52	0.91
6:I:95:DC:N3	7:J:53:DG:N1	2.19	0.91
7:J:135:DC:H2''	7:J:136:DG:H5''	1.53	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:I:14:DG:N2	7:J:134:DC:O2	2.04	0.89
6:I:53:DC:N3	7:J:95:DG:N1	2.20	0.89
8:L:119:MET:HE1	8:L:134:VAL:HG11	1.52	0.89
6:I:70:DC:O2	7:J:78:DG:N2	2.04	0.89
6:I:23:DC:N3	7:J:125:DG:N1	2.20	0.88
1:A:994:TYR:CB	1:A:1272:MET:HE3	2.02	0.88
6:I:125:DC:H2''	6:I:126:DG:H5''	1.54	0.88
1:A:1310:LEU:HG	1:A:1311:PRO:HD2	1.53	0.88
6:I:47:DC:H2''	6:I:48:DT:C7	2.03	0.88
6:I:74:DC:H2'	6:I:75:DT:H71	1.56	0.88
7:J:96:DT:H1'	7:J:97:DG:H5'	1.55	0.87
6:I:70:DC:N3	7:J:78:DG:N1	2.23	0.86
1:A:1300:ARG:HE	1:A:1301:LYS:H	1.20	0.86
2:F:68:ASP:OD2	2:F:93:GLN:NE2	2.08	0.86
4:H:38:ALA:HA	4:H:59:MET:HE2	1.55	0.86
1:A:878:MET:HE3	1:A:880:VAL:HG23	1.58	0.85
1:A:900:HIS:NE2	6:I:17:DC:OP1	2.09	0.85
6:I:37:DG:H2''	6:I:38:DT:H71	1.59	0.85
7:J:126:DC:H4'	7:J:127:DC:OP1	1.76	0.85
1:A:1084:LEU:O	1:A:1088:ILE:HG12	1.75	0.85
1:A:1275:ARG:N	1:A:1279:GLU:OE1	2.11	0.84
6:I:23:DC:O2	7:J:125:DG:N2	2.10	0.84
6:I:17:DC:H2''	6:I:18:DC:C5	2.12	0.84
1:A:977:LEU:HD11	1:A:979:ARG:HE	1.40	0.84
1:A:781:MET:O	1:A:1192:ARG:NH1	2.11	0.83
1:A:758:GLN:HA	1:A:788:GLN:HE21	1.42	0.83
1:A:953:LYS:HG2	1:A:1251:LEU:HB3	1.60	0.83
6:I:55:DG:H1'	6:I:56:DC:H5'	1.60	0.83
1:A:1208:ASN:N	1:A:1212:GLU:OE2	2.12	0.82
6:I:14:DG:N1	7:J:134:DC:N3	2.27	0.82
1:A:807:LEU:HD11	1:A:878:MET:HG3	1.60	0.82
10:O:32:GLU:OE2	10:O:34:LYS:NZ	2.14	0.81
5:K:106:ASP:OD2	5:K:131:ARG:NH1	2.12	0.81
1:A:1293:GLU:OE2	1:A:1296:ARG:NH2	2.14	0.81
1:A:981:LYS:NZ	1:A:1191:HIS:O	2.14	0.81
1:A:887:LYS:NZ	6:I:97:DA:OP2	2.10	0.80
1:A:765:LEU:HB3	1:A:792:LEU:HD12	1.63	0.80
3:G:112:GLN:HB2	3:G:115:LEU:HD13	1.61	0.80
1:A:1110:THR:HG22	2:B:17:ARG:HH21	1.44	0.79
1:A:893:LEU:HA	1:A:896:VAL:HG12	1.63	0.79
1:A:943:PHE:HA	1:A:956:LEU:HD21	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:735:ALA:O	1:A:771:ASN:ND2	2.15	0.79
1:A:1069:ILE:HD13	2:B:15:ALA:HA	1.62	0.79
3:C:78:ILE:HB	4:D:54:ILE:HD12	1.64	0.79
2:B:38:ALA:HB1	2:B:43:VAL:HG21	1.63	0.78
1:A:953:LYS:HE2	1:A:1251:LEU:HB3	1.64	0.78
7:J:123:DC:H2'	7:J:124:DG:C8	2.17	0.78
1:A:1076:TYR:OH	1:A:1301:LYS:NZ	2.14	0.77
6:I:31:DT:C6	6:I:32:DT:H72	2.19	0.77
4:H:41:VAL:HB	4:H:59:MET:HE1	1.66	0.77
9:N:280:MET:SD	9:N:300:LEU:HD11	2.25	0.77
1:A:979:ARG:HB3	1:A:984:VAL:HG21	1.67	0.76
2:B:38:ALA:HB1	2:B:43:VAL:CG2	2.15	0.76
1:A:1037:ASN:O	1:A:1041:GLN:HG2	1.85	0.76
7:J:49:DC:H2''	7:J:50:DT:C7	2.13	0.76
1:A:955:ASP:OD2	1:A:1227:LYS:NZ	2.18	0.76
10:O:21:VAL:HG13	10:O:22:MET:SD	2.25	0.76
1:A:929:LEU:HD22	1:A:933:PHE:HB2	1.67	0.76
1:A:1088:ILE:HD12	1:A:1273:ILE:CD1	2.14	0.76
1:A:1100:LEU:HD11	1:A:1171:VAL:HG22	1.68	0.76
3:G:102:ILE:HG23	4:H:61:ILE:HD13	1.68	0.76
3:G:111:ILE:CD1	5:K:51:ILE:HG21	2.15	0.76
6:I:116:DC:H2'	6:I:117:DT:H71	1.69	0.75
1:A:1288:LEU:HB3	1:A:1292:ARG:HH21	1.49	0.75
9:N:205:ARG:NH2	9:N:254:ASN:OD1	2.19	0.75
7:J:44:DA:H1'	7:J:45:DT:H5'	1.68	0.75
1:A:886:MET:HG3	1:A:894:THR:HG22	1.68	0.75
1:A:841:ARG:NE	1:A:866:ASP:OD2	2.19	0.75
1:A:878:MET:HE2	1:A:906:ARG:HB2	1.68	0.75
1:A:1083:GLU:O	1:A:1087:ARG:HG3	1.87	0.75
1:A:1202:LEU:HD22	1:A:1272:MET:HE2	1.69	0.75
6:I:12:DC:H2'	6:I:13:DG:C8	2.22	0.74
6:I:78:DC:H2''	6:I:79:DC:C5	2.22	0.74
1:A:1014:LYS:HG3	1:A:1016:VAL:HG12	1.69	0.74
7:J:69:DG:OP1	5:K:42:ARG:NH1	2.19	0.74
1:A:740:GLU:OE2	1:A:742:VAL:HB	1.87	0.74
7:J:139:DA:H2''	7:J:140:DT:H71	1.69	0.74
1:A:1126:LEU:HB3	1:A:1154:LEU:CD2	2.18	0.74
6:I:48:DT:H4'	6:I:49:DA:OP1	1.87	0.74
1:A:762:LEU:HD21	1:A:791:ALA:HB3	1.69	0.74
5:K:41:TYR:HB3	5:K:45:THR:CG2	2.18	0.74
6:I:101:DG:H2''	6:I:102:DG:C8	2.22	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1072:GLY:HA2	1:A:1118:TYR:CZ	2.23	0.74
1:A:1122:LYS:NZ	1:A:1148:GLU:OE1	2.20	0.74
6:I:111:DC:H2''	6:I:112:DT:H71	1.70	0.74
8:L:2:ASP:OD2	10:O:20:ARG:NH1	2.21	0.74
1:A:1202:LEU:CD2	1:A:1272:MET:HE2	2.17	0.73
7:J:14:DA:H2'	7:J:15:DT:H71	1.69	0.73
1:A:1301:LYS:HB3	1:A:1302:PRO:HD3	1.71	0.73
2:B:78:ARG:NH2	2:B:85:ASP:OD2	2.20	0.73
1:A:757:TYR:OH	1:A:985:GLU:OE2	2.04	0.73
2:B:37:LEU:HD23	5:K:61:LEU:HD12	1.70	0.73
1:A:1187:GLN:OE1	1:A:1201:VAL:HG21	1.89	0.72
1:A:1300:ARG:HG3	1:A:1302:PRO:HD2	1.71	0.72
1:A:935:SER:HB2	1:A:938:THR:HG23	1.71	0.72
1:A:1135:ARG:NH2	7:J:56:DG:OP2	2.22	0.72
6:I:53:DC:N4	7:J:95:DG:O6	2.11	0.72
6:I:129:DT:H2''	6:I:130:DC:C5	2.24	0.72
1:A:744:LYS:HG3	1:A:759:ILE:HG21	1.71	0.72
1:A:897:LEU:HD22	1:A:927:PHE:HZ	1.52	0.72
1:A:1126:LEU:HD11	1:A:1135:ARG:HG2	1.72	0.71
1:A:1280:PHE:HB3	1:A:1284:MET:HE1	1.70	0.71
6:I:123:DC:H2''	6:I:124:DA:C8	2.26	0.71
5:K:42:ARG:O	5:K:45:THR:HG22	1.90	0.71
1:A:1088:ILE:HG23	1:A:1273:ILE:CD1	2.19	0.71
5:E:65:LEU:HD23	7:J:92:DG:OP2	1.90	0.71
5:K:48:LEU:O	5:K:51:ILE:HG12	1.91	0.71
1:A:1063:LEU:HD22	1:A:1065:PHE:HD1	1.53	0.71
3:C:101:THR:HG23	2:F:97:LEU:HD12	1.71	0.71
1:A:898:ASN:OD1	1:A:899:THR:HG23	1.90	0.71
10:O:9:GLU:OE1	10:O:13:ARG:NH2	2.24	0.71
1:A:834:TYR:OH	1:A:869:ILE:HD11	1.91	0.71
3:G:32:ARG:NH2	4:H:35:GLU:OE1	2.23	0.71
6:I:49:DA:H1'	6:I:50:DG:C8	2.26	0.71
1:A:760:LYS:HE3	1:A:1237:LYS:HE3	1.72	0.71
1:A:916:ASN:HB2	1:A:1221:LYS:NZ	2.06	0.71
1:A:929:LEU:HB3	1:A:932:ILE:HG13	1.73	0.71
1:A:1091:LYS:HB3	1:A:1283:PHE:CE1	2.26	0.71
1:A:1154:LEU:HD22	1:A:1159:GLY:HA3	1.73	0.71
3:C:77:ARG:NH1	7:J:20:DC:H4'	2.06	0.71
6:I:109:DC:H2''	6:I:110:DC:C5	2.25	0.70
7:J:78:DG:H2''	7:J:79:DT:C5	2.26	0.70
1:A:1163:LEU:H	1:A:1189:ARG:HH11	1.39	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:I:34:DG:H2''	6:I:35:DT:H5'	1.72	0.70
1:A:924:LEU:HD23	1:A:928:LEU:HD13	1.73	0.70
1:A:1063:LEU:HD22	1:A:1065:PHE:CD1	2.26	0.70
7:J:140:DT:H2'	7:J:141:DT:C6	2.26	0.70
1:A:748:LEU:HD21	1:A:798:GLU:HG3	1.74	0.70
3:G:16:THR:O	3:G:19:SER:OG	2.10	0.70
1:A:1226:GLN:OE1	1:A:1230:GLN:NE2	2.24	0.70
1:A:1225:ASP:O	1:A:1229:ILE:N	2.24	0.70
1:A:1035:LEU:HD13	1:A:1041:GLN:CD	2.17	0.70
1:A:914:LEU:HD21	1:A:1224:VAL:HG12	1.72	0.70
1:A:838:PRO:O	1:A:842:ARG:HG2	1.92	0.69
8:L:125:GLU:HA	10:O:28:VAL:HG21	1.74	0.69
6:I:95:DC:N4	7:J:53:DG:O6	2.24	0.69
1:A:949:MET:N	1:A:1220:TYR:OH	2.24	0.69
1:A:1003:LEU:HD22	1:A:1059:PHE:CZ	2.27	0.69
3:G:90:ASP:OD2	10:O:11:ARG:NH2	2.25	0.69
1:A:807:LEU:HD22	1:A:875:TRP:HB3	1.74	0.69
1:A:880:VAL:HG11	1:A:886:MET:HE1	1.73	0.69
1:A:1010:HIS:CD2	1:A:1018:LEU:HD21	2.27	0.69
1:A:929:LEU:HD23	1:A:932:ILE:HG13	1.74	0.69
1:A:953:LYS:HA	1:A:1251:LEU:HD22	1.73	0.69
6:I:53:DC:O2	7:J:95:DG:N2	2.22	0.69
7:J:26:DC:H2''	7:J:27:DC:C5	2.28	0.69
1:A:914:LEU:HD13	1:A:921:LEU:CD1	2.22	0.69
3:C:42:ARG:HH11	7:J:39:DG:H4'	1.56	0.69
6:I:26:DC:H2''	6:I:27:DT:C6	2.28	0.69
1:A:748:LEU:O	1:A:750:VAL:HG13	1.93	0.68
6:I:133:DA:H2''	6:I:134:DT:H5'	1.75	0.68
6:I:79:DC:H2''	6:I:80:DC:C5	2.27	0.68
1:A:1040:MET:SD	7:J:53:DG:H5'	2.33	0.68
1:A:544:GLN:O	1:A:545:LYS:HE2	1.93	0.68
1:A:1251:LEU:O	1:A:1254:GLU:HG2	1.92	0.68
7:J:140:DT:H2''	7:J:141:DT:C5'	2.23	0.68
1:A:755:LYS:N	1:A:758:GLN:OE1	2.20	0.68
1:A:893:LEU:HA	1:A:896:VAL:CG1	2.24	0.68
7:J:111:DC:H2''	7:J:112:DG:C8	2.29	0.68
7:J:145:DC:H2''	7:J:146:DA:C8	2.28	0.68
1:A:1339:ARG:NE	3:C:61:GLU:OE2	2.16	0.68
7:J:34:DC:H2''	7:J:35:DT:H71	1.74	0.68
1:A:1126:LEU:HB3	1:A:1154:LEU:HD23	1.75	0.68
5:E:73:GLU:OE1	2:F:25:ASN:HB2	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:J:97:DG:H1'	7:J:98:DC:H5''	1.75	0.68
1:A:749:MET:HE2	1:A:797:MET:HE1	1.74	0.67
1:A:973:ARG:HD2	1:A:973:ARG:O	1.94	0.67
1:A:1106:THR:HA	1:A:1109:MET:CG	2.24	0.67
7:J:128:DT:H2''	7:J:129:DC:C5	2.29	0.67
8:L:287:VAL:HG22	8:L:290:ARG:NH2	2.09	0.67
1:A:861:GLU:HG2	1:A:862:TYR:N	2.11	0.66
1:A:1246:PHE:O	1:A:1250:ILE:HD12	1.95	0.66
7:J:15:DT:H4'	7:J:16:DC:OP1	1.94	0.66
1:A:550:LEU:HD12	1:A:553:LEU:HD11	1.77	0.66
7:J:104:DC:C2'	7:J:105:DT:H71	2.25	0.66
7:J:140:DT:H2''	7:J:141:DT:H5'	1.78	0.66
1:A:1101:LEU:HD11	1:A:1174:PHE:HB2	1.76	0.66
1:A:1107:SER:O	1:A:1111:ILE:HD12	1.95	0.66
1:A:888:ASN:HB3	1:A:891:CYS:HB2	1.77	0.65
6:I:49:DA:H1'	6:I:50:DG:N7	2.11	0.65
1:A:935:SER:HB2	1:A:938:THR:CG2	2.27	0.65
1:A:1253:HIS:O	1:A:1256:GLN:HG2	1.95	0.65
1:A:916:ASN:O	1:A:1221:LYS:HD2	1.96	0.65
4:H:36:SER:HB2	4:H:63:ASN:ND2	2.10	0.65
1:A:1289:ASP:O	1:A:1292:ARG:HG2	1.96	0.65
1:A:1100:LEU:HD12	1:A:1100:LEU:O	1.97	0.65
2:B:24:ASP:OD2	2:B:26:ILE:HG22	1.97	0.64
9:N:54:ILE:HG22	9:N:55:ASP:H	1.61	0.64
1:A:550:LEU:O	1:A:553:LEU:HG	1.98	0.64
1:A:1304:LEU:HD23	1:A:1304:LEU:O	1.98	0.64
3:G:91:GLU:OE2	3:G:91:GLU:N	2.27	0.64
6:I:37:DG:H2''	6:I:38:DT:C7	2.26	0.64
6:I:104:DT:H2''	6:I:105:DT:H5'	1.78	0.64
8:L:363:ASP:O	10:O:29:ARG:NH2	2.30	0.64
1:A:991:LYS:HD3	1:A:991:LYS:O	1.98	0.64
6:I:30:DA:C8	6:I:31:DT:H72	2.32	0.64
