



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 11:49 PM UTC

PDB ID : 9UOY / pdb_00009uoy
EMDB ID : EMD-64385
Title : Structure of C. elegans piezo channel
Authors : Liu, Y.; Guo, Y.R.
Deposited on : 2025-04-27
Resolution : 3.40 Å(reported)

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

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A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.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

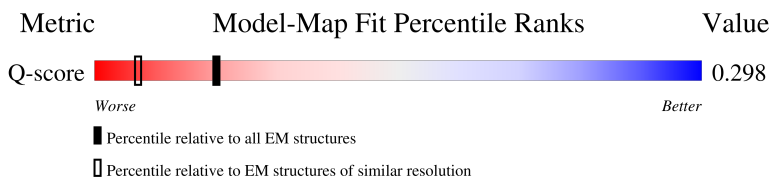
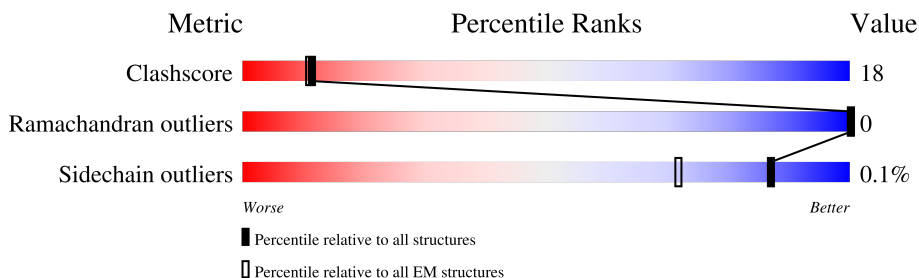
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	2442	10% 49% 29% 21%
1	B	2442	11% 50% 29% 21%
1	C	2442	10% 50% 29% 21%

2 Entry composition

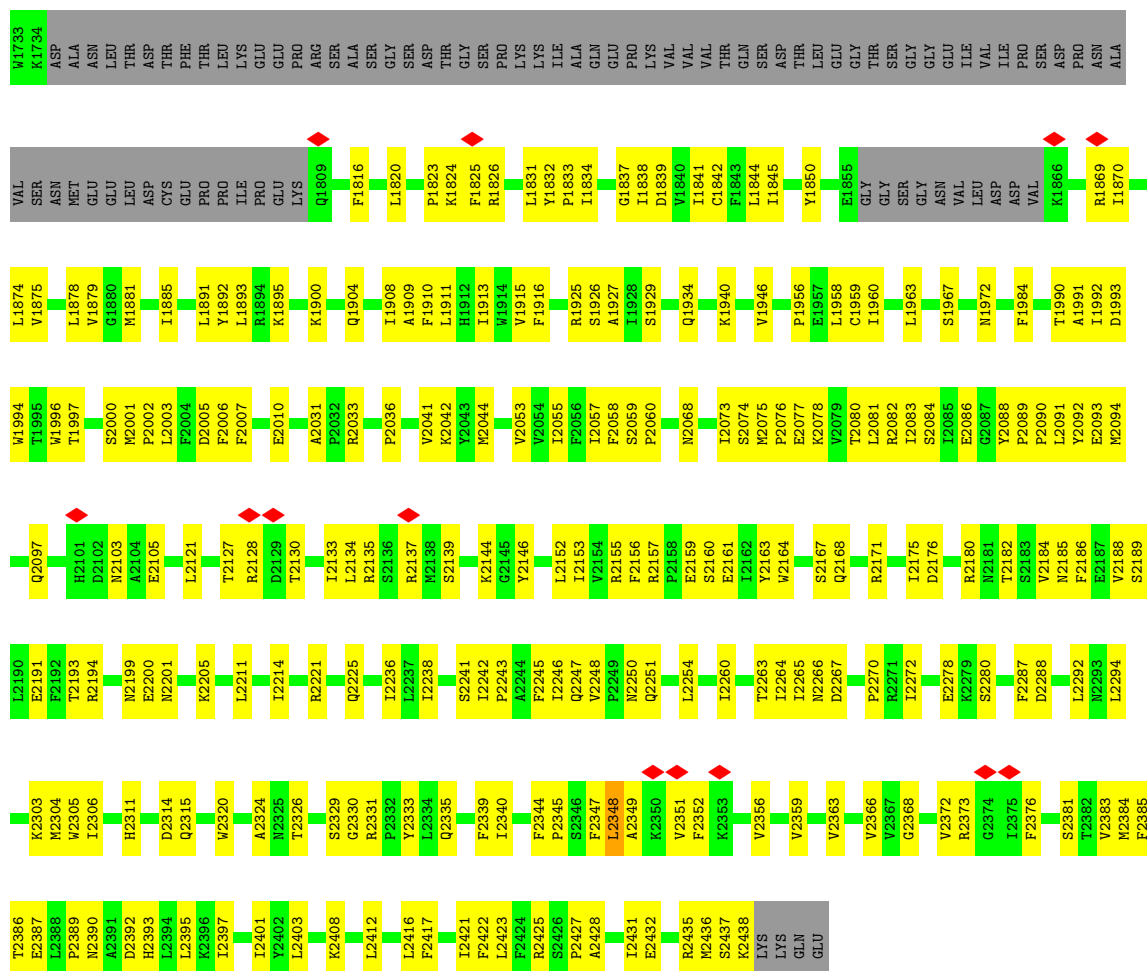
There is only 1 type of molecule in this entry. The entry contains 46695 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

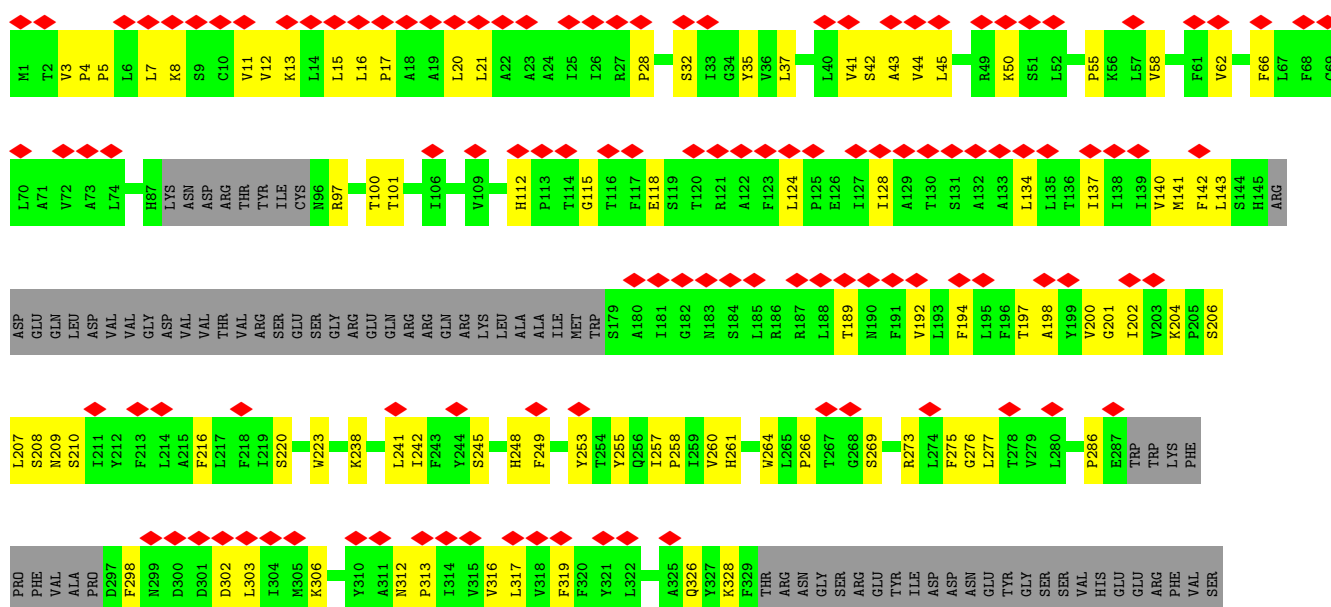
- Molecule 1 is a protein called Piezo-type mechanosensitive ion channel component 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1919	Total	C	N	O	S	0	0
			15565	10325	2510	2643	87		
1	B	1919	Total	C	N	O	S	0	0
			15565	10325	2510	2643	87		
1	C	1919	Total	C	N	O	S	0	0
			15565	10325	2510	2643	87		





• Molecule 1: Piezo-type mechanosensitive ion channel component 1



G1383	M1299	F1111	L922	Y850	ASP	T695	PHE	V553	S483	GLU	ALA
A1384	I1300	F1112	K923	I851	PRO	S696	GLN	H554	I484	GLU	GLY
E1385	G1301	L1116	G924	P852	THR	I697	ASP	A555	F485	GLN	THR
E1386	F1302	L1117	E925	L853	THR	V698	PRO	V556	G486	GLY	VAL
R1387	D1303	A1117	V926	V854	SER	I699	LYS	I557	L487	THR	THR
Y1389	V1304	L1121	E927	S858	THR	I700		I558	I488	ASN	ASN
A1396	H1219	A1021	G928	I861	THR	Y705		L559	L489	VAL	VAL
L1397	T1220	A1022	T929	P864	GLU	F706		L560	L490	ASP	ASP
G1401	W1224	C1025	E930	S865	ALA	G707		V561	L491	LYS	LYS
Y1404	Y1230	L1028	Y933	A866	VAL	S711		S562	L492	THR	GLY
M1405	F1231	V1029	N934	I870	ALA	N717		L564	T493	GLN	GLN
F1406	L1232	G1138	I935	S871	SER	T718		L565	C494	LEU	LEU
F1409	F1233	M1146	F936	S872	THR	S719		T566		ILE	ILE
D1410	T1234	P1147	G937	M875	GLY	L720		L567		ASP	ASP
E1411	I1236	Q1148	Y940		THR			P568		ARG	ARG
ASN	M1237	R1036			GLN			F499		ASN	GLU
ASP	M1237	F1038			GLY			R500		SER	SER
ASP	L1241	D1153	L945		ARG			D501		ALA	ALA
ASP	Q1242	T1154	A946		ALA					ALA	ALA
LEU	K1156	I1042	F947	Y878	HIS			K504		ILE	ILE
VAL	K1156	W1043	Q948	F880	ALA			S505		PHE	PRO
GLU	S1157	V1047	S949	F881	ALA			S506		ASN	ASN
PRO	Y1158		I950	L882	GLY			F507		THR	THR
ASP	V1159		Y951	V882	ASP			A508		GLY	GLY
ASP	D1160	L1053	A883	L884	LEU			M509		ALA	ALA
ASP	Y1161	Y1054	Y953		THR			A510		ARG	ARG
SER	F1162	P1055	I954	M887	LEU			P511		GLY	GLY
VAL	V1166	L1056	Q955	I888	ASP			I512		ASN	ASN
VAL	F1167	Q1057	R956	I889	THR			I513		LYS	LYS
PRO		F1058	Y957	L891	LEU			I514		LEU	LEU
ASP	G1252	V1062	M887	L892	THR			P515		LEU	LEU
GLU	D1253		I888	I891	ASP			A451		SER	SER
VAL			I889	L892	LEU			S452		ALA	ALA
ASP	G1259		I895	I893	THR			K453		SER	SER
ASP	L1262	P1065	E896		LEU			I454		ALA	ALA
PRO	C1263	P1066	LEU		LEU			I456		ASN	ASN
LYS	I1264	D1067	SER		LEU			H465		ASP	ASP
THR	V1265	S1068	GLN		LEU			S468		GLU	GLU
ALA	R1266	C1069	ILE		LEU			T469		GLN	GLN
TVR	Q1267	I1070	ASP		LEU			A470		ARG	ARG
ASP	L1268	W1074	ARG		LEU			L471		ALA	ALA
LEU	I1271		GLY		LEU			A473		SER	SER
ASP			VAL		LEU			M474		ARG	ARG
ASP	V1274	W1077	VAL		LEU			M475		PRO	PRO
PRO	N1276	D1083	ALA		LEU			T476		LEU	LEU
GLY	E1277	R1086	ASP		LEU			M477		ARG	ARG
GLN		L1089	ASN		LEU			L479		ASN	ASN
ILE	V1280	L1198	CYS		LEU			E547		GLY	GLY
MET	L1281	W1202	H911		LEU			M548		ALA	ALA
TVR	K1282	N1206	G912		LEU			T549		LYS	LYS
ALA		L1207	N913		LEU			L551			
ALA	D1286	F1287	M916		LEU			P552			
THR		V1209	P917		LEU						
ALA	Q1377		F920		LEU						
HIS	K1378		G921		LEU						
ASP	G1379				LEU						
LEU	I1380				LEU						
ASP	E1381				LEU						
LEU	R1382				LEU						

L70	A71	V72	L74	H87	LYS	ASP	GLU	GLN	LEU	ASP	PRO	VAL	VAL	GLY	ASP	ASN	ASP	ARG	THR	THR	ILE	CYS	N96	R97	T100	T101	I106	V109	H112	P113	T114	G115	T116	F117	E118	S119	T120	R121	A122	F123	L124	P125	E126	L127	I128	A129	T130	S131	A132	F133	L134	L135	T136	I137	I138	I139	V140	M141	F142	L143	S144	H145	ARG																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
L207	S208	N209	S210	I211	Y212	F213	L214	A215	F216	L217	F218	I219	S220	W223	K238	L241	I242	F243	Y244	S245	H248	F249	Y253	T254	Y255	Q256	I257	P258	N183	S184	A122	L185	R186	L187	L188	T189	N190	F191	V192	L193	F275	G276	L277	T278	V279	L280	P286	E287	TTP	TTP	LYS	PHE	S206																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
PRO	PHE	VAL	ALA	PRO	D297	F298	N299	D300	D301	L303	I304	M305	K306	Y310	A311	N312	P313	I314	Y315	V316	V317	L317	V318	F319	F320	Y321	L322	A325	Q326	Y327	K328	F329	THR	ARG	ASN	GLY	ARG	ARG	GLU	GLU	TYR	ILE	ASP	ASP	GLN	ARG	ALA	ALA	ASN	ASP	ASP	GLY	PRO	SER	LEU	ARG	ASN	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
ALA	GLY	GLN	VAL	THR	ASN	VAL	VAL	ASP	VAL	VAL	GLN	LEU	ILE	SER	ILE	GLU	THR	ALA	SER	ALA	PRO	GLY	GLY	GLY	GLY	ASN	THR	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LE

K2303	D2197	H2101	V1996	M1881	GLU	LEU	THR	PRO	GLN	E1381	M1299	S1212	L116
K2304	P2198	D2102	T1997	T1885	LEU	ASP	ASP	SER	LYS	R1382	I1300	T1213	A1117
V2305	N2199	N2103	S2000	L1891	THR	THR	THR	GLN	ILE	A1384	G1301	L1214	L1121
E2306	E2200	E2105	M2001	Y1892	PHE	PHE	PHE	LEU	ALA	A1385	F1302	R1215	R1125
H2311	N2201	L2121	L2003	L1893	THR	THR	THR	VAL	SER	E1386	V1303	E1218	H1219
D2314	K2205	T2127	F2004	R1894	LEU	LEU	LEU	GLN	ALA	R1387	I1305	T1220	N1131
Q2315	L2211	R2128	F2006	K1895	LYS	GLU	GLU	ALA	VAL	Y1394	A1306	W1224	Y1135
V2320	F2007	T2129	F2007	K1900	LYS	GLU	PRO	ASN	CYS	A1397	L1310	W1230	N1136
A2324	E2010	D2130	E2010	Q1904	ARG	ARG	ARG	VAL	GLY	G1401	F1312	T1231	D1137
K2325	A2031	T2133	A2031	I1908	SER	SER	SER	GLU	VAL	Y1404	Q1313	L1232	G1138
T2326	P2032	L2134	P2032	A1909	ALA	ALA	ALA	MET	THR	H1405	I1314	F1233	N1146
S2329	R2033	S2136	F1910	F1912	GLY	GLY	GLY	GLU	LEU	F1406	I1316	T1234	P1147
Q2330	P2036	R2137	P2036	I1911	SER	SER	SER	THR	PRO	D1409	F1317	I1235	Q1148
R2331	V2041	R2138	V2041	H1912	ASP	ASP	ASP	ALA	CYS	P1410	Q1323	M1237	D1153
F2332	M2044	F2138	M2044	I1913	THR	THR	THR	VAL	ARG	E1411	I1326	Y1247	T1154
L2334	Y2146	F2139	Y2146	W1914	GLY	GLY	GLY	VAL	GLU	ASN	M1326	Q1242	K1156
Q2335	Y2153	R1826	Y2153	F1915	PRO	PRO	PRO	TRP	ALA	ASP	ASP	F1244	S1157
F2339	L2152	L1831	L2053	F1916	LYS	LYS	LYS	Q1594	ILE	ASP	R1330	V1248	Y1159
I2340	T2155	Y1832	V2054	V1917	ALA	ALA	ALA	Q1595	VAL	ASP	E1332	F1248	Y1161
F2344	W2154	P1833	I2055	F1918	GLN	GLN	GLN	K1596	GLY	LEU	L1335	L1249	F1162
P2345	F2056	G1837	I2055	R1925	PRO	PRO	PRO	S1597	PHE	GLU	ASP	V1247	V1166
V2346	I2057	I1838	I2057	S1926	THR	THR	THR	S1598	LEU	PRO	ASP	F1248	F1167
S2347	F2058	I1840	F2058	A1927	VAL	VAL	VAL	I1610	SER	GLU	R1338	D1253	H1172
F2347	S2059	V1840	S2059	I1928	VAL	VAL	VAL	H1613	ARG	ALA	V1341	L1262	L1175
L2348	P2060	I1841	P2060	S1929	VAL	VAL	VAL	T1614	LYS	SER	L1342	I1264	M1176
A2349	N2068	C1842	N2068	Q1934	THR	THR	THR	D1615	PRO	PHE	K1343	R1266	S1177
K2350	I2162	I1845	I2162	K1940	GLN	GLN	GLN	I1616	GLY	PRO	M1344	Q1267	T1178
V2351	Y2163	Y1845	Y2163	V1946	SER	SER	SER	Y1619	LEU	GLY	Q1345	L1268	G1182
F2352	W2164	Y1850	Y2164	V1946	THR	THR	THR	F1620	SER	THR	ASP	I1271	I1183
K2353	S2167	E1855	S2167	P1956	LEU	LEU	LEU	F1621	GLU	ASP	K1349	A1190	A1190
V2356	Q2168	GLY	Q2168	E1957	GLY	GLY	GLY	A1622	GLY	ASP	L1350	V1274	L1191
V2359	R2171	SER	R2171	L1958	THR	THR	THR	I1623	THR	ALA	M1351	N1276	G1192
V2363	I2175	GLY	I2175	C1959	ASN	ASN	ASN	T1624	ASP	ALA	K1352	Y1193	Y1194
V2366	D2176	VAL	D2176	I1960	LEU	LEU	LEU	T1625	THR	ALA	Q1354	E1277	I1195
V2372	R2180	ASP	R2180	L1963	VAL	VAL	VAL	Q1626	SER	GLY	Q1355	V1280	L1198
R2373	T2181	VAL	T2181	S1967	ASP	ASP	ASP	V1627	LEU	GLY	E1356	L1281	L1202
Q2374	S2182	K1866	Q2374	M1972	VAL	VAL	VAL	T1628	ASP	ASP	K1359	K1282	W1202
I2375	W2184	R1869	I2375	F1984	ASP	ASP	ASP	Q1626	THR	LYS	D1364	D1286	N1206
F2376	N2185	P2089	F2376	E1987	SER	SER	SER	V1627	VAL	ILE	I1365	F1287	L1207
S2381	F2186	P2090	S2381	I1874	PRO	PRO	PRO	L1634	GLU	THR	R1367	C1291	V1209
T2382	R2187	L2091	T2382	L1875	ASP	ASP	ASP	T1632	LEU	SER	R1368	E1294	L2388
V2383	Y2188	N2091	V2383	I1874	ASN	ASN	ASN	I1633	THR	LYS	A1373	D1286	N1206
N2384	S2189	E2093	N2384	V1875	ALA	ALA	ALA	T1634	ARG	ALA	R1373	F1287	L1207
F2385	I1991	I1992	F2385	I1874	VAL	VAL	VAL	P1636	SER	THR	Q1377	L1207	L1207
T2386	L2190	L1992	T2386	V1875	SER	SER	SER	P1637	ALA	THR	K1378	V1209	V1209
E2387	E2191	W1994	E2387	L1878	ASN	ASN	ASN	I1638	ALA	THR	Q1377	E1294	L2388
L2388	F2192	T1995	L2388	V1879	MET	MET	MET	M1640	VAL	PHE	G1379	E1294	L2388
	T2193	T1995		G1880	GLU	GLU	GLU	W1644	LEU	ILE	I1380		

P2389	N2390	A2391	D2392	H2393	L2394	L2395	R2396	L2397		I2401	Y2402	L2403		K2408		L2412		L2416	F2417		I2421	F2422	L2423	F2424	R2425	S2426	P2427		I2431	E2432		R2435	N2436	S2437	K2438	LYS	LYS	GLN	GLU
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	163221	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.401	Depositor
Minimum map value	-0.140	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.075	Depositor
Map size (Å)	532.0, 532.0, 532.0	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	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	0.15	0/16001	0.39	0/21741
1	B	0.15	0/16001	0.39	0/21741
1	C	0.15	0/16001	0.39	0/21741
All	All	0.15	0/48003	0.39	0/65223

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	15565	0	15810	581	0
1	B	15565	0	15810	593	0
1	C	15565	0	15810	582	0
All	All	46695	0	47430	1687	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 18.

