



## Full wwPDB EM Validation Report ⓘ

Nov 14, 2022 – 05:31 PM JST

PDB ID : 6JGZ  
EMDB ID : EMD-9824  
Title : Structure of RyR2 (F/P/Ca<sup>2+</sup> dataset)  
Authors : Chi, X.M.; Gong, D.S.; Ren, K.; Zhou, G.W.; Huang, G.X.Y.; Lei, J.L.; Zhou, Q.; Yan, N.  
Deposited on : 2019-02-16  
Resolution : 4.60 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

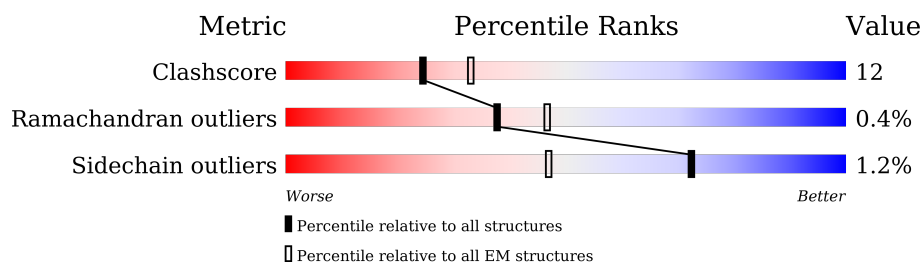
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.60 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	108	 67% 32% .
1	C	108	 67% 32% .
1	E	108	 65% 34% .
1	G	108	 68% 31% .
2	B	4968	 6% 52% 18% . 30%
2	D	4968	 6% 52% 18% . 30%
2	F	4968	 6% 52% 18% . 30%
2	H	4968	 5% 51% 18% . 30%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 109824 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 Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	107	Total	C	N	O	S	0	0
			819	516	144	155	4		
1	C	107	Total	C	N	O	S	0	0
			819	516	144	155	4		
1	E	107	Total	C	N	O	S	0	0
			819	516	144	155	4		
1	G	107	Total	C	N	O	S	0	0
			819	516	144	155	4		

- Molecule 2 is a protein called RyR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	3485	Total	C	N	O	S	0	0
			26636	16958	4556	4964	158		
2	D	3485	Total	C	N	O	S	0	0
			26636	16958	4556	4964	158		
2	F	3485	Total	C	N	O	S	0	0
			26636	16958	4556	4964	158		
2	H	3485	Total	C	N	O	S	0	0
			26636	16958	4556	4964	158		

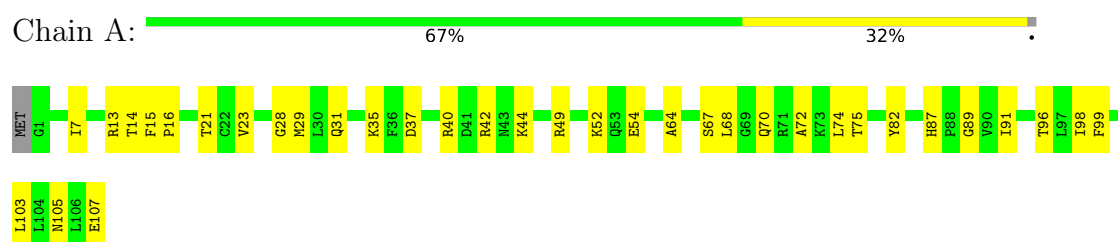
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	B	1	Total	Zn	0
			1	1	
3	D	1	Total	Zn	0
			1	1	
3	F	1	Total	Zn	0
			1	1	
3	H	1	Total	Zn	0
			1	1	

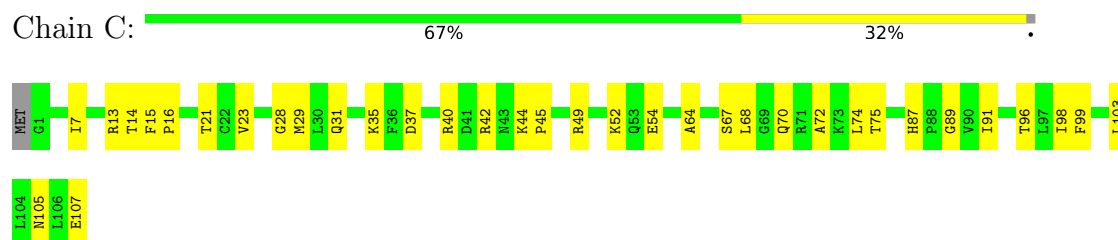
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

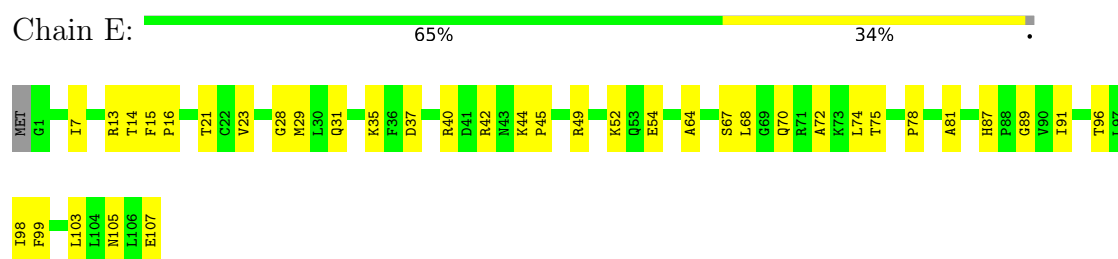
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