1:A:765:LEU:HB3	1:A:792:LEU:CD1	2.28	0.64
1:A:807:LEU:HA	1:A:856:LEU:CD2	2.28	0.64
1:A:1180:PRO:HG3	1:A:1218:ALA:HB1	1.79	0.64
2:B:22:LEU:HD12	2:B:22:LEU:O	1.97	0.64
1:A:1150:PHE:CD2	1:A:1151:ILE:HG23	2.33	0.64
6:I:137:DA:H2'	6:I:138:DT:H71	1.78	0.64
1:A:878:MET:HE3	1:A:880:VAL:CG2	2.26	0.64
1:A:1124:LEU:HD22	1:A:1138:LEU:CD1	2.28	0.64
6:I:112:DT:H2''	6:I:113:DA:C8	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:877:TYR:CE2	1:A:879:ILE:HD11	2.33	0.63
1:A:1019:THR:OG1	1:A:1031:GLY:O	2.14	0.63
1:A:1110:THR:HG22	2:B:17:ARG:NH2	2.12	0.63
9:N:386:GLU:O	9:N:390:SER:OG	2.12	0.63
1:A:980:LEU:HB2	1:A:983:GLU:CD	2.23	0.63
7:J:81:DC:H2''	7:J:82:DG:C8	2.32	0.63
5:K:41:TYR:HB3	5:K:45:THR:HG21	1.81	0.63
2:B:94:GLY:O	3:G:99:ARG:NH2	2.32	0.63
3:G:68:ASN:OD1	3:G:71:ARG:NH2	2.29	0.63
7:J:104:DC:H2''	7:J:105:DT:H71	1.80	0.63
6:I:36:DC:H2''	6:I:37:DG:C8	2.34	0.63
7:J:128:DT:H2''	7:J:129:DC:C6	2.34	0.63
1:A:1106:THR:HA	1:A:1109:MET:HG2	1.80	0.63
1:A:921:LEU:O	1:A:925:LEU:HD23	1.99	0.62
1:A:1034:THR:HG21	5:K:81:ASP:OD2	1.99	0.62
1:A:1180:PRO:HG3	1:A:1218:ALA:CB	2.29	0.62
1:A:1266:ASP:O	1:A:1269:VAL:HG12	1.99	0.62
3:G:32:ARG:HD3	6:I:30:DA:OP2	1.97	0.62
1:A:895:GLN:HA	1:A:898:ASN:HD21	1.65	0.62
7:J:51:DT:H2''	7:J:52:DG:H8	1.65	0.62
1:A:1106:THR:O	1:A:1109:MET:HB2	1.98	0.62
1:A:1180:PRO:HG3	1:A:1218:ALA:CA	2.29	0.62
1:A:1240:SER:HB3	1:A:1242:GLU:OE1	1.99	0.62
7:J:93:DC:H2''	7:J:94:DG:H8	1.64	0.62
1:A:1127:ASP:OD1	1:A:1128:GLY:N	2.33	0.62
7:J:152:DG:H2''	7:J:153:DC:C6	2.34	0.62
1:A:780:GLU:CB	1:A:783:LEU:HD13	2.19	0.62
1:A:952:GLU:OE2	1:A:1227:LYS:NZ	2.23	0.62
7:J:95:DG:H2'	7:J:96:DT:C6	2.35	0.62
6:I:57:DT:H6	6:I:57:DT:H5'	1.63	0.62
1:A:741:ARG:HD3	1:A:763:GLU:CD	2.24	0.62
1:A:1158:ALA:HB2	7:J:55:DG:OP1	2.00	0.62
6:I:-5:DG:H2''	6:I:-4:DC:C5	2.34	0.62
9:N:275:GLN:NE2	9:N:276:VAL:HG23	2.15	0.62
1:A:886:MET:HG3	1:A:894:THR:CG2	2.29	0.61
1:A:1311:PRO:HA	1:A:1314:ILE:HB	1.81	0.61
1:A:879:ILE:HD13	1:A:907:LEU:HB2	1.81	0.61
1:A:1037:ASN:OD1	7:J:52:DG:H5'	2.01	0.61
4:D:68:ASP:OD1	2:F:98:TYR:OH	2.18	0.61
1:A:836:GLY:O	1:A:841:ARG:NH1	2.34	0.61
1:A:892:LYS:H	6:I:95:DC:P	2.24	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:I:89:DT:H2''	6:I:90:DA:C8	2.36	0.61
6:I:127:DT:H2''	6:I:128:DG:C8	2.36	0.61
7:J:152:DG:H2''	7:J:153:DC:C5	2.36	0.61
1:A:849:ARG:NH2	1:A:872:LYS:HE3	2.15	0.61
3:C:99:ARG:HG3	3:C:99:ARG:HH11	1.66	0.61
7:J:1:DT:H2''	7:J:2:DC:C5	2.35	0.61
1:A:764:TRP:O	1:A:768:LEU:HD23	2.00	0.61
6:I:29:DA:H1'	6:I:30:DA:C8	2.35	0.61
1:A:732:TYR:HD1	1:A:974:PRO:HA	1.66	0.61
1:A:776:ILE:HD11	1:A:924:LEU:HD22	1.81	0.61
1:A:1157:ARG:O	1:A:1161:LEU:HD23	2.00	0.61
1:A:1315:ILE:O	1:A:1316:LYS:HG3	2.01	0.61
1:A:762:LEU:O	1:A:766:VAL:HG13	2.01	0.61
2:B:25:ASN:HD21	5:K:73:GLU:HB2	1.66	0.61
3:C:77:ARG:HH12	7:J:20:DC:H4'	1.65	0.61
3:C:101:THR:HG22	2:F:96:THR:O	2.01	0.61
1:A:550:LEU:HA	1:A:553:LEU:HD21	1.82	0.61
1:A:1177:ASP:OD1	1:A:1178:TRP:N	2.33	0.61
6:I:26:DC:H2''	6:I:27:DT:C5	2.36	0.61
7:J:95:DG:H2'	7:J:96:DT:H71	1.83	0.61
1:A:865:LYS:NZ	7:J:57:DT:O3'	2.33	0.60
1:A:871:ALA:HB1	1:A:900:HIS:O	2.01	0.60
1:A:1065:PHE:CZ	1:A:1070:VAL:HG22	2.35	0.60
1:A:878:MET:SD	1:A:897:LEU:HD21	2.40	0.60
1:A:936:CYS:HA	1:A:939:PHE:CE1	2.36	0.60
1:A:1088:ILE:HD11	1:A:1269:VAL:HG21	1.82	0.60
1:A:778:ALA:O	1:A:978:ARG:HD2	2.02	0.60
1:A:786:THR:O	1:A:789:THR:HG22	2.00	0.60
1:A:777:LEU:CD1	1:A:977:LEU:HD23	2.31	0.60
5:E:106:ASP:OD2	5:E:131:ARG:NH1	2.32	0.60
4:H:41:VAL:HB	4:H:59:MET:CE	2.31	0.60
7:J:135:DC:C2'	7:J:136:DG:H5''	2.28	0.60
8:L:138:ALA:CB	8:L:163:VAL:HG21	2.31	0.60
1:A:1335:GLY:HA2	4:D:109:HIS:ND1	2.17	0.60
7:J:53:DG:H2''	7:J:54:DC:O5'	2.02	0.60
7:J:127:DC:H2''	7:J:128:DT:C6	2.36	0.60
1:A:781:MET:SD	1:A:911:GLY:HA3	2.42	0.60
1:A:807:LEU:HA	1:A:856:LEU:HD21	1.82	0.60
1:A:1010:HIS:CE1	1:A:1018:LEU:HD11	2.37	0.60
3:C:102:ILE:HG23	4:D:61:ILE:HD13	1.83	0.60
7:J:109:DT:H2''	7:J:110:DA:C8	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:J:138:DG:H2''	7:J:139:DA:OP2	2.02	0.60
9:N:405:GLN:NE2	9:N:406:GLN:OE1	2.35	0.60
1:A:760:LYS:HE3	1:A:1237:LYS:CE	2.32	0.60
6:I:79:DC:H4'	6:I:80:DC:OP1	2.02	0.59
9:N:72:ALA:O	9:N:75:VAL:HG12	2.01	0.59
1:A:1274:ALA:HB3	1:A:1280:PHE:CE1	2.36	0.59
2:B:19:ARG:HA	2:B:22:LEU:CD2	2.32	0.59
1:A:895:GLN:HA	1:A:898:ASN:ND2	2.18	0.59
1:A:1180:PRO:HG3	1:A:1218:ALA:HA	1.83	0.59
2:B:17:ARG:HA	2:B:20:LYS:NZ	2.18	0.59
10:O:43:LEU:HD23	10:O:44:ARG:N	2.17	0.59
1:A:1019:THR:OG1	1:A:1032:THR:HA	2.02	0.59
1:A:758:GLN:HA	1:A:788:GLN:NE2	2.16	0.59
6:I:82:DC:H2''	6:I:83:DG:C8	2.38	0.59
1:A:879:ILE:CD1	1:A:907:LEU:HB2	2.32	0.59
2:B:59:LYS:NZ	2:B:63:GLU:OE2	2.35	0.59
2:B:98:TYR:OH	4:H:68:ASP:OD2	2.20	0.59
4:D:115:THR:O	4:D:118:VAL:HG12	2.03	0.59
6:I:23:DC:N4	7:J:125:DG:O6	2.20	0.59
6:I:103:DA:H2'	6:I:104:DT:H71	1.83	0.59
1:A:891:CYS:SG	1:A:893:LEU:CD2	2.91	0.58
6:I:133:DA:H2''	6:I:134:DT:C5'	2.33	0.58
10:O:7:ARG:NH2	10:O:13:ARG:HD2	2.18	0.58
1:A:550:LEU:HA	1:A:553:LEU:CD2	2.33	0.58
1:A:781:MET:HB3	1:A:1189:ARG:NH2	2.18	0.58
8:L:80:ASP:OD1	8:L:81:ASP:N	2.36	0.58
1:A:776:ILE:HD11	1:A:924:LEU:CD2	2.33	0.58
1:A:1101:LEU:HD13	1:A:1172:ILE:CG2	2.33	0.58
1:A:1169:ASP:O	1:A:1199:VAL:HA	2.03	0.58
7:J:27:DC:H2''	7:J:28:DT:C5	2.39	0.58
1:A:929:LEU:HB3	1:A:933:PHE:H	1.68	0.58
6:I:13:DG:H2''	6:I:14:DG:C5'	2.24	0.58
6:I:60:DA:H2''	6:I:61:DA:C8	2.38	0.58
1:A:878:MET:HB2	1:A:903:ALA:CB	2.34	0.58
2:B:19:ARG:HA	2:B:22:LEU:HD21	1.84	0.58
4:D:73:ILE:HD13	4:D:101:LEU:CD1	2.34	0.58
7:J:37:DG:H2''	7:J:38:DG:C8	2.39	0.58
1:A:748:LEU:HG	1:A:749:MET:CE	2.34	0.58
6:I:-4:DC:H2''	6:I:-3:DC:C6	2.38	0.58
8:L:78:ASN:ND2	8:L:81:ASP:OD2	2.37	0.58
1:A:991:LYS:HB2	1:A:1191:HIS:NE2	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1058:SER:O	1:A:1061:GLU:HG3	2.03	0.58
1:A:1143:ASN:ND2	1:A:1164:ASN:O	2.19	0.58
1:A:1311:PRO:HA	1:A:1314:ILE:CG1	2.34	0.58
1:A:929:LEU:HG	1:A:932:ILE:HD11	1.85	0.58
1:A:980:LEU:HB2	1:A:983:GLU:HG2	1.84	0.58
2:B:19:ARG:O	2:B:22:LEU:HG	2.04	0.58
1:A:1166:GLN:NE2	1:A:1193:ILE:O	2.37	0.57
7:J:101:DG:H2''	7:J:102:DA:C8	2.38	0.57
1:A:1271:GLN:HA	1:A:1280:PHE:HE1	1.70	0.57
1:A:806:PHE:CD1	1:A:877:TYR:HB3	2.40	0.57
4:H:68:ASP:O	4:H:71:GLU:HG2	2.04	0.57
6:I:66:DC:H2''	6:I:67:DG:C8	2.40	0.57
4:H:97:ALA:O	4:H:101:LEU:HD23	2.05	0.57
6:I:125:DC:C2'	6:I:126:DG:H5''	2.31	0.57
1:A:976:LEU:HD22	1:A:1234:PHE:CD1	2.40	0.57
9:N:277:ALA:CB	9:N:300:LEU:HD12	2.34	0.57
1:A:809:ILE:HD12	1:A:863:ILE:HG13	1.87	0.57
1:A:952:GLU:HB3	1:A:1254:GLU:OE1	2.04	0.57
6:I:90:DA:H1'	6:I:91:DA:C8	2.40	0.57
1:A:969:HIS:NE2	1:A:1231:ALA:HB3	2.20	0.57
2:F:78:ARG:NH2	2:F:85:ASP:OD2	2.38	0.57
7:J:78:DG:H2''	7:J:79:DT:C7	2.35	0.57
1:A:748:LEU:HD23	1:A:748:LEU:H	1.70	0.56
1:A:1134:ASP:O	1:A:1138:LEU:HD23	2.05	0.56
2:B:68:ASP:OD2	2:B:93:GLN:NE2	2.38	0.56
6:I:104:DT:H2'	6:I:105:DT:C6	2.40	0.56
1:A:1126:LEU:HB3	1:A:1154:LEU:HD21	1.86	0.56
1:A:878:MET:HB2	1:A:903:ALA:HB1	1.87	0.56
1:A:1048:HIS:ND1	1:A:1049:PRO:HD2	2.20	0.56
6:I:80:DC:H2''	6:I:81:DC:C5	2.40	0.56
6:I:90:DA:H1'	6:I:91:DA:N7	2.19	0.56
7:J:94:DG:H2''	7:J:95:DG:OP1	2.05	0.56
10:O:7:ARG:HH22	10:O:13:ARG:HD2	1.70	0.56
1:A:755:LYS:HB2	1:A:758:GLN:HG3	1.86	0.56
1:A:1301:LYS:HB3	1:A:1302:PRO:CD	2.34	0.56
1:A:953:LYS:HE2	1:A:1251:LEU:CB	2.33	0.56
7:J:23:DG:C8	7:J:24:DT:H72	2.41	0.56
5:K:51:ILE:HG13	5:K:52:ARG:N	2.19	0.56
1:A:887:LYS:HB2	1:A:920:GLU:HG3	1.87	0.56
1:A:749:MET:HE1	1:A:798:GLU:CG	2.36	0.56
1:A:834:TYR:HB3	1:A:858:THR:OG1	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:I:130:DC:H4'	6:I:131:DA:OP1	2.06	0.56
9:N:124:PRO:HG2	9:N:178:ILE:HD13	1.87	0.56
10:O:18:ILE:O	10:O:21:VAL:HG12	2.06	0.56
1:A:1074:ASP:O	1:A:1303:ARG:NH2	2.38	0.55
3:G:117:PRO:HD3	5:K:48:LEU:CD1	2.36	0.55
3:C:78:ILE:HB	4:D:54:ILE:CD1	2.36	0.55
8:L:138:ALA:HB1	8:L:163:VAL:HG21	1.87	0.55
1:A:1105:MET:HG3	1:A:1107:SER:H	1.72	0.55
3:G:26:PRO:HB2	3:G:29:ARG:HB3	1.88	0.55
10:O:17:ASP:O	10:O:20:ARG:HG2	2.07	0.55
2:F:59:LYS:O	2:F:63:GLU:HG3	2.07	0.55
6:I:109:DC:H4'	6:I:110:DC:OP1	2.06	0.55
7:J:34:DC:C2'	7:J:35:DT:H71	2.36	0.55
1:A:893:LEU:CA	1:A:896:VAL:HG12	2.34	0.55
1:A:1006:VAL:HA	1:A:1009:ARG:HG2	1.89	0.55
2:B:35:ARG:O	2:B:39:ARG:HG2	2.07	0.55
3:G:63:LEU:HD13	4:H:45:LEU:HB2	1.88	0.55
6:I:12:DC:H2''	6:I:13:DG:H8	1.71	0.55
1:A:1331:GLU:O	4:D:108:LYS:NZ	2.28	0.55
4:H:90:THR:OG1	4:H:93:GLU:OE1	2.23	0.55
6:I:10:DC:H2''	6:I:11:DC:C6	2.42	0.55
9:N:322:GLY:O	9:N:326:VAL:HG23	2.06	0.55
1:A:1046:CYS:SG	1:A:1209:SER:HB2	2.47	0.55
6:I:62:DC:H2''	6:I:63:DG:C8	2.42	0.55
6:I:141:DA:C8	6:I:142:DT:H72	2.42	0.55
5:K:47:ALA:O	5:K:50:GLU:HG3	2.07	0.55
1:A:980:LEU:HB2	1:A:983:GLU:CG	2.37	0.55
