



Full wwPDB EM Validation Report ⓘ

Sep 9, 2026 – 04:54 PM EDT

PDB ID : 9ZP0 / pdb_00009zp0
EMDB ID : EMD-74512
Title : CryoEM structure of DNA-PK bound to N0 nucleosome
Authors : Lu, W.; He, Y.
Deposited on : 2025-12-16
Resolution : 4.11 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.dev133
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) : 2.50

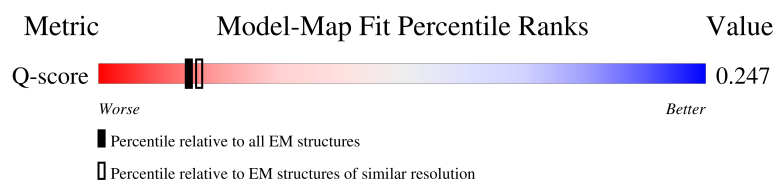
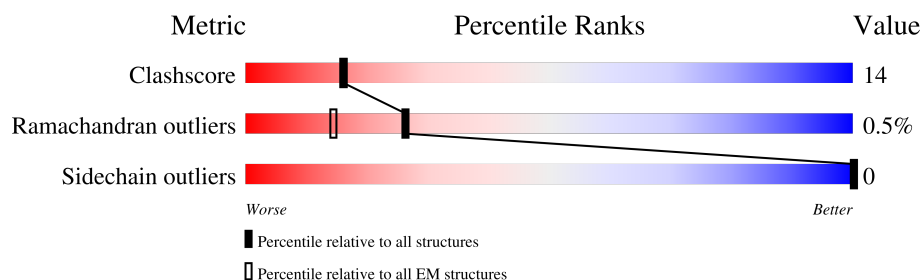
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.11 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	5659 (3.62 - 4.61)

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	I	147	 6% 44% 56%
2	A	99	 22% 77% 23%
2	E	99	 16% 75% 23% ..
3	B	87	 17% 70% 28% ..

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Mol	Chain	Length	Quality of chain
3	F	87	
4	C	111	
4	G	111	
5	D	96	
5	H	96	
6	J	147	
7	M	4128	
8	N	20	
9	K	609	
10	L	732	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 97746 atoms, of which 47931 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 DNA chain called DNA (147-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
1	I	147	Total	C	H	N	O	P	0	0
			4682	1435	1651	566	883	147		

- Molecule 2 is a protein called Histone H3.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	A	99	Total	C	H	N	O	S	0	0
			1678	515	861	158	141	3		
2	E	98	Total	C	H	N	O	S	0	0
			1667	512	856	157	139	3		

- Molecule 3 is a protein called Histone H4.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	B	86	Total	C	H	N	O	S	0	0
			1453	440	755	141	116	1		
3	F	83	Total	C	H	N	O	S	0	0
			1372	418	710	129	114	1		

- Molecule 4 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	C	108	Total	C	H	N	O		0	0
			1701	520	876	159	146			
4	G	111	Total	C	H	N	O		0	0
			1783	539	925	169	150			

- Molecule 5 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	D	96	Total	C	H	N	O	S	0	0
			1547	475	789	140	141	2		

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Mol	Chain	Residues	Atoms						AltConf	Trace
5	H	95	Total	C	H	N	O	S	0	0
			1521	469	774	136	140	2		

- Molecule 6 is a DNA chain called DNA (147-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
6	J	147	Total	C	H	N	O	P	0	0
			4646	1423	1650	545	881	147		

- Molecule 7 is a protein called DNA-dependent protein kinase catalytic subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	M	3662	Total	C	H	N	O	S	0	0
			58977	18776	29693	4946	5370	192		

- Molecule 8 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	20	Total	C	H	N	O	0	0
			141	60	40	20	21		

- Molecule 9 is a protein called X-ray repair cross-complementing protein 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	K	490	Total	C	H	N	O	S	0	0
			7999	2533	4045	671	733	17		

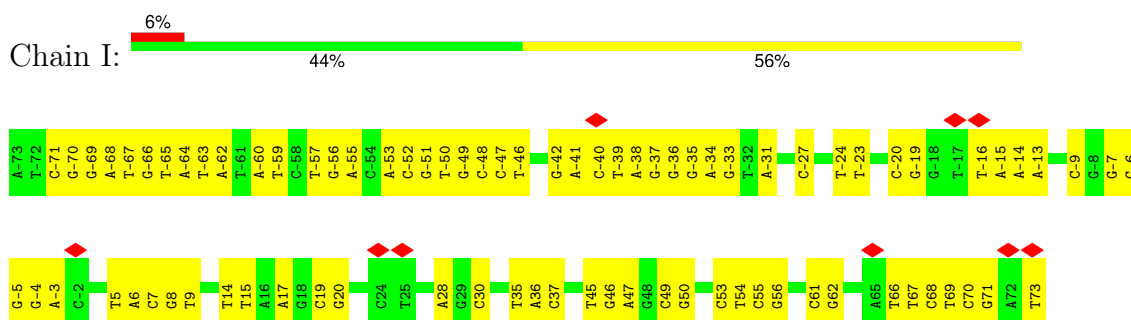
- Molecule 10 is a protein called DNA repair protein Ku80.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	L	535	Total	C	H	N	O	S	0	0
			8579	2736	4306	713	800	24		

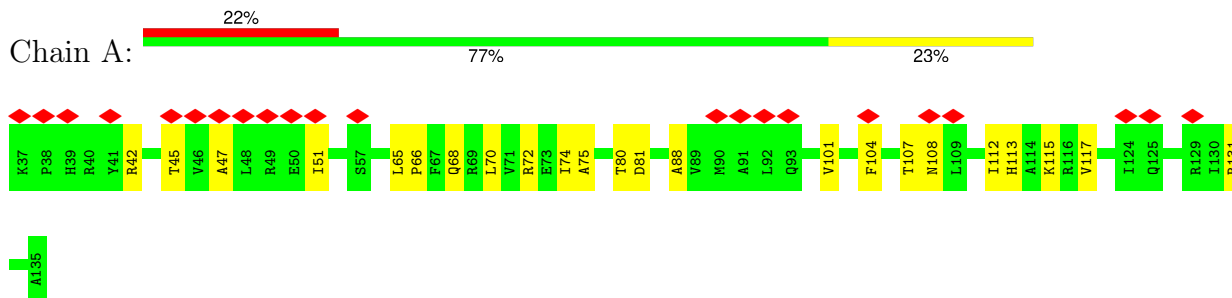
3 Residue-property plots

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.

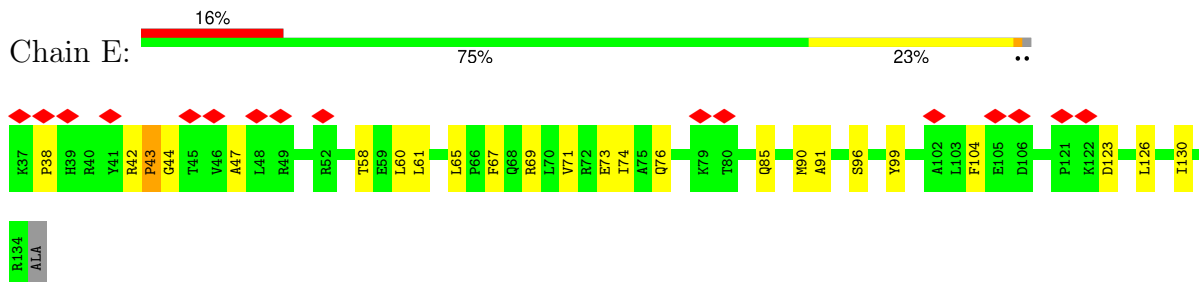
• Molecule 1: DNA (147-MER)



• Molecule 2: Histone H3

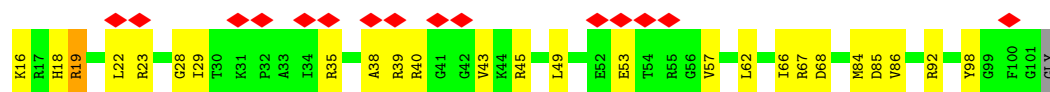


• Molecule 2: Histone H3



• Molecule 3: Histone H4

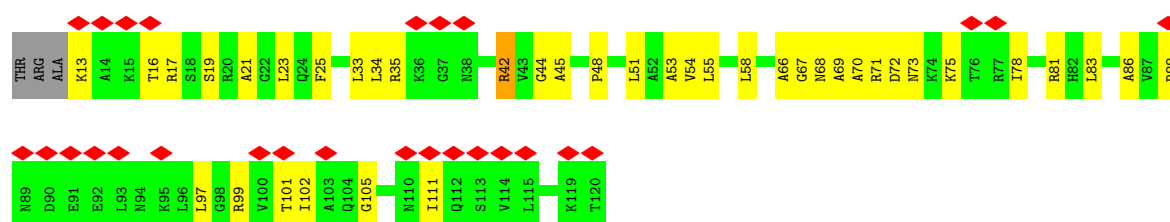




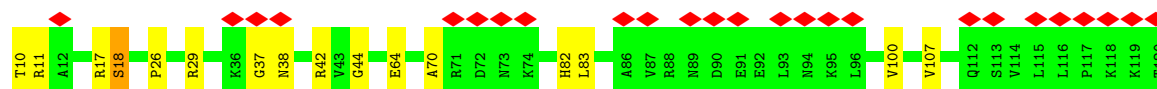
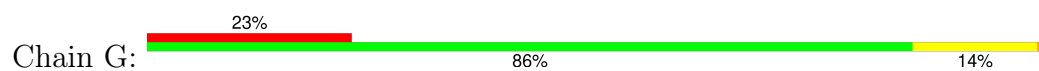
• Molecule 3: Histone H4



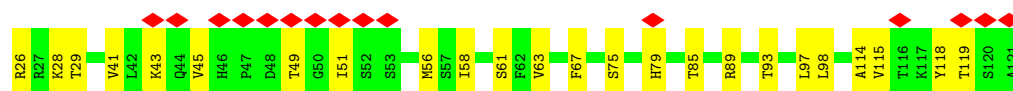
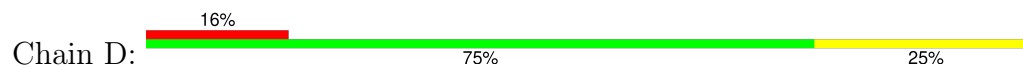
• Molecule 4: Histone H2A



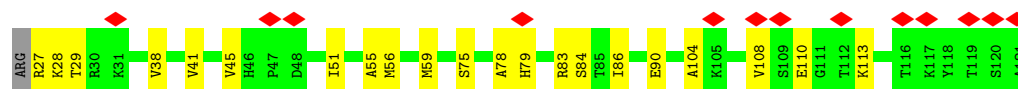
• Molecule 4: Histone H2A



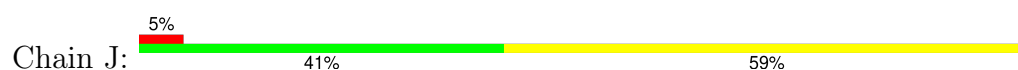
• Molecule 5: Histone H2B

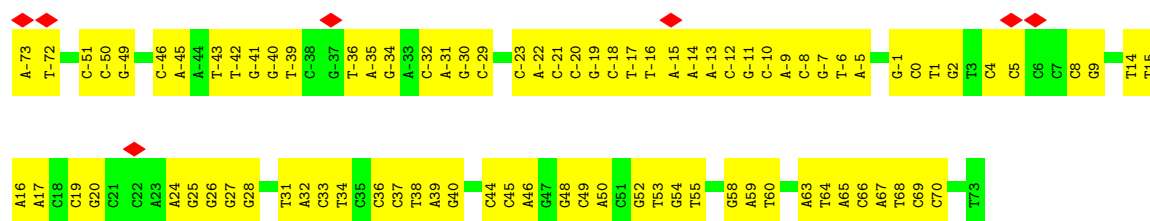


• Molecule 5: Histone H2B

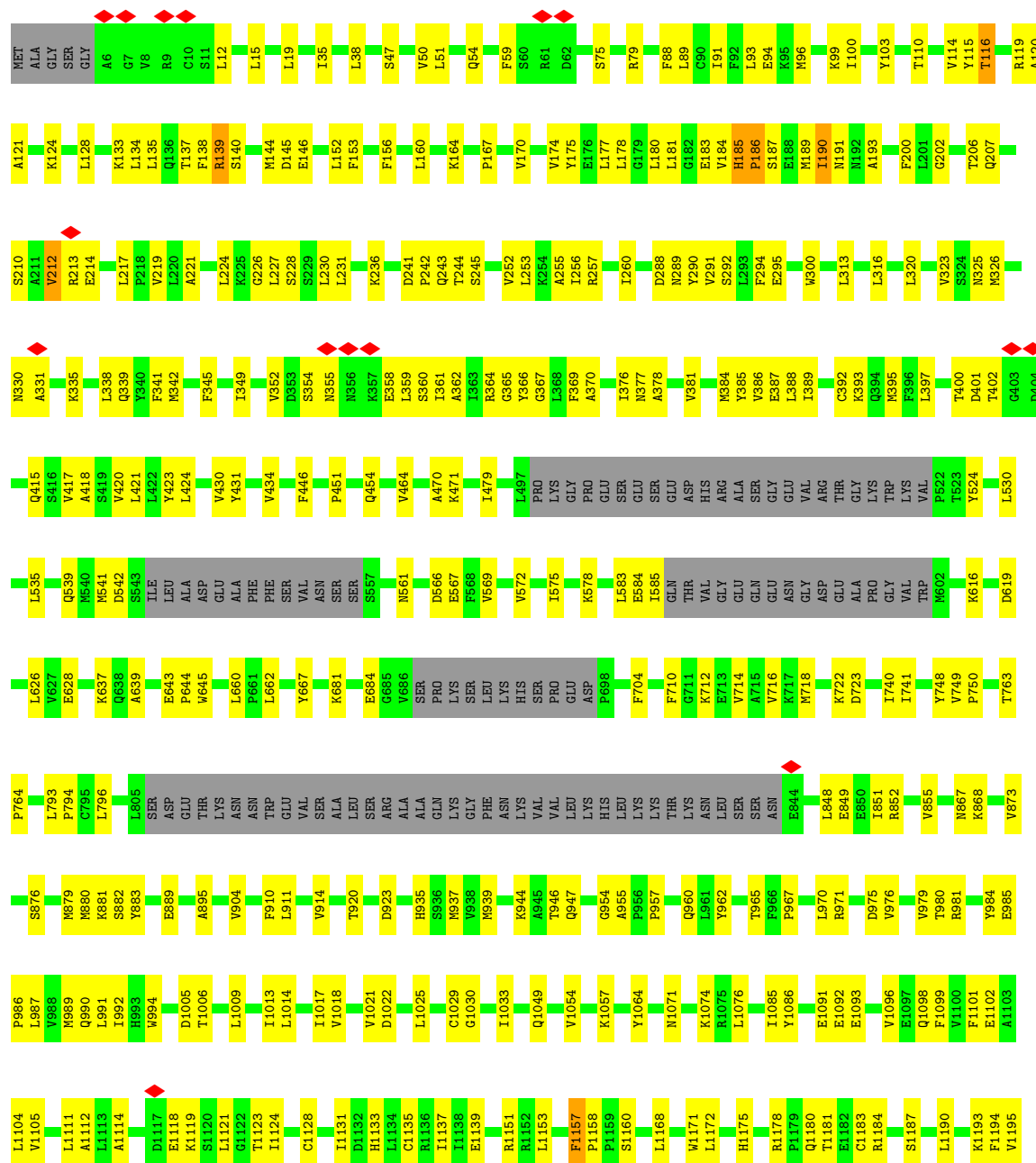


• Molecule 6: DNA (147-MER)





• Molecule 7: DNA-dependent protein kinase catalytic subunit

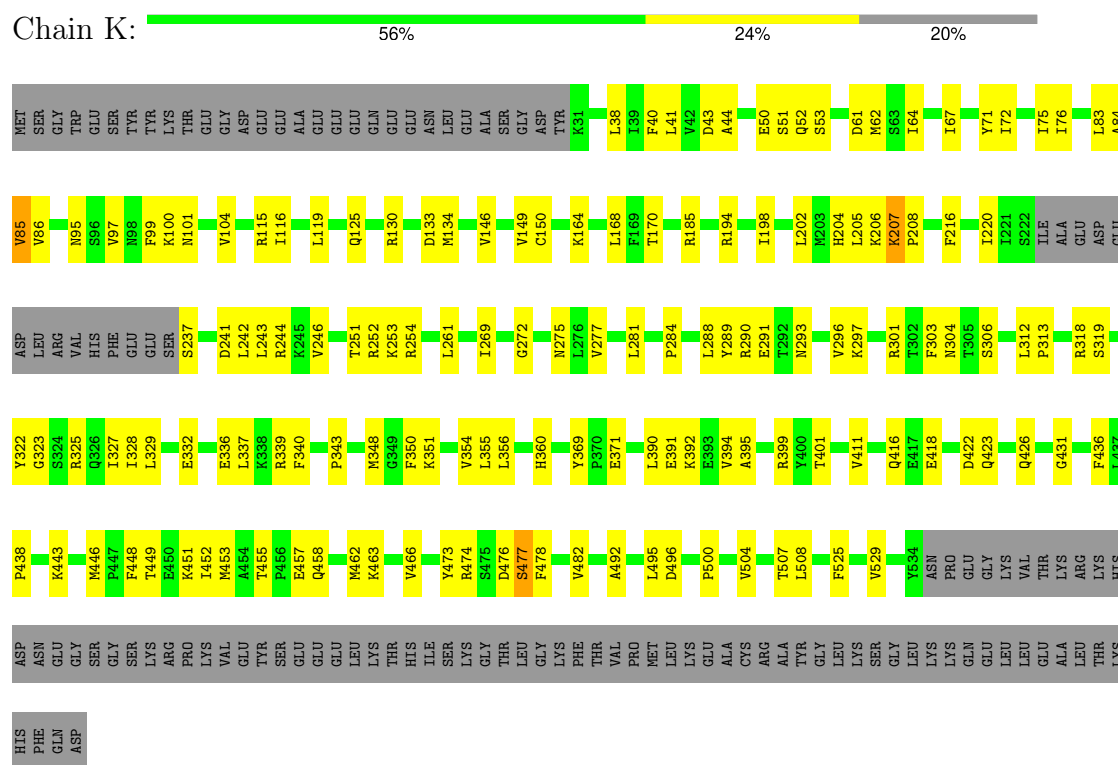


H2527	F2413	A2346	W2245	GLU	MET	L1981	I1876	M1738	L1623	L1528	I1414	I1307	P1196
E2528	D2419	K2347	C2248	ASP	SER	I1982	L1877	Y1739	W1626	V1529	I1415	I1307	R1202
T2529	F2420	Q2348	L2249	PHE	GLN	D1983	D1878	L1747	K1627	S1530	L1418	K1311	D1210
R2530	N2423	Q2350	S2250	ASP	ASP	L1984	W1879	L1750	C1629	S1539	T1424	PHE	G1216
P2532	N2424	H2352	N2266	SER	SER	K1985	V1881	L1765	W1632	T1540	L1431	GLY	V1217
T2536	D2428	Q2353	S2267	THR	THR	ARG	S1882	L1759	E1640	ALA	L1432	THR	S1218
D2537	D2429	N2354	K2268	GLY	GLY	TYR	R1883	E1640	E1640	SER	GLY	GLY	G1219
R2538	Q2432	M2356	L2129	GLN	GLN	PHE	K1886	M1762	V1645	LEU	A1433	ALA	L1220
L2542	T2439	E2357	V2138	SER	SER	PRO	V1889	V1765	L1646	SER	GLY	ASN	N1221
N2543	T2439	Q2275	R2143	TYR	TYR	VAL	V1889	L1766	L1646	GLN	L1436	ARG	N1222
N2544	M2443	L2277	L2144	SER	SER	VAL	S1894	C1767	L1649	GLY	Y1437	THR	T1223
P2544	P2444	G2278	K2162	SER	SER	GLU	G1902	M1774	A1650	I1550	G1438	ARG	F1224
E2551	K2445	T2279	H2165	GLN	GLN	PRO	S1903	E1775	I1652	I1551	D1440	THR	E1225
A2558	L2451	W2281	S2166	ASP	ASP	MET	T1906	G1789	T1655	H1552	A1441	E1326	Q1231
P2575	R2452	Q2295	P2167	ARG	ARG	GLU	E1910	Q1794	D1656	F1553	D1444	P1232	P1232
M2576	L2455	S2296	L2168	PRO	PRO	LYS	E1910	Q1794	F1661	H1555	L1448	G1294	S1233
L2581	V2458	S2297	Q2170	ALA	ALA	LYS	K1917	R1805	F1669	G1556	L1448	I1235	P1238
S2582	V2462	E2298	L2171	THR	THR	TYR	L1918	R1805	T1663	E1557	A1449	T1336	Q1238
E2583	S2463	Y2299	F2300	GLY	GLY	ILE	C1919	K1807	G1666	Y1558	Y1452	V1337	P1239
C2584	H2464	Q2301	E2175	ARG	ARG	ILE	T1920	R1816	S1667	L1562	L1458	V1338	Y1243
Y2589	Q2373	W2304	N2176	PHE	PHE	ILE	A1922	Q1817	F1668	E1565	L1464	V1339	LEU
T2590	D2374	W2307	H2183	ARG	ARG	LYS	F1923	S1818	F1669	I1566	L1467	R1340	ARG
I2591	A2375	E2368	M2185	GLU	GLU	LYS	L1933	R1819	F1672	I1567	L1475	I1341	GLY
D2592	D2376	F2309	V2186	GLN	GLN	ALA	L1934	V1820	Y1675	L1571	L1476	E1343	PHE
ASP	R2377	F2309	W2187	ARG	ARG	ARG	E1935	D1821	L1678	N1574	H1476	M1350	L1249
TRP	D2378	W2187	E2310	ASP	ASP	ALA	R1936	R1822	L1679	L1575	H1477	T1351	L1250
ARG	M2379	R2311	E2188	PRO	PRO	ALA	R1937	L1824	D1685	D1576	S1478	A1252	A1252
THR	N2380	R2311	T2192	THR	THR	ASN	R1938	W1829	Y1479	L1577	Y1479	G1364	L1267
THR	A2381	V2315	I2193	VAL	VAL	GLY	H1941	D1834	G1480	L1580	G1480	H1367	L1267
THR	V2382	Y2316	W2196	ASP	ASP	ASP	Y1945	E1834	T1481	E1581	T1481	L1368	L1261
THR	F2383	A2317	T2197	SER	SER	ASP	N1946	D1834	L1688	L1582	E1482	M1369	A1262
THR	A2318	A2319	Q2198	VAL	VAL	GLY	K1947	R1837	G1689	L1582	L1483	G1387	Y1271
THR	A2320	E2321	L2199	LEU	LEU	PRO	A1948	F1839	G1690	M1583	L1484	L1372	Y1267
THR	E2321	L2327	A2200	GLU	GLU	SER	I1949	F1840	V1693	D1588	Y1488	F1384	I1271
THR	L2327	R2328	T2201	LEU	LEU	TYR	I1952	I1843	L1696	M1589	P1493	M1385	R1274
THR	R2328	Y2329	P2202	MET	MET	TYR	V1955	E1843	P1697	T1590	P1493	I1386	R1274
THR	Y2329	V2330	G2204	SER	SER	LEU	F1956	L1851	E1708	K1591	P1493	G1387	R1274
THR	V2330	W2205	G2204	SER	SER	LEU	N1957	K1852	E1708	M1592	C1499	V1391	L1282
THR	M2331	M2305	P2206	LEU	LEU	ASP	L1959	R1855	R1712	V1596	L1500	M1392	G1283
THR	K2334	L2216	L2216	GLY	GLY	ASP	Q1963	T1856	Q1716	L1597	P1501	L1395	T1284
THR	E2338	M2220	M2220	GLY	GLY	THR	F1967	D1864	V1719	M1600	L1515	V1398	Q1287
THR	E2339	V2223	V2223	PRO	PRO	THR	S1968	T1865	P1723	K1612	A1518	V1398	S1288
THR	S2340	L2341	L2341	GLY	GLY	THR	F1967	D1864	P1723	K1612	A1518	V1398	S1288
THR	E2340	C2342	C2342	PRO	PRO	THR	S1968	T1865	P1723	K1612	A1518	V1398	S1288
THR	E2343	L2344	L2344	GLY	GLY	THR	F1967	D1864	P1723	K1612	A1518	V1398	S1288
THR	V2345	L2241	L2241	GLY	GLY	THR	S1968	T1865	P1723	K1612	A1518	V1398	S1288
THR	Y2412	Y2412	Y2412	GLY	GLY	THR	S1968	T1865	P1723	K1612	A1518	V1398	S1288