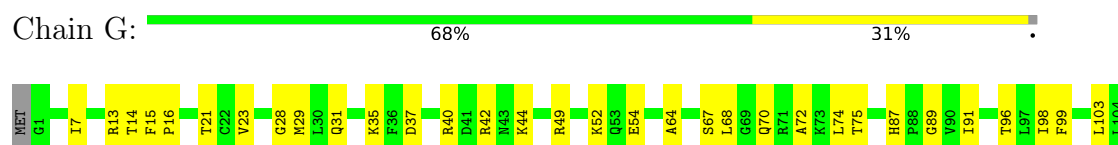
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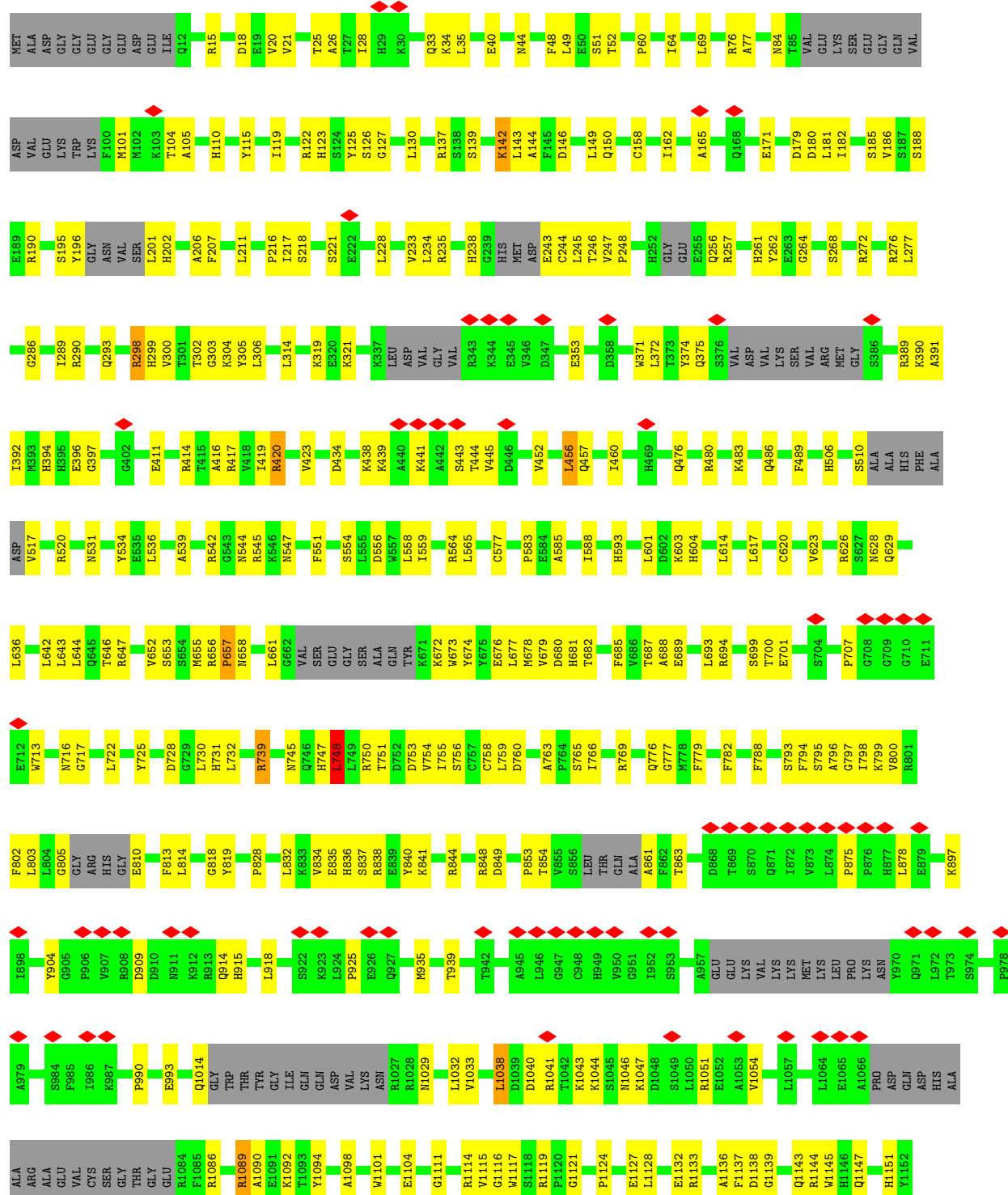