All (1687) 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:966:GLU:HG2	1:A:969:ARG:NH1	1.54	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:966:GLU:HG2	1:C:969:ARG:NH1	1.54	1.21
1:B:966:GLU:HG2	1:B:969:ARG:NH1	1.54	1.19
1:B:959:ARG:NH2	1:B:969:ARG:HD3	1.61	1.15
1:A:959:ARG:NH2	1:A:969:ARG:HD3	1.62	1.13
1:B:32:SER:CB	1:B:253:TYR:HE2	1.61	1.13
1:C:32:SER:CB	1:C:253:TYR:HE2	1.61	1.12
1:C:959:ARG:NH2	1:C:969:ARG:HD3	1.62	1.12
1:B:966:GLU:CG	1:B:969:ARG:HH22	1.67	1.07
1:C:32:SER:CB	1:C:253:TYR:CE2	2.38	1.07
1:C:966:GLU:CG	1:C:969:ARG:HH22	1.68	1.07
1:A:966:GLU:CG	1:A:969:ARG:HH22	1.67	1.06
1:B:2372:VAL:O	1:B:2376:PHE:HB3	1.55	1.06
1:B:32:SER:CB	1:B:253:TYR:CE2	2.38	1.06
1:A:2372:VAL:O	1:A:2376:PHE:HB3	1.55	1.05
1:C:2372:VAL:O	1:C:2376:PHE:HB3	1.55	1.05
1:B:964:LEU:CD1	1:B:968:MET:HG3	1.87	1.04
1:C:964:LEU:HD12	1:C:968:MET:HG3	1.04	1.04
1:A:966:GLU:CG	1:A:969:ARG:HH12	1.72	1.03
1:C:964:LEU:CD1	1:C:968:MET:HG3	1.87	1.03
1:C:966:GLU:CG	1:C:969:ARG:HH12	1.72	1.03
1:A:964:LEU:HD12	1:A:968:MET:HG3	1.04	1.02
1:A:964:LEU:CD1	1:A:968:MET:HG3	1.88	1.02
1:C:966:GLU:HG2	1:C:969:ARG:HH12	0.87	1.02
1:B:964:LEU:HD12	1:B:968:MET:HG3	1.04	1.01
1:B:32:SER:HB3	1:B:253:TYR:HE2	1.25	1.01
1:B:966:GLU:HG2	1:B:969:ARG:HH12	0.88	1.01
1:B:966:GLU:CG	1:B:969:ARG:HH12	1.72	1.01
1:A:966:GLU:HB3	1:A:969:ARG:NH2	1.77	0.99
1:C:966:GLU:HB3	1:C:969:ARG:NH2	1.77	0.99
1:A:966:GLU:HG2	1:A:969:ARG:HH12	0.87	0.99
1:C:32:SER:HB2	1:C:253:TYR:CE2	1.98	0.99
1:B:32:SER:HB2	1:B:253:TYR:CE2	1.98	0.99
1:C:32:SER:HB3	1:C:253:TYR:HE2	1.25	0.98
1:B:966:GLU:HB3	1:B:969:ARG:NH2	1.77	0.98
1:A:966:GLU:CD	1:A:969:ARG:HH22	1.73	0.96
1:B:966:GLU:CD	1:B:969:ARG:HH22	1.73	0.96
1:B:32:SER:HB3	1:B:253:TYR:CE2	2.01	0.96
1:C:32:SER:HB3	1:C:253:TYR:CE2	2.01	0.95
1:C:966:GLU:CD	1:C:969:ARG:HH22	1.73	0.95
1:C:32:SER:HB2	1:C:253:TYR:CD2	2.05	0.92
1:B:32:SER:HB2	1:B:253:TYR:CD2	2.05	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:959:ARG:HH22	1:A:969:ARG:HD3	1.37	0.89
1:C:959:ARG:HH22	1:C:969:ARG:HD3	1.37	0.89
1:B:966:GLU:CG	1:B:969:ARG:NH2	2.36	0.88
1:C:966:GLU:CG	1:C:969:ARG:NH2	2.37	0.88
1:C:959:ARG:CZ	1:C:969:ARG:HD3	2.04	0.88
1:A:966:GLU:CG	1:A:969:ARG:NH2	2.36	0.88
1:B:202:ILE:HG12	1:B:559:LEU:HD22	1.56	0.87
1:A:959:ARG:CZ	1:A:969:ARG:HD3	2.04	0.87
1:A:202:ILE:HG12	1:A:559:LEU:HD22	1.56	0.87
1:B:959:ARG:CZ	1:B:969:ARG:HD3	2.03	0.86
1:C:964:LEU:HD12	1:C:968:MET:CG	2.00	0.86
1:B:959:ARG:HH22	1:B:969:ARG:HD3	1.37	0.85
1:A:966:GLU:CB	1:A:969:ARG:NH2	2.40	0.85
1:C:202:ILE:HG12	1:C:559:LEU:HD22	1.56	0.85
1:B:964:LEU:HD12	1:B:968:MET:CG	2.00	0.84
1:A:964:LEU:HD12	1:A:968:MET:CG	2.00	0.84
1:B:966:GLU:HG2	1:B:969:ARG:CZ	2.08	0.84
1:B:966:GLU:CB	1:B:969:ARG:NH2	2.40	0.84
1:A:966:GLU:HG2	1:A:969:ARG:CZ	2.08	0.83
1:A:968:MET:HE1	1:A:974:PRO:HB2	1.61	0.83
1:C:966:GLU:CB	1:C:969:ARG:NH2	2.40	0.83
1:C:966:GLU:HG2	1:C:969:ARG:CZ	2.08	0.82
1:C:959:ARG:NH2	1:C:969:ARG:HH11	1.78	0.81
1:A:959:ARG:NH2	1:A:969:ARG:HH11	1.79	0.81
1:B:959:ARG:NH2	1:B:969:ARG:HH11	1.78	0.81
1:C:968:MET:HE1	1:C:974:PRO:HB2	1.61	0.81
1:B:968:MET:HE1	1:B:974:PRO:CB	2.11	0.80
1:B:968:MET:HE1	1:B:974:PRO:HB2	1.61	0.80
1:C:968:MET:HE1	1:C:974:PRO:CB	2.11	0.80
1:A:1183:ILE:HG21	1:A:1714:ILE:HD11	1.64	0.80
1:A:968:MET:HE1	1:A:974:PRO:CB	2.11	0.79
1:A:966:GLU:CG	1:A:969:ARG:NH1	2.39	0.79
1:C:1183:ILE:HG21	1:C:1714:ILE:HD11	1.64	0.79
1:B:1183:ILE:HG21	1:B:1714:ILE:HD11	1.64	0.78
1:B:2196:TYR:OH	1:B:2201:ASN:CG	2.27	0.78
1:B:1047:VAL:HG11	1:B:1121:LEU:HD22	1.66	0.78
1:C:966:GLU:CG	1:C:969:ARG:NH1	2.39	0.77
1:C:207:LEU:HB2	1:C:275:PHE:HA	1.65	0.77
1:C:968:MET:CE	1:C:974:PRO:CB	2.63	0.77
1:A:1047:VAL:HG11	1:A:1121:LEU:HD22	1.66	0.77
1:A:207:LEU:HB2	1:A:275:PHE:HA	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:968:MET:CE	1:A:974:PRO:CB	2.63	0.77
1:A:968:MET:CE	1:A:974:PRO:HB3	2.15	0.77
1:B:207:LEU:HB2	1:B:275:PHE:HA	1.65	0.77
1:B:968:MET:CE	1:B:974:PRO:CB	2.63	0.76
1:B:968:MET:CE	1:B:974:PRO:HB3	2.15	0.76
1:C:959:ARG:NH1	1:C:969:ARG:HG2	2.01	0.75
1:C:968:MET:CE	1:C:974:PRO:HB3	2.15	0.75
1:C:1047:VAL:HG11	1:C:1121:LEU:HD22	1.66	0.75
1:A:1029:VAL:HA	1:A:1232:LEU:HD23	1.69	0.75
1:A:966:GLU:CB	1:A:969:ARG:HH22	1.98	0.75
1:B:959:ARG:NH1	1:B:969:ARG:HG2	2.01	0.75
1:C:1029:VAL:HA	1:C:1232:LEU:HD23	1.69	0.75
1:B:966:GLU:CB	1:B:969:ARG:HH22	1.99	0.74
1:C:966:GLU:CB	1:C:969:ARG:HH22	1.99	0.74
1:A:959:ARG:NH1	1:A:969:ARG:HG2	2.01	0.74
1:B:223:TRP:O	1:B:574:ARG:NH1	2.21	0.73
1:B:1029:VAL:HA	1:B:1232:LEU:HD23	1.69	0.73
1:C:223:TRP:O	1:C:574:ARG:NH1	2.21	0.73
1:C:12:VAL:HG13	1:C:16:LEU:HD12	1.71	0.73
1:A:223:TRP:O	1:A:574:ARG:NH1	2.21	0.72
1:B:966:GLU:CG	1:B:969:ARG:NH1	2.40	0.72
1:A:1850:TYR:HB2	1:A:1874:LEU:HD11	1.72	0.72
1:B:12:VAL:HG13	1:B:16:LEU:HD12	1.71	0.72
1:A:2385:PHE:HE2	1:B:2381:SER:HA	1.55	0.72
1:B:1850:TYR:HB2	1:B:1874:LEU:HD11	1.72	0.72
1:C:2093:GLU:O	1:C:2094:MET:HE2	1.90	0.72
1:A:12:VAL:HG13	1:A:16:LEU:HD12	1.71	0.72
1:A:510:ALA:HB1	1:A:573:LEU:HG	1.72	0.72
1:B:2385:PHE:HE2	1:C:2381:SER:HA	1.55	0.71
1:A:2243:PRO:HG2	1:A:2246:ILE:HD11	1.72	0.71
1:A:2381:SER:HA	1:C:2385:PHE:HE2	1.55	0.71
1:A:1351:MET:SD	1:A:1354:GLN:NE2	2.64	0.71
1:A:1595:GLN:HG3	1:A:1596:LYS:H	1.56	0.71
1:C:1351:MET:SD	1:C:1354:GLN:NE2	2.64	0.71
1:B:1595:GLN:HG3	1:B:1596:LYS:H	1.56	0.71
1:B:2243:PRO:HG2	1:B:2246:ILE:HD11	1.72	0.71
1:C:510:ALA:HB1	1:C:573:LEU:HG	1.72	0.71
1:C:1595:GLN:HG3	1:C:1596:LYS:H	1.56	0.71
1:C:2243:PRO:HG2	1:C:2246:ILE:HD11	1.72	0.71
1:C:968:MET:HE3	1:C:974:PRO:HB3	1.73	0.70
1:A:2093:GLU:O	1:A:2094:MET:HE2	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:510:ALA:HB1	1:B:573:LEU:HG	1.72	0.70
1:B:1351:MET:SD	1:B:1354:GLN:NE2	2.64	0.70
1:B:847:ASN:HD22	1:B:921:GLY:HA3	1.56	0.70
1:C:1850:TYR:HB2	1:C:1874:LEU:HD11	1.72	0.70
1:B:2093:GLU:O	1:B:2094:MET:HE2	1.90	0.69
1:C:1057:GLN:NE2	1:C:1110:ASP:OD2	2.26	0.69
1:A:847:ASN:HD22	1:A:921:GLY:HA3	1.56	0.69
1:C:847:ASN:HD22	1:C:921:GLY:HA3	1.56	0.69
1:A:968:MET:HE3	1:A:974:PRO:HB3	1.73	0.69
1:B:11:VAL:HG13	1:B:15:LEU:HD12	1.74	0.69
1:B:1057:GLN:NE2	1:B:1110:ASP:OD2	2.26	0.69
1:C:189:THR:HA	1:C:192:VAL:HG22	1.75	0.69
1:B:968:MET:HE3	1:B:974:PRO:HB3	1.73	0.69
1:B:189:THR:HA	1:B:192:VAL:HG22	1.75	0.68
1:B:2383:VAL:HG23	1:B:2387:GLU:HG3	1.75	0.68
1:C:2383:VAL:HG23	1:C:2387:GLU:HG3	1.75	0.68
1:A:11:VAL:HG13	1:A:15:LEU:HD12	1.74	0.68
1:A:1057:GLN:NE2	1:A:1110:ASP:OD2	2.26	0.68
1:C:1651:ARG:NE	1:C:1732:LEU:HD23	2.08	0.68
1:B:1146:ASN:ND2	1:B:1148:GLN:O	2.27	0.68
1:C:11:VAL:HG13	1:C:15:LEU:HD12	1.74	0.68
1:A:1651:ARG:NE	1:A:1732:LEU:HD23	2.08	0.68
1:B:1651:ARG:NE	1:B:1732:LEU:HD23	2.08	0.68
1:A:1649:ASN:HB2	1:A:1820:LEU:HA	1.76	0.68
1:A:2383:VAL:HG23	1:A:2387:GLU:HG3	1.75	0.68
1:B:1198:LEU:O	1:B:1202:TRP:HB2	1.94	0.68
1:A:1083:ASP:OD1	1:A:1086:ARG:NH2	2.27	0.68
1:B:1649:ASN:HB2	1:B:1820:LEU:HA	1.76	0.68
1:C:1146:ASN:ND2	1:C:1148:GLN:O	2.27	0.68
1:C:273:ARG:HG3	1:C:531:ILE:HA	1.77	0.67
1:B:273:ARG:HG3	1:B:531:ILE:HA	1.77	0.67
1:A:1198:LEU:O	1:A:1202:TRP:HB2	1.94	0.67
1:C:2092:TYR:CE1	1:C:2094:MET:HE3	2.30	0.67
1:A:189:THR:HA	1:A:192:VAL:HG22	1.75	0.67
1:A:2236:ILE:HB	1:A:2292:LEU:HB2	1.77	0.67
1:C:688:TRP:HB3	1:C:760:LEU:HD21	1.76	0.67
1:A:1146:ASN:ND2	1:A:1148:GLN:O	2.27	0.67
1:C:1083:ASP:OD1	1:C:1086:ARG:NH2	2.28	0.67
1:B:688:TRP:HB3	1:B:760:LEU:HD21	1.76	0.66
1:C:966:GLU:HG2	1:C:969:ARG:NH2	2.10	0.66
1:A:1294:GLU:OE2	1:A:1294:GLU:N	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2159:GLU:OE2	1:A:2331:ARG:NH1	2.27	0.66
1:B:1626:GLN:NE2	1:B:1626:GLN:O	2.28	0.66
1:A:688:TRP:HB3	1:A:760:LEU:HD21	1.76	0.66
1:B:2159:GLU:OE2	1:B:2331:ARG:NH1	2.27	0.66
1:C:1649:ASN:HB2	1:C:1820:LEU:HA	1.76	0.66
1:C:2159:GLU:OE2	1:C:2331:ARG:NH1	2.27	0.66
1:A:2092:TYR:CE1	1:A:2094:MET:HE3	2.30	0.66
1:C:839:ALA:HA	1:C:842:ILE:HG22	1.76	0.66
1:B:1083:ASP:OD1	1:B:1086:ARG:NH2	2.28	0.66
1:C:1198:LEU:O	1:C:1202:TRP:HB2	1.94	0.66
1:A:1834:ILE:O	1:A:1838:ILE:HG13	1.96	0.66
1:B:1294:GLU:N	1:B:1294:GLU:OE2	2.28	0.66
1:B:2236:ILE:HB	1:B:2292:LEU:HB2	1.77	0.66
1:C:1626:GLN:NE2	1:C:1626:GLN:O	2.28	0.66
1:C:1834:ILE:O	1:C:1838:ILE:HG13	1.96	0.66
1:C:2372:VAL:O	1:C:2376:PHE:CB	2.40	0.66
1:A:2137:ARG:HE	1:C:1687:ARG:NH1	1.94	0.66
1:B:1834:ILE:O	1:B:1838:ILE:HG13	1.96	0.66
1:B:2092:TYR:CE1	1:B:2094:MET:HE3	2.30	0.66
1:A:1626:GLN:O	1:A:1626:GLN:NE2	2.28	0.66
1:A:1909:ALA:O	1:A:1913:ILE:HG12	1.96	0.66
1:B:1687:ARG:NH1	1:C:2137:ARG:HE	1.94	0.66
1:B:1730:LEU:HB3	1:B:1732:LEU:HD13	1.78	0.66
1:B:1909:ALA:O	1:B:1913:ILE:HG12	1.96	0.66
1:C:2097:GLN:O	1:C:2103:ASN:ND2	2.29	0.66
1:A:696:SER:O	1:A:700:ILE:HG12	1.96	0.66
1:B:696:SER:O	1:B:700:ILE:HG12	1.96	0.66
1:B:2182:THR:O	1:B:2221:ARG:NH2	2.29	0.66
1:C:1730:LEU:HB3	1:C:1732:LEU:HD13	1.78	0.66
1:A:839:ALA:HA	1:A:842:ILE:HG22	1.76	0.65
1:B:839:ALA:HA	1:B:842:ILE:HG22	1.76	0.65
1:A:836:VAL:HA	1:A:1111:PHE:HE2	1.62	0.65
1:A:2182:THR:O	1:A:2221:ARG:NH2	2.29	0.65
1:C:1294:GLU:N	1:C:1294:GLU:OE2	2.28	0.65
1:C:1909:ALA:O	1:C:1913:ILE:HG12	1.96	0.65
1:C:2182:THR:O	1:C:2221:ARG:NH2	2.29	0.65
1:B:646:LEU:HD22	1:B:666:TRP:HB2	1.78	0.65
1:B:2097:GLN:O	1:B:2103:ASN:ND2	2.29	0.65
1:C:2236:ILE:HB	1:C:2292:LEU:HB2	1.77	0.65
1:A:966:GLU:HG2	1:A:969:ARG:NH2	2.09	0.65
1:A:2097:GLN:O	1:A:2103:ASN:ND2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:487:LEU:HD11	1:B:700:ILE:HG23	1.78	0.65
1:A:891:LEU:HD23	1:A:893:ILE:H	1.62	0.65
1:A:1730:LEU:HB3	1:A:1732:LEU:HD13	1.78	0.65
1:A:1687:ARG:NH1	1:B:2137:ARG:HE	1.94	0.64
1:C:42:SER:O	1:C:45:LEU:HG	1.98	0.64
1:B:1651:ARG:HE	1:B:1732:LEU:HD23	1.62	0.64
1:C:1651:ARG:HE	1:C:1732:LEU:HD23	1.62	0.64
1:A:42:SER:O	1:A:45:LEU:HG	1.98	0.64
1:B:42:SER:HA	1:B:45:LEU:HD21	1.79	0.64
1:A:723:GLU:HG2	1:A:724:TRP:HD1	1.62	0.64
1:C:836:VAL:HA	1:C:1111:PHE:HE2	1.62	0.64
1:A:273:ARG:HG3	1:A:531:ILE:HA	1.77	0.64
1:A:1002:LEU:O	1:A:1006:MET:HG2	1.97	0.64
1:B:1280:VAL:HG23	1:C:2128:ARG:CZ	2.27	0.64
1:B:42:SER:O	1:B:45:LEU:HG	1.98	0.64
1:C:696:SER:O	1:C:700:ILE:HG12	1.96	0.64
1:A:2128:ARG:CZ	1:C:1280:VAL:HG23	2.28	0.64
1:B:836:VAL:HA	1:B:1111:PHE:HE2	1.62	0.64
1:B:966:GLU:HG2	1:B:969:ARG:NH2	2.09	0.64
1:C:487:LEU:HD11	1:C:700:ILE:HG23	1.78	0.64
1:A:646:LEU:HD22	1:A:666:TRP:HB2	1.79	0.64
1:B:1002:LEU:O	1:B:1006:MET:HG2	1.97	0.64
1:C:646:LEU:HD22	1:C:666:TRP:HB2	1.79	0.64
1:A:487:LEU:HD11	1:A:700:ILE:HG23	1.78	0.64
1:C:891:LEU:HD23	1:C:893:ILE:H	1.62	0.64
1:C:1002:LEU:O	1:C:1006:MET:HG2	1.97	0.64
1:C:1274:VAL:HG11	1:C:1299:ASN:HB3	1.80	0.64
1:A:1280:VAL:HG23	1:B:2128:ARG:CZ	2.27	0.63
1:B:220:SER:HB2	1:B:570:PHE:HE2	1.64	0.63
1:B:891:LEU:HD23	1:B:893:ILE:H	1.62	0.63
1:C:42:SER:HA	1:C:45:LEU:HD21	1.79	0.63
1:A:42:SER:HA	1:A:45:LEU:HD21	1.79	0.63
1:A:966:GLU:CG	1:A:969:ARG:CZ	2.74	0.63
1:B:1274:VAL:HG11	1:B:1299:ASN:HB3	1.80	0.63
1:A:1684:ILE:HD12	1:A:1687:ARG:HH21	1.64	0.63
1:B:477:TRP:HE3	1:B:565:LEU:HD22	1.64	0.63
1:B:723:GLU:HG2	1:B:724:TRP:HD1	1.62	0.63
1:B:2088:TYR:HB3	1:B:2089:PRO:HD2	1.81	0.63
1:A:2193:THR:HG22	1:A:2205:LYS:HG3	1.81	0.63
1:B:2372:VAL:O	1:B:2376:PHE:CB	2.40	0.63
1:C:115:GLY:HA3	1:C:118:GLU:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:477:TRP:HE3	1:C:565:LEU:HD22	1.64	0.62
1:C:1244:PHE:HA	1:C:1248:PHE:HB2	1.81	0.62
1:C:2088:TYR:HB3	1:C:2089:PRO:HD2	1.81	0.62
1:B:115:GLY:HA3	1:B:118:GLU:HB2	1.81	0.62
1:B:1992:ILE:HG23	1:B:1996:TRP:HD1	1.65	0.62
1:C:578:ARG:HA	1:C:581:PHE:CE1	2.34	0.62
1:A:2270:PRO:HG2	1:A:2314:ASP:HB2	1.81	0.62
1:C:140:VAL:HG13	1:C:141:MET:HE2	1.81	0.62
1:A:220:SER:HB2	1:A:570:PHE:HE2	1.64	0.62
1:A:578:ARG:HA	1:A:581:PHE:CE1	2.34	0.62
1:B:2270:PRO:HG2	1:B:2314:ASP:HB2	1.81	0.62
1:A:140:VAL:HG13	1:A:141:MET:HE2	1.81	0.62
1:A:1274:VAL:HG11	1:A:1299:ASN:HB3	1.80	0.62
1:B:2193:THR:HG22	1:B:2205:LYS:HG3	1.81	0.62
1:C:220:SER:HB2	1:C:570:PHE:HE2	1.64	0.62
1:C:723:GLU:HG2	1:C:724:TRP:HD1	1.62	0.62
1:A:2088:TYR:HB3	1:A:2089:PRO:HD2	1.81	0.62
1:C:959:ARG:CZ	1:C:969:ARG:CD	2.78	0.62
1:C:2270:PRO:HG2	1:C:2314:ASP:HB2	1.81	0.62
1:A:477:TRP:HE3	1:A:565:LEU:HD22	1.64	0.62
1:C:1684:ILE:HD12	1:C:1687:ARG:HH21	1.64	0.62
1:A:115:GLY:HA3	1:A:118:GLU:HB2	1.81	0.62
1:C:966:GLU:CG	1:C:969:ARG:CZ	2.74	0.61
1:C:1992:ILE:HG23	1:C:1996:TRP:HD1	1.65	0.61
1:A:1651:ARG:HE	1:A:1732:LEU:HD23	1.62	0.61
1:A:4:PRO:HB2	1:A:7:LEU:HB3	1.82	0.61
1:B:835:PHE:HB3	1:B:1111:PHE:HZ	1.65	0.61
1:C:2193:THR:HG22	1:C:2205:LYS:HG3	1.81	0.61
1:A:835:PHE:HB3	1:A:1111:PHE:HZ	1.65	0.61
1:C:842:ILE:HD12	1:C:853:LEU:HD23	1.82	0.61
1:C:1265:VAL:HA	1:C:1268:LEU:HG	1.82	0.61
1:B:966:GLU:CG	1:B:969:ARG:CZ	2.74	0.61
1:A:1190:ALA:O	1:A:1194:ILE:HD12	2.01	0.61
1:B:140:VAL:HG13	1:B:141:MET:HE2	1.81	0.61
1:B:578:ARG:HA	1:B:581:PHE:CE1	2.35	0.61
1:B:842:ILE:HD12	1:B:853:LEU:HD23	1.82	0.61
1:A:1992:ILE:HG23	1:A:1996:TRP:HD1	1.65	0.61
1:A:2372:VAL:O	1:A:2376:PHE:CB	2.40	0.61
1:B:1312:PHE:O	1:B:1316:ILE:HG12	2.00	0.61
1:B:1684:ILE:HD12	1:B:1687:ARG:HH21	1.64	0.61
1:C:639:ILE:H	1:C:639:ILE:HD12	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1632:LEU:HA	1:C:1635:LEU:HD13	1.82	0.61
1:C:1667:VAL:HA	1:C:1670:ILE:HG22	1.82	0.61
1:A:959:ARG:CZ	1:A:969:ARG:CD	2.78	0.61
1:A:1632:LEU:HA	1:A:1635:LEU:HD13	1.82	0.61
1:B:884:LEU:O	1:B:888:ILE:HG12	2.01	0.61
1:C:28:PRO:HB2	1:C:257:ILE:HG12	1.83	0.61
1:C:824:ARG:HA	1:C:827:GLU:HG2	1.82	0.61
1:A:842:ILE:HD12	1:A:853:LEU:HD23	1.82	0.61
1:B:639:ILE:H	1:B:639:ILE:HD12	1.66	0.61
1:B:830:ILE:HG23	1:B:948:GLN:HG2	1.83	0.61
1:A:639:ILE:H	1:A:639:ILE:HD12	1.66	0.61
1:B:1003:GLU:O	1:B:1007:ILE:HG12	2.01	0.61
1:B:1383:GLY:HA3	1:B:1404:TYR:HB2	1.82	0.61
1:C:884:LEU:O	1:C:888:ILE:HG12	2.01	0.61
1:C:1190:ALA:O	1:C:1194:ILE:HD12	2.01	0.61
1:C:1312:PHE:O	1:C:1316:ILE:HG12	2.00	0.61
1:A:1244:PHE:HA	1:A:1248:PHE:HB2	1.81	0.60
1:A:1312:PHE:O	1:A:1316:ILE:HG12	2.00	0.60
1:A:1383:GLY:HA3	1:A:1404:TYR:HB2	1.82	0.60
1:B:824:ARG:HA	1:B:827:GLU:HG2	1.82	0.60
1:B:1667:VAL:HA	1:B:1670:ILE:HG22	1.82	0.60
1:C:4:PRO:HB2	1:C:7:LEU:HB3	1.82	0.60
1:C:835:PHE:HB3	1:C:1111:PHE:HZ	1.65	0.60
1:C:717:ASN:OD1	1:C:718:THR:N	2.35	0.60
1:C:1003:GLU:O	1:C:1007:ILE:HG12	2.01	0.60
1:B:4:PRO:HB2	1:B:7:LEU:HB3	1.82	0.60
1:B:1244:PHE:HA	1:B:1248:PHE:HB2	1.81	0.60
1:B:2263:THR:O	1:B:2267:ASP:HB2	2.02	0.60
1:A:1667:VAL:HA	1:A:1670:ILE:HG22	1.82	0.60
1:B:1632:LEU:HA	1:B:1635:LEU:HD13	1.82	0.60
1:C:1383:GLY:HA3	1:C:1404:TYR:HB2	1.82	0.60
1:A:884:LEU:O	1:A:888:ILE:HG12	2.01	0.60
1:A:2152:LEU:HD13	1:A:2340:ILE:HD13	1.83	0.60
1:B:655:PRO:HG3	1:B:890:GLN:HG3	1.83	0.60
1:C:2152:LEU:HD13	1:C:2340:ILE:HD13	1.83	0.60
1:A:1003:GLU:O	1:A:1007:ILE:HG12	2.01	0.60
1:B:1265:VAL:HA	1:B:1268:LEU:HG	1.83	0.60
1:A:824:ARG:HA	1:A:827:GLU:HG2	1.82	0.60
1:A:959:ARG:HH21	1:A:969:ARG:HH11	1.49	0.60
1:A:2263:THR:O	1:A:2267:ASP:HB2	2.02	0.60
1:B:28:PRO:HB2	1:B:257:ILE:HG12	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:959:ARG:CZ	1:B:969:ARG:CD	2.77	0.60
1:B:1190:ALA:O	1:B:1194:ILE:HD12	2.01	0.60
1:B:1649:ASN:HD21	1:B:1823:PRO:HB3	1.67	0.60
1:B:2152:LEU:HD13	1:B:2340:ILE:HD13	1.83	0.60
1:C:655:PRO:HG3	1:C:890:GLN:HG3	1.83	0.60
1:C:830:ILE:HG23	1:C:948:GLN:HG2	1.82	0.60
1:A:1649:ASN:HD21	1:A:1823:PRO:HB3	1.67	0.60
1:A:655:PRO:HG3	1:A:890:GLN:HG3	1.83	0.59
1:A:717:ASN:OD1	1:A:718:THR:N	2.35	0.59
1:B:2000:SER:HA	1:C:2036:PRO:HA	1.84	0.59