1:A:1101:LEU:HD13	1:A:1172:ILE:HB	1.89	0.55
1:A:781:MET:HB3	1:A:1189:ARG:HH22	1.71	0.54
6:I:68:DT:H2''	6:I:69:DA:N7	2.22	0.54
6:I:91:DA:H2''	6:I:92:DC:H5'	1.90	0.54
7:J:7:DT:H2'	7:J:8:DG:C8	2.42	0.54
1:A:914:LEU:HD13	1:A:921:LEU:HG	1.90	0.54
3:C:42:ARG:HH21	6:I:112:DT:C4'	2.20	0.54
1:A:765:LEU:CB	1:A:792:LEU:HD12	2.36	0.54
1:A:914:LEU:HB2	1:A:921:LEU:HD11	1.89	0.54
6:I:27:DT:H2''	6:I:28:DC:C6	2.43	0.54
7:J:81:DC:H2''	7:J:82:DG:H8	1.71	0.54
1:A:849:ARG:HH22	1:A:873:ILE:HD11	1.73	0.54
1:A:1310:LEU:HD23	1:A:1312:SER:N	2.13	0.54
5:E:119:ILE:O	5:E:119:ILE:HG13	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:I:108:DT:H2''	6:I:109:DC:C5	2.43	0.54
6:I:110:DC:H2''	6:I:111:DC:C5	2.42	0.54
1:A:1100:LEU:HD13	1:A:1102:PHE:CE2	2.42	0.54
7:J:17:DT:H2''	7:J:18:DG:N7	2.23	0.54
7:J:54:DC:H1'	7:J:55:DG:H5'	1.88	0.54
7:J:82:DG:C8	7:J:83:DT:H72	2.42	0.54
7:J:93:DC:H2''	7:J:94:DG:C8	2.43	0.54
1:A:1126:LEU:O	1:A:1154:LEU:HD23	2.08	0.54
2:F:30:THR:HB	2:F:32:PRO:HD2	1.90	0.54
7:J:11:DT:H2''	7:J:12:DA:C8	2.43	0.54
7:J:29:DG:H2''	7:J:30:DG:C8	2.43	0.54
7:J:60:DA:H2''	7:J:61:DA:H8	1.73	0.54
1:A:781:MET:HE2	1:A:1188:ASP:OD2	2.07	0.54
1:A:914:LEU:HD13	1:A:921:LEU:HD12	1.89	0.54
1:A:1180:PRO:HB2	1:A:1222:LEU:HD21	1.89	0.54
2:B:51:TYR:O	2:B:54:THR:HG22	2.08	0.54
9:N:261:GLN:HG3	9:N:265:LEU:HD12	1.90	0.54
1:A:898:ASN:OD1	1:A:899:THR:N	2.40	0.53
1:A:916:ASN:HB2	1:A:1221:LYS:HZ2	1.69	0.53
1:A:997:LYS:NZ	1:A:1207:VAL:HA	2.23	0.53
1:A:1081:LYS:NZ	1:A:1206:THR:OG1	2.29	0.53
1:A:1271:GLN:HA	1:A:1280:PHE:CE1	2.43	0.53
7:J:1:DT:H2''	7:J:2:DC:H5	1.72	0.53
1:A:1044:LYS:HB3	1:A:1051:MET:SD	2.48	0.53
1:A:1200:ARG:NH2	1:A:1272:MET:O	2.41	0.53
5:E:59:GLU:OE1	5:E:59:GLU:N	2.32	0.53
6:I:12:DC:H2''	6:I:13:DG:O4'	2.08	0.53
1:A:763:GLU:O	1:A:766:VAL:HG22	2.08	0.53
7:J:153:DC:H2''	7:J:154:DC:C5	2.43	0.53
5:K:61:LEU:N	5:K:97:GLU:OE1	2.41	0.53
5:E:74:ILE:HD12	2:F:62:LEU:HD23	1.90	0.53
7:J:113:DA:H2''	7:J:114:DC:H5'	1.89	0.53
1:A:989:PRO:CB	1:A:1198:GLU:HA	2.39	0.53
3:C:99:ARG:HG3	3:C:99:ARG:NH1	2.24	0.53
6:I:126:DG:H2'	6:I:127:DT:H72	1.90	0.53
1:A:858:THR:CG2	1:A:862:TYR:HB2	2.38	0.53
1:A:953:LYS:CG	1:A:1251:LEU:HB3	2.37	0.53
2:B:31:LYS:HG3	2:B:51:TYR:CE1	2.43	0.53
6:I:28:DC:H4'	6:I:29:DA:OP1	2.07	0.53
1:A:549:ARG:NH1	1:A:934:LYS:HE3	2.24	0.53
1:A:914:LEU:HB2	1:A:1229:ILE:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1344:VAL:HG11	1:A:1346:TYR:CE1	2.44	0.53
1:A:822:PHE:HB2	1:A:831:LYS:HE3	1.91	0.53
7:J:52:DG:H2'	7:J:53:DG:C8	2.44	0.53
1:A:1018:LEU:HD13	1:A:1312:SER:HB2	1.90	0.53
7:J:142:DC:C2'	7:J:143:DT:H72	2.38	0.53
8:L:359:LYS:HZ1	10:O:26:GLU:HB3	1.74	0.53
3:G:54:VAL:O	3:G:58:LEU:HD23	2.09	0.52
7:J:26:DC:H2''	7:J:27:DC:C6	2.44	0.52
9:N:71:ASN:OD1	9:N:72:ALA:N	2.41	0.52
9:N:421:CYS:SG	9:N:424:ARG:NH2	2.82	0.52
7:J:17:DT:H2''	7:J:18:DG:C8	2.44	0.52
10:O:7:ARG:CZ	10:O:13:ARG:HH11	2.22	0.52
7:J:126:DC:H2''	7:J:127:DC:H5''	1.91	0.52
7:J:11:DT:H2''	7:J:12:DA:H8	1.74	0.52
1:A:1269:VAL:O	1:A:1273:ILE:HG13	2.08	0.52
2:F:48:GLY:N	7:J:81:DC:OP1	2.42	0.52
6:I:84:DC:H2''	6:I:85:DG:C8	2.44	0.52
1:A:814:THR:HG22	1:A:1162:GLY:O	2.09	0.52
1:A:998:CYS:SG	1:A:1084:LEU:HD13	2.49	0.52
6:I:57:DT:H5'	6:I:57:DT:C6	2.43	0.52
6:I:94:DG:H1'	6:I:95:DC:H5'	1.92	0.52
6:I:103:DA:H4'	6:I:103:DA:OP1	2.10	0.52
1:A:969:HIS:CE1	1:A:1231:ALA:HB3	2.44	0.52
6:I:70:DC:N4	7:J:78:DG:O6	2.32	0.52
3:C:102:ILE:CG2	4:D:61:ILE:HD13	2.40	0.52
6:I:16:DG:H2''	6:I:17:DC:C5	2.44	0.52
6:I:49:DA:H4'	6:I:50:DG:OP1	2.09	0.52
1:A:810:VAL:O	1:A:859:THR:HA	2.10	0.52
3:G:62:ILE:HD12	4:H:65:PHE:CE2	2.45	0.52
3:G:111:ILE:HD11	5:K:51:ILE:CG2	2.28	0.52
1:A:914:LEU:CD1	1:A:921:LEU:HG	2.39	0.52
1:A:1086:ASP:OD1	1:A:1115:TYR:OH	2.28	0.52
5:K:116:ARG:NH2	5:K:123:ASP:OD1	2.44	0.52
9:N:175:THR:OG1	9:N:195:LEU:O	2.17	0.52
4:H:41:VAL:CB	4:H:59:MET:HE1	2.39	0.51
6:I:74:DC:C2'	6:I:75:DT:H71	2.35	0.51
6:I:101:DG:H2''	6:I:102:DG:H8	1.72	0.51
6:I:48:DT:H2''	6:I:49:DA:N7	2.25	0.51
7:J:96:DT:OP2	7:J:96:DT:H2'	2.11	0.51
9:N:363:ASN:HB2	9:N:378:LEU:HD13	1.92	0.51
1:A:843:ALA:O	1:A:846:PRO:HD2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:906:ARG:C	1:A:907:LEU:HD22	2.35	0.51
7:J:28:DT:H2''	7:J:29:DG:C8	2.46	0.51
1:A:1253:HIS:HB3	1:A:1256:GLN:NE2	2.26	0.51
1:A:953:LYS:HG2	1:A:1251:LEU:CB	2.38	0.51
1:A:1020:ASP:OD1	1:A:1310:LEU:HD21	2.11	0.51
1:A:1087:ARG:O	1:A:1091:LYS:HG3	2.11	0.51
1:A:1200:ARG:HH11	1:A:1275:ARG:HG2	1.76	0.51
4:D:73:ILE:HD13	4:D:101:LEU:HD13	1.93	0.51
8:L:105:LEU:HB2	8:L:134:VAL:HG12	1.90	0.51
2:F:95:ARG:HG3	2:F:95:ARG:O	2.11	0.51
7:J:107:DT:H5'	7:J:107:DT:C6	2.45	0.51
4:D:115:THR:HA	4:D:118:VAL:HG12	1.91	0.51
1:A:489:TYR:O	1:A:492:SER:OG	2.22	0.51
1:A:552:TYR:O	1:A:555:GLN:HG2	2.11	0.51
1:A:765:LEU:HD13	1:A:792:LEU:HD13	1.92	0.51
1:A:867:LYS:HA	1:A:901:TYR:OH	2.11	0.51
1:A:973:ARG:N	1:A:974:PRO:HD2	2.25	0.51
9:N:266:GLN:OE1	9:N:299:ARG:NH1	2.43	0.51
1:A:1006:VAL:HA	1:A:1009:ARG:NH1	2.25	0.51
6:I:3:DG:H2''	6:I:4:DG:C8	2.46	0.51
6:I:12:DC:H2''	6:I:13:DG:OP1	2.10	0.51
6:I:52:DA:H2''	6:I:53:DC:O5'	2.11	0.51
6:I:120:DA:H2''	6:I:121:DG:N7	2.26	0.51
1:A:929:LEU:CB	1:A:932:ILE:HG13	2.40	0.50
5:K:50:GLU:O	5:K:54:TYR:N	2.24	0.50
8:L:153:MET:SD	8:L:278:THR:OG1	2.69	0.50
1:A:808:ILE:CD1	1:A:879:ILE:HB	2.41	0.50
7:J:8:DG:C8	7:J:9:DT:H72	2.45	0.50
1:A:1073:LEU:HD12	1:A:1076:TYR:HB3	1.94	0.50
8:L:37:ARG:NH2	8:L:81:ASP:OD1	2.39	0.50
8:L:236:LEU:O	8:L:254:ARG:NH1	2.40	0.50
10:O:36:VAL:HG21	10:O:49:VAL:HG11	1.94	0.50
1:A:897:LEU:HD22	1:A:927:PHE:CZ	2.41	0.50
1:A:1239:SER:HA	1:A:1243:ARG:NH2	2.27	0.50
8:L:311:ASP:OD1	8:L:312:ARG:N	2.44	0.50
1:A:834:TYR:CE2	1:A:841:ARG:HD2	2.46	0.50
1:A:862:TYR:OH	7:J:57:DT:OP1	2.16	0.50
1:A:1114:ASP:OD2	2:B:17:ARG:NH2	2.45	0.50
8:L:359:LYS:NZ	10:O:26:GLU:HB3	2.26	0.50
1:A:1225:ASP:HA	1:A:1229:ILE:HG12	1.94	0.50
9:N:92:GLU:OE2	9:N:130:LYS:NZ	2.38	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1137:MET:O	1:A:1141:THR:HG23	2.11	0.50
2:B:25:ASN:HD21	5:K:73:GLU:CB	2.23	0.50
7:J:110:DA:H2''	7:J:111:DC:C6	2.47	0.50
1:A:917:LYS:HE2	1:A:917:LYS:HA	1.94	0.50
1:A:925:LEU:HD11	1:A:975:PHE:HE2	1.77	0.50
1:A:1020:ASP:OD1	1:A:1311:PRO:HG2	2.12	0.50
1:A:1116:PHE:CE2	1:A:1151:ILE:HD12	2.46	0.50
6:I:-4:DC:H2''	6:I:-3:DC:C5	2.47	0.50
6:I:14:DG:C2'	6:I:15:DT:H5''	2.35	0.50
6:I:141:DA:N9	6:I:142:DT:H72	2.27	0.50
1:A:805:PRO:HB2	1:A:875:TRP:CZ3	2.47	0.49
1:A:807:LEU:CD1	1:A:878:MET:HG3	2.36	0.49
6:I:-2:DG:H2''	6:I:-1:DC:C6	2.47	0.49
7:J:15:DT:H2''	7:J:16:DC:C6	2.47	0.49
1:A:786:THR:HA	1:A:789:THR:HG22	1.93	0.49
5:E:46:VAL:HB	7:J:83:DT:OP1	2.12	0.49
6:I:116:DC:C2'	6:I:117:DT:H71	2.40	0.49
7:J:135:DC:H6	7:J:135:DC:H5'	1.76	0.49
5:K:60:LEU:HD12	5:K:64:LYS:HE2	1.93	0.49
1:A:966:ARG:HH12	1:A:1247:LEU:HB3	1.77	0.49
1:A:968:LEU:O	1:A:971:VAL:HG12	2.11	0.49
1:A:1108:LEU:HD11	1:A:1174:PHE:CE2	2.47	0.49
1:A:780:GLU:HG2	1:A:979:ARG:O	2.12	0.49
1:A:916:ASN:HB2	1:A:1221:LYS:HZ3	1.76	0.49
1:A:953:LYS:HG2	1:A:1251:LEU:HD22	1.95	0.49
6:I:48:DT:H2''	6:I:49:DA:C8	2.46	0.49
6:I:121:DG:H2''	6:I:122:DG:C8	2.47	0.49
7:J:10:DA:H2''	7:J:11:DT:H71	1.94	0.49
6:I:-3:DC:H2''	6:I:-2:DG:C8	2.47	0.49
9:N:39:ILE:HD11	9:N:96:SER:HB3	1.94	0.49
1:A:929:LEU:HG	1:A:932:ILE:CD1	2.43	0.49
1:A:953:LYS:CE	1:A:1251:LEU:HB3	2.39	0.49
1:A:1017:LEU:O	1:A:1032:THR:HB	2.13	0.49
7:J:12:DA:C8	7:J:13:DT:H72	2.48	0.49
1:A:949:MET:HG3	1:A:950:THR:N	2.27	0.49
1:A:1344:VAL:HG12	1:A:1345:ASP:N	2.27	0.49
6:I:14:DG:H2'	6:I:15:DT:H72	1.95	0.49
7:J:135:DC:H5'	7:J:135:DC:C6	2.47	0.49
1:A:1296:ARG:HG2	1:A:1297:ASN:OD1	2.12	0.49
9:N:122:GLU:OE1	9:N:149:LEU:HD21	2.13	0.49
1:A:1098:LYS:NZ	1:A:1167:SER:HB2	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:J:52:DG:H2'	7:J:53:DG:H8	1.78	0.49
1:A:761:GLY:N	1:A:979:ARG:HH22	2.10	0.48
1:A:1287:ASP:HB2	1:A:1291:ARG:HH12	1.78	0.48
3:G:65:LEU:HB3	3:G:86:ALA:HB1	1.94	0.48
7:J:71:DA:OP1	5:K:116:ARG:HB2	2.13	0.48
1:A:1010:HIS:ND1	1:A:1018:LEU:HD11	2.28	0.48
8:L:124:PHE:O	10:O:28:VAL:HG21	2.13	0.48
1:A:886:MET:CG	1:A:894:THR:HG22	2.42	0.48
6:I:0:DC:H1'	6:I:1:DC:H5'	1.95	0.48
9:N:68:ILE:HG22	9:N:69:ASP:N	2.27	0.48
1:A:1239:SER:HA	1:A:1243:ARG:HH21	1.78	0.48
2:B:50:ILE:HD11	5:K:120:MET:CA	2.43	0.48
3:G:15:LYS:HB3	3:G:20:ARG:HH21	1.79	0.48
7:J:102:DA:H2''	7:J:103:DG:H8	1.79	0.48
7:J:103:DG:H2''	7:J:104:DC:O5'	2.13	0.48
1:A:953:LYS:HG3	1:A:1254:GLU:OE2	2.12	0.48
1:A:999:ASP:O	1:A:1080:GLY:HA3	2.14	0.48
1:A:1083:GLU:CD	1:A:1301:LYS:HG3	2.39	0.48
6:I:60:DA:H2''	6:I:61:DA:H8	1.77	0.48
8:L:62:ARG:NH1	8:L:204:ALA:O	2.46	0.48
1:A:914:LEU:HD13	1:A:921:LEU:CG	2.44	0.48
1:A:742:VAL:HG12	1:A:742:VAL:O	2.13	0.48
1:A:859:THR:OG1	1:A:861:GLU:OE1	2.30	0.48