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



M105  
L106  
E107

• Molecule 2: RyR2



D2301	ILE	A2071	CYS	Q2072	M1907	P1820	L1719	Q1620	A1545	L1459	LYS	ALA	E1237	G1153
R2304	THR	Q2072	CYS	F2190	C1908	L1821	I1726	C1621	V1552	ASP	GLN	SER	N1242	R1154
I2326	M2193	V2075	PRO	M2193	L1910	T1827	I1736	L1622	E1556	PHE	LEU	GLY	R1245	Q1157
R2327	N2196	Q2083	GLY	Q1912	L1911	I1830	I1737	F1627	LEU	VAL	LEU	PRO	R1245	A1158
R2328	C2197	R2083	ILE	Q1912	L1911	I1830	I1737	M1627	GLY	ARG	ARG	LYS	M1249	G1159
F2329	C2197	R2083	ILE	Q1912	L1911	I1830	I1737	M1627	GLY	ARG	ARG	LYS	M1249	D1160
E2330	C2197	R2083	ILE	Q1912	L1911	I1830	I1737	M1627	GLY	ARG	ARG	LYS	M1249	C1164
CYS	R2199	L2088	Q1996	H1921	H1921	H1835	L1738	S1629	ARG	V1465	ASN	ASP	W1250	M1165
PHE	F2200	Q2091	L1997	R1922	R1922	L1843	P1740	H1631	LYS	V1466	PRO	ASP	S1252	T1169
GLY	L2201	Q2092	L1997	R1922	R1922	L1843	P1741	H1631	ASN	V1467	GLY	ASP	K1253	E1170
PRO	C2202	Q2092	L1997	R1922	R1922	L1843	P1741	H1631	VAL	G1470	ASP	ASP	R1254	M1174
ALA	Y2203	Q2096	F2013	F1929	F1929	E1847	ASN	E1634	MET	K1473	TYR	TYR	L1255	F1175
LEU	F2204	Q2096	ASP	F1929	F1929	E1847	LYS	E1635	PRO	K1473	SER	ASP	P1256	L1177
ARG	C2205	V2100	GLY	V1934	V1934	E1847	HIS	S1638	SER	K1475	THR	ALA	Q1257	H1171
GLY	R2206	R2101	SER	Q1938	Q1938	E1847	L1748	E1640	LEU	K1475	SER	ASP	F1258	T1172
GLY	I2207	A2102	LEU	Q1938	Q1938	E1847	P1749	E1641	SER	K1475	HIS	SER	ASP	M1173
GLY	L2103	L2103	ASP	R1942	R1942	E1847	GLY	E1642	GLY	K1475	SER	ASP	ASP	M1174
GLY	N2211	T2106	GLY	R1942	R1942	E1847	L1753	E1643	GLY	K1475	ALA	PHE	V1261	F1176
ASN	Q2212	T2106	ASN	R1942	R1942	E1847	L1753	E1643	GLY	K1475	ALA	PHE	V1261	T1176
G2343	Y2221	D2116	S2022	V1948	V1948	E1847	S1756	E1648	H1587	R1482	ARG	GLY	R1272	L1177
L2344	L2222	T2117	D2023	V1948	V1948	E1847	L1757	E1648	GLY	R1482	LEU	VAL	I1273	N1178
M2348	N2225	I2118	T2025	V1948	V1948	E1847	R1758	E1648	CYS	R1482	THR	THR	D1274	G1179
I2354	S2226	L2121	I2026	V1948	V1948	E1847	M1761	E1654	GLY	R1482	VAL	ALA	ILE	E1180
ALA	A2122	A2123	R2027	V1948	V1948	E1847	S1764	Y1655	GLY	R1482	LEU	ALA	ASP	L1181
ASP	S2232	S2123	L2030	V1948	V1948	E1847	S1765	Y1655	GLY	R1482	LEU	HIS	SER	L1182
PRO	Q2126	I2127	V2034	V1948	V1948	E1847	P1766	R1659	ASP	R1482	LEU	ASP	PRO	L1183
SER	I2127	I2127	T2038	V1948	V1948	E1847	S1767	R1659	ASP	R1482	LEU	VAL	GLY	L1184
ARG	M2135	M2136	Y2039	V1948	V1948	E1847	F1768	R1659	ASP	R1482	LEU	VAL	GLY	D1185
GLY	G2136	G2136	L2040	V1948	V1948	E1847	N1772	H1667	ASP	R1482	LEU	VAL	GLY	S1188
PRO	L2142	L2142	LYS	V2034	V1948	E1847	N1773	H1667	ASP	R1482	LEU	VAL	GLY	A1191
SER	N2143	N2143	LYS	V2034	V1948	E1847	E1774	H1670	ASP	R1482	LEU	VAL	GLY	F1192
THR	I2144	I2144	GLN	V2034	V1948	E1847	C1775	R1671	ASP	R1482	LEU	VAL	GLY	K1193
SER	R2145	R2145	ALA	V2034	V1948	E1847	Y1776	L1676	ASP	R1482	LEU	VAL	GLY	D1194
GLY	G2148	G2148	GLY	V2034	V1948	E1847	Q1777	E1682	ASP	R1482	LEU	VAL	GLY	F1195
SER	N2152	N2152	VAL	V2034	V1948	E1847	Y1778	E1682	ASP	R1482	LEU	VAL	GLY	D1196
MET	N2153	N2153	GLY	V2034	V1948	E1847	S1779	E1682	ASP	R1482	LEU	VAL	GLY	V1197
PRO	K2154	K2154	GLY	V2034	V1948	E1847	A1789	E1682	ASP	R1482	LEU	VAL	GLY	F1201
ASP	Y2157	Y2157	ASP	V2034	V1948	E1847	I1792	E1682	ASP	R1482	LEU	VAL	GLY	S1206
THR	P2160	P2160	ILE	V2034	V1948	E1847	E1797	E1682	ASP	R1482	LEU	VAL	GLY	V1209
GLY	Q2160	Q2160	ASN	V2034	V1948	E1847	A1798	E1682	ASP	R1482	LEU	VAL	GLY	A1210
GLY	V2177	V2177	MET	V2034	V1948	E1847	V1799	E1682	ASP	R1482	LEU	VAL	GLY	Q1211
GLY	V2177	V2177	LEU	V2034	V1948	E1847	S1803	E1682	ASP	R1482	LEU	VAL	GLY	N1216
ASP	G2181	G2181	ASN	V2034	V1948	E1847	S1803	E1682	ASP	R1482	LEU	VAL	GLY	V1221
ASN	GLY	GLY	ASN	V2034	V1948	E1847	S1803	E1682	ASP	R1482	LEU	VAL	GLY	L1224
THR	P2293	P2293	PHE	V2034	V1948	E1847	R1807	E1682	ASP	R1482	LEU	VAL	GLY	ALA
ILE	GLY	GLY	ASP	V2034	V1948	E1847	D1808	E1682	ASP	R1482	LEU	VAL	GLY	LYS
HIS	G2296	G2296	ASP	V2034	V1948	E1847	P1809	E1682	ASP	R1482	LEU	VAL	GLY	PRO
MET	Y2299	Y2299	LYS	V2034	V1948	E1847	F1816	E1682	ASP	R1482	LEU	VAL	GLY	ILE
G2386	L2300	L2300	GLY	V2034	V1948	E1847	L1817	E1682	ASP	R1482	LEU	VAL	GLY	PRO

[illegible]