1:C:1649:ASN:HD21	1:C:1823:PRO:HB3	1.67	0.59
1:B:28:PRO:HA	1:B:253:TYR:OH	2.02	0.59
1:B:717:ASN:OD1	1:B:718:THR:N	2.34	0.59
1:A:830:ILE:HG23	1:A:948:GLN:HG2	1.82	0.59
1:A:1265:VAL:HA	1:A:1268:LEU:HG	1.82	0.59
1:B:477:TRP:HZ3	1:B:566:THR:HB	1.67	0.59
1:B:1043:TRP:HZ2	1:B:1117:ALA:HA	1.67	0.59
1:B:2351:VAL:O	1:B:2351:VAL:HG12	2.02	0.59
1:A:20:LEU:HG	1:A:35:TYR:CE2	2.37	0.59
1:A:477:TRP:HZ3	1:A:566:THR:HB	1.67	0.59
1:A:28:PRO:HB2	1:A:257:ILE:HG12	1.83	0.59
1:A:2351:VAL:HG12	1:A:2351:VAL:O	2.02	0.59
1:C:966:GLU:CB	1:C:969:ARG:CZ	2.81	0.59
1:C:20:LEU:HG	1:C:35:TYR:CE2	2.37	0.59
1:B:966:GLU:CB	1:B:969:ARG:CZ	2.81	0.59
1:C:1043:TRP:HZ2	1:C:1117:ALA:HA	1.67	0.59
1:C:2263:THR:O	1:C:2267:ASP:HB2	2.02	0.59
1:A:966:GLU:HA	1:A:969:ARG:NH1	2.17	0.59
1:B:966:GLU:HA	1:B:969:ARG:NH1	2.17	0.59
1:A:966:GLU:CB	1:A:969:ARG:CZ	2.81	0.59
1:B:514:LEU:HD22	1:B:573:LEU:HD22	1.85	0.59
1:C:28:PRO:HA	1:C:253:TYR:OH	2.02	0.59
1:A:44:VAL:HG13	1:A:328:LYS:HB2	1.84	0.59
1:A:2036:PRO:HA	1:C:2000:SER:HA	1.84	0.59
1:B:20:LEU:HG	1:B:35:TYR:CE2	2.37	0.59
1:B:44:VAL:HG13	1:B:328:LYS:HB2	1.85	0.59
1:B:959:ARG:HH21	1:B:969:ARG:HH11	1.49	0.58
1:A:1043:TRP:HZ2	1:A:1117:ALA:HA	1.67	0.58
1:A:2000:SER:HA	1:B:2036:PRO:HA	1.84	0.58
1:C:966:GLU:HA	1:C:969:ARG:NH1	2.18	0.58
1:A:514:LEU:HD22	1:A:573:LEU:HD22	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1694:PRO:HB3	1:C:1926:SER:HA	1.86	0.58
1:C:2246:ILE:O	1:C:2339:PHE:N	2.35	0.58
1:C:477:TRP:HZ3	1:C:566:THR:HB	1.67	0.58
1:C:514:LEU:HD22	1:C:573:LEU:HD22	1.85	0.58
1:A:1637:LEU:HB2	1:A:1638:PRO:HD3	1.86	0.58
1:B:841:PHE:CD1	1:B:937:GLY:HA3	2.39	0.58
1:A:968:MET:CE	1:A:974:PRO:HB2	2.28	0.58
1:C:1881:MET:O	1:C:1885:ILE:HG12	2.04	0.58
1:C:1262:LEU:HA	1:C:1265:VAL:HG12	1.86	0.58
1:B:2246:ILE:O	1:B:2339:PHE:N	2.35	0.58
1:C:1300:ILE:HB	1:C:1303:ASP:HB3	1.86	0.58
1:C:2351:VAL:O	1:C:2351:VAL:HG12	2.02	0.58
1:C:1637:LEU:HB2	1:C:1638:PRO:HD3	1.86	0.58
1:A:2246:ILE:O	1:A:2339:PHE:N	2.35	0.57
1:B:1637:LEU:HB2	1:B:1638:PRO:HD3	1.86	0.57
1:B:1870:ILE:HG13	1:B:1874:LEU:HD13	1.86	0.57
1:B:2390:ASN:HB2	1:B:2436:MET:HG2	1.86	0.57
1:C:44:VAL:HG13	1:C:328:LYS:HB2	1.84	0.57
1:C:1870:ILE:HG13	1:C:1874:LEU:HD13	1.86	0.57
1:A:959:ARG:NH1	1:A:969:ARG:CG	2.68	0.57
1:A:1694:PRO:HB3	1:A:1926:SER:HA	1.86	0.57
1:A:2121:LEU:HD21	1:A:2139:SER:HB3	1.86	0.57
1:A:2128:ARG:NH2	1:C:1280:VAL:HG23	2.20	0.57
1:A:2390:ASN:ND2	1:A:2392:ASP:OD2	2.38	0.57
1:B:1694:PRO:HB3	1:B:1926:SER:HA	1.85	0.57
1:C:959:ARG:HH21	1:C:969:ARG:HH11	1.49	0.57
1:A:2390:ASN:HB2	1:A:2436:MET:HG2	1.87	0.57
1:A:194:PHE:O	1:A:197:THR:OG1	2.21	0.57
1:C:661:LEU:HD23	1:C:694:TYR:CZ	2.39	0.57
1:C:2238:ILE:HG12	1:C:2241:SER:OG	2.04	0.57
1:A:1300:ILE:HB	1:A:1303:ASP:HB3	1.86	0.57
1:C:2390:ASN:ND2	1:C:2392:ASP:OD2	2.38	0.57
1:B:681:ARG:NH1	1:B:771:THR:O	2.38	0.57
1:B:2053:VAL:O	1:B:2057:ILE:HG12	2.05	0.57
1:A:2251:GLN:OE1	1:C:2201:ASN:ND2	2.38	0.57
1:B:2401:ILE:HG12	1:B:2416:LEU:HB3	1.87	0.57
1:C:2401:ILE:HG12	1:C:2416:LEU:HB3	1.87	0.57
1:A:661:LEU:HD23	1:A:694:TYR:CZ	2.40	0.57
1:C:529:MET:HB2	1:C:531:ILE:HG12	1.87	0.57
1:C:1166:VAL:HG13	1:C:1167:PHE:CD1	2.40	0.57
1:C:2053:VAL:O	1:C:2057:ILE:HG12	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:959:ARG:CZ	1:A:969:ARG:CG	2.83	0.57
1:A:2053:VAL:O	1:A:2057:ILE:HG12	2.04	0.57
1:A:2201:ASN:ND2	1:B:2251:GLN:OE1	2.38	0.57
1:B:2196:TYR:CE1	1:B:2201:ASN:HA	2.40	0.57
1:C:841:PHE:CD1	1:C:937:GLY:HA3	2.39	0.57
1:C:2390:ASN:HB2	1:C:2436:MET:HG2	1.87	0.57
1:A:841:PHE:CD1	1:A:937:GLY:HA3	2.39	0.56
1:A:1262:LEU:HA	1:A:1265:VAL:HG12	1.86	0.56
1:B:194:PHE:O	1:B:197:THR:OG1	2.21	0.56
1:B:2390:ASN:ND2	1:B:2392:ASP:OD2	2.38	0.56
1:C:474:MET:HE3	1:C:489:LEU:HB3	1.87	0.56
1:A:474:MET:HE3	1:A:489:LEU:HB3	1.87	0.56
1:A:681:ARG:NH1	1:A:771:THR:O	2.38	0.56
1:A:1823:PRO:HB2	1:A:1826:ARG:HB3	1.87	0.56
1:B:1280:VAL:HG23	1:C:2128:ARG:NH2	2.19	0.56
1:B:1300:ILE:HB	1:B:1303:ASP:HB3	1.86	0.56
1:B:1881:MET:O	1:B:1885:ILE:HG12	2.04	0.56
1:B:2196:TYR:CZ	1:B:2201:ASN:HA	2.40	0.56
1:B:2238:ILE:HG12	1:B:2241:SER:OG	2.05	0.56
1:A:1280:VAL:HG23	1:B:2128:ARG:NH2	2.20	0.56
1:A:1881:MET:O	1:A:1885:ILE:HG12	2.04	0.56
1:A:2401:ILE:HG12	1:A:2416:LEU:HB3	1.87	0.56
1:B:1018:ASP:H	1:B:1021:ALA:HB3	1.70	0.56
1:B:1166:VAL:HG13	1:B:1167:PHE:CD1	2.40	0.56
1:B:1992:ILE:HG23	1:B:1996:TRP:CD1	2.40	0.56
1:C:486:GLY:HA2	1:C:489:LEU:HG	1.88	0.56
1:C:1302:PHE:HA	1:C:1305:ILE:HG12	1.88	0.56
1:A:1992:ILE:HG23	1:A:1996:TRP:CD1	2.41	0.56
1:B:473:ALA:O	1:B:565:LEU:HD21	2.06	0.56
1:B:661:LEU:HD23	1:B:694:TYR:CZ	2.40	0.56
1:B:959:ARG:CZ	1:B:969:ARG:CG	2.83	0.56
1:C:959:ARG:CZ	1:C:969:ARG:CG	2.83	0.56
1:A:1166:VAL:HG13	1:A:1167:PHE:CD1	2.40	0.56
1:B:1262:LEU:HA	1:B:1265:VAL:HG12	1.86	0.56
1:C:681:ARG:NH1	1:C:771:THR:O	2.38	0.56
1:A:542:ASN:OD1	1:A:543:PHE:N	2.39	0.56
1:A:1018:ASP:H	1:A:1021:ALA:HB3	1.69	0.56
1:B:2121:LEU:HD21	1:B:2139:SER:HB3	1.86	0.56
1:C:1018:ASP:H	1:C:1021:ALA:HB3	1.70	0.56
1:C:2121:LEU:HD21	1:C:2139:SER:HB3	1.86	0.56
1:B:1074:TRP:HA	1:B:1077:TRP:CD1	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:194:PHE:O	1:C:197:THR:OG1	2.20	0.56
1:C:473:ALA:O	1:C:565:LEU:HD21	2.06	0.56
1:C:2081:LEU:HB3	1:C:2094:MET:HB2	1.88	0.56
1:A:1300:ILE:HG13	1:A:1301:GLY:H	1.71	0.56
1:A:1824:LYS:HG3	1:A:1825:PHE:HD1	1.71	0.56
1:B:959:ARG:NH1	1:B:969:ARG:CG	2.67	0.56
1:B:1684:ILE:O	1:B:1687:ARG:HG3	2.06	0.56
1:A:486:GLY:HA2	1:A:489:LEU:HG	1.88	0.56
1:A:1870:ILE:HG13	1:A:1874:LEU:HD13	1.86	0.56
1:B:968:MET:CE	1:B:974:PRO:HB2	2.28	0.56
1:A:529:MET:HB2	1:A:531:ILE:HG12	1.87	0.55
1:A:966:GLU:HB3	1:A:969:ARG:CZ	2.36	0.55
1:A:2238:ILE:HG12	1:A:2241:SER:OG	2.05	0.55
1:B:529:MET:HB2	1:B:531:ILE:HG12	1.87	0.55
1:C:638:PHE:CZ	1:C:755:VAL:HG13	2.41	0.55
1:C:483:SER:OG	1:C:486:GLY:N	2.37	0.55
1:B:542:ASN:OD1	1:B:543:PHE:N	2.39	0.55
1:B:1824:LYS:HG3	1:B:1825:PHE:HD1	1.71	0.55
1:C:968:MET:CE	1:C:974:PRO:HB2	2.28	0.55
1:C:1685:THR:O	1:C:1689:GLU:HG3	2.07	0.55
1:C:1823:PRO:HB2	1:C:1826:ARG:HB3	1.87	0.55
1:B:1300:ILE:HG13	1:B:1301:GLY:H	1.71	0.55
1:B:1302:PHE:HA	1:B:1305:ILE:HG12	1.87	0.55
1:B:1823:PRO:HB2	1:B:1826:ARG:HB3	1.88	0.55
1:B:1991:ALA:HB2	1:B:2007:PHE:HZ	1.71	0.55
1:C:542:ASN:OD1	1:C:543:PHE:N	2.39	0.55
1:C:966:GLU:HB3	1:C:969:ARG:CZ	2.36	0.55
1:C:2349:ALA:HB3	1:C:2352:PHE:HB2	1.88	0.55
1:A:473:ALA:O	1:A:565:LEU:HD21	2.05	0.55
1:A:1684:ILE:O	1:A:1687:ARG:HG3	2.06	0.55
1:C:484:ILE:HD13	1:C:544:VAL:HA	1.89	0.55
1:C:959:ARG:NH1	1:C:969:ARG:CG	2.68	0.55
1:C:1300:ILE:HG13	1:C:1301:GLY:H	1.71	0.55
1:A:638:PHE:CZ	1:A:755:VAL:HG13	2.41	0.55
1:A:1302:PHE:HA	1:A:1305:ILE:HG12	1.87	0.55
1:A:1991:ALA:HB2	1:A:2007:PHE:HZ	1.71	0.55
1:B:484:ILE:HD13	1:B:544:VAL:HA	1.89	0.55
1:A:1615:ASP:OD1	1:A:1616:ILE:N	2.40	0.55
1:C:62:VAL:HG12	1:C:66:PHE:HE2	1.72	0.55
1:C:513:ILE:HD11	1:C:572:LEU:HD11	1.89	0.55
1:C:875:MET:HE3	1:C:945:LEU:HD21	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1074:TRP:HA	1:C:1077:TRP:CD1	2.41	0.55
1:C:1157:SER:HA	1:C:1594:GLN:HG2	1.88	0.55
1:C:1615:ASP:OD1	1:C:1616:ILE:N	2.39	0.55
1:C:1824:LYS:HG3	1:C:1825:PHE:HD1	1.71	0.55
1:A:483:SER:OG	1:A:486:GLY:N	2.37	0.55
1:A:1869:ARG:NH2	1:B:2068:ASN:OD1	2.38	0.55
1:B:62:VAL:HG12	1:B:66:PHE:HE2	1.72	0.55
1:B:1925:ARG:NH2	1:B:1929:SER:O	2.40	0.55
1:C:1925:ARG:NH2	1:C:1929:SER:O	2.40	0.55
1:A:847:ASN:ND2	1:A:921:GLY:HA3	2.22	0.55
1:B:1157:SER:HA	1:B:1594:GLN:HG2	1.89	0.55
1:B:1837:GLY:O	1:B:1841:ILE:HG12	2.07	0.55
1:B:2081:LEU:HB3	1:B:2094:MET:HB2	1.88	0.55
1:C:2155:ARG:HH12	1:C:2324:ALA:HB3	1.71	0.55
1:A:875:MET:HE3	1:A:945:LEU:HD21	1.89	0.54
1:A:1074:TRP:HA	1:A:1077:TRP:CD1	2.41	0.54
1:A:1925:ARG:NH2	1:A:1929:SER:O	2.40	0.54
1:B:474:MET:HE3	1:B:489:LEU:HB3	1.87	0.54
1:B:660:ILE:HD12	1:B:887:MET:HB3	1.90	0.54
1:C:1992:ILE:HG23	1:C:1996:TRP:CD1	2.41	0.54
1:C:2160:SER:HB3	1:C:2304:MET:HG3	1.89	0.54
1:A:1915:VAL:HG12	1:A:1916:PHE:CD2	2.42	0.54
1:B:638:PHE:CZ	1:B:755:VAL:HG13	2.41	0.54
1:B:1915:VAL:HG12	1:B:1916:PHE:CD2	2.42	0.54
1:C:1684:ILE:O	1:C:1687:ARG:HG3	2.06	0.54
1:C:1837:GLY:O	1:C:1841:ILE:HG12	2.07	0.54
1:C:1915:VAL:HG12	1:C:1916:PHE:CD2	2.42	0.54
1:A:484:ILE:HD13	1:A:544:VAL:HA	1.89	0.54
1:A:1157:SER:HA	1:A:1594:GLN:HG2	1.88	0.54
1:A:2329:SER:OG	1:A:2331:ARG:NH1	2.41	0.54
1:B:486:GLY:HA2	1:B:489:LEU:HG	1.88	0.54
1:B:513:ILE:HD11	1:B:572:LEU:HD11	1.89	0.54
1:B:2160:SER:HB3	1:B:2304:MET:HG3	1.90	0.54
1:C:1207:LEU:O	1:C:1220:THR:OG1	2.26	0.54
1:C:1991:ALA:HB2	1:C:2007:PHE:HZ	1.71	0.54
1:C:2175:ILE:HG23	1:C:2225:GLN:HG3	1.89	0.54
1:A:1837:GLY:O	1:A:1841:ILE:HG12	2.07	0.54
1:A:2135:ARG:NE	1:A:2266:ASN:OD1	2.41	0.54
1:B:2155:ARG:HH12	1:B:2324:ALA:HB3	1.72	0.54
1:B:2349:ALA:HB3	1:B:2352:PHE:HB2	1.89	0.54
1:A:660:ILE:HD12	1:A:887:MET:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2349:ALA:HB3	1:A:2352:PHE:HB2	1.89	0.54
1:B:966:GLU:HB3	1:B:969:ARG:CZ	2.37	0.54
1:B:2329:SER:OG	1:B:2331:ARG:NH1	2.41	0.54
1:C:1824:LYS:HG3	1:C:1825:PHE:CD1	2.43	0.54
1:C:2329:SER:OG	1:C:2331:ARG:NH1	2.41	0.54
1:A:1824:LYS:HG3	1:A:1825:PHE:CD1	2.43	0.54
1:B:198:ALA:O	1:B:202:ILE:HG13	2.08	0.54
1:B:968:MET:HE1	1:B:974:PRO:HB3	1.84	0.54
1:C:201:GLY:HA2	1:C:209:ASN:HB3	1.89	0.54
1:A:1895:LYS:NZ	1:A:1956:PRO:O	2.40	0.54
1:A:2081:LEU:HB3	1:A:2094:MET:HB2	1.88	0.54
1:A:2155:ARG:HH12	1:A:2324:ALA:HB3	1.71	0.54
1:A:2160:SER:HB3	1:A:2304:MET:HG3	1.89	0.54
1:B:875:MET:HE3	1:B:945:LEU:HD21	1.89	0.54
1:B:1615:ASP:OD1	1:B:1616:ILE:N	2.39	0.54
1:B:2175:ILE:HG23	1:B:2225:GLN:HG3	1.89	0.54
1:C:660:ILE:HD12	1:C:887:MET:HB3	1.89	0.54
1:B:32:SER:HB2	1:B:253:TYR:HD2	1.65	0.54
1:C:1895:LYS:NZ	1:C:1956:PRO:O	2.40	0.54
1:A:201:GLY:HA2	1:A:209:ASN:HB3	1.89	0.54
1:B:488:ILE:HA	1:B:491:ILE:HG12	1.90	0.54
1:B:966:GLU:HB3	1:B:969:ARG:HH22	1.62	0.54
1:B:2243:PRO:HB3	1:B:2287:PHE:CE1	2.43	0.54
1:C:1967:SER:O	1:C:1972:ASN:ND2	2.41	0.54
1:A:62:VAL:HG12	1:A:66:PHE:HE2	1.72	0.54
1:A:1967:SER:O	1:A:1972:ASN:ND2	2.41	0.54
1:B:1215:ARG:HG2	1:B:1218:GLU:HB3	1.90	0.54
1:B:959:ARG:NH2	1:B:969:ARG:NH1	2.53	0.53
1:B:1065:PRO:HG2	1:B:1068:SER:HB3	1.90	0.53
1:B:1824:LYS:HG3	1:B:1825:PHE:CD1	2.43	0.53
1:B:1895:LYS:NZ	1:B:1956:PRO:O	2.40	0.53
1:C:2243:PRO:HB3	1:C:2287:PHE:CE1	2.43	0.53
1:B:1891:LEU:HD13	1:B:1900:LYS:HA	1.91	0.53
1:B:2084:SER:HB3	1:B:2090:PRO:HA	1.90	0.53
1:C:1068:SER:HB2	1:C:1070:ILE:HD12	1.91	0.53
1:A:513:ILE:HD11	1:A:572:LEU:HD11	1.89	0.53
1:A:1365:ILE:HG23	1:A:2403:LEU:HD21	1.90	0.53
1:A:1823:PRO:HG2	1:A:1826:ARG:HD2	1.91	0.53
1:A:2175:ILE:HG23	1:A:2225:GLN:HG3	1.89	0.53
1:B:13:LYS:NZ	1:B:43:ALA:O	2.34	0.53
1:B:201:GLY:HA2	1:B:209:ASN:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:483:SER:OG	1:B:486:GLY:N	2.37	0.53
1:B:1155:LYS:HD2	1:B:1161:TYR:CZ	2.44	0.53
1:B:2155:ARG:HH22	1:B:2324:ALA:H	1.55	0.53
1:C:1891:LEU:HD13	1:C:1900:LYS:HA	1.91	0.53
1:C:2135:ARG:NE	1:C:2266:ASN:OD1	2.41	0.53
1:A:206:SER:O	1:A:210:SER:N	2.41	0.53
1:A:2155:ARG:HH22	1:A:2324:ALA:H	1.55	0.53
1:B:1009:ILE:HG23	1:B:1024:GLN:HG2	1.90	0.53
1:B:2135:ARG:NE	1:B:2266:ASN:OD1	2.41	0.53
1:C:204:LYS:HG3	1:C:312:ASN:ND2	2.24	0.53
1:C:2084:SER:HB3	1:C:2090:PRO:HA	1.90	0.53
1:C:2164:TRP:HB3	1:C:2303:LYS:HB2	1.91	0.53
1:A:198:ALA:O	1:A:202:ILE:HG13	2.08	0.53
1:B:204:LYS:HG3	1:B:312:ASN:ND2	2.24	0.53
1:B:206:SER:O	1:B:210:SER:N	2.41	0.53
1:B:2363:VAL:HA	1:B:2366:VAL:HG12	1.91	0.53
1:C:260:VAL:HA	1:C:264:TRP:HD1	1.74	0.53
1:C:734:ARG:CZ	1:C:734:ARG:HA	2.39	0.53
1:C:1155:LYS:HD2	1:C:1161:TYR:CZ	2.44	0.53
1:A:8:LYS:HZ2	1:A:142:PHE:HB3	1.73	0.53
1:A:2243:PRO:HB3	1:A:2287:PHE:CE1	2.43	0.53
1:B:266:PRO:HG2	1:B:269:SER:HB3	1.91	0.53
1:C:488:ILE:HA	1:C:491:ILE:HG12	1.90	0.53
1:C:2245:PHE:HB3	1:C:2339:PHE:HE2	1.73	0.53
1:A:1068:SER:HB2	1:A:1070:ILE:HD12	1.91	0.53
1:B:685:TYR:O	1:B:689:LEU:HG	2.09	0.53
1:C:198:ALA:O	1:C:202:ILE:HG13	2.08	0.53
1:A:1215:ARG:HG2	1:A:1218:GLU:HB3	1.90	0.53
1:A:1232:LEU:O	1:A:1235:ILE:HG22	2.09	0.53
1:B:521:LEU:HD13	1:B:524:GLN:HE21	1.74	0.53
1:B:1247:VAL:HG23	1:B:1248:PHE:CD2	2.44	0.53
1:B:1967:SER:O	1:B:1972:ASN:ND2	2.41	0.53
1:C:32:SER:HB2	1:C:253:TYR:HD2	1.65	0.53
1:C:1005:THR:O	1:C:1009:ILE:HG12	2.09	0.53
1:C:1373:ARG:O	1:C:1377:GLN:HG2	2.09	0.53
1:C:1823:PRO:HG2	1:C:1826:ARG:HD2	1.91	0.53
1:B:835:PHE:HE1	1:B:875:MET:HE1	1.74	0.52
1:B:1823:PRO:HG2	1:B:1826:ARG:HD2	1.91	0.52
1:C:1365:ILE:HG23	1:C:2403:LEU:HD21	1.90	0.52
1:A:685:TYR:O	1:A:689:LEU:HG	2.09	0.52
1:A:1247:VAL:HG23	1:A:1248:PHE:CD2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2245:PHE:HB3	1:A:2339:PHE:HE2	1.73	0.52
1:B:1397:ALA:HB2	1:C:2033:ARG:HD2	1.91	0.52
1:C:206:SER:O	1:C:210:SER:N	2.41	0.52
1:C:1038:PHE:O	1:C:1042:ILE:HG12	2.10	0.52
1:C:1247:VAL:HG23	1:C:1248:PHE:CD2	2.44	0.52
1:B:1232:LEU:O	1:B:1235:ILE:HG22	2.09	0.52
1:B:1869:ARG:NH2	1:C:2068:ASN:OD1	2.38	0.52
1:C:266:PRO:HG2	1:C:269:SER:HB3	1.91	0.52
1:C:1232:LEU:O	1:C:1235:ILE:HG22	2.09	0.52
1:C:2326:THR:HA	1:C:2333:TYR:HE1	1.75	0.52
1:A:488:ILE:HA	1:A:491:ILE:HG12	1.90	0.52
1:A:864:PRO:O	1:A:866:ALA:N	2.41	0.52
1:A:1065:PRO:HG2	1:A:1068:SER:HB3	1.90	0.52
1:A:2084:SER:HB3	1:A:2090:PRO:HA	1.90	0.52
1:A:2425:ARG:NH2	1:B:2389:PRO:HD2	2.25	0.52
1:C:676:SER:HB3	1:C:679:LEU:HD12	1.91	0.52
1:C:2155:ARG:HH22	1:C:2324:ALA:H	1.55	0.52
1:A:1038:PHE:O	1:A:1042:ILE:HG12	2.10	0.52
1:A:1155:LYS:HD2	1:A:1161:TYR:CZ	2.44	0.52
1:C:835:PHE:HE1	1:C:875:MET:HE1	1.74	0.52
1:B:734:ARG:HA	1:B:734:ARG:CZ	2.39	0.52
1:B:2326:THR:HA	1:B:2333:TYR:HE1	1.75	0.52
1:C:968:MET:HE1	1:C:974:PRO:HB3	1.84	0.52
1:C:1009:ILE:HG23	1:C:1024:GLN:HG2	1.91	0.52
1:A:266:PRO:HG2	1:A:269:SER:HB3	1.91	0.52
1:B:872:SER:HA	1:B:875:MET:HE2	1.92	0.52
1:B:2245:PHE:HB3	1:B:2339:PHE:HE2	1.73	0.52
1:B:1068:SER:HB2	1:B:1070:ILE:HD12	1.91	0.52
1:B:1365:ILE:HG23	1:B:2403:LEU:HD21	1.90	0.52
1:B:2265:ILE:HA	1:B:2272:ILE:HD13	1.92	0.52
1:B:2385:PHE:CE2	1:C:2381:SER:HA	2.43	0.52
1:C:2265:ILE:HA	1:C:2272:ILE:HD13	1.92	0.52
1:A:2164:TRP:HB3	1:A:2303:LYS:HB2	1.91	0.52
1:B:20:LEU:HG	1:B:35:TYR:CD2	2.45	0.52
1:B:2164:TRP:HB3	1:B:2303:LYS:HB2	1.91	0.52
1:A:204:LYS:HG3	1:A:312:ASN:ND2	2.24	0.52
1:A:260:VAL:HA	1:A:264:TRP:HD1	1.74	0.52
1:A:835:PHE:HE1	1:A:875:MET:HE1	1.74	0.52
1:A:2326:THR:HA	1:A:2333:TYR:HE1	1.75	0.52
1:B:1005:THR:O	1:B:1009:ILE:HG12	2.10	0.52
1:C:471:LEU:O	1:C:475:MET:HG3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:959:ARG:NH2	1:C:969:ARG:NH1	2.53	0.52
1:C:1648:SER:HA	1:C:1816:PHE:HE2	1.75	0.52
1:A:42:SER:HB2	1:A:45:LEU:HD11	1.92	0.51
1:A:1373:ARG:O	1:A:1377:GLN:HG2	2.09	0.51
1:B:1267:GLN:HE21	1:B:1291:CYS:HA	1.75	0.51
1:C:1065:PRO:HG2	1:C:1068:SER:HB3	1.91	0.51
1:A:471:LEU:O	1:A:475:MET:HG3	2.10	0.51
1:A:734:ARG:CZ	1:A:734:ARG:HA	2.39	0.51
1:A:959:ARG:NH2	1:A:969:ARG:NH1	2.53	0.51
1:A:2389:PRO:HD2	1:C:2425:ARG:NH2	2.25	0.51
1:C:2363:VAL:HA	1:C:2366:VAL:HG12	1.91	0.51
1:A:20:LEU:HG	1:A:35:TYR:CD2	2.45	0.51
1:A:526:PHE:HA	1:A:529:MET:HG2	1.92	0.51
1:A:676:SER:HB3	1:A:679:LEU:HD12	1.92	0.51
1:A:1009:ILE:HG23	1:A:1024:GLN:HG2	1.90	0.51
1:C:521:LEU:HD13	1:C:524:GLN:HE21	1.74	0.51
1:A:872:SER:HA	1:A:875:MET:HE2	1.92	0.51
1:A:1891:LEU:HD13	1:A:1900:LYS:HA	1.91	0.51
1:A:2265:ILE:HA	1:A:2272:ILE:HD13	1.92	0.51
1:B:302:ASP:OD1	1:B:303:LEU:N	2.44	0.51
1:B:649:VAL:HG12	1:B:748:ALA:HB1	1.93	0.51
1:B:847:ASN:ND2	1:B:921:GLY:HA3	2.22	0.51