1:A:971:VAL:HG13	1:A:972:LEU:HD13	1.95	0.48
1:A:996:ILE:HD12	1:A:1084:LEU:HD11	1.96	0.48
6:I:71:DG:H1'	6:I:72:DC:H5'	1.95	0.48
1:A:877:TYR:CE1	1:A:907:LEU:HD23	2.49	0.48
1:A:1086:ASP:HB2	1:A:1115:TYR:OH	2.14	0.48
1:A:949:MET:H	1:A:1220:TYR:HH	1.62	0.48
1:A:1014:LYS:CG	1:A:1016:VAL:HG12	2.40	0.48
1:A:1085:LEU:HD11	1:A:1089:LEU:HD11	1.96	0.47
1:A:1163:LEU:H	1:A:1189:ARG:NH1	2.07	0.47
1:A:1311:PRO:HA	1:A:1314:ILE:CB	2.43	0.47
3:C:32:ARG:NH2	4:D:35:GLU:OE1	2.47	0.47
3:C:75:LYS:HE3	6:I:132:DG:H3'	1.94	0.47
1:A:823:ASP:O	1:A:827:PRO:HG3	2.14	0.47
1:A:876:LYS:HA	1:A:876:LYS:HE2	1.95	0.47
1:A:935:SER:N	1:A:938:THR:OG1	2.46	0.47
1:A:1287:ASP:OD1	1:A:1288:LEU:N	2.46	0.47
1:A:545:LYS:HB2	1:A:942:TRP:CH2	2.49	0.47
1:A:991:LYS:HB2	1:A:1191:HIS:CD2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1223:ASN:O	1:A:1227:LYS:HG2	2.14	0.47
3:G:45:ALA:O	3:G:48:PRO:HD2	2.14	0.47
6:I:97:DA:H2''	6:I:98:DA:OP2	2.12	0.47
9:N:334:CYS:SG	9:N:335:ASP:N	2.87	0.47
1:A:834:TYR:CZ	1:A:841:ARG:HD2	2.50	0.47
5:E:119:ILE:O	2:F:50:ILE:HD11	2.14	0.47
4:D:119:THR:O	4:D:122:THR:HG22	2.14	0.47
5:K:111:ALA:HB2	5:K:123:ASP:OD2	2.15	0.47
1:A:781:MET:HG2	1:A:1185:GLN:OE1	2.14	0.47
1:A:1332:LYS:HA	4:D:108:LYS:HE3	1.97	0.47
7:J:4:DG:H2''	7:J:5:DG:C8	2.50	0.47
7:J:126:DC:H2''	7:J:127:DC:C5'	2.45	0.47
1:A:787:ILE:HD12	1:A:787:ILE:H	1.79	0.47
2:B:38:ALA:O	2:B:43:VAL:HG22	2.15	0.47
8:L:163:VAL:HG23	8:L:163:VAL:O	2.15	0.47
1:A:807:LEU:CD2	1:A:878:MET:HA	2.45	0.47
1:A:1003:LEU:O	1:A:1006:VAL:HG12	2.15	0.47
2:B:83:ALA:HB2	5:K:87:SER:OG	2.14	0.47
3:C:101:THR:HG23	2:F:97:LEU:CD1	2.44	0.47
7:J:60:DA:H2''	7:J:61:DA:C8	2.50	0.47
1:A:822:PHE:CB	1:A:831:LYS:HD3	2.45	0.47
1:A:880:VAL:HG11	1:A:886:MET:CE	2.43	0.47
1:A:1043:ARG:HH11	1:A:1214:ILE:HD13	1.79	0.47
1:A:1287:ASP:HB2	1:A:1291:ARG:NH1	2.30	0.47
4:D:105:GLU:OE2	4:D:109:HIS:NE2	2.48	0.47
6:I:123:DC:H2''	6:I:124:DA:H8	1.76	0.47
7:J:7:DT:H2''	7:J:8:DG:O4'	2.14	0.47
8:L:5:ILE:CD1	10:O:20:ARG:HH22	2.28	0.47
1:A:755:LYS:HB2	1:A:758:GLN:CG	2.45	0.46
1:A:1206:THR:N	1:A:1211:GLU:OE1	2.47	0.46
3:G:57:TYR:HD2	3:G:58:LEU:HD22	1.79	0.46
7:J:139:DA:H2''	7:J:140:DT:C7	2.42	0.46
8:L:35:VAL:CG2	8:L:85:ILE:HD11	2.45	0.46
1:A:838:PRO:HG3	7:J:58:DT:OP1	2.15	0.46
1:A:1108:LEU:HD23	1:A:1112:MET:HG2	1.97	0.46
1:A:808:ILE:HD13	1:A:879:ILE:HB	1.96	0.46
1:A:977:LEU:HD21	1:A:979:ARG:NH2	2.29	0.46
6:I:26:DC:H2''	6:I:27:DT:H71	1.97	0.46
6:I:38:DT:H4'	6:I:39:DA:OP1	2.15	0.46
7:J:60:DA:H4'	5:K:63:ARG:NH2	2.31	0.46
1:A:897:LEU:O	1:A:901:TYR:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:50:ILE:HD11	5:K:120:MET:HA	1.98	0.46
4:D:46:LYS:HA	4:D:46:LYS:HE2	1.98	0.46
1:A:808:ILE:HG22	1:A:810:VAL:HG13	1.98	0.46
1:A:1124:LEU:HD11	1:A:1149:TYR:CD2	2.51	0.46
2:B:24:ASP:O	2:B:26:ILE:N	2.49	0.46
6:I:82:DC:H2''	6:I:83:DG:H8	1.81	0.46
1:A:748:LEU:HG	1:A:749:MET:HE3	1.97	0.46
4:H:36:SER:HB2	4:H:63:ASN:HD21	1.81	0.46
4:H:39:ILE:O	4:H:43:LYS:HG3	2.16	0.46
6:I:34:DG:H2''	6:I:35:DT:C5'	2.43	0.46
7:J:61:DA:H2''	7:J:62:DA:H8	1.80	0.46
1:A:748:LEU:HD21	1:A:798:GLU:CG	2.44	0.46
1:A:856:LEU:H	1:A:856:LEU:HD23	1.80	0.46
9:N:280:MET:HE2	9:N:299:ARG:NH2	2.31	0.46
1:A:777:LEU:HD21	1:A:788:GLN:OE1	2.16	0.46
3:G:32:ARG:NH1	6:I:30:DA:OP1	2.48	0.46
8:L:5:ILE:HD12	10:O:20:ARG:HH22	1.81	0.46
10:O:6:VAL:HG22	10:O:6:VAL:O	2.16	0.46
1:A:807:LEU:HD21	1:A:878:MET:HG3	1.97	0.46
1:A:813:SER:OG	1:A:1135:ARG:NH1	2.49	0.46
1:A:849:ARG:NH2	1:A:873:ILE:HD11	2.31	0.46
1:A:1108:LEU:O	1:A:1112:MET:HG2	2.16	0.46
1:A:1288:LEU:HB3	1:A:1292:ARG:NH2	2.26	0.46
3:C:21:ALA:HB2	4:D:121:TYR:HB2	1.98	0.46
3:G:73:ASN:OD1	3:G:73:ASN:O	2.34	0.46
7:J:132:DC:H2''	7:J:133:DA:H8	1.81	0.46
1:A:887:LYS:HA	1:A:920:GLU:HG2	1.97	0.45
1:A:929:LEU:CD2	1:A:932:ILE:HG13	2.44	0.45
1:A:982:LYS:HA	1:A:982:LYS:HE2	1.97	0.45
1:A:1310:LEU:CG	1:A:1311:PRO:HD2	2.37	0.45
5:E:90:MET:O	5:E:94:GLU:HG2	2.16	0.45
7:J:13:DT:H2''	7:J:14:DA:C8	2.51	0.45
8:L:278:THR:HG21	8:L:317:ILE:HD11	1.97	0.45
1:A:544:GLN:O	1:A:545:LYS:CE	2.62	0.45
1:A:1095:THR:HG1	1:A:1097:HIS:CE1	2.34	0.45
4:D:73:ILE:HD13	4:D:101:LEU:HD12	1.98	0.45
5:E:57:SER:HB2	5:E:59:GLU:OE1	2.17	0.45
7:J:29:DG:H2''	7:J:30:DG:H8	1.81	0.45
7:J:63:DC:H2''	7:J:64:DG:H8	1.81	0.45
1:A:554:LEU:O	1:A:557:THR:OG1	2.32	0.45
1:A:906:ARG:O	1:A:907:LEU:HD22	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:925:LEU:CD1	1:A:975:PHE:HE2	2.29	0.45
1:A:975:PHE:O	1:A:975:PHE:CD2	2.69	0.45
2:F:46:ILE:HG22	2:F:47:SER:O	2.17	0.45
3:G:117:PRO:HD3	5:K:48:LEU:HD11	1.97	0.45
7:J:153:DC:H2''	7:J:154:DC:C6	2.51	0.45
1:A:777:LEU:HD13	1:A:977:LEU:HD23	1.98	0.45
1:A:891:CYS:SG	1:A:893:LEU:HD23	2.57	0.45
6:I:131:DA:H2''	6:I:132:DG:C8	2.52	0.45
6:I:146:DG:H2''	6:I:147:DA:O5'	2.16	0.45
1:A:765:LEU:HD13	1:A:792:LEU:CD1	2.46	0.45
1:A:929:LEU:HB2	1:A:933:PHE:HB2	1.97	0.45
1:A:997:LYS:HE3	1:A:1205:CYS:SG	2.56	0.45
1:A:1135:ARG:O	1:A:1139:LEU:HD23	2.16	0.45
6:I:13:DG:C2'	6:I:14:DG:H5''	2.27	0.45
6:I:31:DT:H2'	6:I:32:DT:H72	1.98	0.45
1:A:545:LYS:HG3	1:A:942:TRP:CH2	2.51	0.45
1:A:1060:SER:HB3	1:A:1070:VAL:CG2	2.47	0.45
6:I:117:DT:H2''	6:I:118:DC:O5'	2.17	0.45
1:A:774:ASN:ND2	1:A:928:LEU:O	2.44	0.45
1:A:807:LEU:HD22	1:A:875:TRP:CB	2.46	0.45
1:A:973:ARG:HD2	1:A:973:ARG:C	2.42	0.45
1:A:1202:LEU:HD23	1:A:1272:MET:HE2	1.93	0.45
1:A:1291:ARG:O	1:A:1294:GLU:HG2	2.16	0.45
6:I:26:DC:H2''	6:I:27:DT:C7	2.47	0.45
7:J:37:DG:H2''	7:J:38:DG:N7	2.32	0.45
7:J:53:DG:H2''	7:J:54:DC:C5'	2.46	0.45
7:J:139:DA:H1'	7:J:140:DT:H5'	1.99	0.45
1:A:1100:LEU:CD1	1:A:1171:VAL:HG13	2.46	0.45
5:K:59:GLU:OE1	5:K:59:GLU:N	2.44	0.45
1:A:553:LEU:HD12	1:A:554:LEU:N	2.31	0.45
1:A:1172:ILE:CD1	1:A:1202:LEU:HD12	2.47	0.45
4:D:102:LEU:HB2	4:D:107:ALA:HB2	1.98	0.45
7:J:141:DT:H2''	7:J:142:DC:C6	2.51	0.45
8:L:125:GLU:OE2	10:O:30:LYS:HG2	2.17	0.45
1:A:807:LEU:CA	1:A:856:LEU:HD21	2.45	0.45
2:B:31:LYS:N	2:B:32:PRO:HD2	2.32	0.45
3:C:115:LEU:HB3	2:F:44:LYS:HD2	1.99	0.45
3:G:67:GLY:HA3	4:H:49:HIS:CD2	2.52	0.45
6:I:134:DT:H2''	6:I:135:DA:C8	2.51	0.45
6:I:143:DC:H2''	6:I:144:DC:C6	2.52	0.45
7:J:109:DT:H2''	7:J:110:DA:N7	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:J:117:DA:H1'	7:J:118:DT:C5'	2.35	0.45
1:A:764:TRP:NE1	1:A:768:LEU:HD21	2.31	0.44
1:A:864:ILE:HG12	1:A:896:VAL:HG11	1.99	0.44
1:A:1101:LEU:HD12	1:A:1172:ILE:O	2.17	0.44
6:I:70:DC:H2''	6:I:71:DG:N7	2.32	0.44
1:A:784:GLY:HA3	1:A:787:ILE:HD13	1.99	0.44
1:A:896:VAL:HG13	1:A:897:LEU:N	2.32	0.44
1:A:976:LEU:HD23	1:A:977:LEU:N	2.32	0.44
1:A:1048:HIS:HE1	1:A:1050:TYR:CD2	2.35	0.44
6:I:27:DT:C2'	6:I:28:DC:C5	3.00	0.44
6:I:120:DA:H4'	6:I:121:DG:OP1	2.17	0.44
1:A:826:ALA:N	1:A:827:PRO:HD3	2.32	0.44
7:J:90:DA:H1'	7:J:91:DA:C8	2.53	0.44
8:L:353:GLN:N	8:L:353:GLN:OE1	2.50	0.44
1:A:879:ILE:HG23	1:A:909:LEU:CD1	2.47	0.44
7:J:112:DG:H2''	7:J:113:DA:OP2	2.18	0.44
8:L:90:PHE:O	8:L:95:ARG:N	2.50	0.44
1:A:997:LYS:HZ1	1:A:1207:VAL:HA	1.81	0.44
6:I:-3:DC:H2''	6:I:-2:DG:H8	1.83	0.44
6:I:27:DT:H2'	6:I:28:DC:C5	2.52	0.44
6:I:45:DC:H1'	6:I:46:DT:H5'	2.00	0.44
6:I:119:DC:H4'	6:I:120:DA:OP1	2.18	0.44
1:A:822:PHE:CG	1:A:831:LYS:HD3	2.53	0.44
1:A:991:LYS:HG3	1:A:1191:HIS:CG	2.53	0.44
3:G:63:LEU:HD23	3:G:63:LEU:HA	1.82	0.44
6:I:37:DG:H2''	6:I:38:DT:C5	2.52	0.44
7:J:117:DA:C8	7:J:117:DA:H5'	2.52	0.44
1:A:892:LYS:HB2	6:I:95:DC:OP2	2.18	0.44
1:A:1133:GLU:HG2	1:A:1134:ASP:N	2.32	0.44
2:B:31:LYS:HG3	2:B:51:TYR:CZ	2.53	0.44
1:A:1157:ARG:HD2	7:J:54:DC:H4'	1.98	0.44
2:B:50:ILE:HD11	5:K:120:MET:C	2.43	0.44
4:H:39:ILE:HG13	4:H:40:TYR:N	2.32	0.44
1:A:484:LYS:O	1:A:488:GLU:OE1	2.35	0.44
1:A:1155:SER:OG	1:A:1158:ALA:HB3	2.17	0.44
3:G:39:TYR:O	4:H:78:SER:HB2	2.18	0.44
4:H:80:LEU:HD21	4:H:96:THR:HG21	1.99	0.44
1:A:929:LEU:CD2	1:A:933:PHE:HB2	2.42	0.43
1:A:1035:LEU:HD13	1:A:1041:GLN:CG	2.48	0.43
8:L:229:THR:O	8:L:233:SER:N	2.45	0.43
1:A:755:LYS:HB3	1:A:757:TYR:CE1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:805:PRO:HG2	1:A:875:TRP:HE3	1.82	0.43
3:C:75:LYS:HE3	6:I:133:DA:OP2	2.17	0.43
6:I:58:DT:H2''	6:I:59:DA:N7	2.33	0.43
6:I:129:DT:H2''	6:I:130:DC:H5	1.78	0.43
6:I:31:DT:C2'	6:I:32:DT:H72	2.47	0.43
7:J:142:DC:H2'	7:J:143:DT:H72	2.00	0.43
7:J:151:DG:H2''	7:J:152:DG:C8	2.54	0.43
1:A:755:LYS:O	1:A:758:GLN:HB2	2.19	0.43
1:A:873:ILE:HB	1:A:875:TRP:CZ2	2.54	0.43
1:A:976:LEU:HD22	1:A:1234:PHE:CG	2.52	0.43
3:C:59:THR:O	3:C:62:ILE:HG22	2.18	0.43
5:K:68:GLN:HG3	5:K:89:VAL:HG11	2.00	0.43
9:N:267:VAL:HG22	9:N:303:PRO:HB2	2.00	0.43
9:N:403:THR:O	9:N:406:GLN:NE2	2.51	0.43
1:A:965:ILE:CD1	1:A:1247:LEU:HD21	2.49	0.43
1:A:995:VAL:CG2	1:A:1203:ARG:HD2	2.48	0.43
1:A:1100:LEU:HD11	1:A:1171:VAL:HG13	2.00	0.43
6:I:37:DG:C2'	6:I:38:DT:H71	2.40	0.43