- Molecule 2: RyR2









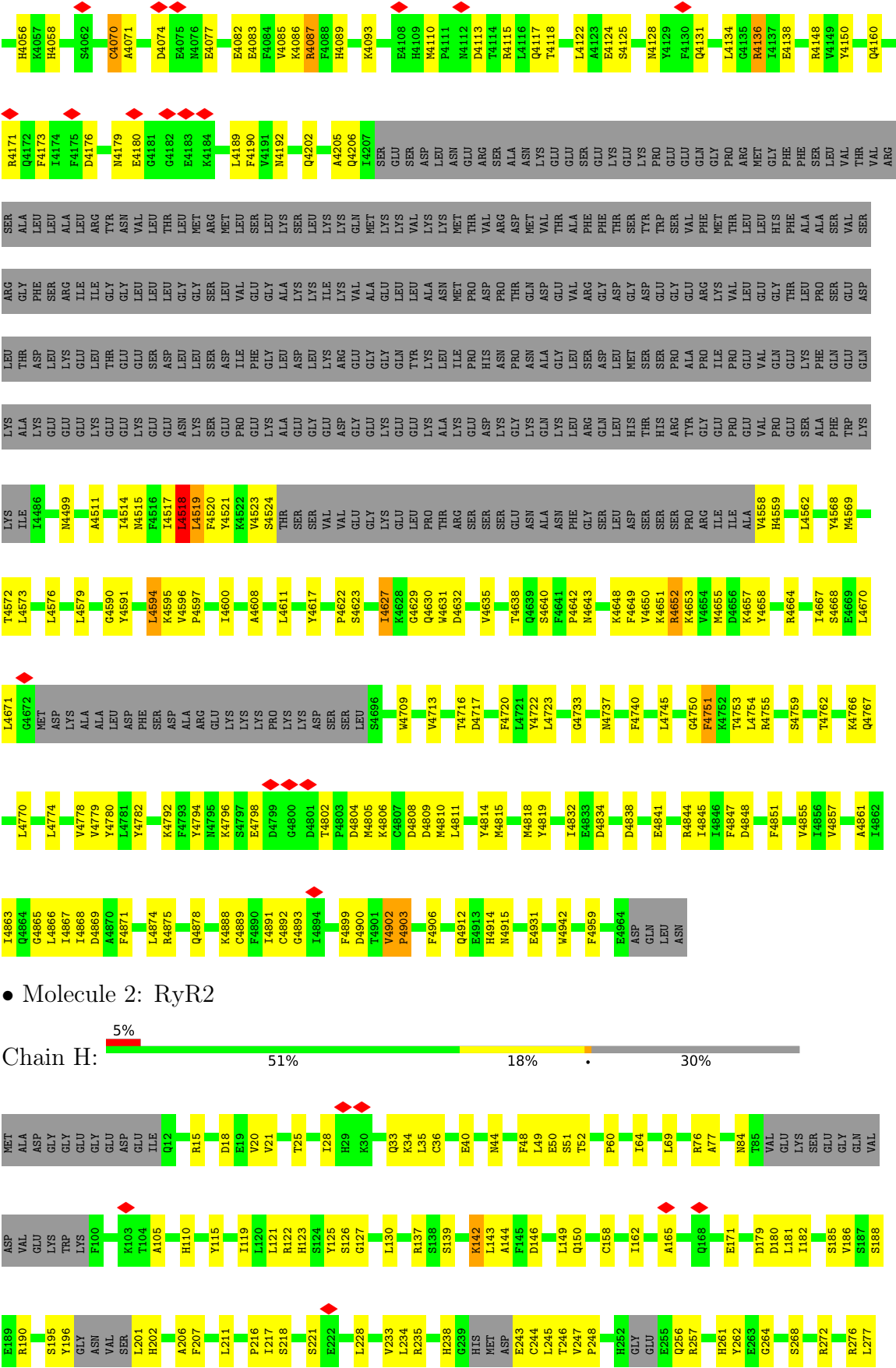
















WORLDWIDE  
**PDB**  
PROTEIN DATA BANK



R4844	G4750	K4651	PHE	V4650	L4874	K4875	Q4878	K4888	I4891	C4892	G4893	I4894	F4899	D4900	T4901	V4902	P4903	F4906	Q4912	E4913	H4914	N4915	E4931	W4942	F4959	E4964	ASP	GLN	LEU	ASN								
I4845	F4751	R4652	SER	K4652	L4867	L4868	Q4879	I4795	I4794	K4796	S4797	E4798	D4799	G4800	D4801	T4802	P4803	D4804	M4805	K4806	C4807	D4808	D4809	M4810	L4811	Y4814	M4815	Y4818	Y4819	L4832	E4833	D4834	D4838	E4841				
I4846	K4752	K4653	ASP	V4654	L4670	L4671	G4672	MET	ASP	LYS	LYS	LYS	D4799	G4800	D4801	T4802	P4803	D4804	M4805	K4806	C4807	D4808	D4809	M4810	L4811	Y4814	M4815	Y4818	Y4819	L4832	E4833	D4834	D4838	E4841				
F4847	T4753	M4655	SER	HIS	L4670	L4671	G4672	ASP	LYS	LYS	LYS	LYS	D4799	G4800	D4801	T4802	P4803	D4804	M4805	K4806	C4807	D4808	D4809	M4810	L4811	Y4814	M4815	Y4818	Y4819	L4832	E4833	D4834	D4838	E4841				
D4848	L4754	R4755	SER	HIS	L4656	K4657	Y4658	R4664	L4762	K4766	Q4767	L4770	L4774	V4778	V4779	Y4780	L4781	Y4782	K4792	F4793	Y4794	K4796	S4797	E4798	D4799	G4800	D4801	T4802	P4803	D4804	M4805	K4806	C4807	D4808	D4809	M4810	L4811	
F4851	S4759	Y4658	PRO	TYR	K4657	Y4658	R4664	L4762	K4766	Q4767	L4770	L4774	V4778	V4779	Y4780	L4781	Y4782	K4792	F4793	Y4794	K4796	S4797	E4798	D4799	G4800	D4801	T4802	P4803	D4804	M4805	K4806	C4807	D4808	D4809	M4810	L4811		
V4855	S4759	Y4658	PRO	TYR	K4657	Y4658	R4664	L4762	K4766	Q4767	L4770	L4774	V4778	V4779	Y4780	L4781	Y4782	K4792	F4793	Y4794	K4796	S4797	E4798	D4799	G4800	D4801	T4802	P4803	D4804	M4805	K4806	C4807	D4808	D4809	M4810	L4811		
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A4861	K4766	S4668	ALA	V4558	H4559	L4562	Y4568	M4569	T4572	L4573	L4576	L4579	G4590	Y4591	L4594	K4595	V4596	P4597	I4600	A4608	L4611	Y4617	P4622	S4623	I4627	Q4628	Q4629	Q4630	W4631	S4640	F4641	N4642	N4643	K4648	F4649			
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G4865	L4774	L4671	SER	ALA	GLY	L4562	Y4568	M4569	T4572	L4573	L4576	L4579	G4590	Y4591	L4594	K4595	V4596	P4597	I4600	A4608	L4611	Y4617	P4622	S4623	I4627	Q4628	Q4629	Q4630	W4631	S4640	F4641	N4642	N4643	K4648	F4649			
L4866	L4774	G4672	ASP	ILE	GLY	L4562	Y4568	M4569	T4572	L4573	L4576	L4579	G4590	Y4591	L4594	K4595	V4596	P4597	I4600	A4608	L4611	Y4617	P4622	S4623	I4627	Q4628	Q4629	Q4630	W4631	S4640	F4641	N4642	N4643	K4648	F4649			
I4867	Q4767	MET	GLY	PRO	GLY	L4562	Y4568	M4569	T4572	L4573	L4576	L4579	G4590	Y4591	L4594	K4595	V4596	P4597	I4600	A4608	L4611	Y4617	P4622	S4623	I4627	Q4628	Q4629	Q4630	W4631	S4640	F4641	N4642	N4643	K4648	F4649			
D4868	V4779	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS			
D4869	Y4779	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS			
A4870	Y4780	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		
F4871	Y4781	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		
L4874	Y4782	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
R4875	K4792	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	
Q4878	F4793	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
K4888	Y4794	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
I4891	D4799	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	
C4892	D4799	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	
G4893	G4800	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	
I4894	D4801	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	
F4899	T4802	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS																			