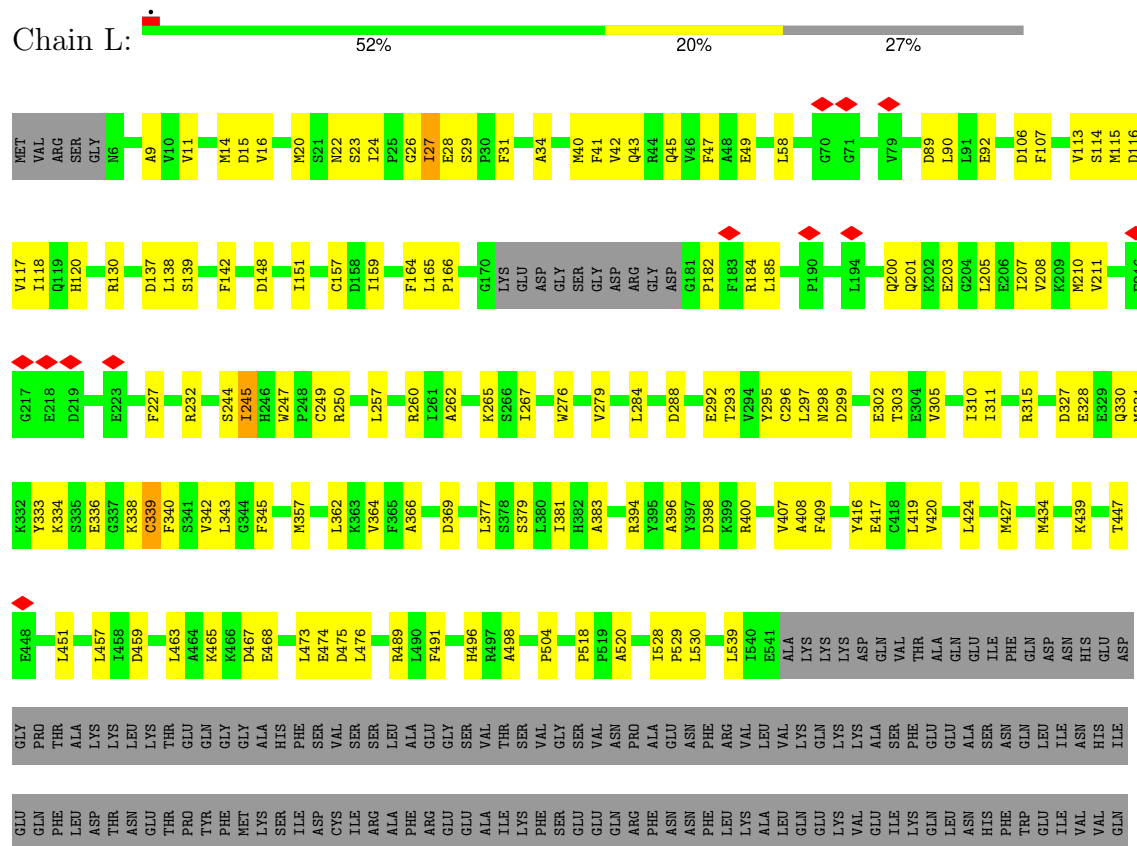
• Molecule 9: X-ray repair cross-complementing protein 6

Chain K:



• Molecule 10: DNA repair protein Ku80

Chain L:



ASP	GLY	ILE	THR	LEU	ILE	THR	LYS	GLU	GLU	ALA	SER	GLY	SER	SER	VAL	THR	ALA	GLU	GLU	ALA	LYS	LYS	PHE	LEU	ALA	PRO	LYS	LYS	ASP	LYS	PRO	SER	GLY	ASP	THR	ALA	ALA	VAL	PHE	GLU	GLU	GLY	GLY	D724	V725	L728	L729	D730	M731	L732
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	96187	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.843	Depositor
Minimum map value	-0.364	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.25	Depositor
Map size ($\text{\AA}$)	446.4, 446.4, 446.4	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.86, 1.86, 1.86	Depositor

5 Model quality

5.1 Standard geometry

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	I	0.23	0/3403	0.47	0/5255
2	A	0.13	0/829	0.37	0/1111
2	E	0.17	0/823	0.47	0/1104
3	B	0.14	0/706	0.47	0/943
3	F	0.15	0/669	0.45	0/894
4	C	0.16	0/835	0.47	0/1127
4	G	0.14	0/868	0.40	0/1169
5	D	0.13	0/769	0.39	0/1032
5	H	0.13	0/758	0.33	0/1018
6	J	0.24	0/3357	0.47	0/5174
7	M	0.19	0/29884	0.48	3/40387 (0.0%)
9	K	0.15	0/4031	0.43	0/5429
10	L	0.16	0/4359	0.45	2/5881 (0.0%)
All	All	0.19	0/51291	0.47	5/70524 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	E	0	1
3	B	0	1
4	C	0	1
7	M	0	8
9	K	0	1
All	All	0	12

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	L	339	CYS	CA-C-N	6.74	133.82	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	L	339	CYS	C-N-CA	6.74	133.82	121.70
7	M	1221	ILE	N-CA-C	-6.34	106.79	112.12
7	M	190	ILE	N-CA-C	-6.24	105.26	111.88
7	M	212	VAL	N-CA-C	-5.80	107.03	111.62

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	19	ARG	Sidechain
4	C	42	ARG	Peptide
2	E	38	PRO	Peptide
9	K	207	LYS	Peptide
7	M	185	HIS	Peptide
7	M	2197	THR	Peptide
7	M	2351	GLN	Peptide
7	M	2378	PHE	Peptide
7	M	2403	CYS	Peptide
7	M	2779	ASP	Peptide
7	M	2780	LEU	Peptide
7	M	3313	SER	Peptide

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	I	3031	1651	1651	96	0
2	A	817	861	858	26	0
2	E	811	856	853	25	0
3	B	698	755	752	30	0
3	F	662	710	709	26	0
4	C	825	876	875	30	0
4	G	858	925	922	13	0
5	D	758	789	786	22	0
5	H	747	774	773	16	0
6	J	2996	1650	1650	102	0
7	M	29284	29693	29680	873	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	N	101	40	24	4	0
9	K	3954	4045	4042	142	0
10	L	4273	4306	4303	128	0
All	All	49815	47931	47878	1388	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 14.