6:I:133:DA:H2'	6:I:134:DT:C6	2.54	0.43
9:N:283:VAL:HG13	9:N:299:ARG:CZ	2.49	0.43
1:A:871:ALA:CB	1:A:900:HIS:HB3	2.48	0.43
1:A:949:MET:HG3	1:A:950:THR:H	1.82	0.43
6:I:28:DC:H2''	6:I:29:DA:N7	2.34	0.43
8:L:286:ASP:OD1	8:L:287:VAL:N	2.52	0.43
1:A:749:MET:O	1:A:749:MET:HG2	2.17	0.43
1:A:757:TYR:HD2	1:A:979:ARG:HH11	1.67	0.43
1:A:790:ILE:CD1	1:A:821:GLU:HG3	2.49	0.43
1:A:1109:MET:HE1	1:A:1154:LEU:C	2.43	0.43
6:I:28:DC:H1'	6:I:29:DA:C8	2.54	0.43
7:J:96:DT:H1'	7:J:97:DG:C5'	2.37	0.43
7:J:118:DT:H6	7:J:118:DT:H2'	1.69	0.43
7:J:63:DC:H2''	7:J:64:DG:C8	2.53	0.43
1:A:881:ASP:OD1	1:A:882:GLU:N	2.52	0.42
1:A:1052:PHE:O	1:A:1053:GLN:HB2	2.18	0.42
1:A:1065:PHE:CE2	1:A:1070:VAL:HG22	2.54	0.42
1:A:1101:LEU:HD13	1:A:1172:ILE:CB	2.48	0.42
2:B:17:ARG:HA	2:B:20:LYS:HZ3	1.81	0.42
3:C:67:GLY:HA2	3:C:78:ILE:HD11	2.01	0.42
6:I:66:DC:H2''	6:I:67:DG:H8	1.84	0.42
6:I:104:DT:H2'	6:I:105:DT:H71	2.00	0.42
7:J:78:DG:H2''	7:J:79:DT:C6	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L:246:GLN:N	8:L:246:GLN:OE1	2.52	0.42
1:A:815:LEU:HD23	1:A:835:LYS:HD3	2.00	0.42
1:A:819:ALA:HA	1:A:831:LYS:HE3	2.01	0.42
1:A:1250:ILE:HD12	1:A:1250:ILE:H	1.84	0.42
6:I:14:DG:O6	7:J:134:DC:N4	2.43	0.42
1:A:977:LEU:HD11	1:A:979:ARG:NE	2.21	0.42
2:B:34:ILE:HD13	2:B:54:THR:CG2	2.49	0.42
3:C:32:ARG:HD3	7:J:30:DG:OP2	2.18	0.42
8:L:35:VAL:HG23	8:L:85:ILE:HD11	2.01	0.42
9:N:378:LEU:H	9:N:378:LEU:HD23	1.85	0.42
1:A:1065:PHE:HZ	1:A:1070:VAL:HG22	1.80	0.42
7:J:47:DC:H1'	7:J:48:DC:C5	2.54	0.42
8:L:172:PRO:HA	8:L:175:ILE:HD12	2.01	0.42
8:L:330:ILE:HG22	8:L:332:PRO:HD3	2.01	0.42
1:A:829:VAL:HG13	1:A:854:ASN:HB2	2.01	0.42
1:A:849:ARG:HA	1:A:849:ARG:NE	2.35	0.42
1:A:871:ALA:HA	1:A:901:TYR:CD2	2.55	0.42
1:A:921:LEU:CD1	1:A:1229:ILE:HD11	2.35	0.42
1:A:965:ILE:HG22	1:A:969:HIS:CD2	2.54	0.42
4:H:46:LYS:HA	4:H:46:LYS:HD3	1.76	0.42
6:I:121:DG:H2''	6:I:122:DG:N7	2.34	0.42
7:J:130:DG:H2''	7:J:131:DG:N7	2.34	0.42
9:N:41:MET:CE	9:N:83:ILE:HD13	2.50	0.42
5:E:126:LEU:HD22	5:K:113:HIS:CG	2.54	0.42
9:N:260:PHE:CE1	9:N:264:VAL:HG11	2.54	0.42
1:A:749:MET:HE2	1:A:797:MET:CE	2.44	0.42
6:I:23:DC:H2''	6:I:24:DC:C6	2.54	0.42
6:I:133:DA:H4'	6:I:133:DA:OP1	2.18	0.42
7:J:56:DG:H2''	7:J:57:DT:OP2	2.20	0.42
5:K:120:MET:HB3	5:K:121:PRO:HD2	2.00	0.42
1:A:545:LYS:HB2	1:A:942:TRP:HH2	1.85	0.42
1:A:941:GLN:O	1:A:944:ASN:ND2	2.52	0.42
1:A:952:GLU:O	1:A:1227:LYS:NZ	2.52	0.42
1:A:1246:PHE:O	1:A:1250:ILE:CD1	2.65	0.42
1:A:1288:LEU:CB	1:A:1292:ARG:HH21	2.27	0.42
6:I:18:DC:H1'	6:I:19:DG:C8	2.55	0.42
7:J:95:DG:H2'	7:J:96:DT:C7	2.50	0.42
1:A:1058:SER:HB2	1:A:1310:LEU:HD11	2.02	0.42
1:A:1309:GLU:OE1	1:A:1309:GLU:N	2.52	0.42
6:I:52:DA:H2''	6:I:53:DC:C5'	2.50	0.42
1:A:966:ARG:HH12	1:A:1247:LEU:CB	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:970:LYS:O	1:A:973:ARG:HB3	2.20	0.42
1:A:1152:PHE:CE2	1:A:1154:LEU:HD11	2.55	0.42
2:F:31:LYS:HB3	2:F:32:PRO:HD3	2.02	0.42
6:I:16:DG:H2''	6:I:17:DC:C6	2.55	0.42
6:I:59:DA:H2''	6:I:60:DA:C8	2.55	0.42
6:I:84:DC:H2''	6:I:85:DG:H8	1.83	0.42
8:L:153:MET:CE	8:L:278:THR:HG23	2.49	0.42
1:A:929:LEU:CG	1:A:932:ILE:HG13	2.50	0.41
1:A:976:LEU:HD22	1:A:1234:PHE:HB2	2.01	0.41
1:A:1065:PHE:CZ	1:A:1070:VAL:HG13	2.55	0.41
1:A:1344:VAL:HG11	1:A:1346:TYR:CZ	2.55	0.41
7:J:123:DC:H2'	7:J:124:DG:H8	1.78	0.41
1:A:1124:LEU:HB2	1:A:1152:PHE:HD1	1.84	0.41
6:I:121:DG:H1'	6:I:122:DG:C8	2.55	0.41
8:L:357:ILE:HD11	8:L:374:CYS:SG	2.60	0.41
9:N:15:ASP:OD2	9:N:22:ARG:NH1	2.53	0.41
1:A:1016:VAL:HG21	1:A:1032:THR:OG1	2.21	0.41
3:C:30:VAL:HG13	4:D:70:PHE:HE2	1.85	0.41
10:O:26:GLU:HG3	10:O:27:LYS:N	2.35	0.41
1:A:924:LEU:CD2	1:A:928:LEU:HD13	2.48	0.41
1:A:929:LEU:CB	1:A:933:PHE:HB2	2.50	0.41
1:A:1280:PHE:O	1:A:1284:MET:CE	2.68	0.41
6:I:142:DT:H2''	6:I:143:DC:OP2	2.20	0.41
7:J:98:DC:H5'	7:J:98:DC:C6	2.55	0.41
1:A:805:PRO:HD2	1:A:876:LYS:H	1.86	0.41
1:A:1076:TYR:HE1	1:A:1086:ASP:CB	2.34	0.41
1:A:1109:MET:HE1	1:A:1154:LEU:O	2.21	0.41
4:H:41:VAL:CG1	4:H:59:MET:HE1	2.50	0.41
7:J:135:DC:H2''	7:J:136:DG:C8	2.56	0.41
1:A:914:LEU:HB3	1:A:1229:ILE:HG13	2.03	0.41
3:G:29:ARG:NH1	4:H:36:SER:O	2.54	0.41
6:I:10:DC:H2''	6:I:11:DC:C5	2.55	0.41
6:I:121:DG:H2'	6:I:121:DG:O5'	2.21	0.41
9:N:277:ALA:HB2	9:N:300:LEU:HD12	2.03	0.41
1:A:808:ILE:HB	1:A:857:LEU:HD23	2.03	0.41
1:A:858:THR:HG22	1:A:859:THR:N	2.35	0.41
1:A:1336:ARG:HD3	4:D:113:GLU:OE2	2.21	0.41
1:A:1341:ARG:NH2	3:C:64:GLU:OE1	2.53	0.41
2:F:64:ASN:OD1	2:F:67:ARG:NH2	2.54	0.41
6:I:8:DA:C8	6:I:9:DT:H72	2.55	0.41
6:I:45:DC:C2'	6:I:46:DT:H72	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:I:134:DT:H2''	6:I:135:DA:H8	1.86	0.41
1:A:790:ILE:HD12	1:A:821:GLU:HG3	2.02	0.41
1:A:792:LEU:C	1:A:792:LEU:HD23	2.45	0.41
1:A:805:PRO:HB2	1:A:875:TRP:CE3	2.56	0.41
1:A:807:LEU:HD21	1:A:878:MET:HA	2.03	0.41
1:A:998:CYS:N	1:A:1205:CYS:O	2.54	0.41
1:A:1082:PHE:CE1	1:A:1112:MET:HE1	2.56	0.41
1:A:1247:LEU:HA	1:A:1250:ILE:CD1	2.51	0.41
3:G:57:TYR:CD2	3:G:58:LEU:HD22	2.56	0.41
7:J:94:DG:H2''	7:J:95:DG:O5'	2.19	0.41
7:J:95:DG:H2'	7:J:96:DT:C5	2.55	0.41
9:N:80:MET:HE1	9:N:248:TRP:CD1	2.56	0.41
10:O:27:LYS:HD3	10:O:27:LYS:HA	1.90	0.41
1:A:542:ILE:HA	1:A:942:TRP:CZ3	2.56	0.41
1:A:918:LEU:N	1:A:919:PRO:CD	2.84	0.41
1:A:1263:VAL:HG23	1:A:1263:VAL:O	2.20	0.41
2:B:95:ARG:O	2:B:96:THR:C	2.64	0.41
3:C:68:ASN:OD1	3:C:71:ARG:NH2	2.54	0.41
5:E:118:THR:HA	2:F:45:ARG:O	2.20	0.41
6:I:27:DT:OP1	6:I:27:DT:H4'	2.21	0.41
6:I:133:DA:H2'	6:I:134:DT:H6	1.86	0.41
7:J:20:DC:H2''	7:J:21:DA:C8	2.56	0.41
7:J:47:DC:H2''	7:J:48:DC:C5	2.56	0.41
7:J:51:DT:H2''	7:J:52:DG:C8	2.50	0.41
8:L:82:MET:HE3	8:L:82:MET:O	2.20	0.41
1:A:915:GLN:OE1	1:A:1179:ASN:ND2	2.53	0.41
1:A:965:ILE:HD12	1:A:1247:LEU:HD21	2.03	0.41
1:A:993:GLU:OE1	1:A:993:GLU:N	2.54	0.41
1:A:1103:CYS:O	1:A:1155:SER:HA	2.21	0.41
6:I:8:DA:C2'	6:I:9:DT:H72	2.50	0.41
1:A:732:TYR:CD1	1:A:974:PRO:HA	2.52	0.40
1:A:892:LYS:N	6:I:95:DC:OP1	2.55	0.40
1:A:1018:LEU:HB3	1:A:1312:SER:HB2	2.04	0.40
1:A:1036:MET:HE1	5:K:83:ARG:HE	1.85	0.40
1:A:1050:TYR:OH	1:A:1303:ARG:NH2	2.54	0.40
1:A:1152:PHE:CE2	1:A:1154:LEU:HD21	2.56	0.40
1:A:1171:VAL:HG11	1:A:1187:GLN:HA	2.03	0.40
1:A:1335:GLY:HA2	4:D:109:HIS:CG	2.55	0.40
6:I:95:DC:H2''	6:I:96:DC:C6	2.56	0.40
7:J:40:DA:H2''	7:J:41:DG:C8	2.56	0.40
1:A:924:LEU:HD23	1:A:924:LEU:C	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1069:ILE:HD13	2:B:15:ALA:CA	2.41	0.40
4:D:123:SER:O	4:D:124:ALA:HB2	2.21	0.40
3:G:65:LEU:HD23	3:G:65:LEU:HA	1.93	0.40
6:I:110:DC:H1'	6:I:111:DC:C5	2.56	0.40
8:L:140:LEU:CD2	8:L:346:LEU:HD12	2.51	0.40
1:A:806:PHE:CE1	1:A:877:TYR:HB3	2.56	0.40
1:A:807:LEU:HD21	1:A:878:MET:CB	2.51	0.40
1:A:918:LEU:HB3	1:A:919:PRO:HD3	2.03	0.40
1:A:1035:LEU:HB3	1:A:1041:GLN:HE21	1.85	0.40
4:D:115:THR:O	4:D:116:LYS:C	2.64	0.40
5:E:61:LEU:HD12	2:F:37:LEU:HD23	2.04	0.40
7:J:139:DA:H2''	7:J:140:DT:OP2	2.20	0.40
1:A:881:ASP:OD1	1:A:882:GLU:HG2	2.22	0.40
1:A:969:HIS:HE2	1:A:1231:ALA:HB3	1.86	0.40
1:A:972:LEU:C	1:A:974:PRO:HD2	2.47	0.40
1:A:996:ILE:HG21	1:A:1272:MET:SD	2.61	0.40
7:J:1:DT:H2''	7:J:2:DC:C6	2.56	0.40
1:A:1247:LEU:HA	1:A:1250:ILE:HD13	2.04	0.40
5:E:113:HIS:CG	5:K:126:LEU:HD22	2.56	0.40
2:F:84:MET:HE2	2:F:88:TYR:CZ	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	671/1614 (42%)	629 (94%)	42 (6%)	0	100	100
2	B	85/102 (83%)	81 (95%)	4 (5%)	0	100	100
2	F	84/102 (82%)	83 (99%)	1 (1%)	0	100	100
3	C	105/129 (81%)	103 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	G	106/129 (82%)	105 (99%)	1 (1%)	0	100	100
4	D	91/125 (73%)	91 (100%)	0	0	100	100
4	H	91/125 (73%)	89 (98%)	2 (2%)	0	100	100
5	E	93/135 (69%)	93 (100%)	0	0	100	100
5	K	96/135 (71%)	92 (96%)	4 (4%)	0	100	100
8	L	373/375 (100%)	369 (99%)	4 (1%)	0	100	100
9	N	425/429 (99%)	417 (98%)	8 (2%)	0	100	100
10	O	40/210 (19%)	38 (95%)	2 (5%)	0	100	100
All	All	2260/3610 (63%)	2190 (97%)	70 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	610/1396 (44%)	610 (100%)	0	100	100
2	B	72/78 (92%)	72 (100%)	0	100	100
2	F	67/78 (86%)	67 (100%)	0	100	100
3	C	81/101 (80%)	81 (100%)	0	100	100
3	G	84/101 (83%)	84 (100%)	0	100	100
4	D	77/105 (73%)	77 (100%)	0	100	100
4	H	79/105 (75%)	79 (100%)	0	100	100
5	E	82/110 (74%)	82 (100%)	0	100	100
5	K	84/110 (76%)	84 (100%)	0	100	100
8	L	318/318 (100%)	318 (100%)	0	100	100
9	N	362/364 (100%)	362 (100%)	0	100	100
10	O	41/182 (22%)	41 (100%)	0	100	100
All	All	1957/3048 (64%)	1957 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	473	GLN
1	A	508	HIS
1	A	756	GLN
1	A	799	HIS
1	A	944	ASN
1	A	969	HIS
1	A	1164	ASN
1	A	1230	GLN
1	A	1248	GLN
1	A	1253	HIS
3	C	104	GLN
3	G	73	ASN
8	L	73	HIS
9	N	108	HIS
9	N	212	ASN
9	N	318	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