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	60287	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 ( $e^-/\text{\AA}^2$ )	48.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.085	Depositor
Minimum map value	-0.039	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	522.616, 522.616, 522.616	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.30654, 1.30654, 1.30654	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

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	0.35	0/835	0.58	0/1123
1	C	0.35	0/835	0.58	0/1123
1	E	0.35	0/835	0.58	0/1123
1	G	0.35	0/835	0.58	0/1123
2	B	0.38	0/27132	0.62	12/36687 (0.0%)
2	D	0.38	0/27132	0.62	12/36687 (0.0%)
2	F	0.38	0/27132	0.62	12/36687 (0.0%)
2	H	0.38	0/27132	0.62	12/36687 (0.0%)
All	All	0.38	0/111868	0.61	48/151240 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	29
2	D	0	29
2	F	0	29
2	H	0	29
All	All	0	116

There are no bond length outliers.

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1753	LEU	CA-CB-CG	6.30	129.80	115.30
2	B	1753	LEU	CA-CB-CG	6.30	129.79	115.30
2	D	1753	LEU	CA-CB-CG	6.30	129.78	115.30
2	F	1753	LEU	CA-CB-CG	6.29	129.76	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	814	LEU	CA-CB-CG	5.94	128.97	115.30
2	F	814	LEU	CA-CB-CG	5.94	128.96	115.30
2	B	814	LEU	CA-CB-CG	5.92	128.92	115.30
2	D	814	LEU	CA-CB-CG	5.92	128.92	115.30
2	D	2517	LEU	CA-CB-CG	5.47	127.88	115.30
2	B	2517	LEU	CA-CB-CG	5.45	127.84	115.30
2	F	2517	LEU	CA-CB-CG	5.45	127.84	115.30
2	H	2517	LEU	CA-CB-CG	5.45	127.84	115.30
2	H	1738	LEU	CA-CB-CG	5.40	127.72	115.30
2	F	1738	LEU	CA-CB-CG	5.39	127.69	115.30
2	B	1738	LEU	CA-CB-CG	5.38	127.67	115.30
2	D	1738	LEU	CA-CB-CG	5.37	127.65	115.30
2	B	1038	LEU	CA-CB-CG	5.32	127.54	115.30
2	H	1038	LEU	CA-CB-CG	5.32	127.54	115.30
2	D	1038	LEU	CA-CB-CG	5.32	127.54	115.30
2	F	1038	LEU	CA-CB-CG	5.31	127.52	115.30
2	H	3925	ILE	CG1-CB-CG2	-5.27	99.80	111.40
2	B	3925	ILE	CG1-CB-CG2	-5.27	99.81	111.40
2	D	3925	ILE	CG1-CB-CG2	-5.27	99.81	111.40
2	F	3925	ILE	CG1-CB-CG2	-5.25	99.84	111.40
2	B	2088	LEU	CA-CB-CG	5.20	127.26	115.30
2	F	2088	LEU	CA-CB-CG	5.20	127.26	115.30
2	D	2039	TYR	C-N-CA	5.20	134.69	121.70
2	D	2088	LEU	CA-CB-CG	5.19	127.24	115.30
2	F	2039	TYR	C-N-CA	5.19	134.66	121.70
2	H	2088	LEU	CA-CB-CG	5.19	127.23	115.30
2	B	2039	TYR	C-N-CA	5.18	134.66	121.70
2	D	748	LEU	CA-CB-CG	5.18	127.21	115.30
2	F	2022	SER	C-N-CA	5.17	134.64	121.70
2	F	748	LEU	CA-CB-CG	5.17	127.20	115.30
2	B	748	LEU	CA-CB-CG	5.17	127.19	115.30
2	H	748	LEU	CA-CB-CG	5.17	127.19	115.30
2	D	2022	SER	C-N-CA	5.17	134.62	121.70
2	B	2022	SER	C-N-CA	5.16	134.60	121.70
2	H	2022	SER	C-N-CA	5.16	134.60	121.70
2	H	2039	TYR	C-N-CA	5.16	134.59	121.70
2	D	139	SER	C-N-CA	5.15	134.56	121.70
2	B	456	LEU	CA-CB-CG	5.14	127.13	115.30
2	F	456	LEU	CA-CB-CG	5.14	127.13	115.30
2	B	139	SER	C-N-CA	5.14	134.54	121.70
2	D	456	LEU	CA-CB-CG	5.14	127.11	115.30
2	H	139	SER	C-N-CA	5.13	134.54	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	456	LEU	CA-CB-CG	5.13	127.11	115.30
2	F	139	SER	C-N-CA	5.12	134.51	121.70

There are no chirality outliers.