All (1388) 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)
7:M:2216:LEU:HD21	7:M:2241:LEU:HD22	1.45	0.96
4:C:17:ARG:NH1	6:J:45:DC:OP1	2.02	0.92
7:M:3499:ILE:HD11	7:M:3521:ILE:HD13	1.52	0.91
7:M:879:MET:HE3	7:M:879:MET:O	1.71	0.90
7:M:2424:MET:O	7:M:2432:GLN:NE2	2.04	0.90
4:C:35:ARG:NH2	6:J:40:DG:OP2	2.05	0.90
1:I:-9:DC:O2	6:J:9:DG:N2	2.05	0.88
7:M:358:GLU:OE2	7:M:360:SER:OG	1.92	0.88
7:M:1484:LEU:HD21	7:M:1531:LEU:HD21	1.57	0.87
7:M:923:ASP:OD2	7:M:2800:ARG:NH2	2.07	0.86
9:K:194:ARG:NH2	9:K:220:ILE:O	2.09	0.86
10:L:400:ARG:O	10:L:400:ARG:NH1	2.09	0.86
7:M:236:LYS:O	7:M:245:SER:OG	1.93	0.85
7:M:1557:GLU:OE2	7:M:1591:LYS:NZ	2.09	0.85
7:M:1829:TRP:O	7:M:1883:ARG:NH2	2.09	0.85
7:M:681:LYS:NZ	7:M:684:GLU:OE2	2.09	0.85
2:A:131:ARG:NE	2:E:130:ILE:O	2.09	0.84
9:K:492:ALA:O	9:K:496:ASP:N	2.11	0.84
1:I:30:DC:OP1	5:D:28:LYS:NZ	2.10	0.83
7:M:992:ILE:HD13	7:M:1009:LEU:HD21	1.59	0.83
1:I:17:DA:OP1	2:E:69:ARG:NH1	2.12	0.82
1:I:-53:DA:N6	6:J:54:DG:C2	2.48	0.82
7:M:3326:GLN:NE2	7:M:3327:ASN:OD1	2.12	0.82
10:L:184:ARG:NH2	10:L:518:PRO:O	2.13	0.82
7:M:3499:ILE:HD13	7:M:3502:MET:HE3	1.63	0.81
7:M:2462:VAL:HG23	7:M:2473:MET:HE1	1.62	0.81
5:H:38:VAL:HG11	5:H:59:MET:HE3	1.62	0.80
7:M:3828:TYR:OH	7:M:4125:GLU:OE2	1.97	0.80
9:K:325:ARG:NH2	10:L:92:GLU:OE2	2.15	0.79
7:M:2857:CYS:O	7:M:2861:ILE:HD12	1.83	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:27:DC:OP1	5:H:27:ARG:NH2	2.16	0.78
3:B:19:ARG:HD2	6:J:15:DT:H2"	1.64	0.78
7:M:364:ARG:NH1	7:M:415:GLN:OE1	2.16	0.78
7:M:849:GLU:N	7:M:849:GLU:OE1	2.17	0.77
7:M:2825:THR:OG1	7:M:2828:GLU:OE2	2.03	0.77
1:I:3:DA:OP1	2:A:117:VAL:N	2.17	0.77
1:I:34:DA:OP1	5:D:85:THR:N	2.18	0.76
10:L:297:LEU:O	10:L:303:THR:OG1	2.01	0.76
7:M:1112:ALA:HB1	7:M:1180:GLN:NE2	2.00	0.76
7:M:134:LEU:O	7:M:137:THR:OG1	2.03	0.75
9:K:284:PRO:O	10:L:315:ARG:NH2	2.19	0.75
1:I:9:DC:N3	6:J:9:DG:N1	2.33	0.74
7:M:2340:SER:O	7:M:2344:LEU:HD23	1.88	0.74
7:M:139:ARG:NH1	7:M:140:SER:OG	2.21	0.74
7:M:1612:LYS:NZ	7:M:1656:ASP:OD2	2.21	0.74
7:M:2862:SER:HA	7:M:2868:LEU:HD22	1.69	0.74
7:M:3530:VAL:HG22	7:M:3562:LEU:HD11	1.69	0.73
7:M:2216:LEU:HD21	7:M:2241:LEU:CD2	2.18	0.73
1:I:19:DG:N7	3:B:16:LYS:N	2.36	0.73
7:M:962:TYR:HA	7:M:965:THR:HG22	1.68	0.73
7:M:3290:SER:OG	7:M:3291:GLN:OE1	2.07	0.73
7:M:2351:GLN:N	7:M:2351:GLN:OE1	2.22	0.72
7:M:378:ALA:O	7:M:381:VAL:HG22	1.88	0.72
7:M:1017:ILE:HG23	7:M:1018:VAL:HG13	1.71	0.72
7:M:3455:LYS:NZ	7:M:3485:LYS:O	2.23	0.72
7:M:2523:ASN:OD1	7:M:2524:PHE:N	2.22	0.72
7:M:3971:MET:O	7:M:3974:MET:N	2.20	0.72
7:M:1274:ARG:NH1	7:M:1351:THR:HG22	2.04	0.72
7:M:2374:LEU:O	7:M:2377:ARG:N	2.23	0.71
1:I:55:DA:N1	6:J:54:DG:N2	2.39	0.71
4:C:13:LYS:O	4:C:17:ARG:NE	2.24	0.71
7:M:2582:SER:OG	7:M:2583:GLU:OE1	2.08	0.71
7:M:1565:GLU:N	7:M:1565:GLU:OE1	2.23	0.71
7:M:2274:ILE:HD11	7:M:2318:ALA:HB1	1.73	0.70
3:B:35:ARG:NH2	6:J:8:DC:OP2	2.25	0.70
7:M:2183:HIS:CE1	7:M:2186:VAL:HG23	2.27	0.70
7:M:1484:LEU:HD13	7:M:1488:TYR:CZ	2.26	0.70
10:L:137:ASP:OD2	10:L:139:SER:OG	2.09	0.69
9:K:288:LEU:O	10:L:311:ILE:N	2.26	0.69
7:M:3170:ASP:N	7:M:3174:ASP:OD2	2.23	0.69
1:I:37:DC:O2	4:G:42:ARG:NH2	2.24	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:1855:PHE:O	7:M:1856:THR:HG23	1.93	0.69
9:K:206:LYS:NZ	9:K:237:SER:O	2.20	0.69
9:K:418:GLU:OE1	9:K:426:GLN:NE2	2.26	0.68
7:M:1478:SER:O	7:M:1479:VAL:HG22	1.93	0.68
7:M:4081:ALA:O	7:M:4090:ARG:NH2	2.26	0.68
7:M:341:PHE:O	7:M:345:PHE:N	2.26	0.68
7:M:2379:MET:HE3	7:M:2403:CYS:SG	2.34	0.68
7:M:2589:TYR:O	7:M:2775:TYR:OH	2.10	0.68
7:M:3499:ILE:HD13	7:M:3502:MET:CE	2.24	0.68
9:K:416:GLN:N	9:K:431:GLY:O	2.27	0.68
6:J:58:DG:N3	10:L:400:ARG:NH2	2.41	0.68
7:M:1894:SER:O	7:M:1903:SER:OG	2.12	0.68
7:M:2379:MET:HE1	7:M:2405:VAL:HG12	1.74	0.68
7:M:1304:HIS:NE2	7:M:1307:ILE:O	2.27	0.68
7:M:2239:LYS:HB2	7:M:2279:ILE:HD12	1.75	0.67
7:M:320:LEU:HA	7:M:323:VAL:HG12	1.76	0.67
7:M:2899:ARG:O	7:M:2899:ARG:NE	2.27	0.67
1:I:8:DG:OP1	3:F:39:ARG:NH1	2.26	0.67
9:K:458:GLN:HB3	9:K:529:VAL:HG12	1.76	0.67
7:M:1910:GLU:N	7:M:1910:GLU:OE1	2.26	0.67
9:K:272:GLY:N	9:K:369:TYR:O	2.28	0.67
9:K:463:LYS:HA	9:K:466:VAL:HG12	1.75	0.67
7:M:2201:THR:HG22	7:M:2245:TRP:CZ3	2.30	0.67
10:L:26:GLY:O	10:L:28:GLU:N	2.27	0.67
10:L:417:GLU:OE1	10:L:417:GLU:N	2.28	0.67
7:M:2320:ALA:HB1	7:M:2362:VAL:HG21	1.77	0.67
7:M:1112:ALA:HB1	7:M:1180:GLN:CD	2.20	0.66
7:M:370:ALA:HB3	7:M:423:TYR:CD2	2.31	0.66
5:H:84:SER:N	6:J:-34:DG:OP1	2.29	0.66
7:M:3788:LEU:HD11	7:M:3911:ILE:HD13	1.77	0.66
4:C:111:ILE:O	4:C:111:ILE:HG22	1.96	0.66
7:M:1864:ASP:OD1	7:M:1865:THR:N	2.29	0.66
7:M:3689:ASP:OD1	7:M:3690:PHE:N	2.29	0.66
9:K:476:ASP:HA	10:L:427:MET:SD	2.36	0.66
7:M:2330:VAL:HG11	7:M:2342:CYS:HB3	1.77	0.66
9:K:133:ASP:OD1	9:K:134:MET:N	2.29	0.66
7:M:2201:THR:HG22	7:M:2245:TRP:CE3	2.30	0.66
7:M:3176:MET:HE3	7:M:3246:ALA:HA	1.76	0.65
7:M:2351:GLN:O	7:M:2355:THR:OG1	2.10	0.65
7:M:2930:TYR:HA	7:M:2933:ILE:HG22	1.78	0.65
7:M:3919:GLY:O	7:M:3946:PHE:N	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:3531:TYR:O	7:M:3535:ILE:HD12	1.97	0.65
7:M:4012:ASP:OD1	7:M:4013:TRP:N	2.30	0.65
10:L:339:CYS:HB3	10:L:340:PHE:HA	1.76	0.65
7:M:139:ARG:HG2	7:M:140:SER:H	1.62	0.65
7:M:970:LEU:HD23	7:M:970:LEU:O	1.95	0.65
9:K:242:LEU:O	9:K:246:VAL:HG22	1.97	0.65
7:M:290:TYR:OH	7:M:295:GLU:OE2	2.09	0.65
7:M:15:LEU:HB3	7:M:38:LEU:HD21	1.78	0.65
7:M:3029:LYS:O	7:M:3032:SER:OG	2.14	0.65
7:M:1369:MET:HE1	7:M:1415:LEU:HA	1.78	0.65
7:M:1588:ASP:OD1	7:M:1589:ASN:N	2.28	0.64
10:L:200:GLN:NE2	10:L:203:GLU:OE2	2.29	0.64
7:M:575:ILE:HD11	7:M:626:LEU:HD22	1.78	0.64
7:M:2375:ALA:HB1	7:M:2403:CYS:SG	2.37	0.64
9:K:448:PHE:HB2	10:L:416:TYR:CD1	2.32	0.64
7:M:1343:GLU:OE1	7:M:1398:VAL:HG23	1.96	0.64
7:M:400:THR:HG22	7:M:401:ASP:H	1.62	0.64
7:M:1289:SER:O	7:M:1292:LYS:NZ	2.30	0.64
3:F:37:LEU:HD13	3:F:40:ARG:HD3	1.79	0.64
7:M:2376:ASP:OD1	7:M:2377:ARG:N	2.31	0.64
9:K:40:PHE:CZ	9:K:83:LEU:HD22	2.33	0.64
9:K:455:THR:OG1	9:K:457:GLU:OE1	2.14	0.64
7:M:3816:LEU:O	7:M:3819:THR:HG22	1.97	0.64
7:M:984:TYR:O	7:M:987:LEU:N	2.31	0.63
9:K:41:LEU:HD23	9:K:168:LEU:HD21	1.79	0.63
7:M:1805:PHE:O	7:M:1816:ARG:NH2	2.31	0.63
7:M:2363:CYS:O	7:M:2367:VAL:N	2.31	0.63
7:M:4003:ASP:HA	7:M:4044:ILE:HD12	1.81	0.63
9:K:41:LEU:HD23	9:K:168:LEU:CD2	2.28	0.63
6:J:54:DG:H2"	6:J:55:DT:H71	1.81	0.63
10:L:20:MET:HE1	10:L:227:PHE:CE2	2.33	0.63
2:A:88:ALA:HB1	3:B:86:VAL:HG11	1.81	0.63
7:M:349:ILE:HA	7:M:352:VAL:HG13	1.79	0.63
7:M:2409:THR:OG1	7:M:2410:GLU:OE1	2.15	0.63
1:I:8:DG:OP2	3:F:39:ARG:NH2	2.32	0.62
7:M:967:PRO:O	7:M:971:ARG:NH1	2.32	0.62
7:M:1484:LEU:HD13	7:M:1488:TYR:CE1	2.34	0.62
7:M:3133:GLN:HE22	7:M:3182:ILE:HD13	1.64	0.62
7:M:1049:GLN:HG2	7:M:1054:VAL:HG23	1.81	0.62
7:M:2389:PHE:O	7:M:2390:HIS:ND1	2.31	0.62
7:M:3937:VAL:HG23	7:M:3937:VAL:O	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:3442:TYR:O	7:M:3446:VAL:HG22	1.99	0.62
7:M:1350:ASN:O	7:M:1351:THR:OG1	2.11	0.62
7:M:987:LEU:HD23	7:M:991:LEU:HD23	1.80	0.62
7:M:1092:GLU:N	7:M:1092:GLU:OE1	2.32	0.62
7:M:3470:GLN:HG2	7:M:4004:VAL:HG11	1.81	0.62
9:K:251:THR:O	9:K:252:ARG:HG2	1.99	0.62
10:L:463:LEU:HD12	10:L:476:LEU:HB3	1.82	0.61
1:I:-67:DT:OP1	7:M:119:ARG:NH2	2.33	0.61
7:M:3880:ALA:HB1	7:M:3969:ASN:HD21	1.65	0.61
9:K:277:VAL:HG11	10:L:357:MET:SD	2.40	0.61
9:K:290:ARG:HA	10:L:311:ILE:HG13	1.82	0.61
7:M:3570:ASP:OD2	7:M:3686:TRP:NE1	2.32	0.61
10:L:164:PHE:C	10:L:165:LEU:HD12	2.25	0.61
7:M:1738:ASN:OD1	7:M:1739:TYR:N	2.34	0.61
7:M:2481:HIS:HA	7:M:2484:TYR:CE1	2.35	0.61
10:L:284:LEU:O	10:L:284:LEU:HD12	1.99	0.61
7:M:2353:GLN:O	7:M:2353:GLN:NE2	2.33	0.61
7:M:2868:LEU:HD23	7:M:2868:LEU:O	2.00	0.61
10:L:245:ILE:O	10:L:245:ILE:HG23	2.00	0.61
7:M:1902:GLY:O	7:M:1906:THR:HG23	2.00	0.61
7:M:2428:ASP:O	7:M:2429:ASP:OD1	2.18	0.61
9:K:297:LYS:NZ	10:L:299:ASP:OD1	2.34	0.61
7:M:2869:LEU:HD13	7:M:2896:ALA:HA	1.82	0.60
7:M:1880:MET:SD	7:M:1881:TYR:N	2.74	0.60
5:D:61:SER:OG	3:F:101:GLY:N	2.27	0.60
10:L:16:VAL:HG12	10:L:16:VAL:O	2.01	0.60
7:M:1283:GLY:O	7:M:1284:THR:HG22	2.01	0.60
7:M:3793:VAL:HG22	7:M:3803:ILE:HG23	1.84	0.60
7:M:3470:GLN:NE2	7:M:3498:TRP:CD2	2.70	0.59
7:M:3243:ILE:HG21	7:M:3259:LEU:HD21	1.84	0.59
7:M:1151:ARG:NH2	7:M:1160:SER:O	2.35	0.59
7:M:1937:ARG:O	7:M:1941:HIS:ND1	2.33	0.59
7:M:1458:LEU:HD13	7:M:1467:ILE:HG21	1.84	0.59
7:M:3758:LEU:HD21	7:M:3801:GLY:HA3	1.85	0.59
7:M:2424:MET:HE1	7:M:2439:ILE:HD11	1.85	0.59
7:M:1525:CYS:SG	7:M:1574:ASN:ND2	2.76	0.59
7:M:3468:LEU:O	7:M:3472:ILE:HD12	2.03	0.59
7:M:1364:CYS:O	7:M:1367:HIS:N	2.35	0.59
7:M:2304:VAL:O	7:M:2307:MET:HE2	2.02	0.59
7:M:3234:CYS:SG	7:M:3238:MET:HE2	2.43	0.58
9:K:337:LEU:O	10:L:489:ARG:NE	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:462:MET:SD	10:L:383:ALA:HB1	2.42	0.58
7:M:388:LEU:HD22	7:M:420:VAL:HG11	1.85	0.58
7:M:880:MET:HE1	7:M:3896:ALA:HB1	1.85	0.58
7:M:1118:GLU:OE2	7:M:1119:LYS:N	2.36	0.58
7:M:2464:HIS:O	7:M:2470:ARG:NH2	2.36	0.58
7:M:3544:ASP:O	7:M:3549:HIS:NE2	2.36	0.58
7:M:1304:HIS:O	7:M:1334:LYS:NZ	2.36	0.58
7:M:3755:GLY:N	7:M:3799:ARG:O	2.36	0.58
7:M:1105:VAL:HG23	7:M:1171:TRP:CZ2	2.39	0.58
7:M:2170:GLN:O	7:M:2170:GLN:NE2	2.32	0.58
10:L:296:CYS:O	10:L:298:ASN:ND2	2.36	0.58
7:M:2451:LEU:O	7:M:2455:LEU:HD23	2.03	0.58
9:K:354:VAL:HG13	9:K:355:LEU:HD12	1.85	0.58
7:M:2542:LEU:HD21	7:M:2558:ALA:HB2	1.86	0.58
7:M:3499:ILE:HD11	7:M:3521:ILE:CD1	2.28	0.58
9:K:418:GLU:OE2	10:L:439:LYS:NZ	2.34	0.58
9:K:500:PRO:HB2	10:L:331:MET:HE1	1.86	0.58
6:J:14:DT:O3'	6:J:15:DT:H2'	2.04	0.58
7:M:3789:ARG:HH21	7:M:3806:LEU:HD11	1.67	0.58
10:L:148:ASP:HA	10:L:151:ILE:HD12	1.84	0.58
7:M:47:SER:OG	7:M:50:VAL:HG22	2.03	0.58
7:M:3729:MET:HE2	7:M:3729:MET:HA	1.85	0.58
7:M:873:VAL:HG23	7:M:876:SER:HB3	1.86	0.57
7:M:2362:VAL:HA	7:M:2365:ASN:HB3	1.85	0.57
7:M:3489:SER:O	7:M:3490:VAL:HG13	2.04	0.57
7:M:3912:CYS:HG	7:M:3961:PHE:HD1	1.46	0.57
7:M:3912:CYS:SG	7:M:3961:PHE:CD1	2.95	0.57
7:M:193:ALA:HB2	7:M:230:LEU:HD11	1.84	0.57
7:M:352:VAL:HB	7:M:362:ALA:HB2	1.86	0.57
7:M:970:LEU:HD23	7:M:1025:LEU:HD11	1.87	0.57
7:M:1135:CYS:SG	7:M:1190:LEU:HD13	2.44	0.57
5:D:41:VAL:O	5:D:45:VAL:HG23	2.05	0.57
7:M:2307:MET:SD	7:M:2360:PHE:CZ	2.98	0.57
9:K:306:SER:OG	10:L:288:ASP:OD1	2.22	0.57
9:K:328:ILE:C	9:K:329:LEU:HD12	2.30	0.57
1:I:8:DG:O3'	2:E:44:GLY:N	2.38	0.57
7:M:3467:ARG:HE	7:M:3471:ILE:CD1	2.17	0.57
5:D:93:THR:O	5:D:97:LEU:HD23	2.05	0.57
7:M:1529:VAL:HG11	7:M:1581:GLU:OE1	2.05	0.57
7:M:2462:VAL:CG2	7:M:2473:MET:HE1	2.33	0.57
5:D:115:VAL:O	5:D:119:THR:HG23	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:354:SER:OG	7:M:358:GLU:O	2.21	0.57
7:M:3144:PHE:CE1	7:M:3193:ILE:HD11	2.39	0.57
7:M:3838:GLU:O	7:M:3838:GLU:HG2	2.04	0.57
7:M:3856:MET:HB3	7:M:3859:TYR:CE1	2.39	0.57
7:M:1411:TYR:O	7:M:1414:ILE:HG22	2.05	0.57
9:K:246:VAL:HG23	9:K:246:VAL:O	2.05	0.57
7:M:970:LEU:HD21	7:M:1029:CYS:SG	2.44	0.56
7:M:3326:GLN:O	7:M:3330:LEU:HD23	2.04	0.56
7:M:4101:GLU:OE2	7:M:4101:GLU:N	2.34	0.56
7:M:566:ASP:OD1	7:M:645:TRP:NE1	2.37	0.56
7:M:3619:ASP:OD1	7:M:3622:ALA:N	2.36	0.56
9:K:86:VAL:HG22	9:K:104:VAL:HG12	1.86	0.56
4:C:34:LEU:HD21	4:C:51:LEU:HD22	1.85	0.56
7:M:867:ASN:OD1	7:M:868:LYS:N	2.38	0.56
7:M:1372:LEU:HD21	7:M:1403:MET:HE2	1.88	0.56
7:M:3161:LEU:HD12	7:M:3234:CYS:SG	2.46	0.56
7:M:4112:THR:HG22	7:M:4112:THR:O	2.05	0.56
1:I:8:DG:H2'	1:I:9:DT:H71	1.88	0.56
4:G:83:LEU:HD11	5:H:55:ALA:HB1	1.86	0.56
7:M:994:TRP:CZ2	7:M:2581:LEU:HD12	2.41	0.56
7:M:2529:THR:HG23	7:M:2530:ARG:H	1.70	0.56
7:M:291:VAL:O	7:M:294:PHE:N	2.37	0.56
7:M:1593:VAL:HA	7:M:1596:VAL:HG12	1.88	0.56
7:M:2458:VAL:O	7:M:2473:MET:HE3	2.06	0.56
10:L:89:ASP:OD1	10:L:90:LEU:N	2.38	0.56
10:L:327:ASP:OD1	10:L:328:GLU:N	2.39	0.56
7:M:219:VAL:HG12	7:M:221:ALA:H	1.70	0.56
7:M:920:THR:HG22	7:M:920:THR:O	2.06	0.56
7:M:3526:PRO:O	7:M:3530:VAL:HG23	2.06	0.56
7:M:4008:GLU:OE1	7:M:4010:SER:OG	2.15	0.56
7:M:1484:LEU:CD2	7:M:1531:LEU:HD21	2.33	0.55
7:M:3681:LYS:HD2	7:M:3687:MET:HB2	1.88	0.55
10:L:379:SER:O	10:L:383:ALA:HB2	2.05	0.55
4:G:83:LEU:HD11	5:H:55:ALA:CB	2.36	0.55
7:M:1424:THR:O	7:M:1424:THR:HG22	2.06	0.55
7:M:2944:THR:O	7:M:2944:THR:HG22	2.06	0.55
7:M:2584:CYS:SG	7:M:2780:LEU:N	2.74	0.55
7:M:3621:LYS:O	7:M:3621:LYS:HD3	2.05	0.55
9:K:83:LEU:O	9:K:115:ARG:NH2	2.40	0.55
4:C:55:LEU:HD11	5:D:63:VAL:HG13	1.86	0.55
7:M:325:ASN:OD1	7:M:326:MET:N	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:572:VAL:HG23	7:M:626:LEU:HD11	1.86	0.55
7:M:796:LEU:HD23	7:M:796:LEU:O	2.06	0.55
2:A:80:THR:HG22	2:A:81:ASP:N	2.22	0.55
3:B:19:ARG:HD2	6:J:15:DT:C2'	2.35	0.55
3:B:84:MET:HE2	3:B:85:ASP:OD1	2.07	0.55
7:M:430:VAL:HG11	7:M:1640:GLU:HB3	1.89	0.55
7:M:3288:SER:HB2	7:M:3296:GLN:HG3	1.88	0.55
7:M:848:LEU:HD11	7:M:852:ARG:NH2	2.22	0.55
7:M:935:HIS:N	7:M:984:TYR:OH	2.40	0.55
7:M:3065:ILE:HG22	7:M:3069:MET:HE2	1.87	0.55
7:M:1195:VAL:HG23	7:M:1196:PRO:HD3	1.88	0.55
7:M:2405:VAL:HG22	7:M:2406:GLU:N	2.22	0.55
4:G:44:GLY:N	5:H:86:ILE:O	2.39	0.55
7:M:1484:LEU:HD21	7:M:1531:LEU:CD2	2.35	0.55
7:M:1493:PRO:HD3	7:M:1500:LEU:HD12	1.88	0.55
7:M:1955:VAL:HG23	7:M:1956:PHE:H	1.72	0.55
7:M:3271:ASP:OD1	7:M:3272:TRP:N	2.39	0.55
7:M:3634:GLN:NE2	7:M:3635:THR:OG1	2.40	0.55
4:G:70:ALA:HA	4:G:82:HIS:CE1	2.42	0.54
7:M:291:VAL:HG22	7:M:294:PHE:HB3	1.89	0.54
7:M:1483:LEU:HD11	7:M:1514:LEU:HD13	1.89	0.54
7:M:1575:LEU:HD12	7:M:1618:LEU:HA	1.89	0.54
7:M:2361:ILE:O	7:M:2364:LEU:N	2.41	0.54
7:M:2529:THR:HG23	7:M:2530:ARG:N	2.23	0.54
7:M:3458:SER:HB3	7:M:3468:LEU:HD11	1.89	0.54
7:M:1775:GLU:OE2	7:M:1822:ARG:NH2	2.36	0.54
7:M:3595:GLU:O	7:M:3602:ASN:ND2	2.38	0.54
10:L:14:MET:HE3	10:L:15:ASP:O	2.07	0.54
10:L:338:LYS:NZ	10:L:398:ASP:OD2	2.37	0.54
7:M:3269:ARG:NH2	7:M:3271:ASP:OD2	2.41	0.54
7:M:1335:CYS:SG	7:M:1384:PHE:HA	2.48	0.54
7:M:796:LEU:HD21	7:M:855:VAL:CG2	2.37	0.54
7:M:970:LEU:HD11	7:M:1013:ILE:HD13	1.89	0.54
7:M:2327:LEU:HD11	7:M:2345:VAL:HG11	1.88	0.54
7:M:3176:MET:HE3	7:M:3246:ALA:CA	2.38	0.54
9:K:64:ILE:HA	9:K:67:ILE:HG22	1.89	0.54
10:L:11:VAL:HG11	10:L:114:SER:HA	1.88	0.54
1:I:53:DA:H62	6:J:52:DG:N2	2.05	0.54
7:M:1952:ILE:HA	7:M:1955:VAL:HG22	1.89	0.54
7:M:2958:LEU:HD11	7:M:4101:GLU:HG2	1.88	0.54
2:A:68:GLN:OE1	2:A:72:ARG:NH2	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:160:LEU:HD23	7:M:164:LYS:NZ	2.23	0.54
7:M:3961:PHE:CE2	7:M:4107:LEU:HG	2.43	0.54
5:D:29:THR:O	5:D:29:THR:HG22	2.08	0.54
1:I:-24:DT:H2'	1:I:-23:DT:H72	1.90	0.54
8:N:2:UNK:O	8:N:5:UNK:N	2.41	0.54
10:L:465:LYS:NZ	10:L:467:ASP:OD2	2.36	0.54
7:M:796:LEU:HD21	7:M:855:VAL:HG22	1.90	0.53
7:M:1225:GLU:OE2	7:M:1233:SER:OG	2.26	0.53
7:M:3170:ASP:O	7:M:3171:ALA:HB3	2.09	0.53
9:K:97:VAL:HG12	9:K:97:VAL:O	2.08	0.53
7:M:944:LYS:O	7:M:947:GLN:NE2	2.41	0.53
7:M:393:LYS:HE3	7:M:397:LEU:HD11	1.90	0.53
9:K:71:TYR:OH	9:K:115:ARG:NE	2.39	0.53
3:B:53:GLU:O	3:B:57:VAL:HG23	2.08	0.53
7:M:364:ARG:O	7:M:369:PHE:CD1	2.61	0.53
7:M:3953:LEU:O	7:M:3954:PRO:C	2.51	0.53
9:K:476:ASP:C	10:L:427:MET:HE3	2.33	0.53
10:L:467:ASP:O	10:L:468:GLU:HG2	2.08	0.53
1:I:73:DT:N3	6:J:-73:DA:N1	2.57	0.53
7:M:400:THR:HG22	7:M:401:ASP:N	2.23	0.53
7:M:3462:ARG:O	7:M:3464:LYS:NZ	2.40	0.53
7:M:3831:ASP:OD1	7:M:3832:PRO:HD2	2.09	0.53
9:K:446:MET:HE3	10:L:265:LYS:O	2.09	0.53
1:I:-50:DT:H2'	1:I:-49:DG:C8	2.44	0.53
7:M:133:LYS:O	7:M:137:THR:HG23	2.08	0.53
7:M:616:LYS:HG3	7:M:619:ASP:HB3	1.91	0.53
7:M:868:LYS:NZ	7:M:3174:ASP:OD1	2.41	0.53
7:M:1331:ASN:OD1	7:M:1332:TYR:N	2.42	0.53
7:M:1600:MET:SD	7:M:1618:LEU:HD11	2.49	0.53
