



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 03:14 PM UTC

PDB ID : 7PQH / pdb_00007pqh
EMDB ID : EMD-13594
Title : Cryo-EM structure of *Saccharomyces cerevisiae* TOROID (TORC1 Organized in Inhibited Domains).
Authors : Felix, J.; Prouteau, M.; Bourgoint, C.; Bonadei, L.; Desfosses, A.; Gabus, C.; Sadian, Y.; Savvides, S.N.; Gutsche, I.; Loewith, R.
Deposited on : 2021-09-17
Resolution : 3.87 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

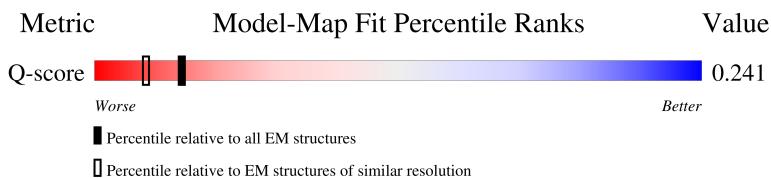
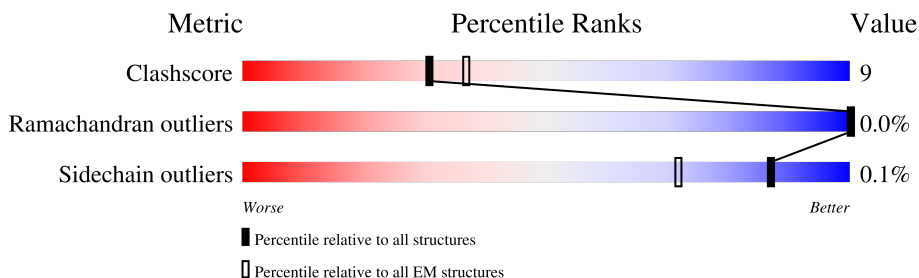
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

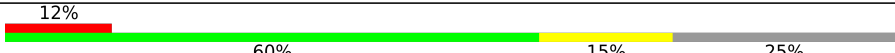
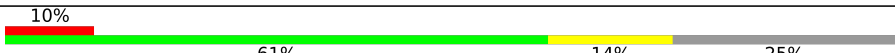
The reported resolution of this entry is 3.87 Å.

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	8831 (3.37 - 4.37)

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	1608	
1	B	1608	
1	G	1608	
1	J	1608	

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Mol	Chain	Length	Quality of chain
2	C	303	
2	D	303	
2	I	303	
2	L	303	
3	E	2474	
3	F	2474	
3	H	2474	
3	K	2474	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 102671 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 Target of rapamycin complex 1 subunit KOG1, Target of rapamycin complex 1 subunit Kog1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1209	Total	C	N	O	S	0	0
			9693	6225	1638	1784	46		
1	B	1208	Total	C	N	O	S	0	0
			9686	6223	1636	1781	46		
1	G	1212	Total	C	N	O	S	0	0
			9705	6239	1639	1781	46		
1	J	1213	Total	C	N	O	S	0	0
			9711	6242	1641	1782	46		

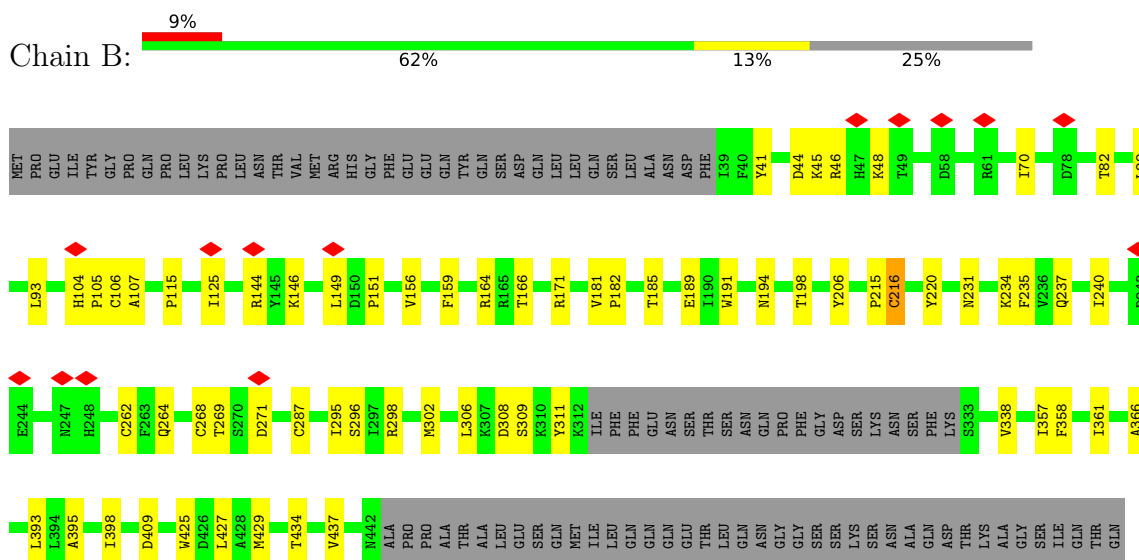
- Molecule 2 is a protein called Target of rapamycin complex subunit LST8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	300	Total	C	N	O	S	0	0
			2366	1465	430	460	11		
2	D	300	Total	C	N	O	S	0	0
			2366	1465	430	460	11		
2	I	300	Total	C	N	O	S	0	0
			2366	1465	430	460	11		
2	L	300	Total	C	N	O	S	0	0
			2366	1465	430	460	11		

- Molecule 3 is a protein called Serine/threonine-protein kinase TOR2.

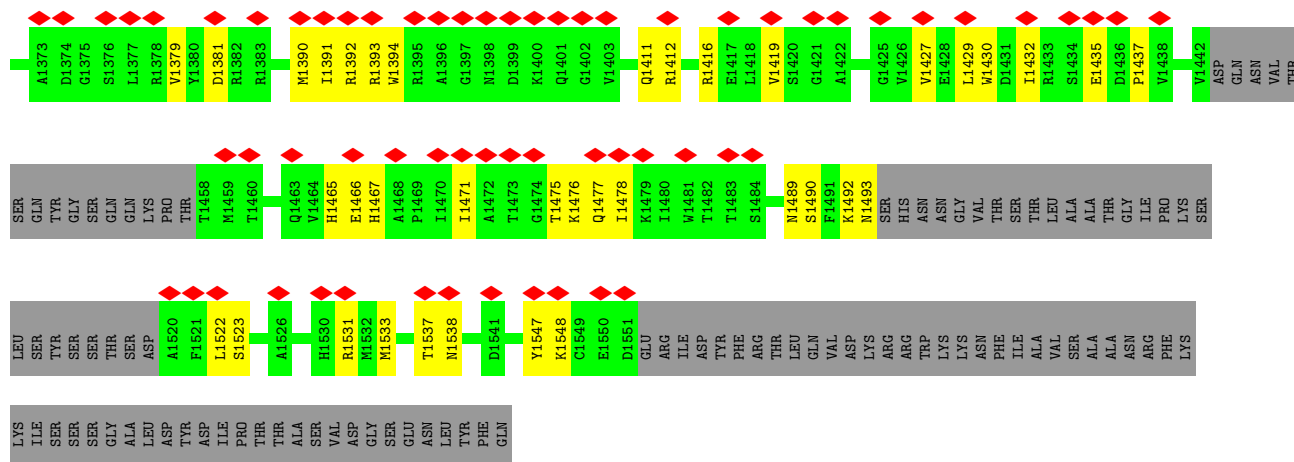
Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	2238	Total	C	N	O	S	0	0
			17910	11494	3058	3275	83		
3	F	2238	Total	C	N	O	S	0	0
			17904	11491	3055	3275	83		
3	H	1157	Total	C	N	O	S	0	0
			9299	5981	1588	1684	46		
3	K	1157	Total	C	N	O	S	0	0
			9299	5981	1588	1684	46		

- Molecule 1: Target of rapamycin complex 1 subunit KOG1,Target of rapamycin complex 1 subunit Kog1

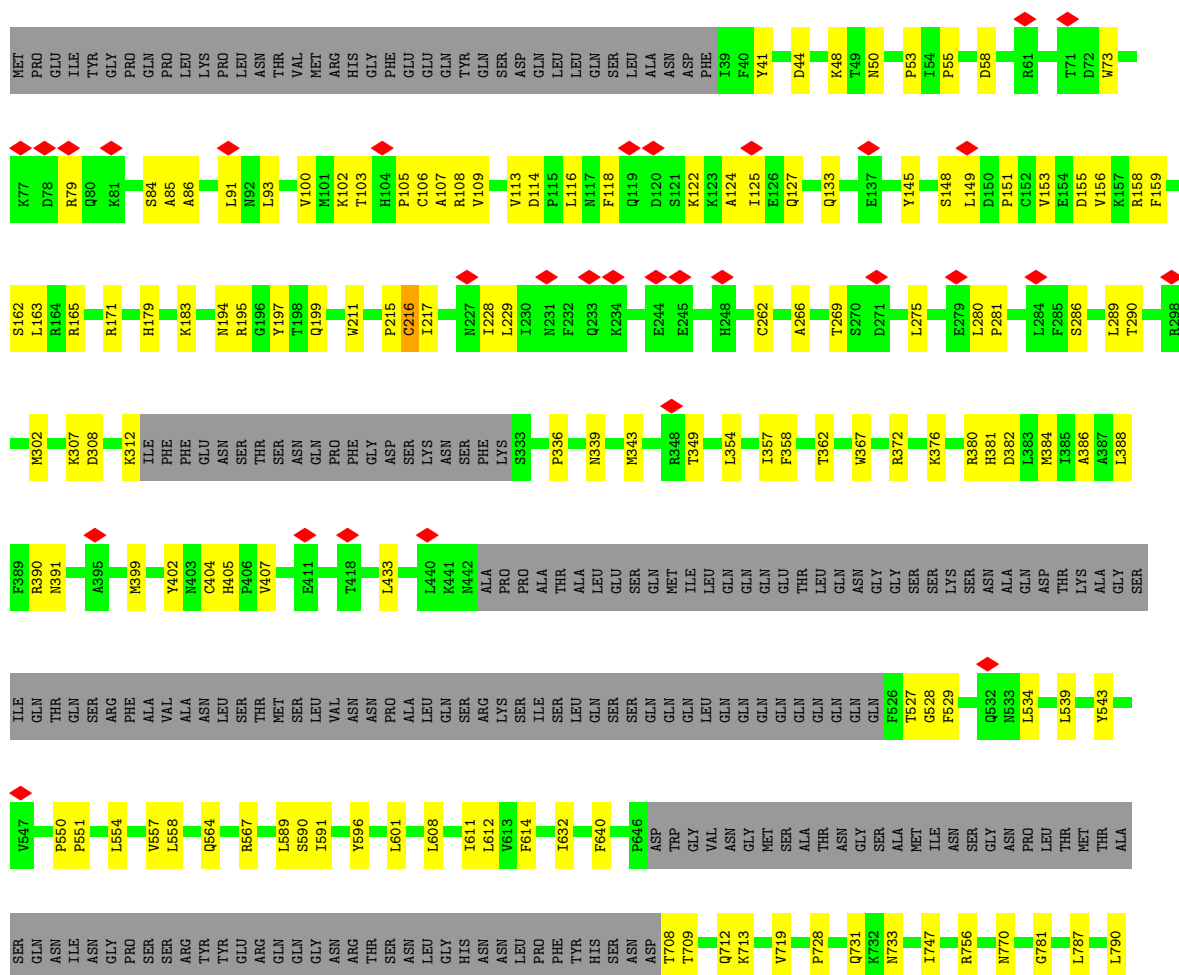






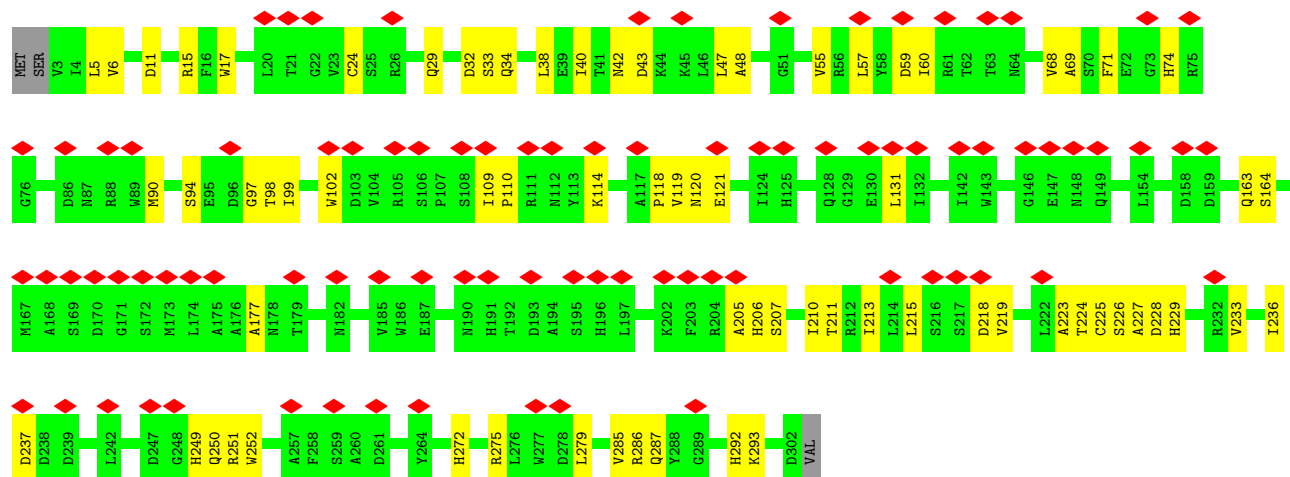
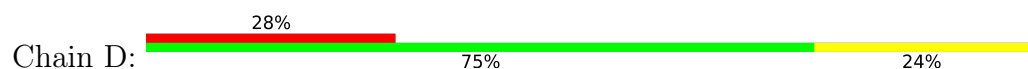


- Molecule 1: Target of rapamycin complex 1 subunit KOG1, Target of rapamycin complex 1 subunit Kog1

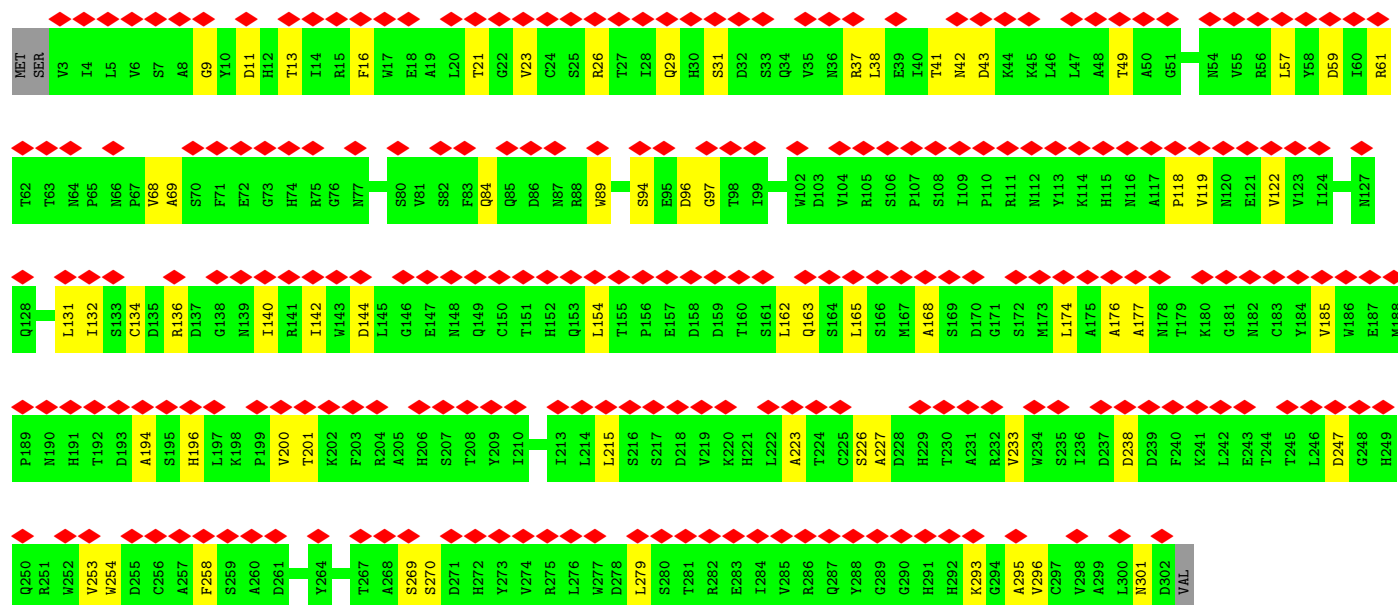
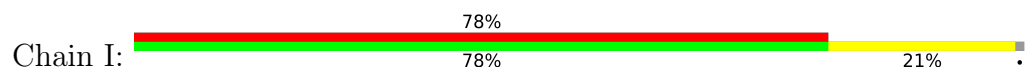




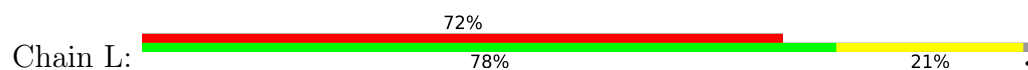
• Molecule 2: Target of rapamycin complex subunit LST8

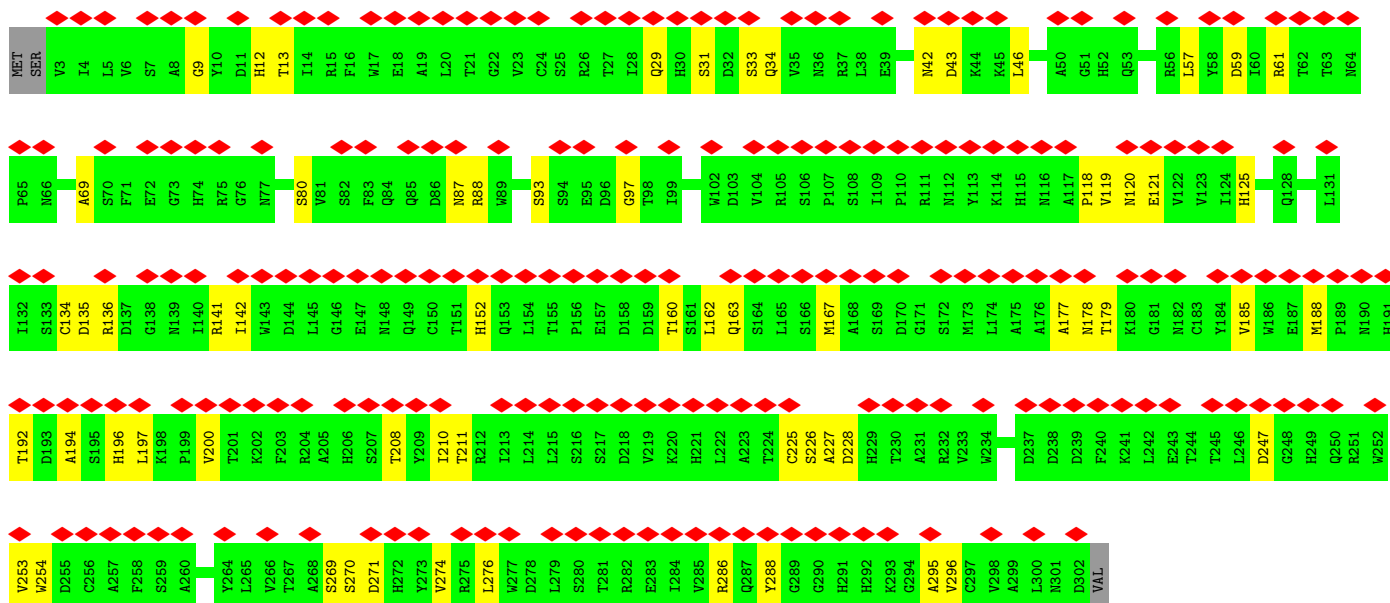


• Molecule 2: Target of rapamycin complex subunit LST8

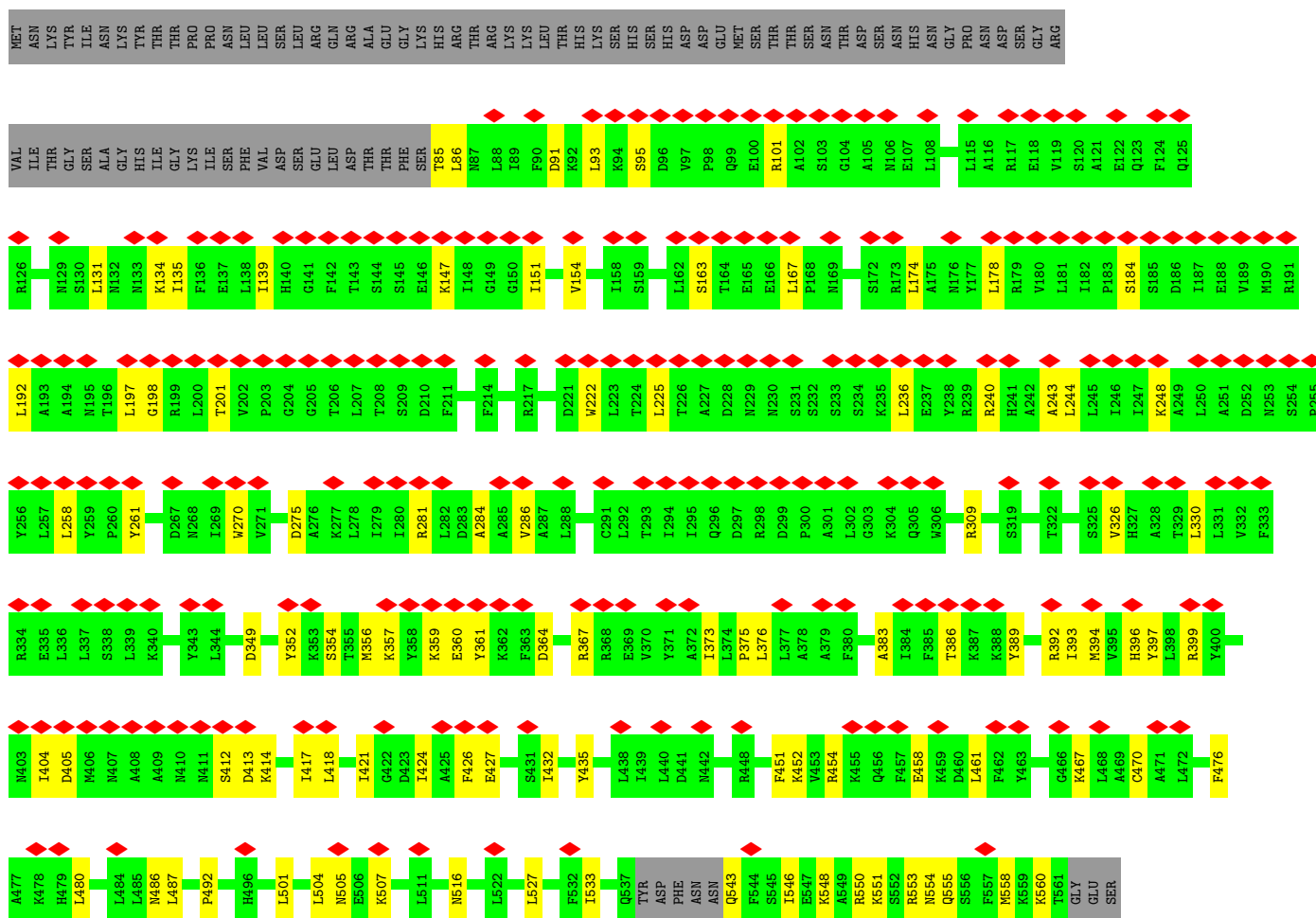


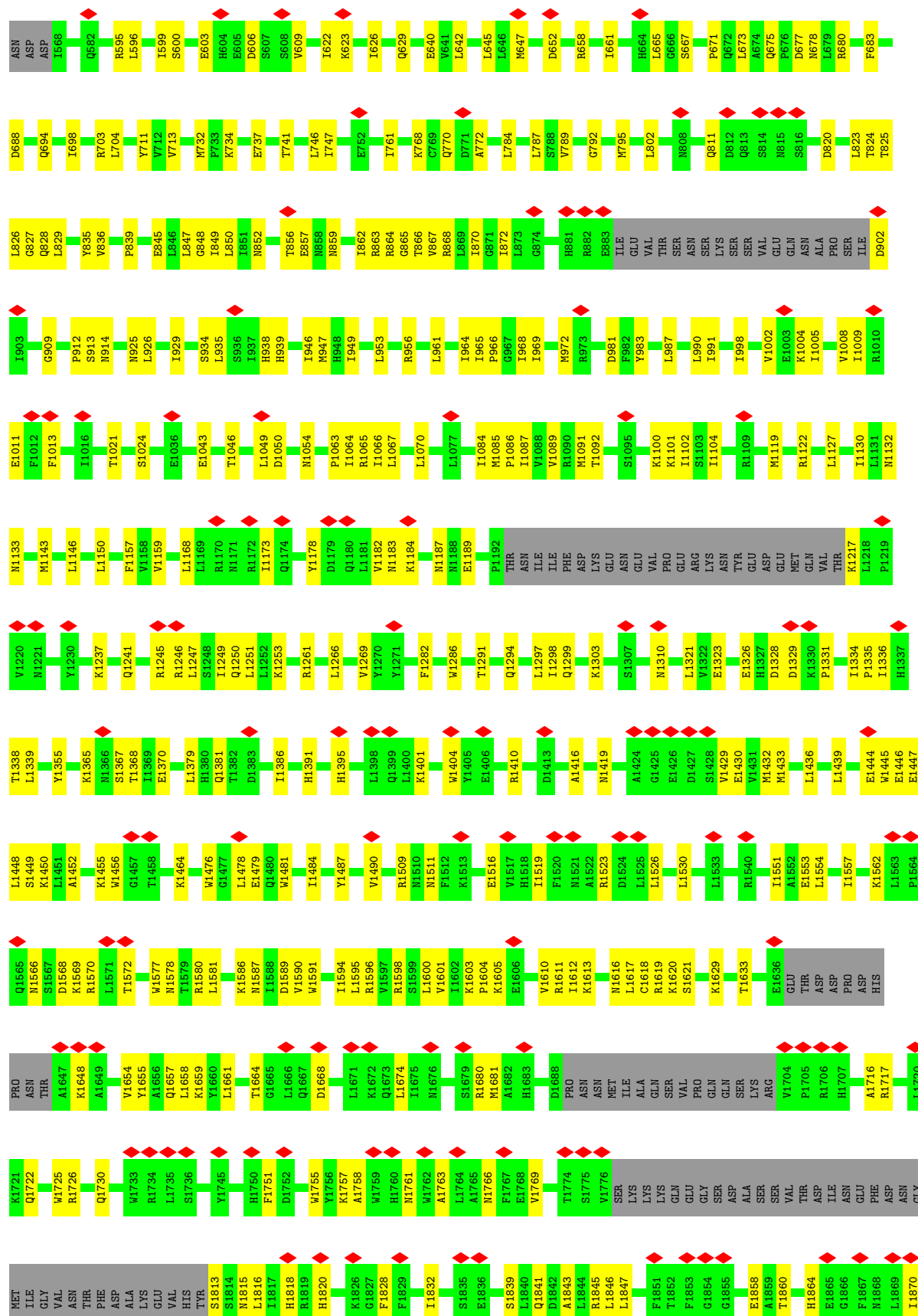
• Molecule 2: Target of rapamycin complex subunit LST8

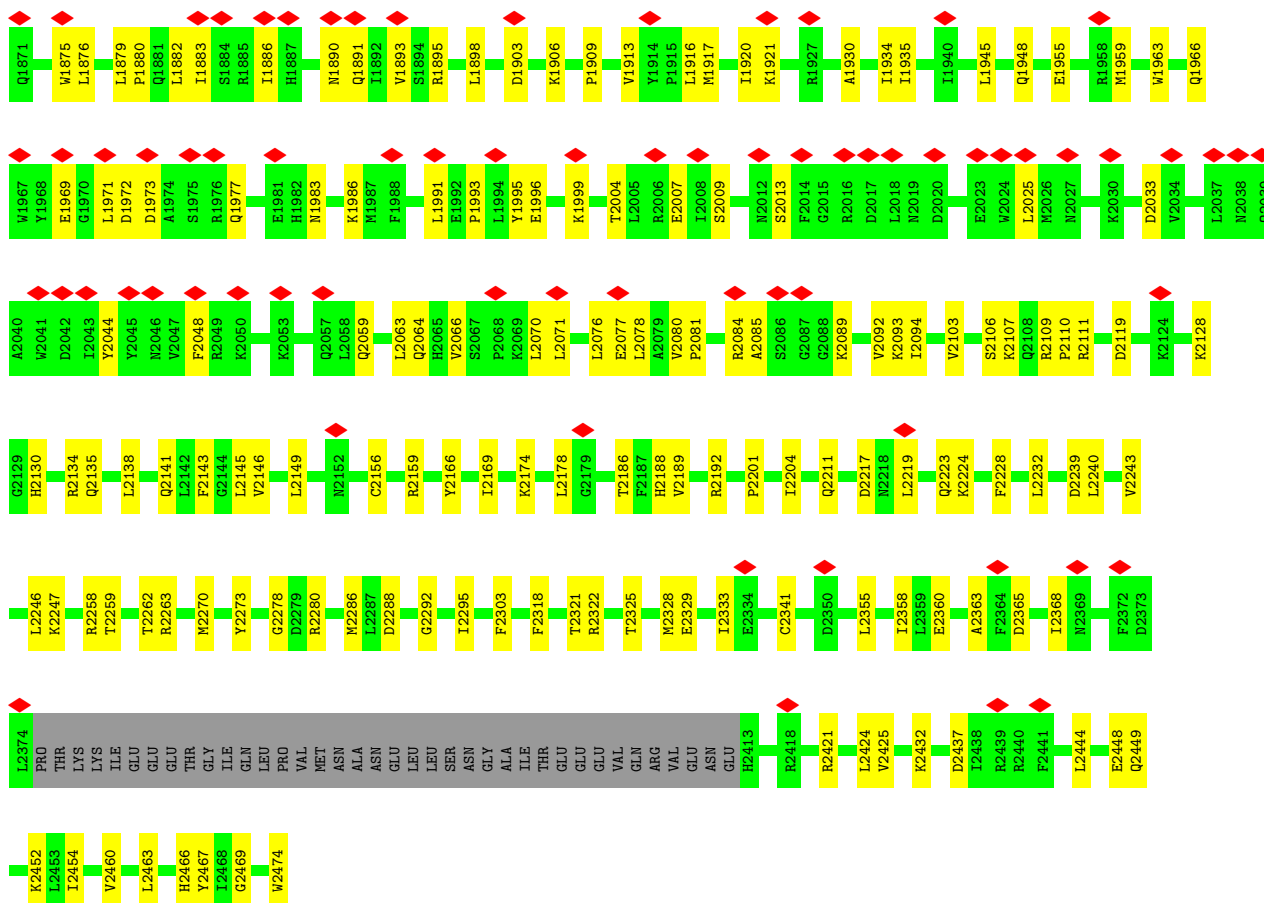




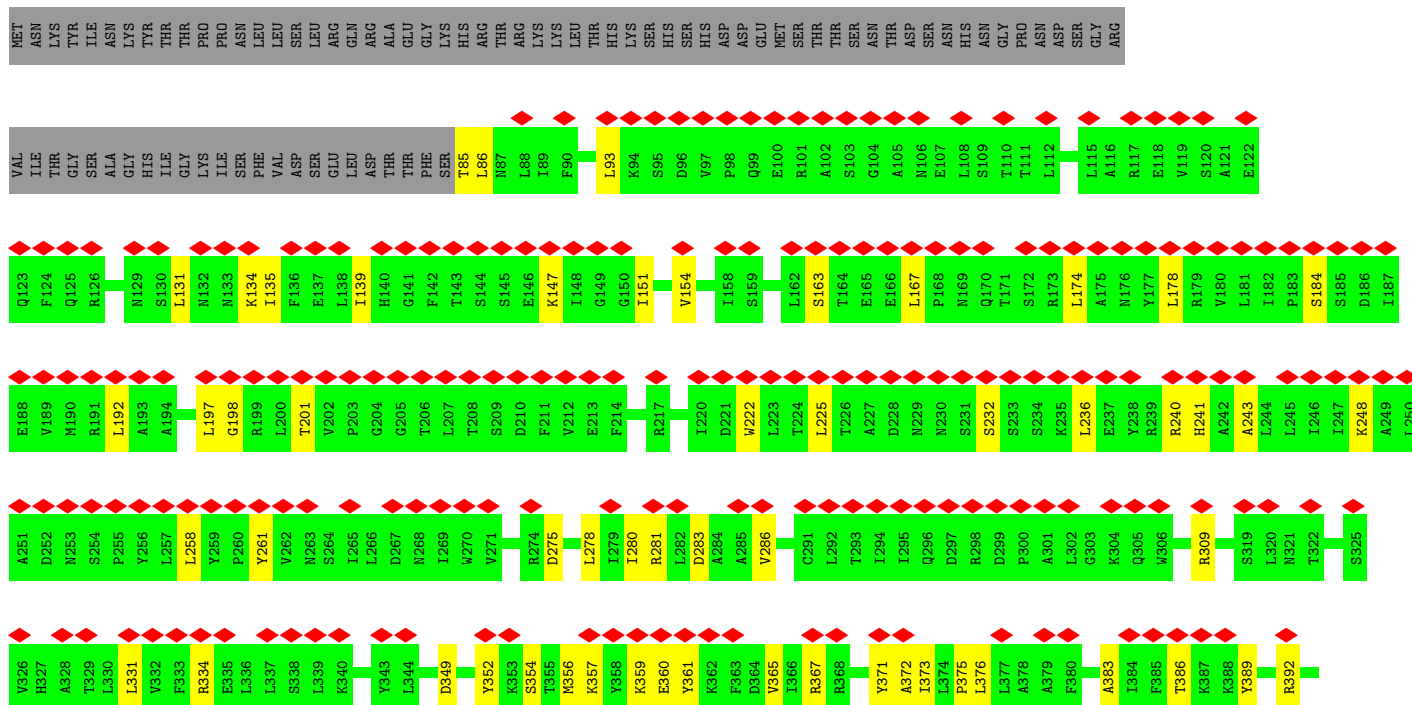
• Molecule 3: Serine/threonine-protein kinase TOR2