All (116) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	105	ALA	Peptide
2	B	142	LYS	Peptide
2	B	1475	LYS	Peptide
2	B	1579	VAL	Peptide
2	B	1607	ASP	Peptide
2	B	1635	GLU	Peptide
2	B	1756	SER	Peptide
2	B	1758	ARG	Peptide
2	B	1777	GLN	Peptide
2	B	1835	HIS	Peptide
2	B	1847	GLU	Peptide
2	B	2075	VAL	Peptide
2	B	221	SER	Peptide
2	B	2232	SER	Peptide
2	B	2462	CYS	Peptide
2	B	321	LYS	Peptide
2	B	4070	CYS	Peptide
2	B	4074	ASP	Peptide
2	B	4594	LEU	Peptide
2	B	4627	ILE	Peptide
2	B	4751	PHE	Peptide
2	B	657	PRO	Peptide
2	B	728	ASP	Peptide
2	B	739	ARG	Peptide
2	B	748	LEU	Peptide
2	B	777	GLY	Peptide
2	B	818	GLY	Peptide
2	B	819	TYR	Peptide
2	B	838	ARG	Peptide
2	D	105	ALA	Peptide
2	D	142	LYS	Peptide
2	D	1475	LYS	Peptide
2	D	1579	VAL	Peptide
2	D	1607	ASP	Peptide
2	D	1635	GLU	Peptide

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Mol	Chain	Res	Type	Group
2	D	1756	SER	Peptide
2	D	1758	ARG	Peptide
2	D	1777	GLN	Peptide
2	D	1835	HIS	Peptide
2	D	1847	GLU	Peptide
2	D	2075	VAL	Peptide
2	D	221	SER	Peptide
2	D	2232	SER	Peptide
2	D	2462	CYS	Peptide
2	D	321	LYS	Peptide
2	D	4070	CYS	Peptide
2	D	4074	ASP	Peptide
2	D	4594	LEU	Peptide
2	D	4627	ILE	Peptide
2	D	4751	PHE	Peptide
2	D	657	PRO	Peptide
2	D	728	ASP	Peptide
2	D	739	ARG	Peptide
2	D	748	LEU	Peptide
2	D	777	GLY	Peptide
2	D	818	GLY	Peptide
2	D	819	TYR	Peptide
2	D	838	ARG	Peptide
2	F	105	ALA	Peptide
2	F	142	LYS	Peptide
2	F	1475	LYS	Peptide
2	F	1579	VAL	Peptide
2	F	1607	ASP	Peptide
2	F	1635	GLU	Peptide
2	F	1756	SER	Peptide
2	F	1758	ARG	Peptide
2	F	1777	GLN	Peptide
2	F	1835	HIS	Peptide
2	F	1847	GLU	Peptide
2	F	2075	VAL	Peptide
2	F	221	SER	Peptide
2	F	2232	SER	Peptide
2	F	2462	CYS	Peptide
2	F	321	LYS	Peptide
2	F	4070	CYS	Peptide
2	F	4074	ASP	Peptide
2	F	4594	LEU	Peptide

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Mol	Chain	Res	Type	Group
2	F	4627	ILE	Peptide
2	F	4751	PHE	Peptide
2	F	657	PRO	Peptide
2	F	728	ASP	Peptide
2	F	739	ARG	Peptide
2	F	748	LEU	Peptide
2	F	777	GLY	Peptide
2	F	818	GLY	Peptide
2	F	819	TYR	Peptide
2	F	838	ARG	Peptide
2	H	105	ALA	Peptide
2	H	142	LYS	Peptide
2	H	1475	LYS	Peptide
2	H	1579	VAL	Peptide
2	H	1607	ASP	Peptide
2	H	1635	GLU	Peptide
2	H	1756	SER	Peptide
2	H	1758	ARG	Peptide
2	H	1777	GLN	Peptide
2	H	1835	HIS	Peptide
2	H	1847	GLU	Peptide
2	H	2075	VAL	Peptide
2	H	221	SER	Peptide
2	H	2232	SER	Peptide
2	H	2462	CYS	Peptide
2	H	321	LYS	Peptide
2	H	4070	CYS	Peptide
2	H	4074	ASP	Peptide
2	H	4594	LEU	Peptide
2	H	4627	ILE	Peptide
2	H	4751	PHE	Peptide
2	H	657	PRO	Peptide
2	H	728	ASP	Peptide
2	H	739	ARG	Peptide
2	H	748	LEU	Peptide
2	H	777	GLY	Peptide
2	H	818	GLY	Peptide
2	H	819	TYR	Peptide
2	H	838	ARG	Peptide

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	819	0	824	25	0
1	C	819	0	824	25	0
1	E	819	0	824	26	0
1	G	819	0	824	24	0
2	B	26636	0	25174	673	0
2	D	26636	0	25174	667	0
2	F	26636	0	25174	671	0
2	H	26636	0	25174	682	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
All	All	109824	0	103992	2512	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 12.

All (2512) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:4520:PHE:CD1	2:F:4562:LEU:HD21	1.50	1.47
2:B:4520:PHE:CD1	2:B:4562:LEU:HD21	1.50	1.47
2:D:4520:PHE:CD1	2:D:4562:LEU:HD21	1.50	1.46
2:H:4520:PHE:CD1	2:H:4562:LEU:HD21	1.50	1.44
2:B:4808:ASP:HB3	2:D:4523:VAL:CG2	1.55	1.36
2:F:207:PHE:CZ	2:H:2326:ILE:HG23	1.60	1.35
2:D:4808:ASP:HB3	2:F:4523:VAL:CG2	1.54	1.35
2:B:2326:ILE:HG23	2:H:207:PHE:CZ	1.61	1.34
2:D:207:PHE:CZ	2:F:2326:ILE:HG23	1.60	1.34
2:B:4523:VAL:CG2	2:H:4808:ASP:HB3	1.57	1.34
2:B:207:PHE:CZ	2:D:2326:ILE:HG23	1.61	1.33
2:F:4808:ASP:HB3	2:H:4523:VAL:CG2	1.58	1.30
2:B:4902:VAL:HG12	2:B:4903:PRO:CD	1.65	1.27
2:H:4902:VAL:HG12	2:H:4903:PRO:CD	1.64	1.25
2:F:4902:VAL:HG12	2:F:4903:PRO:CD	1.64	1.25