7:M:2201:THR:HG23	7:M:2248:CYS:HB3	1.89	0.53
7:M:3129:LEU:O	7:M:3132:VAL:HG12	2.08	0.53
7:M:3417:ALA:HA	7:M:3450:MET:HG2	1.89	0.53
7:M:1282:LEU:HD22	7:M:1291:LEU:HD23	1.90	0.53
7:M:1629:CYS:HA	7:M:1632:TRP:CZ3	2.44	0.53
7:M:2188:GLU:O	7:M:2192:THR:HG23	2.09	0.53
7:M:2770:VAL:HG22	7:M:2771:LEU:H	1.72	0.53
1:I:-51:DG:H2'	1:I:-50:DT:H72	1.91	0.53
7:M:2196:TRP:O	7:M:2197:THR:OG1	2.17	0.53
7:M:3023:ASN:O	7:M:3025:PRO:HD3	2.09	0.53
7:M:3475:TYR:N	7:M:3476:PRO:HD2	2.24	0.53
7:M:3793:VAL:HG13	7:M:3803:ILE:CD1	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:354:SER:N	7:M:358:GLU:O	2.37	0.53
7:M:2576:MET:SD	7:M:2785:ILE:HG23	2.49	0.53
7:M:206:THR:HG23	7:M:207:GLN:N	2.22	0.52
7:M:446:PHE:CE2	7:M:454:GLN:OE1	2.62	0.52
7:M:985:GLU:HG3	7:M:986:PRO:HD3	1.92	0.52
7:M:1539:SER:OG	7:M:1553:PHE:N	2.42	0.52
7:M:1850:VAL:O	7:M:1853:SER:OG	2.23	0.52
10:L:407:VAL:HG23	10:L:424:LEU:HG	1.91	0.52
2:E:74:ILE:HD11	3:F:59:LYS:NZ	2.24	0.52
7:M:1332:TYR:O	7:M:1336:THR:HG23	2.09	0.52
10:L:339:CYS:HB3	10:L:340:PHE:CA	2.39	0.52
10:L:142:PHE:CD1	10:L:207:ILE:HD11	2.45	0.52
1:I:-52:DC:H2''	1:I:-51:DG:C8	2.43	0.52
7:M:3329:LEU:O	7:M:3332:THR:OG1	2.23	0.52
7:M:3424:LEU:O	7:M:3427:GLU:C	2.52	0.52
7:M:3470:GLN:CG	7:M:4004:VAL:HG11	2.39	0.52
3:B:19:ARG:O	3:B:19:ARG:HG2	2.09	0.52
3:F:35:ARG:HG2	3:F:51:TYR:CE2	2.44	0.52
9:K:84:ALA:O	9:K:85:VAL:HG12	2.09	0.52
7:M:160:LEU:O	7:M:164:LYS:NZ	2.37	0.52
7:M:342:MET:HE2	7:M:342:MET:HA	1.91	0.52
7:M:3447:VAL:HG23	7:M:3448:GLU:H	1.73	0.52
7:M:3912:CYS:SG	7:M:3961:PHE:HD1	2.32	0.52
9:K:185:ARG:O	9:K:185:ARG:HD2	2.09	0.52
6:J:69:DC:H1'	6:J:70:DC:C6	2.45	0.52
7:M:228:SER:OG	7:M:231:LEU:HD23	2.09	0.52
7:M:1114:ALA:CB	7:M:1124:ILE:HG21	2.39	0.52
9:K:61:ASP:HA	9:K:64:ILE:HG22	1.92	0.52
9:K:422:ASP:OD1	9:K:423:GLN:N	2.43	0.52
7:M:2511:ILE:O	7:M:2511:ILE:HG22	2.09	0.52
9:K:291:GLU:N	9:K:291:GLU:OE1	2.42	0.52
9:K:504:VAL:HG23	9:K:504:VAL:O	2.09	0.52
2:A:101:VAL:HG11	3:B:40:ARG:HD2	1.92	0.52
7:M:848:LEU:HD12	7:M:851:ILE:HD11	1.90	0.52
9:K:448:PHE:HB2	10:L:416:TYR:CG	2.45	0.52
2:E:90:MET:SD	2:E:91:ALA:N	2.83	0.52
7:M:3137:GLU:OE2	7:M:3167:ARG:NH2	2.42	0.52
7:M:939:MET:HA	7:M:939:MET:HE2	1.91	0.51
7:M:1104:LEU:HD22	7:M:1168:LEU:HD11	1.90	0.51
7:M:1386:ILE:HA	7:M:1392:MET:HE1	1.92	0.51
7:M:1567:ILE:O	7:M:1571:LEU:HD23	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:3144:PHE:HE1	7:M:3193:ILE:HD11	1.74	0.51
7:M:2330:VAL:HG13	7:M:2331:MET:N	2.25	0.51
7:M:3137:GLU:HG3	7:M:3182:ILE:HD11	1.92	0.51
7:M:3243:ILE:HD11	7:M:3258:LEU:HB3	1.91	0.51
9:K:100:LYS:NZ	9:K:101:ASN:OD1	2.43	0.51
2:A:113:HIS:CD2	2:E:126:LEU:HD22	2.45	0.51
7:M:2364:LEU:O	7:M:2367:VAL:HG12	2.09	0.51
7:M:3772:ASN:ND2	7:M:3787:GLN:OE1	2.40	0.51
9:K:318:ARG:HD2	10:L:276:TRP:HB3	1.91	0.51
2:E:42:ARG:NE	6:J:-5:DA:OP1	2.43	0.51
7:M:170:VAL:O	7:M:174:VAL:HG23	2.10	0.51
7:M:320:LEU:HD11	7:M:369:PHE:HE2	1.74	0.51
7:M:1981:LEU:HD21	7:M:2088:LEU:HD21	1.93	0.51
7:M:3259:LEU:HD12	7:M:3283:LEU:HD23	1.92	0.51
6:J:67:DA:C8	6:J:68:DT:H72	2.45	0.51
7:M:2168:LEU:HA	7:M:2171:LEU:HB3	1.92	0.51
7:M:2888:VAL:HG23	7:M:3894:PRO:HG2	1.91	0.51
10:L:115:MET:HE1	10:L:157:CYS:SG	2.50	0.51
1:I:61:DC:N4	1:I:62:DG:O6	2.43	0.51
7:M:1235:ILE:HB	7:M:1292:LYS:HE2	1.93	0.51
10:L:116:ASP:OD2	10:L:120:HIS:NE2	2.44	0.51
4:C:69:ALA:HB1	4:C:75:LYS:HB2	1.93	0.51
6:J:-21:DC:C2	6:J:-20:DC:C5	2.99	0.51
7:M:2345:VAL:O	7:M:2349:LEU:HD23	2.10	0.51
7:M:2405:VAL:HG22	7:M:2406:GLU:H	1.75	0.51
4:C:66:ALA:O	4:C:86:ALA:HB3	2.11	0.51
7:M:200:PHE:HB3	7:M:227:LEU:HD22	1.92	0.51
7:M:1111:LEU:HD11	7:M:1131:ILE:HD12	1.92	0.51
7:M:1807:LYS:O	7:M:1816:ARG:NH1	2.44	0.51
2:A:113:HIS:NE2	2:E:123:ASP:OD1	2.41	0.51
7:M:960:GLN:O	7:M:960:GLN:NE2	2.42	0.51
7:M:1190:LEU:HD11	7:M:1194:PHE:CZ	2.46	0.51
7:M:2371:PHE:CD2	7:M:2374:LEU:HB2	2.46	0.51
7:M:3411:ASP:HA	7:M:3414:MET:HE2	1.93	0.51
9:K:478:PHE:O	10:L:427:MET:HG2	2.11	0.51
3:F:81:VAL:HG12	3:F:85:ASP:OD2	2.11	0.51
7:M:578:LYS:CG	7:M:578:LYS:O	2.58	0.51
7:M:2488:GLU:O	7:M:2493:ASN:ND2	2.41	0.50
7:M:3855:TYR:OH	7:M:4122:GLU:N	2.45	0.50
9:K:281:LEU:HD23	9:K:281:LEU:H	1.77	0.50
6:J:-18:DC:H2"	6:J:-17:DT:H71	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:49:DC:H2'	6:J:50:DA:C8	2.45	0.50
9:K:319:SER:OG	10:L:279:VAL:HG21	2.11	0.50
1:I:-69:DG:H4'	7:M:121:ALA:HB3	1.93	0.50
1:I:70:DC:H2''	1:I:71:DG:C8	2.46	0.50
2:E:61:LEU:H	2:E:61:LEU:HD23	1.76	0.50
7:M:852:ARG:HB3	7:M:3111:MET:SD	2.52	0.50
7:M:1342:MET:HE1	7:M:1402:LEU:CD2	2.41	0.50
7:M:2274:ILE:CD1	7:M:2318:ALA:HB1	2.42	0.50
9:K:71:TYR:HD2	9:K:116:ILE:HG22	1.77	0.50
4:C:70:ALA:HA	4:C:78:ILE:HD11	1.93	0.50
7:M:2220:MET:HA	7:M:2223:VAL:HG23	1.93	0.50
7:M:3515:GLN:HG2	7:M:3516:HIS:N	2.26	0.50
7:M:3256:MET:HE2	7:M:3256:MET:HA	1.94	0.50
2:A:66:PRO:HG3	6:J:17:DA:OP1	2.12	0.50
7:M:110:THR:O	7:M:110:THR:HG22	2.12	0.50
7:M:288:ASP:OD1	7:M:288:ASP:C	2.54	0.50
7:M:4068:HIS:O	7:M:4070:LYS:N	2.45	0.50
9:K:296:VAL:HG11	10:L:295:TYR:HB3	1.92	0.50
9:K:351:LYS:NZ	10:L:476:LEU:O	2.37	0.50
10:L:260:ARG:O	10:L:377:LEU:HD12	2.11	0.50
7:M:1483:LEU:CD1	7:M:1514:LEU:HD13	2.42	0.50
7:M:1576:ASP:OD1	7:M:1577:LEU:N	2.44	0.50
7:M:2266:ASN:O	7:M:2311:ARG:NH2	2.45	0.50
7:M:2315:VAL:CG1	7:M:2318:ALA:HB2	2.42	0.50
7:M:2364:LEU:HA	7:M:2367:VAL:HG12	1.94	0.50
10:L:14:MET:HE1	10:L:34:ALA:HB3	1.93	0.50
4:C:16:THR:HG23	4:C:17:ARG:HG3	1.94	0.50
5:H:75:SER:O	5:H:79:HIS:ND1	2.45	0.50
6:J:0:DC:C2'	6:J:1:DT:H71	2.42	0.50
7:M:1101:PHE:CG	7:M:1101:PHE:O	2.64	0.50
7:M:1224:PHE:O	7:M:1231:GLN:NE2	2.42	0.50
7:M:1478:SER:C	7:M:1480:GLY:H	2.20	0.50
10:L:210:MET:SD	10:L:211:VAL:HG23	2.52	0.50
7:M:402:THR:HG22	7:M:402:THR:O	2.12	0.50
7:M:1439:PRO:O	7:M:1441:ALA:N	2.41	0.50
10:L:185:LEU:O	10:L:232:ARG:NH1	2.41	0.50
10:L:407:VAL:HG12	10:L:408:ALA:N	2.27	0.50
1:I:55:DC:H2''	1:I:56:DG:N7	2.27	0.49
7:M:1335:CYS:HA	7:M:1338:VAL:HG22	1.92	0.49
7:M:3475:TYR:O	7:M:3479:THR:N	2.41	0.49
7:M:3940:ILE:HG21	7:M:3942:PHE:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:-53:DA:H5'	10:L:245:ILE:HD11	1.93	0.49
4:C:99:ARG:NH1	4:C:101:THR:OG1	2.44	0.49
7:M:1093:GLU:O	7:M:1096:VAL:HG12	2.12	0.49
7:M:1921:ASP:OD1	7:M:1922:ALA:N	2.45	0.49
7:M:2575:PRO:HA	7:M:2786:LYS:HA	1.93	0.49
4:C:78:ILE:HD12	4:C:78:ILE:H	1.77	0.49
6:J:38:DT:H2'	6:J:39:DA:H8	1.76	0.49
7:M:975:ASP:OD1	7:M:976:VAL:N	2.42	0.49
7:M:1251:GLN:O	7:M:1252:ALA:HB3	2.12	0.49
7:M:1481:THR:HG22	7:M:1531:LEU:HD22	1.94	0.49
7:M:1632:TRP:HB3	7:M:1645:VAL:CG2	2.42	0.49
7:M:2352:HIS:O	7:M:2355:THR:N	2.45	0.49
7:M:4014:LYS:O	7:M:4018:GLN:NE2	2.45	0.49
10:L:41:PHE:O	10:L:45:GLN:HG2	2.12	0.49
6:J:64:DT:H2''	6:J:65:DA:C8	2.48	0.49
7:M:152:LEU:HD11	7:M:156:PHE:HE2	1.77	0.49
7:M:852:ARG:HH11	7:M:3111:MET:HE1	1.77	0.49
7:M:914:VAL:HG21	7:M:937:MET:HE1	1.94	0.49
7:M:3330:LEU:O	7:M:3333:THR:OG1	2.24	0.49
9:K:449:THR:HG22	9:K:449:THR:O	2.11	0.49
1:I:-49:DG:H2'	1:I:-48:DC:C6	2.47	0.49
7:M:1668:PHE:CZ	7:M:1672:PHE:CE2	3.01	0.49
7:M:4001:THR:O	7:M:4004:VAL:HG12	2.13	0.49
9:K:40:PHE:CB	9:K:67:ILE:HD11	2.43	0.49
1:I:-42:DG:OP1	4:C:21:ALA:N	2.39	0.49
1:I:-7:DG:H2''	1:I:-6:DG:N7	2.27	0.49
6:J:58:DG:C2	10:L:400:ARG:NH2	2.80	0.49
7:M:160:LEU:CD2	7:M:164:LYS:HZ1	2.25	0.49
7:M:718:MET:SD	7:M:718:MET:C	2.95	0.49
7:M:1342:MET:HE1	7:M:1402:LEU:HB3	1.94	0.49
7:M:1843:ILE:CD1	7:M:1876:ILE:HD12	2.42	0.49
7:M:2123:PRO:HD3	7:M:2163:HIS:CE1	2.47	0.49
7:M:2542:LEU:HD21	7:M:2558:ALA:CB	2.43	0.49
7:M:3447:VAL:HG23	7:M:3448:GLU:N	2.28	0.49
7:M:3512:VAL:C	7:M:3515:GLN:OE1	2.55	0.49
9:K:253:LYS:NZ	10:L:434:MET:O	2.44	0.49
10:L:408:ALA:HB1	10:L:419:LEU:HG	1.94	0.49
1:I:-14:DA:H2	6:J:15:DT:O2	1.95	0.49
1:I:9:DT:P	2:E:47:ALA:HB3	2.53	0.49
3:B:39:ARG:NH2	6:J:8:DC:OP1	2.45	0.49
7:M:1878:ASP:OD1	7:M:1947:CYS:HA	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:2972:TYR:O	7:M:2976:LEU:HD23	2.13	0.49
7:M:3176:MET:HE1	7:M:3245:SER:OG	2.13	0.49
7:M:3107:ILE:HD13	7:M:3135:LEU:HD23	1.93	0.49
3:B:67:ARG:NH1	3:B:68:ASP:OD1	2.45	0.49
6:J:8:DC:N4	6:J:9:DG:O6	2.46	0.49
7:M:1919:CYS:O	7:M:1923:PHE:CD1	2.66	0.49
7:M:1963:GLN:N	7:M:1963:GLN:OE1	2.46	0.49
7:M:2201:THR:HA	7:M:2204:GLY:HA2	1.95	0.49
7:M:2779:ASP:OD1	7:M:2782:ASP:HB3	2.13	0.49
7:M:2300:PHE:CD2	7:M:2341:LEU:HD11	2.47	0.49
7:M:3458:SER:CB	7:M:3468:LEU:HD11	2.43	0.49
9:K:476:ASP:O	9:K:477:SER:CB	2.60	0.49
10:L:42:VAL:HG13	10:L:90:LEU:HD23	1.95	0.49
1:I:-53:DA:N6	6:J:54:DG:N2	2.61	0.48
7:M:289:ASN:ND2	7:M:292:SER:OG	2.45	0.48
7:M:1386:ILE:HG22	7:M:1387:GLY:N	2.28	0.48
7:M:3180:ASP:HA	7:M:3242:MET:HE1	1.95	0.48
7:M:3190:LEU:HD12	7:M:3231:ILE:HD12	1.94	0.48
7:M:3291:GLN:OE1	7:M:3291:GLN:N	2.45	0.48
9:K:492:ALA:HB3	9:K:500:PRO:HG3	1.95	0.48
6:J:4:DC:H2''	6:J:5:DC:C5	2.48	0.48
7:M:446:PHE:CE2	7:M:530:LEU:HB2	2.48	0.48
7:M:619:ASP:O	7:M:619:ASP:OD2	2.31	0.48
7:M:1917:LYS:HB2	10:L:729:LEU:HD22	1.95	0.48
7:M:2311:ARG:HA	7:M:2311:ARG:NE	2.27	0.48
9:K:261:LEU:N	9:K:269:ILE:O	2.45	0.48
10:L:201:GLN:O	10:L:205:LEU:HD23	2.13	0.48
10:L:330:GLN:O	10:L:334:LYS:NZ	2.29	0.48
7:M:1774:MET:HG2	7:M:1774:MET:O	2.13	0.48
9:K:170:THR:O	9:K:204:HIS:HA	2.13	0.48
9:K:356:LEU:HD23	9:K:356:LEU:H	1.78	0.48
3:B:19:ARG:NH1	6:J:15:DT:H1'	2.28	0.48
7:M:1184:ARG:O	7:M:1187:SER:OG	2.29	0.48
7:M:2361:ILE:HG22	7:M:2365:ASN:HB2	1.95	0.48
7:M:2530:ARG:NH2	7:M:2544:SER:OG	2.46	0.48
7:M:3758:LEU:O	7:M:3758:LEU:HD12	2.13	0.48
7:M:3844:THR:HG21	7:M:3850:HIS:CD2	2.49	0.48
9:K:64:ILE:O	9:K:67:ILE:HG22	2.13	0.48
1:I:53:DC:H2'	1:I:54:DT:H71	1.95	0.48
3:B:19:ARG:HB3	6:J:16:DA:C8	2.48	0.48
7:M:160:LEU:HD13	7:M:178:LEU:HD22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:359:LEU:HD11	7:M:1734:PRO:HG3	1.94	0.48
7:M:539:GLN:NE2	7:M:542:ASP:O	2.45	0.48
7:M:881:LYS:O	7:M:882:SER:HB2	2.13	0.48
7:M:1956:PHE:O	7:M:1957:ASN:HB2	2.14	0.48
7:M:2359:LYS:C	7:M:2361:ILE:N	2.70	0.48
7:M:3179:TRP:O	7:M:3182:ILE:HG22	2.13	0.48
7:M:4113:ASP:OD1	7:M:4115:ASN:N	2.46	0.48
9:K:339:ARG:HE	9:K:340:PHE:N	2.12	0.48
10:L:343:LEU:HD23	10:L:343:LEU:H	1.78	0.48
7:M:939:MET:HE3	7:M:987:LEU:HD11	1.94	0.48
7:M:1175:HIS:O	7:M:1178:ARG:HG3	2.14	0.48
7:M:1391:VAL:O	7:M:1395:LEU:HG	2.14	0.48
7:M:1021:VAL:HG13	7:M:1022:ASP:N	2.29	0.48
7:M:1171:TRP:CZ3	7:M:1172:LEU:HD23	2.48	0.48
7:M:1342:MET:HE1	7:M:1402:LEU:HD23	1.96	0.48
7:M:2327:LEU:HD12	7:M:2327:LEU:N	2.29	0.48
7:M:2406:GLU:CD	7:M:2406:GLU:O	2.56	0.48
7:M:2455:LEU:HD11	7:M:2480:ILE:HD13	1.95	0.48
7:M:3495:PHE:HB3	7:M:3502:MET:CE	2.44	0.48
9:K:207:LYS:O	9:K:208:PRO:C	2.56	0.48
2:A:88:ALA:HB1	3:B:86:VAL:CG1	2.43	0.48
6:J:-10:DC:C4	6:J:-9:DA:N6	2.81	0.48
7:M:1219:PHE:O	7:M:1223:THR:HG23	2.14	0.48
7:M:1464:LEU:O	7:M:1467:ILE:HG22	2.14	0.48
7:M:2361:ILE:O	7:M:2364:LEU:HD23	2.14	0.48
7:M:3006:ALA:O	7:M:3257:LYS:NZ	2.44	0.48
7:M:3499:ILE:O	7:M:3503:VAL:HG22	2.13	0.48
10:L:366:ALA:HA	10:L:377:LEU:HD22	1.95	0.48
1:I:-33:DG:N2	6:J:34:DT:C2	2.82	0.48
1:I:9:DT:OP1	2:E:47:ALA:HB3	2.13	0.48
4:C:42:ARG:O	4:C:44:GLY:N	2.40	0.48
4:C:83:LEU:CD1	5:D:58:ILE:HG21	2.44	0.48
7:M:160:LEU:HD23	7:M:164:LYS:HZ1	1.79	0.48
7:M:1663:THR:O	7:M:1666:GLY:N	2.43	0.48
7:M:2361:ILE:O	7:M:2363:CYS:N	2.46	0.48
7:M:2410:GLU:O	7:M:2413:PHE:N	2.46	0.48
7:M:2481:HIS:HA	7:M:2484:TYR:CD1	2.49	0.48
9:K:318:ARG:N	9:K:329:LEU:O	2.46	0.48
7:M:291:VAL:HG22	7:M:294:PHE:CB	2.43	0.48
7:M:880:MET:HE3	7:M:883:TYR:O	2.13	0.48
7:M:1323:SER:N	7:M:1326:GLU:OE2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:2364:LEU:HA	7:M:2367:VAL:CG1	2.44	0.48
7:M:3050:LYS:NZ	7:M:3181:ASP:OD1	2.37	0.48
7:M:3421:ASP:O	7:M:3425:ARG:HG2	2.14	0.48
7:M:3834:ALA:HB3	7:M:3835:PRO:CD	2.44	0.48
5:D:43:LYS:HD3	5:D:49:THR:HB	1.96	0.47
6:J:-20:DC:C2	6:J:-19:DG:N7	2.82	0.47
7:M:202:GLY:O	7:M:206:THR:HG22	2.13	0.47
7:M:1431:LEU:HD23	7:M:1444:ASP:OD2	2.14	0.47
9:K:301:ARG:NH1	10:L:292:GLU:OE2	2.46	0.47
2:A:80:THR:HG22	2:A:81:ASP:H	1.79	0.47
2:E:73:GLU:OE2	3:F:23:ARG:N	2.40	0.47
6:J:-73:DA:N3	6:J:-73:DA:H2'	2.28	0.47
7:M:12:LEU:HD12	7:M:54:GLN:OE1	2.14	0.47
7:M:341:PHE:CD1	7:M:369:PHE:HB3	2.50	0.47
7:M:662:LEU:N	7:M:662:LEU:HD12	2.28	0.47
7:M:1195:VAL:N	7:M:1196:PRO:HD2	2.29	0.47
7:M:1873:TYR:O	7:M:1877:LEU:HD23	2.13	0.47
7:M:2443:MET:N	7:M:2444:PRO:CD	2.77	0.47
7:M:3012:GLU:OE2	7:M:3048:LYS:NZ	2.47	0.47
7:M:3180:ASP:CB	7:M:3242:MET:HE1	2.44	0.47
7:M:384:MET:O	7:M:387:GLU:N	2.41	0.47
7:M:1623:LEU:H	7:M:1623:LEU:HD23	1.80	0.47
9:K:149:VAL:HG13	9:K:150:CYS:N	2.29	0.47
6:J:-14:DA:C6	6:J:-13:DA:C6	3.02	0.47
7:M:1716:GLN:HA	7:M:1719:VAL:HG22	1.96	0.47
7:M:1959:LEU:HD21	7:M:2124:SER:OG	2.15	0.47
7:M:3519:GLU:O	7:M:3522:THR:OG1	2.29	0.47
7:M:4060:THR:O	7:M:4064:LEU:HD23	2.13	0.47
9:K:466:VAL:HG23	10:L:345:PHE:CD2	2.50	0.47
10:L:465:LYS:O	10:L:474:GLU:N	2.41	0.47
2:A:70:LEU:HD11	2:A:74:ILE:HD12	1.96	0.47
3:B:19:ARG:NH1	6:J:16:DA:O4'	2.48	0.47
7:M:181:LEU:C	7:M:183:GLU:N	2.72	0.47
7:M:749:VAL:N	7:M:750:PRO:HD2	2.29	0.47
7:M:990:GLN:OE1	7:M:2781:PRO:HA	2.15	0.47
7:M:1646:LEU:HD23	7:M:1688:LEU:CD1	2.44	0.47
7:M:1882:SER:C	7:M:1883:ARG:HD3	2.39	0.47
7:M:2939:LEU:HD11	7:M:2943:PHE:CE2	2.50	0.47
7:M:3450:MET:HE1	7:M:3475:TYR:OH	2.14	0.47
9:K:207:LYS:HB3	9:K:208:PRO:HD2	1.96	0.47
2:A:104:PHE:O	2:A:108:ASN:ND2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:38:VAL:HB	5:H:56:MET:HE1	1.97	0.47
7:M:120:ALA:O	7:M:121:ALA:HB3	2.15	0.47
7:M:660:LEU:O	7:M:662:LEU:HD12	2.14	0.47
7:M:1588:ASP:O	7:M:1590:THR:N	2.48	0.47
7:M:2484:TYR:HE2	7:M:2486:ASP:HA	1.79	0.47
7:M:2484:TYR:CE2	7:M:2499:PHE:CD1	3.02	0.47
7:M:124:LYS:O	7:M:128:LEU:HD23	2.15	0.47
7:M:184:VAL:HB	7:M:191:ASN:HD22	1.79	0.47
7:M:206:THR:O	7:M:210:SER:OG	2.31	0.47
7:M:335:LYS:O	7:M:339:GLN:HB2	2.14	0.47
7:M:364:ARG:C	7:M:367:GLY:H	2.20	0.47
7:M:376:ILE:HG22	7:M:377:ASN:N	2.30	0.47
7:M:539:GLN:O	7:M:541:MET:N	2.48	0.47
7:M:722:LYS:O	7:M:723:ASP:OD1	2.33	0.47
7:M:1102:GLU:HG3	7:M:1153:LEU:HD11	1.95	0.47
7:M:2334:LYS:O	7:M:2334:LYS:HD3	2.15	0.47
7:M:2890:ILE:HG21	7:M:3898:LEU:HD11	1.97	0.47
7:M:3329:LEU:HD12	7:M:3330:LEU:HD22	1.95	0.47
7:M:3627:ALA:O	7:M:3628:PHE:CD1	2.68	0.47
7:M:3959:MET:O	7:M:3959:MET:HG2	2.15	0.47
9:K:62:MET:SD	9:K:205:LEU:HD22	2.55	0.47
10:L:106:ASP:OD1	10:L:107:PHE:N	2.47	0.47
4:C:53:ALA:HB2	5:D:114:ALA:CB	2.45	0.47
3:F:32:PRO:CG	6:J:-12:DC:OP1	2.63	0.47
7:M:1091:GLU:OE1	7:M:1091:GLU:N	2.46	0.47
7:M:1121:LEU:HD22	7:M:1123:THR:HG23	1.97	0.47
7:M:1918:LEU:O	7:M:1922:ALA:HB2	2.15	0.47
7:M:2268:LYS:O	7:M:2268:LYS:NZ	2.45	0.47
7:M:2366:LYS:O	7:M:2370:SER:OG	2.30	0.47
9:K:202:LEU:HD12	9:K:202:LEU:C	2.39	0.47
9:K:392:LYS:NZ	10:L:459:ASP:OD1	2.39	0.47
3:B:19:ARG:HB3	6:J:16:DA:N7	2.30	0.47
6:J:31:DT:H2"	6:J:32:DA:C8	2.50	0.47
7:M:313:LEU:HD11	7:M:364:ARG:HD3	1.95	0.47
7:M:2330:VAL:HG13	7:M:2331:MET:H	1.79	0.47
7:M:3495:PHE:HB3	7:M:3502:MET:HE2	1.97	0.47
10:L:297:LEU:N	10:L:303:THR:O	2.47	0.47
10:L:447:THR:O	10:L:451:LEU:HD23	2.14	0.47
1:I:-66:DG:H21	9:K:254:ARG:NH2	2.12	0.47
1:I:-65:DT:H2"	1:I:-64:DA:C8	2.50	0.47
1:I:-57:DT:C2	1:I:-56:DG:N7	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:1098:GLN:C	7:M:1153:LEU:HD13	2.40	0.47
7:M:1558:TYR:CE1	7:M:1562:LEU:HD21	2.50	0.47
7:M:2410:GLU:OE1	7:M:2410:GLU:N	2.45	0.47
7:M:2527:HIS:CG	7:M:2528:GLU:N	2.81	0.47
7:M:3921:GLY:O	7:M:3922:ASP:OD1	2.33	0.47
8:N:9:UNK:O	8:N:12:UNK:N	2.48	0.47
7:M:852:ARG:O	7:M:855:VAL:HG12	2.14	0.46
7:M:976:VAL:O	7:M:981:ARG:NH2	2.47	0.46
7:M:1014:LEU:O	7:M:1017:ILE:HG22	2.16	0.46
7:M:2825:THR:OG1	7:M:2828:GLU:CD	2.58	0.46