1:B:2425:ARG:NH2	1:C:2389:PRO:HD2	2.25	0.51
1:C:1215:ARG:HG2	1:C:1218:GLU:HB3	1.90	0.51
1:C:2002:PRO:HD2	1:C:2005:ASP:HB2	1.92	0.51
1:A:1648:SER:HA	1:A:1816:PHE:HE2	1.76	0.51
1:A:2031:ALA:O	1:C:1394:TYR:N	2.42	0.51
1:A:2363:VAL:HA	1:A:2366:VAL:HG12	1.91	0.51
1:B:676:SER:HB3	1:B:679:LEU:HD12	1.92	0.51
1:B:1232:LEU:HA	1:B:1235:ILE:HG22	1.92	0.51
1:C:685:TYR:O	1:C:689:LEU:HG	2.09	0.51
1:C:872:SER:HA	1:C:875:MET:HE2	1.92	0.51
1:A:1005:THR:O	1:A:1009:ILE:HG12	2.10	0.51
1:A:1267:GLN:HE21	1:A:1291:CYS:HA	1.75	0.51
1:B:200:VAL:O	1:B:209:ASN:ND2	2.43	0.51
1:B:1038:PHE:O	1:B:1042:ILE:HG12	2.10	0.51
1:C:260:VAL:HA	1:C:264:TRP:CD1	2.46	0.51
1:C:1017:MET:HB3	1:C:1242:GLN:HG2	1.92	0.51
1:A:28:PRO:HG2	1:A:258:PRO:HD3	1.93	0.51
1:A:1025:CYS:SG	1:A:1235:ILE:HG23	2.51	0.51
1:A:2385:PHE:CE2	1:B:2381:SER:HA	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:864:PRO:O	1:B:866:ALA:N	2.41	0.51
1:C:42:SER:HB2	1:C:45:LEU:HD11	1.93	0.51
1:C:649:VAL:HG12	1:C:748:ALA:HB1	1.93	0.51
1:C:2408:LYS:HA	1:C:2408:LYS:HE2	1.93	0.51
1:A:200:VAL:O	1:A:209:ASN:ND2	2.43	0.51
1:A:477:TRP:CE3	1:A:565:LEU:HD22	2.45	0.51
1:A:521:LEU:HD13	1:A:524:GLN:HE21	1.74	0.51
1:A:2068:ASN:OD1	1:C:1869:ARG:NH2	2.38	0.51
1:B:42:SER:HB2	1:B:45:LEU:HD11	1.93	0.51
1:B:1373:ARG:O	1:B:1377:GLN:HG2	2.09	0.51
1:B:2002:PRO:HD2	1:B:2005:ASP:HB2	1.92	0.51
1:C:28:PRO:HG2	1:C:258:PRO:HD3	1.93	0.51
1:C:1074:TRP:CE2	1:C:1095:LEU:HB3	2.46	0.51
1:C:1267:GLN:HE21	1:C:1291:CYS:HA	1.75	0.51
1:A:649:VAL:HG12	1:A:748:ALA:HB1	1.93	0.51
1:A:2002:PRO:HD2	1:A:2005:ASP:HB2	1.92	0.51
1:A:2408:LYS:HE2	1:A:2408:LYS:HA	1.93	0.51
1:B:28:PRO:HG2	1:B:258:PRO:HD3	1.93	0.51
1:B:959:ARG:NH1	1:B:969:ARG:HD3	2.26	0.51
1:B:1025:CYS:SG	1:B:1235:ILE:HG23	2.51	0.51
1:C:477:TRP:CE3	1:C:565:LEU:HD22	2.45	0.51
1:C:740:GLY:HA2	1:C:743:PHE:HD2	1.76	0.51
1:C:847:ASN:ND2	1:C:921:GLY:HA3	2.22	0.51
1:C:1025:CYS:SG	1:C:1235:ILE:HG23	2.51	0.51
1:A:302:ASP:OD1	1:A:303:LEU:N	2.44	0.51
1:B:260:VAL:HA	1:B:264:TRP:HD1	1.74	0.51
1:B:1074:TRP:CE2	1:B:1095:LEU:HB3	2.46	0.51
1:C:959:ARG:NH1	1:C:969:ARG:HD3	2.26	0.51
1:C:1349:LYS:HA	1:C:1352:LYS:HD2	1.93	0.51
1:C:1833:PRO:HG3	1:C:1963:LEU:HD12	1.93	0.51
1:A:1349:LYS:HA	1:A:1352:LYS:HD2	1.93	0.50
1:A:2168:GLN:OE1	1:A:2171:ARG:NH2	2.39	0.50
1:B:471:LEU:O	1:B:475:MET:HG3	2.10	0.50
1:C:200:VAL:O	1:C:209:ASN:ND2	2.43	0.50
1:C:864:PRO:O	1:C:866:ALA:N	2.41	0.50
1:A:312:ASN:HB3	1:A:313:PRO:HD3	1.94	0.50
1:A:1074:TRP:CE2	1:A:1095:LEU:HB3	2.46	0.50
1:A:1207:LEU:O	1:A:1220:THR:OG1	2.26	0.50
1:A:1232:LEU:HA	1:A:1235:ILE:HG22	1.92	0.50
1:A:2033:ARG:HD2	1:C:1397:ALA:HB2	1.92	0.50
1:B:202:ILE:HG22	1:B:556:VAL:HG23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:20:LEU:HG	1:C:35:TYR:CD2	2.45	0.50
1:C:202:ILE:HG22	1:C:556:VAL:HG23	1.93	0.50
1:B:112:HIS:HE2	1:B:118:GLU:HB3	1.77	0.50
1:C:2260:ILE:O	1:C:2264:ILE:HG13	2.11	0.50
1:A:1397:ALA:HB2	1:B:2033:ARG:HD2	1.91	0.50
1:A:2392:ASP:OD1	1:A:2393:HIS:N	2.45	0.50
1:B:134:LEU:HA	1:B:137:ILE:HD12	1.94	0.50
1:C:1326:MET:O	1:C:1330:ARG:N	2.34	0.50
1:A:13:LYS:NZ	1:A:43:ALA:O	2.34	0.50
1:A:1029:VAL:HG22	1:A:1232:LEU:HB3	1.93	0.50
1:A:2427:PRO:HG2	1:B:2427:PRO:HG2	1.93	0.50
1:B:526:PHE:HA	1:B:529:MET:HG2	1.92	0.50
1:B:1349:LYS:HA	1:B:1352:LYS:HD2	1.93	0.50
1:B:2168:GLN:OE1	1:B:2171:ARG:NH2	2.39	0.50
1:A:948:GLN:HE22	1:A:952:ILE:HD11	1.77	0.50
1:A:2260:ILE:O	1:A:2264:ILE:HG13	2.11	0.50
1:B:2392:ASP:OD1	1:B:2393:HIS:N	2.45	0.50
1:C:112:HIS:HE2	1:C:118:GLU:HB3	1.76	0.50
1:B:260:VAL:HA	1:B:264:TRP:CD1	2.46	0.50
1:B:477:TRP:CE3	1:B:565:LEU:HD22	2.45	0.50
1:B:1175:LEU:HA	1:B:1178:THR:HG22	1.93	0.50
1:B:1648:SER:HA	1:B:1816:PHE:HE2	1.75	0.50
1:C:526:PHE:HA	1:C:529:MET:HG2	1.92	0.50
1:C:1175:LEU:HA	1:C:1178:THR:HG22	1.94	0.50
1:C:1232:LEU:HA	1:C:1235:ILE:HG22	1.92	0.50
1:A:202:ILE:HG22	1:A:556:VAL:HG23	1.93	0.50
1:A:1017:MET:HB3	1:A:1242:GLN:HG2	1.93	0.50
1:B:947:PHE:HA	1:B:950:ILE:HG12	1.94	0.50
1:B:1157:SER:HB3	1:B:1159:VAL:HG12	1.94	0.50
1:B:2134:LEU:O	1:B:2137:ARG:HB2	2.11	0.50
1:B:2408:LYS:HE2	1:B:2408:LYS:HA	1.93	0.50
1:C:8:LYS:HZ2	1:C:142:PHE:HB3	1.76	0.50
1:A:947:PHE:HA	1:A:950:ILE:HG12	1.94	0.50
1:B:1017:MET:HB3	1:B:1242:GLN:HG2	1.93	0.50
1:C:1162:PHE:O	1:C:1166:VAL:HG12	2.12	0.50
1:C:2134:LEU:O	1:C:2137:ARG:HB2	2.11	0.50
1:A:238:LYS:NZ	1:A:326:GLN:HG3	2.27	0.49
1:A:740:GLY:HA2	1:A:743:PHE:HD2	1.77	0.49
1:A:1157:SER:HB3	1:A:1159:VAL:HG12	1.94	0.49
1:A:1833:PRO:HG3	1:A:1963:LEU:HD12	1.93	0.49
1:A:1993:ASP:O	1:A:1997:THR:HG22	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:563:THR:HA	1:B:566:THR:HG22	1.94	0.49
1:B:2427:PRO:HG2	1:C:2427:PRO:HG2	1.93	0.49
1:A:1353:GLU:O	1:A:1356:GLU:HG3	2.12	0.49
1:A:1664:THR:HA	1:A:1667:VAL:HG12	1.95	0.49
1:A:1915:VAL:HG12	1:A:1916:PHE:HD2	1.76	0.49
1:A:2427:PRO:HG2	1:C:2427:PRO:HG2	1.93	0.49
1:B:312:ASN:HB3	1:B:313:PRO:HD3	1.94	0.49
1:B:1009:ILE:HG21	1:B:1028:LEU:HB2	1.94	0.49
1:C:302:ASP:OD1	1:C:303:LEU:N	2.44	0.49
1:C:563:THR:HA	1:C:566:THR:HG22	1.94	0.49
1:C:1157:SER:HB3	1:C:1159:VAL:HG12	1.94	0.49
1:B:97:ARG:O	1:B:101:THR:HG23	2.12	0.49
1:B:1162:PHE:O	1:B:1166:VAL:HG12	2.12	0.49
1:B:1326:MET:O	1:B:1330:ARG:N	2.34	0.49
1:B:1833:PRO:HG3	1:B:1963:LEU:HD12	1.93	0.49
1:C:312:ASN:HB3	1:C:313:PRO:HD3	1.94	0.49
1:C:817:GLN:O	1:C:821:LEU:HG	2.12	0.49
1:C:1401:GLY:HA3	1:C:2422:PHE:HB2	1.94	0.49
1:C:2392:ASP:OD1	1:C:2393:HIS:N	2.45	0.49
1:A:260:VAL:HA	1:A:264:TRP:CD1	2.46	0.49
1:A:959:ARG:NH1	1:A:969:ARG:HD3	2.26	0.49
1:A:1162:PHE:O	1:A:1166:VAL:HG12	2.12	0.49
1:A:1326:MET:O	1:A:1330:ARG:N	2.34	0.49
1:B:8:LYS:HZ2	1:B:142:PHE:HB3	1.76	0.49
1:B:501:ASP:HB3	1:B:504:LYS:HB3	1.95	0.49
1:B:1380:ILE:HG22	1:B:1404:TYR:HE1	1.78	0.49
1:B:1394:TYR:N	1:C:2031:ALA:O	2.42	0.49
1:B:2326:THR:HG1	1:B:2331:ARG:H	1.59	0.49
1:C:501:ASP:HB3	1:C:504:LYS:HB3	1.94	0.49
1:A:5:PRO:HG3	1:A:50:LYS:HD3	1.95	0.49
1:A:134:LEU:HA	1:A:137:ILE:HD12	1.94	0.49
1:A:1707:ASP:OD1	1:A:1708:SER:N	2.46	0.49
1:A:2134:LEU:O	1:A:2137:ARG:HB2	2.11	0.49
1:C:97:ARG:O	1:C:101:THR:HG23	2.12	0.49
1:A:872:SER:HA	1:A:875:MET:HG2	1.95	0.49
1:A:1636:PRO:O	1:A:1640:MET:HG2	2.13	0.49
1:A:1911:LEU:HD13	1:A:1940:LYS:HG2	1.94	0.49
1:B:238:LYS:NZ	1:B:326:GLN:HG3	2.27	0.49
1:B:1029:VAL:HG22	1:B:1232:LEU:HB3	1.93	0.49
1:B:2425:ARG:HH22	1:C:2389:PRO:HD2	1.78	0.49
1:C:1353:GLU:O	1:C:1356:GLU:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1364:ASP:OD1	1:C:1367:ARG:NH2	2.38	0.49
1:A:112:HIS:HE2	1:A:118:GLU:HB3	1.76	0.49
1:A:966:GLU:CD	1:A:969:ARG:NH2	2.57	0.49
1:B:817:GLN:O	1:B:821:LEU:HG	2.13	0.49
1:B:1915:VAL:HG12	1:B:1916:PHE:HD2	1.76	0.49
1:B:2260:ILE:O	1:B:2264:ILE:HG13	2.11	0.49
1:C:5:PRO:HG3	1:C:50:LYS:HD3	1.95	0.49
1:C:134:LEU:HA	1:C:137:ILE:HD12	1.94	0.49
1:C:947:PHE:HA	1:C:950:ILE:HG12	1.94	0.49
1:A:1009:ILE:HG21	1:A:1028:LEU:HB2	1.94	0.49
1:B:740:GLY:HA2	1:B:743:PHE:HD2	1.76	0.49
1:B:872:SER:HA	1:B:875:MET:HG2	1.95	0.49
1:B:948:GLN:HE22	1:B:952:ILE:HD11	1.77	0.49
1:C:872:SER:HA	1:C:875:MET:HG2	1.95	0.49
1:C:1029:VAL:HG22	1:C:1232:LEU:HB3	1.93	0.49
1:A:817:GLN:O	1:A:821:LEU:HG	2.13	0.49
1:B:44:VAL:CG1	1:B:328:LYS:HB2	2.43	0.49
1:B:255:TYR:CG	1:B:277:LEU:HD23	2.48	0.49
1:B:748:ALA:HB3	1:B:749:PRO:HD3	1.95	0.49
1:B:1993:ASP:O	1:B:1997:THR:HG22	2.13	0.49
1:C:948:GLN:HE22	1:C:952:ILE:HD11	1.77	0.49
1:C:1663:TYR:HA	1:C:1666:CYS:SG	2.53	0.49
1:A:501:ASP:HB3	1:A:504:LYS:HB3	1.94	0.49
1:B:42:SER:HB2	1:B:45:LEU:CD1	2.43	0.49
1:B:959:ARG:NH1	1:B:969:ARG:CD	2.76	0.49
1:B:1267:GLN:NE2	1:B:1291:CYS:SG	2.86	0.49
1:C:238:LYS:NZ	1:C:326:GLN:HG3	2.27	0.49
1:C:1009:ILE:HG21	1:C:1028:LEU:HB2	1.94	0.49
1:C:1664:THR:HA	1:C:1667:VAL:HG12	1.95	0.49
1:C:2188:VAL:HG21	1:C:2241:SER:HB3	1.94	0.49
1:A:44:VAL:CG1	1:A:328:LYS:HB2	2.43	0.48
1:A:97:ARG:O	1:A:101:THR:HG23	2.12	0.48
1:A:1175:LEU:HA	1:A:1178:THR:HG22	1.93	0.48
1:A:1620:PHE:O	1:A:1624:MET:HG2	2.13	0.48
1:A:2186:PHE:HB3	1:A:2238:ILE:HD11	1.95	0.48
1:C:1636:PRO:O	1:C:1640:MET:HG2	2.13	0.48
1:C:2080:THR:HG22	1:C:2191:GLU:HB2	1.95	0.48
1:C:2176:ASP:O	1:C:2180:ARG:NH1	2.46	0.48
1:A:42:SER:HB2	1:A:45:LEU:CD1	2.43	0.48
1:B:1664:THR:HA	1:B:1667:VAL:HG12	1.95	0.48
1:B:2188:VAL:HG21	1:B:2241:SER:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:521:LEU:HD13	1:C:524:GLN:NE2	2.28	0.48
1:C:1267:GLN:NE2	1:C:1291:CYS:SG	2.86	0.48
1:C:1911:LEU:HD13	1:C:1940:LYS:HG2	1.95	0.48
1:A:37:LEU:O	1:A:41:VAL:HG23	2.13	0.48
1:A:208:SER:HB2	1:A:248:HIS:CD2	2.48	0.48
1:A:1267:GLN:NE2	1:A:1291:CYS:SG	2.86	0.48
1:A:2001:MET:HE2	1:A:2006:PHE:HA	1.94	0.48
1:B:208:SER:HB2	1:B:248:HIS:CD2	2.48	0.48
1:B:1353:GLU:O	1:B:1356:GLU:HG3	2.12	0.48
1:B:1648:SER:HA	1:B:1816:PHE:CE2	2.48	0.48
1:B:1663:TYR:HA	1:B:1666:CYS:SG	2.53	0.48
1:B:2163:TYR:CE1	1:C:2167:SER:HA	2.48	0.48
1:B:2176:ASP:O	1:B:2180:ARG:NH1	2.46	0.48
1:C:255:TYR:CG	1:C:277:LEU:HD23	2.48	0.48
1:A:521:LEU:HD13	1:A:524:GLN:NE2	2.28	0.48
1:A:959:ARG:NH1	1:A:969:ARG:CD	2.77	0.48
1:A:2077:GLU:O	1:A:2097:GLN:HB2	2.14	0.48
1:B:1401:GLY:HA3	1:B:2422:PHE:HB2	1.94	0.48
1:B:1707:ASP:OD1	1:B:1708:SER:N	2.46	0.48
1:B:2080:THR:HG22	1:B:2191:GLU:HB2	1.95	0.48
1:C:44:VAL:CG1	1:C:328:LYS:HB2	2.43	0.48
1:C:748:ALA:HB3	1:C:749:PRO:HD3	1.95	0.48
1:C:1648:SER:HA	1:C:1816:PHE:CE2	2.48	0.48
1:C:1915:VAL:HG12	1:C:1916:PHE:HD2	1.76	0.48
1:C:2001:MET:HE2	1:C:2006:PHE:HA	1.95	0.48
1:A:948:GLN:NE2	1:A:952:ILE:HD11	2.29	0.48
1:A:1020:LEU:HD13	1:A:1053:LEU:HD21	1.96	0.48
1:A:1341:VAL:O	1:A:1345:GLN:HG2	2.14	0.48
1:A:1648:SER:HA	1:A:1816:PHE:CE2	2.48	0.48
1:A:1875:VAL:O	1:A:1879:VAL:HG23	2.14	0.48
1:C:453:LYS:HA	1:C:456:ILE:HG22	1.96	0.48
1:C:1380:ILE:HG22	1:C:1404:TYR:HE1	1.78	0.48
1:C:1875:VAL:O	1:C:1879:VAL:HG23	2.14	0.48
1:C:1993:ASP:O	1:C:1997:THR:HG22	2.13	0.48
1:A:255:TYR:CG	1:A:277:LEU:HD23	2.48	0.48
1:A:563:THR:HA	1:A:566:THR:HG22	1.94	0.48
1:A:748:ALA:HB3	1:A:749:PRO:HD3	1.95	0.48
1:A:1401:GLY:HA3	1:A:2422:PHE:HB2	1.94	0.48
1:A:1616:ILE:HA	1:A:1619:TYR:CD2	2.49	0.48
1:A:2167:SER:HA	1:C:2163:TYR:CE1	2.49	0.48
1:B:1636:PRO:O	1:B:1640:MET:HG2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1687:ARG:HD2	1:B:1688:THR:N	2.29	0.48
1:B:1911:LEU:HD13	1:B:1940:LYS:HG2	1.95	0.48
1:B:2186:PHE:HB3	1:B:2238:ILE:HD11	1.96	0.48
1:B:2425:ARG:HG2	1:C:2384:MET:HA	1.95	0.48
1:C:501:ASP:O	1:C:505:SER:N	2.34	0.48
1:C:547:GLU:HG2	1:C:549:THR:H	1.78	0.48
1:C:1341:VAL:O	1:C:1345:GLN:HG2	2.14	0.48
1:B:1355:ASN:O	1:B:1359:LYS:HG2	2.13	0.48
1:B:1875:VAL:O	1:B:1879:VAL:HG23	2.14	0.48
1:B:2001:MET:HE2	1:B:2006:PHE:HA	1.94	0.48
1:C:887:MET:HA	1:C:887:MET:HE2	1.96	0.48
1:C:948:GLN:NE2	1:C:952:ILE:HD11	2.29	0.48
1:C:959:ARG:NH1	1:C:969:ARG:CD	2.77	0.48
1:B:1020:LEU:HD13	1:B:1053:LEU:HD21	1.96	0.48
1:B:1616:ILE:HA	1:B:1619:TYR:CD2	2.49	0.48
1:C:37:LEU:O	1:C:41:VAL:HG23	2.13	0.48
1:C:42:SER:HB2	1:C:45:LEU:CD1	2.43	0.48
1:C:869:GLY:O	1:C:872:SER:OG	2.26	0.48
1:C:1616:ILE:HA	1:C:1619:TYR:CD2	2.49	0.48
1:C:2294:LEU:HD12	1:C:2305:TRP:CZ2	2.48	0.48
1:A:453:LYS:HA	1:A:456:ILE:HG22	1.96	0.48
1:A:2042:LYS:HD3	1:C:1995:THR:HA	1.94	0.48
1:A:2075:MET:HG3	1:A:2152:LEU:HD11	1.96	0.48
1:A:2294:LEU:HD12	1:A:2305:TRP:CZ2	2.49	0.48
1:A:2384:MET:HA	1:C:2425:ARG:HG2	1.95	0.48
1:A:2437:SER:OG	1:A:2438:LYS:N	2.46	0.48
1:B:521:LEU:HD13	1:B:524:GLN:NE2	2.28	0.48
1:B:2315:GLN:OE1	1:B:2315:GLN:N	2.47	0.48
1:C:1687:ARG:HD2	1:C:1688:THR:N	2.29	0.48
1:C:2315:GLN:OE1	1:C:2315:GLN:N	2.47	0.48
1:A:24:ALA:O	1:A:253:TYR:OH	2.32	0.48
1:A:724:TRP:HA	1:A:893:ILE:HD11	1.96	0.48
1:A:2389:PRO:HD2	1:C:2425:ARG:HH22	1.78	0.48
1:B:5:PRO:HG3	1:B:50:LYS:HD3	1.95	0.48
1:B:37:LEU:O	1:B:41:VAL:HG23	2.13	0.48
1:A:1171:HIS:O	1:A:1175:LEU:HG	2.14	0.47
1:A:1663:TYR:HA	1:A:1666:CYS:SG	2.53	0.47
1:A:2163:TYR:CE1	1:B:2167:SER:HA	2.49	0.47
1:A:2176:ASP:O	1:A:2180:ARG:NH1	2.46	0.47
1:A:2425:ARG:HH22	1:B:2389:PRO:HD2	1.78	0.47
1:B:773:PRO:HG2	1:B:957:HIS:NE2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:948:GLN:NE2	1:B:952:ILE:HD11	2.29	0.47
1:B:1620:PHE:O	1:B:1624:MET:HG2	2.13	0.47
1:C:724:TRP:HA	1:C:893:ILE:HD11	1.96	0.47
1:A:2137:ARG:HE	1:C:1687:ARG:HH11	1.62	0.47
1:B:547:GLU:HG2	1:B:549:THR:H	1.78	0.47
1:B:646:LEU:HA	1:B:649:VAL:HG22	1.96	0.47
1:B:724:TRP:HA	1:B:893:ILE:HD11	1.96	0.47
1:B:1016:ARG:NH1	1:B:1110:ASP:OD2	2.47	0.47
1:B:1341:VAL:O	1:B:1345:GLN:HG2	2.14	0.47
1:C:1355:ASN:O	1:C:1359:LYS:HG2	2.13	0.47
1:A:851:ILE:HD11	1:A:1062:VAL:HG11	1.96	0.47
1:A:1355:ASN:O	1:A:1359:LYS:HG2	2.13	0.47
1:A:1626:GLN:NE2	1:A:1916:PHE:CE1	2.82	0.47
1:A:2188:VAL:HG21	1:A:2241:SER:HB3	1.95	0.47
1:B:827:GLU:HB3	1:B:955:GLN:HG3	1.96	0.47
1:B:1171:HIS:O	1:B:1175:LEU:HG	2.14	0.47
1:B:1958:LEU:HD23	1:B:1959:CYS:N	2.29	0.47
1:C:854:VAL:HG11	1:C:1058:PHE:CD2	2.49	0.47
1:C:1016:ARG:NH1	1:C:1110:ASP:OD2	2.48	0.47
1:C:1286:ASP:OD1	1:C:1287:PHE:N	2.48	0.47
1:C:1620:PHE:O	1:C:1624:MET:HG2	2.13	0.47
1:A:827:GLU:HB3	1:A:955:GLN:HG3	1.96	0.47
1:A:2080:THR:HG22	1:A:2191:GLU:HB2	1.95	0.47
1:A:2326:THR:HG1	1:A:2331:ARG:H	1.59	0.47
1:B:453:LYS:HA	1:B:456:ILE:HG22	1.96	0.47
1:B:1207:LEU:O	1:B:1220:THR:OG1	2.26	0.47
1:B:2073:ILE:HG22	1:B:2074:SER:O	2.15	0.47
1:B:2077:GLU:O	1:B:2097:GLN:HB2	2.14	0.47
1:C:208:SER:HB2	1:C:248:HIS:CD2	2.48	0.47
1:C:646:LEU:HA	1:C:649:VAL:HG22	1.97	0.47
1:C:1958:LEU:HD23	1:C:1959:CYS:N	2.29	0.47
1:C:2199:ASN:OD1	1:C:2200:GLU:N	2.46	0.47
1:A:62:VAL:HG12	1:A:66:PHE:CE2	2.49	0.47
1:A:1016:ARG:NH1	1:A:1110:ASP:OD2	2.47	0.47
1:B:841:PHE:CE1	1:B:937:GLY:HA3	2.49	0.47
1:B:2294:LEU:HD12	1:B:2305:TRP:CZ2	2.48	0.47
1:C:569:VAL:HA	1:C:572:LEU:HD23	1.97	0.47
1:C:1266:ARG:HA	1:C:1271:ILE:HD12	1.97	0.47
1:C:2077:GLU:O	1:C:2097:GLN:HB2	2.14	0.47
1:C:2186:PHE:HB3	1:C:2238:ILE:HD11	1.96	0.47
1:A:547:GLU:HG2	1:A:549:THR:H	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1380:ILE:HG22	1:A:1404:TYR:HE1	1.78	0.47
1:A:2073:ILE:HG22	1:A:2074:SER:O	2.15	0.47
1:A:2389:PRO:HB2	1:A:2436:MET:HG3	1.96	0.47
1:B:653:PHE:CZ	1:B:745:GLN:HB2	2.50	0.47
1:B:959:ARG:NH2	1:B:969:ARG:CD	2.55	0.47
1:A:1286:ASP:OD1	1:A:1287:PHE:N	2.48	0.47
1:A:1958:LEU:HD23	1:A:1959:CYS:N	2.29	0.47
1:A:1994:TRP:HB2	1:A:2006:PHE:CD1	2.50	0.47
1:A:2425:ARG:HG2	1:B:2384:MET:HA	1.95	0.47
1:B:569:VAL:HA	1:B:572:LEU:HD23	1.97	0.47
1:B:1137:ASP:OD1	1:B:1138:GLY:N	2.48	0.47
1:C:2073:ILE:HG22	1:C:2074:SER:O	2.15	0.47
1:C:2075:MET:HG3	1:C:2152:LEU:HD11	1.96	0.47
1:C:2139:SER:OG	1:C:2263:THR:OG1	2.31	0.47
1:A:1394:TYR:HB3	1:B:2031:ALA:HB3	1.97	0.47
1:A:1687:ARG:HD2	1:A:1688:THR:N	2.29	0.47
1:A:1687:ARG:HH11	1:B:2137:ARG:HE	1.62	0.47
1:B:1286:ASP:OD1	1:B:1287:PHE:N	2.48	0.47
1:B:2075:MET:HG3	1:B:2152:LEU:HD11	1.97	0.47
1:C:656:ASN:O	1:C:660:ILE:HG12	2.15	0.47
1:C:1171:HIS:O	1:C:1175:LEU:HG	2.14	0.47
1:A:2315:GLN:OE1	1:A:2315:GLN:N	2.47	0.47
1:B:1266:ARG:HA	1:B:1271:ILE:HD12	1.97	0.47
1:B:1626:GLN:NE2	1:B:1916:PHE:CE1	2.82	0.47
1:B:1633:ILE:HG12	1:B:1701:PHE:O	2.15	0.47
1:B:2437:SER:OG	1:B:2438:LYS:N	2.46	0.47
1:C:1626:GLN:NE2	1:C:1916:PHE:CE1	2.82	0.47
1:A:656:ASN:O	1:A:660:ILE:HG12	2.15	0.47
1:A:1310:LEU:O	1:A:1314:ILE:HG12	2.15	0.47
1:B:1687:ARG:HH11	1:C:2137:ARG:HE	1.62	0.47
1:B:1994:TRP:HB2	1:B:2006:PHE:CD1	2.50	0.47
1:C:773:PRO:HG2	1:C:957:HIS:NE2	2.30	0.47
1:C:841:PHE:CE1	1:C:937:GLY:HA3	2.49	0.47
1:C:2389:PRO:HB2	1:C:2436:MET:HG3	1.96	0.47
1:A:569:VAL:HA	1:A:572:LEU:HD23	1.97	0.46