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:4902:VAL:HG12	2:D:4903:PRO:CD	1.67	1.25
2:H:4779:VAL:HG11	2:H:4818:MET:SD	1.86	1.16
2:B:4779:VAL:HG11	2:B:4818:MET:SD	1.86	1.15
2:F:4779:VAL:HG11	2:F:4818:MET:SD	1.86	1.14
2:F:4808:ASP:HB3	2:H:4523:VAL:HG23	1.23	1.14
2:B:4523:VAL:HG23	2:H:4808:ASP:HB3	1.19	1.14
2:D:4779:VAL:HG11	2:D:4818:MET:SD	1.86	1.13
2:B:4808:ASP:HB3	2:D:4523:VAL:HG23	1.18	1.12
2:B:4808:ASP:CB	2:D:4523:VAL:HG21	1.79	1.12
2:D:4808:ASP:CB	2:F:4523:VAL:HG21	1.79	1.12
2:D:4808:ASP:HB3	2:F:4523:VAL:HG23	1.19	1.11
2:B:4808:ASP:CG	2:D:4523:VAL:HG21	1.72	1.10
2:D:207:PHE:CE2	2:F:2326:ILE:HG23	1.86	1.10
2:F:207:PHE:CE2	2:H:2326:ILE:HG23	1.85	1.10
2:B:4523:VAL:HG21	2:H:4808:ASP:CB	1.82	1.09
2:D:207:PHE:CE1	2:F:2326:ILE:HG23	1.86	1.09
2:F:207:PHE:CE1	2:H:2326:ILE:HG23	1.87	1.09
2:B:4523:VAL:HG21	2:H:4808:ASP:CG	1.73	1.09
2:D:4808:ASP:CG	2:F:4523:VAL:HG21	1.73	1.09
2:B:2326:ILE:HG23	2:H:207:PHE:CE1	1.87	1.08
2:B:207:PHE:CE2	2:D:2326:ILE:HG23	1.89	1.07
2:B:2326:ILE:HG23	2:H:207:PHE:CE2	1.87	1.07
2:B:207:PHE:CE1	2:D:2326:ILE:HG23	1.87	1.07
2:F:4808:ASP:CB	2:H:4523:VAL:HG21	1.83	1.06
2:D:4808:ASP:CB	2:F:4523:VAL:CG2	2.34	1.05
2:B:4774:LEU:CD2	2:D:4754:LEU:HD21	1.86	1.05
2:B:4808:ASP:CB	2:D:4523:VAL:CG2	2.34	1.05
2:B:4754:LEU:HD21	2:H:4774:LEU:CD2	1.87	1.04
2:B:4523:VAL:CG2	2:H:4808:ASP:CB	2.36	1.03
2:D:4774:LEU:CD2	2:F:4754:LEU:HD21	1.89	1.03
2:F:4774:LEU:CD2	2:H:4754:LEU:HD21	1.88	1.03
2:F:4808:ASP:CG	2:H:4523:VAL:HG21	1.76	1.03
2:D:4902:VAL:CG1	2:D:4903:PRO:HD2	1.89	1.03
2:H:4902:VAL:CG1	2:H:4903:PRO:HD2	1.89	1.02
2:D:207:PHE:CE1	2:F:2326:ILE:CG2	2.42	1.02
2:B:4902:VAL:CG1	2:B:4903:PRO:HD2	1.89	1.02
2:D:4808:ASP:HB3	2:F:4523:VAL:HG21	1.37	1.02
2:B:2326:ILE:CG2	2:H:207:PHE:CE1	2.43	1.01
2:F:4902:VAL:CG1	2:F:4903:PRO:HD2	1.89	1.01
2:B:207:PHE:CE1	2:D:2326:ILE:CG2	2.44	1.01
2:F:207:PHE:CE1	2:H:2326:ILE:CG2	2.42	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:4902:VAL:HG12	2:H:4903:PRO:HD2	1.00	0.99
2:F:4902:VAL:HG12	2:F:4903:PRO:HD2	0.99	0.99
2:F:4808:ASP:CB	2:H:4523:VAL:CG2	2.38	0.98
2:B:4902:VAL:HG12	2:B:4903:PRO:HD2	0.99	0.98
2:F:4520:PHE:HD1	2:F:4562:LEU:CD2	1.76	0.98
2:B:4774:LEU:HD22	2:D:4754:LEU:CD2	1.93	0.98
2:H:4520:PHE:CD1	2:H:4562:LEU:CD2	2.46	0.98
2:H:4520:PHE:HD1	2:H:4562:LEU:CD2	1.76	0.98
2:B:4520:PHE:HB3	2:B:4562:LEU:HD23	1.45	0.98
2:B:4754:LEU:CD2	2:H:4774:LEU:HD22	1.93	0.98
2:D:4520:PHE:CD1	2:D:4562:LEU:CD2	2.46	0.98
2:D:4520:PHE:HD1	2:D:4562:LEU:CD2	1.76	0.98
2:D:4774:LEU:HD22	2:F:4754:LEU:HD21	0.99	0.98
2:F:4774:LEU:HD22	2:H:4754:LEU:CD2	1.94	0.97
2:B:4520:PHE:CD1	2:B:4562:LEU:CD2	2.46	0.97
2:D:4902:VAL:HG12	2:D:4903:PRO:HD2	0.97	0.97
2:F:4520:PHE:HB3	2:F:4562:LEU:HD23	1.45	0.97
2:D:207:PHE:CZ	2:F:2326:ILE:HD12	2.00	0.97
2:F:4520:PHE:CD1	2:F:4562:LEU:CD2	2.46	0.97
2:F:4774:LEU:HD22	2:H:4754:LEU:HD21	0.97	0.97
2:H:4520:PHE:HB3	2:H:4562:LEU:HD23	1.45	0.97
2:B:4520:PHE:HD1	2:B:4562:LEU:CD2	1.76	0.97
2:D:207:PHE:CZ	2:F:2326:ILE:CG2	2.48	0.96