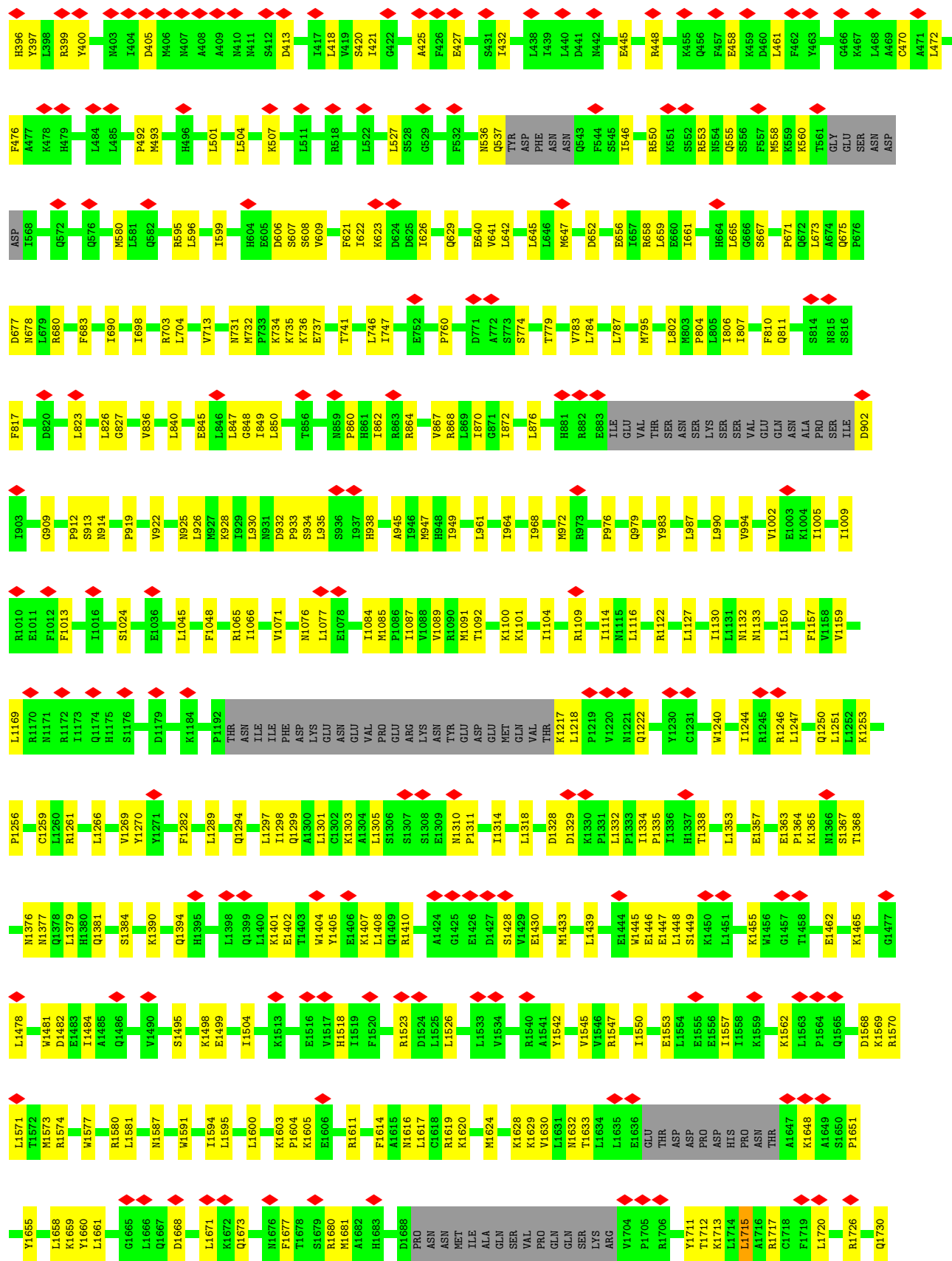






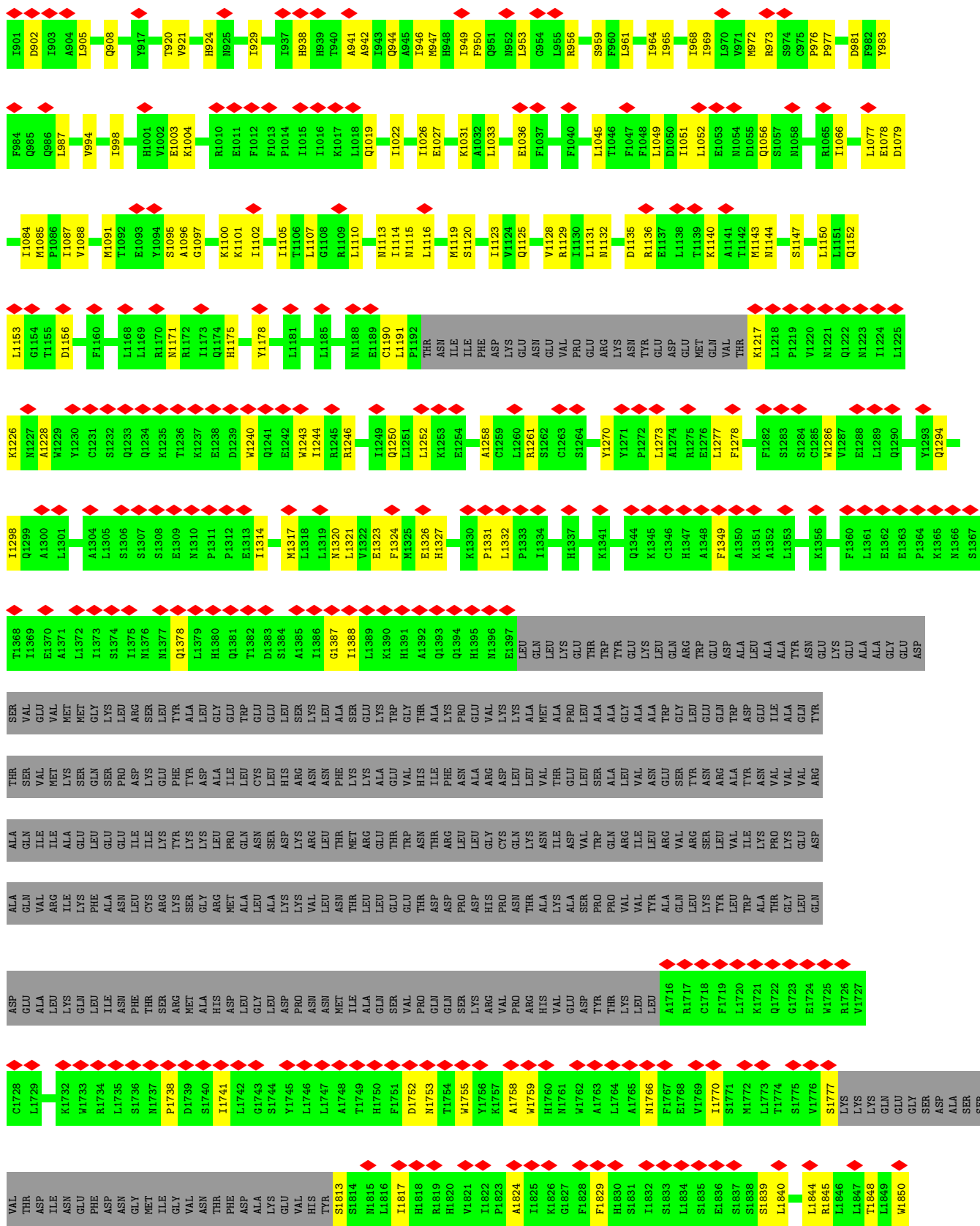
• Molecule 3: Serine/threonine-protein kinase TOR2

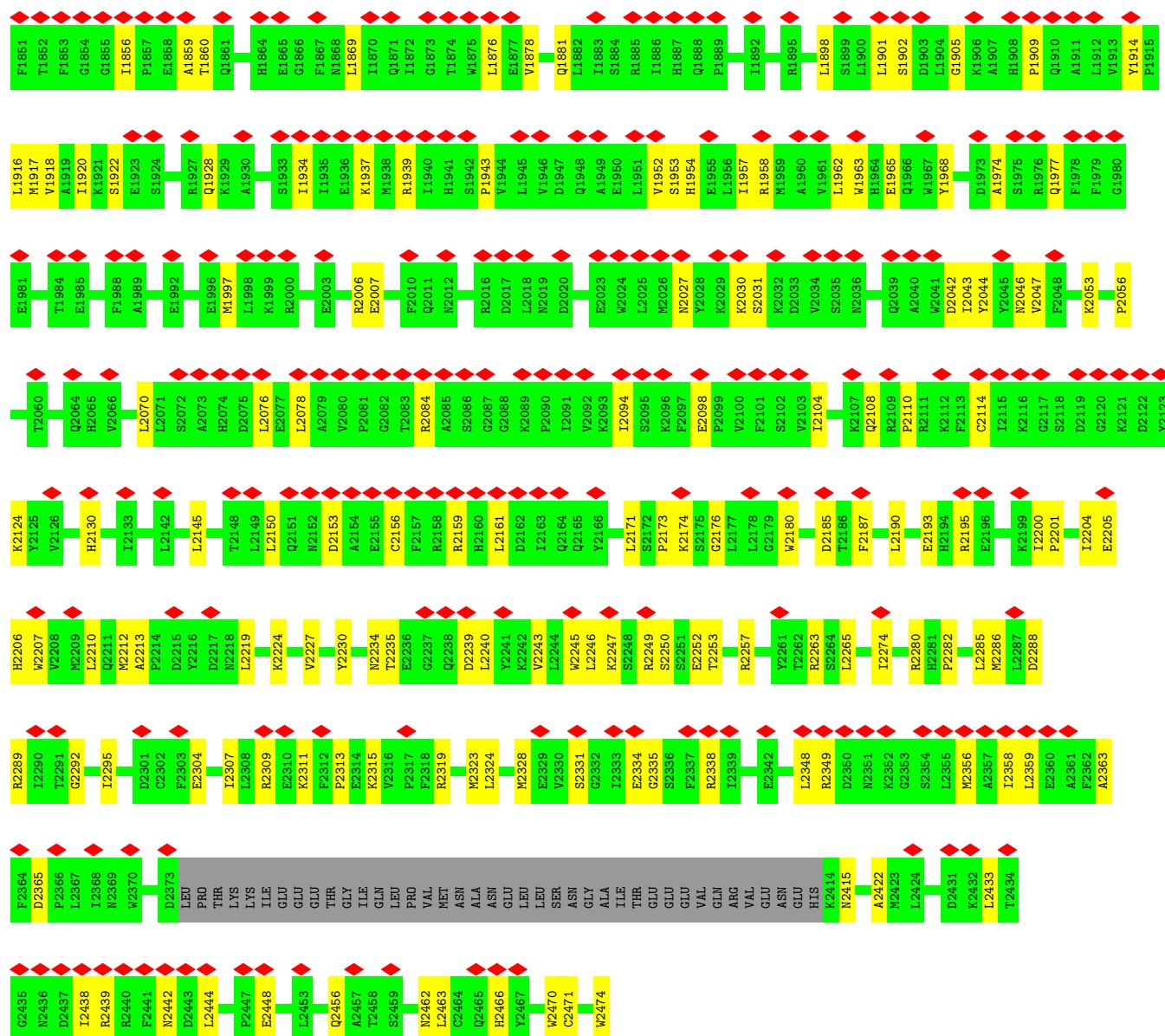






T2262	H2188	F2048	K2117	G1980	L1912	L1847	GLY	ALA	LYS	ASN	ASN	GLU	ALA
R2263	V2189	R2049	G2117	E1981	V1913	L1847	SER	THR	PRO	VAL	VAL	THR	ALA
A2266	I2191	K2050	S2118	H1982	Y1914	W1850	ASP	GLY	LYS	GLY	GLY	THR	GLY
W2270	E2193	K2053	D2119	H1983	Y1915	F1851	SER	GLN	ASP	ASP	ASP	SER	SER
V2273	R2192	Q2054	G2120	T1984	L1916	T1852	VAL	ALA	ALA	ALA	ALA	VAL	VAL
I2274	E2194	L2055	K2121	E1985	V1917	W1853	THR	GLU	GLN	GLN	GLN	SER	GLU
R2280	R2195	P2056	D2122	K1986	Y1918	G1854	ASP	ALA	VAL	VAL	VAL	MET	MET
P2281	E2196	Q2059	Y2123	M1987	A1919	G1854	THR	LEU	ARG	ARG	ARG	LYS	LYS
S2283	A2197	T2060	Y2123	F1988	I1920	G1855	ASN	GLN	LYS	LYS	LYS	SER	MET
W2284	K2198	T2061	H2130	A1990	S1922	I1856	GLU	LEU	PHE	PHE	ALA	SER	GLY
L2285	R2199	Q2064	R2134	L1991	E1923	P1857	ASP	ASN	ASN	GLY	GLY	PRO	LEU
W2286	I2200	H2065	Q2135	P1993	S1924	E1858	ASP	PHE	LEU	LEU	LEU	ASP	ARG
H2287	E2203	V2066	D2136	L1994	R1927	A1859	GLY	THR	THR	THR	THR	LYS	SER
D2288	H2206	S2072	S2137	Y1995	Q1928	T1860	MET	ARG	ARG	LYS	LYS	PHE	TYR
R2289	W2207	A2073	V2138	M1997	K1929	H1864	GLY	VAL	GLY	LYS	LYS	TYR	ALA
T2290	W2207	H2074	W2139	L1998	A1930	E1865	ASN	ASN	VAL	VAL	LEU	ASP	LEU
T2291	M2209	D2075	H2140	K1999	A1931	G1866	THR	THR	THR	THR	LEU	PRO	GLY
G2292	M2209	L2076	W2143	R2000	S1933	F1867	ASP	PHE	ALA	ALA	ALA	LEU	TRP
D2301	W2212	E2077	V2146	E2003	I1935	N1868	LYS	LYS	ASP	LEU	LEU	SER	GLU
C2302	D2215	L2078	W2147	L2016	E1936	L1869	GLU	PRO	PRO	ASP	LEU	HIS	LEU
F2303	Y2216	A2079	T2148	D2017	E1937	I1870	VAL	ASN	VAL	VAL	VAL	ARG	SER
R2309	D2217	V2080	L2149	I2008	K1937	Q1871	THR	ASN	ASN	ASN	ASN	ASN	LYS
F2310	W2218	P2081	L2150	S2009	H1938	I1872	THR	THR	THR	THR	THR	PHE	ALA
T2311	L2219	G2082	T2151	Q2011	R1939	G1873	PHE	ILE	THR	THR	THR	LYS	SER
K2224	K2224	T2083	W2152	N2012	I1940	T1874	ALA	ALA	LEU	LEU	LEU	ARG	GLY
V2227	V2227	A2084	D2153	R2016	H1941	W1875	LYS	VAL	LYS	LYS	LYS	LEU	GLU
L2232	L2232	R2085	A2154	D2017	S1942	L1876	GLU	ASN	ASN	ASN	ASN	HIS	LEU
T2235	E2236	S2086	E2155	L2018	P1943	E1877	VAL	THR	THR	THR	THR	THR	ALA
G2237	G2237	G2088	C2156	N2019	V1944	V1878	THR	GLN	ASP	ASP	ASP	ILE	ALA
Q2238	Q2238	K2089	F2157	W2019	V1946	Q1881	VAL	GLN	PRO	PRO	PRO	THR	LYS
D2239	L2240	R2090	R2158	D2020	D1947	L1882	LYS	SER	ASN	ASN	ASN	ASN	LYS
L2241	Y2241	P2091	R2159	E2023	Q1948	I1883	THR	THR	THR	THR	THR	THR	ALA
K2242	K2242	L2091	H2160	W2024	A1949	S1884	VAL	VAL	VAL	VAL	VAL	VAL	ALA
L2244	L2244	V2092	L2161	L2025	E1950	R1885	ARG	ARG	ARG	ARG	ARG	ARG	ALA
W2245	W2245	K2093	D2162	L2026	L1951	I1886	THR	THR	THR	THR	THR	THR	LEU
K2247	K2247	S2095	I2163	N2027	V1952	H1887	LYS	LYS	LYS	LYS	LYS	VAL	LEU
S2246	S2246	K2096	Q2164	Y2028	S1953	Q1888	ASP	ASP	ASP	ASP	ASP	THR	ALA
R2249	R2249	P2097	Y2166	K2028	H1954	P1889	THR	THR	THR	THR	THR	SER	ALA
S2250	S2250	E2098	P2167	K2030	L1956	I1892	PRO	PRO	PRO	PRO	PRO	VAL	ALA
T2253	T2253	P2099	A2168	D2033	I1957	R1895	LEU	LEU	LEU	LEU	LEU	VAL	ALA
W2254	W2254	V2100	I2169	W2034	A1960	L1898	THR	THR	THR	THR	THR	THR	ALA
L2255	L2255	F2101	P2170	S2035	V1961	S1899	VAL	VAL	VAL	VAL	VAL	VAL	ALA
E2256	E2256	S2102	P2173	N2036	L1962	L1900	GLN	GLN	GLN	GLN	GLN	GLN	ARG
R2257	R2257	V2103	K2174	W2037	W1963	L1901	LYS	LYS	LYS	LYS	LYS	LYS	ARG
T2258	T2258	I2104	R2174	N2038	Q1966	S1902	THR	THR	THR	THR	THR	THR	SER
K2338	K2338	K2107	L2178	Q2039	Q1966	D1903	ASN	ASN	ASN	ASN	ASN	ASN	ASN
L2339	L2339	Q2108	G2179	A2040	D1973	L1904	THR	THR	THR	THR	THR	THR	THR
T2340	T2340	R2109	W2180	W2041	A1974	Q1905	VAL	VAL	VAL	VAL	VAL	VAL	GLY
C2341	C2341	P2110	P2110	D2042	S1975	K1906	GLY	GLY	GLY	GLY	GLY	GLY	GLY
E2342	E2342	R2111	R2111	T2043	S1976	A1907	LYS	LYS	LYS	LYS	LYS	LYS	GLY
		K2112	K2112	Y2044	R1976	H1908	THR	THR	THR	THR	THR	THR	THR
		F2113	F2113	W2045	Q1977	P1909	ASN	ASN	ASN	ASN	ASN	ASN	ASN
		C2114	C2114	N2046	F1978	Q1910	LEU	LEU	LEU	LEU	LEU	LEU	LEU
		T2115	T2115	V2047	F1979	A1911	TRP	TRP	TRP	TRP	TRP	TRP	TRP





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D2	Depositor
Number of particles used	218872	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	37000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.344	Depositor
Minimum map value	-0.057	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	405.0, 405.0, 405.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.18	0/9911	0.47	0/13437
1	B	0.19	0/9904	0.47	1/13427 (0.0%)
1	G	0.20	0/9923	0.47	4/13455 (0.0%)
1	J	0.20	0/9929	0.46	2/13463 (0.0%)
2	C	0.16	0/2422	0.47	0/3302
2	D	0.16	0/2422	0.45	0/3302
2	I	0.15	0/2422	0.44	2/3302 (0.1%)
2	L	0.15	0/2422	0.44	0/3302
3	E	0.19	0/18271	0.50	3/24746 (0.0%)
3	F	0.19	0/18265	0.50	2/24739 (0.0%)
3	H	0.18	0/9509	0.48	1/12893 (0.0%)
3	K	0.17	0/9509	0.47	1/12893 (0.0%)
All	All	0.19	0/104909	0.48	16/142261 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	J	0	1
All	All	0	3

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	998	ILE	N-CA-C	-7.33	105.39	111.91
2	I	238	ASP	CA-C-N	5.98	132.96	121.54
2	I	238	ASP	C-N-CA	5.98	132.96	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	1715	LEU	CA-CB-CG	5.46	135.41	116.30
1	G	60	GLN	N-CA-CB	5.45	118.23	110.16
3	F	2368	ILE	N-CA-C	-5.31	108.67	113.71
1	G	630	GLU	N-CA-C	-5.30	106.68	112.72
1	G	1107	GLY	CA-C-N	5.21	126.35	119.84
1	G	1107	GLY	C-N-CA	5.21	126.35	119.84
3	K	2193	GLU	N-CA-CB	5.20	118.34	110.28
1	B	865	GLU	N-CA-CB	5.15	118.80	110.40
3	E	1572	THR	CA-C-N	-5.11	114.26	122.08
3	E	1572	THR	C-N-CA	-5.11	114.26	122.08
1	J	1107	GLY	CA-C-N	5.09	126.20	119.84
1	J	1107	GLY	C-N-CA	5.09	126.20	119.84
3	E	1011	GLU	N-CA-CB	5.05	118.63	110.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	216	CYS	Peptide
1	B	216	CYS	Peptide
1	J	216	CYS	Peptide

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	9693	0	9655	142	0
1	B	9686	0	9656	134	0
1	G	9705	0	9676	164	0
1	J	9711	0	9683	157	0
2	C	2366	0	2251	47	0
2	D	2366	0	2251	43	0
2	I	2366	0	2251	37	0
2	L	2366	0	2251	38	0
3	E	17910	0	18236	366	0
3	F	17904	0	18225	347	0
3	H	9299	0	9374	186	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	9299	0	9374	176	0
All	All	102671	0	102883	1822	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 9.