7:M:2958:LEU:HD11	7:M:4101:GLU:HB3	1.96	0.46
10:L:138:LEU:HD21	10:L:208:VAL:HG23	1.96	0.46
10:L:342:VAL:HG11	10:L:345:PHE:CE1	2.50	0.46
7:M:741:ILE:HD13	7:M:748:TYR:CD2	2.49	0.46
7:M:1817:GLN:OE1	7:M:1936:ARG:NH1	2.35	0.46
7:M:2360:PHE:C	7:M:2362:VAL:N	2.70	0.46
7:M:2484:TYR:CE2	7:M:2499:PHE:CE1	3.03	0.46
9:K:350:PHE:HB3	9:K:394:VAL:HG21	1.97	0.46
10:L:137:ASP:OD1	10:L:138:LEU:N	2.48	0.46
1:I:-69:DG:C2	1:I:-68:DA:C5	3.03	0.46
1:I:-5:DG:OP1	2:A:42:ARG:NH2	2.49	0.46
5:D:58:ILE:HG23	3:F:98:TYR:CD2	2.50	0.46
6:J:66:DC:O2	6:J:67:DA:C5	2.68	0.46
7:M:185:HIS:C	7:M:187:SER:N	2.73	0.46
7:M:1181:THR:HG22	7:M:1184:ARG:HH21	1.80	0.46
7:M:2338:GLU:HA	7:M:2342:CYS:SG	2.55	0.46
1:I:-53:DA:C8	1:I:-52:DC:H1'	2.50	0.46
7:M:290:TYR:CG	7:M:291:VAL:N	2.84	0.46
7:M:291:VAL:HG21	7:M:338:LEU:HD23	1.96	0.46
7:M:637:LYS:CG	7:M:639:ALA:HB2	2.46	0.46
7:M:2868:LEU:HD23	7:M:2868:LEU:C	2.40	0.46
7:M:2871:LEU:HD22	7:M:2876:VAL:CG2	2.46	0.46
7:M:3381:ALA:O	7:M:3385:LEU:HG	2.14	0.46
7:M:4121:TRP:CE2	7:M:4122:GLU:O	2.69	0.46
9:K:476:ASP:O	9:K:477:SER:OG	2.28	0.46
10:L:24:ILE:HG22	10:L:29:SER:HB2	1.97	0.46
7:M:93:LEU:CD2	7:M:100:ILE:HD12	2.46	0.46
7:M:93:LEU:HD21	7:M:100:ILE:HD12	1.98	0.46
7:M:1369:MET:HE3	7:M:1418:HIS:HB3	1.96	0.46
7:M:3622:ALA:N	7:M:3623:PRO:HD2	2.30	0.46
9:K:289:TYR:O	9:K:293:ASN:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:247:TRP:HD1	10:L:362:LEU:HD21	1.80	0.46
1:I:28:DA:P	1:I:28:DA:H8	2.38	0.46
2:A:104:PHE:CZ	3:B:38:ALA:HB1	2.50	0.46
7:M:88:PHE:O	7:M:89:LEU:C	2.57	0.46
7:M:578:LYS:O	7:M:578:LYS:HG2	2.15	0.46
7:M:2296:SER:O	7:M:2299:TYR:HB3	2.15	0.46
7:M:2328:ARG:HD3	7:M:2371:PHE:CD1	2.51	0.46
7:M:3190:LEU:HD12	7:M:3231:ILE:HG23	1.97	0.46
7:M:3458:SER:C	7:M:3461:ALA:H	2.23	0.46
7:M:3701:ILE:HG23	7:M:3701:ILE:O	2.16	0.46
7:M:4068:HIS:C	7:M:4070:LYS:H	2.23	0.46
9:K:348:MET:HE3	9:K:399:ARG:HB2	1.98	0.46
10:L:20:MET:HE3	10:L:31:PHE:HA	1.97	0.46
10:L:182:PRO:HG2	10:L:520:ALA:HB3	1.97	0.46
10:L:293:THR:HG23	10:L:293:THR:O	2.16	0.46
10:L:394:ARG:HH12	10:L:396:ALA:HB2	1.81	0.46
7:M:35:ILE:HG22	7:M:88:PHE:CE2	2.50	0.46
7:M:339:GLN:HG2	7:M:339:GLN:O	2.16	0.46
7:M:451:PRO:HA	7:M:454:GLN:HB2	1.97	0.46
7:M:1076:LEU:HD13	7:M:1123:THR:O	2.15	0.46
7:M:3348:LEU:O	7:M:3349:ALA:HB3	2.16	0.46
7:M:3633:ILE:HG23	7:M:3637:GLY:HA3	1.97	0.46
7:M:3738:ILE:HG13	7:M:3738:ILE:O	2.15	0.46
1:I:-64:DA:C8	1:I:-63:DT:H72	2.51	0.46
7:M:12:LEU:HD12	7:M:54:GLN:CD	2.41	0.46
7:M:175:TYR:HB3	7:M:226:GLY:O	2.16	0.46
7:M:431:TYR:O	7:M:434:VAL:HG12	2.15	0.46
7:M:763:THR:N	7:M:764:PRO:HD2	2.31	0.46
7:M:987:LEU:CD2	7:M:991:LEU:HD23	2.46	0.46
7:M:1629:CYS:O	7:M:1632:TRP:HE3	1.98	0.46
7:M:1675:TYR:O	7:M:1679:LEU:HD13	2.16	0.46
9:K:360:HIS:HB3	9:K:438:PRO:HD2	1.98	0.46
7:M:3614:TYR:O	7:M:3615:ALA:HB3	2.15	0.46
7:M:3958:LEU:HD12	7:M:4060:THR:HB	1.98	0.46
7:M:3992:ARG:NH1	7:M:4100:GLU:OE2	2.48	0.46
4:G:17:ARG:O	4:G:18:SER:C	2.59	0.46
6:J:63:DA:H2'	6:J:64:DT:H71	1.98	0.46
7:M:1690:GLY:O	7:M:1693:VAL:HG22	2.16	0.46
7:M:1945:TYR:CE2	7:M:2097:LEU:HD21	2.51	0.46
7:M:2927:ALA:HB1	7:M:2939:LEU:CD1	2.46	0.46
7:M:3350:GLU:OE1	7:M:3350:GLU:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:97:VAL:HG11	9:K:99:PHE:CZ	2.50	0.46
9:K:446:MET:HE1	10:L:244:SER:HB2	1.97	0.46
4:C:68:ASN:O	4:C:73:ASN:ND2	2.49	0.45
3:F:82:THR:HG22	3:F:82:THR:O	2.17	0.45
6:J:-7:DG:H2''	6:J:-6:DT:H71	1.98	0.45
7:M:1333:SER:O	7:M:1336:THR:OG1	2.32	0.45
7:M:1438:GLY:N	7:M:1439:PRO:CD	2.79	0.45
7:M:2129:LEU:HD23	7:M:2129:LEU:O	2.16	0.45
7:M:2175:GLU:O	7:M:2176:ASN:OD1	2.34	0.45
7:M:2276:LEU:O	7:M:2280:VAL:HG23	2.16	0.45
9:K:297:LYS:NZ	10:L:298:ASN:OD1	2.47	0.45
9:K:319:SER:HA	9:K:327:ILE:O	2.16	0.45
9:K:355:LEU:HD11	10:L:473:LEU:HB3	1.98	0.45
1:I:-40:DC:H2'	1:I:-39:DT:H72	1.98	0.45
4:C:45:ALA:C	4:C:48:PRO:HD2	2.41	0.45
6:J:14:DT:H4'	6:J:15:DT:OP1	2.16	0.45
7:M:1171:TRP:HZ3	7:M:1172:LEU:HD23	1.81	0.45
7:M:1750:LEU:HD11	7:M:1759:LEU:HA	1.98	0.45
7:M:2452:ARG:NH2	7:M:2494:ASP:O	2.48	0.45
7:M:2857:CYS:O	7:M:2861:ILE:CD1	2.59	0.45
7:M:3438:GLU:OE1	7:M:3438:GLU:N	2.43	0.45
7:M:3496:ILE:HA	7:M:3499:ILE:HG12	1.99	0.45
10:L:45:GLN:O	10:L:49:GLU:N	2.49	0.45
7:M:207:GLN:HG3	7:M:214:GLU:O	2.16	0.45
7:M:1478:SER:O	7:M:1479:VAL:CG2	2.63	0.45
7:M:2380:ASN:O	7:M:2381:ALA:C	2.59	0.45
7:M:3962:ARG:O	7:M:3962:ARG:HG2	2.15	0.45
9:K:84:ALA:O	9:K:85:VAL:O	2.34	0.45
3:B:40:ARG:HD3	4:G:107:VAL:HG21	1.98	0.45
7:M:370:ALA:HB3	7:M:423:TYR:HD2	1.79	0.45
7:M:619:ASP:OD2	7:M:619:ASP:C	2.59	0.45
7:M:1157:PHE:H	7:M:1158:PRO:CD	2.29	0.45
7:M:2871:LEU:HD23	7:M:2872:ASP:N	2.32	0.45
7:M:3493:TRP:O	7:M:3495:PHE:N	2.50	0.45
9:K:474:ARG:HE	9:K:478:PHE:HD2	1.64	0.45
7:M:848:LEU:O	7:M:852:ARG:HG2	2.15	0.45
7:M:1747:LEU:HD22	7:M:1762:MET:SD	2.57	0.45
7:M:3696:ARG:H	7:M:3696:ARG:HD3	1.81	0.45
9:K:328:ILE:O	9:K:329:LEU:HD12	2.16	0.45
1:I:-37:DG:H1'	1:I:-36:DG:C6	2.51	0.45
2:A:104:PHE:O	2:A:107:THR:HG22	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:96:SER:HA	2:E:99:TYR:CE1	2.52	0.45
7:M:704:PHE:CE1	7:M:740:ILE:HD13	2.52	0.45
7:M:946:THR:HG21	7:M:2581:LEU:HD13	1.98	0.45
7:M:979:VAL:HG13	7:M:980:THR:N	2.32	0.45
7:M:1133:HIS:O	7:M:1137:ILE:HG12	2.17	0.45
7:M:1917:LYS:HD2	7:M:1917:LYS:O	2.16	0.45
7:M:2328:ARG:O	7:M:2329:TYR:C	2.60	0.45
7:M:2443:MET:HE1	7:M:2479:TRP:CZ3	2.52	0.45
7:M:3914:SER:HA	7:M:3917:ILE:HG22	1.97	0.45
9:K:323:GLY:N	10:L:49:GLU:OE2	2.38	0.45
7:M:164:LYS:HE2	9:K:313:PRO:HD2	1.99	0.45
7:M:2428:ASP:OD1	7:M:2429:ASP:N	2.44	0.45
7:M:3729:MET:SD	7:M:3737:ARG:NH2	2.90	0.45
7:M:3914:SER:O	7:M:3918:LEU:HD23	2.16	0.45
1:I:-16:DT:O3'	1:I:-15:DA:C8	2.70	0.45
7:M:19:LEU:HD21	7:M:35:ILE:HD11	1.99	0.45
7:M:1685:ASP:HB3	7:M:1688:LEU:HB3	1.99	0.45
7:M:2104:MET:SD	7:M:2104:MET:C	3.00	0.45
7:M:3038:GLU:OE1	7:M:3038:GLU:HA	2.17	0.45
10:L:528:ILE:HB	10:L:529:PRO:HD3	1.97	0.45
1:I:7:DC:H2''	1:I:8:DG:N7	2.32	0.45
3:B:28:GLY:O	3:B:29:ILE:HG23	2.17	0.45
4:C:23:LEU:HA	5:D:118:TYR:CZ	2.52	0.45
5:H:90:GLU:OE1	5:H:90:GLU:N	2.47	0.45
7:M:193:ALA:CB	7:M:230:LEU:HD11	2.47	0.45
7:M:2300:PHE:CE2	7:M:2341:LEU:HD21	2.52	0.45
7:M:3577:GLN:NE2	7:M:3684:SER:OG	2.36	0.45
2:A:47:ALA:O	2:A:51:ILE:HG12	2.17	0.45
7:M:153:PHE:CE2	7:M:191:ASN:OD1	2.70	0.45
7:M:643:GLU:N	7:M:644:PRO:HD2	2.32	0.45
7:M:989:MET:HA	7:M:989:MET:HE2	1.98	0.45
7:M:3334:TYR:CB	7:M:3381:ALA:HB2	2.47	0.45
7:M:3552:LYS:HA	7:M:3555:VAL:HG22	1.98	0.45
10:L:113:VAL:O	10:L:117:VAL:HG23	2.17	0.45
5:D:51:ILE:HG12	5:D:56:MET:SD	2.57	0.44
7:M:2201:THR:HG23	7:M:2248:CYS:CB	2.47	0.44
7:M:2309:PHE:HB2	7:M:2317:ALA:HA	1.99	0.44
7:M:2361:ILE:O	7:M:2362:VAL:C	2.61	0.44
7:M:2371:PHE:CD1	7:M:2373:PRO:HD2	2.52	0.44
7:M:2419:ASP:O	7:M:2423:VAL:HG13	2.16	0.44
9:K:95:ASN:HD21	9:K:99:PHE:HB2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:525:PHE:CE1	9:K:529:VAL:HG11	2.52	0.44
10:L:249:CYS:SG	10:L:340:PHE:N	2.90	0.44
1:I:-38:DA:H2''	1:I:-37:DG:N7	2.32	0.44
1:I:5:DT:H2''	1:I:6:DA:N7	2.32	0.44
1:I:69:DT:O3'	2:A:45:THR:HG21	2.16	0.44
3:F:22:LEU:HD23	3:F:22:LEU:H	1.82	0.44
7:M:212:VAL:HG13	7:M:213:ARG:H	1.82	0.44
7:M:991:LEU:HD12	7:M:992:ILE:N	2.32	0.44
7:M:1528:LEU:HD23	7:M:1528:LEU:C	2.42	0.44
7:M:1839:PHE:CE2	7:M:1843:ILE:HD13	2.52	0.44
7:M:2241:LEU:HG	7:M:2245:TRP:CD1	2.53	0.44
7:M:2249:LEU:HD12	7:M:2250:SER:N	2.32	0.44
7:M:2360:PHE:CG	7:M:2360:PHE:O	2.70	0.44
9:K:325:ARG:NH1	10:L:498:ALA:O	2.51	0.44
10:L:327:ASP:O	10:L:331:MET:HG3	2.18	0.44
1:I:-33:DG:OP1	5:D:89:ARG:NH1	2.50	0.44
3:B:19:ARG:NH2	6:J:16:DA:C4	2.86	0.44
7:M:354:SER:CB	7:M:358:GLU:O	2.65	0.44
7:M:479:ILE:HG22	7:M:567:GLU:OE2	2.17	0.44
7:M:662:LEU:HD23	7:M:667:TYR:CE1	2.51	0.44
7:M:1934:LEU:HD23	7:M:1934:LEU:H	1.82	0.44
7:M:2402:LEU:O	7:M:2403:CYS:C	2.60	0.44
6:J:52:DG:N3	6:J:53:DT:H71	2.32	0.44
7:M:1178:ARG:HD3	7:M:1183:CYS:SG	2.57	0.44
7:M:1369:MET:HE2	7:M:1414:ILE:HG13	2.00	0.44
7:M:1432:CYS:H	7:M:1448:LEU:HD11	1.83	0.44
7:M:3542:PHE:CZ	7:M:3555:VAL:HG21	2.52	0.44
7:M:3793:VAL:HG13	7:M:3803:ILE:HD13	2.00	0.44
7:M:3923:ARG:HA	7:M:3923:ARG:CZ	2.48	0.44
9:K:411:VAL:HG12	9:K:436:PHE:CD1	2.53	0.44
9:K:495:LEU:O	9:K:496:ASP:OD1	2.36	0.44
1:I:-69:DG:P	7:M:167:PRO:HB3	2.58	0.44
7:M:1114:ALA:HB2	7:M:1124:ILE:HG21	1.99	0.44
7:M:1675:TYR:CZ	7:M:1679:LEU:HD11	2.52	0.44
7:M:1820:VAL:HA	7:M:1824:LEU:HB3	1.99	0.44
7:M:2471:GLU:OE2	7:M:2475:ASN:ND2	2.51	0.44
7:M:2947:ILE:HG23	7:M:2947:ILE:O	2.17	0.44
9:K:40:PHE:CD2	9:K:67:ILE:HD11	2.52	0.44
10:L:27:ILE:HG23	10:L:28:GLU:N	2.33	0.44
1:I:-71:DC:H2''	1:I:-70:DG:C8	2.53	0.44
1:I:66:DT:C2'	1:I:67:DT:H71	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:65:LEU:HD12	6:J:17:DA:H2''	2.00	0.44
2:E:67:PHE:O	2:E:71:VAL:HG23	2.18	0.44
5:H:78:ALA:O	5:H:83:ARG:N	2.50	0.44
7:M:1646:LEU:HD13	7:M:1678:LEU:CD1	2.48	0.44
7:M:2393:LEU:O	7:M:2394:LYS:C	2.60	0.44
9:K:303:PHE:CG	9:K:304:ASN:N	2.86	0.44
9:K:332:GLU:O	9:K:336:GLU:HG2	2.18	0.44
10:L:118:ILE:CG2	10:L:159:ILE:HD13	2.47	0.44
2:E:73:GLU:OE2	2:E:76:GLN:NE2	2.51	0.44
6:J:66:DC:O2	6:J:67:DA:N7	2.51	0.44
7:M:206:THR:CG2	7:M:207:GLN:N	2.80	0.44
7:M:253:LEU:O	7:M:257:ARG:HG2	2.18	0.44
7:M:355:ASN:N	7:M:361:ILE:HD12	2.33	0.44
7:M:446:PHE:CD1	7:M:446:PHE:C	2.95	0.44
7:M:1851:LEU:O	7:M:1854:ARG:HG3	2.18	0.44
7:M:2144:LEU:HD11	7:M:2185:MET:HG3	2.00	0.44
7:M:3433:VAL:HG11	7:M:3438:GLU:OE1	2.18	0.44
7:M:4056:PRO:O	7:M:4060:THR:HG23	2.18	0.44
9:K:72:ILE:O	9:K:76:ILE:HD12	2.18	0.44
9:K:86:VAL:CG2	9:K:104:VAL:HG12	2.46	0.44
10:L:245:ILE:O	10:L:245:ILE:CG2	2.65	0.44
10:L:298:ASN:O	10:L:299:ASP:HB2	2.17	0.44
1:I:-40:DC:C2'	1:I:-39:DT:H72	2.48	0.44
3:B:92:ARG:NH2	5:D:98:LEU:HD23	2.33	0.44
6:J:-21:DC:C2	6:J:-20:DC:C4	3.05	0.44
7:M:352:VAL:HB	7:M:362:ALA:CB	2.47	0.44
7:M:1231:GLN:N	7:M:1232:PRO:CD	2.81	0.44
7:M:2347:LYS:O	7:M:2351:GLN:OE1	2.35	0.44
7:M:3117:ILE:HD11	7:M:3124:SER:OG	2.18	0.44
9:K:394:VAL:HG22	9:K:395:ALA:N	2.33	0.44
3:F:20:LYS:NZ	6:J:-22:DA:OP2	2.32	0.44
6:J:8:DC:H2''	6:J:9:DG:H8	1.82	0.44
7:M:386:VAL:HA	7:M:389:ILE:HG22	1.99	0.44
7:M:1139:GLU:OE2	7:M:1193:LYS:NZ	2.40	0.44
7:M:1238:GLN:HB2	7:M:1239:PRO:HD3	2.00	0.44
7:M:1818:SER:O	7:M:1819:PHE:C	2.61	0.44
7:M:2360:PHE:O	7:M:2361:ILE:C	2.60	0.44
7:M:3170:ASP:OD1	7:M:3172:LYS:HB2	2.18	0.44
7:M:3467:ARG:HE	7:M:3471:ILE:HD11	1.82	0.44
7:M:3523:ASP:OD1	7:M:3561:LYS:NZ	2.48	0.44
10:L:40:MET:SD	10:L:43:GLN:NE2	2.90	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:69:DT:H2''	1:I:70:DC:C6	2.52	0.43
3:B:49:LEU:H	3:B:49:LEU:HD23	1.83	0.43
7:M:2897:LEU:HD21	7:M:2923:TRP:CZ2	2.53	0.43
7:M:3069:MET:SD	7:M:3090:TYR:OH	2.76	0.43
7:M:3281:CYS:O	7:M:3285:HIS:ND1	2.47	0.43
9:K:355:LEU:HD11	10:L:473:LEU:CB	2.48	0.43
9:K:443:LYS:HA	10:L:267:ILE:HG22	2.00	0.43
9:K:462:MET:CE	10:L:383:ALA:HB1	2.48	0.43
2:A:65:LEU:HD12	6:J:17:DA:C2'	2.48	0.43
3:B:19:ARG:CZ	6:J:16:DA:C4	3.01	0.43
7:M:1550:VAL:O	7:M:1551:ILE:O	2.36	0.43
9:K:43:ASP:OD1	9:K:44:ALA:N	2.51	0.43
9:K:241:ASP:OD1	9:K:244:ARG:NH2	2.48	0.43
9:K:371:GLU:OE1	9:K:371:GLU:N	2.52	0.43
6:J:-12:DC:OP1	6:J:-12:DC:H3'	2.18	0.43
6:J:1:DT:C2	6:J:2:DG:C5	3.06	0.43
7:M:241:ASP:HB3	7:M:242:PRO:HD3	2.00	0.43
7:M:1099:PHE:HA	7:M:1153:LEU:HD13	2.00	0.43
7:M:1261:LEU:CD1	7:M:1340:ARG:HG3	2.48	0.43
7:M:2470:ARG:HG2	7:M:2474:TYR:CE2	2.52	0.43
7:M:2806:LYS:HG3	7:M:2857:CYS:HB2	1.98	0.43
7:M:3914:SER:O	7:M:3917:ILE:HG22	2.17	0.43
3:F:43:VAL:HB	3:F:46:ILE:HG12	2.00	0.43
7:M:115:TYR:O	7:M:116:THR:HB	2.19	0.43
7:M:326:MET:O	7:M:326:MET:HG2	2.17	0.43
7:M:1596:VAL:HG13	7:M:1597:LEU:N	2.33	0.43
7:M:1843:ILE:HD12	7:M:1876:ILE:HD12	1.99	0.43
7:M:2274:ILE:O	7:M:2277:LEU:N	2.51	0.43
7:M:2382:VAL:HG12	7:M:2382:VAL:O	2.17	0.43
7:M:3531:TYR:HB2	7:M:3532:PRO:HD3	2.00	0.43
7:M:3747:GLU:N	7:M:3747:GLU:OE1	2.52	0.43
7:M:3767:LEU:HD11	7:M:3918:LEU:HD13	2.00	0.43
6:J:-40:DG:H2'	6:J:-39:DT:H71	2.00	0.43
6:J:64:DT:C2'	6:J:65:DA:C8	3.02	0.43
7:M:955:ALA:O	7:M:957:PRO:HD3	2.18	0.43
7:M:2301:GLN:HA	7:M:2304:VAL:HG22	2.00	0.43
7:M:3448:GLU:OE2	7:M:3482:LEU:N	2.51	0.43
7:M:3654:MET:SD	7:M:3654:MET:N	2.92	0.43
7:M:3655:LYS:O	7:M:3655:LYS:HG3	2.18	0.43
9:K:296:VAL:HG21	10:L:310:ILE:CD1	2.48	0.43
9:K:473:TYR:CG	9:K:474:ARG:N	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:-23:DC:C2	6:J:-22:DA:N7	2.86	0.43
7:M:2328:ARG:CD	7:M:2371:PHE:CD1	3.01	0.43
7:M:2362:VAL:O	7:M:2366:LYS:HB2	2.18	0.43
7:M:2389:PHE:C	7:M:2390:HIS:CG	2.97	0.43
7:M:3535:ILE:HD12	7:M:3535:ILE:H	1.83	0.43
7:M:3807:GLU:OE2	7:M:3807:GLU:HA	2.19	0.43
9:K:275:ASN:ND2	9:K:277:VAL:O	2.49	0.43
1:I:-23:DT:P	2:A:72:ARG:HH12	2.41	0.43
1:I:46:DG:H4'	1:I:47:DA:OP1	2.19	0.43
7:M:364:ARG:O	7:M:365:GLY:C	2.62	0.43
9:K:277:VAL:CG1	10:L:357:MET:SD	3.07	0.43
10:L:336:GLU:OE2	10:L:394:ARG:NH2	2.52	0.43
1:I:-68:DA:N1	6:J:68:DT:C2	2.86	0.43
6:J:53:DT:H2''	6:J:54:DG:C5'	2.48	0.43
6:J:69:DC:H2''	6:J:70:DC:OP2	2.18	0.43
7:M:96:MET:SD	7:M:99:LYS:HB2	2.59	0.43
7:M:114:VAL:HG13	7:M:128:LEU:HD21	2.01	0.43
7:M:385:TYR:CE2	7:M:434:VAL:HG13	2.54	0.43
7:M:710:PHE:O	7:M:714:VAL:HG12	2.19	0.43
7:M:712:LYS:O	7:M:716:VAL:HG23	2.19	0.43
7:M:895:ALA:HA	7:M:904:VAL:HA	2.01	0.43
7:M:1071:ASN:HB3	7:M:1074:LYS:CG	2.49	0.43
7:M:1092:GLU:HG2	7:M:1093:GLU:HG2	2.00	0.43
7:M:1195:VAL:HG23	7:M:1196:PRO:CD	2.47	0.43
7:M:2367:VAL:HA	7:M:2370:SER:HG	1.84	0.43
7:M:2520:ILE:O	7:M:2523:ASN:OD1	2.37	0.43
7:M:3695:LEU:HD23	7:M:3695:LEU:H	1.83	0.43
7:M:3859:TYR:HB3	7:M:4073:ALA:HB2	2.01	0.43
7:M:4128:MET:HE2	7:M:4128:MET:HA	1.99	0.43
9:K:343:PRO:HA	9:K:401:THR:O	2.18	0.43
9:K:452:ILE:O	9:K:453:MET:HE2	2.18	0.43
9:K:492:ALA:HB3	9:K:500:PRO:CB	2.49	0.43
7:M:75:SER:O	7:M:79:ARG:N	2.52	0.43
7:M:1101:PHE:HB3	7:M:1153:LEU:HD21	2.01	0.43
7:M:1661:PHE:O	7:M:1663:THR:HG23	2.19	0.43
7:M:1767:CYS:HG	7:M:1819:PHE:HE1	1.67	0.43
7:M:2278:GLY:O	7:M:2281:MET:HG3	2.19	0.43
7:M:2344:LEU:O	7:M:2348:GLN:HG2	2.18	0.43
7:M:2410:GLU:O	7:M:2411:LEU:C	2.62	0.43
9:K:296:VAL:HG13	10:L:305:VAL:HG22	2.01	0.43
9:K:477:SER:OG	9:K:478:PHE:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:-47:DC:N4	6:J:46:DA:N7	2.67	0.43
1:I:67:DT:H2''	1:I:68:DC:C5	2.54	0.43
2:A:113:HIS:CG	2:E:126:LEU:HD22	2.54	0.43
2:E:85:GLN:OE1	2:E:85:GLN:N	2.46	0.43
6:J:24:DA:H2''	6:J:25:DG:C8	2.53	0.43
6:J:48:DG:H2'	6:J:49:DC:C6	2.53	0.43
7:M:320:LEU:HD11	7:M:369:PHE:CE2	2.54	0.43
7:M:1257:LEU:HD21	7:M:1334:LYS:HA	2.01	0.43
7:M:1820:VAL:HG23	7:M:1821:ASP:N	2.33	0.43
7:M:2930:TYR:CE2	7:M:2938:VAL:HG11	2.54	0.43
7:M:3680:LEU:O	7:M:3682:GLU:N	2.52	0.43
1:I:-42:DG:H4'	4:C:19:SER:H	1.84	0.42
1:I:-14:DA:C2	1:I:-13:DA:C6	3.07	0.42
5:H:41:VAL:O	5:H:45:VAL:HG23	2.18	0.42
7:M:138:PHE:O	7:M:139:ARG:C	2.62	0.42
7:M:910:PHE:O	7:M:911:LEU:C	2.62	0.42
7:M:1054:VAL:O	7:M:1054:VAL:HG13	2.19	0.42
7:M:1231:GLN:O	7:M:1233:SER:N	2.52	0.42
7:M:1696:LEU:N	7:M:1697:PRO:CD	2.82	0.42
7:M:2535:THR:HG23	7:M:2536:LEU:N	2.33	0.42
7:M:3568:ILE:HD12	7:M:3568:ILE:H	1.83	0.42
7:M:3608:LYS:O	7:M:3609:MET:C	2.62	0.42
9:K:64:ILE:HD11	9:K:119:LEU:HD11	2.01	0.42
9:K:355:LEU:HD23	10:L:475:ASP:HA	2.01	0.42
9:K:474:ARG:CG	9:K:476:ASP:O	2.67	0.42
4:C:81:ARG:NH1	4:C:105:GLY:O	2.40	0.42
5:D:26:ARG:O	5:D:29:THR:N	2.46	0.42
2:E:104:PHE:CE2	3:F:41:GLY:HA2	2.54	0.42
6:J:67:DA:C8	6:J:68:DT:C5	3.06	0.42
7:M:212:VAL:HG13	7:M:213:ARG:N	2.34	0.42
7:M:388:LEU:O	7:M:392:CYS:N	2.37	0.42
7:M:1434:VAL:C	7:M:1436:LEU:H	2.27	0.42
7:M:1475:LEU:O	7:M:1477:HIS:N	2.52	0.42
7:M:2205:VAL:O	7:M:2206:PRO:C	2.61	0.42
7:M:2389:PHE:C	7:M:2390:HIS:ND1	2.77	0.42