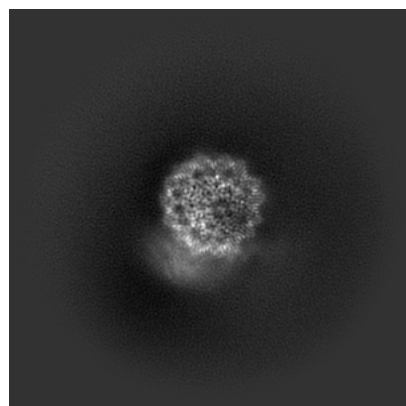
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65851. These allow visual inspection of the internal detail of the map and identification of artifacts.

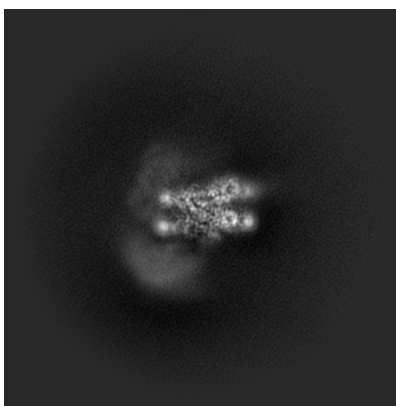
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

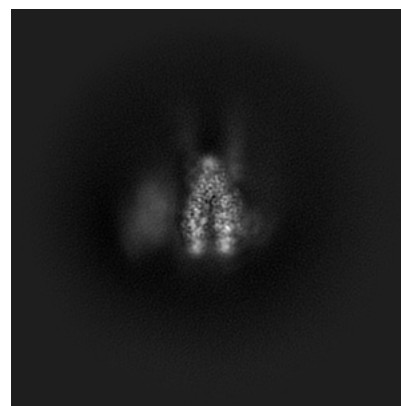
6.1.1 Primary map



X

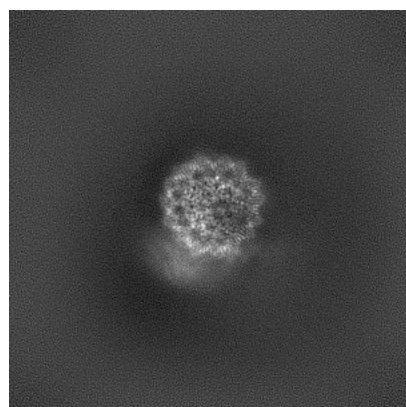


Y

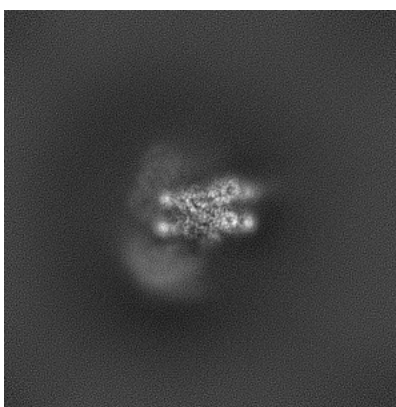


Z

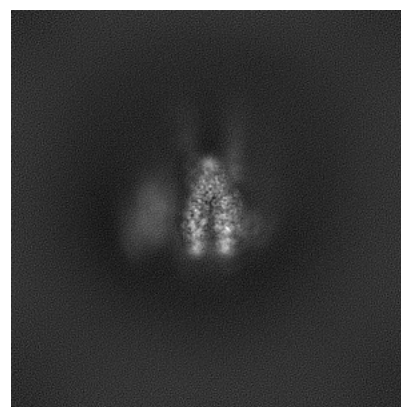
6.1.2 Raw map



X



Y

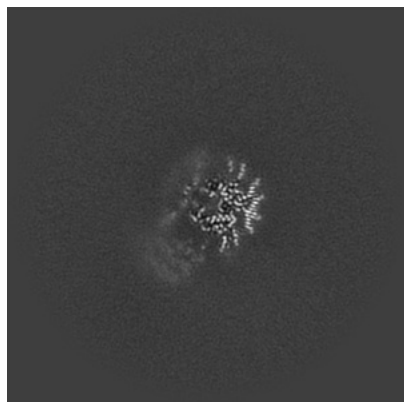


Z

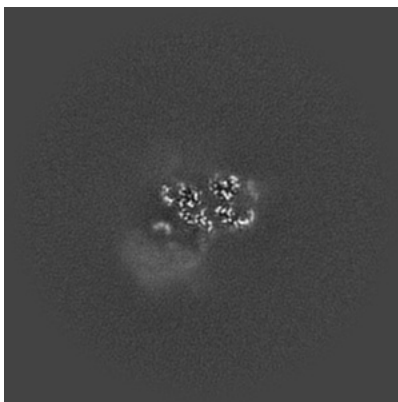
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

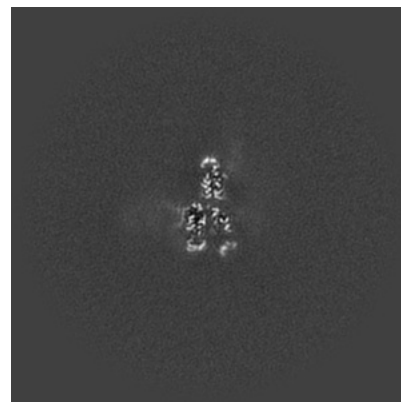
6.2.1 Primary map



X Index: 180

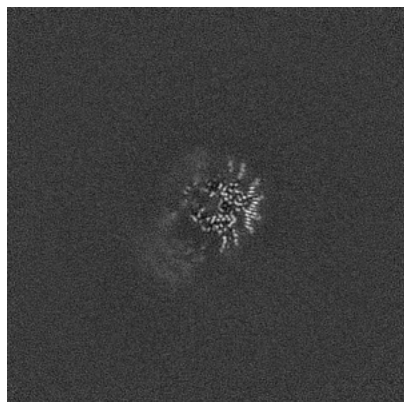


Y Index: 180

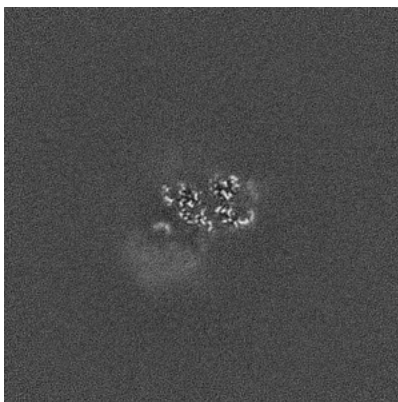


Z Index: 180

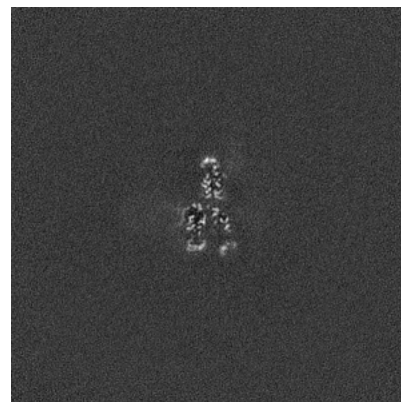
6.2.2 Raw map



X Index: 180



Y Index: 180

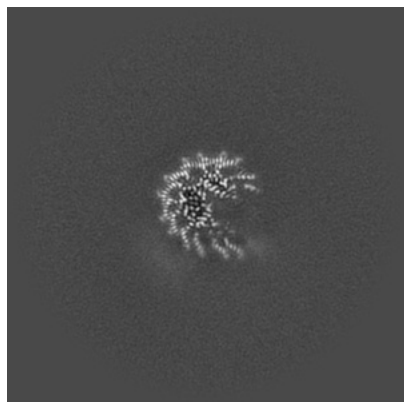


Z Index: 180

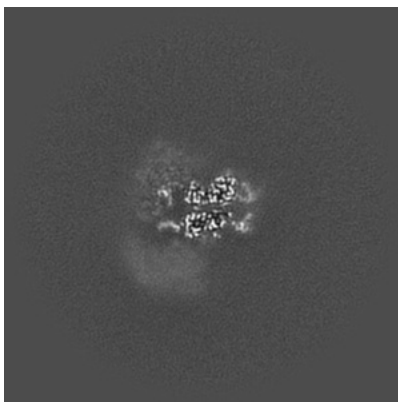
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