All (1822) 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:J:632:ILE:HD11	1:J:733:ASN:HD22	1.26	0.97
1:J:1105:LYS:HZ1	1:J:1306:LEU:HD11	1.36	0.90
1:G:630:GLU:N	1:G:630:GLU:OE1	2.08	0.85
3:H:971:VAL:O	3:H:975:CYS:HB3	1.80	0.82
3:E:2286:MET:HB2	3:E:2295:ILE:HB	1.62	0.82
3:E:1680:ARG:NH1	3:E:1681:MET:SD	2.57	0.78
3:F:1619:ARG:HH12	3:F:1659:LYS:HB3	1.49	0.78
3:K:2247:LYS:HB3	3:K:2289:ARG:HH12	1.47	0.78
1:B:585:VAL:HG11	1:B:622:ILE:HG13	1.68	0.76
1:J:1105:LYS:NZ	1:J:1306:LEU:HD11	2.01	0.75
3:K:1777:SER:HG	3:K:1813:SER:N	1.85	0.75
3:E:626:ILE:HA	3:E:629:GLN:HE21	1.51	0.75
1:J:1106:LYS:HD2	1:J:1106:LYS:N	2.03	0.74
1:J:1105:LYS:NZ	1:J:1306:LEU:CD1	2.51	0.73
3:H:1939:ARG:HH21	3:H:1943:PRO:HA	1.54	0.73
3:H:1326:GLU:HG2	3:H:1331:PRO:HB3	1.71	0.72
3:E:824:THR:HG22	3:E:828:GLN:HE22	1.54	0.72
2:L:12:HIS:HE1	2:L:31:SER:HA	1.54	0.71
2:L:57:LEU:HB2	2:L:69:ALA:HB3	1.72	0.71
1:B:1482:THR:HG22	1:B:1484:SER:H	1.53	0.71
3:F:1619:ARG:HE	3:F:1620:LYS:HD2	1.54	0.71
1:B:1081:LEU:O	1:B:1085:GLU:HG2	1.90	0.71
1:A:750:SER:O	1:A:756:ARG:NH2	2.24	0.70
3:H:1777:SER:HG	3:H:1813:SER:N	1.88	0.70
1:B:811:GLY:H	1:B:922:ARG:HH12	1.40	0.70
3:E:2063:LEU:HD22	3:E:2071:LEU:HD12	1.74	0.69
1:J:632:ILE:CD1	1:J:733:ASN:HD22	2.02	0.69
1:B:237:GLN:HA	1:B:240:ILE:HG12	1.73	0.69
1:J:882:ASP:CG	1:J:885:LYS:HB2	2.18	0.69
3:F:626:ILE:HA	3:F:629:GLN:HE21	1.58	0.69
3:H:2134:ARG:HH12	3:H:2138:LEU:HD23	1.57	0.69
3:K:1963:TRP:HE1	3:K:1997:MET:HE1	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:219:VAL:HG12	2:C:236:ILE:HG21	1.76	0.68
1:G:1264:ASN:H	1:G:1319:GLN:HE22	1.42	0.68
1:J:1105:LYS:HE2	1:J:1306:LEU:HD12	1.74	0.68
3:E:533:ILE:HG13	3:E:543:GLN:HE21	1.59	0.68
3:F:1717:ARG:HH21	3:F:1720:LEU:HD13	1.57	0.68
1:A:1176:ARG:O	1:A:1180:ASN:ND2	2.26	0.68
1:J:1214:LEU:HB2	1:J:1227:ALA:HB3	1.76	0.68
3:E:658:ARG:HA	3:E:661:ILE:HG22	1.75	0.68
3:E:961:LEU:HA	3:E:964:ILE:HG22	1.76	0.67
3:E:424:ILE:HG13	3:E:432:ILE:HD11	1.76	0.67
3:K:1120:SER:HA	3:K:1123:ILE:HG12	1.76	0.67
2:I:9:GLY:HA2	2:I:296:VAL:HG22	1.75	0.67
1:J:302:MET:HE2	1:J:336:PRO:HD3	1.75	0.67
3:F:2134:ARG:HH12	3:F:2367:LEU:HB2	1.59	0.67
3:E:1860:THR:O	3:E:1864:HIS:ND1	2.23	0.67
3:H:1085:MET:HG3	3:H:1119:MET:HG3	1.77	0.67
1:J:41:TYR:O	1:J:1264:ASN:ND2	2.28	0.67
3:E:1447:GLU:HA	3:E:1450:LYS:HG2	1.77	0.66
3:F:546:ILE:HG12	3:F:596:LEU:HD23	1.76	0.66
3:K:1840:LEU:HD13	3:K:1878:VAL:HG22	1.77	0.66
3:K:2053:LYS:O	3:K:2056:PRO:HD2	1.95	0.66
3:E:867:VAL:HA	3:E:870:ILE:HG12	1.76	0.66
3:F:972:MET:HE1	3:F:983:TYR:HB3	1.77	0.66
2:I:122:VAL:HB	2:I:131:LEU:HD11	1.75	0.66
3:F:658:ARG:HA	3:F:661:ILE:HG22	1.76	0.66
3:E:1587:ASN:HB2	3:E:1590:VAL:HG12	1.77	0.66
3:E:2186:THR:HG22	3:E:2188:HIS:H	1.59	0.66
3:K:1097:GLY:HA2	3:K:1100:LYS:HB2	1.77	0.66
1:J:1105:LYS:HZ1	1:J:1306:LEU:CD1	2.05	0.66
3:E:947:MET:HE1	3:E:990:LEU:HG	1.78	0.66
1:B:1479:LYS:HZ3	1:B:1487:LEU:HD13	1.60	0.66
1:G:929:VAL:HG11	1:G:1078:PHE:HB2	1.77	0.66
3:E:1581:LEU:HD13	3:E:1594:ILE:HD11	1.77	0.65
3:H:1228:ALA:O	3:H:1243:TRP:NE1	2.28	0.65
3:H:2047:VAL:HA	3:H:2050:LYS:HG2	1.78	0.65
3:K:2201:PRO:HG2	3:K:2204:ILE:HB	1.78	0.65
1:A:264:GLN:HB2	1:A:409:ASP:HB2	1.79	0.65
3:E:2110:PRO:HB3	3:E:2128:LYS:HG2	1.78	0.65
1:G:1478:ILE:HG12	1:G:1522:LEU:HD11	1.78	0.65
2:C:118:PRO:HG2	2:C:136:ARG:HE	1.61	0.65
3:E:1523:ARG:HH21	3:E:1526:LEU:HD23	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:1122:ARG:HA	3:H:1125:GLN:HE22	1.62	0.65
3:E:1336:ILE:HD11	3:E:1355:TYR:HB3	1.78	0.65
3:K:953:LEU:HD13	3:K:956:ARG:HB3	1.77	0.65
3:H:2219:LEU:HD23	3:H:2224:LYS:HG2	1.77	0.65
3:F:1713:LYS:HZ2	3:F:1717:ARG:HG2	1.61	0.65
3:E:2288:ASP:HB3	3:E:2292:GLY:H	1.62	0.65
3:E:2262:THR:HG21	3:E:2329:GLU:HG2	1.79	0.65
1:A:1318:LEU:HD11	1:A:1365:GLY:HA2	1.79	0.64
1:B:819:LEU:HD13	1:B:822:GLN:NE2	2.12	0.64
1:B:822:GLN:O	1:B:822:GLN:HG2	1.94	0.64
1:G:399:MET:HB3	1:G:404:CYS:HB2	1.78	0.64
3:E:1127:LEU:HA	3:E:1130:ILE:HD12	1.79	0.64
3:F:922:VAL:HG11	3:F:1259:CYS:HB3	1.78	0.64
1:A:1261:LYS:HE3	1:A:1316:GLU:HA	1.79	0.64
1:B:181:VAL:HG13	1:B:191:TRP:HB2	1.78	0.64
3:K:1974:ALA:HA	3:K:1977:GLN:HE21	1.62	0.64
3:K:2265:LEU:HD21	3:K:2328:MET:HE1	1.79	0.64
1:A:898:LEU:HD21	1:A:967:VAL:HG22	1.80	0.64
3:E:824:THR:O	3:E:828:GLN:NE2	2.31	0.64
3:E:826:LEU:HA	3:E:829:LEU:HG	1.79	0.64
1:J:50:ASN:ND2	1:J:981:GLU:OE2	2.31	0.64
3:H:1097:GLY:HA2	3:H:1100:LYS:HB2	1.79	0.64
3:K:956:ARG:NH1	3:K:959:SER:OG	2.29	0.64
1:A:361:ILE:HD13	1:A:425:TRP:HB2	1.80	0.64
2:C:135:ASP:HB3	2:C:139:ASN:H	1.63	0.63
3:E:1009:ILE:O	3:E:1013:PHE:HB2	1.98	0.63
2:L:9:GLY:HA2	2:L:296:VAL:HG12	1.79	0.63
1:B:823:GLN:OE1	1:J:195:ARG:NH1	2.30	0.63
3:F:1439:LEU:HD13	3:F:1447:GLU:HG2	1.79	0.63
2:D:38:LEU:HD12	2:D:47:LEU:HD11	1.79	0.63
3:F:1983:ASN:HB2	3:F:1986:LYS:HG2	1.80	0.63
2:L:163:GLN:N	2:L:177:ALA:O	2.30	0.63
3:E:868:ARG:NH2	3:E:1523:ARG:HD3	2.14	0.63
3:H:2423:MET:SD	3:H:2427:LYS:NZ	2.72	0.63
1:B:1489:ASN:OD1	1:B:1490:SER:N	2.31	0.63
3:F:1246:ARG:O	3:F:1250:GLN:NE2	2.31	0.63
3:F:840:LEU:HG	3:F:876:LEU:HD21	1.81	0.63
2:C:205:ALA:O	2:C:206:HIS:ND1	2.32	0.63
3:E:1983:ASN:HB2	3:E:1986:LYS:HG2	1.80	0.63
3:F:774:SER:HB2	3:F:817:PHE:HB3	1.80	0.63
3:K:1922:SER:O	3:K:1928:GLN:NE2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:268:CYS:SG	1:B:269:THR:N	2.72	0.63
1:B:819:LEU:HD13	1:B:822:GLN:HE21	1.63	0.63
1:B:859:GLN:HA	1:B:862:MET:HG2	1.80	0.63
3:E:1452:ALA:HA	3:E:1455:LYS:HE3	1.80	0.63
3:E:1553:GLU:OE2	3:E:1577:TRP:NE1	2.32	0.63
1:G:106:CYS:SG	1:G:107:ALA:N	2.72	0.63
3:H:2288:ASP:HB3	3:H:2292:GLY:H	1.64	0.63
3:H:1918:VAL:HG13	3:H:2173:PRO:HD3	1.79	0.62
3:K:2124:LYS:HG3	3:K:2180:TRP:HB3	1.81	0.62
1:A:164:ARG:HH22	1:A:215:PRO:HD2	1.64	0.62
1:B:914:VAL:HG12	1:B:1140:LEU:HD23	1.81	0.62
3:E:1619:ARG:HH12	3:E:1659:LYS:HB3	1.63	0.62
1:G:747:ILE:HD12	1:G:756:ARG:HG2	1.81	0.62
2:C:59:ASP:HB2	2:C:68:VAL:HG21	1.81	0.62
1:G:298:ARG:NH1	1:G:336:PRO:O	2.32	0.62
1:G:361:ILE:HG23	1:G:421:MET:HE2	1.81	0.62
3:K:938:HIS:HB3	3:K:942:ALA:HB2	1.81	0.62
3:K:1246:ARG:O	3:K:1250:GLN:NE2	2.32	0.62
1:G:164:ARG:HH12	1:G:215:PRO:HD2	1.64	0.62
3:F:371:TYR:HB3	3:F:420:SER:HB3	1.82	0.62
1:G:1411:GLN:HB2	1:G:1416:ARG:HA	1.79	0.62
2:L:13:THR:HG22	2:L:29:GLN:HA	1.80	0.62
3:E:1439:LEU:HD13	3:E:1447:GLU:HG2	1.81	0.62
1:J:156:VAL:HA	1:J:159:PHE:HB3	1.82	0.62
1:J:539:LEU:O	1:J:543:TYR:HB2	1.99	0.62
3:F:1071:VAL:HB	3:F:1109:ARG:HD2	1.81	0.62
3:F:1996:GLU:O	3:F:2000:ARG:NH1	2.32	0.62
1:B:164:ARG:HH22	1:B:215:PRO:HD2	1.65	0.61
3:F:1818:HIS:ND1	3:F:1858:GLU:OE2	2.33	0.61
3:E:595:ARG:NH2	3:E:640:GLU:OE1	2.34	0.61
3:K:1323:GLU:HA	3:K:1326:GLU:HG2	1.81	0.61
3:K:1918:VAL:HG13	3:K:2173:PRO:HD3	1.81	0.61
3:F:947:MET:HE1	3:F:990:LEU:HG	1.82	0.61
1:J:372:ARG:NH1	1:J:590:SER:OG	2.32	0.61
1:J:1264:ASN:H	1:J:1319:GLN:NE2	1.98	0.61
1:J:1406:ASN:ND2	1:J:1459:MET:SD	2.72	0.61
2:C:213:ILE:HG12	2:C:224:THR:HG22	1.81	0.61
1:G:799:THR:HG23	1:G:911:GLU:HG3	1.81	0.61
3:K:953:LEU:HD22	3:K:956:ARG:HE	1.64	0.61
3:E:373:ILE:HA	3:E:376:LEU:HD12	1.82	0.61
3:K:1140:LYS:O	3:K:1144:ASN:ND2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:2145:LEU:HD22	3:K:2358:ILE:HG13	1.82	0.61
1:B:814:ASP:HA	1:B:817:VAL:HG12	1.83	0.61
1:G:171:ARG:HH12	1:G:262:CYS:HA	1.66	0.61
2:I:163:GLN:N	2:I:177:ALA:O	2.33	0.61
1:B:156:VAL:HA	1:B:159:PHE:HB3	1.83	0.61
3:F:732:MET:HE3	3:F:735:LYS:HG2	1.83	0.61
3:H:2108:GLN:OE1	3:H:2130:HIS:NE2	2.34	0.61
3:K:1003:GLU:OE1	3:K:1004:LYS:NZ	2.33	0.61
1:G:194:ASN:ND2	1:G:199:GLN:O	2.34	0.61
1:A:181:VAL:HG13	1:A:191:TRP:HB2	1.82	0.61
3:F:2456:GLN:O	3:F:2462:ASN:ND2	2.33	0.61
1:B:1191:LYS:HE2	1:B:1467:HIS:HB3	1.81	0.61
3:F:1390:LYS:HE2	3:F:1394:GLN:HE22	1.65	0.61
3:K:961:LEU:HA	3:K:964:ILE:HG12	1.80	0.61
1:B:1003:LEU:HD11	1:B:1074:LEU:HD21	1.81	0.60
3:E:2360:GLU:HA	3:E:2363:ALA:HB3	1.83	0.60
3:F:1365:LYS:NZ	3:F:1367:SER:OG	2.26	0.60
3:H:2319:ARG:NH2	3:H:2471:CYS:O	2.34	0.60
1:J:564:GLN:HG2	1:J:567:ARG:HH21	1.65	0.60
3:K:2309:ARG:NH1	3:K:2311:LYS:O	2.34	0.60
3:E:1557:ILE:HD12	3:E:1601:VAL:HG11	1.83	0.60
3:H:1922:SER:O	3:H:1928:GLN:NE2	2.34	0.60
3:H:2349:ARG:NH2	3:H:2433:LEU:O	2.32	0.60
3:K:1131:LEU:O	3:K:1171:ASN:ND2	2.35	0.60
2:L:253:VAL:HA	2:L:269:SER:HB2	1.83	0.60
1:A:1191:LYS:HE2	1:A:1467:HIS:HB3	1.83	0.60
1:B:44:ASP:OD2	1:B:46:ARG:NH1	2.34	0.60
1:B:1085:GLU:OE1	1:B:1085:GLU:HA	2.01	0.60
3:F:1365:LYS:HE3	3:F:1368:THR:HG23	1.83	0.60
1:G:1106:LYS:HD2	1:G:1106:LYS:N	2.16	0.60
1:J:794:VAL:HG12	1:J:796:GLU:H	1.67	0.60
1:B:264:GLN:HB2	1:B:409:ASP:HB2	1.84	0.60
3:E:935:LEU:O	3:E:939:HIS:NE2	2.35	0.60
3:E:827:GLY:HA2	3:E:872:ILE:HD13	1.83	0.60
3:K:1314:ILE:HB	3:K:1317:MET:HE2	1.83	0.60
3:K:2153:ASP:HB3	3:K:2156:CYS:HB2	1.84	0.60
2:C:55:VAL:HG21	2:C:81:VAL:HG11	1.84	0.60
3:E:1717:ARG:HH22	3:E:1755:TRP:CD1	2.18	0.60
3:H:2320:LEU:HA	3:H:2324:LEU:HD12	1.83	0.60
1:J:155:ASP:OD1	1:J:158:ARG:NH2	2.35	0.60
3:E:1391:HIS:O	3:E:1395:HIS:HB2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1603:LYS:HD2	3:F:1604:PRO:HD2	1.84	0.60
3:H:1136:ARG:O	3:H:1140:LYS:NZ	2.35	0.60
3:K:2230:TYR:O	3:K:2234:ASN:ND2	2.34	0.60
3:H:953:LEU:HD13	3:H:956:ARG:HB3	1.83	0.59
1:A:552:GLU:OE2	3:E:711:TYR:OH	2.21	0.59
1:B:231:ASN:OD1	1:B:234:LYS:NZ	2.34	0.59
2:D:219:VAL:HG12	2:D:236:ILE:HG21	1.83	0.59
1:J:799:THR:HG23	1:J:911:GLU:HG3	1.84	0.59
3:K:1147:SER:HA	3:K:1150:LEU:HD12	1.84	0.59
2:L:162:LEU:HA	2:L:178:ASN:HA	1.84	0.59
1:G:710:ASP:HB2	1:G:752:ILE:HD12	1.83	0.59
3:F:275:ASP:O	3:F:281:ARG:NH2	2.35	0.59
1:J:1478:ILE:HG12	1:J:1522:LEU:HD11	1.84	0.59
2:D:11:ASP:HB3	2:D:293:LYS:HB2	1.85	0.59
3:F:1581:LEU:HD13	3:F:1594:ILE:HD11	1.85	0.59
2:C:231:ALA:O	2:C:246:LEU:HB3	2.02	0.59
3:E:458:GLU:HG2	3:E:461:LEU:HD13	1.84	0.59
3:F:919:PRO:HA	3:F:922:VAL:HG12	1.85	0.59
1:J:1105:LYS:CE	1:J:1306:LEU:HD12	2.32	0.59
1:J:1179:ARG:HH12	1:J:1220:PHE:HB3	1.67	0.59
3:F:836:VAL:HG21	3:F:1580:ARG:HE	1.67	0.59
3:F:1816:LEU:O	3:F:1820:HIS:ND1	2.35	0.59
3:F:1958:ARG:HH12	3:F:2004:THR:HB	1.66	0.59
3:H:1150:LEU:HD23	3:H:1157:PHE:HD2	1.68	0.59
2:D:211:THR:HG1	2:D:225:CYS:HG	1.50	0.59
3:E:1876:LEU:HD12	3:E:2084:ARG:HH21	1.68	0.59
3:F:642:LEU:HD21	3:F:673:LEU:HB3	1.84	0.59
3:H:924:HIS:HA	3:H:927:MET:HE3	1.85	0.59
3:H:1190:CYS:SG	3:H:1191:LEU:N	2.76	0.59
1:B:1533:MET:HE3	1:B:1546:ILE:HG22	1.85	0.59
2:D:205:ALA:O	2:D:206:HIS:ND1	2.36	0.59
3:E:2333:ILE:HD12	3:E:2454:ILE:HD12	1.85	0.59
3:F:2304:GLU:HG3	3:F:2308:LEU:HD23	1.83	0.59
3:E:836:VAL:HG11	3:E:1580:ARG:HE	1.67	0.59
3:F:2156:CYS:SG	3:F:2159:ARG:NH1	2.76	0.59
3:K:1217:LYS:O	3:K:1261:ARG:NH2	2.36	0.59
3:K:2043:ILE:HA	3:K:2046:ASN:HD22	1.65	0.59
1:A:914:VAL:HG12	1:A:1140:LEU:HD23	1.84	0.58
1:A:1378:ARG:HG2	1:A:1390:MET:HE1	1.84	0.58
1:J:194:ASN:HD21	1:J:199:GLN:H	1.50	0.58
2:I:118:PRO:HB2	2:I:136:ARG:HH12	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1332:VAL:HG11	1:A:1346:ASP:HB3	1.85	0.58
1:B:1332:VAL:HA	1:B:1348:PRO:HA	1.86	0.58
1:J:614:PHE:HE2	1:J:1157:MET:HE3	1.68	0.58
3:E:492:PRO:HD3	3:E:560:LYS:HG2	1.85	0.58
3:E:642:LEU:HD21	3:E:673:LEU:HB3	1.84	0.58
3:F:501:LEU:HD23	3:F:504:LEU:HD21	1.85	0.58
3:K:2108:GLN:OE1	3:K:2130:HIS:NE2	2.37	0.58
1:A:918:HIS:NE2	1:A:1140:LEU:O	2.35	0.58
3:E:1365:LYS:HE3	3:E:1368:THR:HG23	1.86	0.58
3:F:2278:GLY:O	3:F:2280:ARG:NH1	2.36	0.58
3:H:2186:THR:HA	3:H:2286:MET:HA	1.86	0.58
1:J:55:PRO:HG2	1:J:58:ASP:HB2	1.84	0.58
1:B:361:ILE:HD13	1:B:425:TRP:HB2	1.86	0.58
3:E:2278:GLY:O	3:E:2280:ARG:NH1	2.36	0.58
3:H:1257:SER:HG	3:H:1259:CYS:HG	1.51	0.58
3:E:1577:TRP:HB2	3:E:1598:ARG:HH21	1.69	0.58
3:F:1624:MET:HE3	3:F:1628:LYS:HD3	1.86	0.58
2:L:194:ALA:HB3	2:L:196:HIS:HD2	1.68	0.58
3:F:823:LEU:HD11	3:F:862:ILE:HG23	1.86	0.58
1:A:353:GLU:HG2	1:A:526:PHE:HB2	1.86	0.58
3:F:1377:ASN:OD1	3:F:1407:LYS:NZ	2.37	0.58
3:E:850:LEU:HD22	3:E:870:ILE:HG22	1.85	0.58
3:H:1101:LYS:HG3	3:H:1102:ILE:HD12	1.86	0.58
3:H:2104:ILE:HB	3:H:2110:PRO:HG2	1.86	0.58
1:J:1411:GLN:HB2	1:J:1416:ARG:HA	1.86	0.58
3:K:1845:ARG:NH1	3:K:1848:THR:OG1	2.37	0.58
1:B:805:LEU:HD22	1:B:897:ILE:HD11	1.86	0.57
3:F:241:HIS:ND1	3:F:283:ASP:OD2	2.32	0.57
3:F:747:ILE:HG12	3:F:787:LEU:HD23	1.85	0.57
3:F:1574:ARG:HA	3:F:1577:TRP:CD1	2.39	0.57
1:B:618:ARG:NH1	1:B:1152:PHE:O	2.37	0.57
3:F:1883:ILE:HA	3:F:1886:ILE:HB	1.86	0.57
3:F:2085:ALA:HB3	3:F:2089:LYS:HB2	1.86	0.57
1:G:1523:SER:HB3	1:G:1537:THR:HG23	1.85	0.57
3:K:2257:ARG:NH2	3:K:2288:ASP:O	2.37	0.57
1:A:616:TRP:HA	1:A:619:ILE:HG22	1.86	0.57
1:A:770:ASN:HB3	1:A:773:ASN:HB2	1.85	0.57
3:E:356:MET:HG2	3:E:360:GLU:HG3	1.86	0.57
3:F:151:ILE:HG21	3:F:192:LEU:HG	1.85	0.57
1:A:41:TYR:O	1:A:1264:ASN:ND2	2.31	0.57
3:E:789:VAL:HB	3:E:828:GLN:HB3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:2424:LEU:HA	3:F:2427:LYS:HZ3	1.69	0.57
1:G:1294:ILE:HD11	1:G:1297:ALA:HB2	1.87	0.57
3:H:1053:GLU:O	3:H:1056:GLN:NE2	2.37	0.57
3:H:1120:SER:HA	3:H:1123:ILE:HG12	1.85	0.57
3:E:823:LEU:HD13	3:E:865:GLY:HA3	1.87	0.57
3:F:1603:LYS:HE3	3:F:1605:LYS:HG2	1.86	0.57
1:A:1214:LEU:HB2	1:A:1227:ALA:HB3	1.86	0.57
1:G:194:ASN:HD21	1:G:199:GLN:H	1.53	0.57
1:G:538:GLU:HB3	1:G:573:LEU:HD11	1.86	0.57
1:J:1264:ASN:H	1:J:1319:GLN:HE22	1.52	0.57
1:J:1427:VAL:HG11	1:J:1471:ILE:HG21	1.87	0.57
1:A:1523:SER:HB3	1:A:1537:THR:HG23	1.85	0.57
2:C:211:THR:OG1	2:C:225:CYS:SG	2.62	0.57
1:B:1351:THR:HB	1:B:1378:ARG:HH12	1.70	0.57
3:E:1237:LYS:O	3:E:1241:GLN:NE2	2.36	0.57
3:E:2134:ARG:NH2	3:E:2365:ASP:OD2	2.38	0.57
3:E:2258:ARG:NH2	3:E:2328:MET:O	2.38	0.57
2:L:9:GLY:HA3	2:L:295:ALA:HA	1.87	0.57
3:F:2138:LEU:HD21	3:F:2362:PHE:CG	2.40	0.56
1:G:537:PHE:HD2	1:G:573:LEU:HD21	1.70	0.56
2:C:215:LEU:HD21	2:C:219:VAL:HG13	1.87	0.56
3:E:236:LEU:HD23	3:E:240:ARG:HG3	1.87	0.56
3:F:811:GLN:HB3	3:F:849:ILE:HG12	1.87	0.56
1:G:55:PRO:HG2	1:G:58:ASP:HB2	1.88	0.56
1:G:1381:ASP:HB2	1:G:1391:ILE:HD11	1.86	0.56
3:H:2352:LYS:HG3	3:H:2356:MET:HE2	1.87	0.56
1:J:836:LEU:HB2	1:J:864:ILE:HG21	1.87	0.56
3:K:994:VAL:HG13	3:K:998:ILE:HD11	1.87	0.56
3:K:1753:ASN:O	3:K:1759:TRP:NE1	2.34	0.56
3:K:2104:ILE:HB	3:K:2110:PRO:HG2	1.85	0.56
3:K:2456:GLN:OE1	3:K:2462:ASN:ND2	2.38	0.56
1:B:1263:ILE:HD11	1:B:1272:LEU:HD12	1.87	0.56
2:D:215:LEU:HD21	2:D:219:VAL:HG13	1.88	0.56
3:F:396:HIS:O	3:F:399:ARG:NH1	2.38	0.56
3:F:425:ALA:HA	3:F:432:ILE:HD13	1.87	0.56
3:F:1855:GLY:HA2	3:F:1892:ILE:HD11	1.86	0.56
1:G:925:ASN:HA	1:G:928:ILE:HD12	1.87	0.56
3:H:1878:VAL:O	3:H:1881:GLN:NE2	2.35	0.56
3:H:2050:LYS:O	3:H:2054:GLN:NE2	2.38	0.56
1:J:1294:ILE:HD11	1:J:1297:ALA:HB2	1.88	0.56
3:K:1136:ARG:O	3:K:1140:LYS:NZ	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:1326:GLU:HB2	3:K:1331:PRO:HB3	1.87	0.56
3:E:151:ILE:HG21	3:E:192:LEU:HG	1.87	0.56
3:E:1603:LYS:HD2	3:E:1604:PRO:HD2	1.87	0.56
1:J:1105:LYS:NZ	1:J:1306:LEU:HD12	2.20	0.56
1:B:306:LEU:HD13	3:F:760:PRO:HB3	1.87	0.56
3:E:93:LEU:HD21	3:E:135:ILE:HG12	1.87	0.56
3:H:1116:LEU:O	3:H:1120:SER:OG	2.23	0.56
2:I:223:ALA:HB3	2:I:258:PHE:HZ	1.70	0.56
3:K:1258:ALA:HA	3:K:1261:ARG:HH11	1.71	0.56
3:K:2319:ARG:NH2	3:K:2471:CYS:O	2.38	0.56
3:K:2439:ARG:HB2	3:K:2442:ASN:HB2	1.87	0.56
2:L:59:ASP:OD1	2:L:61:ARG:NH1	2.38	0.56
1:A:1532:MET:HB3	1:A:1549:CYS:HB3	1.87	0.56
1:B:1304:MET:HG3	1:B:1329:ASP:HB2	1.86	0.56
3:F:1890:ASN:HB3	3:F:1893:VAL:HB	1.87	0.56
3:H:2309:ARG:NH1	3:H:2311:LYS:O	2.39	0.56
1:J:194:ASN:ND2	1:J:199:GLN:O	2.39	0.56
3:F:1547:ARG:HA	3:F:1550:ILE:HG12	1.88	0.56
3:F:2338:ARG:NH1	3:F:2451:ASP:OD1	2.39	0.56
3:H:953:LEU:HD22	3:H:956:ARG:HE	1.71	0.56
1:J:1321:ARG:NH1	1:J:1323:SER:OG	2.39	0.56
2:D:275:ARG:NH1	2:D:287:GLN:OE1	2.38	0.56
1:G:287:CYS:HB3	1:G:295:ILE:HG21	1.87	0.56
1:A:1263:ILE:HB	1:A:1270:LEU:HB2	1.86	0.56
1:B:194:ASN:HD21	1:B:198:THR:HG1	1.51	0.56
3:E:1523:ARG:HE	3:E:1526:LEU:HD21	1.71	0.56
3:E:1969:GLU:OE1	3:E:2130:HIS:NE2	2.38	0.56
3:K:1101:LYS:HG3	3:K:1102:ILE:HD12	1.87	0.56
3:K:1905:GLY:HA2	3:K:1909:PRO:HB3	1.87	0.56
3:K:2159:ARG:O	3:K:2263:ARG:NH1	2.38	0.56
3:K:2219:LEU:HD23	3:K:2224:LYS:HG2	1.88	0.56
1:B:882:ASP:OD1	1:B:884:ARG:NH2	2.39	0.56
2:I:59:ASP:HB2	2:I:68:VAL:HG21	1.87	0.56
1:A:710:ASP:HB3	1:A:752:ILE:HD13	1.88	0.55
3:E:2325:THR:HA	3:E:2328:MET:HE3	1.87	0.55
3:F:976:PRO:HD2	3:F:979:GLN:HE22	1.70	0.55
3:H:2439:ARG:HB2	3:H:2442:ASN:HB2	1.87	0.55
1:B:1523:SER:HB3	1:B:1537:THR:HG23	1.86	0.55
3:E:2004:THR:HG23	3:E:2007:GLU:H	1.71	0.55
3:K:2042:ASP:O	3:K:2046:ASN:ND2	2.39	0.55
3:K:2349:ARG:NH2	3:K:2433:LEU:O	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:458:GLU:HG2	3:F:461:LEU:HD13	1.87	0.55
3:K:2150:LEU:HD11	3:K:2161:LEU:HB2	1.88	0.55
3:K:2212:MET:HE3	3:K:2227:VAL:HG12	1.87	0.55
3:K:2257:ARG:NH1	3:K:2289:ARG:O	2.38	0.55
3:E:147:LYS:NZ	3:E:184:SER:O	2.39	0.55
3:E:972:MET:HE1	3:E:983:TYR:HB3	1.87	0.55
1:G:1379:VAL:HG12	1:G:1391:ILE:HD12	1.87	0.55
3:H:956:ARG:NH1	3:H:959:SER:OG	2.40	0.55
1:A:64:ASN:O	1:A:64:ASN:ND2	2.30	0.55
1:A:152:CYS:SG	1:A:195:ARG:NH1	2.79	0.55
1:A:814:ASP:HA	1:A:817:VAL:HG12	1.87	0.55
1:A:1213:LYS:NZ	1:A:1229:ASP:OD1	2.31	0.55
3:F:2004:THR:HG23	3:F:2007:GLU:H	1.72	0.55
3:H:1020:ILE:HD13	3:H:1062:VAL:HG22	1.88	0.55
3:K:1045:LEU:HD21	3:K:1077:LEU:HD11	1.88	0.55
1:B:1214:LEU:HB2	1:B:1227:ALA:HB3	1.88	0.55
3:E:1246:ARG:O	3:E:1250:GLN:NE2	2.39	0.55
3:F:2257:ARG:HD2	3:F:2292:GLY:HA3	1.87	0.55
3:E:1479:GLU:OE2	3:E:1596:ARG:NH1	2.40	0.55
1:G:354:LEU:HD11	1:G:432:VAL:HG21	1.88	0.55
3:H:1298:ILE:HD11	3:H:1332:LEU:HD22	1.88	0.55
3:K:2098:GLU:HB2	3:K:2114:CYS:HB3	1.88	0.55
1:B:216:CYS:HB2	1:B:262:CYS:HA	1.89	0.55
3:F:359:LYS:HG3	3:F:361:TYR:H	1.72	0.55
3:F:2424:LEU:HD23	3:F:2427:LYS:HZ3	1.72	0.55
1:G:731:GLN:NE2	1:G:770:ASN:OD1	2.40	0.55
1:J:927:PHE:HA	1:J:930:VAL:HG22	1.87	0.55
3:K:2240:LEU:HA	3:K:2243:VAL:HG12	1.87	0.55
1:A:934:ASP:OD2	1:A:968:TRP:NE1	2.26	0.55
1:A:1177:ARG:HA	1:A:1180:ASN:HD22	1.72	0.55
2:C:200:VAL:HG12	2:C:201:THR:HG23	1.88	0.55
3:E:375:PRO:HB3	3:E:427:GLU:HG3	1.89	0.55
3:E:1386:ILE:HD12	3:E:1410:ARG:HH21	1.71	0.55
3:F:1217:LYS:O	3:F:1261:ARG:NH2	2.40	0.55
3:E:418:LEU:HA	3:E:421:ILE:HG12	1.89	0.55
3:F:1266:LEU:HA	3:F:1269:VAL:HG12	1.88	0.55
3:H:2162:ASP:OD1	3:H:2263:ARG:NH2	2.39	0.55
3:H:2212:MET:HE3	3:H:2227:VAL:HG12	1.88	0.55
1:J:84:SER:HB3	1:J:163:LEU:HD22	1.89	0.55
2:L:33:SER:OG	2:L:34:GLN:N	2.40	0.55
1:B:171:ARG:HA	1:B:215:PRO:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:163:GLN:N	2:C:177:ALA:O	2.36	0.54
2:C:226:SER:OG	2:C:227:ALA:N	2.40	0.54
1:G:44:ASP:O	1:G:48:LYS:NZ	2.40	0.54
3:H:1128:VAL:HA	3:H:1131:LEU:HB2	1.89	0.54
2:C:121:GLU:HG3	2:C:164:SER:HA	1.88	0.54
1:A:784:GLU:HG2	2:I:13:THR:HG21	1.89	0.54
1:B:41:TYR:O	1:B:1264:ASN:ND2	2.38	0.54
1:B:1257:VAL:HA	1:B:1275:SER:HA	1.90	0.54
2:D:59:ASP:OD1	2:D:60:ILE:N	2.40	0.54
3:F:2333:ILE:HD12	3:F:2454:ILE:HD12	1.88	0.54
3:K:921:VAL:HA	3:K:924:HIS:CE1	2.41	0.54
1:A:823:GLN:HE22	1:G:195:ARG:HH12	1.56	0.54
3:E:354:SER:HB3	3:E:357:LYS:HZ1	1.71	0.54
3:E:359:LYS:HG3	3:E:361:TYR:H	1.72	0.54
1:G:186:LYS:O	1:G:231:ASN:ND2	2.40	0.54
3:H:1019:GLN:HA	3:H:1022:ILE:HD12	1.90	0.54
2:I:59:ASP:OD1	2:I:61:ARG:NH1	2.41	0.54
1:J:904:GLY:HA3	1:J:1341:GLU:HB3	1.90	0.54
1:A:805:LEU:HD12	1:A:897:ILE:HD11	1.89	0.54
1:B:616:TRP:HA	1:B:619:ILE:HG22	1.88	0.54
3:F:925:ASN:OD1	3:F:926:LEU:N	2.40	0.54
3:H:2186:THR:HG23	3:H:2189:VAL:H	1.73	0.54
1:B:1215:MET:HE3	1:B:1224:LEU:HD11	1.89	0.54
1:B:1302:THR:HG23	1:B:1334:ARG:HH12	1.73	0.54
2:C:90:MET:HB2	2:C:102:TRP:HB2	1.90	0.54
2:C:275:ARG:NH1	2:C:287:GLN:OE1	2.41	0.54
1:A:257:SER:O	1:A:260:GLN:NE2	2.41	0.54
3:F:236:LEU:HD23	3:F:240:ARG:HG3	1.90	0.54
3:F:595:ARG:NH2	3:F:640:GLU:OE1	2.41	0.54
2:I:37:ARG:O	2:I:49:THR:OG1	2.25	0.54
1:J:275:LEU:HD23	1:J:280:LEU:HD22	1.90	0.54
1:J:1525:MET:HA	1:J:1535:ALA:O	2.08	0.54
2:L:135:ASP:OD1	2:L:136:ARG:N	2.38	0.54
1:B:1391:ILE:HG22	1:B:1392:ARG:HG3	1.89	0.54
3:E:1616:ASN:OD1	3:E:1617:LEU:N	2.41	0.54
3:F:2145:LEU:HD21	3:F:2358:ILE:HG12	1.88	0.54
1:G:171:ARG:NH1	1:G:216:CYS:O	2.40	0.54
2:L:87:ASN:OD1	2:L:88:ARG:NH2	2.40	0.54
2:L:120:ASN:ND2	2:L:163:GLN:O	2.41	0.54
2:L:125:HIS:HD2	2:L:167:MET:HE2	1.73	0.54
3:F:527:LEU:O	3:F:553:ARG:NH2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:211:THR:OG1	2:L:225:CYS:SG	2.58	0.54
1:A:156:VAL:HA	1:A:159:PHE:HB3	1.90	0.54
1:B:805:LEU:HD23	1:B:893:ASN:HB3	1.90	0.54
3:E:1476:TRP:HE1	3:E:1600:LEU:HD13	1.73	0.54
2:I:9:GLY:HA3	2:I:295:ALA:HA	1.90	0.54
3:F:1856:ILE:HG22	3:F:1859:ALA:H	1.73	0.53
1:G:70:ILE:HD11	1:G:590:SER:HB3	1.89	0.53
2:I:165:LEU:HD12	2:I:174:LEU:HD11	1.91	0.53
3:E:820:ASP:OD1	3:E:820:ASP:N	2.42	0.53
1:G:108:ARG:HD2	1:G:116:LEU:HB2	1.89	0.53
1:J:79:ARG:NH1	1:J:381:HIS:O	2.41	0.53
3:E:966:PRO:HA	3:E:969:ILE:HG12	1.89	0.53
3:E:1655:TYR:HA	3:E:1658:LEU:HB2	1.91	0.53
3:K:1019:GLN:HA	3:K:1022:ILE:HD12	1.91	0.53
3:E:2219:LEU:HB2	3:E:2224:LYS:HG3	1.91	0.53
3:F:1024:SER:OG	3:F:1065:ARG:NH2	2.41	0.53
3:H:1730:GLN:NE2	3:H:1731:PRO:O	2.40	0.53
2:I:38:LEU:HA	2:I:49:THR:HA	1.90	0.53
1:J:125:ILE:HG21	1:J:149:LEU:HA	1.90	0.53
3:K:1876:LEU:O	3:K:2084:ARG:NH2	2.42	0.53
3:K:2365:ASP:N	3:K:2365:ASP:OD1	2.39	0.53
1:A:746:TYR:HB3	1:A:755:LEU:HD21	1.89	0.53
1:B:144:ARG:HH21	1:B:166:THR:HG21	1.72	0.53
3:E:1291:THR:HA	3:E:1294:GLN:HG2	1.91	0.53
3:E:2146:VAL:HG12	3:E:2355:LEU:HD11	1.91	0.53
1:J:854:GLN:HA	1:J:857:LEU:HD12	1.90	0.53
2:C:3:VAL:HG12	2:C:302:ASP:HA	1.90	0.53
3:F:1428:SER:OG	3:F:1430:GLU:OE1	2.27	0.53
3:H:2043:ILE:HA	3:H:2046:ASN:HD22	1.73	0.53
3:H:2240:LEU:HA	3:H:2243:VAL:HG12	1.90	0.53
2:I:162:LEU:HD11	2:I:176:ALA:HB1	1.90	0.53
3:K:920:THR:O	3:K:924:HIS:ND1	2.42	0.53
3:K:1049:LEU:HD12	3:K:1087:ILE:HD11	1.88	0.53
2:L:254:TRP:HE1	2:L:270:SER:HB3	1.74	0.53
1:A:1391:ILE:HG22	1:A:1392:ARG:HG3	1.91	0.53
2:D:121:GLU:HG3	2:D:164:SER:HA	1.90	0.53
3:E:1050:ASP:O	3:E:1054:ASN:HB2	2.08	0.53
3:E:1569:LYS:HE2	3:E:1570:ARG:HH22	1.73	0.53
3:E:1766:ASN:HA	3:E:1769:VAL:HG12	1.90	0.53
3:F:622:ILE:HG13	3:F:623:LYS:H	1.74	0.53
3:F:698:ILE:HD11	3:F:746:LEU:HD13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1132:ASN:OD1	3:F:1133:ASN:N	2.42	0.53
3:F:2463:LEU:O	3:F:2466:HIS:ND1	2.41	0.53
3:K:1085:MET:HG3	3:K:1119:MET:HG3	1.91	0.53
1:B:1537:THR:HB	1:B:1544:VAL:HG13	1.89	0.53
3:E:1365:LYS:NZ	3:E:1367:SER:OG	2.27	0.53
3:F:93:LEU:HD21	3:F:135:ILE:HG12	1.90	0.53
3:F:1301:LEU:HD21	3:F:1318:LEU:HD12	1.91	0.53
3:F:1402:GLU:HG3	3:F:1405:TYR:HD2	1.74	0.53
1:G:787:LEU:HA	1:G:790:LEU:HD12	1.91	0.53
1:G:854:GLN:HA	1:G:857:LEU:HD12	1.91	0.53
3:K:1175:HIS:HB3	3:K:1178:TYR:HB3	1.91	0.53
1:B:710:ASP:HB3	1:B:752:ILE:HD13	1.91	0.53
2:D:59:ASP:HB2	2:D:68:VAL:HG21	1.90	0.53
2:D:177:ALA:HB2	2:D:213:ILE:HD12	1.89	0.53
3:E:673:LEU:HD12	3:E:704:LEU:HD21	1.91	0.53
3:E:2085:ALA:HB3	3:E:2089:LYS:HB2	1.90	0.53
3:F:827:GLY:HA2	3:F:872:ILE:HD11	1.91	0.53
3:F:2329:GLU:HG3	3:F:2336:SER:HB3	1.91	0.53
1:G:217:ILE:HA	1:G:263:PHE:O	2.09	0.53
3:H:1175:HIS:HB3	3:H:1178:TYR:HB3	1.89	0.53
3:H:1777:SER:OG	3:H:1813:SER:N	2.41	0.53
3:H:2130:HIS:N	3:H:2174:LYS:O	2.41	0.53
3:K:1839:SER:O	3:K:1839:SER:OG	2.27	0.53
2:D:97:GLY:HA2	2:D:118:PRO:HA	1.91	0.53
2:D:120:ASN:ND2	2:D:163:GLN:O	2.42	0.53
3:E:533:ILE:CG1	3:E:543:GLN:HE21	2.19	0.53
3:E:1401:LYS:HB2	3:E:1404:TRP:CE2	2.44	0.53
3:E:1726:ARG:HD3	3:E:1730:GLN:HE22	1.74	0.53
3:E:2109:ARG:O	3:E:2111:ARG:NH1	2.42	0.53
3:H:1042:PRO:HA	3:H:1045:LEU:HD12	1.90	0.53
1:J:376:LYS:HD3	1:J:380:ARG:HG3	1.91	0.53
1:A:567:ARG:HH22	1:A:600:LEU:HG	1.74	0.52
1:A:1362:GLN:HG3	1:A:1412:ARG:HG2	1.91	0.52
1:B:220:TYR:OH	1:B:264:GLN:OE1	2.27	0.52
2:C:6:VAL:HG21	2:C:40:ILE:HD11	1.91	0.52
3:F:198:GLY:O	3:F:201:THR:OG1	2.26	0.52
1:G:284:LEU:HB3	1:G:399:MET:HE1	1.91	0.52
1:G:811:GLY:O	1:G:922:ARG:NH1	2.42	0.52
3:H:2193:GLU:HA	3:H:2196:GLU:HG3	1.91	0.52
2:I:226:SER:OG	2:I:227:ALA:N	2.42	0.52
3:K:1125:GLN:HA	3:K:1128:VAL:HG22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:640:PHE:HA	1:A:643:VAL:HG12	1.91	0.52
3:E:761:ILE:HD13	3:E:787:LEU:HD21	1.91	0.52
3:E:1654:VAL:HA	3:E:1657:GLN:HE22	1.74	0.52
3:E:2063:LEU:HD21	3:E:2070:LEU:HB2	1.90	0.52
3:F:2084:ARG:HA	3:F:2089:LYS:HZ3	1.74	0.52
2:I:94:SER:OG	2:I:96:ASP:OD1	2.26	0.52
2:L:188:MET:HE1	2:L:192:THR:HG22	1.90	0.52
1:A:894:LEU:HD21	1:A:967:VAL:HG21	1.90	0.52
2:C:220:LYS:O	2:C:221:HIS:ND1	2.42	0.52
3:E:91:ASP:O	3:E:95:SER:HB2	2.10	0.52
3:E:198:GLY:O	3:E:201:THR:OG1	2.26	0.52
1:G:794:VAL:HG12	1:G:796:GLU:H	1.74	0.52
1:J:354:LEU:HA	1:J:357:ILE:HG22	1.91	0.52
3:K:1140:LYS:HA	3:K:1143:MET:HE3	1.90	0.52
3:K:1755:TRP:CE3	3:K:1758:ALA:HB2	2.44	0.52
3:E:792:GLY:H	3:E:795:MET:HE1	1.75	0.52
3:E:969:ILE:CG2	3:E:1004:LYS:HZ2	2.23	0.52
3:E:2211:GLN:HE21	1:J:888:ARG:HH12	1.57	0.52
3:F:1002:VAL:HA	3:F:1005:ILE:HG22	1.91	0.52
3:F:2080:VAL:HG12	3:F:2092:VAL:HG11	1.91	0.52
2:I:168:ALA:HA	2:I:215:LEU:HD11	1.91	0.52
1:J:308:ASP:OD1	1:J:308:ASP:N	2.41	0.52
2:C:268:ALA:HB2	2:C:298:VAL:HB	1.92	0.52
3:E:1132:ASN:OD1	3:E:1133:ASN:N	2.43	0.52
3:E:1217:LYS:O	3:E:1261:ARG:NH2	2.42	0.52
3:E:1816:LEU:O	3:E:1820:HIS:ND1	2.42	0.52
3:E:1948:GLN:HE22	3:E:2077:GLU:HG2	1.74	0.52
3:F:397:TYR:HA	3:F:400:TYR:HD2	1.75	0.52
3:H:1986:LYS:NZ	3:H:1990:ALA:HB2	2.25	0.52
1:J:747:ILE:HD12	1:J:756:ARG:HG2	1.90	0.52
1:J:968:TRP:HE1	1:J:990:ILE:HD11	1.75	0.52
3:K:941:ALA:HA	3:K:944:GLN:HG2	1.91	0.52
3:K:1190:CYS:SG	3:K:1191:LEU:N	2.82	0.52
1:A:1478:ILE:HG12	1:A:1522:LEU:HD11	1.92	0.52
3:E:1449:SER:HB3	3:E:1478:LEU:HD22	1.92	0.52
3:F:1955:GLU:OE1	3:F:2067:SER:OG	2.24	0.52
3:K:1829:PHE:HB3	3:K:1869:LEU:HD23	1.92	0.52
3:K:2076:LEU:HB3	3:K:2094:ILE:HB	1.92	0.52
2:L:118:PRO:HB2	2:L:136:ARG:HH12	1.73	0.52
3:E:2189:VAL:HA	3:E:2192:ARG:HG2	1.90	0.52
3:F:375:PRO:HB3	3:F:427:GLU:HG3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:667:SER:OG	3:F:703:ARG:NH1	2.42	0.52
3:H:1019:GLN:HG2	3:H:1051:ILE:HD11	1.92	0.52
3:H:2363:ALA:HB1	3:H:2422:ALA:HB1	1.92	0.52
1:G:307:LYS:NZ	1:G:312:LYS:O	2.38	0.52
1:G:1523:SER:N	1:G:1537:THR:O	2.40	0.52
3:H:1049:LEU:HD12	3:H:1087:ILE:HD11	1.91	0.52
1:J:1106:LYS:N	1:J:1106:LYS:CD	2.72	0.52
3:E:622:ILE:HG13	3:E:623:LYS:H	1.74	0.52
3:E:1249:ILE:O	3:E:1253:LYS:NZ	2.35	0.52
3:E:1977:GLN:HB3	3:E:1986:LYS:HZ3	1.75	0.52
3:F:864:ARG:O	3:F:868:ARG:NH1	2.42	0.52
1:G:91:LEU:HD21	1:G:179:HIS:HB2	1.91	0.52
1:G:156:VAL:HA	1:G:159:PHE:HB3	1.92	0.52
1:G:185:THR:HG22	1:G:187:SER:H	1.74	0.52
3:H:1898:LEU:HD23	3:H:1901:LEU:HD21	1.92	0.52
3:H:2444:LEU:HD22	3:H:2448:GLU:HG2	1.92	0.52
3:K:2130:HIS:N	3:K:2174:LYS:O	2.42	0.52
3:E:2145:LEU:HD21	3:E:2358:ILE:HG21	1.92	0.52
3:F:356:MET:HG2	3:F:360:GLU:HG3	1.91	0.52
3:F:1009:ILE:O	3:F:1013:PHE:HB2	2.09	0.52
1:G:624:TYR:O	1:G:628:GLN:HB3	2.10	0.52
3:H:981:ASP:OD1	3:H:982:PHE:N	2.42	0.52
1:J:1523:SER:N	1:J:1537:THR:O	2.39	0.52
1:A:824:GLU:OE1	1:A:824:GLU:N	2.35	0.51
3:E:396:HIS:O	3:E:399:ARG:NH1	2.43	0.51
3:F:1087:ILE:O	3:F:1091:MET:HG3	2.10	0.51
3:F:1614:PHE:CE2	3:F:1630:VAL:HG21	2.44	0.51
3:F:1757:LYS:O	3:F:1761:ASN:ND2	2.43	0.51
1:G:237:GLN:HA	1:G:240:ILE:HG12	1.92	0.51
1:G:792:ASP:OD1	1:G:798:ARG:NH1	2.43	0.51
3:K:2444:LEU:HD22	3:K:2448:GLU:HG2	1.91	0.51
1:B:1263:ILE:HB	1:B:1270:LEU:HB2	1.91	0.51
1:B:1314:LEU:HD13	1:B:1355:ILE:HG22	1.91	0.51
3:E:86:LEU:HD23	3:E:131:LEU:HD13	1.92	0.51
3:E:688:ASP:H	3:E:694:GLN:HE21	1.58	0.51
3:E:2217:ASP:N	3:E:2217:ASP:OD1	2.43	0.51
1:G:813:GLN:HB3	1:G:816:GLU:HB3	1.92	0.51
1:J:811:GLY:O	1:J:922:ARG:NH1	2.44	0.51
1:J:1419:VAL:HG22	1:J:1429:LEU:HG	1.92	0.51
1:A:1006:PRO:O	1:A:1010:MET:HG2	2.11	0.51
2:D:99:ILE:HD11	2:D:119:VAL:HB	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:864:ARG:HA	3:E:867:VAL:HG12	1.91	0.51
3:E:1184:LYS:NZ	3:E:1189:GLU:OE2	2.44	0.51
3:E:1763:ALA:HB1	3:E:1828:PHE:HE1	1.76	0.51
3:E:2463:LEU:O	3:E:2466:HIS:ND1	2.43	0.51
3:F:278:LEU:HD11	3:F:365:VAL:HG13	1.92	0.51
3:H:1327:HIS:HD2	3:H:2246:LEU:HA	1.75	0.51
3:H:2201:PRO:HG2	3:H:2204:ILE:HB	1.91	0.51
1:J:100:VAL:HG23	1:J:102:LYS:HZ1	1.74	0.51
2:L:226:SER:OG	2:L:227:ALA:N	2.44	0.51
2:L:276:LEU:HB3	2:L:286:ARG:HB2	1.91	0.51