7:M:2886:GLN:N	7:M:2887:PRO:CD	2.82	0.42
7:M:3180:ASP:CA	7:M:3242:MET:HE1	2.48	0.42
7:M:3295:GLU:O	7:M:3299:THR:HG23	2.19	0.42
9:K:451:LYS:HE3	9:K:453:MET:HE3	2.01	0.42
10:L:22:ASN:O	10:L:23:SER:C	2.62	0.42
10:L:409:PHE:C	10:L:419:LEU:HD12	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:75:ALA:HB2	3:B:66:ILE:HD11	2.00	0.42
7:M:114:VAL:HG11	7:M:156:PHE:CE1	2.54	0.42
7:M:164:LYS:CE	9:K:312:LEU:HD12	2.49	0.42
7:M:911:LEU:HA	7:M:914:VAL:CG2	2.49	0.42
7:M:1723:PRO:HD2	7:M:1739:TYR:CE1	2.54	0.42
7:M:2316:TYR:OH	7:M:2358:ASP:HB2	2.19	0.42
7:M:3410:ILE:HG23	7:M:3464:LYS:HZ2	1.84	0.42
7:M:3971:MET:O	7:M:3972:LEU:C	2.62	0.42
7:M:4039:TYR:CE2	7:M:4041:ARG:HB2	2.54	0.42
7:M:4046:TYR:CB	7:M:4059:ILE:HD11	2.49	0.42
9:K:304:ASN:O	10:L:288:ASP:O	2.37	0.42
9:K:390:LEU:HD12	9:K:391:GLU:N	2.35	0.42
10:L:728:LEU:O	10:L:731:MET:HE3	2.18	0.42
1:I:-4:DG:H5"	3:B:45:ARG:HE	1.84	0.42
2:E:42:ARG:O	2:E:43:PRO:C	2.61	0.42
2:E:65:LEU:C	2:E:65:LEU:HD23	2.43	0.42
7:M:2584:CYS:SG	7:M:2781:PRO:O	2.77	0.42
7:M:3599:THR:OG1	7:M:3602:ASN:OD1	2.35	0.42
7:M:3960:PRO:HD2	7:M:4110:GLN:OE1	2.20	0.42
9:K:243:LEU:C	9:K:243:LEU:HD23	2.45	0.42
9:K:339:ARG:HE	9:K:340:PHE:H	1.66	0.42
7:M:190:ILE:HG13	7:M:190:ILE:O	2.20	0.42
7:M:260:ILE:HG23	7:M:260:ILE:O	2.18	0.42
7:M:470:ALA:O	7:M:1551:ILE:HD11	2.20	0.42
7:M:1238:GLN:HB2	7:M:1239:PRO:CD	2.49	0.42
7:M:1282:LEU:CD2	7:M:1291:LEU:HD23	2.50	0.42
7:M:1880:MET:O	7:M:1881:TYR:C	2.62	0.42
7:M:1938:ARG:CD	7:M:1977:ILE:HG23	2.50	0.42
7:M:1945:TYR:CZ	7:M:1949:ILE:HD11	2.54	0.42
7:M:1967:PHE:CG	7:M:1968:SER:N	2.84	0.42
7:M:3030:ILE:HG22	7:M:3031:TRP:N	2.34	0.42
7:M:3383:GLN:O	7:M:3387:GLU:HG2	2.18	0.42
7:M:3609:MET:O	7:M:3609:MET:HG2	2.19	0.42
7:M:3639:GLU:O	7:M:3643:HIS:ND1	2.53	0.42
9:K:462:MET:HE1	10:L:383:ALA:HB1	2.01	0.42
1:I:-33:DG:N1	6:J:33:DC:O2	2.48	0.42
1:I:45:DT:H2"	1:I:46:DG:N7	2.35	0.42
4:C:102:ILE:HA	3:F:98:TYR:CE1	2.55	0.42
3:F:98:TYR:CD2	3:F:98:TYR:C	2.98	0.42
6:J:36:DC:H2"	6:J:37:DC:C4	2.55	0.42
7:M:1449:ALA:O	7:M:1452:VAL:HG12	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:1539:SER:HB2	7:M:1553:PHE:CZ	2.55	0.42
7:M:2319:ALA:HB3	7:M:2360:PHE:HE1	1.85	0.42
7:M:2320:ALA:HB1	7:M:2321:GLU:OE1	2.20	0.42
10:L:302:GLU:O	10:L:303:THR:HG23	2.19	0.42
1:I:-60:DA:H2'	1:I:-59:DT:H71	1.99	0.42
1:I:-39:DT:O4	1:I:-38:DA:N6	2.53	0.42
7:M:1030:GLY:O	7:M:1033:ILE:HG22	2.20	0.42
7:M:1287:GLN:CG	7:M:1287:GLN:O	2.67	0.42
7:M:1655:ILE:O	7:M:1656:ASP:C	2.62	0.42
7:M:2383:PHE:O	7:M:2386:LEU:HD13	2.19	0.42
7:M:3069:MET:HA	7:M:3075:LYS:HB2	2.02	0.42
7:M:3427:GLU:OE2	7:M:3433:VAL:HG23	2.19	0.42
9:K:446:MET:HB2	9:K:448:PHE:HD1	1.84	0.42
10:L:463:LEU:HD12	10:L:476:LEU:CB	2.49	0.42
10:L:496:HIS:NE2	10:L:504:PRO:O	2.53	0.42
1:I:-35:DG:C8	1:I:-35:DG:H5''	2.55	0.42
1:I:-20:DC:C2	1:I:-19:DG:N7	2.87	0.42
1:I:28:DA:OP1	3:F:79:LYS:HG2	2.20	0.42
4:G:37:GLY:O	4:G:38:ASN:OD1	2.38	0.42
5:H:28:LYS:O	5:H:29:THR:OG1	2.33	0.42
5:H:104:ALA:O	5:H:108:VAL:HG23	2.20	0.42
7:M:93:LEU:HD21	7:M:100:ILE:CG1	2.49	0.42
7:M:1111:LEU:HD11	7:M:1128:CYS:HB2	2.02	0.42
7:M:2315:VAL:HG13	7:M:2318:ALA:HB2	2.02	0.42
7:M:2551:GLU:OE1	7:M:2847:THR:OG1	2.36	0.42
7:M:3600:PRO:O	7:M:3601:VAL:C	2.62	0.42
7:M:3908:HIS:O	7:M:3912:CYS:HB2	2.20	0.42
10:L:9:ALA:HB3	10:L:130:ARG:HG3	2.00	0.42
10:L:381:ILE:HD12	10:L:381:ILE:H	1.85	0.42
1:I:-47:DC:H2''	1:I:-46:DT:C4	2.55	0.42
1:I:-41:DA:C4	1:I:-40:DC:C6	3.07	0.42
1:I:49:DC:H2''	1:I:50:DG:C8	2.55	0.42
6:J:45:DC:H1'	6:J:46:DA:C5	2.55	0.42
7:M:569:VAL:O	7:M:572:VAL:HG12	2.20	0.42
7:M:793:LEU:N	7:M:794:PRO:HD2	2.34	0.42
7:M:1851:LEU:O	7:M:1854:ARG:CG	2.68	0.42
7:M:1886:LYS:HA	7:M:1889:VAL:HG22	2.02	0.42
7:M:2402:LEU:O	7:M:2402:LEU:HD23	2.19	0.42
7:M:2869:LEU:HD12	7:M:2869:LEU:C	2.45	0.42
7:M:2943:PHE:O	7:M:2944:THR:HB	2.19	0.42
7:M:3008:TRP:HB2	7:M:3051:LEU:CD2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:38:LEU:O	9:K:83:LEU:HD23	2.20	0.42
10:L:457:LEU:HD11	10:L:530:LEU:CD2	2.50	0.42
3:F:31:LYS:HB3	3:F:32:PRO:HD3	2.01	0.42
6:J:-36:DT:O3'	6:J:-35:DA:C8	2.73	0.42
7:M:184:VAL:C	7:M:186:PRO:HD2	2.44	0.42
7:M:3432:SER:OG	7:M:3435:ASP:O	2.36	0.42
7:M:3470:GLN:N	7:M:3470:GLN:CD	2.78	0.42
7:M:3569:GLN:OE1	7:M:3573:ASN:ND2	2.50	0.42
7:M:3921:GLY:O	7:M:3923:ARG:NH1	2.53	0.42
10:L:539:LEU:HD23	10:L:539:LEU:H	1.85	0.42
4:C:88:ARG:NH1	4:C:97:LEU:O	2.48	0.41
5:H:110:GLU:O	5:H:113:LYS:HG3	2.20	0.41
6:J:-13:DA:C6	6:J:-12:DC:N4	2.87	0.41
6:J:-1:DG:C4	6:J:0:DC:C5	3.08	0.41
7:M:1350:ASN:C	7:M:1351:THR:HG23	2.45	0.41
7:M:4014:LYS:O	7:M:4018:GLN:HG2	2.20	0.41
1:I:-63:DT:C2	1:I:-62:DA:N7	2.88	0.41
1:I:-62:DA:C2	6:J:63:DA:C2	3.08	0.41
3:B:22:LEU:O	3:B:23:ARG:HB3	2.20	0.41
6:J:44:DC:H1'	6:J:45:DC:C4	2.54	0.41
7:M:59:PHE:CD2	7:M:103:TYR:CD2	3.08	0.41
7:M:144:MET:O	7:M:145:ASP:HB2	2.20	0.41
7:M:880:MET:HG2	7:M:3933:GLU:O	2.21	0.41
7:M:1111:LEU:CD1	7:M:1131:ILE:HD12	2.50	0.41
7:M:1580:LEU:O	7:M:1583:MET:HB3	2.20	0.41
7:M:1878:ASP:O	7:M:1881:TYR:CE1	2.73	0.41
7:M:2406:GLU:O	7:M:2407:GLY:C	2.62	0.41
7:M:2420:PHE:O	7:M:2420:PHE:CG	2.73	0.41
7:M:3776:ALA:HB2	7:M:3787:GLN:HE22	1.86	0.41
9:K:52:GLN:O	9:K:53:SER:OG	2.24	0.41
9:K:72:ILE:HA	9:K:75:ILE:HG22	2.02	0.41
9:K:507:THR:C	9:K:508:LEU:HD22	2.45	0.41
10:L:165:LEU:HB3	10:L:166:PRO:HD2	2.02	0.41
4:C:71:ARG:HD3	5:D:49:THR:HA	2.01	0.41
4:C:72:ASP:OD1	5:D:45:VAL:CG1	2.69	0.41
3:F:32:PRO:HB3	6:J:-12:DC:P	2.60	0.41
4:G:26:PRO:HB2	4:G:29:ARG:HG3	2.02	0.41
5:H:51:ILE:HD13	5:H:59:MET:CE	2.50	0.41
6:J:25:DG:H2''	6:J:26:DG:N7	2.35	0.41
7:M:395:MET:HE2	7:M:401:ASP:HB3	2.02	0.41
7:M:1054:VAL:HG13	7:M:1057:LYS:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:1184:ARG:HD3	7:M:1262:ALA:HB1	2.02	0.41
7:M:2200:ALA:C	7:M:2202:PRO:HD2	2.45	0.41
7:M:2359:LYS:O	7:M:2359:LYS:HG3	2.20	0.41
7:M:4110:GLN:HE21	7:M:4116:ILE:HD13	1.84	0.41
10:L:43:GLN:OE1	10:L:491:PHE:HB3	2.20	0.41
1:I:-39:DT:C4	1:I:-38:DA:N6	2.89	0.41
6:J:-46:DC:H1'	6:J:-45:DA:C8	2.55	0.41
7:M:51:LEU:HD11	7:M:96:MET:HG3	2.01	0.41
7:M:139:ARG:CG	7:M:140:SER:H	2.31	0.41
7:M:421:LEU:HG	7:M:464:VAL:HG22	2.02	0.41
7:M:889:GLU:OE2	7:M:3889:ARG:NH2	2.48	0.41
7:M:987:LEU:O	7:M:990:GLN:HG3	2.19	0.41
7:M:1104:LEU:O	7:M:1104:LEU:HD23	2.21	0.41
7:M:1267:TYR:O	7:M:1271:ILE:HD12	2.21	0.41
7:M:1372:LEU:C	7:M:1372:LEU:HD23	2.45	0.41
7:M:1488:TYR:CD1	7:M:1555:HIS:HB3	2.56	0.41
7:M:1626:TRP:HA	7:M:1629:CYS:HB3	2.02	0.41
7:M:1662:ASN:OD1	7:M:1662:ASN:C	2.63	0.41
7:M:2360:PHE:O	7:M:2360:PHE:CD2	2.73	0.41
7:M:2389:PHE:O	7:M:2390:HIS:CB	2.68	0.41
7:M:2785:ILE:HG12	7:M:2789:SER:OG	2.21	0.41
7:M:3240:MET:HE1	7:M:3276:TRP:HA	2.02	0.41
7:M:4040:PRO:HA	7:M:4043:LYS:HG2	2.02	0.41
9:K:322:TYR:CE1	10:L:47:PHE:O	2.74	0.41
1:I:-51:DG:C2'	1:I:-50:DT:H72	2.50	0.41
1:I:19:DC:H2''	1:I:20:DG:H8	1.85	0.41
2:E:42:ARG:NH2	6:J:-5:DA:OP1	2.54	0.41
7:M:91:ILE:O	7:M:94:GLU:HG2	2.20	0.41
7:M:535:LEU:O	7:M:561:ASN:ND2	2.50	0.41
7:M:1514:LEU:HD12	7:M:1514:LEU:C	2.45	0.41
7:M:1668:PHE:N	7:M:1669:PRO:HD2	2.36	0.41
7:M:1933:LEU:HD12	7:M:1933:LEU:O	2.20	0.41
7:M:2801:ASP:OD1	7:M:2801:ASP:C	2.63	0.41
7:M:3470:GLN:CD	7:M:3470:GLN:H	2.29	0.41
7:M:3828:TYR:O	7:M:3836:PRO:HA	2.21	0.41
2:E:42:ARG:HA	2:E:42:ARG:CZ	2.51	0.41
6:J:39:DA:H2'	6:J:40:DG:O4'	2.20	0.41
6:J:54:DG:H1'	6:J:55:DT:C6	2.55	0.41
6:J:59:DA:C2'	6:J:60:DT:H71	2.51	0.41
7:M:100:ILE:HD11	7:M:134:LEU:HD13	2.01	0.41
7:M:135:LEU:HD23	7:M:180:LEU:HG	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:345:PHE:HB2	7:M:366:TYR:OH	2.20	0.41
7:M:364:ARG:O	7:M:367:GLY:N	2.43	0.41
7:M:954:GLY:O	7:M:955:ALA:C	2.62	0.41
7:M:984:TYR:O	7:M:987:LEU:HB3	2.21	0.41
7:M:1121:LEU:HD23	7:M:1121:LEU:O	2.20	0.41
7:M:2200:ALA:HB3	7:M:2202:PRO:HD2	2.01	0.41
7:M:2331:MET:HB3	7:M:2371:PHE:CZ	2.55	0.41
7:M:2374:LEU:O	7:M:2375:ALA:C	2.63	0.41
7:M:2443:MET:O	7:M:2444:PRO:C	2.62	0.41
7:M:3334:TYR:HB3	7:M:3381:ALA:HB2	2.03	0.41
7:M:3465:PHE:N	7:M:3466:PRO:CD	2.84	0.41
7:M:3813:LYS:HD2	7:M:3813:LYS:C	2.45	0.41
7:M:3858:MET:SD	7:M:4077:TYR:CD1	3.13	0.41
7:M:3917:ILE:HD11	7:M:4051:LEU:HD13	2.03	0.41
7:M:3958:LEU:HD11	7:M:4064:LEU:HD21	2.02	0.41
7:M:3972:LEU:N	7:M:3973:PRO:HD2	2.36	0.41
10:L:118:ILE:HG21	10:L:159:ILE:HD13	2.01	0.41
10:L:262:ALA:O	10:L:364:VAL:HG23	2.21	0.41
10:L:409:PHE:O	10:L:420:VAL:HG22	2.21	0.41
1:I:-68:DA:H2'	1:I:-67:DT:H71	2.01	0.41
7:M:583:LEU:C	7:M:584:GLU:HG3	2.46	0.41
7:M:1216:GLY:C	7:M:1218:SER:N	2.78	0.41
7:M:1287:GLN:O	7:M:1289:SER:N	2.54	0.41
7:M:1342:MET:HE1	7:M:1402:LEU:CB	2.50	0.41
7:M:3455:LYS:HE3	7:M:3489:SER:O	2.20	0.41
7:M:3633:ILE:HA	7:M:3637:GLY:H	1.85	0.41
8:N:17:UNK:O	8:N:18:UNK:CB	2.69	0.41
9:K:50:GLU:HG2	9:K:51:SER:N	2.35	0.41
9:K:130:ARG:O	9:K:133:ASP:OD1	2.39	0.41
1:I:-49:DG:H2'	1:I:-48:DC:O4'	2.20	0.41
1:I:-42:DG:H5''	4:C:19:SER:HA	2.03	0.41
1:I:-31:DA:N1	6:J:32:DA:N3	2.69	0.41
1:I:61:DC:H2''	1:I:62:DG:H5'	2.03	0.41
2:A:117:VAL:O	3:B:43:VAL:HG22	2.19	0.41
4:C:99:ARG:O	4:C:99:ARG:HG3	2.21	0.41
6:J:-15:DA:C6	6:J:-14:DA:C6	3.09	0.41
7:M:160:LEU:HD13	7:M:178:LEU:CD2	2.51	0.41
7:M:1436:LEU:CB	7:M:1439:PRO:HG3	2.51	0.41
7:M:1571:LEU:HB3	7:M:1600:MET:HE2	2.02	0.41
7:M:1982:ILE:HG22	7:M:1984:LEU:HD22	2.02	0.41
7:M:2171:LEU:O	7:M:2171:LEU:HD23	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:3097:ASP:OD1	7:M:3097:ASP:N	2.54	0.41
1:I:-53:DA:C2	6:J:55:DT:H1'	2.56	0.41
1:I:-41:DA:C2	1:I:-40:DC:C2	3.09	0.41
1:I:-6:DG:H2''	1:I:-5:DG:C8	2.56	0.41
1:I:35:DT:H2''	1:I:36:DA:N7	2.36	0.41
2:A:70:LEU:HD21	3:B:62:LEU:HD22	2.03	0.41
3:B:19:ARG:CZ	6:J:16:DA:C5	3.04	0.41
5:D:75:SER:O	5:D:79:HIS:ND1	2.54	0.41
2:E:58:THR:O	2:E:60:LEU:HD22	2.21	0.41
3:F:43:VAL:HG12	3:F:44:LYS:N	2.35	0.41
4:G:64:GLU:HG2	5:H:45:VAL:HG13	2.02	0.41
6:J:-73:DA:P	6:J:-72:DT:H73	2.61	0.41
6:J:-50:DC:C4	6:J:-49:DG:O6	2.73	0.41
6:J:-32:DC:C4	6:J:-31:DA:N6	2.88	0.41
6:J:-30:DG:C4	6:J:-29:DC:C4	3.09	0.41
6:J:-12:DC:C2	6:J:-11:DG:C5	3.09	0.41
6:J:27:DG:C2	6:J:28:DG:C6	3.08	0.41
6:J:32:DA:H2''	6:J:33:DC:H5'	2.02	0.41
7:M:138:PHE:C	7:M:139:ARG:HD3	2.46	0.41
7:M:417:VAL:HG23	7:M:418:ALA:N	2.36	0.41
7:M:524:TYR:OH	7:M:628:GLU:HB3	2.20	0.41
7:M:1005:ASP:OD1	7:M:1006:THR:N	2.54	0.41
7:M:1064:TYR:N	7:M:1064:TYR:CD1	2.89	0.41
7:M:1202:ARG:NH1	7:M:1210:ASP:OD2	2.48	0.41
7:M:1515:LEU:O	7:M:1518:ALA:HB3	2.19	0.41
7:M:1747:LEU:HA	7:M:1762:MET:HE1	2.01	0.41
7:M:1789:GLY:O	7:M:1794:GLN:NE2	2.49	0.41
7:M:1834:ASP:OD2	7:M:1837:ARG:NH2	2.49	0.41
7:M:1956:PHE:C	7:M:1958:GLU:H	2.29	0.41
7:M:2162:LYS:O	7:M:2163:HIS:C	2.63	0.41
7:M:2192:THR:OG1	7:M:2193:ILE:N	2.54	0.41
7:M:2196:TRP:C	7:M:2198:GLY:H	2.29	0.41
7:M:2357:GLU:N	7:M:2357:GLU:OE1	2.53	0.41
7:M:2943:PHE:O	7:M:2944:THR:CB	2.69	0.41
7:M:3963:LEU:HD11	7:M:3968:ILE:HG22	2.03	0.41
9:K:50:GLU:HG2	9:K:51:SER:H	1.86	0.41
9:K:356:LEU:HG	9:K:356:LEU:O	2.20	0.41
2:A:112:ILE:O	2:A:115:LYS:N	2.53	0.41
2:E:61:LEU:HD21	3:F:40:ARG:CG	2.51	0.41
6:J:-16:DT:H2''	6:J:-15:DA:N7	2.36	0.41
7:M:128:LEU:CD1	7:M:177:LEU:HD13	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:144:MET:C	7:M:146:GLU:H	2.29	0.41
7:M:243:GLN:OE1	7:M:244:THR:HG23	2.20	0.41
7:M:364:ARG:C	7:M:369:PHE:CE1	2.99	0.41
7:M:1881:TYR:CG	7:M:1882:SER:N	2.86	0.41
7:M:2295:GLN:OE1	7:M:2297:SER:N	2.42	0.41
7:M:2532:PRO:O	7:M:2538:ARG:NH1	2.54	0.41
7:M:3503:VAL:HG12	7:M:3518:VAL:HG21	2.03	0.41
9:K:146:VAL:O	9:K:149:VAL:HG12	2.21	0.41
9:K:482:VAL:HG22	10:L:333:TYR:CD1	2.55	0.41
10:L:249:CYS:O	10:L:250:ARG:C	2.63	0.41
1:I:-33:DG:OP1	5:D:89:ARG:NH2	2.54	0.40
1:I:-16:DT:C2	1:I:-15:DA:C6	3.09	0.40
1:I:14:DT:H4'	1:I:15:DT:OP1	2.20	0.40
1:I:66:DT:H2'	1:I:67:DT:H71	2.03	0.40
3:B:98:TYR:CE2	4:G:100:VAL:HG21	2.56	0.40
6:J:-32:DC:C2	6:J:-31:DA:N7	2.89	0.40
7:M:207:GLN:HG2	7:M:217:LEU:HA	2.02	0.40
7:M:424:LEU:HD21	7:M:471:LYS:HG3	2.03	0.40
7:M:584:GLU:O	7:M:585:ILE:C	2.62	0.40
7:M:1651:LYS:NZ	8:N:13:UNK:O	2.54	0.40
7:M:3608:LYS:C	7:M:3609:MET:SD	3.04	0.40
7:M:3752:VAL:O	7:M:3753:LYS:C	2.64	0.40
7:M:3961:PHE:CZ	7:M:3984:MET:SD	3.14	0.40
9:K:164:LYS:HG3	9:K:198:ILE:HA	2.03	0.40
9:K:202:LEU:HD13	9:K:204:HIS:CD2	2.57	0.40
4:C:54:VAL:O	4:C:58:LEU:HD23	2.21	0.40
3:F:81:VAL:HG23	3:F:82:THR:N	2.36	0.40
6:J:-42:DT:H2''	6:J:-41:DG:H8	1.85	0.40
6:J:-8:DC:H4'	6:J:-7:DG:OP1	2.21	0.40
7:M:207:GLN:HA	7:M:210:SER:O	2.22	0.40
7:M:341:PHE:CG	7:M:369:PHE:HB3	2.56	0.40
7:M:1583:MET:HE2	7:M:1628:LYS:HE2	2.03	0.40
7:M:1708:GLU:O	7:M:1712:ARG:HG2	2.21	0.40
7:M:1840:PHE:CG	7:M:1880:MET:HE3	2.56	0.40
7:M:2166:SER:N	7:M:2167:PRO:CD	2.84	0.40
7:M:2394:LYS:O	7:M:2398:LEU:HD13	2.20	0.40
7:M:3425:ARG:NH2	7:M:4000:ASN:OD1	2.54	0.40
7:M:3427:GLU:O	7:M:3428:GLU:HG3	2.21	0.40
7:M:3516:HIS:HA	7:M:3519:GLU:HG2	2.03	0.40
7:M:3953:LEU:O	7:M:3955:VAL:N	2.54	0.40
9:K:495:LEU:O	9:K:496:ASP:C	2.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:725:VAL:HG12	10:L:725:VAL:O	2.21	0.40
1:I:-63:DT:C2	1:I:-62:DA:C8	3.09	0.40
1:I:-48:DC:H2''	1:I:-47:DC:C6	2.56	0.40
3:F:36:ARG:HD3	6:J:-13:DA:OP1	2.20	0.40
3:F:37:LEU:O	3:F:40:ARG:HB2	2.22	0.40
4:G:10:THR:O	4:G:11:ARG:HG2	2.21	0.40
6:J:-43:DT:H2''	6:J:-42:DT:C6	2.56	0.40
7:M:224:LEU:HD21	7:M:255:ALA:HB3	2.03	0.40
7:M:256:ILE:O	7:M:300:TRP:NE1	2.55	0.40
7:M:330:ASN:O	7:M:331:ALA:HB3	2.21	0.40
7:M:946:THR:HG23	7:M:946:THR:O	2.20	0.40
7:M:2443:MET:O	7:M:2445:LYS:N	2.53	0.40
7:M:2523:ASN:OD1	7:M:2523:ASN:C	2.65	0.40
7:M:3024:PRO:O	7:M:3025:PRO:C	2.64	0.40
7:M:3041:LEU:N	7:M:3042:PRO:HD2	2.37	0.40
7:M:3410:ILE:HD12	7:M:3410:ILE:H	1.86	0.40
7:M:3599:THR:HB	7:M:3600:PRO:HD2	2.02	0.40
7:M:3878:VAL:HG21	7:M:4128:MET:HE1	2.04	0.40
4:C:67:GLY:O	4:C:69:ALA:N	2.53	0.40
2:E:73:GLU:OE2	3:F:22:LEU:HA	2.22	0.40
4:G:38:ASN:OD1	4:G:38:ASN:C	2.64	0.40
6:J:19:DC:H2''	6:J:20:DG:H8	1.87	0.40
7:M:294:PHE:CE1	7:M:316:LEU:HD11	2.56	0.40
7:M:323:VAL:HA	7:M:326:MET:HE1	2.03	0.40
7:M:1085:ILE:O	7:M:1086:TYR:C	2.62	0.40
7:M:1678:LEU:HD12	7:M:1679:LEU:HD12	2.03	0.40
7:M:2428:ASP:C	7:M:2429:ASP:OD1	2.65	0.40
9:K:61:ASP:O	9:K:64:ILE:HG22	2.21	0.40
10:L:14:MET:HB3	10:L:58:LEU:HD12	2.04	0.40
1:I:-5:DG:H4'	1:I:-4:DG:OP1	2.22	0.40
4:C:33:LEU:HB3	5:D:67:PHE:CZ	2.57	0.40
6:J:-51:DC:C2	6:J:-50:DC:C4	3.09	0.40
6:J:-20:DC:O2	6:J:-19:DG:N7	2.54	0.40
7:M:252:VAL:HG12	7:M:256:ILE:HD12	2.04	0.40
7:M:1649:LEU:HA	7:M:1652:ILE:HG12	2.04	0.40
7:M:1762:MET:O	7:M:1765:VAL:HB	2.22	0.40
7:M:2138:VAL:O	7:M:2143:ARG:NH2	2.52	0.40
7:M:2241:LEU:O	7:M:2245:TRP:HD1	2.05	0.40
7:M:2309:PHE:CZ	7:M:2318:ALA:HB3	2.56	0.40
7:M:2517:LEU:C	7:M:2517:LEU:HD23	2.47	0.40
7:M:2780:LEU:HB2	7:M:2781:PRO:CD	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:3066:ASP:HA	7:M:3069:MET:HE3	2.03	0.40
7:M:3470:GLN:HE22	7:M:3498:TRP:CG	2.40	0.40
7:M:3506:LEU:HD21	7:M:3555:VAL:HG12	2.03	0.40
9:K:125:GLN:OE1	9:K:125:GLN:N	2.52	0.40
9:K:133:ASP:OD1	9:K:133:ASP:C	2.65	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	
2	A	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
2	E	96/99 (97%)	86 (90%)	9 (9%)	1 (1%)	12	46
3	B	84/87 (97%)	82 (98%)	1 (1%)	1 (1%)	10	42
3	F	81/87 (93%)	78 (96%)	3 (4%)	0	100	100
4	C	106/111 (96%)	86 (81%)	19 (18%)	1 (1%)	14	48
4	G	109/111 (98%)	99 (91%)	9 (8%)	1 (1%)	14	48
5	D	94/96 (98%)	87 (93%)	7 (7%)	0	100	100
5	H	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
7	M	3632/4128 (88%)	3203 (88%)	412 (11%)	17 (0%)	24	61
9	K	486/609 (80%)	429 (88%)	54 (11%)	3 (1%)	21	58
10	L	529/732 (72%)	464 (88%)	61 (12%)	4 (1%)	16	52
All	All	5407/6255 (86%)	4794 (89%)	585 (11%)	28 (0%)	26	61