1:A:646:LEU:HA	1:A:649:VAL:HG22	1.96	0.46
1:A:773:PRO:HG2	1:A:957:HIS:NE2	2.29	0.46
1:A:887:MET:HE3	1:A:935:LEU:HD22	1.98	0.46
1:B:276:GLY:C	1:B:277:LEU:HD12	2.40	0.46
1:C:1994:TRP:HB2	1:C:2006:PHE:CD1	2.50	0.46
1:A:653:PHE:CZ	1:A:745:GLN:HB2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:695:THR:HA	1:A:698:VAL:HG12	1.97	0.46
1:A:841:PHE:CE1	1:A:937:GLY:HA3	2.49	0.46
1:A:854:VAL:HG11	1:A:1058:PHE:CD2	2.49	0.46
1:A:2031:ALA:HB3	1:C:1394:TYR:HB3	1.97	0.46
1:B:887:MET:HE2	1:B:887:MET:HA	1.96	0.46
1:B:1680:PRO:HD2	1:B:1681:TYR:H	1.80	0.46
1:B:2389:PRO:HB2	1:B:2436:MET:HG3	1.96	0.46
1:C:633:LYS:HD3	1:C:633:LYS:HA	1.75	0.46
1:C:1020:LEU:HD13	1:C:1053:LEU:HD21	1.96	0.46
1:C:1121:LEU:O	1:C:1125:ARG:HG2	2.15	0.46
1:C:2127:THR:OG1	1:C:2128:ARG:N	2.48	0.46
1:A:966:GLU:CB	1:A:969:ARG:NH1	2.79	0.46
1:A:1121:LEU:O	1:A:1125:ARG:HG2	2.15	0.46
1:A:1394:TYR:N	1:B:2031:ALA:O	2.42	0.46
1:A:2250:ASN:OD1	1:A:2251:GLN:N	2.49	0.46
1:B:854:VAL:HG11	1:B:1058:PHE:CD2	2.49	0.46
1:B:1364:ASP:OD1	1:B:1367:ARG:NH2	2.38	0.46
1:B:2127:THR:OG1	1:B:2128:ARG:N	2.48	0.46
1:A:276:GLY:C	1:A:277:LEU:HD12	2.40	0.46
1:A:1633:ILE:HG12	1:A:1701:PHE:O	2.15	0.46
1:B:501:ASP:O	1:B:505:SER:N	2.34	0.46
1:B:1121:LEU:O	1:B:1125:ARG:HG2	2.15	0.46
1:C:723:GLU:HG2	1:C:724:TRP:N	2.30	0.46
1:C:842:ILE:HD11	1:C:850:TYR:HB3	1.97	0.46
1:C:887:MET:HE3	1:C:935:LEU:HD22	1.98	0.46
1:C:1626:GLN:NE2	1:C:1630:GLY:HA2	2.31	0.46
1:C:1691:GLN:HG3	1:C:1692:MET:SD	2.56	0.46
1:C:1707:ASP:OD1	1:C:1708:SER:N	2.46	0.46
1:A:1869:ARG:NH1	1:B:2345:PRO:HA	2.31	0.46
1:A:2246:ILE:HG23	1:A:2254:LEU:HB3	1.97	0.46
1:B:21:LEU:HD13	1:B:317:LEU:HD21	1.98	0.46
1:B:1310:LEU:O	1:B:1314:ILE:HG12	2.15	0.46
1:B:1987:GLU:OE1	1:B:1987:GLU:N	2.35	0.46
1:C:966:GLU:CD	1:C:969:ARG:NH2	2.57	0.46
1:C:1633:ILE:HG12	1:C:1701:PHE:O	2.15	0.46
1:C:2168:GLN:OE1	1:C:2171:ARG:NH2	2.39	0.46
1:C:2250:ASN:OD1	1:C:2251:GLN:N	2.49	0.46
1:C:2347:PHE:O	1:C:2348:LEU:C	2.59	0.46
1:A:2153:ILE:HG23	1:A:2335:GLN:HE21	1.81	0.46
1:B:1691:GLN:HG3	1:B:1692:MET:SD	2.56	0.46
1:C:695:THR:HA	1:C:698:VAL:HG12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:851:ILE:HD11	1:C:1062:VAL:HG11	1.96	0.46
1:C:1310:LEU:O	1:C:1314:ILE:HG12	2.15	0.46
1:A:685:TYR:CE1	1:A:689:LEU:HD21	2.51	0.46
1:A:1691:GLN:HG3	1:A:1692:MET:SD	2.56	0.46
1:B:249:PHE:CE2	1:B:316:VAL:HG12	2.51	0.46
1:B:723:GLU:HG2	1:B:724:TRP:N	2.30	0.46
1:C:62:VAL:HG12	1:C:66:PHE:CE2	2.49	0.46
1:C:276:GLY:C	1:C:277:LEU:HD12	2.40	0.46
1:C:1680:PRO:HD2	1:C:1681:TYR:H	1.80	0.46
1:A:3:VAL:HG11	1:A:143:LEU:HA	1.98	0.46
1:A:2127:THR:OG1	1:A:2128:ARG:N	2.48	0.46
1:A:2347:PHE:O	1:A:2348:LEU:C	2.59	0.46
1:B:567:LEU:HB3	1:B:568:PRO:HD3	1.98	0.46
1:B:851:ILE:HD11	1:B:1062:VAL:HG11	1.96	0.46
1:B:1394:TYR:HB3	1:C:2031:ALA:HB3	1.97	0.46
1:C:567:LEU:HB3	1:C:568:PRO:HD3	1.98	0.46
1:C:653:PHE:CZ	1:C:745:GLN:HB2	2.50	0.46
1:B:887:MET:HE3	1:B:935:LEU:HD22	1.98	0.46
1:B:2250:ASN:OD1	1:B:2251:GLN:N	2.48	0.46
1:C:827:GLU:HB3	1:C:955:GLN:HG3	1.96	0.46
1:A:968:MET:HE1	1:A:974:PRO:HB3	1.84	0.46
1:A:1640:MET:HE3	1:A:1660:MET:HG2	1.98	0.46
1:A:1680:PRO:HD2	1:A:1681:TYR:H	1.80	0.46
1:A:1984:PHE:CD2	1:B:2057:ILE:HD11	2.51	0.46
1:A:2055:ILE:O	1:A:2059:SER:HB3	2.16	0.46
1:B:62:VAL:HG12	1:B:66:PHE:CE2	2.49	0.46
1:B:695:THR:HA	1:B:698:VAL:HG12	1.97	0.46
1:C:966:GLU:CB	1:C:969:ARG:NH1	2.79	0.46
1:C:977:HIS:HB3	1:C:980:HIS:CD2	2.52	0.46
1:A:810:LYS:HE3	1:A:814:LEU:HD23	1.98	0.45
1:A:887:MET:HE2	1:A:887:MET:HA	1.96	0.45
1:A:925:GLU:HG3	1:A:934:MET:HG3	1.98	0.45
1:A:1626:GLN:NE2	1:A:1630:GLY:HA2	2.31	0.45
1:A:2356:VAL:HA	1:A:2359:VAL:HG12	1.98	0.45
1:B:977:HIS:HB3	1:B:980:HIS:CD2	2.52	0.45
1:C:3:VAL:HG11	1:C:143:LEU:HA	1.98	0.45
1:A:723:GLU:HG2	1:A:724:TRP:N	2.30	0.45
1:A:1266:ARG:HA	1:A:1271:ILE:HD12	1.97	0.45
1:A:2105:GLU:OE2	1:A:2157:ARG:NH1	2.41	0.45
1:B:842:ILE:HD11	1:B:850:TYR:HB3	1.97	0.45
1:B:1106:TYR:OH	1:B:1275:ASN:ND2	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1869:ARG:NH1	1:C:2345:PRO:HA	2.31	0.45
1:B:2246:ILE:HG23	1:B:2254:LEU:HB3	1.97	0.45
1:C:1624:MET:HE3	1:C:1628:MET:HE1	1.98	0.45
1:A:642:VAL:HA	1:A:645:VAL:HG12	1.98	0.45
1:A:1020:LEU:HA	1:A:1023:ILE:HG12	1.98	0.45
1:A:1711:LEU:HA	1:A:1714:ILE:HD13	1.98	0.45
1:A:2139:SER:OG	1:A:2263:THR:OG1	2.31	0.45
1:A:2199:ASN:OD1	1:A:2200:GLU:N	2.46	0.45
1:A:2345:PRO:HA	1:C:1869:ARG:NH1	2.31	0.45
1:B:2094:MET:HG3	1:B:2156:PHE:HB3	1.98	0.45
1:C:642:VAL:HA	1:C:645:VAL:HG12	1.98	0.45
1:C:810:LYS:HE3	1:C:814:LEU:HD23	1.97	0.45
1:C:1378:LYS:O	1:C:1382:ARG:NE	2.42	0.45
1:C:2094:MET:HG3	1:C:2156:PHE:HB3	1.99	0.45
1:A:198:ALA:HB2	1:A:216:PHE:CE1	2.52	0.45
1:A:249:PHE:CE2	1:A:316:VAL:HG12	2.51	0.45
1:A:842:ILE:HD11	1:A:850:TYR:HB3	1.98	0.45
1:A:1137:ASP:OD1	1:A:1138:GLY:N	2.48	0.45
1:A:2381:SER:HA	1:C:2385:PHE:CE2	2.42	0.45
1:B:3:VAL:HG11	1:B:143:LEU:HA	1.98	0.45
1:B:2417:PHE:O	1:B:2421:ILE:HG12	2.16	0.45
1:C:1137:ASP:OD1	1:C:1138:GLY:N	2.48	0.45
1:C:1711:LEU:HA	1:C:1714:ILE:HD13	1.98	0.45
1:C:1831:LEU:HD23	1:C:1946:VAL:HG23	1.98	0.45
1:C:1987:GLU:OE1	1:C:1987:GLU:N	2.35	0.45
1:C:2246:ILE:HG23	1:C:2254:LEU:HB3	1.97	0.45
1:A:2057:ILE:HD11	1:C:1984:PHE:CD2	2.51	0.45
1:B:656:ASN:O	1:B:660:ILE:HG12	2.15	0.45
1:B:810:LYS:HE3	1:B:814:LEU:HD23	1.98	0.45
1:B:2055:ILE:O	1:B:2059:SER:HB3	2.16	0.45
1:C:249:PHE:CE2	1:C:316:VAL:HG12	2.51	0.45
1:C:1192:GLY:HA2	1:C:1195:ILE:HG12	1.99	0.45
1:A:2184:VAL:HG23	1:A:2214:ILE:HD12	1.98	0.45
1:A:2397:ILE:O	1:A:2401:ILE:HG13	2.17	0.45
1:B:1406:PHE:HE2	1:B:2423:LEU:HD12	1.82	0.45
1:B:1624:MET:HE3	1:B:1628:MET:HE1	1.98	0.45
1:B:1984:PHE:CD2	1:C:2057:ILE:HD11	2.51	0.45
1:B:2397:ILE:O	1:B:2401:ILE:HG13	2.17	0.45
1:C:1020:LEU:HA	1:C:1023:ILE:HG12	1.98	0.45
1:C:1640:MET:HE3	1:C:1660:MET:HG2	1.98	0.45
1:C:2159:GLU:HA	1:C:2306:ILE:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2184:VAL:HG23	1:C:2214:ILE:HD12	1.98	0.45
1:A:2094:MET:HG3	1:A:2156:PHE:HB3	1.99	0.45
1:A:2417:PHE:O	1:A:2421:ILE:HG12	2.17	0.45
1:A:2427:PRO:O	1:A:2431:ILE:HG12	2.17	0.45
1:B:685:TYR:CE1	1:B:689:LEU:HD21	2.51	0.45
1:B:1626:GLN:NE2	1:B:1630:GLY:HA2	2.31	0.45
1:B:1640:MET:HE3	1:B:1660:MET:HG2	1.98	0.45
1:B:2159:GLU:HA	1:B:2306:ILE:HG22	1.99	0.45
1:C:198:ALA:HB2	1:C:216:PHE:CE1	2.52	0.45
1:C:540:TRP:O	1:C:544:VAL:HB	2.17	0.45
1:C:1301:GLY:O	1:C:1304:VAL:HG12	2.17	0.45
1:A:959:ARG:HH21	1:A:969:ARG:NH1	2.15	0.45
1:A:1249:LEU:HD11	1:A:1287:PHE:HE2	1.82	0.45
1:A:1613:HIS:HB3	1:A:1616:ILE:HG12	1.99	0.45
1:B:198:ALA:HB2	1:B:216:PHE:CE1	2.52	0.45
1:B:966:GLU:CB	1:B:969:ARG:NH1	2.79	0.45
1:C:2288:ASP:OD2	1:C:2311:HIS:ND1	2.49	0.45
1:A:567:LEU:HB3	1:A:568:PRO:HD3	1.98	0.45
1:A:1106:TYR:OH	1:A:1275:ASN:ND2	2.41	0.45
1:B:642:VAL:HA	1:B:645:VAL:HG12	1.99	0.45
1:B:2184:VAL:HG23	1:B:2214:ILE:HD12	1.98	0.45
1:C:21:LEU:HD13	1:C:317:LEU:HD21	1.98	0.45
1:C:1274:VAL:HG21	1:C:1299:ASN:N	2.32	0.45
1:A:1192:GLY:HA2	1:A:1195:ILE:HG12	1.99	0.45
1:A:1301:GLY:O	1:A:1304:VAL:HG12	2.17	0.45
1:B:1274:VAL:HG21	1:B:1299:ASN:N	2.32	0.45
1:B:1613:HIS:HB3	1:B:1616:ILE:HG12	1.99	0.45
1:C:565:LEU:O	1:C:568:PRO:HD2	2.17	0.45
1:C:685:TYR:CE1	1:C:689:LEU:HD21	2.51	0.45
1:C:2086:GLU:HB2	1:C:2185:ASN:O	2.17	0.45
1:A:977:HIS:HB3	1:A:980:HIS:CD2	2.52	0.44
1:A:1406:PHE:HE2	1:A:2423:LEU:HD12	1.82	0.44
1:B:112:HIS:CD2	1:B:286:PRO:HD2	2.52	0.44
1:B:980:HIS:HB3	1:B:983:ARG:NE	2.33	0.44
1:B:1192:GLY:HA2	1:B:1195:ILE:HG12	1.99	0.44
1:B:1301:GLY:O	1:B:1304:VAL:HG12	2.17	0.44
1:B:2153:ILE:HG23	1:B:2335:GLN:HE21	1.81	0.44
1:B:2427:PRO:O	1:B:2431:ILE:HG12	2.17	0.44
1:C:1631:GLY:HA3	1:C:1702:GLY:HA3	1.99	0.44
1:C:2417:PHE:O	1:C:2421:ILE:HG12	2.17	0.44
1:A:2083:ILE:HD12	1:A:2188:VAL:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:849:LEU:HB2	1:B:920:PHE:O	2.18	0.44
1:B:1387:ARG:NH1	1:B:1404:TYR:OH	2.50	0.44
1:B:1631:GLY:HA3	1:B:1702:GLY:HA3	2.00	0.44
1:B:1831:LEU:HD23	1:B:1946:VAL:HG23	1.98	0.44
1:C:849:LEU:HB2	1:C:920:PHE:O	2.18	0.44
1:C:980:HIS:HB3	1:C:983:ARG:NE	2.33	0.44
1:C:1135:TYR:OH	1:C:1323:GLN:OE1	2.26	0.44
1:C:1406:PHE:HE2	1:C:2423:LEU:HD12	1.82	0.44
1:C:1927:ALA:O	1:C:1934:GLN:NE2	2.51	0.44
1:C:2356:VAL:HA	1:C:2359:VAL:HG12	1.98	0.44
1:A:1387:ARG:NH1	1:A:1404:TYR:OH	2.50	0.44
1:B:925:GLU:HG3	1:B:934:MET:HG3	1.98	0.44
1:B:1711:LEU:HA	1:B:1714:ILE:HD13	1.98	0.44
1:B:2086:GLU:HB2	1:B:2185:ASN:O	2.17	0.44
1:B:2356:VAL:HA	1:B:2359:VAL:HG12	1.98	0.44
1:C:657:PHE:HB2	1:C:728:ILE:HA	2.00	0.44
1:C:851:ILE:HA	1:C:854:VAL:HG22	2.00	0.44
1:A:112:HIS:CD2	1:A:286:PRO:HD2	2.52	0.44
1:A:1927:ALA:O	1:A:1934:GLN:NE2	2.50	0.44
1:B:514:LEU:HD12	1:B:517:ILE:HD11	1.99	0.44
1:B:540:TRP:O	1:B:544:VAL:HB	2.17	0.44
1:B:1020:LEU:HA	1:B:1023:ILE:HG12	1.98	0.44
1:B:2199:ASN:OD1	1:B:2200:GLU:N	2.46	0.44
1:C:112:HIS:CD2	1:C:286:PRO:HD2	2.52	0.44
1:C:2055:ILE:O	1:C:2059:SER:HB3	2.16	0.44
1:A:851:ILE:HA	1:A:854:VAL:HG22	2.00	0.44
1:A:1241:LEU:HD13	1:A:1271:ILE:HG12	2.00	0.44
1:A:1274:VAL:HG21	1:A:1299:ASN:N	2.32	0.44
1:A:1378:LYS:O	1:A:1382:ARG:NE	2.42	0.44
1:A:2003:LEU:CD1	1:A:2007:PHE:HE2	2.31	0.44
1:A:2386:THR:HG23	1:A:2387:GLU:HG2	2.00	0.44
1:B:930:GLU:HB2	1:B:933:TYR:CD2	2.53	0.44
1:C:514:LEU:HD12	1:C:517:ILE:HD11	1.99	0.44
1:C:1626:GLN:NE2	1:C:1916:PHE:HE1	2.16	0.44
1:A:21:LEU:HD13	1:A:317:LEU:HD21	1.98	0.44
1:A:501:ASP:O	1:A:505:SER:N	2.34	0.44
1:A:1713:ASP:OD1	1:A:1714:ILE:HD12	2.18	0.44
1:A:1831:LEU:HD23	1:A:1946:VAL:HG23	1.98	0.44
1:A:1990:THR:HG23	1:A:2010:GLU:HG3	2.00	0.44
1:B:1249:LEU:HD11	1:B:1287:PHE:HE2	1.82	0.44
1:B:1893:LEU:HD13	1:B:1993:ASP:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1990:THR:HG23	1:B:2010:GLU:HG3	2.00	0.44
1:B:2078:LYS:HA	1:B:2097:GLN:HB3	2.00	0.44
1:C:2153:ILE:HG23	1:C:2335:GLN:HE21	1.81	0.44
1:C:2326:THR:N	1:C:2331:ARG:O	2.47	0.44
1:C:2386:THR:HG23	1:C:2387:GLU:HG2	2.00	0.44
1:C:2397:ILE:O	1:C:2401:ILE:HG13	2.17	0.44
1:A:1904:GLN:HE22	1:A:1908:ILE:HD11	1.83	0.44
1:A:2086:GLU:HB2	1:A:2185:ASN:O	2.17	0.44
1:B:565:LEU:O	1:B:568:PRO:HD2	2.17	0.44
1:B:1713:ASP:OD1	1:B:1714:ILE:HD12	2.18	0.44
1:B:2003:LEU:CD1	1:B:2007:PHE:HE2	2.31	0.44
1:B:2083:ILE:HD12	1:B:2188:VAL:HG22	1.99	0.44
1:B:2347:PHE:O	1:B:2348:LEU:C	2.59	0.44
1:C:930:GLU:HB2	1:C:933:TYR:CD2	2.53	0.44
1:C:1036:ARG:HH12	1:C:1131:ASN:HB3	1.83	0.44
1:C:1249:LEU:HD11	1:C:1287:PHE:HE2	1.82	0.44
1:A:540:TRP:O	1:A:544:VAL:HB	2.17	0.44
1:A:1631:GLY:HA3	1:A:1702:GLY:HA3	1.99	0.44
1:A:2059:SER:OG	1:A:2060:PRO:HD3	2.18	0.44
1:B:1844:LEU:HD23	1:B:1844:LEU:HA	1.89	0.44
1:B:2082:ARG:HB3	1:B:2189:SER:HB3	1.99	0.44
1:B:2386:THR:HG23	1:B:2387:GLU:HG2	2.00	0.44
1:C:13:LYS:O	1:C:17:PRO:HG2	2.18	0.44
1:C:925:GLU:HG3	1:C:934:MET:HG3	1.98	0.44
1:C:2078:LYS:HA	1:C:2097:GLN:HB3	2.00	0.44
1:A:1036:ARG:HH12	1:A:1131:ASN:HB3	1.83	0.44
1:A:1192:GLY:HA3	1:A:1230:TYR:OH	2.18	0.44
1:A:2078:LYS:HA	1:A:2097:GLN:HB3	2.00	0.44
1:C:645:VAL:O	1:C:649:VAL:HG13	2.18	0.44
1:C:1241:LEU:HD13	1:C:1271:ILE:HG12	2.00	0.44
1:A:565:LEU:O	1:A:568:PRO:HD2	2.17	0.43
1:A:645:VAL:O	1:A:649:VAL:HG13	2.18	0.43
1:A:849:LEU:HB2	1:A:920:PHE:O	2.18	0.43
1:A:980:HIS:HB3	1:A:983:ARG:NE	2.33	0.43
1:B:851:ILE:HA	1:B:854:VAL:HG22	2.00	0.43
1:B:1241:LEU:HD13	1:B:1271:ILE:HG12	2.00	0.43
1:B:1378:LYS:O	1:B:1382:ARG:NE	2.42	0.43
1:B:2083:ILE:O	1:B:2091:LEU:N	2.51	0.43
1:C:1153:ASP:OD1	1:C:1154:THR:N	2.51	0.43
1:C:1192:GLY:HA3	1:C:1230:TYR:OH	2.18	0.43
1:C:1252:PHE:HB3	1:C:1287:PHE:CZ	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:LYS:O	1:A:17:PRO:HG2	2.18	0.43
1:A:917:PRO:HB2	1:A:923:LYS:HA	1.99	0.43
1:A:1153:ASP:OD1	1:A:1154:THR:N	2.51	0.43
1:A:1252:PHE:HB3	1:A:1287:PHE:CZ	2.53	0.43
1:A:1624:MET:HE3	1:A:1628:MET:HE1	1.98	0.43
1:A:1651:ARG:NH1	1:A:1651:ARG:HB2	2.33	0.43
1:B:645:VAL:O	1:B:649:VAL:HG13	2.18	0.43
1:B:879:LEU:HA	1:B:882:VAL:HG12	2.00	0.43
1:B:1192:GLY:HA3	1:B:1230:TYR:OH	2.18	0.43
1:B:1252:PHE:HB3	1:B:1287:PHE:CZ	2.53	0.43
1:B:1927:ALA:O	1:B:1934:GLN:NE2	2.50	0.43
1:C:2083:ILE:O	1:C:2091:LEU:N	2.51	0.43
1:C:2427:PRO:O	1:C:2431:ILE:HG12	2.17	0.43
1:B:471:LEU:HD11	1:B:493:THR:HA	2.00	0.43
1:B:1624:MET:HB3	1:B:1628:MET:HE1	2.00	0.43
1:B:1687:ARG:NH1	1:C:2137:ARG:NE	2.65	0.43
1:B:1904:GLN:HE22	1:B:1908:ILE:HD11	1.82	0.43
1:B:2042:LYS:O	1:B:2043:TYR:C	2.61	0.43
1:B:2326:THR:OG1	1:B:2330:GLY:N	2.50	0.43
1:C:638:PHE:HZ	1:C:755:VAL:HG13	1.83	0.43
1:C:1613:HIS:HB3	1:C:1616:ILE:HG12	1.99	0.43
1:A:471:LEU:HD11	1:A:493:THR:HA	2.01	0.43
1:A:657:PHE:HB2	1:A:728:ILE:HA	2.00	0.43
1:A:2159:GLU:HA	1:A:2306:ILE:HG22	1.99	0.43
1:B:1036:ARG:HH12	1:B:1131:ASN:HB3	1.83	0.43
1:C:455:MET:SD	1:C:455:MET:N	2.91	0.43
1:C:917:PRO:HB2	1:C:923:LYS:HA	2.00	0.43
1:C:2059:SER:OG	1:C:2060:PRO:HD3	2.18	0.43
1:A:930:GLU:HB2	1:A:933:TYR:CD2	2.53	0.43
1:A:1089:LEU:HD12	1:A:1093:LEU:HD23	2.01	0.43
1:A:1626:GLN:NE2	1:A:1916:PHE:HE1	2.16	0.43
1:A:1687:ARG:NH1	1:B:2137:ARG:NE	2.65	0.43
1:B:1368:ARG:HD2	1:B:2403:LEU:HD13	2.00	0.43
1:B:1651:ARG:NH1	1:B:1651:ARG:HB2	2.33	0.43
1:C:879:LEU:HA	1:C:882:VAL:HG12	2.00	0.43
1:C:1387:ARG:NH1	1:C:1404:TYR:OH	2.50	0.43
1:C:1990:THR:HG23	1:C:2010:GLU:HG3	2.00	0.43
1:C:13:LYS:HZ3	1:C:45:LEU:H	1.66	0.43
1:C:1198:LEU:O	1:C:1202:TRP:CB	2.66	0.43
1:C:1644:TRP:O	1:C:1648:SER:OG	2.36	0.43
1:C:1893:LEU:HD13	1:C:1993:ASP:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:869:GLY:O	1:A:872:SER:OG	2.26	0.43
1:A:1879:VAL:HG22	1:B:2058:PHE:HD2	1.84	0.43
1:A:2082:ARG:HB3	1:A:2189:SER:HB3	1.99	0.43
1:B:3:VAL:HG22	1:B:142:PHE:CE2	2.54	0.43
1:B:966:GLU:CD	1:B:969:ARG:NH2	2.57	0.43
1:B:1598:SER:HB2	1:B:1601:ARG:HH11	1.84	0.43
1:C:1368:ARG:HD2	1:C:2403:LEU:HD13	2.00	0.43
1:C:1904:GLN:HE22	1:C:1908:ILE:HD11	1.82	0.43
1:A:514:LEU:HD12	1:A:517:ILE:HD11	1.99	0.43
1:A:1224:TRP:CD2	1:A:1317:PHE:HE2	2.37	0.43
1:A:1364:ASP:OD1	1:A:1367:ARG:NH2	2.38	0.43
1:A:2058:PHE:HD2	1:C:1879:VAL:HG22	1.84	0.43
1:B:657:PHE:HB2	1:B:728:ILE:HA	2.00	0.43
1:B:2059:SER:OG	1:B:2060:PRO:HD3	2.18	0.43
1:C:2083:ILE:HD12	1:C:2188:VAL:HG22	1.99	0.43
1:A:298:PHE:HE2	1:A:306:LYS:HZ3	1.66	0.43
1:A:1373:ARG:HB2	1:A:2412:LEU:HD21	2.01	0.43
1:A:2288:ASP:OD2	1:A:2311:HIS:ND1	2.49	0.43
1:B:1089:LEU:HD12	1:B:1093:LEU:HD23	2.01	0.43
1:C:471:LEU:HD11	1:C:493:THR:HA	2.01	0.43
1:C:1904:GLN:NE2	1:C:1908:ILE:HD11	2.34	0.43
1:A:3:VAL:HG22	1:A:142:PHE:CE2	2.54	0.43
1:A:55:PRO:HB2	1:A:58:VAL:HB	2.01	0.43
1:A:959:ARG:NH2	1:A:969:ARG:CD	2.55	0.43
1:A:2242:ILE:O	1:A:2288:ASP:N	2.48	0.43
1:B:249:PHE:HZ	1:B:317:LEU:HA	1.84	0.43
1:B:1224:TRP:CD2	1:B:1317:PHE:HE2	2.37	0.43
1:B:1409:ASP:OD1	1:B:1409:ASP:N	2.52	0.43
1:B:1904:GLN:NE2	1:B:1908:ILE:HD11	2.34	0.43
1:C:3:VAL:HG22	1:C:142:PHE:CE2	2.54	0.43
1:C:2082:ARG:HB3	1:C:2189:SER:HB3	1.99	0.43
1:C:2082:ARG:N	1:C:2189:SER:O	2.52	0.43
1:C:2326:THR:OG1	1:C:2330:GLY:N	2.50	0.43
1:A:707:PHE:O	1:A:711:SER:OG	2.31	0.42
1:A:2083:ILE:O	1:A:2091:LEU:N	2.51	0.42
1:B:1153:ASP:OD1	1:B:1154:THR:N	2.51	0.42
1:B:1874:LEU:HD23	1:B:1878:LEU:HD23	2.01	0.42
1:C:241:LEU:HD21	1:C:319:PHE:CE2	2.54	0.42
1:C:485:PHE:O	1:C:489:LEU:HG	2.19	0.42
1:C:1089:LEU:HD12	1:C:1093:LEU:HD23	2.01	0.42
1:C:1713:ASP:OD1	1:C:1714:ILE:HD12	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2076:PRO:HA	1:C:2194:ARG:HA	2.01	0.42
1:A:241:LEU:HD21	1:A:319:PHE:CE2	2.54	0.42
1:A:638:PHE:HZ	1:A:755:VAL:HG13	1.83	0.42
1:A:916:MET:HE2	1:A:916:MET:HA	2.01	0.42
1:A:1893:LEU:HD13	1:A:1993:ASP:HA	1.99	0.42