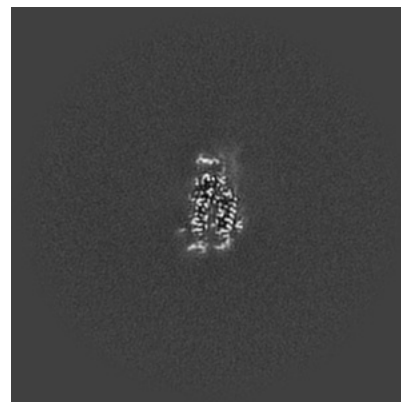
6.3.1 Primary map



X Index: 168

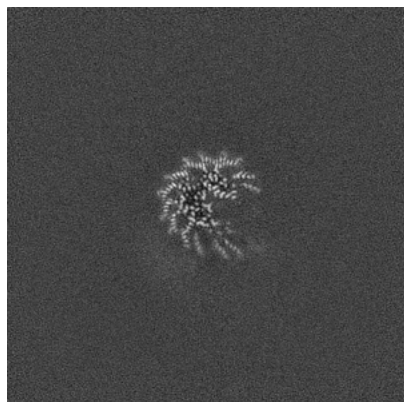


Y Index: 165

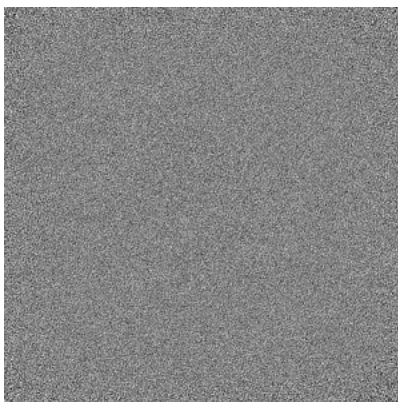


Z Index: 196

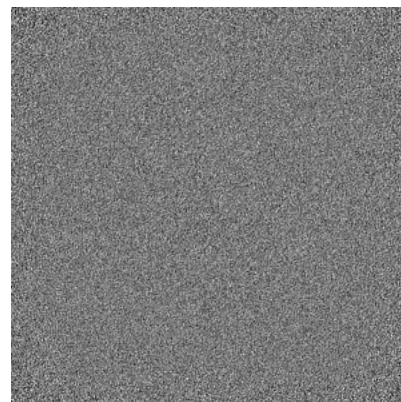
6.3.2 Raw map



X Index: 169



Y Index: 0

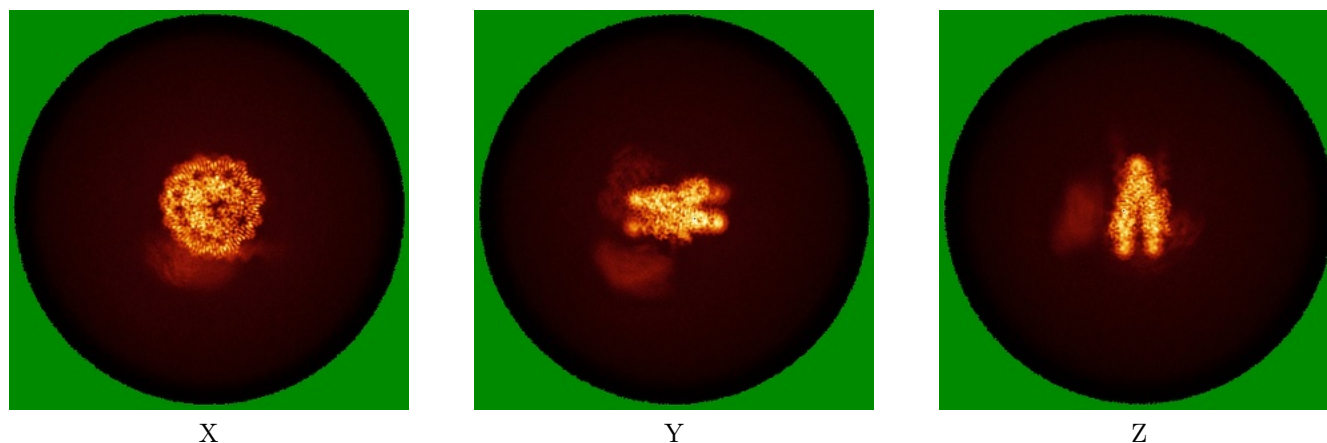


Z Index: 0

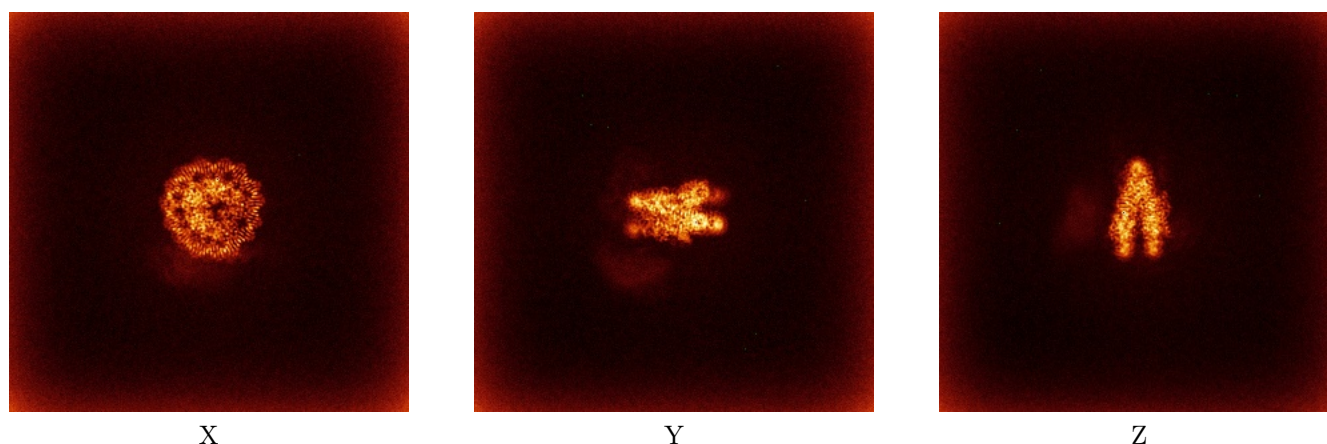
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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

6.5 Orthogonal surface views [i](#)

This section was not generated.

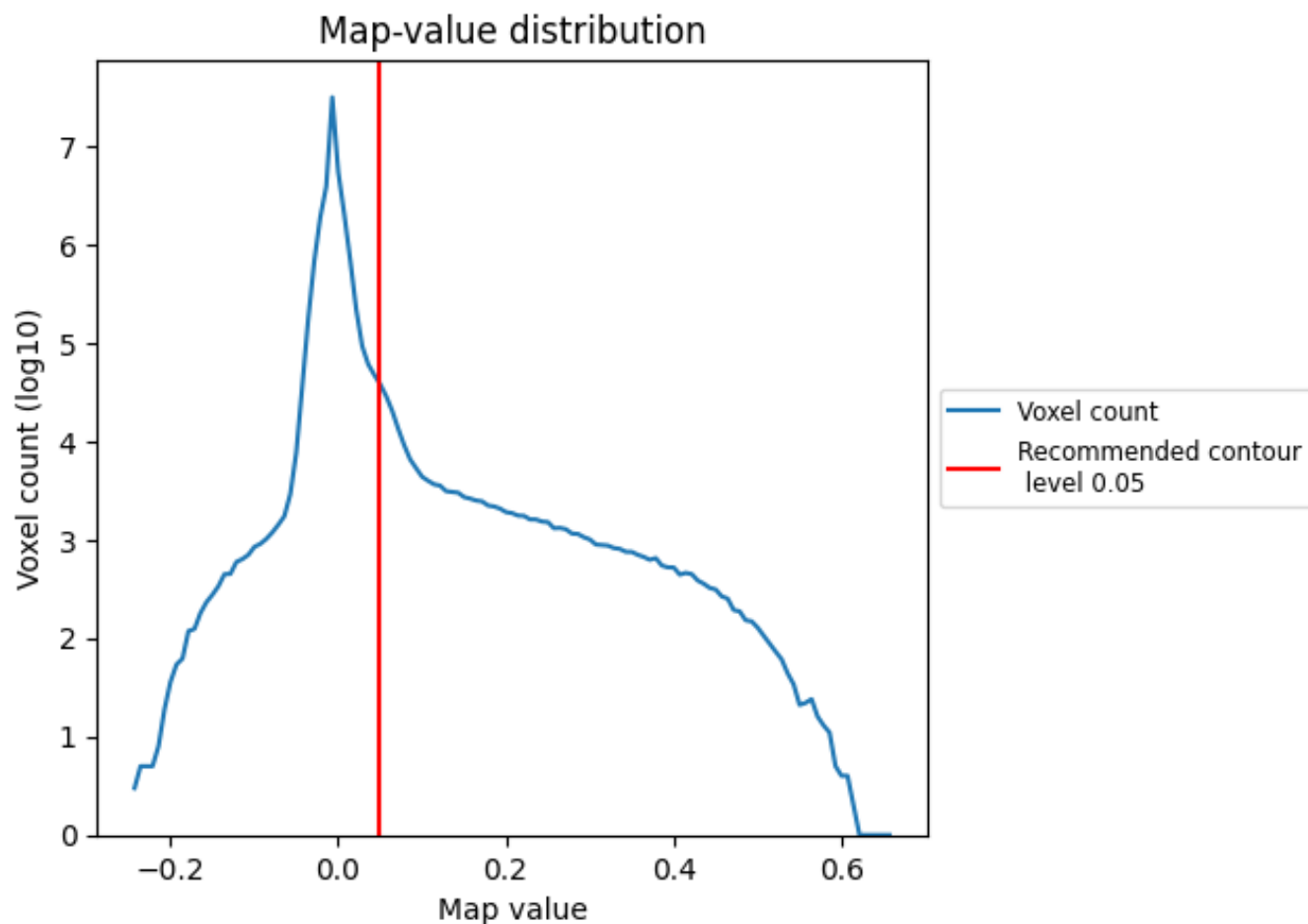
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

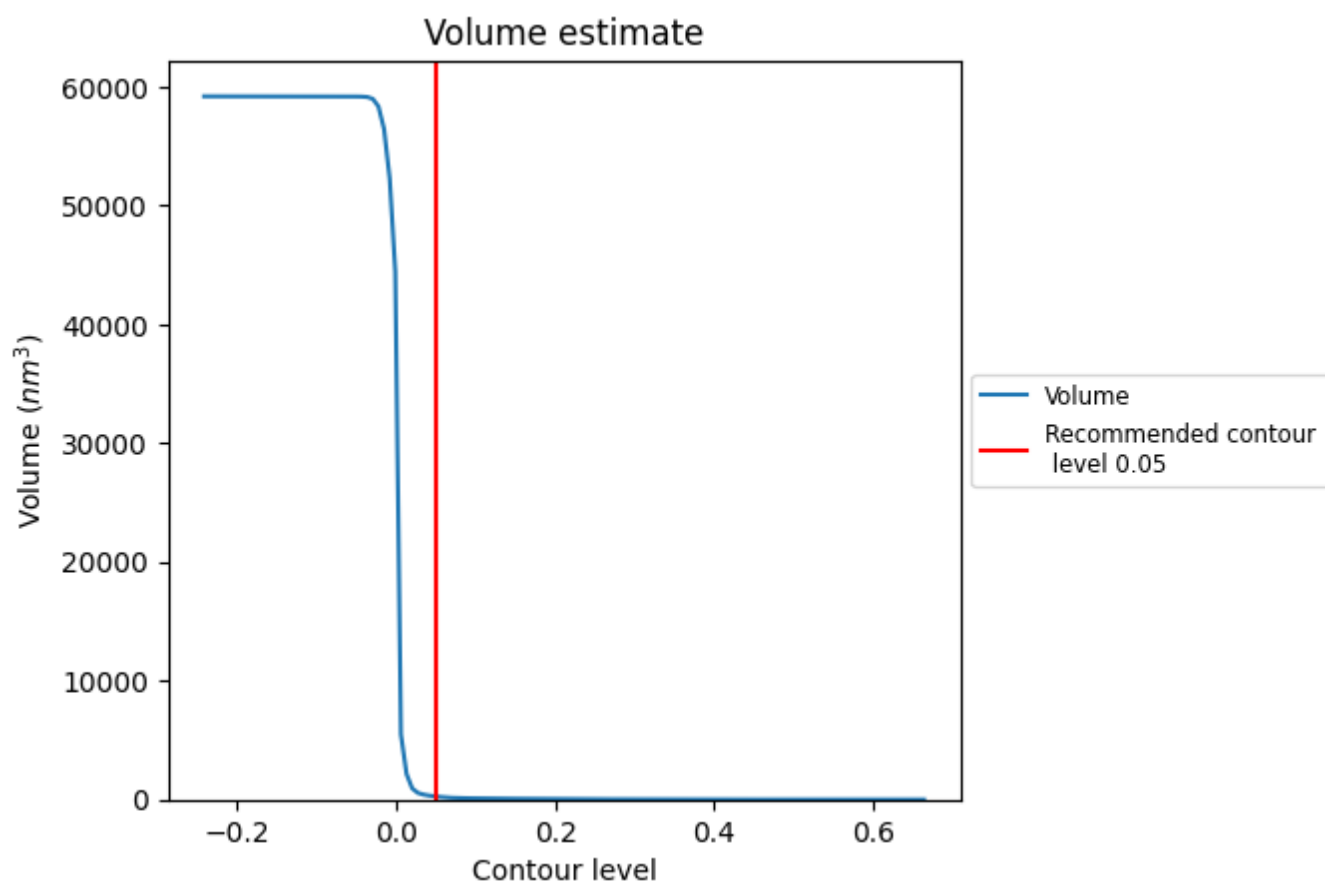
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