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	G	18	SER

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Mol	Chain	Res	Type
7	M	186	PRO
7	M	189	MET
7	M	1479	VAL
7	M	1551	ILE
7	M	1955	VAL
9	K	85	VAL
9	K	216	PHE
9	K	477	SER
3	B	18	HIS
7	M	139	ARG
7	M	4069	GLU
7	M	116	THR
7	M	1157	PHE
7	M	2390	HIS
10	L	245	ILE
10	L	257	LEU
4	C	25	PHE
7	M	1476	HIS
7	M	1967	PHE
10	L	369	ASP
7	M	2576	MET
7	M	2780	LEU
7	M	3461	ALA
10	L	27	ILE
7	M	2781	PRO
2	E	43	PRO
7	M	2362	VAL

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	
2	A	86/86 (100%)	86 (100%)	0	100	100
2	E	86/86 (100%)	86 (100%)	0	100	100
3	B	72/72 (100%)	72 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	68/72 (94%)	68 (100%)	0	100	100
4	C	84/88 (96%)	84 (100%)	0	100	100
4	G	88/88 (100%)	88 (100%)	0	100	100
5	D	82/82 (100%)	82 (100%)	0	100	100
5	H	81/82 (99%)	81 (100%)	0	100	100
7	M	3266/3671 (89%)	3266 (100%)	0	100	100
9	K	444/548 (81%)	444 (100%)	0	100	100
10	L	481/649 (74%)	481 (100%)	0	100	100
All	All	4838/5524 (88%)	4838 (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 (46) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	108	ASN
3	B	93	GLN
2	E	125	GLN
4	G	68	ASN
4	G	82	HIS
5	H	60	ASN
5	H	64	ASN
7	M	74	ASN
7	M	109	ASN
7	M	195	ASN
7	M	250	ASN
7	M	322	GLN
7	M	1049	GLN
7	M	1175	HIS
7	M	1238	GLN
7	M	1457	GLN
7	M	1574	ASN
7	M	1901	HIS
7	M	1926	ASN
7	M	2217	ASN
7	M	2222	HIS
7	M	2283	ASN
7	M	2365	ASN
7	M	2560	ASN

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Mol	Chain	Res	Type
7	M	2799	GLN
7	M	2885	GLN
7	M	3028	ASN
7	M	3037	GLN
7	M	3133	GLN
7	M	3154	GLN
7	M	3379	GLN
7	M	3384	HIS
7	M	3510	GLN
7	M	3569	GLN
7	M	3573	ASN
7	M	3590	ASN
7	M	3634	GLN
7	M	3760	GLN
7	M	3783	GLN
7	M	3944	HIS
7	M	3969	ASN
7	M	4068	HIS
9	K	110	ASN
9	K	128	GLN
10	L	246	HIS
10	L	269	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [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 [i](#)

There are no chain breaks in this entry.

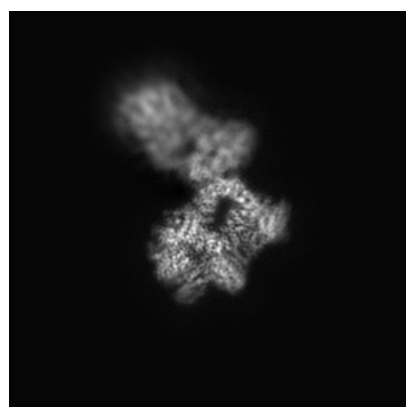
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74512. These allow visual inspection of the internal detail of the map and identification of artifacts.

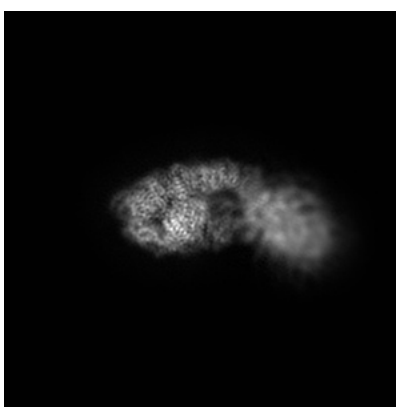
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

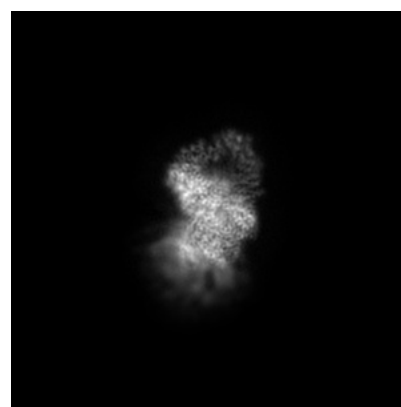
6.1.1 Primary map



X



Y

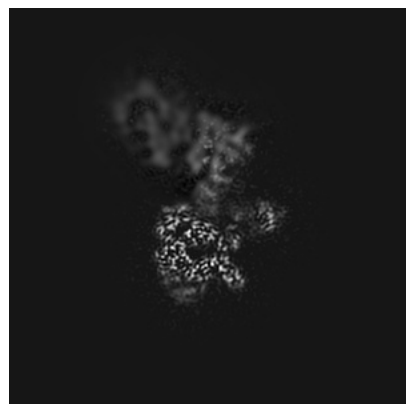


Z

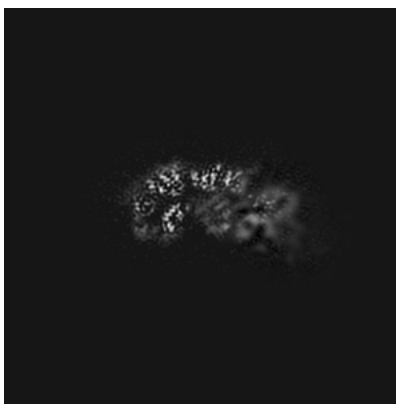
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

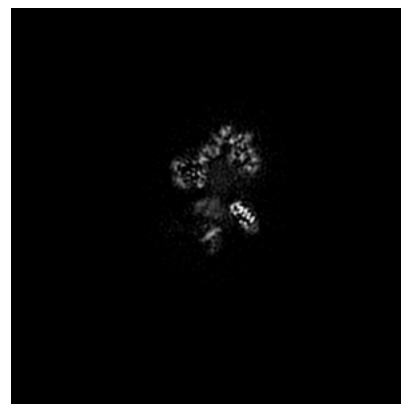
6.2.1 Primary map



X Index: 120



Y Index: 120

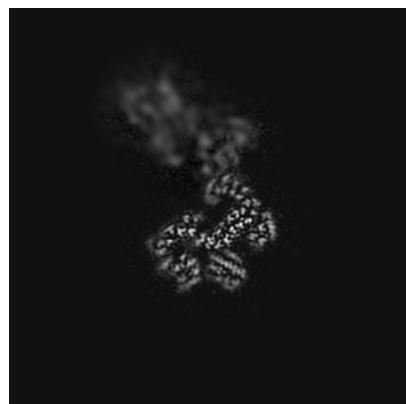


Z Index: 120

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

6.3 Largest variance slices [i](#)

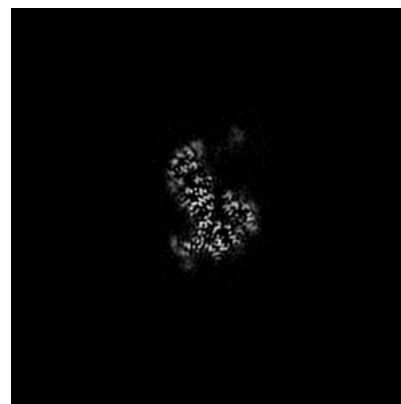
6.3.1 Primary map



X Index: 108



Y Index: 111

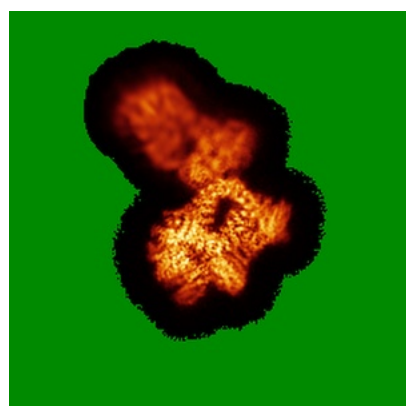


Z Index: 101

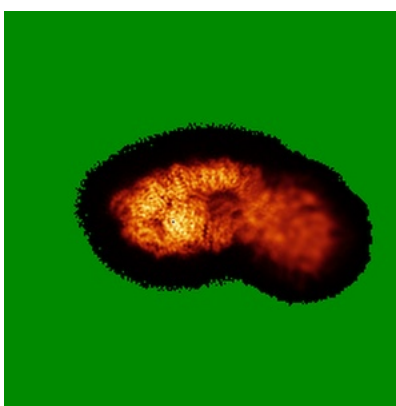
The images above show the largest variance slices of the map in three orthogonal directions.