1:A:2003:LEU:HD12	1:A:2007:PHE:HE2	1.84	0.42
1:B:13:LYS:O	1:B:17:PRO:HG2	2.18	0.42
1:B:55:PRO:HB2	1:B:58:VAL:HB	2.01	0.42
1:B:917:PRO:HB2	1:B:923:LYS:HA	2.00	0.42
1:B:1626:GLN:NE2	1:B:1916:PHE:HE1	2.16	0.42
1:B:1644:TRP:O	1:B:1648:SER:OG	2.36	0.42
1:B:2288:ASP:OD2	1:B:2311:HIS:ND1	2.49	0.42
1:C:1252:PHE:CE2	1:C:1266:ARG:HB2	2.55	0.42
1:C:1624:MET:HB3	1:C:1628:MET:HE1	2.00	0.42
1:C:1651:ARG:NH1	1:C:1651:ARG:HB2	2.33	0.42
1:C:2003:LEU:HD12	1:C:2007:PHE:HE2	1.84	0.42
1:A:1054:TYR:HB3	1:A:1055:PRO:HD3	2.01	0.42
1:A:1598:SER:HB2	1:A:1601:ARG:HH11	1.84	0.42
1:A:1904:GLN:NE2	1:A:1908:ILE:HD11	2.34	0.42
1:A:2373:ARG:HD3	1:A:2373:ARG:HA	1.89	0.42
1:B:673:LEU:HD12	1:B:680:TYR:CZ	2.55	0.42
1:B:692:THR:HA	1:B:695:THR:HG22	2.02	0.42
1:B:959:ARG:HH21	1:B:969:ARG:NH1	2.14	0.42
1:B:2326:THR:N	1:B:2331:ARG:O	2.46	0.42
1:B:2381:SER:OG	1:C:2381:SER:OG	2.35	0.42
1:C:7:LEU:O	1:C:11:VAL:HG23	2.20	0.42
1:C:12:VAL:O	1:C:17:PRO:HD2	2.20	0.42
1:C:692:THR:HA	1:C:695:THR:HG22	2.02	0.42
1:C:1409:ASP:N	1:C:1409:ASP:OD1	2.52	0.42
1:C:2092:TYR:HE1	1:C:2094:MET:HE3	1.82	0.42
1:C:2194:ARG:HH22	1:C:2340:ILE:HG23	1.84	0.42
1:C:2353:LYS:HD2	1:C:2353:LYS:HA	1.84	0.42
1:A:13:LYS:HZ3	1:A:45:LEU:H	1.66	0.42
1:A:485:PHE:O	1:A:489:LEU:HG	2.19	0.42
1:A:1368:ARG:HD2	1:A:2403:LEU:HD13	2.00	0.42
1:A:1624:MET:HB3	1:A:1628:MET:HE1	2.00	0.42
1:A:2144:LYS:HB3	1:A:2144:LYS:HE3	1.94	0.42
1:B:707:PHE:O	1:B:711:SER:OG	2.31	0.42
1:B:1879:VAL:HG22	1:C:2058:PHE:HD2	1.84	0.42
1:B:2082:ARG:N	1:B:2189:SER:O	2.52	0.42
1:B:2155:ARG:HB3	1:B:2333:TYR:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:977:HIS:NE2	1:C:978:HIS:CE1	2.88	0.42
1:C:1224:TRP:CD2	1:C:1317:PHE:HE2	2.37	0.42
1:C:2155:ARG:HB3	1:C:2333:TYR:CD2	2.54	0.42
1:A:12:VAL:O	1:A:17:PRO:HD2	2.20	0.42
1:A:249:PHE:HZ	1:A:317:LEU:HA	1.84	0.42
1:A:977:HIS:NE2	1:A:978:HIS:CE1	2.88	0.42
1:A:1356:GLU:HA	1:A:1359:LYS:HE2	2.02	0.42
1:A:1844:LEU:HD23	1:A:1844:LEU:HA	1.89	0.42
1:A:2146:TYR:CD2	1:A:2339:PHE:HB3	2.55	0.42
1:A:2381:SER:OG	1:B:2381:SER:OG	2.35	0.42
1:B:977:HIS:NE2	1:B:978:HIS:CE1	2.88	0.42
1:B:2146:TYR:CD2	1:B:2339:PHE:HB3	2.55	0.42
1:C:55:PRO:HB2	1:C:58:VAL:HB	2.01	0.42
1:C:249:PHE:HZ	1:C:317:LEU:HA	1.84	0.42
1:C:746:LEU:O	1:C:750:ILE:HD12	2.20	0.42
1:C:834:VAL:HA	1:C:837:ILE:HG22	2.02	0.42
1:C:1106:TYR:OH	1:C:1275:ASN:ND2	2.41	0.42
1:C:1373:ARG:HB2	1:C:2412:LEU:HD21	2.01	0.42
1:C:1839:ASP:HA	1:C:1842:CYS:SG	2.60	0.42
1:A:37:LEU:HD23	1:A:37:LEU:HA	1.86	0.42
1:A:97:ARG:N	1:A:100:THR:OG1	2.50	0.42
1:A:98:SER:O	1:A:101:THR:OG1	2.27	0.42
1:A:879:LEU:HA	1:A:882:VAL:HG12	2.00	0.42
1:A:1332:GLU:HA	1:A:1335:LEU:HG	2.02	0.42
1:A:1660:MET:HE2	1:A:1660:MET:HB3	1.92	0.42
1:A:1839:ASP:HA	1:A:1842:CYS:SG	2.60	0.42
1:A:2155:ARG:HB3	1:A:2333:TYR:CD2	2.54	0.42
1:B:916:MET:HA	1:B:916:MET:HE2	2.02	0.42
1:B:2194:ARG:HH22	1:B:2340:ILE:HG23	1.84	0.42
1:C:13:LYS:NZ	1:C:43:ALA:O	2.34	0.42
1:C:1598:SER:HB2	1:C:1601:ARG:HH11	1.84	0.42
1:C:2197:ASP:OD1	1:C:2197:ASP:N	2.52	0.42
1:A:1892:TYR:OH	1:A:1960:ILE:HD13	2.20	0.42
1:A:2092:TYR:HE1	1:A:2094:MET:HE3	1.82	0.42
1:B:959:ARG:O	1:B:964:LEU:N	2.37	0.42
1:B:1332:GLU:HA	1:B:1335:LEU:HG	2.02	0.42
1:B:2092:TYR:HE1	1:B:2094:MET:HE3	1.82	0.42
1:C:298:PHE:HE2	1:C:306:LYS:HZ3	1.67	0.42
1:C:673:LEU:HD12	1:C:680:TYR:CZ	2.54	0.42
1:C:916:MET:HE2	1:C:916:MET:HA	2.02	0.42
1:C:1356:GLU:HA	1:C:1359:LYS:HE2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1660:MET:HE2	1:C:1660:MET:HB3	1.92	0.42
1:C:1709:PHE:CE2	1:C:1711:LEU:HB3	2.55	0.42
1:C:2146:TYR:CD2	1:C:2339:PHE:HB3	2.54	0.42
1:C:2146:TYR:CE2	1:C:2339:PHE:HB3	2.55	0.42
1:A:1662:THR:O	1:A:1665:GLU:HG2	2.20	0.42
1:A:2381:SER:OG	1:C:2381:SER:OG	2.35	0.42
1:B:12:VAL:O	1:B:17:PRO:HD2	2.20	0.42
1:B:245:SER:O	1:B:249:PHE:HD2	2.03	0.42
1:B:834:VAL:HA	1:B:837:ILE:HG22	2.02	0.42
1:B:980:HIS:HB3	1:B:983:ARG:CZ	2.50	0.42
1:B:1373:ARG:HB2	1:B:2412:LEU:HD21	2.01	0.42
1:B:1709:PHE:CE2	1:B:1711:LEU:HB3	2.55	0.42
1:B:1892:TYR:OH	1:B:1960:ILE:HD13	2.20	0.42
1:C:1874:LEU:HD23	1:C:1878:LEU:HD23	2.01	0.42
1:C:2416:LEU:HD23	1:C:2416:LEU:HA	1.91	0.42
1:A:566:THR:HA	1:A:569:VAL:HG12	2.02	0.42
1:A:1644:TRP:O	1:A:1648:SER:OG	2.36	0.42
1:A:1646:ASN:HD22	1:A:1646:ASN:C	2.28	0.42
1:A:2082:ARG:N	1:A:2189:SER:O	2.52	0.42
1:B:826:PHE:O	1:B:830:ILE:HB	2.20	0.42
1:B:1252:PHE:CE2	1:B:1266:ARG:HB2	2.55	0.42
1:B:1307:LEU:HD12	1:B:1310:LEU:HD11	2.02	0.42
1:B:1628:MET:HE3	1:B:1712:TRP:CE2	2.55	0.42
1:C:517:ILE:O	1:C:521:LEU:HD23	2.20	0.42
1:C:1235:ILE:CD1	1:C:1300:ILE:HG21	2.50	0.42
1:C:1343:LYS:HA	1:C:1343:LYS:HD2	1.92	0.42
1:C:1624:MET:HA	1:C:1627:VAL:HG12	2.02	0.42
1:C:1892:TYR:OH	1:C:1960:ILE:HD13	2.20	0.42
1:A:62:VAL:O	1:A:66:PHE:HD2	2.03	0.42
1:A:1628:MET:HE3	1:A:1712:TRP:CE2	2.55	0.42
1:B:858:SER:HA	1:B:861:ILE:HG22	2.01	0.42
1:B:1167:PHE:CD2	1:B:1316:ILE:HG23	2.55	0.42
1:B:1235:ILE:CD1	1:B:1300:ILE:HG21	2.50	0.42
1:B:1646:ASN:C	1:B:1646:ASN:HD22	2.28	0.42
1:B:2185:ASN:HD22	1:B:2211:LEU:HD23	1.84	0.42
1:B:2278:GLU:OE1	1:B:2280:SER:N	2.53	0.42
1:C:917:PRO:O	1:C:921:GLY:N	2.53	0.42
1:C:2003:LEU:CD1	1:C:2007:PHE:HE2	2.31	0.42
1:A:980:HIS:HB3	1:A:983:ARG:CZ	2.50	0.41
1:A:1259:GLY:HA2	1:A:1262:LEU:HG	2.02	0.41
1:A:1670:ILE:HA	1:A:1673:VAL:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1874:LEU:HD23	1:A:1878:LEU:HD23	2.01	0.41
1:A:2146:TYR:CE2	1:A:2339:PHE:HB3	2.55	0.41
1:A:2278:GLU:OE1	1:A:2280:SER:N	2.53	0.41
1:B:1839:ASP:HA	1:B:1842:CYS:SG	2.60	0.41
1:C:858:SER:HA	1:C:861:ILE:HG22	2.01	0.41
1:C:1054:TYR:HB3	1:C:1055:PRO:HD3	2.01	0.41
1:C:2130:THR:HA	1:C:2133:ILE:HG12	2.02	0.41
1:C:2264:ILE:HD13	1:C:2320:TRP:CH2	2.55	0.41
1:A:245:SER:O	1:A:249:PHE:HD2	2.03	0.41
1:A:670:LEU:HD23	1:A:670:LEU:HA	1.93	0.41
1:A:826:PHE:O	1:A:830:ILE:HB	2.20	0.41
1:A:1709:PHE:CE2	1:A:1711:LEU:HB3	2.55	0.41
1:A:2076:PRO:HA	1:A:2194:ARG:HA	2.01	0.41
1:A:2264:ILE:HD13	1:A:2320:TRP:CH2	2.55	0.41
1:B:633:LYS:HD3	1:B:633:LYS:HA	1.75	0.41
1:B:1356:GLU:HA	1:B:1359:LYS:HE2	2.02	0.41
1:B:1842:CYS:HA	1:B:1845:ILE:HG22	2.02	0.41
1:C:555:ALA:HA	1:C:558:ILE:HG12	2.02	0.41
1:C:1259:GLY:HA2	1:C:1262:LEU:HG	2.02	0.41
1:C:1679:MET:H	1:C:1679:MET:HG2	1.69	0.41
1:C:2185:ASN:HD22	1:C:2211:LEU:HD23	1.84	0.41
1:A:633:LYS:HD3	1:A:633:LYS:HA	1.75	0.41
1:A:953:TYR:HD1	1:A:956:ARG:HH21	1.68	0.41
1:A:1198:LEU:O	1:A:1202:TRP:CB	2.66	0.41
1:A:1235:ILE:CD1	1:A:1300:ILE:HG21	2.50	0.41
1:B:830:ILE:CG2	1:B:948:GLN:HG2	2.49	0.41
1:B:1328:GLU:O	1:B:1332:GLU:HB2	2.21	0.41
1:B:2130:THR:HA	1:B:2133:ILE:HG12	2.02	0.41
1:C:97:ARG:N	1:C:100:THR:OG1	2.50	0.41
1:C:566:THR:HA	1:C:569:VAL:HG12	2.02	0.41
1:C:980:HIS:HB3	1:C:983:ARG:CZ	2.50	0.41
1:C:1206:ASN:O	1:C:1209:VAL:HG22	2.21	0.41
1:C:1910:PHE:O	1:C:1911:LEU:C	2.63	0.41
1:C:2278:GLU:OE1	1:C:2280:SER:N	2.53	0.41
1:A:32:SER:HB2	1:A:253:TYR:CD2	2.55	0.41
1:A:223:TRP:CD1	1:A:574:ARG:HH22	2.39	0.41
1:A:253:TYR:O	1:A:256:GLN:N	2.54	0.41
1:A:258:PRO:HA	1:A:261:HIS:CD2	2.56	0.41
1:A:917:PRO:O	1:A:921:GLY:N	2.53	0.41
1:A:1135:TYR:OH	1:A:1323:GLN:OE1	2.26	0.41
1:A:2194:ARG:HH22	1:A:2340:ILE:HG23	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:LEU:O	1:B:128:ILE:HG12	2.21	0.41
1:B:238:LYS:HZ3	1:B:326:GLN:HG3	1.85	0.41
1:B:455:MET:SD	1:B:455:MET:N	2.91	0.41
1:B:746:LEU:O	1:B:750:ILE:HD12	2.20	0.41
1:B:1206:ASN:O	1:B:1209:VAL:HG22	2.21	0.41
1:B:1259:GLY:HA2	1:B:1262:LEU:HG	2.02	0.41
1:B:1624:MET:HA	1:B:1627:VAL:HG12	2.02	0.41
1:B:2003:LEU:HD12	1:B:2007:PHE:HE2	1.84	0.41
1:B:2076:PRO:HA	1:B:2194:ARG:HA	2.01	0.41
1:B:2146:TYR:CE2	1:B:2339:PHE:HB3	2.55	0.41
1:B:2395:LEU:HD12	1:B:2395:LEU:HA	1.88	0.41
1:C:258:PRO:HA	1:C:261:HIS:CD2	2.56	0.41
1:C:1233:PHE:O	1:C:1237:MET:HG2	2.21	0.41
1:A:7:LEU:O	1:A:11:VAL:HG23	2.20	0.41
1:A:673:LEU:HD12	1:A:680:TYR:CZ	2.55	0.41
1:A:834:VAL:HA	1:A:837:ILE:HG22	2.02	0.41
1:A:858:SER:HA	1:A:861:ILE:HG22	2.01	0.41
1:A:1252:PHE:CE2	1:A:1266:ARG:HB2	2.55	0.41
1:A:2089:PRO:HD3	1:C:2161:GLU:OE2	2.21	0.41
1:A:2185:ASN:HD22	1:A:2211:LEU:HD23	1.84	0.41
1:B:485:PHE:O	1:B:489:LEU:HG	2.20	0.41
1:B:917:PRO:O	1:B:921:GLY:N	2.53	0.41
1:B:936:PHE:O	1:B:940:VAL:HG23	2.21	0.41
1:B:1054:TYR:HB3	1:B:1055:PRO:HD3	2.01	0.41
1:A:1112:PHE:O	1:A:1116:LEU:HD23	2.21	0.41
1:A:1832:TYR:HB2	1:A:1892:TYR:CE1	2.56	0.41
1:A:2395:LEU:HD12	1:A:2395:LEU:HA	1.88	0.41
1:B:62:VAL:O	1:B:66:PHE:HD2	2.03	0.41
1:B:97:ARG:N	1:B:100:THR:OG1	2.49	0.41
1:B:555:ALA:HA	1:B:558:ILE:HG12	2.02	0.41
1:B:566:THR:HA	1:B:569:VAL:HG12	2.02	0.41
1:B:638:PHE:HZ	1:B:755:VAL:HG13	1.83	0.41
1:B:1233:PHE:O	1:B:1237:MET:HG2	2.21	0.41
1:C:1112:PHE:O	1:C:1116:LEU:HD23	2.21	0.41
1:C:1662:THR:O	1:C:1665:GLU:HG2	2.20	0.41
1:C:1842:CYS:HA	1:C:1845:ILE:HG22	2.02	0.41
1:A:455:MET:SD	1:A:455:MET:N	2.91	0.41
1:A:494:CYS:O	1:A:498:ILE:HB	2.21	0.41
1:A:692:THR:HA	1:A:695:THR:HG22	2.02	0.41
1:A:1206:ASN:O	1:A:1209:VAL:HG22	2.20	0.41
1:A:2247:GLN:HA	1:A:2339:PHE:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:LEU:O	1:B:11:VAL:HG23	2.20	0.41
1:B:13:LYS:HZ3	1:B:45:LEU:H	1.67	0.41
1:B:1018:ASP:HB2	1:B:1092:LEU:O	2.21	0.41
1:B:1198:LEU:O	1:B:1202:TRP:CB	2.66	0.41
1:B:1264:ILE:HG23	1:B:1678:PHE:HB3	2.03	0.41
1:B:1910:PHE:O	1:B:1911:LEU:C	2.63	0.41
1:C:124:LEU:O	1:C:128:ILE:HG12	2.21	0.41
1:C:245:SER:O	1:C:249:PHE:HD2	2.03	0.41
1:C:1307:LEU:HD12	1:C:1310:LEU:HD11	2.02	0.41
1:C:2347:PHE:O	1:C:2350:LYS:N	2.49	0.41
1:C:2395:LEU:HD12	1:C:2395:LEU:HA	1.88	0.41
1:A:555:ALA:HA	1:A:558:ILE:HG12	2.02	0.41
1:A:1104:SER:O	1:A:1108:ILE:HG12	2.21	0.41
1:A:1842:CYS:HA	1:A:1845:ILE:HG22	2.02	0.41
1:A:2161:GLU:OE2	1:B:2089:PRO:HD3	2.20	0.41
1:B:484:ILE:CD1	1:B:544:VAL:HA	2.51	0.41
1:B:639:ILE:HA	1:B:642:VAL:HG12	2.03	0.41
1:B:1235:ILE:HD12	1:B:1235:ILE:HA	1.89	0.41
1:B:1662:THR:O	1:B:1665:GLU:HG2	2.20	0.41
1:B:1670:ILE:HA	1:B:1673:VAL:HG12	2.02	0.41
1:B:2161:GLU:OE2	1:C:2089:PRO:HD3	2.21	0.41
1:B:2347:PHE:O	1:B:2348:LEU:HG	2.21	0.41
1:B:2432:GLU:OE2	1:B:2435:ARG:NH2	2.54	0.41
1:C:62:VAL:O	1:C:66:PHE:HD2	2.03	0.41
1:C:1018:ASP:HB2	1:C:1092:LEU:O	2.21	0.41
1:C:1182:GLY:O	1:C:1190:ALA:HB1	2.21	0.41
1:C:1628:MET:HE3	1:C:1712:TRP:CE2	2.55	0.41
1:C:1646:ASN:C	1:C:1646:ASN:HD22	2.28	0.41
1:A:238:LYS:O	1:A:242:ILE:HG12	2.20	0.41
1:A:870:ILE:HG13	1:A:871:PHE:N	2.36	0.41
1:A:1156:LYS:H	1:A:1156:LYS:HG2	1.70	0.41
1:A:1182:GLY:O	1:A:1190:ALA:HB1	2.21	0.41
1:A:1307:LEU:HD12	1:A:1310:LEU:HD11	2.01	0.41
1:A:1409:ASP:OD1	1:A:1409:ASP:N	2.52	0.41
1:A:2326:THR:OG1	1:A:2330:GLY:N	2.50	0.41
1:A:2432:GLU:OE2	1:A:2435:ARG:NH2	2.54	0.41
1:B:223:TRP:CD1	1:B:574:ARG:HH22	2.39	0.41
1:B:241:LEU:HD21	1:B:319:PHE:CE2	2.55	0.41
1:B:494:CYS:O	1:B:498:ILE:HB	2.21	0.41
1:B:517:ILE:O	1:B:521:LEU:HD23	2.20	0.41
1:B:1637:LEU:HA	1:B:1640:MET:HE2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2041:VAL:HA	1:B:2044:MET:SD	2.61	0.41
1:B:2078:LYS:HA	1:B:2097:GLN:CB	2.51	0.41
1:B:2105:GLU:OE2	1:B:2157:ARG:NH1	2.41	0.41
1:B:2250:ASN:HD22	1:B:2344:PHE:HA	1.86	0.41
1:B:2264:ILE:HD13	1:B:2320:TRP:CH2	2.55	0.41
1:B:2353:LYS:HA	1:B:2353:LYS:HD2	1.84	0.41
1:C:223:TRP:CD1	1:C:574:ARG:HH22	2.39	0.41
1:C:1190:ALA:HA	1:C:1193:TYR:HD1	1.86	0.41
1:C:1670:ILE:HA	1:C:1673:VAL:HG12	2.02	0.41
1:C:2250:ASN:HD22	1:C:2344:PHE:HA	1.86	0.41
1:C:2269:ASN:HB2	1:C:2270:PRO:HD3	2.03	0.41
1:A:28:PRO:HB3	1:A:253:TYR:CE2	2.56	0.41
1:A:1167:PHE:CD2	1:A:1316:ILE:HG23	2.55	0.41
1:A:2078:LYS:HA	1:A:2097:GLN:CB	2.51	0.41
1:A:2347:PHE:O	1:A:2348:LEU:HG	2.21	0.41
1:B:238:LYS:O	1:B:242:ILE:HG12	2.21	0.41
1:B:298:PHE:HE2	1:B:306:LYS:HZ3	1.68	0.41
1:B:870:ILE:HG13	1:B:871:PHE:N	2.36	0.41
1:B:1182:GLY:O	1:B:1190:ALA:HB1	2.21	0.41
1:B:1190:ALA:HA	1:B:1193:TYR:HD1	1.86	0.41
1:B:1622:ALA:HA	1:B:1716:LEU:HD12	2.03	0.41
1:B:2248:VAL:HB	1:B:2340:ILE:HG13	2.02	0.41
1:C:494:CYS:O	1:C:498:ILE:HB	2.21	0.41
1:C:514:LEU:HA	1:C:517:ILE:HG12	2.03	0.41
1:C:826:PHE:O	1:C:830:ILE:HB	2.20	0.41
1:C:1104:SER:O	1:C:1108:ILE:HG12	2.21	0.41
1:A:454:GLY:O	1:A:458:VAL:HG23	2.21	0.40
1:A:830:ILE:CG2	1:A:948:GLN:HG2	2.49	0.40
1:B:258:PRO:HA	1:B:261:HIS:CD2	2.56	0.40
1:B:953:TYR:HD1	1:B:956:ARG:HH21	1.68	0.40
1:B:1684:ILE:HD12	1:B:1687:ARG:NH2	2.34	0.40
1:B:1832:TYR:HB2	1:B:1892:TYR:CE1	2.56	0.40
1:C:238:LYS:O	1:C:242:ILE:HG12	2.20	0.40
1:C:639:ILE:HA	1:C:642:VAL:HG12	2.02	0.40
1:C:1064:LEU:HD23	1:C:1064:LEU:HA	1.96	0.40
1:C:1332:GLU:HA	1:C:1335:LEU:HG	2.02	0.40
1:C:1684:ILE:HD12	1:C:1687:ARG:NH2	2.34	0.40
1:C:1832:TYR:HB2	1:C:1892:TYR:CE1	2.56	0.40
1:C:2057:ILE:HG22	1:C:2058:PHE:CD1	2.56	0.40
1:C:2135:ARG:NH2	1:C:2267:ASP:OD1	2.44	0.40
1:C:2247:GLN:HA	1:C:2339:PHE:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:639:ILE:HA	1:A:642:VAL:HG12	2.02	0.40
1:A:2130:THR:HA	1:A:2133:ILE:HG12	2.02	0.40
1:A:2250:ASN:HD22	1:A:2344:PHE:HA	1.86	0.40
1:B:2196:TYR:CD2	1:C:2253:GLU:OE2	2.74	0.40
1:B:2379:SER:O	1:B:2382:THR:OG1	2.38	0.40
1:C:1919:LEU:HD12	1:C:1919:LEU:HA	1.94	0.40
1:C:2078:LYS:HA	1:C:2097:GLN:CB	2.51	0.40
1:C:2105:GLU:OE2	1:C:2157:ARG:NH1	2.41	0.40
1:A:124:LEU:N	1:A:125:PRO:HD2	2.37	0.40
1:A:734:ARG:HA	1:A:734:ARG:NE	2.36	0.40
1:A:936:PHE:O	1:A:940:VAL:HG23	2.21	0.40
1:A:1007:ILE:O	1:A:1011:ILE:HG12	2.22	0.40
1:A:1233:PHE:O	1:A:1237:MET:HG2	2.21	0.40
1:A:1625:THR:HG21	1:A:1716:LEU:HB2	2.04	0.40
1:A:2248:VAL:HB	1:A:2340:ILE:HG13	2.02	0.40
1:B:514:LEU:HA	1:B:517:ILE:HG12	2.03	0.40
1:B:2057:ILE:HG22	1:B:2058:PHE:CD1	2.56	0.40
1:C:734:ARG:HA	1:C:734:ARG:NE	2.36	0.40
1:C:2041:VAL:HA	1:C:2044:MET:SD	2.61	0.40
1:C:2248:VAL:HB	1:C:2340:ILE:HG13	2.02	0.40
1:A:124:LEU:O	1:A:128:ILE:HG12	2.21	0.40
1:A:517:ILE:O	1:A:521:LEU:HD23	2.20	0.40
1:A:1328:GLU:O	1:A:1332:GLU:HB2	2.21	0.40
1:A:1622:ALA:HA	1:A:1716:LEU:HD12	2.04	0.40
1:A:1910:PHE:O	1:A:1911:LEU:C	2.63	0.40
1:A:2368:GLY:O	1:A:2372:VAL:HG22	2.22	0.40
1:A:2428:ALA:O	1:A:2432:GLU:HG2	2.21	0.40
1:B:8:LYS:HB3	1:B:8:LYS:HE2	1.86	0.40
1:B:734:ARG:HA	1:B:734:ARG:NE	2.36	0.40
1:B:2428:ALA:O	1:B:2432:GLU:HG2	2.22	0.40
1:C:1172:TRP:O	1:C:1176:MET:HG3	2.22	0.40
1:A:1172:TRP:O	1:A:1176:MET:HG3	2.22	0.40
1:A:2041:VAL:HA	1:A:2044:MET:SD	2.61	0.40
1:A:2057:ILE:HG22	1:A:2058:PHE:CD1	2.56	0.40
1:B:1112:PHE:O	1:B:1116:LEU:HD23	2.21	0.40
1:B:1172:TRP:O	1:B:1176:MET:HG3	2.22	0.40
1:B:1684:ILE:HD13	1:B:1684:ILE:HA	1.97	0.40
1:B:1832:TYR:HA	1:B:1835:MET:HG2	2.04	0.40
1:B:2247:GLN:HA	1:B:2339:PHE:HB2	2.03	0.40
1:B:2416:LEU:HD23	1:B:2416:LEU:HA	1.90	0.40
1:C:849:LEU:HD13	1:C:920:PHE:CE2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1167:PHE:CD2	1:C:1316:ILE:HG23	2.55	0.40
1:C:1264:ILE:HG23	1:C:1678:PHE:HB3	2.03	0.40
1:C:1622:ALA:HA	1:C:1716:LEU:HD12	2.04	0.40
1:C:2347:PHE:O	1:C:2348:LEU:HG	2.21	0.40
1:C:2432:GLU:OE2	1:C:2435:ARG:NH2	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1897/2442 (78%)	1792 (94%)	105 (6%)	0	100	100
1	B	1897/2442 (78%)	1792 (94%)	105 (6%)	0	100	100
1	C	1897/2442 (78%)	1792 (94%)	105 (6%)	0	100	100
All	All	5691/7326 (78%)	5376 (94%)	315 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1698/2141 (79%)	1697 (100%)	1 (0%)	88	89
1	B	1698/2141 (79%)	1697 (100%)	1 (0%)	88	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	1698/2141 (79%)	1697 (100%)	1 (0%)	88	89
All	All	5094/6423 (79%)	5091 (100%)	3 (0%)	87	89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2348	LEU
1	B	2348	LEU
1	C	2348	LEU