1:B:1219:GLN:HA	1:B:1529:PRO:HG2	1.93	0.51
2:C:50:ALA:HB1	2:C:78:VAL:HG13	1.92	0.51
3:F:147:LYS:NZ	3:F:184:SER:O	2.42	0.51
1:G:1278:GLY:O	1:G:1300:GLY:N	2.40	0.51
1:G:1369:VAL:HG22	1:G:1379:VAL:HG22	1.91	0.51
1:G:1390:MET:HE3	1:G:1391:ILE:H	1.76	0.51
3:H:2240:LEU:HB3	3:H:2323:MET:HE2	1.92	0.51
2:I:200:VAL:HG12	2:I:201:THR:HG23	1.91	0.51
2:I:253:VAL:HA	2:I:269:SER:HB2	1.91	0.51
1:J:1317:TRP:HE1	1:J:1319:GLN:NE2	2.09	0.51
1:A:227:ASN:O	1:A:231:ASN:ND2	2.43	0.51
2:D:57:LEU:HB2	2:D:69:ALA:HB3	1.92	0.51
3:E:258:LEU:HD12	3:E:261:TYR:HB2	1.91	0.51
3:F:652:ASP:O	3:F:658:ARG:NH2	2.43	0.51
3:F:961:LEU:HA	3:F:964:ILE:HG22	1.93	0.51
3:F:1955:GLU:HG3	3:F:1959:MET:HE1	1.92	0.51
3:H:2098:GLU:HB2	3:H:2114:CYS:HB3	1.93	0.51
3:H:2253:THR:O	3:H:2257:ARG:HG2	2.10	0.51
1:A:870:HIS:O	1:A:874:MET:HG2	2.11	0.51
1:B:1460:THR:OG1	1:B:1474:GLY:O	2.29	0.51
3:E:698:ILE:HD11	3:E:746:LEU:HD13	1.92	0.51
3:F:373:ILE:HA	3:F:376:LEU:HD12	1.93	0.51
3:F:806:ILE:HD12	3:F:826:LEU:HG	1.91	0.51
3:F:1948:GLN:HB2	3:F:2076:LEU:HD13	1.93	0.51
3:F:278:LEU:HD23	3:F:281:ARG:HH11	1.76	0.51
3:H:1755:TRP:CE3	3:H:1758:ALA:HB2	2.45	0.51
3:H:1829:PHE:HB3	3:H:1869:LEU:HD22	1.93	0.51
3:H:1905:GLY:HA2	3:H:1909:PRO:HB3	1.93	0.51
3:K:1898:LEU:HD23	3:K:1901:LEU:HD21	1.91	0.51
3:E:606:ASP:HB3	3:E:609:VAL:H	1.76	0.51
3:E:1436:LEU:HD21	3:E:1455:LYS:HZ2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:1519:ILE:O	3:E:1523:ARG:NH1	2.44	0.51
3:E:1916:LEU:HB3	3:E:1935:ILE:HD11	1.93	0.51
3:F:470:CYS:HA	3:F:507:LYS:HG2	1.92	0.51
3:H:1997:MET:HA	3:H:2000:ARG:HB2	1.93	0.51
1:A:1320:ILE:HD12	1:A:1363:LEU:HA	1.92	0.51
1:B:530:PHE:HD1	1:B:560:VAL:HG22	1.75	0.51
3:E:275:ASP:O	3:E:281:ARG:NH2	2.38	0.51
3:E:913:SER:OG	3:E:914:ASN:N	2.44	0.51
3:F:1851:PHE:HE2	3:F:1885:ARG:HE	1.58	0.51
1:G:772:LEU:HB2	1:G:878:LEU:HD13	1.92	0.51
3:H:1381:GLN:HG3	3:H:2258:ARG:HH22	1.76	0.51
1:J:93:LEU:HD12	1:J:124:ALA:HA	1.93	0.51
3:K:1324:PHE:HA	3:K:1327:HIS:CE1	2.45	0.51
3:E:671:PRO:O	3:E:675:GLN:NE2	2.43	0.51
3:E:2033:ASP:OD1	3:E:2033:ASP:N	2.43	0.51
1:G:164:ARG:HH22	1:G:215:PRO:HD2	1.76	0.51
1:G:1475:THR:OG1	1:G:1477:GLN:O	2.29	0.51
3:H:1125:GLN:HA	3:H:1128:VAL:HG22	1.92	0.51
3:H:1353:LEU:HB2	3:H:1375:ILE:HG21	1.93	0.51
1:J:1267:ASP:OD1	1:J:1267:ASP:N	2.43	0.51
2:C:91:VAL:HG21	2:C:124:ILE:HD11	1.93	0.50
2:C:161:SER:O	2:C:178:ASN:ND2	2.44	0.50
3:F:1717:ARG:HH22	3:F:1755:TRP:CD1	2.29	0.50
1:G:1264:ASN:HD22	1:G:1270:LEU:HD12	1.76	0.50
2:I:254:TRP:HE1	2:I:270:SER:HB3	1.76	0.50
2:C:120:ASN:ND2	2:C:163:GLN:O	2.44	0.50
3:F:784:LEU:HD11	3:F:802:LEU:HD21	1.93	0.50
3:H:969:ILE:HG22	3:H:973:ARG:HH22	1.74	0.50
1:A:1167:SER:OG	1:A:1168:VAL:N	2.44	0.50
3:F:961:LEU:HD11	3:F:994:VAL:HG11	1.94	0.50
2:I:194:ALA:HB3	2:I:196:HIS:HD2	1.77	0.50
1:B:870:HIS:O	1:B:874:MET:HG2	2.11	0.50
3:E:451:PHE:H	3:E:454:ARG:HB2	1.77	0.50
3:E:926:LEU:HA	3:E:929:ILE:HG12	1.92	0.50
3:E:2232:LEU:HD13	3:E:2322:ARG:HH21	1.76	0.50
3:E:2084:ARG:HA	3:E:2089:LYS:HZ3	1.76	0.50
3:E:2186:THR:HB	3:E:2189:VAL:HG22	1.93	0.50
3:F:2162:ASP:OD1	3:F:2163:ILE:N	2.44	0.50
1:J:608:LEU:HD13	1:J:611:ILE:HD11	1.94	0.50
1:A:106:CYS:SG	1:A:107:ALA:N	2.84	0.50
1:A:308:ASP:OD1	1:A:309:SER:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:425:TRP:CZ2	1:B:429:MET:HE3	2.47	0.50
1:B:874:MET:O	1:B:878:LEU:HG	2.12	0.50
3:E:349:ASP:N	3:E:349:ASP:OD1	2.43	0.50
3:E:555:GLN:HA	3:E:558:MET:HG3	1.94	0.50
3:F:2342:GLU:HB2	3:F:2446:VAL:HG12	1.94	0.50
1:G:909:ARG:NH1	1:G:1297:ALA:O	2.45	0.50
3:K:2282:PRO:HA	3:K:2285:LEU:HB2	1.93	0.50
1:A:778:MET:HE3	1:A:885:LYS:HE3	1.94	0.50
1:A:859:GLN:HA	1:A:862:MET:SD	2.52	0.50
1:B:1321:ARG:NH1	1:B:1366:ASN:OD1	2.45	0.50
3:E:383:ALA:HB1	3:E:386:THR:HB	1.94	0.50
3:E:1605:LYS:NZ	3:E:1633:THR:O	2.45	0.50
3:E:1891:GLN:O	3:E:1895:ARG:NH1	2.45	0.50
3:E:2085:ALA:H	3:E:2089:LYS:HZ3	1.59	0.50
3:F:1481:TRP:HA	3:F:1484:ILE:HD12	1.94	0.50
3:H:2047:VAL:HG12	3:H:2050:LYS:HE2	1.94	0.50
3:K:1323:GLU:OE2	3:K:2245:TRP:NE1	2.44	0.50
3:E:1519:ILE:O	3:E:1523:ARG:HG2	2.10	0.50
3:F:1449:SER:HB3	3:F:1478:LEU:HD22	1.93	0.50
3:F:1712:THR:O	3:F:1715:LEU:HB3	2.12	0.50
1:G:173:LEU:HA	1:G:217:ILE:HG23	1.94	0.50
3:H:1995:TYR:HE1	3:H:2018:LEU:HB3	1.76	0.50
2:I:57:LEU:HB2	2:I:69:ALA:HB3	1.94	0.50
1:J:194:ASN:OD1	1:J:197:TYR:N	2.44	0.50
3:E:154:VAL:HG13	3:E:174:LEU:HD13	1.94	0.50
3:E:680:ARG:HA	3:E:683:PHE:CE1	2.47	0.50
3:E:1237:LYS:HB2	3:E:1241:GLN:HE22	1.77	0.50
3:E:1328:ASP:OD1	3:E:1329:ASP:N	2.44	0.50
3:E:1883:ILE:HA	3:E:1886:ILE:HB	1.93	0.50
3:F:154:VAL:HG13	3:F:174:LEU:HD13	1.93	0.50
1:G:792:ASP:OD2	1:G:797:VAL:HG23	2.12	0.50
2:L:46:LEU:HD13	2:L:57:LEU:HD13	1.94	0.50
2:L:97:GLY:HA2	2:L:119:VAL:HG22	1.94	0.50
3:E:1444:GLU:HA	3:E:1629:LYS:HE3	1.93	0.49
3:F:934:SER:O	3:F:938:HIS:ND1	2.45	0.49
3:F:1570:ARG:O	3:F:1574:ARG:NH1	2.34	0.49
3:H:1952:VAL:O	3:H:1956:LEU:HD23	2.12	0.49
3:H:2192:ARG:HA	3:H:2202:LEU:HD11	1.93	0.49
1:J:794:VAL:HB	1:J:797:VAL:HG22	1.94	0.49
3:K:961:LEU:O	3:K:965:ILE:HG12	2.12	0.49
3:E:1841:GLN:OE1	3:E:1841:GLN:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:932:ASP:HA	3:F:935:LEU:HB2	1.94	0.49
3:K:905:LEU:O	3:K:908:GLN:NE2	2.45	0.49
3:K:2250:SER:H	3:K:2253:THR:HB	1.78	0.49
3:E:546:ILE:HD13	3:E:599:ILE:HD12	1.92	0.49
3:E:2421:ARG:HD3	3:E:2424:LEU:HD12	1.94	0.49
3:F:645:LEU:HD22	3:F:665:LEU:HD21	1.95	0.49
3:F:1726:ARG:HH21	3:F:1730:GLN:HE22	1.60	0.49
3:F:2085:ALA:H	3:F:2089:LYS:HZ3	1.60	0.49
1:G:79:ARG:NH1	1:G:381:HIS:O	2.45	0.49
1:G:156:VAL:HG23	1:G:211:TRP:HZ3	1.77	0.49
1:A:111:ALA:O	1:A:131:ASN:ND2	2.46	0.49
1:A:113:VAL:HG21	1:A:127:GLN:HG2	1.94	0.49
1:A:882:ASP:OD1	1:A:885:LYS:N	2.37	0.49
3:E:486:ASN:OD1	3:E:487:LEU:N	2.45	0.49
3:E:550:ARG:HA	3:E:553:ARG:HG2	1.94	0.49
3:E:784:LEU:HD21	3:E:802:LEU:HD11	1.93	0.49
3:E:1334:ILE:HD11	3:E:1339:LEU:HD12	1.94	0.49
3:E:1523:ARG:NH2	3:E:1551:ILE:HG12	2.27	0.49
3:F:492:PRO:HD3	3:F:560:LYS:HG2	1.94	0.49
3:H:2033:ASP:OD2	3:H:2036:ASN:ND2	2.40	0.49
3:H:2205:GLU:HB3	3:H:2235:THR:HG21	1.93	0.49
3:K:2205:GLU:HB3	3:K:2235:THR:HG21	1.93	0.49
3:E:845:GLU:O	3:E:848:GLY:N	2.46	0.49
3:E:1903:ASP:HA	3:E:1906:LYS:HD3	1.95	0.49
3:F:1651:PRO:HD2	3:F:1711:TYR:HE1	1.78	0.49
1:G:614:PHE:HE2	1:G:1157:MET:HE3	1.77	0.49
1:G:792:ASP:O	1:G:798:ARG:NH1	2.42	0.49
3:H:932:ASP:OD1	3:H:933:PRO:HD3	2.12	0.49
3:H:978:SER:OG	3:H:979:GLN:OE1	2.30	0.49
3:H:1140:LYS:HA	3:H:1143:MET:HE3	1.92	0.49
3:H:1844:LEU:HD21	3:H:2358:ILE:HD13	1.94	0.49
1:J:399:MET:HB3	1:J:404:CYS:HB2	1.93	0.49
3:E:1183:ASN:O	3:E:1187:ASN:ND2	2.45	0.49
3:F:987:LEU:HD12	3:F:990:LEU:HD12	1.94	0.49
1:G:84:SER:HB3	1:G:172:ILE:HG12	1.93	0.49
1:G:269:THR:HB	1:G:405:HIS:HB2	1.95	0.49
1:G:302:MET:HE2	1:G:336:PRO:HD3	1.94	0.49
1:J:343:MET:H	1:J:349:THR:HG21	1.77	0.49
1:J:708:THR:OG1	1:J:713:LYS:NZ	2.40	0.49
1:A:171:ARG:HA	1:A:215:PRO:HB2	1.95	0.49
1:B:932:PHE:HB3	1:B:1074:LEU:HD13	1.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:210:ILE:HD11	2:C:224:THR:HB	1.93	0.49
3:F:909:GLY:HA2	3:F:912:PRO:HD2	1.95	0.49
1:G:931:VAL:HA	1:G:968:TRP:HZ3	1.76	0.49
3:H:1033:LEU:HB3	3:H:1036:GLU:HB2	1.94	0.49
1:A:299:ILE:HD13	1:A:398:ILE:HG23	1.94	0.49
2:C:233:VAL:HG11	2:C:279:LEU:HD21	1.94	0.49
1:G:1203:LEU:HD11	1:G:1548:LYS:HB2	1.95	0.49
1:G:1267:ASP:OD1	1:G:1268:SER:N	2.45	0.49
3:K:944:GLN:HA	3:K:947:MET:HE2	1.95	0.49
1:B:287:CYS:HB3	1:B:295:ILE:HG21	1.94	0.49
2:C:162:LEU:HD11	2:C:176:ALA:HB1	1.95	0.49
3:E:85:THR:OG1	3:E:86:LEU:N	2.45	0.49
1:G:107:ALA:HB2	1:G:276:MET:HA	1.95	0.49
3:H:1027:GLU:HB2	3:H:1031:LYS:NZ	2.28	0.49
3:H:2027:ASN:HA	3:H:2030:LYS:HG2	1.95	0.49
3:H:2262:THR:HG22	3:H:2328:MET:HE1	1.95	0.49
1:J:1191:LYS:HE2	1:J:1467:HIS:HB3	1.93	0.49
2:L:135:ASP:OD2	2:L:141:ARG:NH2	2.46	0.49
1:A:194:ASN:HD21	1:A:198:THR:HG1	1.59	0.49
3:E:1955:GLU:HG2	3:E:1959:MET:HE1	1.94	0.49
3:E:1993:PRO:HA	3:E:1996:GLU:HG2	1.94	0.49
3:F:847:LEU:HA	3:F:850:LEU:HG	1.94	0.49
3:F:2201:PRO:HB2	3:F:2204:ILE:HB	1.95	0.49
1:G:88:LEU:HD23	1:G:176:TYR:HD1	1.77	0.49
1:G:1261:LYS:HB2	1:G:1272:LEU:HD23	1.95	0.49
1:A:764:GLY:O	1:A:807:HIS:ND1	2.35	0.48
1:A:1095:SER:OG	1:A:1096:ASN:N	2.44	0.48
1:B:1263:ILE:O	1:B:1269:ALA:HA	2.13	0.48
1:B:1359:THR:HG21	1:B:1409:HIS:HA	1.95	0.48
3:E:1024:SER:OG	3:E:1065:ARG:NH2	2.45	0.48
3:E:1445:TRP:HA	3:E:1448:LEU:HD12	1.95	0.48
3:F:1332:LEU:HB3	3:F:1334:ILE:HG23	1.95	0.48
3:F:2325:THR:HA	3:F:2328:MET:HE3	1.95	0.48
1:J:156:VAL:HG13	1:J:211:TRP:HZ3	1.78	0.48
3:K:1088:VAL:HA	3:K:1091:MET:HE2	1.95	0.48
3:K:2304:GLU:HB3	3:K:2307:ILE:HD13	1.95	0.48
3:E:548:LYS:HA	3:E:551:LYS:HE2	1.95	0.48
3:E:1909:PRO:O	3:E:1913:VAL:HG13	2.13	0.48
3:H:1914:TYR:HA	3:H:1917:MET:SD	2.52	0.48
3:K:1349:PHE:HB3	3:K:1378:GLN:HE22	1.78	0.48
3:K:1770:ILE:HG12	3:K:1817:ILE:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:2185:ASP:N	3:K:2185:ASP:OD1	2.45	0.48
1:B:182:PRO:HG2	1:B:191:TRP:CD1	2.48	0.48
1:B:308:ASP:OD1	1:B:309:SER:N	2.44	0.48
1:B:1378:ARG:HG2	1:B:1390:MET:HE1	1.94	0.48
3:H:929:ILE:HG21	3:H:942:ALA:HB1	1.95	0.48
3:K:1878:VAL:O	3:K:1881:GLN:NE2	2.39	0.48
1:B:185:THR:OG1	1:B:189:GLU:OE1	2.31	0.48
1:B:1167:SER:OG	1:B:1168:VAL:N	2.46	0.48
2:C:122:VAL:HG13	2:C:131:LEU:HD11	1.94	0.48
3:E:1266:LEU:HA	3:E:1269:VAL:HG12	1.95	0.48
3:E:1603:LYS:HE3	3:E:1605:LYS:HG2	1.95	0.48
3:F:1244:ILE:HD11	3:F:1314:ILE:HD11	1.94	0.48
1:G:1167:SER:O	1:G:1171:ASN:ND2	2.46	0.48
1:J:931:VAL:HA	1:J:968:TRP:CZ3	2.48	0.48
3:F:1085:MET:HE2	3:F:1116:LEU:HD21	1.95	0.48
3:F:1956:LEU:HA	3:F:1959:MET:HE2	1.95	0.48
3:H:2136:ASP:OD1	3:H:2137:SER:N	2.46	0.48
3:H:2169:ILE:HD12	3:H:2170:PRO:HD2	1.96	0.48
3:K:2356:MET:HA	3:K:2359:LEU:HG	1.94	0.48
1:B:82:THR:HG22	1:B:171:ARG:HB3	1.96	0.48
3:F:546:ILE:HD13	3:F:599:ILE:HD12	1.95	0.48
3:F:671:PRO:O	3:F:675:GLN:NE2	2.46	0.48
3:F:864:ARG:O	3:F:867:VAL:HG22	2.13	0.48
3:F:1401:LYS:HB2	3:F:1404:TRP:CE2	2.48	0.48
1:G:160:CYS:HB2	1:G:211:TRP:HB3	1.94	0.48
1:G:1430:TRP:CD1	1:G:1437:PRO:HA	2.48	0.48
1:B:1225:ILE:HD13	1:B:1271:LEU:HD13	1.95	0.48
2:C:260:ALA:N	2:C:302:ASP:OD2	2.46	0.48
3:E:154:VAL:HG22	3:E:174:LEU:HD22	1.93	0.48
3:E:225:LEU:HB2	3:E:240:ARG:HH22	1.78	0.48
3:F:1616:ASN:OD1	3:F:1617:LEU:N	2.47	0.48
3:F:1671:LEU:HD22	3:F:1726:ARG:HH22	1.78	0.48
1:J:1146:ASP:HA	1:J:1149:ARG:HG2	1.96	0.48
1:J:1261:LYS:HZ2	1:J:1317:TRP:H	1.62	0.48
3:K:1027:GLU:HB2	3:K:1031:LYS:NZ	2.29	0.48
3:K:1116:LEU:O	3:K:1120:SER:OG	2.31	0.48
3:E:991:ILE:HD12	3:E:998:ILE:HD13	1.96	0.48
3:E:1841:GLN:O	3:E:1845:ARG:HG2	2.13	0.48
3:E:2228:PHE:HD2	3:E:2460:VAL:HG13	1.79	0.48
3:F:1446:GLU:O	3:F:1449:SER:OG	2.26	0.48
1:G:275:LEU:HD23	1:G:280:LEU:HD22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:931:VAL:HA	1:G:968:TRP:CZ3	2.49	0.48
3:K:1317:MET:HA	3:K:1320:ASN:HD22	1.78	0.48
3:K:2307:ILE:HA	3:K:2313:PRO:HB3	1.96	0.48
3:E:2064:GLN:HE21	3:E:2071:LEU:HD11	1.78	0.48
3:E:2243:VAL:O	3:E:2247:LYS:HG2	2.13	0.48
3:F:86:LEU:HD23	3:F:131:LEU:HD13	1.95	0.48
1:G:153:VAL:HA	1:G:156:VAL:HG22	1.96	0.48
1:G:194:ASN:OD1	1:G:197:TYR:N	2.47	0.48
3:H:1122:ARG:HA	3:H:1125:GLN:NE2	2.29	0.48
1:J:106:CYS:SG	1:J:107:ALA:N	2.87	0.48
1:J:113:VAL:HG11	1:J:127:GLN:HE22	1.78	0.48
1:A:1219:GLN:HA	1:A:1529:PRO:HG2	1.96	0.48
1:B:1199:TRP:H	1:B:1489:ASN:ND2	2.12	0.48
3:E:1087:ILE:O	3:E:1091:MET:HG3	2.14	0.48
3:F:795:MET:N	3:F:795:MET:SD	2.87	0.48
3:F:2189:VAL:HA	3:F:2192:ARG:HG2	1.96	0.48
3:H:2309:ARG:HD2	3:H:2311:LYS:HG3	1.96	0.48
3:H:2456:GLN:O	3:H:2462:ASN:ND2	2.42	0.48
1:J:1391:ILE:HG22	1:J:1392:ARG:HG3	1.96	0.48
3:K:1051:ILE:O	3:K:1056:GLN:NE2	2.47	0.48
3:K:2363:ALA:HB1	3:K:2422:ALA:HB1	1.94	0.48
1:A:607:GLU:HG2	1:A:608:LEU:HD12	1.95	0.47
2:D:32:ASP:OD1	2:D:33:SER:N	2.47	0.47
3:E:677:ASP:OD1	3:E:678:ASN:N	2.47	0.47
3:E:925:ASN:OD1	3:E:926:LEU:N	2.47	0.47
3:F:1668:ASP:N	3:F:1668:ASP:OD1	2.46	0.47
1:G:308:ASP:OD1	1:G:308:ASP:N	2.46	0.47
1:G:354:LEU:HA	1:G:357:ILE:HG22	1.95	0.47
1:J:228:ILE:HG13	1:J:229:LEU:HD22	1.96	0.47
1:J:357:ILE:HD11	1:J:529:PHE:HB3	1.96	0.47
3:K:981:ASP:OD1	3:K:981:ASP:N	2.46	0.47
3:K:1914:TYR:HA	3:K:1917:MET:SD	2.54	0.47
1:A:287:CYS:HB3	1:A:295:ILE:HG21	1.96	0.47
2:C:285:VAL:O	2:C:286:ARG:NE	2.38	0.47
3:E:1948:GLN:HB2	3:E:2076:LEU:HD13	1.96	0.47
3:E:2174:LYS:HA	3:E:2174:LYS:HE3	1.97	0.47
3:F:1987:MET:HA	3:F:1987:MET:HE3	1.96	0.47
1:G:349:THR:HG23	1:G:352:GLY:H	1.79	0.47
1:J:1359:THR:OG1	1:J:1408:VAL:O	2.31	0.47
3:K:2027:ASN:O	3:K:2031:SER:OG	2.30	0.47
3:E:405:ASP:N	3:E:405:ASP:OD1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:1063:PRO:HA	3:E:1066:ILE:HG22	1.96	0.47
3:E:2080:VAL:HG12	3:E:2092:VAL:HG11	1.95	0.47
3:F:1673:GLN:HB3	3:F:1677:PHE:CE2	2.48	0.47
1:G:109:VAL:HG13	1:G:281:PRO:HA	1.96	0.47
1:G:985:LEU:HD11	1:G:1140:LEU:HD22	1.95	0.47
1:J:1167:SER:O	1:J:1171:ASN:ND2	2.48	0.47
3:K:1228:ALA:O	3:K:1243:TRP:NE1	2.46	0.47
3:E:505:ASN:ND2	3:E:516:ASN:OD1	2.47	0.47
3:E:909:GLY:HA2	3:E:912:PRO:HD2	1.96	0.47
3:E:1064:ILE:HG12	3:E:1102:ILE:HG13	1.96	0.47
3:H:1129:ARG:HA	3:H:1132:ASN:HD21	1.78	0.47
1:J:1288:ASP:OD2	1:J:1291:THR:OG1	2.32	0.47
3:K:1752:ASP:HB3	3:K:1755:TRP:HB2	1.96	0.47
3:K:1953:SER:O	3:K:1957:ILE:HD12	2.15	0.47
3:K:2210:LEU:HA	3:K:2213:ALA:HB3	1.96	0.47
1:B:106:CYS:SG	1:B:107:ALA:N	2.87	0.47
3:E:1595:LEU:HD21	3:E:1611:ARG:CZ	2.45	0.47
3:E:2259:THR:O	3:E:2263:ARG:HG3	2.14	0.47
3:F:248:LYS:HE3	3:F:286:VAL:HB	1.95	0.47
1:G:1419:VAL:HG22	1:G:1429:LEU:HG	1.97	0.47
3:H:1323:GLU:HA	3:H:1326:GLU:HB2	1.95	0.47
1:A:125:ILE:HG13	1:A:149:LEU:HA	1.97	0.47
1:B:609:LYS:O	1:B:613:VAL:HG23	2.15	0.47
1:B:921:SER:HB2	1:B:1138:LEU:HB3	1.96	0.47
3:E:2119:ASP:OD1	3:E:2119:ASP:N	2.47	0.47
3:F:1962:LEU:HD12	3:F:2006:ARG:HG2	1.96	0.47
1:G:728:PRO:HA	1:G:731:GLN:HG2	1.96	0.47
3:H:2274:ILE:HG23	3:H:2433:LEU:HD11	1.95	0.47
1:A:64:ASN:HD22	1:A:64:ASN:C	2.18	0.47
1:A:608:LEU:HB3	1:A:612:LEU:HD23	1.97	0.47
2:D:163:GLN:N	2:D:177:ALA:O	2.46	0.47
3:E:1416:ALA:HA	3:E:1419:ASN:HD22	1.80	0.47
3:E:1587:ASN:O	3:E:1591:TRP:HB2	2.15	0.47
3:E:2081:PRO:HB3	3:E:2169:ILE:HD11	1.95	0.47
3:E:2138:LEU:HD21	3:E:2368:ILE:HD12	1.97	0.47
3:F:383:ALA:HB1	3:F:386:THR:HB	1.97	0.47
3:F:1581:LEU:HD11	3:F:1591:TRP:CE2	2.50	0.47
3:F:1841:GLN:OE1	3:F:1841:GLN:N	2.43	0.47
3:F:2248:SER:OG	3:F:2253:THR:OG1	2.29	0.47
3:F:2275:LEU:HD22	3:F:2277:LEU:HB2	1.96	0.47
3:F:2437:ASP:OD1	3:F:2437:ASP:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:556:ILE:O	1:G:560:VAL:HG23	2.15	0.47
1:G:709:THR:N	1:G:712:GLN:OE1	2.48	0.47
1:J:286:SER:O	1:J:290:THR:HG22	2.14	0.47
3:K:1153:LEU:HG	3:K:1156:ASP:HB2	1.97	0.47
1:A:1194:SER:HB2	1:A:1199:TRP:HZ2	1.79	0.47
1:A:1215:MET:HE3	1:A:1224:LEU:HD11	1.96	0.47
1:A:1358:LEU:HD13	1:A:1370:ALA:HB2	1.95	0.47
1:B:917:SER:OG	1:B:1138:LEU:O	2.28	0.47
2:D:109:ILE:HD12	2:D:110:PRO:HD2	1.97	0.47
3:E:397:TYR:CD1	3:E:417:ILE:HD11	2.50	0.47
3:E:667:SER:OG	3:E:703:ARG:NH1	2.47	0.47
3:E:2130:HIS:N	3:E:2174:LYS:O	2.48	0.47
3:F:225:LEU:HB2	3:F:240:ARG:HH22	1.80	0.47
3:F:1553:GLU:O	3:F:1557:ILE:HG12	2.15	0.47
3:F:1870:ILE:HG21	3:F:1875:TRP:HE1	1.80	0.47
1:G:608:LEU:HD13	1:G:611:ILE:HD11	1.97	0.47
3:H:2134:ARG:HH21	3:H:2367:LEU:HB3	1.80	0.47
3:H:2280:ARG:N	3:H:2470:TRP:HE1	2.13	0.47
3:K:1252:LEU:HD21	3:K:1277:LEU:HD21	1.97	0.47
3:K:2006:ARG:HD3	3:K:2006:ARG:HA	1.63	0.47
1:A:182:PRO:HG2	1:A:191:TRP:CD1	2.50	0.47
1:A:294:GLU:O	1:A:298:ARG:HG3	2.14	0.47
2:D:272:HIS:ND1	2:D:292:HIS:O	2.47	0.47
3:E:902:ASP:N	3:E:902:ASP:OD1	2.47	0.47
3:E:2009:SER:O	3:E:2013:SER:OG	2.31	0.47
3:F:2224:LYS:HB3	3:F:2464:CYS:SG	2.55	0.47
1:G:737:LEU:HA	1:G:740:VAL:HG22	1.95	0.47
1:G:1522:LEU:HA	1:G:1538:ASN:HA	1.96	0.47
2:I:84:GLN:HE22	2:I:89:TRP:HD1	1.63	0.47
1:B:1522:LEU:HD13	1:B:1525:MET:HE3	1.97	0.47
2:D:237:ASP:OD1	2:D:237:ASP:N	2.46	0.47
3:E:1616:ASN:O	3:E:1620:LYS:HG2	2.15	0.47
3:E:1879:LEU:HG	3:E:1880:PRO:HD3	1.96	0.47
3:F:677:ASP:OD1	3:F:678:ASN:N	2.48	0.47
3:F:1430:GLU:HA	3:F:1433:MET:HE2	1.97	0.47
3:H:961:LEU:HA	3:H:964:ILE:HG12	1.96	0.47
3:H:2195:ARG:HH22	3:H:2204:ILE:HG21	1.80	0.47
1:J:109:VAL:HG13	1:J:281:PRO:HA	1.97	0.47
1:J:787:LEU:HA	1:J:790:LEU:HD12	1.96	0.47
1:A:884:ARG:HD2	3:H:2207:TRP:CD2	2.50	0.46
3:E:2138:LEU:O	3:E:2141:GLN:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:2280:ARG:O	3:H:2470:TRP:NE1	2.48	0.46
1:J:171:ARG:HD3	1:J:217:ILE:HG12	1.97	0.46
1:J:1203:LEU:HD11	1:J:1548:LYS:HB2	1.96	0.46
1:B:641:VAL:HG23	1:B:739:LEU:HD13	1.98	0.46
3:E:546:ILE:HG12	3:E:596:LEU:HD23	1.97	0.46
3:E:1972:ASP:OD1	3:E:1973:ASP:N	2.48	0.46
3:F:1655:TYR:HA	3:F:1658:LEU:HB2	1.96	0.46
3:F:2211:GLN:OE1	1:G:888:ARG:NE	2.49	0.46
1:G:218:PHE:HB2	1:G:264:GLN:HB3	1.97	0.46
3:H:1037:PHE:HZ	3:H:1044:THR:HG21	1.81	0.46
2:I:16:PHE:HD2	2:I:26:ARG:HB3	1.80	0.46
1:J:269:THR:HB	1:J:405:HIS:HB2	1.96	0.46
1:J:1156:GLN:HG2	1:J:1157:MET:HE2	1.96	0.46
3:E:1818:HIS:ND1	3:E:1858:GLU:OE2	2.47	0.46
3:E:2093:LYS:NZ	3:E:2094:ILE:O	2.48	0.46
3:E:2239:ASP:OD1	3:E:2240:LEU:N	2.48	0.46
3:F:1879:LEU:HA	3:F:1882:LEU:HB2	1.96	0.46
3:F:1970:GLY:HA3	3:F:1994:LEU:HD11	1.98	0.46
1:G:1392:ARG:HD3	1:G:1435:GLU:HG2	1.97	0.46
3:K:1965:GLU:HA	3:K:1968:TYR:HB3	1.98	0.46
1:A:1378:ARG:HD2	1:A:1393:ARG:HG3	1.97	0.46
3:E:1551:ILE:HD12	3:E:1554:LEU:HD21	1.97	0.46
3:F:248:LYS:HZ1	3:F:283:ASP:HB3	1.81	0.46
3:F:258:LEU:HD12	3:F:261:TYR:HB2	1.98	0.46
3:F:1218:LEU:HD12	3:F:1256:PRO:HD3	1.96	0.46
3:F:1376:ASN:ND2	3:F:1384:SER:OG	2.34	0.46
3:F:1542:TYR:HA	3:F:1545:VAL:HG12	1.96	0.46
3:H:1914:TYR:OH	3:H:2079:ALA:O	2.34	0.46
3:H:2266:ALA:O	3:H:2270:MET:HG2	2.15	0.46
2:I:144:ASP:N	2:I:144:ASP:OD1	2.48	0.46
1:J:527:THR:OG1	1:J:528:GLY:N	2.49	0.46
3:K:2319:ARG:NH2	3:K:2474:TRP:O	2.49	0.46
1:B:750:SER:O	1:B:756:ARG:NE	2.48	0.46
2:C:135:ASP:OD1	2:C:136:ARG:N	2.48	0.46
3:E:404:ILE:HD11	3:E:412:SER:H	1.80	0.46
3:E:2444:LEU:HB3	3:E:2449:GLN:HB2	1.97	0.46
3:F:1282:PHE:HZ	3:F:1297:LEU:HD21	1.79	0.46
3:F:1629:LYS:HE2	3:F:1629:LYS:HB2	1.71	0.46
3:F:1948:GLN:HE22	3:F:2077:GLU:HG2	1.81	0.46
1:G:1264:ASN:N	1:G:1319:GLN:HE22	2.09	0.46
2:I:97:GLY:HA2	2:I:119:VAL:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:216:CYS:N	1:J:262:CYS:HB2	2.31	0.46
1:J:289:LEU:HA	1:J:391:ASN:HB3	1.98	0.46
1:J:882:ASP:OD2	1:J:885:LYS:HB2	2.15	0.46
1:A:874:MET:O	1:A:878:LEU:HG	2.16	0.46
2:D:90:MET:HB2	2:D:102:TRP:HB2	1.96	0.46
3:E:2201:PRO:HB2	3:E:2204:ILE:HB	1.98	0.46
3:F:1455:LYS:HA	3:F:1455:LYS:HD2	1.61	0.46
3:F:1605:LYS:NZ	3:F:1633:THR:O	2.48	0.46
3:F:1909:PRO:O	3:F:1913:VAL:HG13	2.15	0.46
3:F:2219:LEU:HB2	3:F:2224:LYS:HG3	1.98	0.46
1:A:234:LYS:HA	1:A:237:GLN:HG3	1.98	0.46
3:E:1722:GLN:HA	3:E:1725:TRP:HB2	1.97	0.46
3:F:913:SER:OG	3:F:914:ASN:N	2.47	0.46
3:F:1816:LEU:C	3:F:1820:HIS:HD1	2.24	0.46
1:G:927:PHE:O	1:G:931:VAL:HG23	2.16	0.46
3:H:921:VAL:HA	3:H:924:HIS:CE1	2.50	0.46
2:I:132:ILE:HG12	2:I:142:ILE:HG12	1.97	0.46
1:J:1278:GLY:O	1:J:1300:GLY:N	2.39	0.46
3:K:1240:TRP:O	3:K:1244:ILE:HG12	2.16	0.46
1:A:872:GLN:HA	1:A:875:GLN:HB2	1.97	0.46
3:E:867:VAL:HG13	3:E:868:ARG:NH2	2.31	0.46
3:E:2166:TYR:HE2	3:E:2178:LEU:HD12	1.81	0.46
3:F:810:PHE:HE1	3:F:823:LEU:HD23	1.81	0.46
3:F:1305:LEU:HD21	3:F:1318:LEU:HB2	1.97	0.46
1:J:731:GLN:NE2	1:J:770:ASN:OD1	2.48	0.46
1:J:1407:ASN:HB2	1:J:1462:MET:HB3	1.98	0.46
3:K:2044:TYR:HA	3:K:2047:VAL:HG22	1.96	0.46
3:K:2315:LYS:NZ	3:K:2456:GLN:OE1	2.48	0.46
2:L:142:ILE:HB	2:L:152:HIS:HB2	1.97	0.46
1:A:610:PRO:HA	1:A:613:VAL:HG12	1.98	0.46
1:A:1000:HIS:HB3	1:A:1003:LEU:HB3	1.97	0.46
1:B:125:ILE:HG13	1:B:149:LEU:HA	1.98	0.46
1:B:609:LYS:HD3	1:B:643:VAL:HG23	1.97	0.46
3:E:857:GLU:OE1	3:E:859:ASN:N	2.38	0.46
3:E:1335:PRO:HG2	3:E:1338:THR:HG22	1.98	0.46
3:F:2424:LEU:HD23	3:F:2427:LYS:NZ	2.30	0.46
2:I:134:CYS:HB3	2:I:165:LEU:HD22	1.98	0.46
1:J:73:TRP:CE3	1:J:589:LEU:HB3	2.51	0.46
3:K:1079:ASP:OD1	3:K:1079:ASP:N	2.47	0.46
3:K:1755:TRP:HE3	3:K:1758:ALA:HB2	1.79	0.46
3:K:2076:LEU:HG	3:K:2078:LEU:HG	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:55:VAL:HG13	2:D:71:PHE:HD2	1.81	0.46
3:E:1002:VAL:HA	3:E:1005:ILE:HG22	1.97	0.46
3:E:1578:ASN:ND2	3:E:1610:VAL:HG11	2.30	0.46
3:E:1972:ASP:HB3	3:E:2048:PHE:HE2	1.80	0.46
3:F:902:ASP:OD1	3:F:902:ASP:N	2.49	0.46
3:F:1089:VAL:HG11	3:F:1122:ARG:HG2	1.96	0.46
3:F:1127:LEU:HD23	3:F:1130:ILE:HD12	1.97	0.46
1:G:1235:VAL:O	1:G:1244:LEU:N	2.46	0.46
3:H:2076:LEU:HB3	3:H:2094:ILE:HB	1.98	0.46
1:J:358:PHE:O	1:J:362:THR:HG22	2.15	0.46
3:E:622:ILE:HG13	3:E:623:LYS:N	2.31	0.45
3:F:1294:GLN:O	3:F:1298:ILE:HD12	2.16	0.45
1:B:357:ILE:HG23	1:B:425:TRP:HZ3	1.81	0.45
3:E:1589:ASP:OD1	3:E:1589:ASP:N	2.48	0.45
3:E:2318:PHE:HZ	3:E:2454:ILE:HG22	1.81	0.45
1:G:286:SER:O	1:G:290:THR:HG22	2.16	0.45
1:G:1179:ARG:HH22	1:G:1220:PHE:HB3	1.81	0.45
1:G:1215:MET:HG2	1:G:1226:THR:HG22	1.98	0.45
1:J:382:ASP:N	1:J:382:ASP:OD1	2.48	0.45
1:A:1257:VAL:HA	1:A:1275:SER:HA	1.98	0.45
1:B:564:GLN:HB2	1:B:567:ARG:HH12	1.80	0.45
2:C:237:ASP:OD1	2:C:237:ASP:N	2.48	0.45
3:E:647:MET:HG2	3:F:1159:VAL:HG23	1.97	0.45
3:E:934:SER:O	3:E:938:HIS:ND1	2.50	0.45
3:E:1299:GLN:O	3:E:1303:LYS:NZ	2.36	0.45
3:E:1568:ASP:OD1	3:E:1569:LYS:N	2.49	0.45
3:F:154:VAL:HG22	3:F:174:LEU:HD22	1.97	0.45
3:F:1632:ASN:OD1	3:F:1633:THR:N	2.50	0.45
3:F:2154:ALA:HA	3:F:2157:PHE:HB2	1.98	0.45
1:G:125:ILE:HG21	1:G:149:LEU:HA	1.98	0.45
3:H:1976:ARG:NH1	3:H:1977:GLN:HB3	2.31	0.45
1:J:171:ARG:HG3	1:J:215:PRO:HB2	1.97	0.45
1:J:367:TRP:CE2	1:J:591:ILE:HD11	2.51	0.45
1:J:554:LEU:HA	1:J:557:VAL:HG12	1.99	0.45
1:J:601:LEU:HD23	1:J:612:LEU:HD21	1.98	0.45
3:E:1995:TYR:O	3:E:1999:LYS:NZ	2.50	0.45
3:F:550:ARG:HA	3:F:553:ARG:HG2	1.98	0.45
3:F:1247:LEU:O	3:F:1251:LEU:HG	2.17	0.45
3:F:1328:ASP:OD1	3:F:1329:ASP:N	2.49	0.45
3:F:1767:PHE:HD1	3:F:1849:LEU:HD21	1.81	0.45
1:G:103:THR:OG1	1:G:105:PRO:O	2.27	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:216:CYS:HB2	1:G:262:CYS:HB2	1.55	0.45
1:G:578:LEU:O	1:G:618:ARG:NH1	2.49	0.45
1:G:939:ILE:HD13	1:G:1010:MET:HE3	1.98	0.45
3:H:2338:ARG:O	3:H:2341:CYS:HB2	2.16	0.45
1:A:965:TYR:HD2	1:A:1100:LYS:HE2	1.82	0.45
1:B:556:ILE:O	1:B:560:VAL:HG23	2.17	0.45
1:B:921:SER:HA	1:B:1138:LEU:HD23	1.98	0.45
1:B:992:TYR:CD2	1:B:1138:LEU:HD22	2.51	0.45
2:D:6:VAL:HG21	2:D:40:ILE:HD11	1.98	0.45
2:D:42:ASN:OD1	2:D:43:ASP:N	2.50	0.45
3:E:330:LEU:HB3	3:E:373:ILE:HD13	1.99	0.45
3:E:1282:PHE:HZ	3:E:1297:LEU:HD21	1.82	0.45
3:E:1991:LEU:HD13	3:E:2025:LEU:HD21	1.97	0.45
3:E:2156:CYS:HA	3:E:2159:ARG:HH21	1.81	0.45
3:F:673:LEU:HD12	3:F:704:LEU:HD21	1.97	0.45
3:K:1078:GLU:HB3	3:K:1114:ILE:HG22	1.97	0.45
3:K:2334:GLU:HA	3:K:2338:ARG:HG3	1.99	0.45
1:A:1077:LEU:O	1:A:1080:SER:OG	2.34	0.45
3:E:770:GLN:HG2	3:E:772:ALA:H	1.81	0.45
3:E:1430:GLU:HA	3:E:1433:MET:HE3	1.99	0.45
3:E:1758:ALA:HA	3:E:1761:ASN:HD21	1.81	0.45
3:E:1813:SER:OG	3:E:1815:ASN:OD1	2.35	0.45
3:E:2059:GLN:HA	3:E:2103:VAL:HG22	1.97	0.45
3:E:2448:GLU:O	3:E:2452:LYS:HG2	2.16	0.45
3:F:240:ARG:HB2	3:F:280:ILE:HD13	1.99	0.45
3:F:367:ARG:NH1	3:F:413:ASP:OD2	2.49	0.45
3:F:606:ASP:OD1	3:F:608:SER:N	2.46	0.45
3:F:1045:LEU:HD11	3:F:1084:ILE:HG13	1.99	0.45
3:F:1916:LEU:HB3	3:F:1935:ILE:HD11	1.97	0.45
3:F:2303:PHE:HB3	3:F:2425:VAL:HG21	1.98	0.45
1:G:205:LEU:HD23	1:G:232:PHE:HD1	1.82	0.45
3:H:1840:LEU:HD13	3:H:1878:VAL:HG22	1.98	0.45
3:H:1875:TRP:HB2	3:H:1904:LEU:HD21	1.97	0.45
1:J:1459:MET:HE1	1:J:1462:MET:HB2	1.99	0.45
1:A:88:LEU:HD23	1:A:176:TYR:HD1	1.82	0.45
1:A:811:GLY:H	1:A:922:ARG:HH12	1.65	0.45
1:B:1333:ILE:N	1:B:1347:ILE:O	2.44	0.45
2:C:57:LEU:HB2	2:C:69:ALA:HB3	1.98	0.45
2:D:210:ILE:HD11	2:D:224:THR:HB	1.97	0.45
2:D:211:THR:OG1	2:D:225:CYS:SG	2.63	0.45
2:D:218:ASP:OD1	2:D:218:ASP:N	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:732:MET:SD	3:E:734:LYS:HB3	2.57	0.45
3:E:987:LEU:HD12	3:E:990:LEU:HD12	1.98	0.45
3:E:2437:ASP:N	3:E:2437:ASP:OD1	2.50	0.45
3:E:2467:TYR:HD2	3:E:2469:GLY:H	1.63	0.45
3:F:85:THR:OG1	3:F:86:LEU:N	2.47	0.45
3:F:178:LEU:HD13	3:F:197:LEU:HG	1.99	0.45
3:F:925:ASN:HA	3:F:928:LYS:NZ	2.32	0.45
3:F:2081:PRO:HB3	3:F:2169:ILE:HD11	1.97	0.45
1:G:1412:ARG:N	1:G:1466:GLU:O	2.50	0.45
1:G:1493:ASN:OD1	1:G:1547:TYR:OH	2.32	0.45
3:K:968:ILE:HG13	3:K:972:MET:HE3	1.99	0.45
1:A:557:VAL:HA	1:A:560:VAL:HG12	1.98	0.45
1:A:558:LEU:HG	1:A:593:ILE:HD13	1.98	0.45
3:E:527:LEU:O	3:E:553:ARG:NH2	2.50	0.45
3:E:747:ILE:HG12	3:E:787:LEU:HD23	1.99	0.45
3:E:823:LEU:HD11	3:E:862:ILE:HG23	1.98	0.45
3:E:825:THR:HG23	3:E:826:LEU:HD12	1.98	0.45
3:E:1446:GLU:O	3:E:1449:SER:OG	2.27	0.45
3:E:1913:VAL:HA	3:E:1916:LEU:HD12	1.98	0.45
3:E:1963:TRP:HA	3:E:1966:GLN:OE1	2.17	0.45
3:F:945:ALA:O	3:F:949:ILE:HG12	2.16	0.45
1:J:1429:LEU:HD21	1:J:1483:THR:HB	1.99	0.45
3:K:1135:ASP:OD1	3:K:1135:ASP:N	2.49	0.45
1:A:988:GLN:HB3	1:A:1136:LEU:HD21	1.98	0.45
1:B:1249:ASN:HB3	1:B:1251:THR:HG23	1.98	0.45
3:E:501:LEU:HD23	3:E:504:LEU:HD21	1.99	0.45
3:E:768:LYS:HA	3:E:768:LYS:HD2	1.84	0.45
3:E:867:VAL:HG23	3:E:870:ILE:HD11	1.99	0.45
3:E:1370:GLU:HG2	3:E:1404:TRP:HE1	1.82	0.45
3:E:2143:PHE:HA	3:E:2146:VAL:HG22	1.99	0.45
3:F:418:LEU:HA	3:F:421:ILE:HG12	1.97	0.45
3:F:1660:TYR:HD2	3:F:1661:LEU:HD22	1.81	0.45
1:G:433:LEU:HD23	1:G:433:LEU:HA	1.80	0.45
1:G:905:SER:OG	1:G:1341:GLU:OE1	2.25	0.45
3:H:918:TYR:HE2	3:H:1284:SER:HB3	1.82	0.45
3:H:967:GLY:O	3:H:971:VAL:HG23	2.17	0.45
3:H:1102:ILE:HA	3:H:1105:ILE:HG12	1.99	0.45
3:H:2083:THR:HB	3:H:2167:PRO:HG3	1.98	0.45
2:I:185:VAL:HG13	2:I:200:VAL:HB	1.99	0.45
1:J:386:ALA:O	1:J:390:ARG:HB2	2.17	0.45
3:K:1844:LEU:O	3:K:1848:THR:HG23	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:2195:ARG:HE	3:K:2200:ILE:HG13	1.81	0.45
1:A:620:MET:SD	1:A:722:SER:OG	2.73	0.45
1:B:794:VAL:HG23	1:B:797:VAL:HG22	1.98	0.45
2:C:9:GLY:HA2	2:C:296:VAL:HG12	1.99	0.45
3:E:847:LEU:HA	3:E:850:LEU:HG	1.97	0.45
3:F:1310:ASN:C	3:F:1310:ASN:HD22	2.24	0.45
1:G:155:ASP:HA	1:G:158:ARG:NH1	2.32	0.45
1:G:174:PHE:HB3	1:G:218:PHE:CD1	2.52	0.45
1:J:86:ALA:HB1	1:J:159:PHE:CZ	2.52	0.45
1:J:433:LEU:HD23	1:J:433:LEU:HA	1.80	0.45
3:K:1766:ASN:HB2	3:K:1824:ALA:HB2	1.99	0.45
3:K:1939:ARG:HE	3:K:1943:PRO:HB3	1.82	0.45
3:K:2027:ASN:HA	3:K:2030:LYS:HG2	1.98	0.45
2:L:160:THR:OG1	2:L:178:ASN:ND2	2.46	0.45
1:A:376:LYS:HB3	1:A:376:LYS:HE2	1.73	0.44
1:A:834:SER:O	1:A:838:HIS:ND1	2.50	0.44
2:C:109:ILE:HD12	2:C:110:PRO:HD2	1.99	0.44
2:D:99:ILE:HG21	2:D:131:LEU:HD21	1.99	0.44
3:E:383:ALA:HB3	3:E:389:TYR:H	1.82	0.44
3:E:811:GLN:HB3	3:E:849:ILE:HG12	1.99	0.44
3:E:1168:LEU:HD22	3:E:1173:ILE:HB	1.99	0.44
3:E:1178:TYR:O	3:E:1182:VAL:HG23	2.18	0.44
3:E:1247:LEU:HA	3:E:1250:GLN:HE22	1.82	0.44
3:E:1481:TRP:HA	3:E:1484:ILE:HD12	1.99	0.44
3:F:622:ILE:HG13	3:F:623:LYS:N	2.31	0.44
3:F:1353:LEU:O	3:F:1357:GLU:HG2	2.16	0.44
3:F:1972:ASP:OD1	3:F:1972:ASP:N	2.49	0.44
3:H:2134:ARG:NH2	3:H:2367:LEU:HB3	2.31	0.44
1:J:927:PHE:HB3	1:J:993:ILE:HD11	1.98	0.44
2:C:42:ASN:OD1	2:C:42:ASN:N	2.50	0.44
2:D:5:LEU:HG	2:D:17:TRP:HB2	1.98	0.44
2:D:226:SER:OG	2:D:227:ALA:N	2.50	0.44
3:E:1945:LEU:HD12	3:E:1948:GLN:HE21	1.82	0.44
3:F:1405:TYR:HB3	3:F:1410:ARG:HB2	1.98	0.44
1:G:376:LYS:HD3	1:G:380:ARG:HG3	1.98	0.44
1:A:1249:ASN:HB3	1:A:1251:THR:HG23	1.98	0.44
1:A:1314:LEU:HD13	1:A:1355:ILE:HG22	1.99	0.44
1:B:427:LEU:HD11	3:F:713:VAL:HG12	1.98	0.44
1:B:1406:ASN:ND2	1:B:1459:MET:O	2.49	0.44
2:D:229:HIS:NE2	2:D:250:GLN:O	2.46	0.44
3:E:309:ARG:HA	3:E:309:ARG:HD3	1.73	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:737:GLU:O	3:E:741:THR:HG22	2.18	0.44
3:E:863:ARG:O	3:E:866:THR:OG1	2.30	0.44
3:E:1101:LYS:HA	3:E:1104:ILE:HG12	1.97	0.44
3:F:472:LEU:HD23	3:F:472:LEU:HA	1.87	0.44
3:F:1591:TRP:CD1	3:F:1614:PHE:HD1	2.35	0.44
1:G:527:THR:OG1	1:G:528:GLY:N	2.49	0.44
3:H:2017:ASP:OD2	3:H:2050:LYS:NZ	2.43	0.44
1:J:153:VAL:HA	1:J:156:VAL:HG12	2.00	0.44
1:J:1489:ASN:OD1	1:J:1490:SER:N	2.49	0.44
1:A:84:SER:HB3	1:A:163:LEU:HD22	1.99	0.44
1:B:395:ALA:HA	1:B:398:ILE:HG22	1.99	0.44
2:D:250:GLN:C	2:D:251:ARG:HD2	2.42	0.44
3:E:1049:LEU:HD21	3:E:1087:ILE:HG13	1.99	0.44
3:F:281:ARG:HB3	3:F:331:LEU:HD13	1.98	0.44