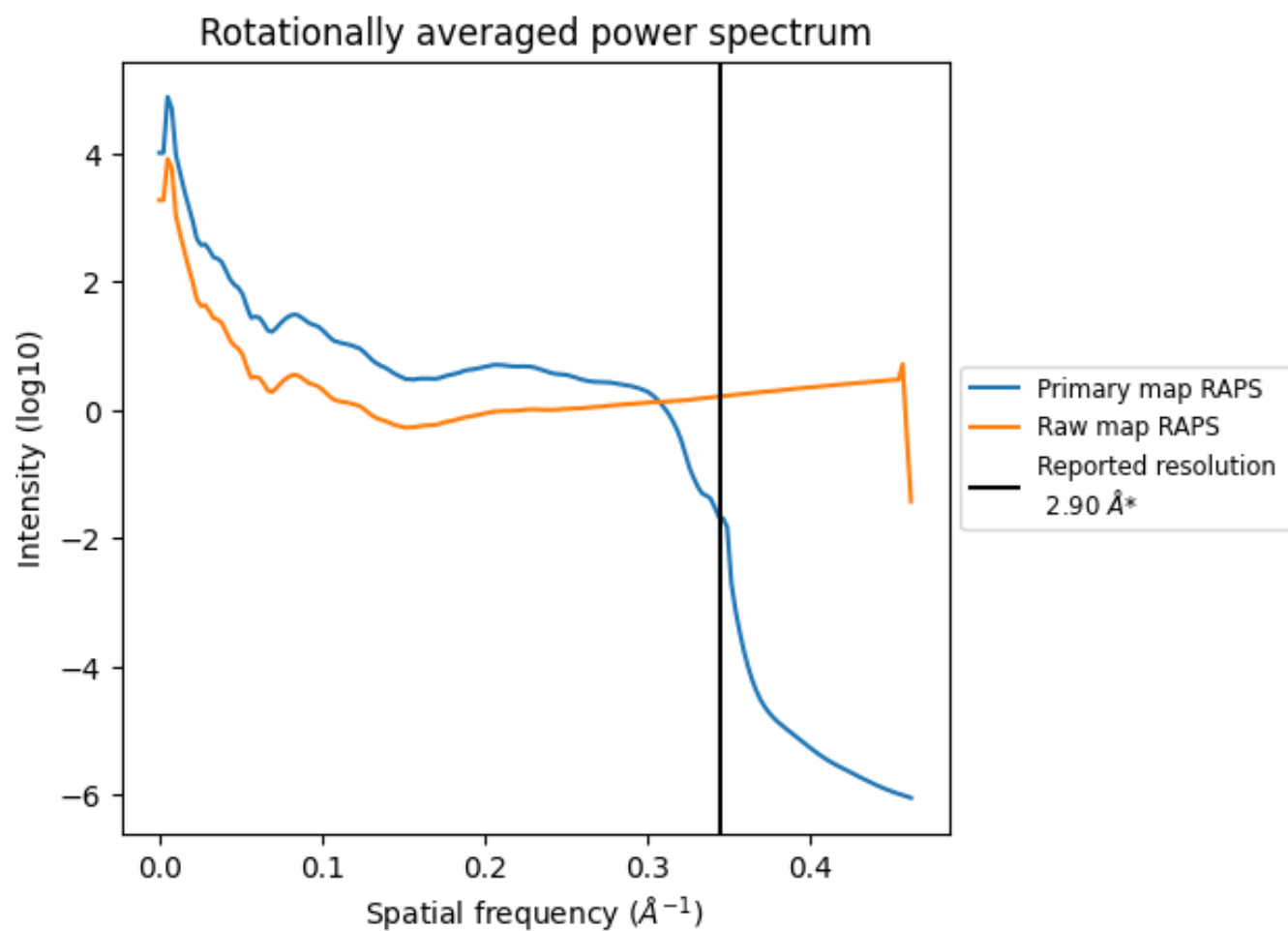
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 259 nm^3 ; this corresponds to an approximate mass of 234 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 ⓘ

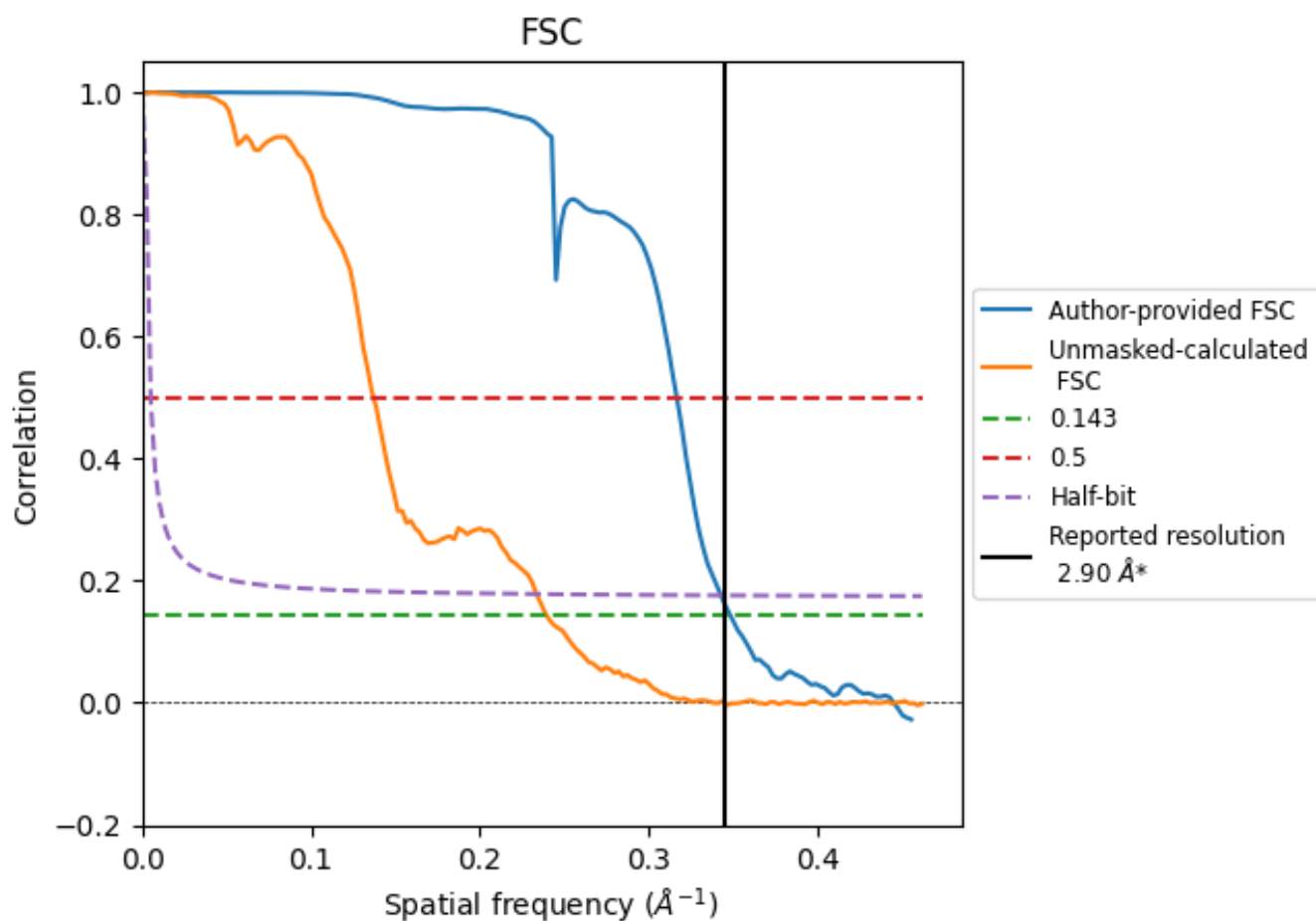


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

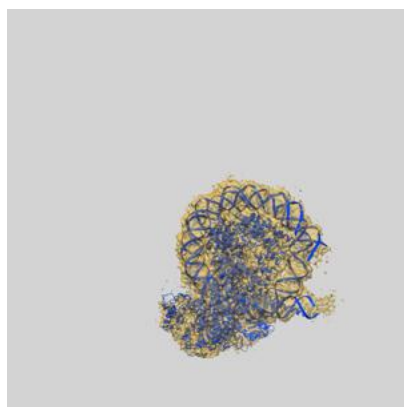
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.87	3.16	2.92
Unmasked-calculated*	4.17	7.30	4.28

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.17 differs from the reported value 2.9 by more than 10 %

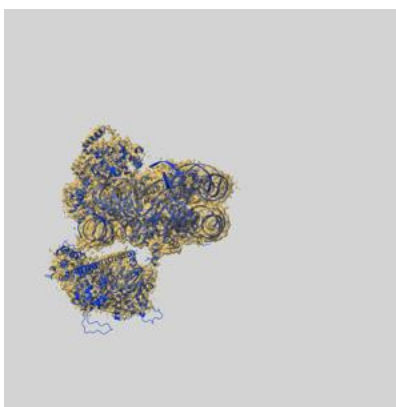
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65851 and PDB model 9WBZ. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

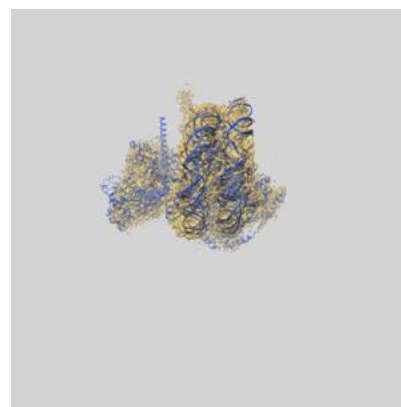
9.1 Map-model overlay [i](#)



X



Y



Z

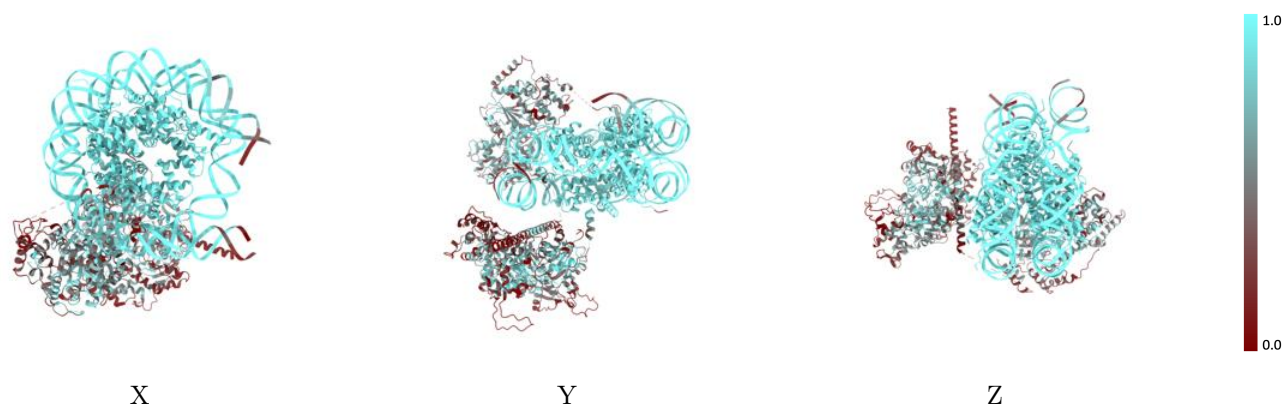
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



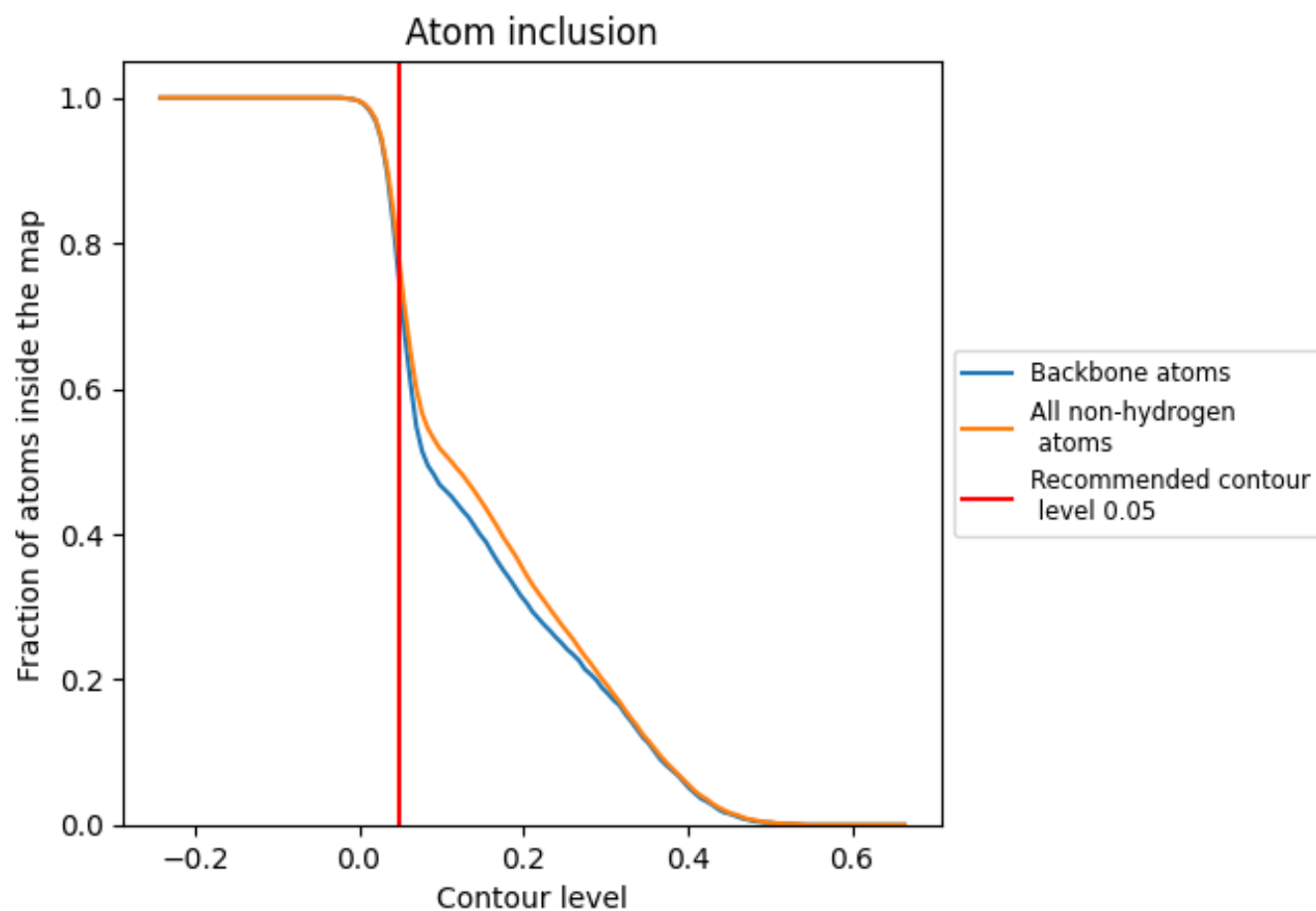
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion ⓘ



At the recommended contour level, 74% of all backbone atoms, 76% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7650	<div></div> 0.3430
A	<div></div> 0.4900	<div></div> 0.2550
B	<div></div> 0.8910	<div></div> 0.5200
C	<div></div> 0.9920	<div></div> 0.5570
D	<div></div> 0.9960	<div></div> 0.5500
E	<div></div> 0.9880	<div></div> 0.5680
F	<div></div> 0.9680	<div></div> 0.5560
G	<div></div> 0.9660	<div></div> 0.5530
H	<div></div> 0.9890	<div></div> 0.5570
I	<div></div> 0.9430	<div></div> 0.4920
J	<div></div> 0.9570	<div></div> 0.4950
K	<div></div> 0.9650	<div></div> 0.5390
L	<div></div> 0.5170	<div></div> 0.0920
N	<div></div> 0.4410	<div></div> 0.0620
O	<div></div> 0.5530	<div></div> 0.2100