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

Mol	Chain	Res	Type
1	A	722	GLN
1	A	817	GLN
1	A	948	GLN
1	A	978	HIS
1	A	1267	GLN
1	A	1318	HIS
1	A	1646	ASN
1	A	1682	ASN
1	A	1818	HIS
1	A	1931	HIS
1	A	2201	ASN
1	A	2301	ASN
1	A	2325	ASN
1	B	722	GLN
1	B	817	GLN
1	B	948	GLN
1	B	978	HIS
1	B	980	HIS
1	B	1267	GLN
1	B	1318	HIS
1	B	1646	ASN
1	B	1682	ASN
1	B	1818	HIS
1	B	1931	HIS
1	C	722	GLN
1	C	817	GLN
1	C	948	GLN
1	C	978	HIS

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Mol	Chain	Res	Type
1	C	980	HIS
1	C	1267	GLN
1	C	1318	HIS
1	C	1646	ASN
1	C	1682	ASN
1	C	1818	HIS
1	C	1931	HIS
1	C	2201	ASN
1	C	2301	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 [i](#)

There are no chain breaks in this entry.

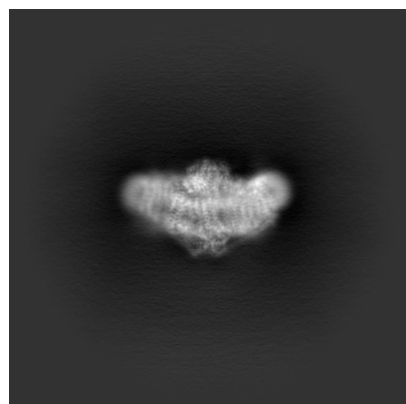
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64385. These allow visual inspection of the internal detail of the map and identification of artifacts.

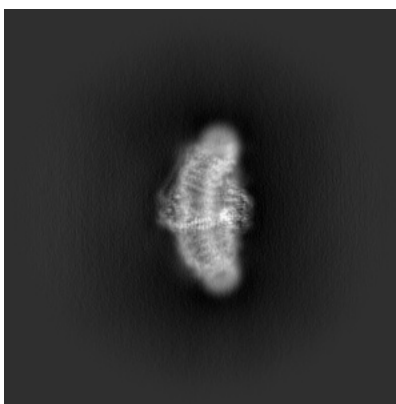
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

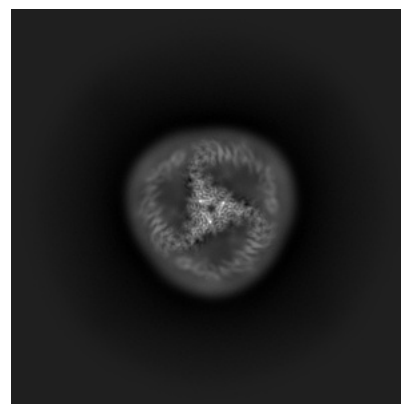
6.1.1 Primary map



X

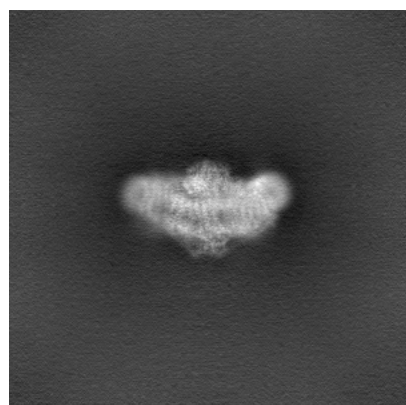


Y

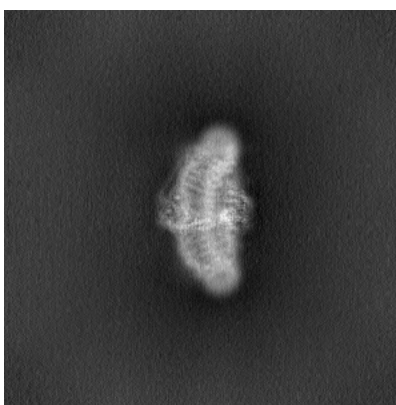


Z

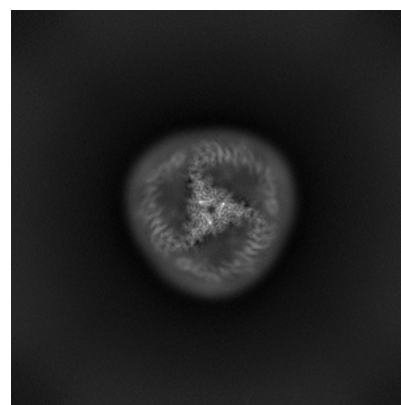
6.1.2 Raw map



X



Y

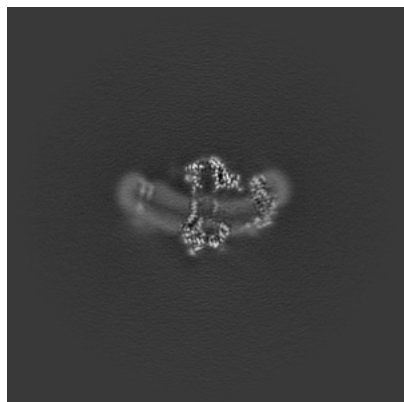


Z

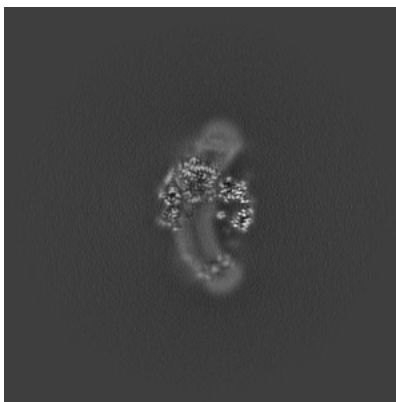
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

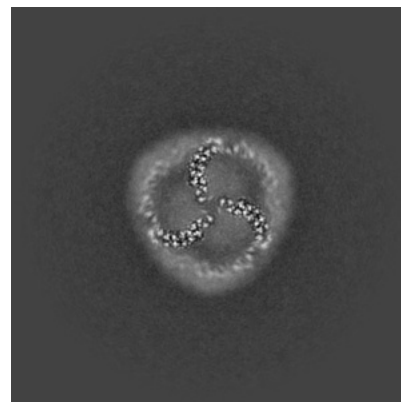
6.2.1 Primary map



X Index: 280



Y Index: 280

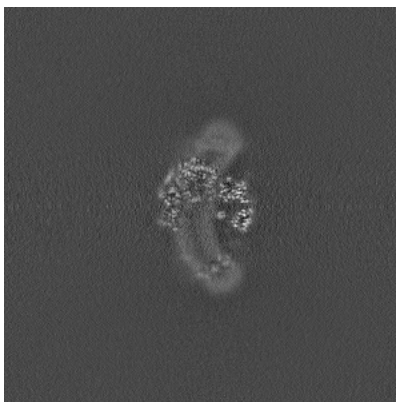


Z Index: 280

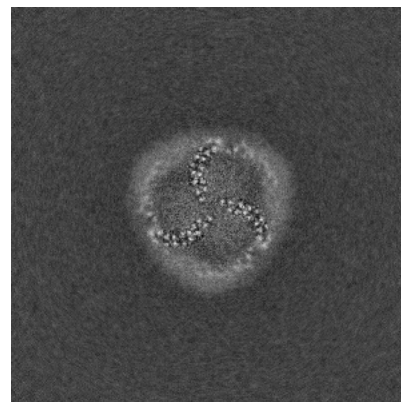
6.2.2 Raw map



X Index: 280



Y Index: 280

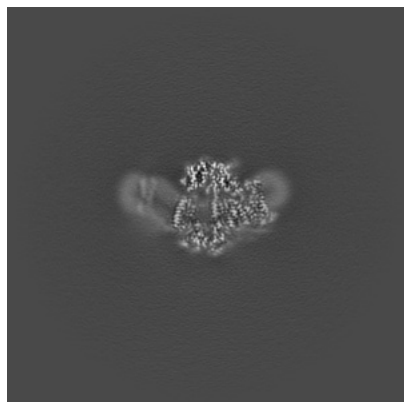


Z Index: 280

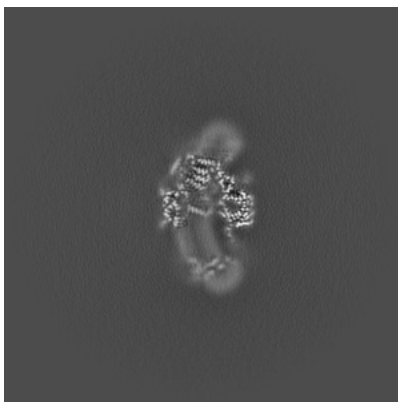
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

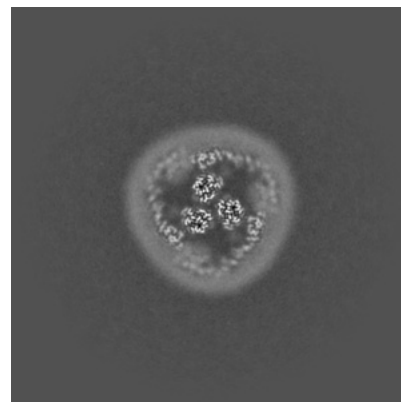
6.3.1 Primary map



X Index: 265

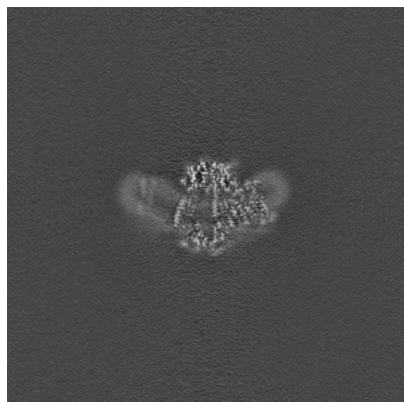


Y Index: 273

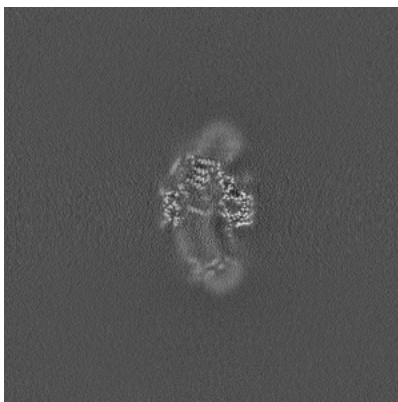


Z Index: 314

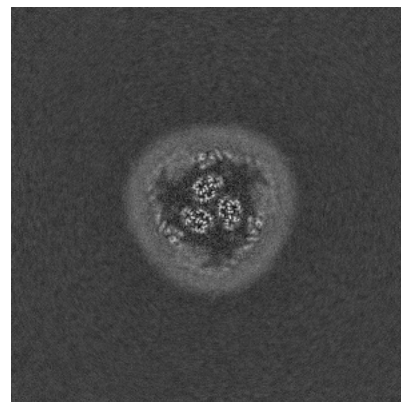
6.3.2 Raw map



X Index: 265



Y Index: 273

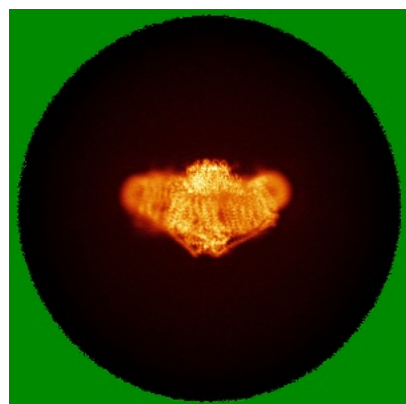


Z Index: 315

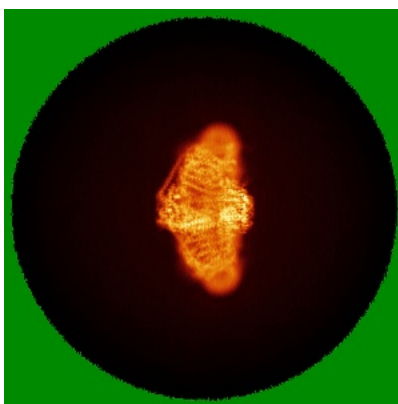
The images above show the largest variance slices of the map in three orthogonal directions.