3:F:1587:ASN:O	3:F:1591:TRP:HB2	2.17	0.44
3:F:1891:GLN:HG2	3:F:1892:ILE:H	1.82	0.44
1:G:356:TRP:HZ2	1:G:560:VAL:HA	1.83	0.44
1:G:1489:ASN:OD1	1:G:1490:SER:N	2.50	0.44
1:G:1531:ARG:HB2	1:G:1533:MET:HE2	1.98	0.44
3:H:1752:ASP:HB3	3:H:1755:TRP:HB2	2.00	0.44
3:H:2053:LYS:O	3:H:2056:PRO:HD2	2.17	0.44
1:J:44:ASP:O	1:J:48:LYS:NZ	2.49	0.44
1:J:148:SER:HB2	1:J:151:PRO:HG3	2.00	0.44
1:J:911:GLU:HA	1:J:914:VAL:HG12	1.99	0.44
3:K:1115:ASN:OD1	3:K:1152:GLN:NE2	2.50	0.44
3:E:367:ARG:NH1	3:E:413:ASP:OD2	2.50	0.44
3:F:606:ASP:OD1	3:F:607:SER:N	2.51	0.44
3:F:2163:ILE:HG23	3:F:2268:MET:HE1	2.00	0.44
1:G:1429:LEU:HD11	1:G:1471:ILE:HD11	2.00	0.44
3:H:2250:SER:H	3:H:2253:THR:HB	1.83	0.44
3:H:2315:LYS:O	3:H:2456:GLN:NE2	2.43	0.44
1:J:367:TRP:CD2	1:J:591:ILE:HD11	2.52	0.44
1:J:934:ASP:HB3	1:J:968:TRP:HZ3	1.82	0.44
1:A:45:LYS:O	1:A:49:THR:OG1	2.23	0.44
1:A:171:ARG:NH1	1:A:261:ASP:OD1	2.39	0.44
3:E:1323:GLU:OE1	3:E:1355:TYR:OH	2.32	0.44
3:H:944:GLN:HA	3:H:947:MET:HE2	1.99	0.44
3:H:1726:ARG:NE	3:H:1730:GLN:OE1	2.42	0.44
3:K:1095:SER:OG	3:K:1096:ALA:N	2.48	0.44
1:A:711:GLU:O	1:A:715:MET:HG2	2.17	0.44
1:A:777:CYS:HA	1:A:780:THR:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:311:TYR:HE1	1:B:338:VAL:HG22	1.83	0.44
1:B:903:ASP:OD1	1:B:903:ASP:N	2.46	0.44
3:E:2135:GLN:HA	3:E:2138:LEU:HG	1.99	0.44
3:F:222:TRP:HE3	3:F:243:ALA:HB2	1.83	0.44
3:F:309:ARG:HD3	3:F:309:ARG:HA	1.71	0.44
3:F:732:MET:SD	3:F:734:LYS:HB3	2.58	0.44
3:F:1439:LEU:HD12	3:F:1448:LEU:HD23	2.00	0.44
3:F:1570:ARG:NH2	3:F:1573:MET:HG3	2.33	0.44
3:F:1738:PRO:HA	3:F:1741:ILE:HG12	2.00	0.44
1:G:645:VAL:HG22	1:G:742:LYS:HG2	2.00	0.44
1:G:794:VAL:HB	1:G:797:VAL:HG22	1.99	0.44
3:H:924:HIS:O	3:H:928:LYS:NZ	2.40	0.44
3:H:1091:MET:HE2	3:H:1103:SER:OG	2.18	0.44
3:H:1157:PHE:O	3:H:1161:VAL:HG23	2.17	0.44
3:H:1953:SER:O	3:H:1957:ILE:HD12	2.18	0.44
1:J:133:GLN:HE21	1:J:145:TYR:HD2	1.66	0.44
1:J:728:PRO:HA	1:J:731:GLN:HG2	1.98	0.44
3:K:1952:VAL:HG23	3:K:2070:LEU:HD22	1.99	0.44
1:A:348:ARG:HH12	1:A:563:SER:HB2	1.83	0.44
1:A:924:SER:O	1:A:928:ILE:HG12	2.18	0.44
3:E:946:ILE:HA	3:E:949:ILE:HG12	1.99	0.44
3:F:334:ARG:HH22	3:F:372:ALA:HB3	1.83	0.44
3:F:555:GLN:HA	3:F:558:MET:HG3	2.00	0.44
3:F:731:ASN:HA	3:F:736:LYS:HE3	2.00	0.44
3:F:1363:GLU:HA	3:F:1364:PRO:HD3	1.91	0.44
3:F:1379:LEU:HB3	3:F:1381:GLN:OE1	2.18	0.44
3:H:977:PRO:HA	3:H:980:LEU:HG	2.00	0.44
3:H:2186:THR:OG1	3:H:2285:LEU:O	2.28	0.44
2:I:42:ASN:OD1	2:I:43:ASP:N	2.51	0.44
3:K:950:PHE:HD1	3:K:953:LEU:HD21	1.82	0.44
3:K:2280:ARG:H	3:K:2470:TRP:HE1	1.66	0.44
1:A:934:ASP:OD1	1:A:965:TYR:OH	2.32	0.44
1:B:884:ARG:HD2	3:K:2207:TRP:CD2	2.53	0.44
2:C:32:ASP:OD1	2:C:33:SER:N	2.51	0.44
3:E:244:LEU:HD22	3:E:284:ALA:HA	1.99	0.44
3:F:536:ASN:OD1	3:F:537:GLN:N	2.51	0.44
3:F:659:LEU:HD21	3:F:690:ILE:HG13	2.00	0.44
3:F:737:GLU:O	3:F:741:THR:HG22	2.18	0.44
1:G:1361:ASP:N	1:G:1361:ASP:OD1	2.45	0.44
1:J:1317:TRP:HE1	1:J:1319:GLN:CD	2.26	0.44
3:K:1298:ILE:HD11	3:K:1332:LEU:HD22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:GLU:HA	1:A:59:LYS:HB2	2.00	0.43
1:B:613:VAL:HG21	1:B:643:VAL:HG21	2.00	0.43
3:F:139:ILE:HG22	3:F:147:LYS:HA	1.98	0.43
3:F:1495:SER:O	3:F:1498:LYS:HG2	2.17	0.43
3:F:1822:ILE:HA	3:F:1825:ILE:HG12	2.00	0.43
3:F:1895:ARG:HA	3:F:1898:LEU:HG	1.99	0.43
1:G:1317:TRP:HE1	1:G:1319:GLN:CD	2.26	0.43
3:H:1761:ASN:HA	3:H:1764:LEU:HG	2.00	0.43
1:A:171:ARG:HD2	1:A:385:ILE:HD11	2.00	0.43
1:A:869:ARG:O	1:A:873:VAL:HG23	2.18	0.43
2:D:29:GLN:OE1	1:J:781:GLY:O	2.36	0.43
3:F:163:SER:HB2	3:F:167:LEU:HG	2.00	0.43
3:F:493:MET:HE1	3:F:580:MET:HG2	1.99	0.43
3:F:1523:ARG:HA	3:F:1526:LEU:HG	1.99	0.43
3:F:1929:LYS:HD3	3:F:1932:LEU:HD21	2.00	0.43
3:H:1020:ILE:HD12	3:H:1023:ILE:HD11	1.99	0.43
3:H:1161:VAL:O	3:H:1165:ASN:ND2	2.51	0.43
1:J:1103:THR:HB	1:J:1105:LYS:HE3	2.00	0.43
1:J:1361:ASP:N	1:J:1361:ASP:OD1	2.48	0.43
3:K:1963:TRP:NE1	3:K:2007:GLU:HG3	2.34	0.43
3:E:1004:LYS:NZ	3:E:1008:VAL:HG21	2.33	0.43
3:F:383:ALA:HB3	3:F:389:TYR:HB2	2.00	0.43
3:F:606:ASP:HB3	3:F:609:VAL:H	1.83	0.43
3:F:1101:LYS:HA	3:F:1104:ILE:HG12	2.00	0.43
3:F:1250:GLN:HA	3:F:1253:LYS:HE2	1.99	0.43
3:F:1571:LEU:HA	3:F:1574:ARG:NH1	2.34	0.43
3:F:1595:LEU:HD21	3:F:1611:ARG:CZ	2.48	0.43
3:F:2237:GLY:N	3:F:2322:ARG:HH21	2.16	0.43
3:F:2353:GLY:HA2	3:F:2356:MET:HE2	2.00	0.43
1:G:1430:TRP:HE1	1:G:1437:PRO:HB3	1.83	0.43
3:H:2249:ARG:H	3:H:2253:THR:HG21	1.83	0.43
1:J:909:ARG:NH1	1:J:1297:ALA:O	2.51	0.43
1:J:1105:LYS:HB2	1:J:1106:LYS:HZ1	1.83	0.43
3:K:2286:MET:HB3	3:K:2295:ILE:HB	2.00	0.43
1:A:936:LEU:HB3	1:A:1010:MET:HE1	2.01	0.43
1:B:358:PHE:HB2	1:B:425:TRP:CH2	2.53	0.43
1:B:638:MET:HA	1:B:641:VAL:HG12	1.99	0.43
1:B:757:GLN:HE22	1:B:1144:PHE:HE2	1.65	0.43
2:C:188:MET:HE3	2:C:192:THR:HA	2.00	0.43
2:D:223:ALA:HA	2:D:233:VAL:HA	2.00	0.43
3:E:389:TYR:O	3:E:393:ILE:HG12	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1445:TRP:HA	3:F:1448:LEU:HD12	2.00	0.43
3:F:1620:LYS:HE3	3:F:1620:LYS:HA	2.00	0.43
3:F:1888:GLN:HG2	3:F:1894:SER:HA	1.99	0.43
3:F:2114:CYS:SG	3:F:2122:ASP:HB3	2.59	0.43
3:H:1078:GLU:HB3	3:H:1114:ILE:HG22	2.00	0.43
3:H:1084:ILE:HD12	3:H:1087:ILE:HD12	1.99	0.43
3:H:1878:VAL:HG12	3:H:1881:GLN:NE2	2.34	0.43
3:H:2319:ARG:HH21	3:H:2474:TRP:C	2.26	0.43
2:I:140:ILE:HB	2:I:154:LEU:HB2	2.00	0.43
3:K:2288:ASP:HB3	3:K:2292:GLY:H	1.83	0.43
1:A:68:GLN:HA	1:A:69:PRO:HD3	1.93	0.43
1:B:861:GLN:HA	1:B:864:ILE:HD12	2.00	0.43
1:B:1358:LEU:HD13	1:B:1370:ALA:HB2	2.01	0.43
2:D:285:VAL:O	2:D:286:ARG:NE	2.44	0.43
3:E:947:MET:HE3	3:E:947:MET:HA	2.00	0.43
3:F:656:GLU:HA	3:F:659:LEU:HD23	1.99	0.43
3:F:1335:PRO:HB2	3:F:1338:THR:HG22	1.99	0.43
3:F:1482:ASP:OD1	3:F:1482:ASP:N	2.47	0.43
3:F:2174:LYS:HE3	3:F:2174:LYS:HA	2.00	0.43
3:F:2467:TYR:HD2	3:F:2469:GLY:H	1.65	0.43
1:G:93:LEU:HD12	1:G:124:ALA:HA	2.01	0.43
1:J:1255:THR:HG21	1:J:1277:ASP:HB3	2.01	0.43
3:E:470:CYS:HA	3:E:507:LYS:HG2	1.99	0.43
3:E:953:LEU:O	3:E:956:ARG:NH2	2.52	0.43
3:E:981:ASP:OD1	3:E:1021:THR:OG1	2.34	0.43
3:E:1043:GLU:O	3:E:1046:THR:OG1	2.31	0.43
3:F:1568:ASP:OD1	3:F:1569:LYS:N	2.52	0.43
3:F:2421:ARG:HA	3:F:2424:LEU:HD12	2.01	0.43
1:G:216:CYS:N	1:G:262:CYS:HB2	2.34	0.43
1:G:225:ALA:O	1:G:229:LEU:HD23	2.19	0.43
1:G:809:ILE:HD11	1:G:915:TYR:HE1	1.82	0.43
3:H:948:HIS:O	3:H:951:GLN:HG3	2.19	0.43
3:H:2076:LEU:HD21	3:H:2078:LEU:HD12	1.99	0.43
3:H:2281:HIS:ND1	3:H:2283:SER:HB2	2.34	0.43
2:I:247:ASP:OD1	2:I:247:ASP:N	2.52	0.43
1:J:384:MET:HE3	1:J:388:LEU:HD21	2.00	0.43
3:K:1954:HIS:O	3:K:1958:ARG:HG2	2.18	0.43
3:K:1962:LEU:O	3:K:1965:GLU:HG2	2.19	0.43
1:A:757:GLN:NE2	1:A:800:ALA:HB2	2.33	0.43
1:B:206:TYR:HB2	1:B:235:PHE:CE2	2.54	0.43
1:B:434:THR:HA	1:B:437:VAL:HG12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:894:LEU:HD21	1:B:967:VAL:HG21	2.01	0.43
3:E:645:LEU:HD22	3:E:665:LEU:HD21	2.01	0.43
3:E:1843:ALA:HA	3:E:1846:LEU:HG	2.01	0.43
3:F:947:MET:HA	3:F:947:MET:HE3	2.00	0.43
3:H:938:HIS:HB3	3:H:942:ALA:HB2	2.01	0.43
1:J:108:ARG:NE	1:J:114:ASP:OD1	2.51	0.43
3:K:2171:LEU:H	3:K:2176:GLY:HA2	1.84	0.43
2:L:188:MET:HB2	2:L:197:LEU:HD23	2.00	0.43
1:A:932:PHE:HE1	1:A:997:LEU:HB2	1.84	0.43
1:B:1138:LEU:HD12	1:B:1138:LEU:HA	1.85	0.43
2:C:99:ILE:HD11	2:C:119:VAL:HB	2.01	0.43
3:E:452:LYS:HD3	3:E:452:LYS:HA	1.77	0.43
3:E:1067:LEU:HD23	3:E:1070:LEU:HD12	1.99	0.43
3:E:1159:VAL:HG23	3:F:647:MET:HG2	2.01	0.43
3:E:1429:VAL:HA	3:E:1432:MET:HE2	1.99	0.43
3:E:1648:LYS:HD2	3:E:1648:LYS:HA	1.88	0.43
3:F:225:LEU:HD13	3:F:232:SER:HB2	2.01	0.43
3:H:2191:ILE:O	3:H:2195:ARG:HG2	2.19	0.43
3:H:2319:ARG:NH2	3:H:2474:TRP:OXT	2.51	0.43
1:J:339:ASN:N	1:J:339:ASN:OD1	2.52	0.43
1:J:534:LEU:HA	1:J:534:LEU:HD23	1.86	0.43
1:J:1106:LYS:HD2	1:J:1106:LYS:H	1.76	0.43
3:K:976:PRO:HA	3:K:977:PRO:HD3	1.89	0.43
1:B:146:LYS:NZ	1:B:159:PHE:HA	2.34	0.43
1:B:366:ALA:HB2	1:B:393:LEU:HD11	2.01	0.43
3:E:248:LYS:HE3	3:E:286:VAL:HB	2.00	0.43
3:E:1456:TRP:CD1	3:E:1464:LYS:HE2	2.54	0.43
3:F:1499:GLU:HG3	3:F:1518:HIS:CD2	2.54	0.43
3:F:2232:LEU:HD13	3:F:2322:ARG:HD2	2.00	0.43
3:F:2246:LEU:HD23	3:F:2246:LEU:HA	1.88	0.43
3:F:2259:THR:O	3:F:2263:ARG:HG3	2.19	0.43
1:J:564:GLN:OE1	1:J:567:ARG:NE	2.52	0.43
3:K:1084:ILE:HD12	3:K:1087:ILE:HD12	2.01	0.43
3:K:2463:LEU:HA	3:K:2466:HIS:CE1	2.54	0.43
2:L:42:ASN:OD1	2:L:43:ASP:N	2.51	0.43
2:L:247:ASP:OD1	2:L:247:ASP:N	2.50	0.43
1:B:1001:LYS:HG3	1:B:1002:GLU:HG3	2.01	0.43
2:C:223:ALA:HA	2:C:233:VAL:HA	2.00	0.43
3:E:139:ILE:HG22	3:E:147:LYS:HA	2.01	0.43
3:E:835:TYR:CE2	3:E:839:PRO:HG3	2.54	0.43
3:E:852:ASN:O	3:E:856:THR:OG1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:1100:LYS:HE3	3:E:1100:LYS:HB2	1.92	0.43
3:E:1516:GLU:HA	3:E:1519:ILE:HG22	2.00	0.43
3:F:968:ILE:HG12	3:F:972:MET:HE3	2.01	0.43
3:F:1240:TRP:CD1	3:F:1311:PRO:HG3	2.54	0.43
3:F:1266:LEU:O	3:F:1270:TYR:HB3	2.19	0.43
3:F:1755:TRP:HD1	3:F:1758:ALA:HB2	1.83	0.43
3:F:2166:TYR:HE2	3:F:2178:LEU:HD12	1.84	0.43
2:I:21:THR:HG23	2:I:23:VAL:H	1.84	0.43
1:J:85:ALA:HB3	1:J:145:TYR:CD1	2.54	0.43
1:J:558:LEU:HD11	1:J:596:TYR:HD2	1.83	0.43
1:J:1412:ARG:N	1:J:1466:GLU:O	2.52	0.43
3:K:1107:LEU:HD23	3:K:1110:LEU:HD21	2.00	0.43
3:K:1327:HIS:HD2	3:K:2246:LEU:HA	1.84	0.43
3:K:2239:ASP:HB2	3:K:2323:MET:HE1	2.01	0.43
2:L:210:ILE:HA	2:L:226:SER:HA	2.01	0.43
1:A:585:VAL:HG11	1:A:622:ILE:HD13	2.01	0.42
1:A:589:LEU:HD11	1:A:619:ILE:HD11	2.01	0.42
1:A:1368:PHE:HE1	1:A:1382:ARG:HG3	1.84	0.42
1:B:271:ASP:OD1	1:B:271:ASP:N	2.44	0.42
2:D:15:ARG:HB2	2:D:24:CYS:SG	2.59	0.42
3:F:930:LEU:HA	3:F:935:LEU:HD11	2.01	0.42
3:F:2317:PRO:HG2	3:F:2457:ALA:HB2	2.01	0.42
1:G:229:LEU:HD11	1:G:264:GLN:OE1	2.19	0.42
1:G:630:GLU:OE1	1:G:630:GLU:CA	2.66	0.42
1:G:1465:HIS:CD2	1:G:1467:HIS:H	2.36	0.42
1:A:148:SER:HB2	1:A:159:PHE:CE2	2.54	0.42
1:B:1227:ALA:HB2	1:B:1260:LEU:HD11	2.00	0.42
3:E:1100:LYS:O	3:E:1104:ILE:HG23	2.20	0.42
3:E:1948:GLN:HG3	3:E:2078:LEU:HD11	2.00	0.42
3:E:2186:THR:HG22	3:E:2188:HIS:N	2.32	0.42
3:F:349:ASP:OD1	3:F:349:ASP:N	2.49	0.42
3:F:352:TYR:HE2	3:F:392:ARG:HE	1.65	0.42
3:F:1246:ARG:HE	3:F:1246:ARG:HB2	1.65	0.42
3:F:2281:HIS:CE1	3:F:2283:SER:HB3	2.54	0.42
1:G:229:LEU:HA	1:G:229:LEU:HD13	1.81	0.42
3:H:1131:LEU:O	3:H:1171:ASN:ND2	2.52	0.42
3:H:1155:THR:HG22	3:H:1185:LEU:HG	2.00	0.42
2:I:196:HIS:O	2:I:196:HIS:ND1	2.52	0.42
1:J:108:ARG:HD3	1:J:116:LEU:HD23	1.99	0.42
3:K:929:ILE:HG21	3:K:942:ALA:HB1	2.01	0.42
3:K:1856:ILE:HG22	3:K:1859:ALA:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:TYR:HE1	1:A:338:VAL:HG22	1.83	0.42
1:B:88:LEU:HD11	1:B:151:PRO:HG3	2.01	0.42
3:E:476:PHE:CZ	3:E:480:LEU:HB2	2.54	0.42
3:E:1150:LEU:HD13	3:E:1157:PHE:CD2	2.54	0.42
3:E:2270:MET:SD	3:E:2341:CYS:HB2	2.59	0.42
3:F:131:LEU:HA	3:F:134:LYS:HG2	2.01	0.42
3:F:1717:ARG:NH2	3:F:1720:LEU:HD13	2.29	0.42
3:F:2195:ARG:NH2	3:F:2205:GLU:OE2	2.47	0.42
3:H:2282:PRO:HA	3:H:2285:LEU:HB2	2.01	0.42
3:H:2321:THR:HG22	3:H:2324:LEU:HG	2.01	0.42
3:K:1850:TRP:HH2	3:K:1860:THR:HG22	1.84	0.42
1:A:370:LEU:HD22	1:A:374:LEU:HD23	2.01	0.42
1:A:805:LEU:HD23	1:A:805:LEU:HA	1.84	0.42
1:A:1489:ASN:OD1	1:A:1490:SER:N	2.52	0.42
1:B:45:LYS:HA	1:B:48:LYS:HG2	2.02	0.42
1:B:530:PHE:CD1	1:B:560:VAL:HG22	2.54	0.42
1:B:1194:SER:HB2	1:B:1199:TRP:HZ2	1.85	0.42
2:D:38:LEU:HA	2:D:48:ALA:O	2.20	0.42
2:D:227:ALA:HB1	2:D:252:TRP:CE2	2.53	0.42
3:E:222:TRP:HE3	3:E:243:ALA:HB2	1.85	0.42
3:E:1004:LYS:HZ3	3:E:1008:VAL:HG21	1.84	0.42
3:E:1143:MET:HA	3:E:1146:LEU:HG	2.00	0.42
3:E:1846:LEU:HD12	3:E:1847:LEU:HD22	2.01	0.42
3:E:1916:LEU:O	3:E:1920:ILE:HG12	2.20	0.42
3:E:1917:MET:O	3:E:1921:LYS:HG2	2.19	0.42
3:F:472:LEU:HB3	3:F:476:PHE:HB2	2.00	0.42
3:F:1100:LYS:HE3	3:F:1100:LYS:HB2	1.90	0.42
1:G:397:ARG:HD2	1:G:422:TRP:CD2	2.54	0.42
1:G:790:LEU:HD11	1:G:805:LEU:HD11	2.01	0.42
1:J:85:ALA:HB3	1:J:145:TYR:HD1	1.84	0.42
1:J:266:ALA:HB3	1:J:407:VAL:H	1.83	0.42
3:K:2150:LEU:HD12	3:K:2156:CYS:HB3	2.00	0.42
3:K:2438:ILE:HG22	3:K:2439:ARG:HG2	2.01	0.42
1:A:1493:ASN:OD1	1:A:1545:ASN:ND2	2.46	0.42
1:B:70:ILE:HG12	1:B:586:TYR:HB3	2.02	0.42
1:B:1157:MET:HE2	1:B:1157:MET:HB3	1.97	0.42
2:D:233:VAL:HG11	2:D:279:LEU:HD21	2.01	0.42
3:E:1326:GLU:HA	3:E:1331:PRO:HG3	2.01	0.42
3:F:1841:GLN:O	3:F:1845:ARG:HG2	2.19	0.42
3:F:2146:VAL:O	3:F:2150:LEU:HG	2.19	0.42
1:G:1362:GLN:HG3	1:G:1412:ARG:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:2184:SER:HA	3:H:2289:ARG:H	1.84	0.42
2:I:41:THR:O	2:I:301:ASN:ND2	2.53	0.42
1:J:53:PRO:HD3	1:J:1143:SER:HB3	2.01	0.42
3:K:1286:TRP:NE1	3:K:1294:GLN:HE22	2.17	0.42
3:K:2274:ILE:HG21	3:K:2348:LEU:HD13	2.01	0.42
1:A:358:PHE:HB2	1:A:425:TRP:CH2	2.54	0.42
1:A:417:THR:HG23	1:A:418:THR:HG23	2.02	0.42
3:E:364:ASP:OD1	3:E:364:ASP:N	2.51	0.42
3:E:600:SER:OG	3:E:603:GLU:OE1	2.30	0.42
3:E:1294:GLN:O	3:E:1298:ILE:HG12	2.19	0.42
3:E:1618:CYS:O	3:E:1621:SER:OG	2.33	0.42
3:E:2273:TYR:O	3:E:2432:LYS:NZ	2.48	0.42
3:F:867:VAL:HA	3:F:870:ILE:HG12	2.01	0.42
3:F:1713:LYS:HA	3:F:1713:LYS:HD2	1.81	0.42
3:F:2074:HIS:ND1	3:F:2075:ASP:OD2	2.46	0.42
3:H:934:SER:HA	3:H:937:ILE:HG12	2.02	0.42
3:H:1068:LYS:HA	3:H:1068:LYS:HD2	1.77	0.42
3:H:1252:LEU:HD21	3:H:1277:LEU:HD21	2.01	0.42
3:H:2198:LYS:HA	3:H:2198:LYS:HD2	1.84	0.42
1:J:367:TRP:HZ2	1:J:372:ARG:HH22	1.68	0.42
3:K:965:ILE:O	3:K:969:ILE:HG12	2.19	0.42
3:K:1102:ILE:HA	3:K:1105:ILE:HG12	2.01	0.42
3:K:1387:GLY:HA3	3:K:2335:GLY:HA2	2.00	0.42
1:A:990:ILE:HD12	1:A:990:ILE:HA	1.93	0.42
1:B:298:ARG:O	1:B:302:MET:HG2	2.20	0.42
2:D:74:HIS:ND1	2:D:94:SER:OG	2.41	0.42
3:E:1668:ASP:OD1	3:E:1668:ASP:N	2.52	0.42
3:F:1377:ASN:HD21	3:F:1408:LEU:HD21	1.84	0.42
3:F:1648:LYS:HD2	3:F:1648:LYS:HA	1.85	0.42
3:F:1959:MET:HE3	3:F:2070:LEU:HD11	2.02	0.42
3:F:2138:LEU:O	3:F:2141:GLN:HG3	2.20	0.42
1:G:164:ARG:NH1	1:G:215:PRO:HD2	2.32	0.42
1:G:792:ASP:OD1	1:G:798:ARG:HG3	2.19	0.42
1:G:1427:VAL:HG11	1:G:1471:ILE:HG21	2.01	0.42
3:H:1300:ALA:O	3:H:1303:LYS:HG3	2.19	0.42
3:H:2238:GLN:HG2	3:H:2326:TYR:HB3	2.01	0.42
1:J:275:LEU:HD11	1:J:402:TYR:HB3	2.01	0.42
1:J:1523:SER:HB3	1:J:1537:THR:HG23	2.02	0.42
1:A:1263:ILE:HD11	1:A:1272:LEU:HD12	2.01	0.42
3:E:131:LEU:HA	3:E:134:LYS:HG2	2.01	0.42
3:E:397:TYR:CE1	3:E:417:ILE:HD11	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:554:ASN:OD1	3:E:555:GLN:N	2.53	0.42
3:E:1379:LEU:HB3	3:E:1381:GLN:OE1	2.20	0.42
3:E:1716:ALA:HB2	3:E:1751:PHE:HB3	2.02	0.42
3:F:1681:MET:HE1	3:F:1715:LEU:HD12	2.01	0.42
3:F:1813:SER:OG	3:F:1815:ASN:OD1	2.29	0.42
3:F:2130:HIS:N	3:F:2174:LYS:O	2.53	0.42
1:G:894:LEU:HA	1:G:897:ILE:HG22	2.01	0.42
1:G:1212:PRO:HG2	1:G:1537:THR:HG21	2.02	0.42
3:K:969:ILE:HG22	3:K:973:ARG:HH12	1.85	0.42
3:K:1052:LEU:HD11	3:K:1066:ILE:HG21	2.02	0.42
3:K:2206:HIS:ND1	3:K:2210:LEU:HD23	2.35	0.42
2:L:185:VAL:HG23	2:L:200:VAL:HB	2.02	0.42
1:A:913:VAL:HG12	1:A:974:LEU:HD13	2.01	0.42
1:B:531:GLU:OE1	1:B:569:ARG:NH1	2.52	0.42
1:B:550:PRO:HA	1:B:551:PRO:HD3	1.89	0.42
1:B:711:GLU:O	1:B:715:MET:HG2	2.19	0.42
1:B:770:ASN:HB3	1:B:773:ASN:HB2	2.02	0.42
3:E:414:LYS:HA	3:E:417:ILE:HG22	2.00	0.42
3:E:652:ASP:O	3:E:658:ARG:NH2	2.35	0.42
3:E:1661:LEU:O	3:E:1664:THR:OG1	2.34	0.42
3:E:1879:LEU:HA	3:E:1882:LEU:HB2	2.01	0.42
3:F:860:PRO:HB2	3:F:864:ARG:HH22	1.85	0.42
3:F:1169:LEU:HD23	3:F:1169:LEU:HA	1.92	0.42
3:F:1881:GLN:O	3:F:1885:ARG:HD3	2.20	0.42
1:G:104:HIS:HB2	1:G:105:PRO:HD3	2.02	0.42
1:G:234:LYS:HA	1:G:234:LYS:HD2	1.77	0.42
1:G:885:LYS:HE2	1:G:885:LYS:HB2	1.65	0.42
1:G:1179:ARG:NH2	1:G:1221:GLU:OE2	2.46	0.42
1:J:103:THR:OG1	1:J:105:PRO:O	2.27	0.42
1:J:709:THR:N	1:J:712:GLN:OE1	2.52	0.42
1:J:1377:LEU:HB2	1:J:1394:TRP:HB2	2.00	0.42
3:K:1226:LYS:HA	3:K:1226:LYS:HD3	1.81	0.42
1:A:346:ASP:OD1	1:A:347:ARG:N	2.51	0.42
1:B:1225:ILE:HG22	1:B:1260:LEU:HD13	2.00	0.42
1:B:1534:ILE:HG23	1:B:1547:TYR:HB2	2.02	0.42
3:E:270:TRP:HH2	3:E:309:ARG:HB3	1.84	0.42
3:E:326:VAL:HG11	3:E:357:LYS:HZ1	1.84	0.42
3:E:1619:ARG:HH22	3:E:1659:LYS:HD3	1.84	0.42
3:E:1930:ALA:O	3:E:1934:ILE:HG12	2.20	0.42
3:F:1916:LEU:O	3:F:1920:ILE:HG12	2.19	0.42
3:F:2309:ARG:NH2	3:F:2312:PHE:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:108:ARG:HG2	1:G:115:PRO:HD2	2.02	0.42
1:G:630:GLU:O	1:G:630:GLU:HG2	2.19	0.42
3:H:1843:ALA:HB3	3:H:1878:VAL:HG11	2.02	0.42
1:J:1385:ASP:OD1	1:J:1388:ASP:N	2.50	0.42
2:L:269:SER:OG	2:L:270:SER:N	2.53	0.42
1:A:190:ILE:HG22	1:A:191:TRP:H	1.84	0.41
1:A:394:LEU:HD21	1:A:398:ILE:HD12	2.02	0.41
1:A:985:LEU:HD12	1:A:985:LEU:HA	1.85	0.41
1:A:1081:LEU:O	1:A:1085:GLU:HG2	2.19	0.41
1:B:918:HIS:NE2	1:B:1140:LEU:O	2.39	0.41
3:E:1237:LYS:H	3:E:1310:ASN:HD22	1.68	0.41
3:E:1586:LYS:HE2	3:E:1586:LYS:HB2	1.82	0.41
3:E:1816:LEU:C	3:E:1820:HIS:HD1	2.28	0.41
3:F:445:GLU:O	3:F:448:ARG:NE	2.50	0.41
3:F:1745:TYR:HB3	3:F:1762:TRP:HB2	2.02	0.41
1:G:1240:LYS:NZ	1:G:1242:LYS:HB3	2.35	0.41
1:J:162:SER:HA	1:J:165:ARG:HG2	2.02	0.41
1:J:1327:THR:HB	1:J:1333:ILE:HG12	2.01	0.41
1:A:1190:GLU:HA	1:A:1193:LEU:HD23	2.01	0.41
3:E:968:ILE:O	3:E:972:MET:HG2	2.20	0.41
3:E:1487:TYR:HA	3:E:1490:VAL:HG22	2.02	0.41
3:E:1612:ILE:HG13	3:E:1613:LYS:HD2	2.02	0.41
3:E:2246:LEU:HA	3:E:2246:LEU:HD23	1.86	0.41
3:F:1299:GLN:O	3:F:1303:LYS:NZ	2.36	0.41
3:F:1504:ILE:HG23	3:F:1600:LEU:HD11	2.02	0.41
3:F:1913:VAL:HA	3:F:1916:LEU:HD12	2.02	0.41
3:F:1917:MET:O	3:F:1921:LYS:HG2	2.20	0.41
3:F:2318:PHE:HZ	3:F:2454:ILE:HG22	1.85	0.41
1:G:593:ILE:HG13	1:G:597:VAL:HG13	2.02	0.41
3:H:1327:HIS:CD2	3:H:2246:LEU:HA	2.53	0.41
1:J:118:PHE:HE2	1:J:122:LYS:HB2	1.84	0.41
1:J:640:PHE:CZ	1:J:719:VAL:HG11	2.55	0.41
1:J:969:LYS:HA	1:J:969:LYS:HD3	1.86	0.41
1:J:1168:VAL:HA	1:J:1171:ASN:HD21	1.84	0.41
3:K:1107:LEU:HA	3:K:1110:LEU:HG	2.00	0.41
1:A:82:THR:HG22	1:A:171:ARG:HB3	2.01	0.41
3:E:352:TYR:HE2	3:E:392:ARG:HE	1.68	0.41
3:E:550:ARG:HD2	3:E:553:ARG:HD2	2.01	0.41
3:E:965:ILE:O	3:E:969:ILE:HG23	2.20	0.41
3:E:1084:ILE:HG22	3:E:1085:MET:HE2	2.03	0.41
3:E:1674:LEU:HD11	3:E:1726:ARG:NH1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:2219:LEU:HB3	3:E:2223:GLN:HB2	2.03	0.41
3:F:845:GLU:O	3:F:848:GLY:N	2.53	0.41
3:F:1828:PHE:O	3:F:1832:ILE:HD12	2.20	0.41
3:H:2134:ARG:NH1	3:H:2138:LEU:HD23	2.29	0.41
3:H:2185:ASP:OD1	3:H:2185:ASP:N	2.53	0.41
3:H:2356:MET:HA	3:H:2359:LEU:HG	2.02	0.41
3:K:946:ILE:HA	3:K:949:ILE:HG12	2.03	0.41
3:K:1270:TYR:HD2	3:K:1273:LEU:HD22	1.85	0.41
1:A:53:PRO:HG3	1:A:1143:SER:HB2	2.01	0.41
1:A:121:SER:O	1:A:121:SER:OG	2.33	0.41
2:D:249:HIS:NE2	2:D:275:ARG:HD2	2.35	0.41
3:E:1509:ARG:NH1	3:E:1511:ASN:HB3	2.34	0.41
3:E:1757:LYS:O	3:E:1761:ASN:ND2	2.53	0.41
3:F:1289:LEU:HD12	3:F:1294:GLN:HG2	2.02	0.41
3:F:2321:THR:OG1	3:F:2322:ARG:N	2.53	0.41
1:G:777:CYS:HA	1:G:780:THR:HG22	2.02	0.41
3:H:943:ILE:HA	3:H:946:ILE:HD13	2.02	0.41
3:H:1218:LEU:HD12	3:H:1219:PRO:HD2	2.03	0.41
3:K:902:ASP:OD1	3:K:2249:ARG:NH2	2.53	0.41
1:A:752:ILE:HG22	1:A:754:LEU:H	1.85	0.41
1:A:1528:HIS:HB2	1:A:1533:MET:HB2	2.02	0.41
1:B:296:SER:OG	1:B:429:MET:HE1	2.21	0.41
1:B:746:TYR:HB3	1:B:755:LEU:HD21	2.03	0.41
3:E:364:ASP:HA	3:E:367:ARG:HE	1.85	0.41
3:E:394:MET:HE2	3:E:435:TYR:HE2	1.85	0.41
3:E:1089:VAL:HG11	3:E:1122:ARG:HG2	2.03	0.41
3:E:1526:LEU:HD13	3:E:1530:LEU:HD11	2.02	0.41
3:E:1895:ARG:HA	3:E:1898:LEU:HG	2.03	0.41
3:F:1048:PHE:HA	3:F:1066:ILE:HD11	2.01	0.41
3:F:2323:MET:HE1	3:F:2474:TRP:C	2.45	0.41
1:G:393:LEU:HD22	1:G:416:ILE:HD12	2.01	0.41
3:H:1916:LEU:O	3:H:1920:ILE:HG12	2.21	0.41
3:H:1935:ILE:O	3:H:1939:ARG:HG2	2.19	0.41
1:J:122:LYS:HA	1:J:122:LYS:HE3	2.03	0.41
3:K:1388:ILE:HG13	3:K:2331:SER:HB3	2.02	0.41
3:K:1902:SER:HA	3:K:1937:LYS:HE3	2.02	0.41
3:K:2324:LEU:O	3:K:2328:MET:HG2	2.21	0.41
3:K:2415:ASN:OD1	3:K:2415:ASN:N	2.53	0.41
1:A:630:GLU:N	1:A:630:GLU:OE1	2.54	0.41
2:C:148:ASN:O	2:C:149:GLN:NE2	2.54	0.41
3:E:1870:ILE:HD13	3:E:1875:TRP:HE1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:2004:THR:OG1	3:E:2066:VAL:O	2.36	0.41
3:F:804:PRO:HA	3:F:807:ILE:HG12	2.02	0.41
3:F:1921:LYS:HD2	3:F:2172:SER:HA	2.03	0.41
3:F:2264:SER:HB3	3:F:2293:LYS:HB2	2.02	0.41
1:G:637:TYR:OH	1:G:733:ASN:O	2.30	0.41
3:H:1016:ILE:HD11	3:H:1018:LEU:HD22	2.02	0.41
3:H:1856:ILE:O	3:H:1860:THR:HG23	2.20	0.41
1:J:969:LYS:HD2	1:J:1102:HIS:CE1	2.56	0.41
1:J:1533:MET:HG3	1:J:1548:LYS:HB2	2.03	0.41
3:K:1110:LEU:HA	3:K:1113:ASN:HB2	2.03	0.41
3:K:1278:PHE:CE2	3:K:1321:LEU:HD22	2.55	0.41
1:A:737:LEU:HA	1:A:740:VAL:HG22	2.01	0.41
2:C:5:LEU:HD21	2:C:300:LEU:HD12	2.03	0.41
3:E:1832:ILE:HG13	3:E:1839:SER:HB2	2.03	0.41
1:G:1168:VAL:HA	1:G:1171:ASN:HD21	1.86	0.41
1:G:1394:TRP:HH2	1:G:1432:ILE:HA	1.85	0.41
3:H:2143:PHE:HA	3:H:2146:VAL:HG12	2.01	0.41
1:J:550:PRO:HA	1:J:551:PRO:HD2	1.80	0.41
1:J:1362:GLN:HG3	1:J:1412:ARG:HG2	2.03	0.41
2:C:6:VAL:HG12	2:C:16:PHE:CD1	2.56	0.41
3:E:178:LEU:HD13	3:E:197:LEU:HG	2.02	0.41
3:E:1247:LEU:O	3:E:1251:LEU:HG	2.20	0.41
3:E:1755:TRP:CD1	3:E:1758:ALA:H	2.39	0.41
3:F:1562:LYS:HG2	3:F:1569:LYS:NZ	2.36	0.41
1:G:810:SER:OG	1:G:811:GLY:N	2.54	0.41
3:H:983:TYR:O	3:H:987:LEU:HG	2.21	0.41
3:H:1107:LEU:HD23	3:H:1110:LEU:HD21	2.03	0.41
2:I:29:GLN:OE1	2:I:31:SER:OG	2.38	0.41
3:K:1022:ILE:O	3:K:1026:ILE:HG12	2.20	0.41
3:K:1033:LEU:HG	3:K:1036:GLU:HB2	2.01	0.41
3:K:1934:ILE:HA	3:K:1937:LYS:HG2	2.02	0.41
2:L:121:GLU:HB2	2:L:134:CYS:SG	2.61	0.41
2:L:178:ASN:OD1	2:L:179:THR:N	2.54	0.41
1:B:93:LEU:HD23	1:B:115:PRO:HB3	2.02	0.41
2:C:218:ASP:OD1	2:C:218:ASP:N	2.45	0.41
2:C:251:ARG:HG2	2:C:271:ASP:HA	2.03	0.41
3:E:197:LEU:O	3:E:201:THR:HG23	2.21	0.41
3:E:426:PHE:HB2	3:E:467:LYS:HD3	2.03	0.41
3:E:1086:PRO:HD3	3:E:1119:MET:HE1	2.01	0.41
3:E:1282:PHE:CE2	3:E:1321:LEU:HD21	2.55	0.41
3:E:1890:ASN:HB3	3:E:1893:VAL:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:2303:PHE:HB3	3:E:2425:VAL:HG21	2.03	0.41
3:E:2321:THR:HG1	3:E:2474:TRP:C	2.28	0.41
3:F:405:ASP:N	3:F:405:ASP:OD1	2.53	0.41
3:F:860:PRO:HB2	3:F:864:ARG:NH2	2.35	0.41
3:F:932:ASP:OD1	3:F:933:PRO:HD3	2.21	0.41
3:F:1150:LEU:HD13	3:F:1157:PHE:CD2	2.55	0.41
3:F:1680:ARG:NH1	3:F:1681:MET:HB3	2.36	0.41
3:F:2190:LEU:HD23	3:F:2190:LEU:HA	1.97	0.41
3:F:2219:LEU:HB3	3:F:2223:GLN:HB2	2.03	0.41
3:F:2239:ASP:OD1	3:F:2239:ASP:N	2.53	0.41
3:F:2346:LYS:HE3	3:F:2346:LYS:HB3	1.92	0.41
1:G:1227:ALA:HB2	1:G:1260:LEU:HD11	2.03	0.41
3:H:1067:LEU:HD11	3:H:1091:MET:HE1	2.03	0.41
3:H:1753:ASN:O	3:H:1759:TRP:NE1	2.48	0.41
3:H:1883:ILE:HG12	3:H:1915:PRO:HB2	2.02	0.41
3:H:2028:TYR:CZ	3:H:2037:LEU:HD22	2.56	0.41
3:H:2438:ILE:HG22	3:H:2439:ARG:HG2	2.03	0.41
2:I:11:ASP:OD1	2:I:293:LYS:N	2.50	0.41
2:I:233:VAL:HG11	2:I:279:LEU:HD21	2.02	0.41
3:K:1110:LEU:HD13	3:K:1114:ILE:HD11	2.03	0.41
3:K:1129:ARG:HA	3:K:1132:ASN:HD21	1.86	0.41
3:K:2315:LYS:HZ2	3:K:2315:LYS:HG3	1.59	0.41
1:A:104:HIS:HB2	1:A:105:PRO:HD3	2.03	0.41
1:A:724:VAL:HG13	1:A:731:GLN:HG2	2.03	0.41
1:A:823:GLN:NE2	1:G:195:ARG:HH12	2.19	0.41
1:B:1098:SER:O	1:B:1100:LYS:N	2.52	0.41
3:E:1089:VAL:O	3:E:1092:THR:HG22	2.20	0.41
3:E:1562:LYS:O	3:E:1566:ASN:ND2	2.39	0.41
3:F:779:THR:O	3:F:783:VAL:HG23	2.21	0.41
3:F:1407:LYS:HG3	3:F:1408:LEU:HG	2.03	0.41
3:F:1930:ALA:O	3:F:1933:SER:OG	2.35	0.41
1:G:792:ASP:OD1	1:G:792:ASP:N	2.54	0.41
3:H:932:ASP:OD1	3:H:932:ASP:N	2.54	0.41
3:H:2042:ASP:O	3:H:2046:ASN:ND2	2.54	0.41
3:H:2255:LEU:O	3:H:2258:ARG:HG3	2.21	0.41
3:H:2368:ILE:O	3:H:2370:TRP:N	2.52	0.41
1:J:1214:LEU:HD13	1:J:1260:LEU:HG	2.03	0.41
3:K:2252:GLU:H	3:K:2252:GLU:CD	2.29	0.41
1:A:1475:THR:OG1	1:A:1477:GLN:O	2.39	0.40
1:B:737:LEU:HA	1:B:740:VAL:HG22	2.03	0.40
2:C:121:GLU:HB2	2:C:134:CYS:SG	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:1241:GLN:O	3:E:1245:ARG:HG2	2.21	0.40
3:F:1077:LEU:HB2	3:F:1114:ILE:HG13	2.03	0.40
3:F:1462:GLU:HA	3:F:1465:LYS:HG2	2.03	0.40
3:F:1905:GLY:HA3	3:F:1937:LYS:NZ	2.36	0.40
3:F:2059:GLN:HA	3:F:2103:VAL:HG22	2.04	0.40
1:J:91:LEU:HD21	1:J:179:HIS:HB2	2.03	0.40
2:L:208:THR:OG1	2:L:228:ASP:OD2	2.31	0.40
1:A:194:ASN:ND2	1:A:198:THR:OG1	2.41	0.40
1:A:427:LEU:HD11	3:E:713:VAL:HG12	2.02	0.40
1:A:1263:ILE:O	1:A:1269:ALA:HA	2.20	0.40
1:B:1214:LEU:HD13	1:B:1260:LEU:HG	2.02	0.40
1:B:1479:LYS:NZ	1:B:1487:LEU:HD13	2.32	0.40
2:D:98:THR:HG22	2:D:114:LYS:HG3	2.03	0.40
3:E:101:ARG:H	3:E:101:ARG:HG2	1.74	0.40
3:E:163:SER:HB2	3:E:167:LEU:HG	2.03	0.40
3:E:1250:GLN:HA	3:E:1253:LYS:HE2	2.03	0.40
3:E:1613:LYS:HD2	3:E:1613:LYS:H	1.85	0.40
3:E:2106:SER:O	3:E:2107:LYS:CB	2.69	0.40
3:F:621:PHE:HE2	3:F:641:VAL:HG11	1.86	0.40
3:F:1247:LEU:HA	3:F:1250:GLN:HE22	1.86	0.40
3:F:1734:ARG:HB2	3:F:1738:PRO:HD3	2.02	0.40
3:F:2164:GLN:HG2	3:F:2293:LYS:NZ	2.37	0.40
3:F:2288:ASP:OD1	3:F:2289:ARG:N	2.54	0.40
1:G:284:LEU:HA	1:G:287:CYS:HB2	2.03	0.40
1:G:1393:ARG:HD2	1:G:1393:ARG:HA	1.86	0.40
3:H:1995:TYR:O	3:H:1999:LYS:NZ	2.54	0.40
1:J:100:VAL:HG13	1:J:183:LYS:NZ	2.36	0.40
3:K:983:TYR:O	3:K:987:LEU:HG	2.20	0.40
2:L:274:VAL:HG23	2:L:288:TYR:HD2	1.86	0.40
1:B:1277:ASP:OD1	1:B:1277:ASP:N	2.49	0.40
3:E:417:ILE:HA	3:E:417:ILE:HD12	1.92	0.40
3:E:1971:LEU:HD11	3:E:2044:TYR:HB3	2.02	0.40
3:F:354:SER:HB3	3:F:357:LYS:HZ1	1.86	0.40
3:F:1089:VAL:O	3:F:1092:THR:HG22	2.22	0.40
3:F:2448:GLU:O	3:F:2452:LYS:HG2	2.22	0.40
1:G:537:PHE:CD1	1:G:553:GLN:HB2	2.56	0.40
3:H:1973:ASP:OD1	3:H:1974:ALA:N	2.54	0.40
3:H:2316:VAL:HG23	3:H:2457:ALA:HA	2.02	0.40
1:J:591:ILE:HD13	1:J:591:ILE:HA	1.91	0.40
1:B:104:HIS:HB2	1:B:105:PRO:HD3	2.04	0.40
1:B:630:GLU:N	1:B:630:GLU:OE1	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:179:THR:HB	2:C:209:TYR:HD1	1.86	0.40
3:F:359:LYS:HE3	3:F:361:TYR:HB3	2.03	0.40
3:H:970:LEU:HD13	3:H:973:ARG:HH21	1.86	0.40
3:H:1730:GLN:HE22	3:H:1737:ASN:HB2	1.84	0.40
1:J:307:LYS:NZ	1:J:312:LYS:O	2.48	0.40
3:K:1738:PRO:HA	3:K:1741:ILE:HG12	2.02	0.40
3:K:2187:PHE:HA	3:K:2190:LEU:HD12	2.04	0.40
1:A:1215:MET:HE2	1:A:1535:ALA:HB1	2.03	0.40
1:A:1381:ASP:HB2	1:A:1391:ILE:HD11	2.02	0.40
1:B:1533:MET:HE1	1:B:1548:LYS:HB2	2.04	0.40
2:D:207:SER:OG	2:D:228:ASP:OD2	2.35	0.40
3:E:1286:TRP:CZ3	3:E:1294:GLN:HB2	2.57	0.40
3:E:2149:LEU:HD22	3:E:2355:LEU:HD21	2.04	0.40
3:F:680:ARG:HA	3:F:683:PHE:CE1	2.57	0.40
3:F:1963:TRP:HA	3:F:1966:GLN:CD	2.47	0.40
3:F:1977:GLN:HB3	3:F:1986:LYS:HZ3	1.87	0.40
1:G:300:PHE:CE2	1:G:433:LEU:HD12	2.57	0.40
1:G:535:THR:HA	1:G:538:GLU:HG2	2.03	0.40
1:G:883:LEU:O	1:G:887:LYS:HG2	2.22	0.40
1:G:969:LYS:NZ	1:G:1100:LYS:O	2.49	0.40
1:G:1476:LYS:O	1:G:1492:LYS:NZ	2.52	0.40
3:H:1079:ASP:OD1	3:H:1079:ASP:N	2.52	0.40
3:H:1962:LEU:HB2	3:H:2111:ARG:HH21	1.86	0.40
3:H:2140:MET:HA	3:H:2143:PHE:HD2	1.86	0.40
3:K:1916:LEU:O	3:K:1920:ILE:HG12	2.21	0.40
2:L:80:SER:OG	2:L:93:SER:OG	2.35	0.40
2:L:271:ASP:OD1	2:L:271:ASP:N	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	1189/1608 (74%)	1121 (94%)	68 (6%)	0	100	100
1	B	1188/1608 (74%)	1128 (95%)	60 (5%)	0	100	100
1	G	1192/1608 (74%)	1131 (95%)	59 (5%)	2 (0%)	43	74
1	J	1193/1608 (74%)	1126 (94%)	65 (5%)	2 (0%)	43	74
2	C	298/303 (98%)	267 (90%)	31 (10%)	0	100	100
2	D	298/303 (98%)	267 (90%)	31 (10%)	0	100	100
2	I	298/303 (98%)	266 (89%)	32 (11%)	0	100	100
2	L	298/303 (98%)	268 (90%)	30 (10%)	0	100	100
3	E	2220/2474 (90%)	2072 (93%)	148 (7%)	0	100	100
3	F	2220/2474 (90%)	2069 (93%)	151 (7%)	0	100	100
3	H	1147/2474 (46%)	1097 (96%)	50 (4%)	0	100	100
3	K	1147/2474 (46%)	1091 (95%)	56 (5%)	0	100	100
All	All	12688/17540 (72%)	11903 (94%)	781 (6%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	1099	MET
1	G	1099	MET
1	J	1108	PRO
1	G	1108	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1080/1458 (74%)	1078 (100%)	2 (0%)	87	87
1	B	1079/1458 (74%)	1079 (100%)	0	100	100
1	G	1079/1458 (74%)	1075 (100%)	4 (0%)	84	83
1	J	1080/1458 (74%)	1075 (100%)	5 (0%)	81	81
2	C	263/267 (98%)	263 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	263/267 (98%)	262 (100%)	1 (0%)	84	83
2	I	263/267 (98%)	263 (100%)	0	100	100
2	L	263/267 (98%)	263 (100%)	0	100	100
3	E	1991/2219 (90%)	1991 (100%)	0	100	100
3	F	1990/2219 (90%)	1988 (100%)	2 (0%)	88	89
3	H	1037/2219 (47%)	1037 (100%)	0	100	100
3	K	1037/2219 (47%)	1037 (100%)	0	100	100
All	All	11425/15776 (72%)	11411 (100%)	14 (0%)	87	89