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

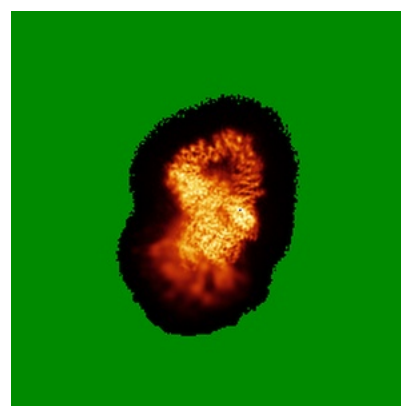
6.4.1 Primary map



X



Y



Z

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

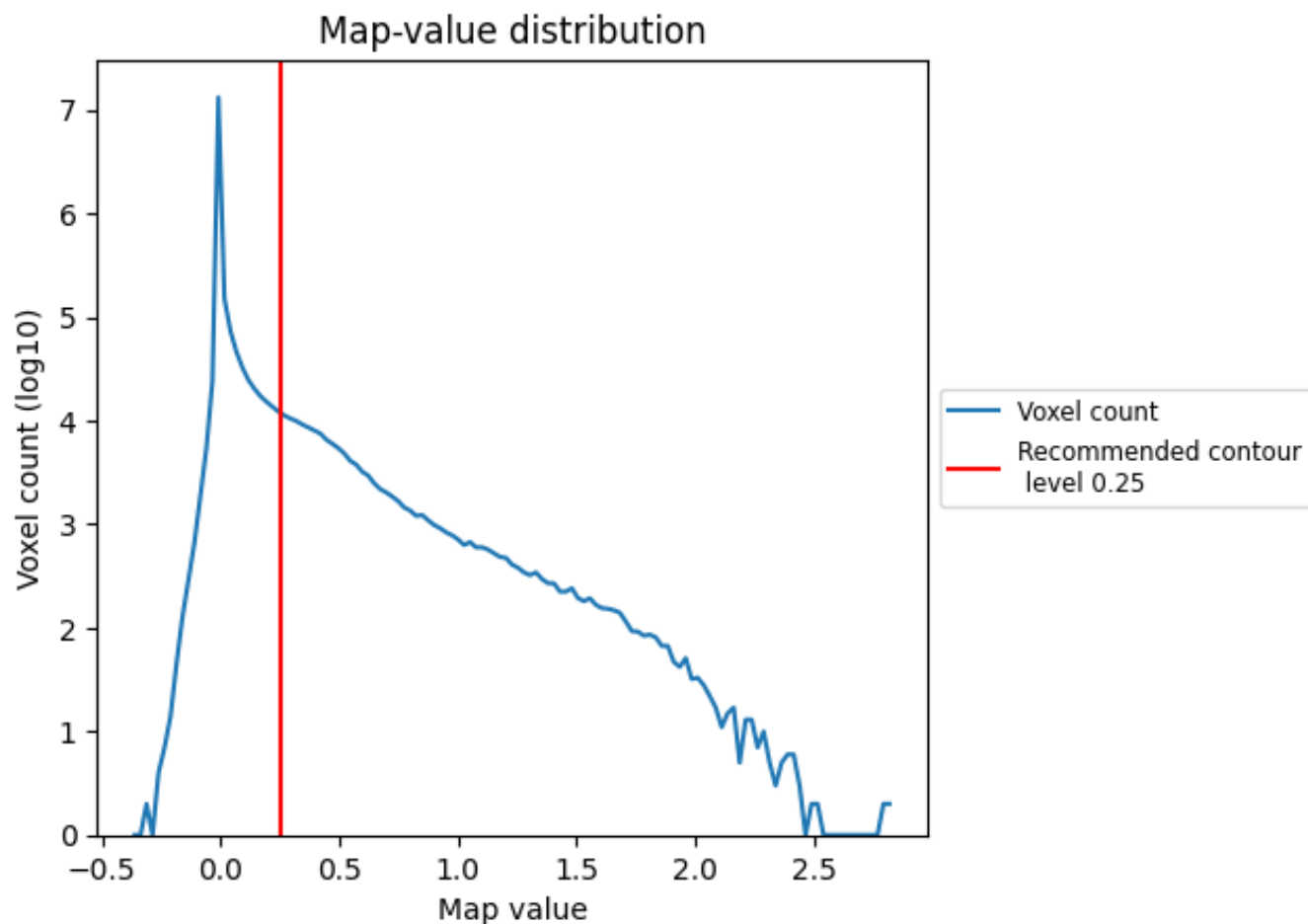
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

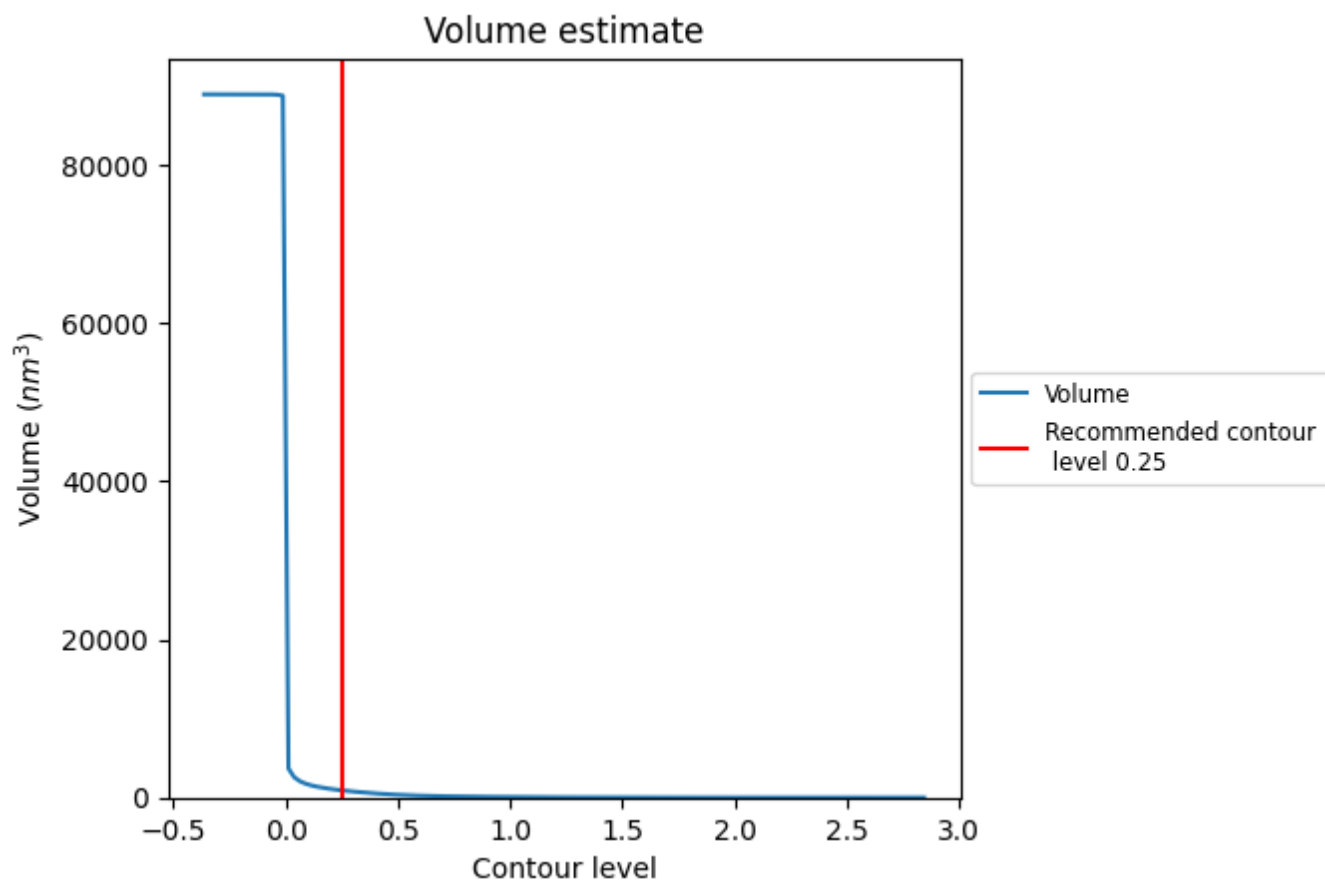
This section contains the results of statistical analysis of the map.

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.

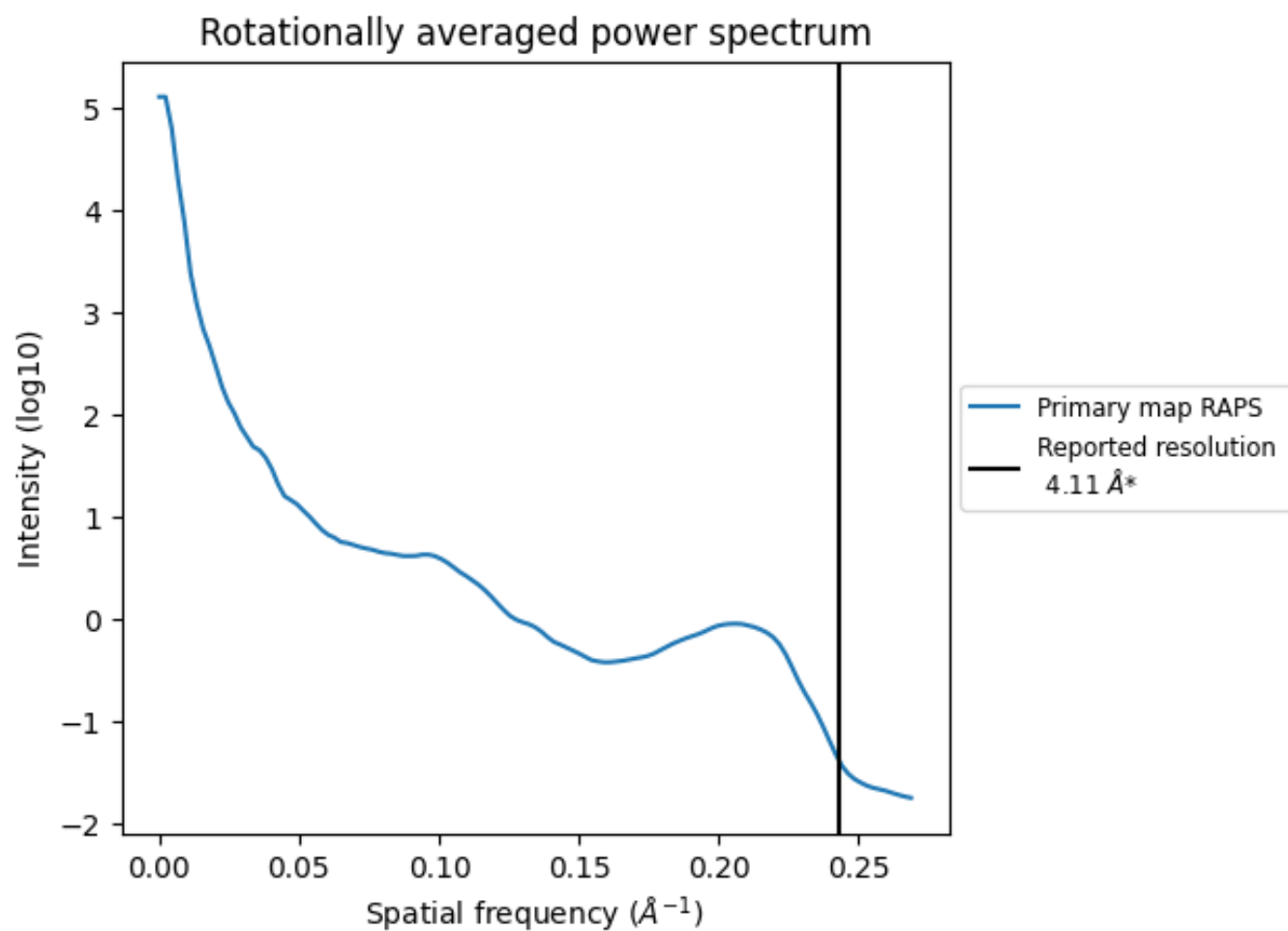
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 912 nm³; this corresponds to an approximate mass of 824 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 0.243 Å⁻¹

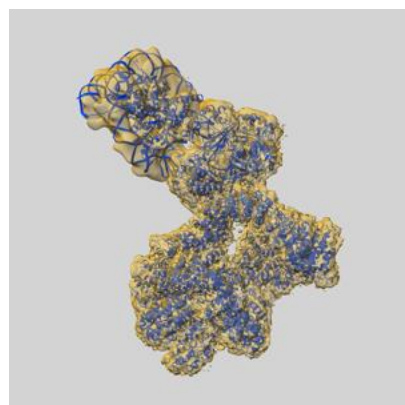
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

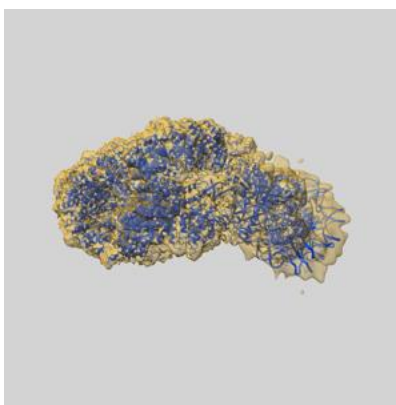
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-74512 and PDB model 9ZP0. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

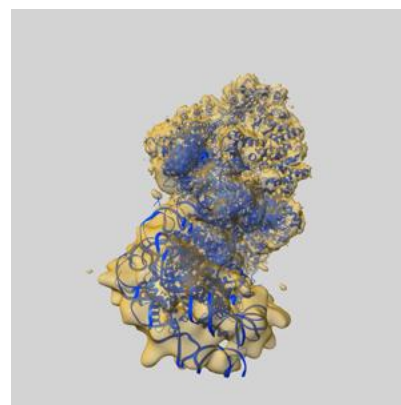
9.1 Map-model overlay [i](#)



X



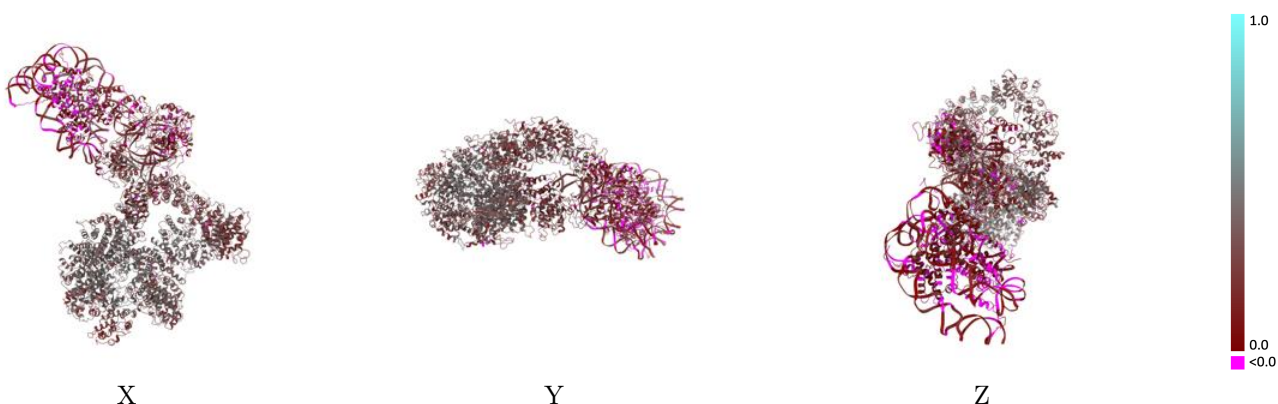
Y



Z

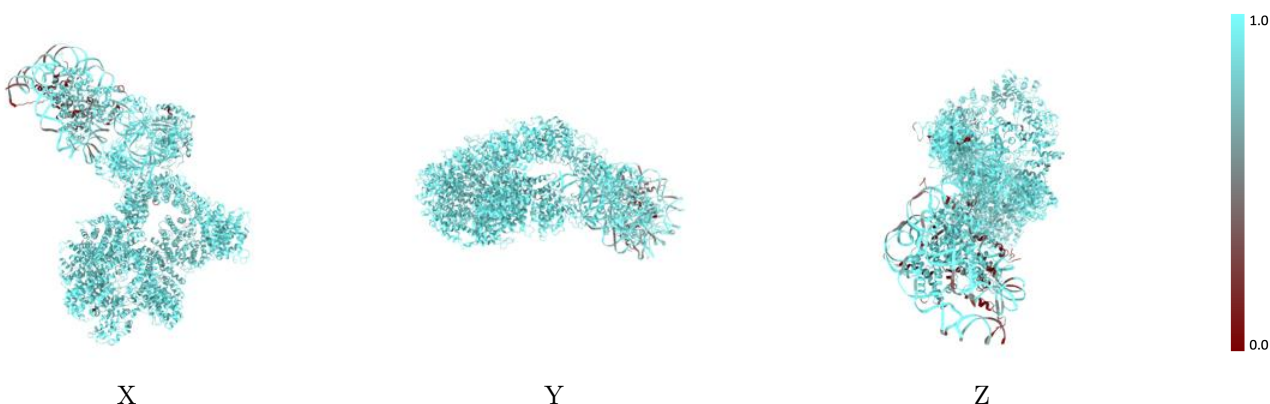
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



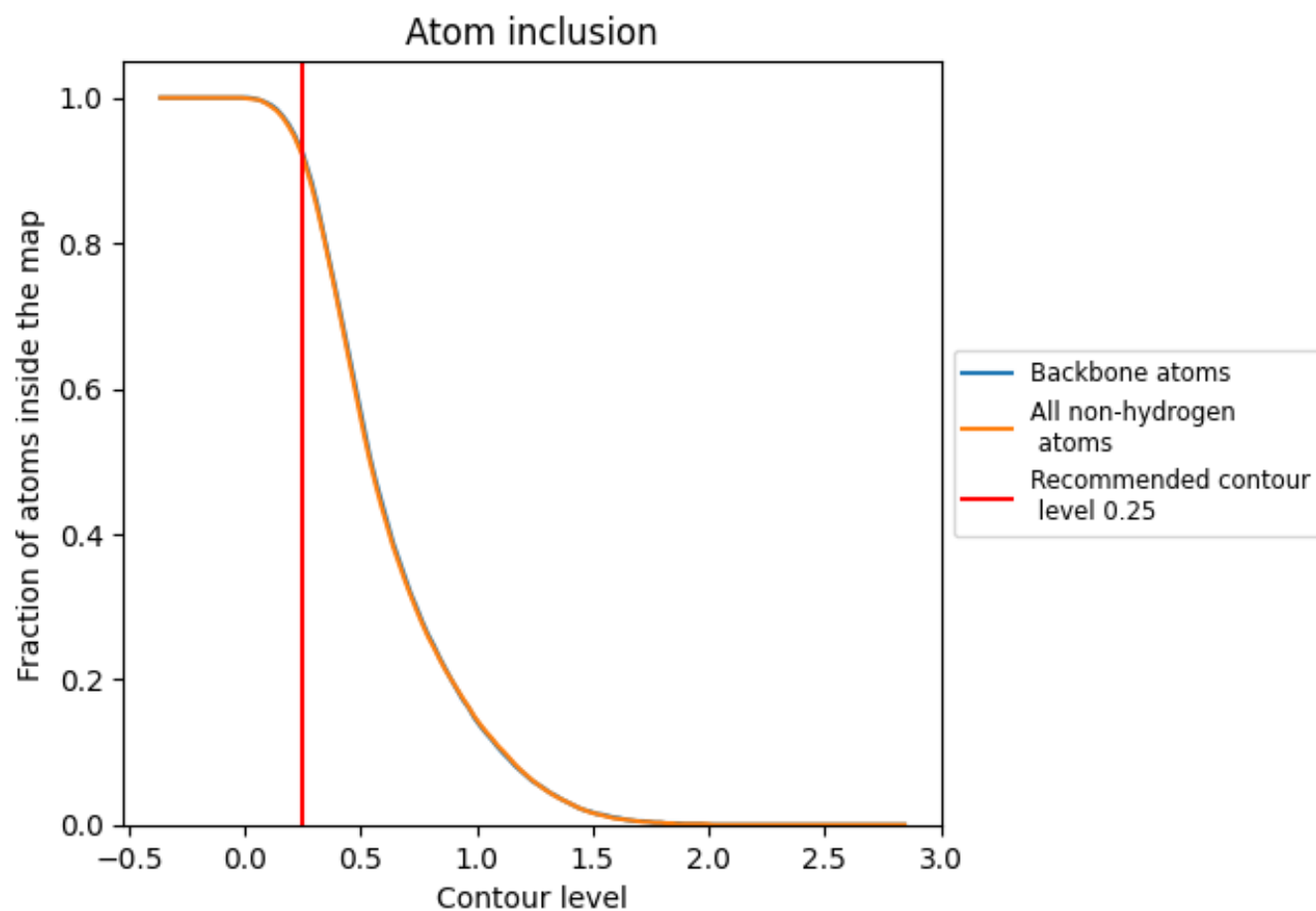
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 92% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9190	0.2470
A	0.7460	0.0030
B	0.7810	0.0420
C	0.7170	0.0480
D	0.8220	0.0820
E	0.7960	0.0400
F	0.8590	0.0560
G	0.7470	0.0420
H	0.8320	0.0510
I	0.8620	0.1070
J	0.8440	0.0960
K	0.9670	0.2100
L	0.9330	0.1500
M	0.9540	0.3380
N	0.9900	0.4440

1.0

0.0

<0.0