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

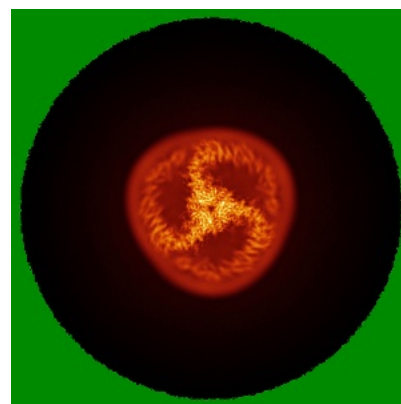
6.4.1 Primary map



X

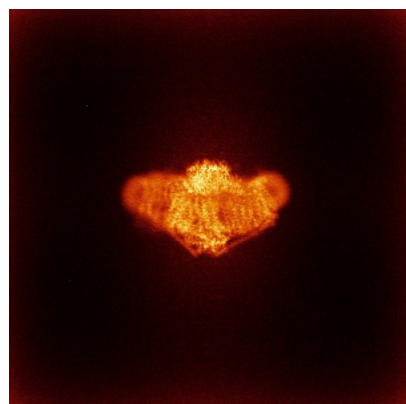


Y

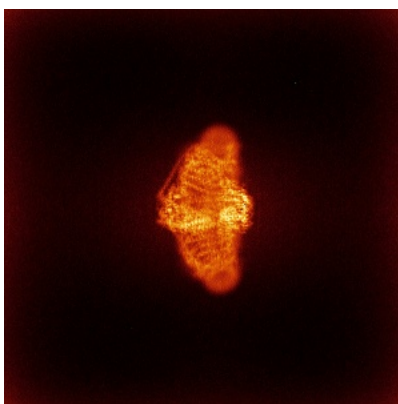


Z

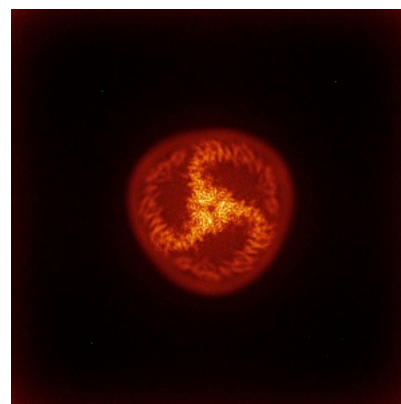
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.075. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

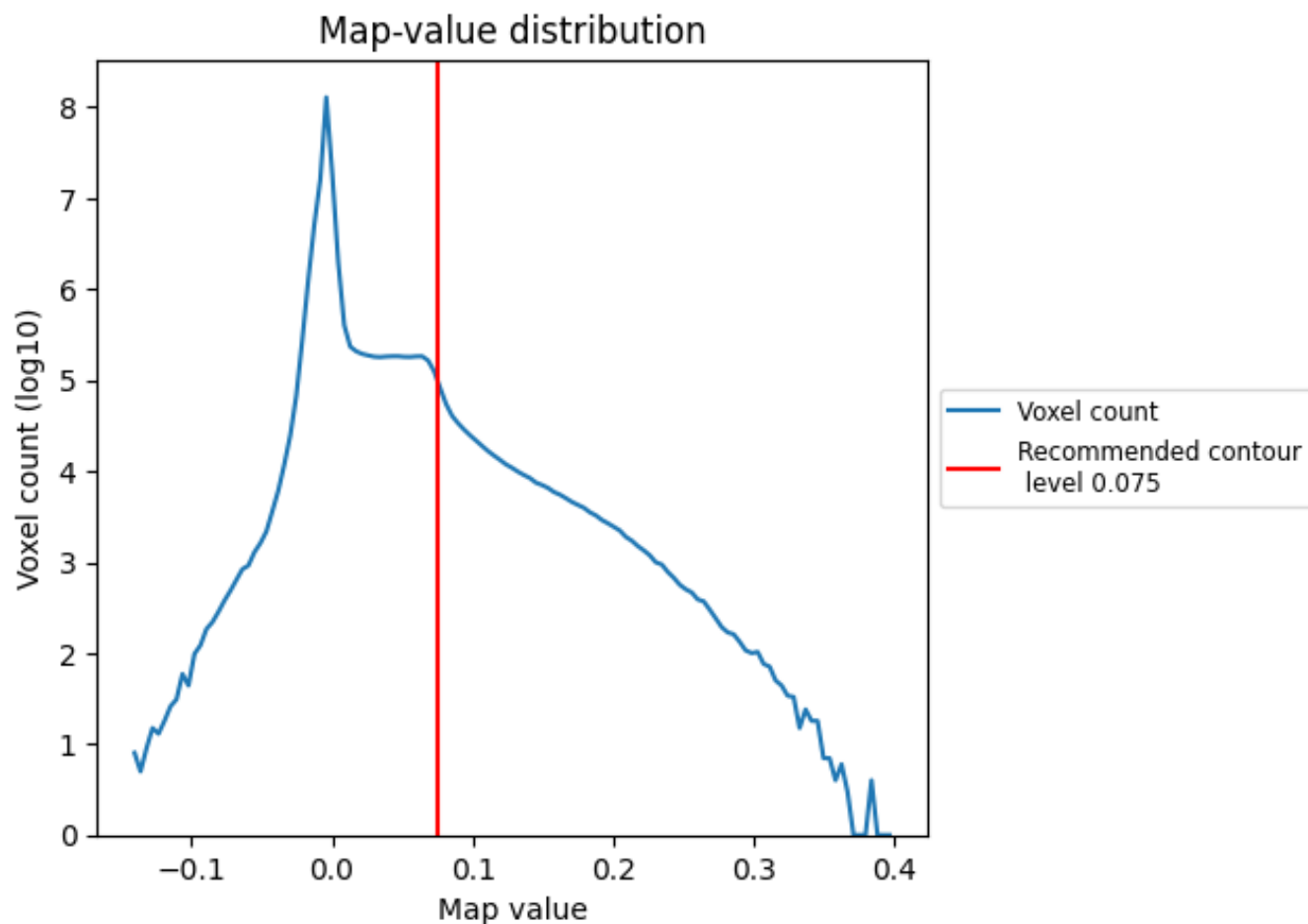
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

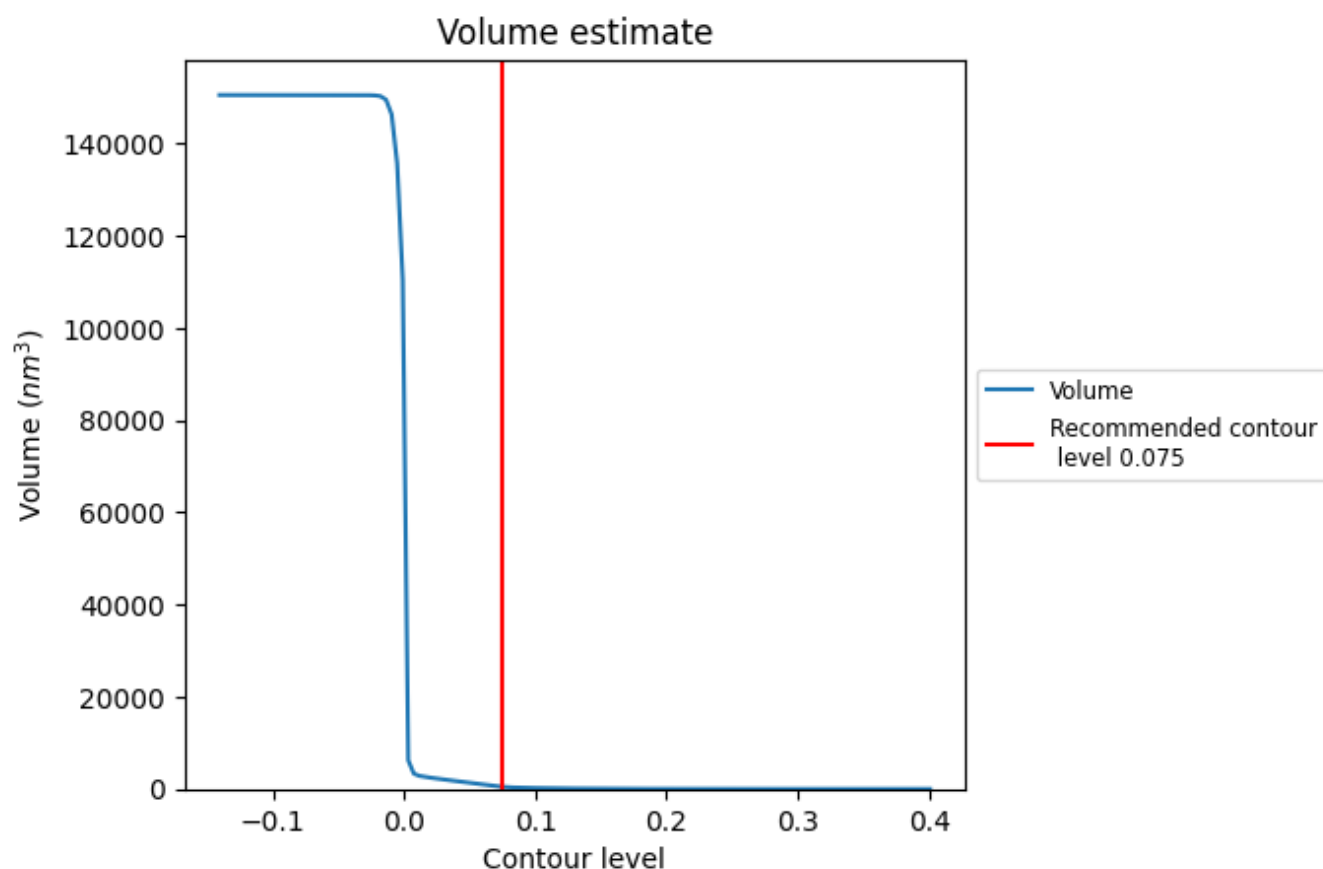
This section contains the results of statistical analysis of the map.

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.

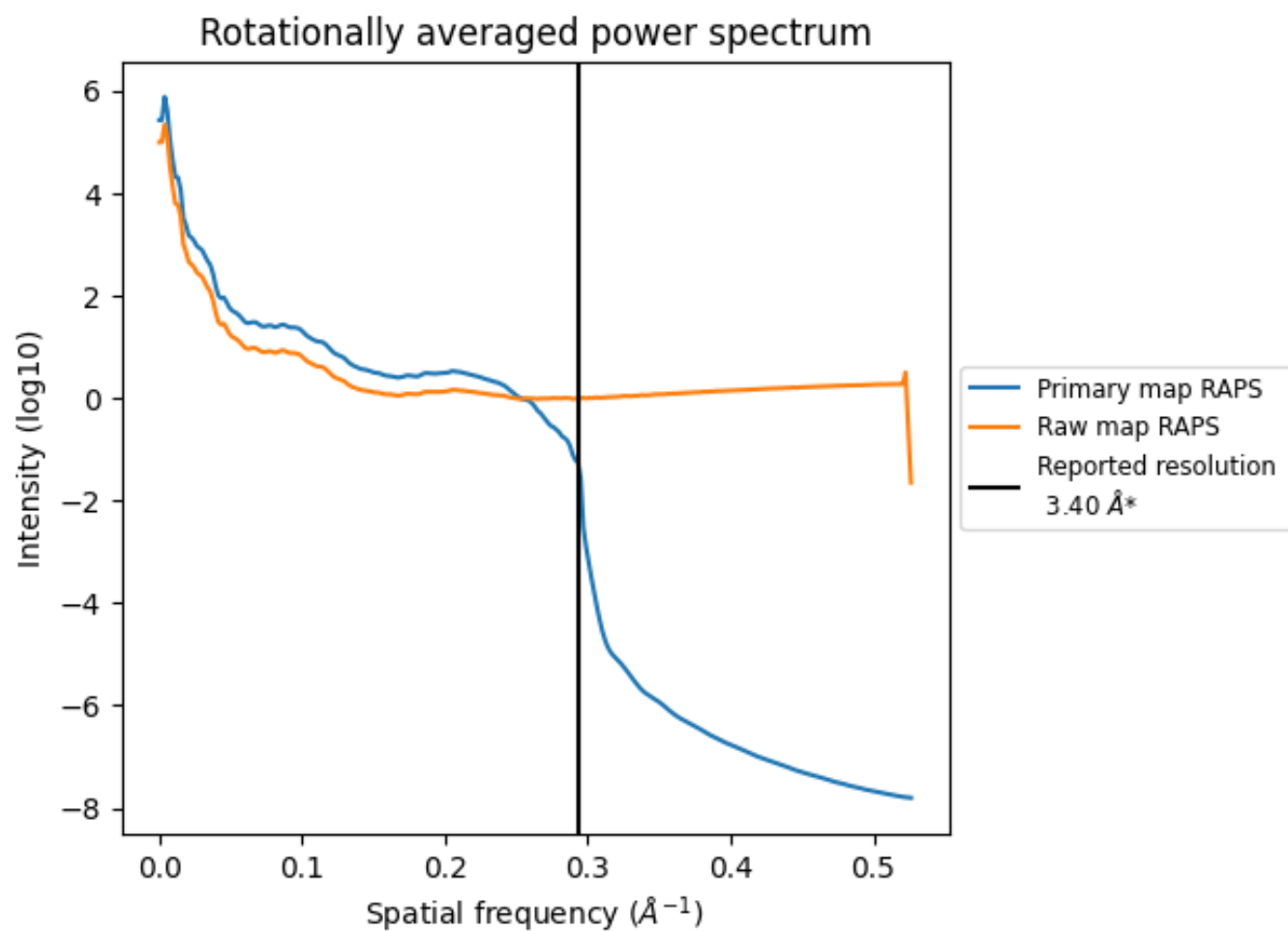
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 458 nm^3 ; this corresponds to an approximate mass of 414 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

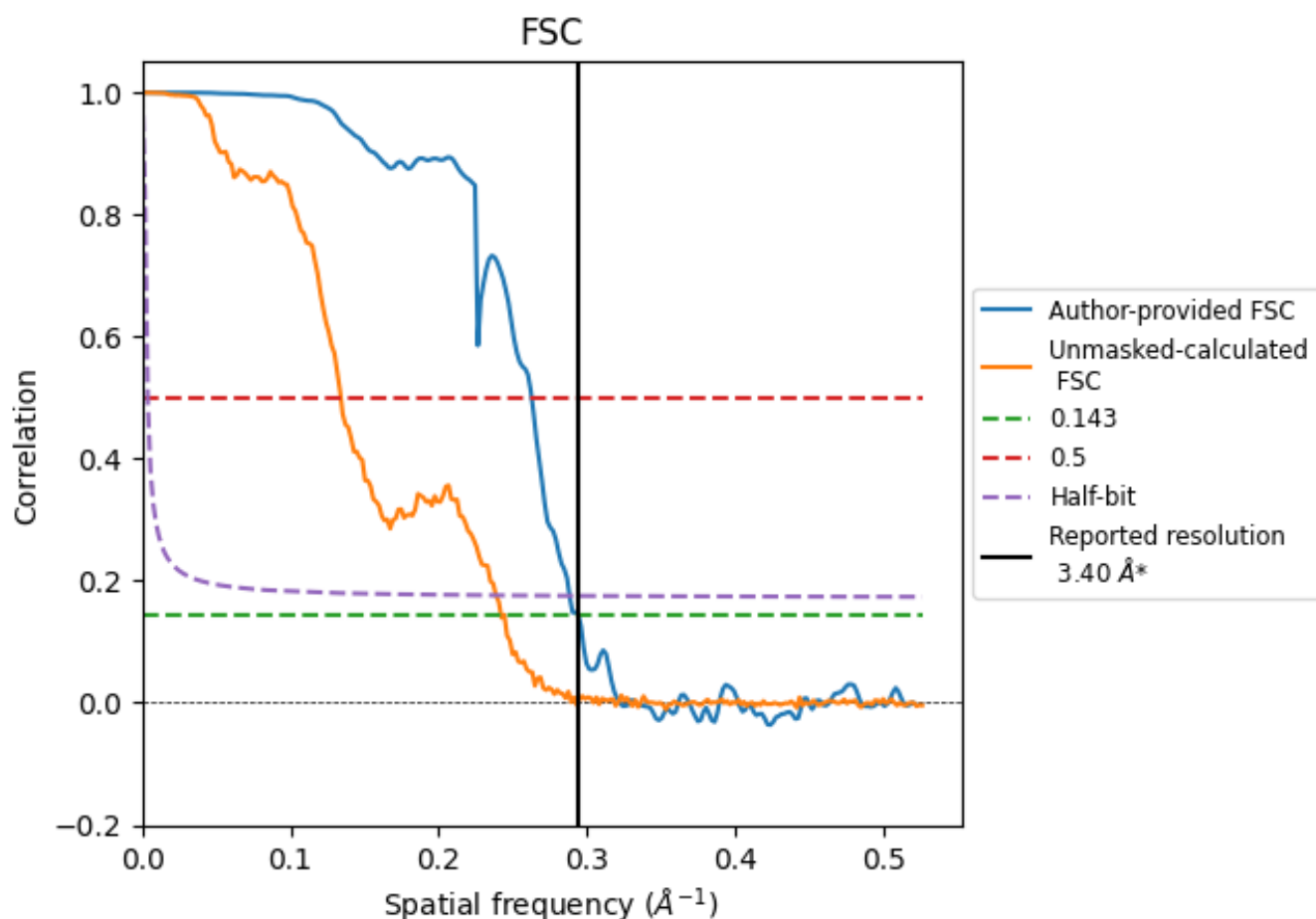


*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.40	3.81	3.47
Unmasked-calculated*	4.13	7.46	4.19

*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 4.13 differs from the reported value 3.4 by more than 10 %

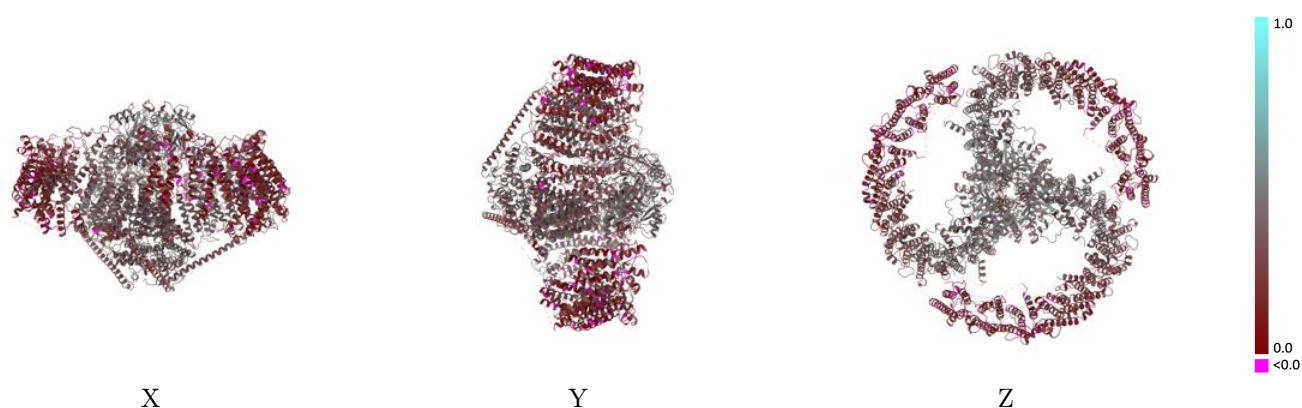
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64385 and PDB model 9UOY. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

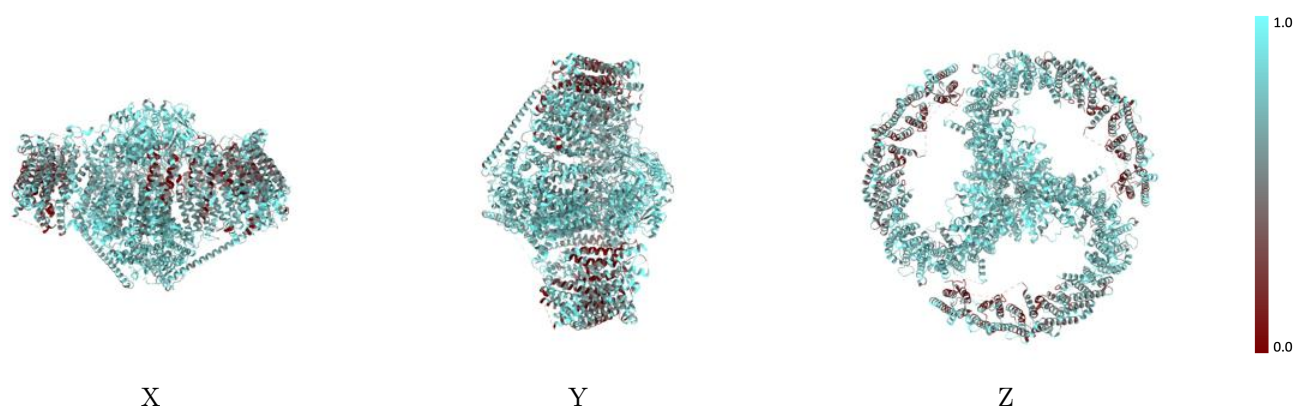
This section was not generated.

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



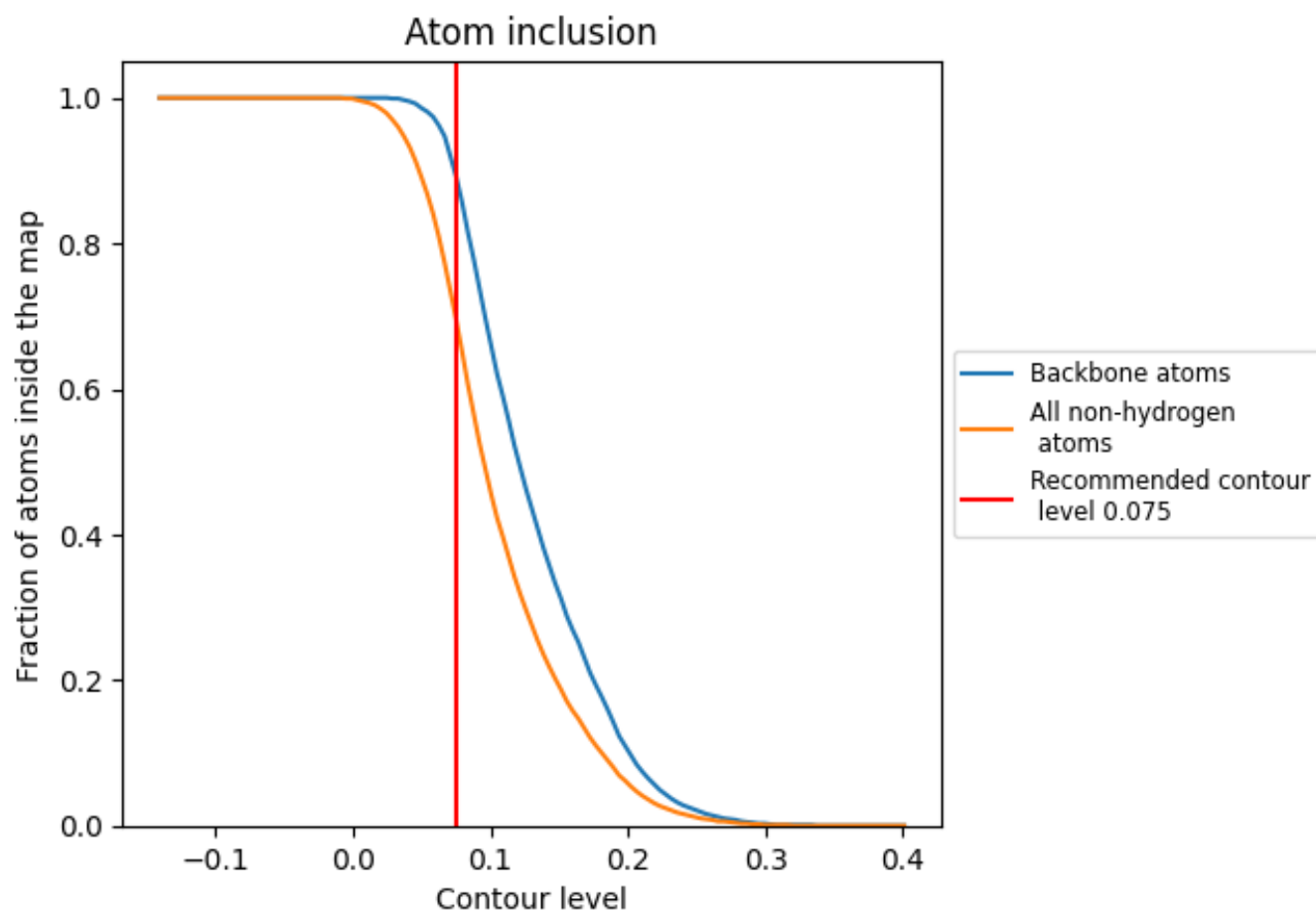
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.075).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 70% 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 (0.075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6960	0.2980
A	0.6960	0.2970
B	0.6960	0.2980
C	0.6970	0.2980