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	209	GLN
1	A	749	ASN
2	D	34	GLN
3	F	1076	ASN
3	F	1222	GLN
1	G	630	GLU
1	G	1104	SER
1	G	1106	LYS
1	G	1108	PRO
1	J	822	GLN
1	J	1104	SER
1	J	1105	LYS
1	J	1106	LYS
1	J	1108	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (146) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	161	ASN
1	A	559	GLN
1	A	712	GLN
1	A	733	ASN
1	A	749	ASN
1	A	822	GLN
1	A	823	GLN
1	A	840	GLN

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Mol	Chain	Res	Type
1	A	877	GLN
1	A	902	ASN
1	A	1180	ASN
1	A	1208	ASN
1	A	1463	GLN
1	B	161	ASN
1	B	248	HIS
1	B	559	GLN
1	B	712	GLN
1	B	1096	ASN
1	B	1406	ASN
1	B	1463	GLN
2	C	12	HIS
2	C	29	GLN
2	C	149	GLN
2	C	196	HIS
2	C	249	HIS
2	D	29	GLN
2	D	149	GLN
2	D	196	HIS
3	E	125	GLN
3	E	230	ASN
3	E	253	ASN
3	E	442	ASN
3	E	543	GLN
3	E	629	GLN
3	E	828	GLN
3	E	1125	GLN
3	E	1174	GLN
3	E	1222	GLN
3	E	1241	GLN
3	E	1354	HIS
3	E	1486	GLN
3	E	1761	ASN
3	E	1948	GLN
3	E	2057	GLN
3	E	2211	GLN
3	E	2343	ASN
3	E	2436	ASN
3	F	253	ASN
3	F	312	GLN
3	F	410	ASN

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Mol	Chain	Res	Type
3	F	629	GLN
3	F	813	GLN
3	F	1019	GLN
3	F	1347	HIS
3	F	1394	GLN
3	F	1486	GLN
3	F	1521	ASN
3	F	1750	HIS
3	F	1761	ASN
3	F	1766	ASN
3	F	1948	GLN
3	F	2147	ASN
3	F	2165	GLN
3	F	2206	HIS
3	F	2436	ASN
3	F	2462	ASN
1	G	68	GLN
1	G	131	ASN
1	G	147	GLN
1	G	161	ASN
1	G	175	HIS
1	G	532	GLN
1	G	822	GLN
1	G	823	GLN
1	G	837	GLN
1	G	842	GLN
1	G	960	GLN
1	G	1137	GLN
1	G	1171	ASN
1	G	1188	GLN
1	G	1319	GLN
1	G	1528	HIS
3	H	908	GLN
3	H	997	HIS
3	H	1082	HIS
3	H	1376	ASN
3	H	1377	ASN
3	H	1393	GLN
3	H	1396	ASN
3	H	1737	ASN
3	H	1750	HIS
3	H	1753	ASN

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Mol	Chain	Res	Type
3	H	1910	GLN
3	H	1964	HIS
3	H	2038	ASN
3	H	2059	GLN
3	H	2194	HIS
3	H	2351	ASN
3	H	2436	ASN
2	I	30	HIS
2	I	84	GLN
2	I	128	GLN
2	I	182	ASN
2	I	206	HIS
2	I	287	GLN
2	I	301	ASN
1	J	52	ASN
1	J	68	GLN
1	J	80	GLN
1	J	147	GLN
1	J	175	HIS
1	J	227	ASN
1	J	532	GLN
1	J	733	ASN
1	J	822	GLN
1	J	823	GLN
1	J	838	HIS
1	J	842	GLN
1	J	1102	HIS
1	J	1171	ASN
1	J	1188	GLN
1	J	1319	GLN
3	K	1054	ASN
3	K	1082	HIS
3	K	1187	ASN
3	K	1233	GLN
3	K	1294	GLN
3	K	1320	ASN
3	K	1337	HIS
3	K	1376	ASN
3	K	1377	ASN
3	K	1378	GLN
3	K	1393	GLN
3	K	1396	ASN

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Mol	Chain	Res	Type
3	K	1753	ASN
3	K	1761	ASN
3	K	1871	GLN
3	K	1910	GLN
3	K	1977	GLN
3	K	2165	GLN
3	K	2436	ASN
2	L	12	HIS
2	L	29	GLN
2	L	163	GLN
2	L	206	HIS
2	L	287	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

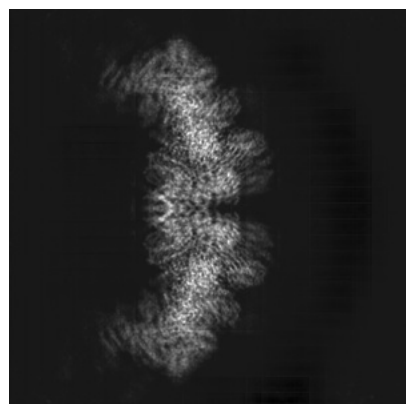
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13594. These allow visual inspection of the internal detail of the map and identification of artifacts.

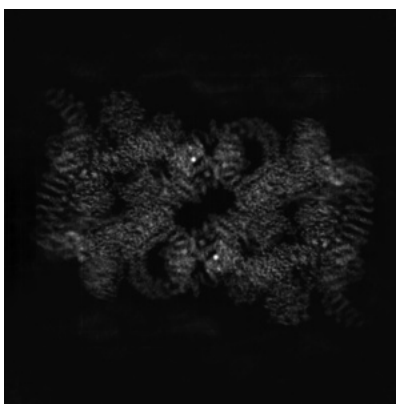
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

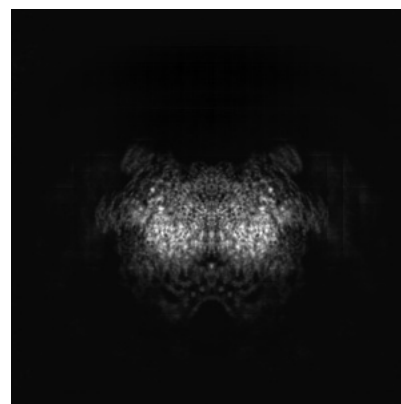
6.1.1 Primary map



X

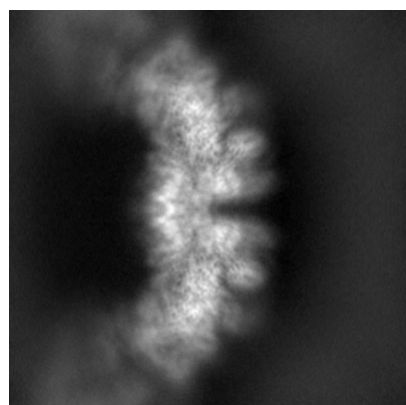


Y

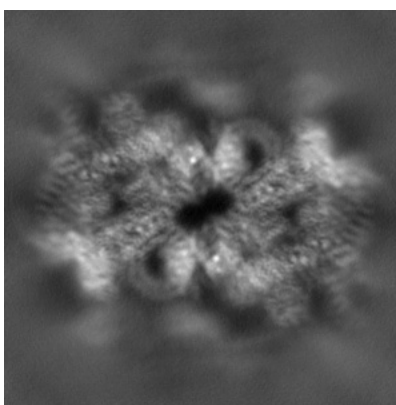


Z

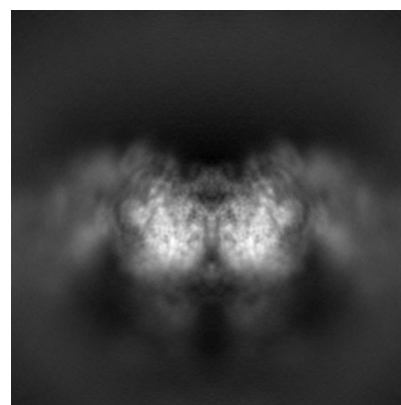
6.1.2 Raw map



X



Y

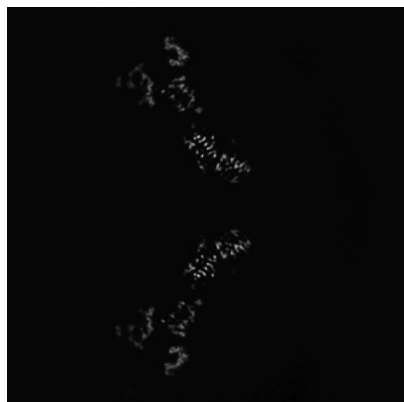


Z

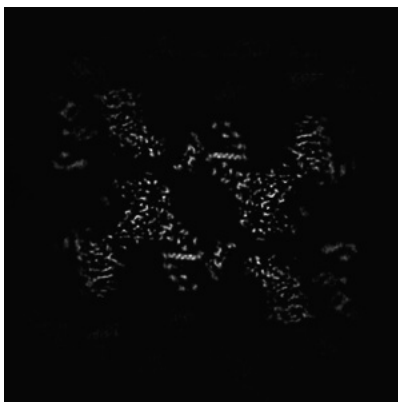
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 150

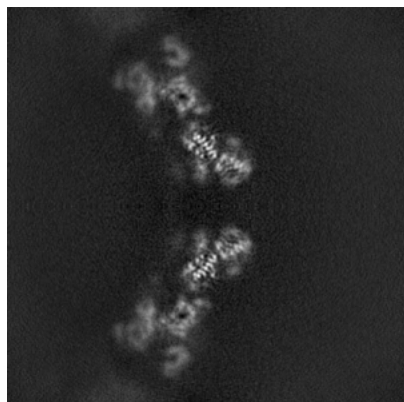


Y Index: 150

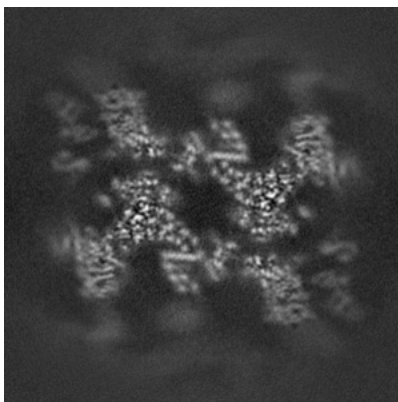


Z Index: 150

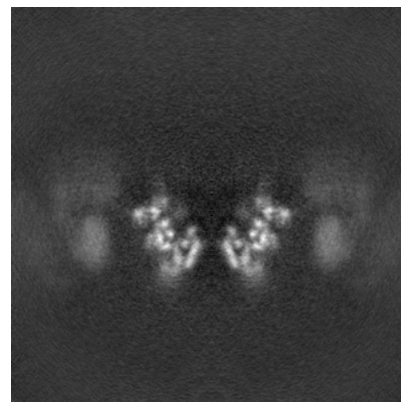
6.2.2 Raw map



X Index: 150



Y Index: 150



Z Index: 150

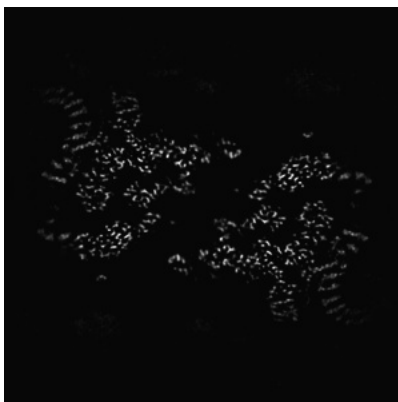
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 187



Y Index: 136

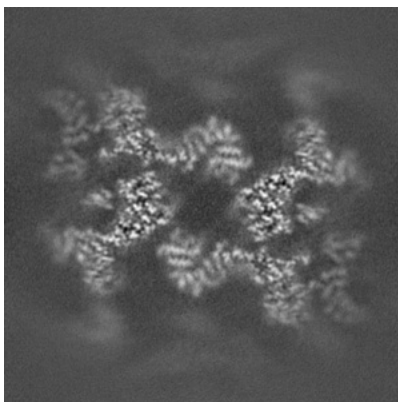


Z Index: 195

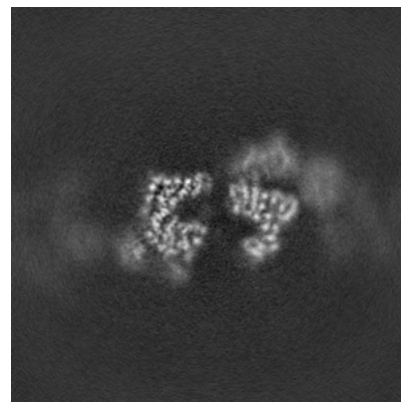
6.3.2 Raw map



X Index: 187



Y Index: 143

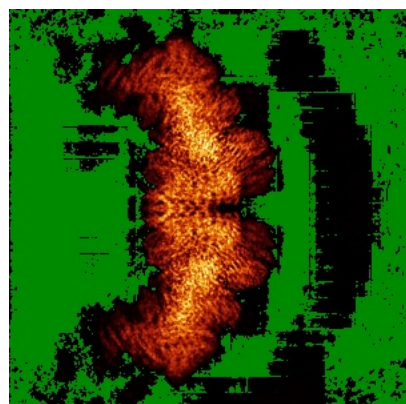


Z Index: 166

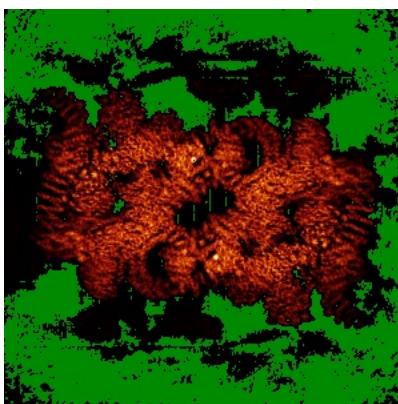
The images above show the largest variance slices of the map in three orthogonal directions.

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

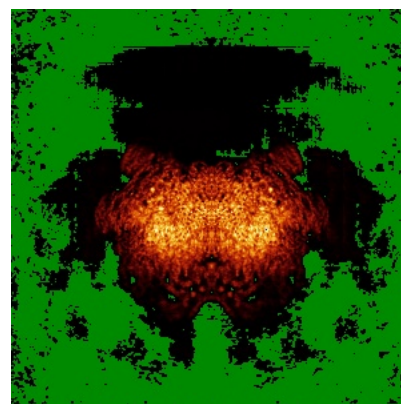
6.4.1 Primary map



X

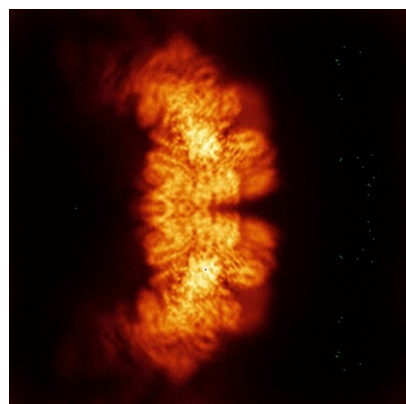


Y

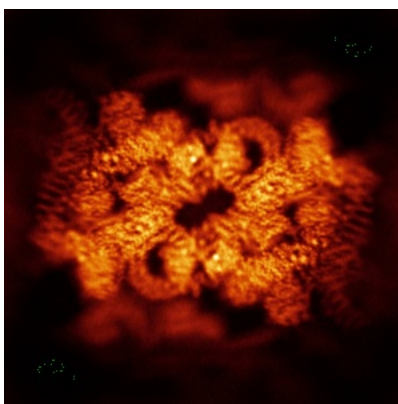


Z

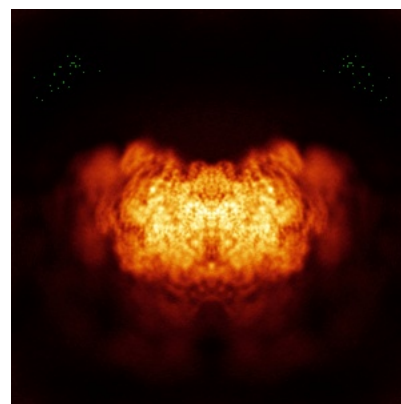
6.4.2 Raw map



X



Y

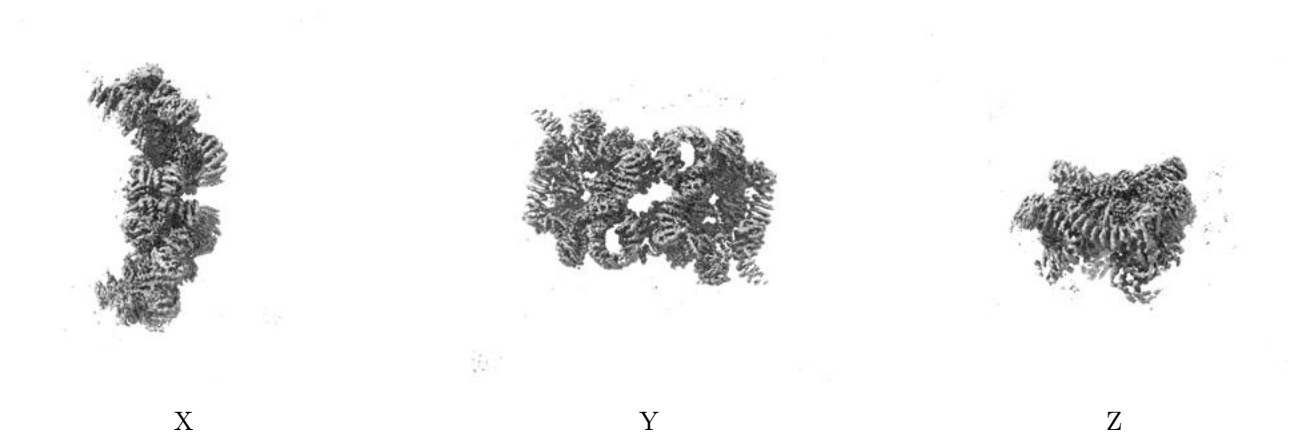


Z

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.

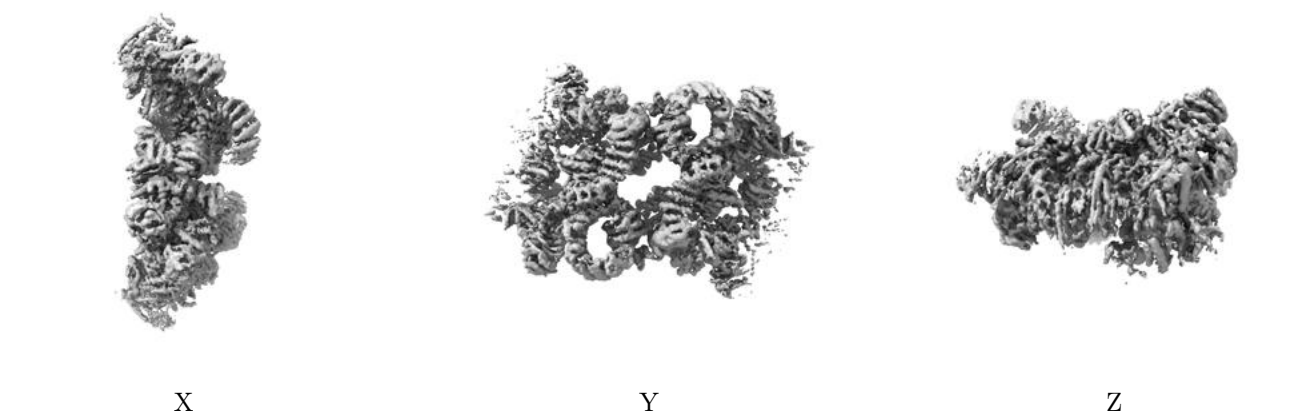
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

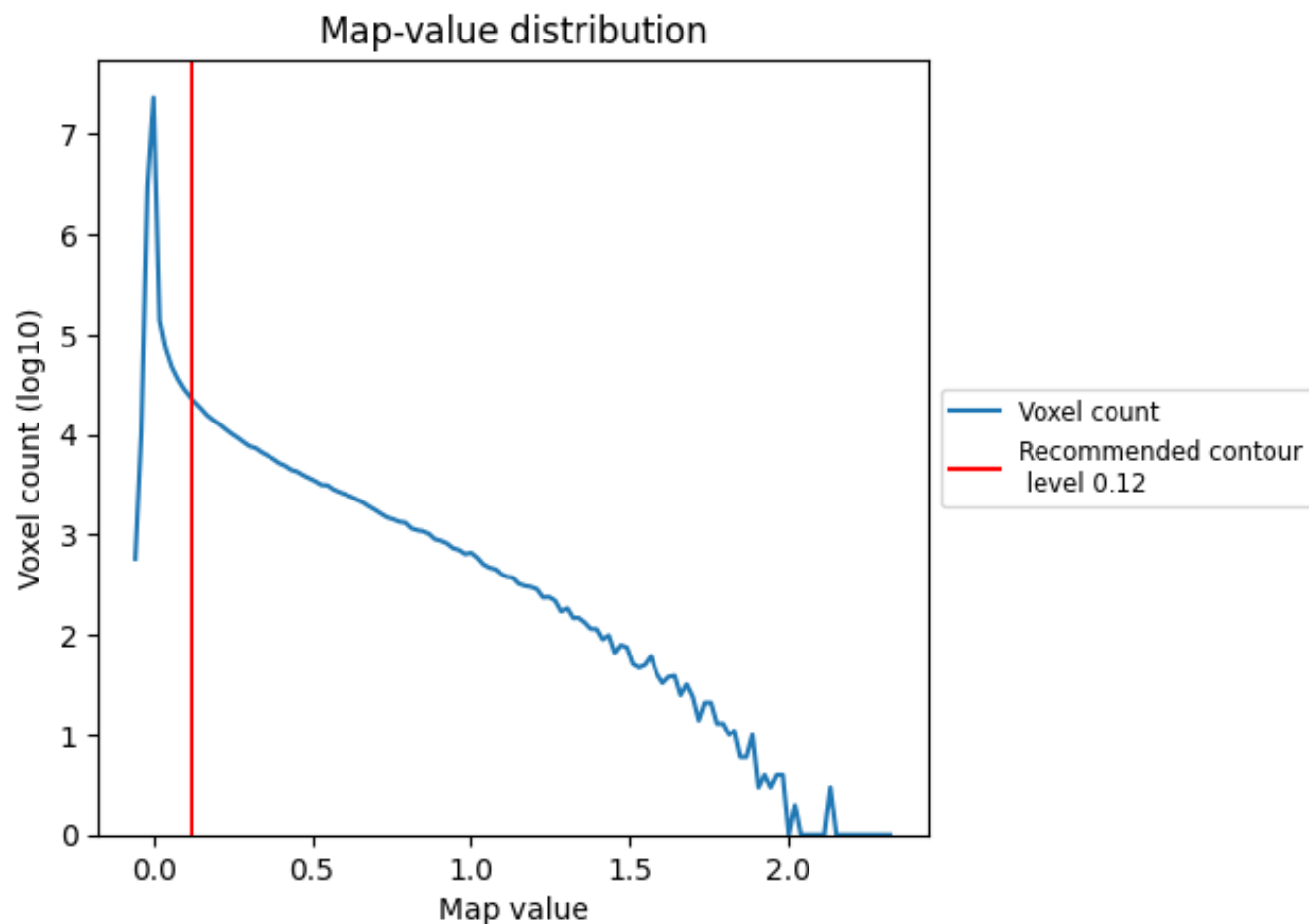
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

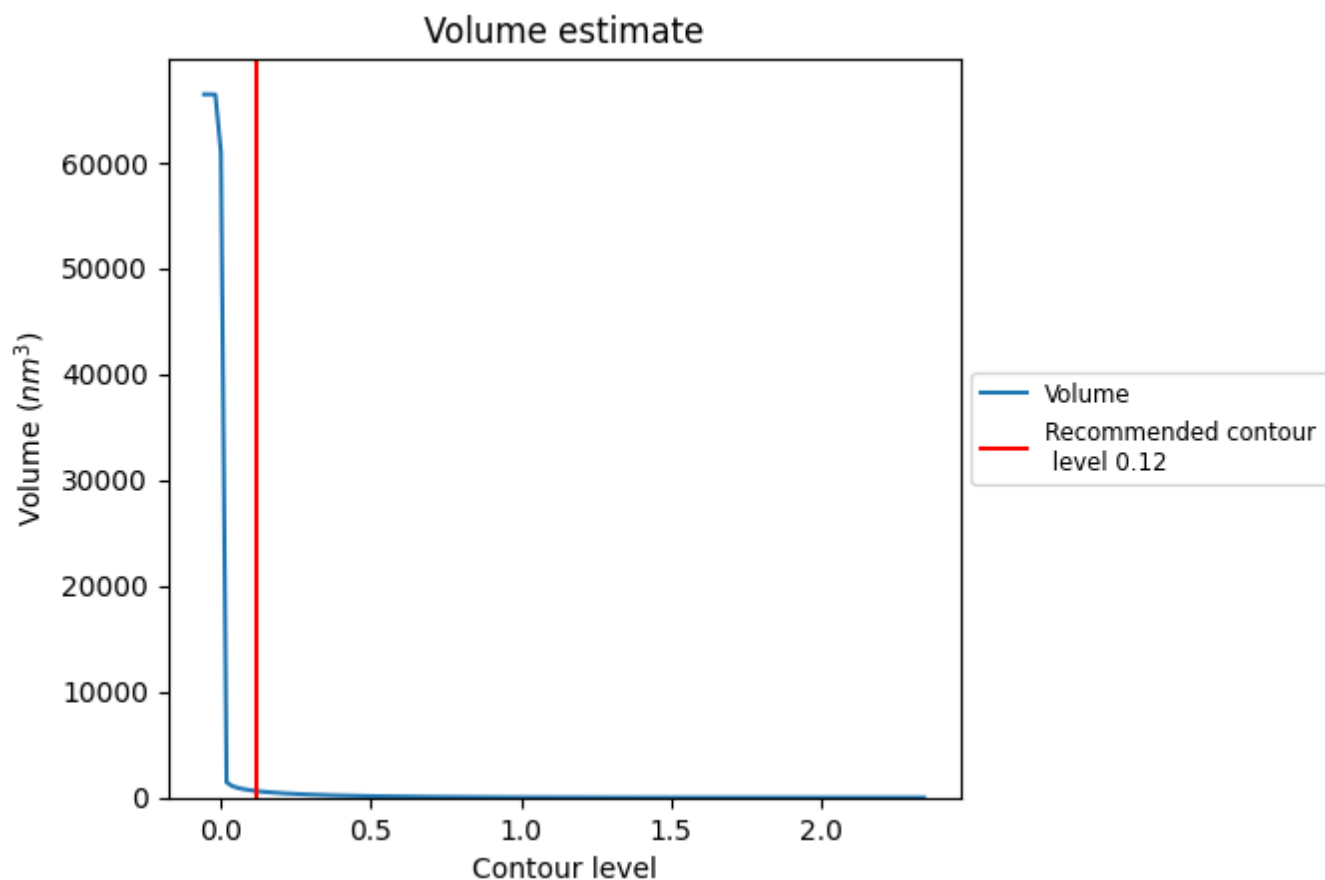
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

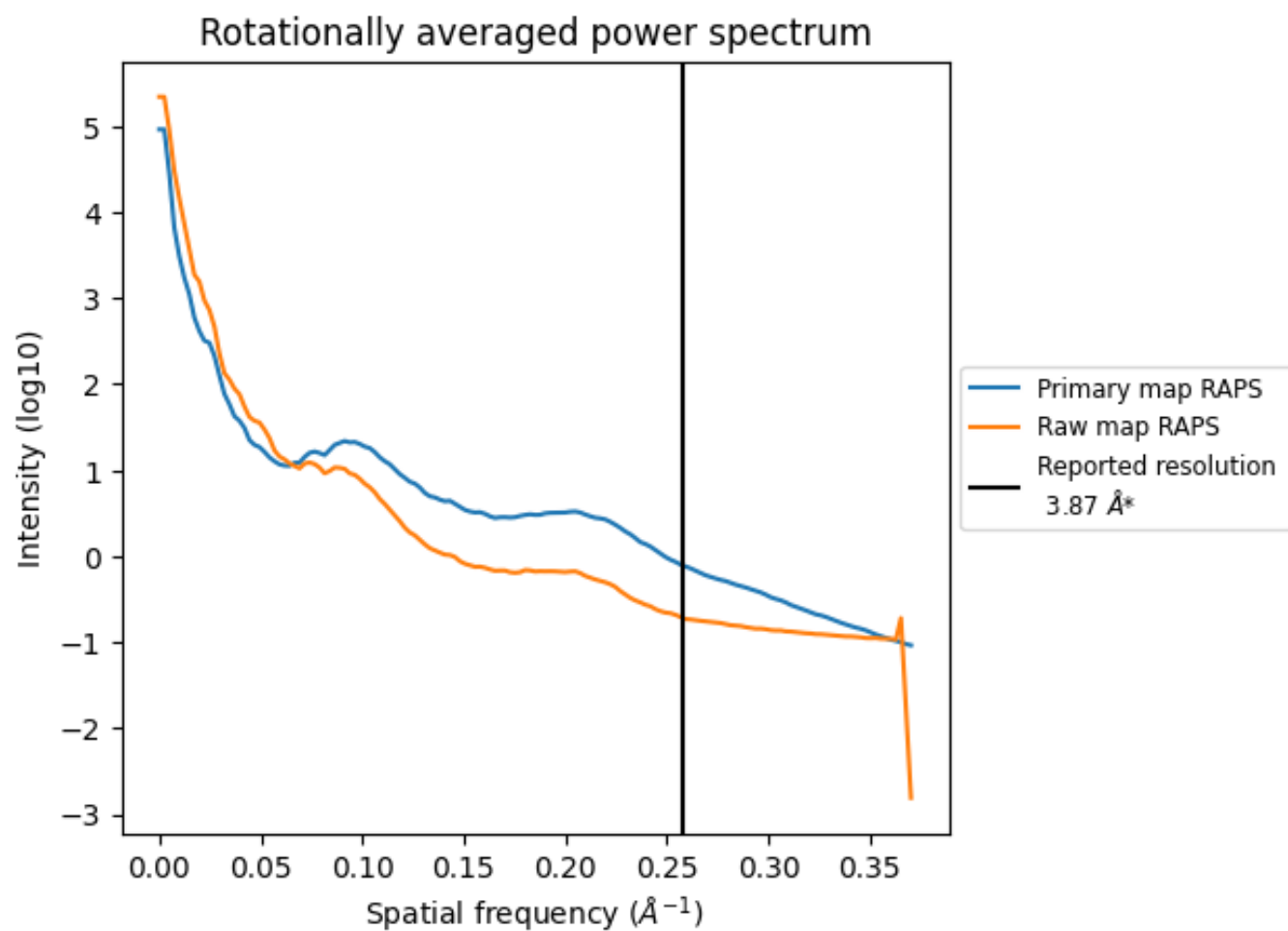
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 609 nm^3 ; this corresponds to an approximate mass of 550 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 ⓘ

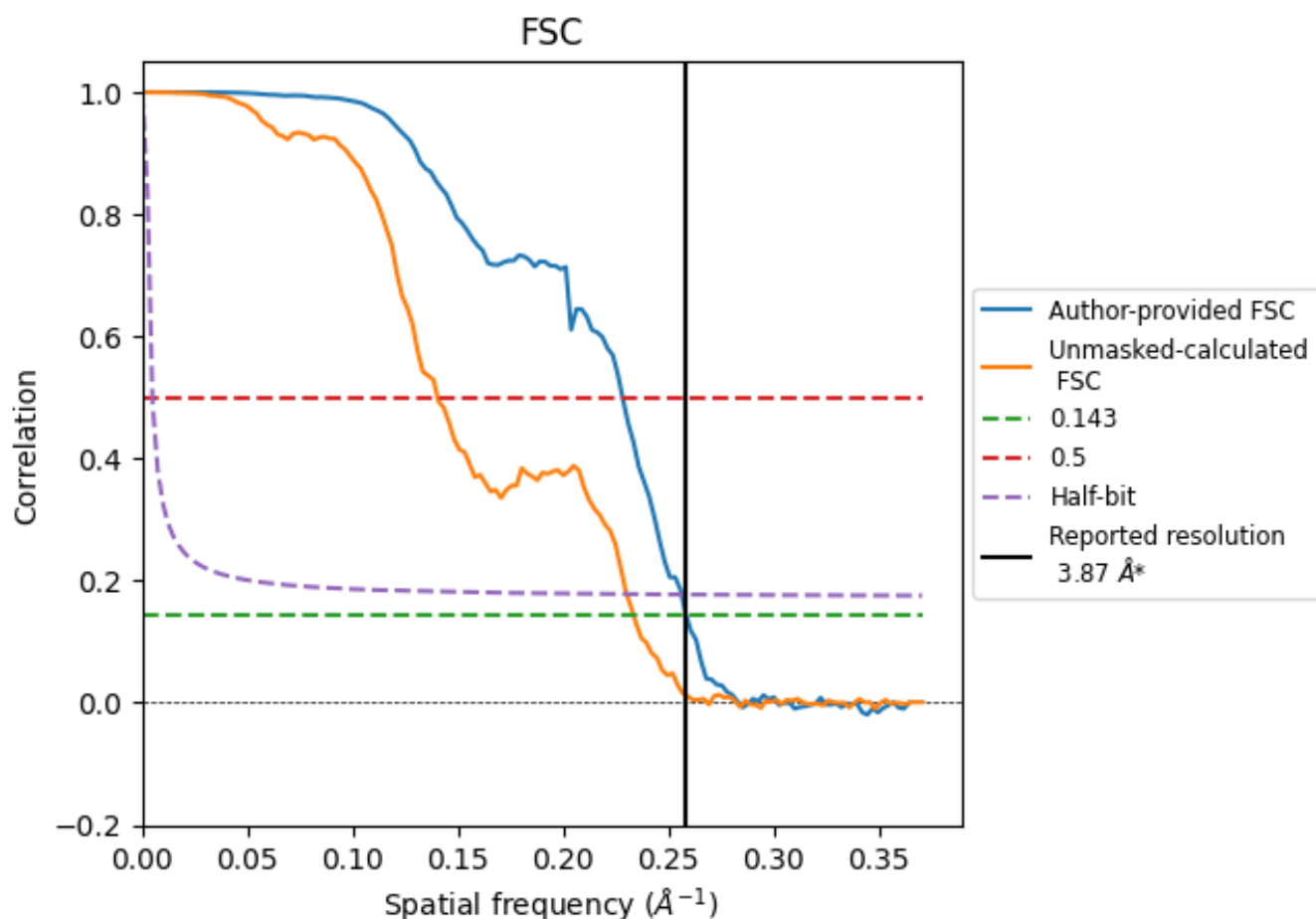


*Reported resolution corresponds to spatial frequency of 0.258 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.258 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

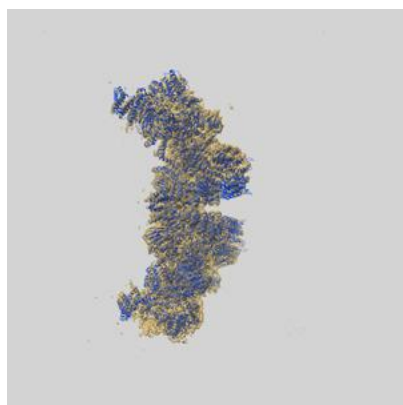
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.87	-	-
Author-provided FSC curve	3.87	4.38	3.90
Unmasked-calculated*	4.28	7.13	4.35

*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 4.28 differs from the reported value 3.87 by more than 10 %

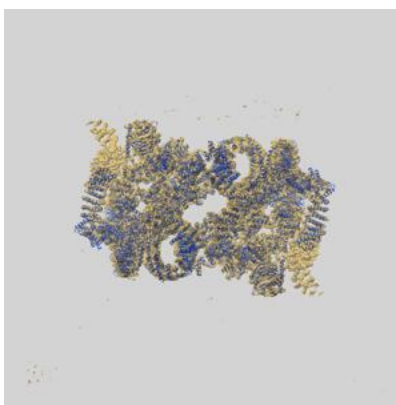
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13594 and PDB model 7PQH. Per-residue inclusion information can be found in section [3](#) on page [5](#).

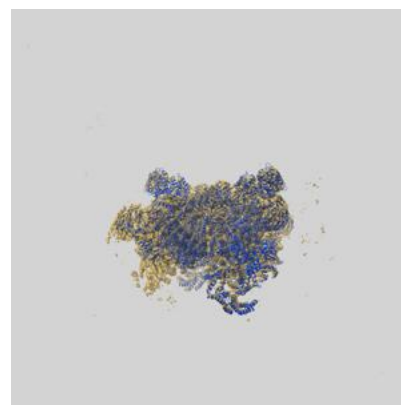
9.1 Map-model overlay [i](#)



X



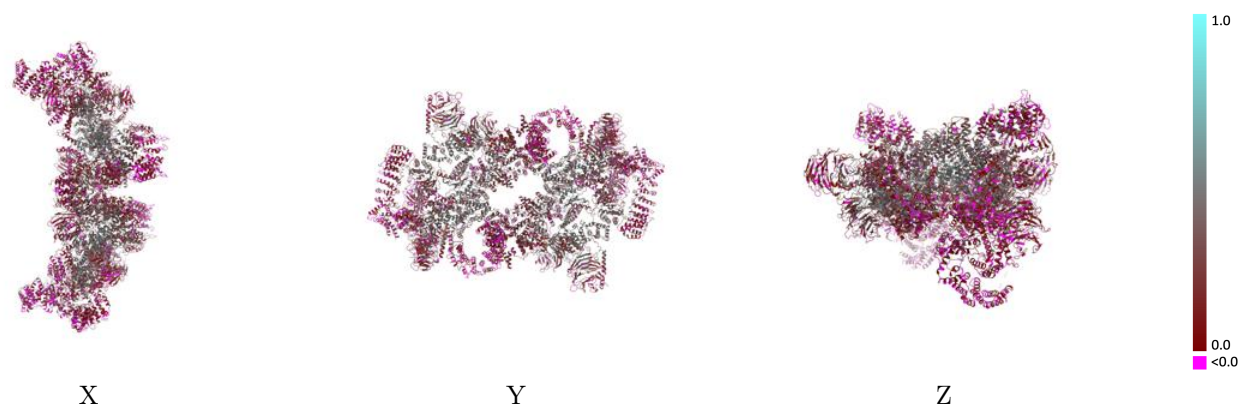
Y



Z

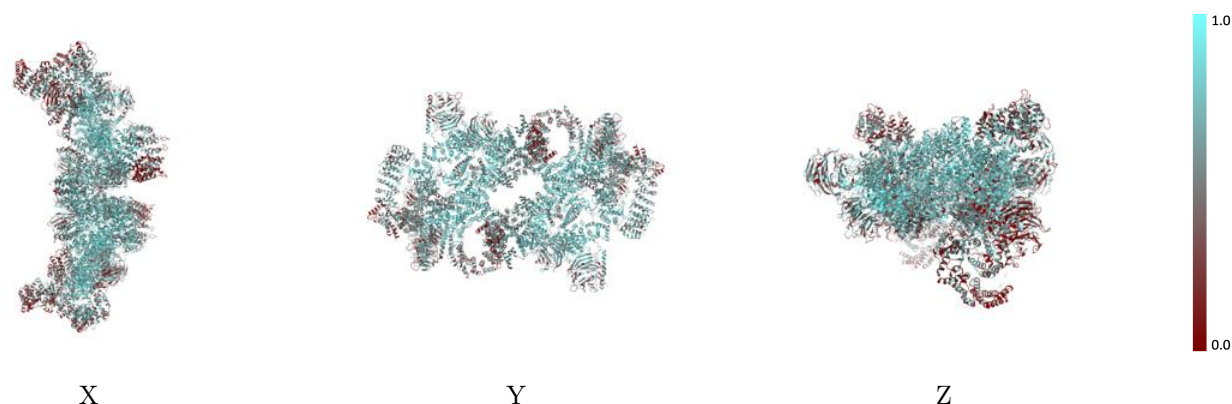
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



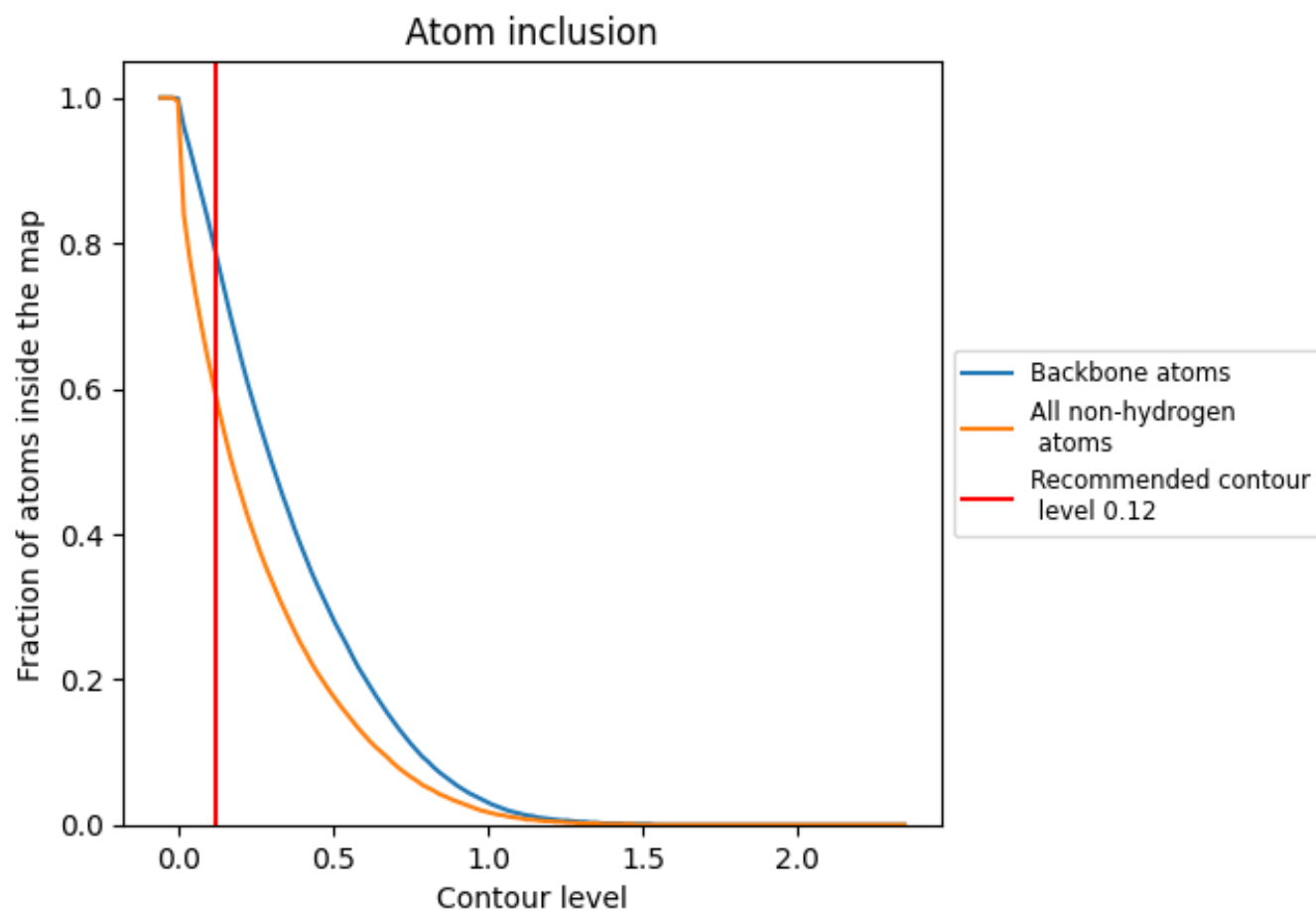
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 59% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5920	0.2410
A	0.7000	0.3320
B	0.7190	0.3360
C	0.5660	0.2680
D	0.5480	0.2640
E	0.6180	0.2290
F	0.6110	0.2270
G	0.6840	0.3160
H	0.4170	0.1110
I	0.2020	0.1100
J	0.6970	0.3160
K	0.4350	0.1150
L	0.2450	0.1250

1.0

0.0

<0.0