2:F:207:PHE:CZ	2:H:2326:ILE:CG2	2.48	0.96
2:F:4808:ASP:HB3	2:H:4523:VAL:HG21	1.40	0.96
2:F:207:PHE:CZ	2:H:2326:ILE:HD12	2.01	0.95
2:B:4754:LEU:HD21	2:H:4774:LEU:HD22	0.96	0.95
2:B:4808:ASP:HB3	2:D:4523:VAL:HG21	1.39	0.95
2:B:2326:ILE:HD12	2:H:207:PHE:CZ	2.02	0.95
2:D:4520:PHE:HB3	2:D:4562:LEU:HD23	1.45	0.95
2:B:207:PHE:CZ	2:D:2326:ILE:CG2	2.50	0.94
2:B:2326:ILE:CG2	2:H:207:PHE:CZ	2.50	0.94
2:B:207:PHE:CZ	2:D:2326:ILE:HD12	2.03	0.94
2:B:4774:LEU:HD22	2:D:4754:LEU:HD21	0.96	0.92
2:D:4865:GLY:HA2	2:F:4868:ILE:HG12	1.54	0.90
2:F:4857:VAL:HG22	2:H:4863:ILE:HG21	1.53	0.90
2:B:4863:ILE:HG21	2:H:4857:VAL:HG22	1.55	0.89
2:B:4865:GLY:HA2	2:D:4868:ILE:HG12	1.55	0.89
2:D:4774:LEU:HD22	2:F:4754:LEU:CD2	1.96	0.89
2:F:4865:GLY:HA2	2:H:4868:ILE:HG12	1.55	0.88
2:B:4868:ILE:HG12	2:H:4865:GLY:HA2	1.56	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4857:VAL:HG22	2:D:4863:ILE:HG21	1.53	0.88
2:D:4857:VAL:HG22	2:F:4863:ILE:HG21	1.54	0.87
2:F:4902:VAL:CG1	2:F:4903:PRO:CD	2.52	0.86
2:F:4857:VAL:HG13	2:H:4863:ILE:CG2	2.07	0.85
2:B:4902:VAL:CG1	2:B:4903:PRO:CD	2.52	0.85
2:D:4857:VAL:HG13	2:F:4863:ILE:CG2	2.07	0.84
2:H:4902:VAL:CG1	2:H:4903:PRO:CD	2.51	0.84
2:D:76:ARG:CB	2:F:3891:TRP:HB3	2.08	0.83
2:F:76:ARG:CB	2:H:3891:TRP:HB3	2.08	0.83
2:B:4857:VAL:HG13	2:D:4863:ILE:CG2	2.09	0.82
2:B:4863:ILE:CG2	2:H:4857:VAL:HG13	2.10	0.82
2:B:3891:TRP:HB3	2:H:76:ARG:CB	2.10	0.81
2:D:207:PHE:CE2	2:F:2326:ILE:HD12	2.15	0.81
2:F:207:PHE:CE2	2:H:2326:ILE:HD12	2.16	0.80
2:F:4520:PHE:HB3	2:F:4562:LEU:CD2	2.12	0.80
2:H:4520:PHE:HB3	2:H:4562:LEU:CD2	2.12	0.80
2:B:76:ARG:CB	2:D:3891:TRP:HB3	2.11	0.80
2:D:4520:PHE:HB3	2:D:4562:LEU:CD2	2.12	0.79
2:B:4520:PHE:HB3	2:B:4562:LEU:CD2	2.12	0.79
2:F:4779:VAL:CG1	2:F:4818:MET:SD	2.71	0.79
2:B:207:PHE:CE2	2:D:2326:ILE:HD12	2.19	0.78
2:H:4627:ILE:O	2:H:4631:TRP:HB2	1.84	0.78
2:B:4627:ILE:O	2:B:4631:TRP:HB2	1.84	0.78
2:F:4520:PHE:CG	2:F:4562:LEU:HD21	2.17	0.78
2:B:2326:ILE:HD12	2:H:207:PHE:CE2	2.17	0.78
2:H:4520:PHE:CG	2:H:4562:LEU:HD21	2.17	0.78
2:D:4902:VAL:CG1	2:D:4903:PRO:CD	2.54	0.77
2:F:4857:VAL:CG2	2:H:4863:ILE:HG21	2.14	0.77
2:B:4857:VAL:CG2	2:D:4863:ILE:HG21	2.15	0.77
2:F:4627:ILE:O	2:F:4631:TRP:HB2	1.84	0.77
2:H:4779:VAL:CG1	2:H:4818:MET:SD	2.71	0.77
2:F:4857:VAL:HG13	2:H:4863:ILE:HB	1.67	0.77
2:B:4779:VAL:CG1	2:B:4818:MET:SD	2.71	0.76
2:D:4520:PHE:CG	2:D:4562:LEU:HD21	2.17	0.76
2:D:4810:MET:HG2	2:F:4521:TYR:HB2	1.65	0.76
2:B:4810:MET:HG2	2:D:4521:TYR:HB2	1.66	0.76
2:D:4627:ILE:O	2:D:4631:TRP:HB2	1.84	0.76
2:H:4902:VAL:HG12	2:H:4903:PRO:HD3	1.66	0.76
2:D:207:PHE:CD1	2:F:2326:ILE:CG2	2.69	0.75
2:B:4520:PHE:CG	2:B:4562:LEU:HD21	2.17	0.75
2:D:4779:VAL:CG1	2:D:4818:MET:SD	2.71	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4521:TYR:HB2	2:H:4810:MET:HG2	1.68	0.75
2:D:4857:VAL:CG2	2:F:4863:ILE:HG21	2.16	0.75
2:B:4863:ILE:HG21	2:H:4857:VAL:CG2	2.16	0.74
2:B:4863:ILE:HB	2:H:4857:VAL:HG13	1.70	0.74
2:F:4810:MET:HG2	2:H:4521:TYR:HB2	1.69	0.74
2:B:2326:ILE:CG2	2:H:207:PHE:CD1	2.71	0.73
2:F:76:ARG:CB	2:H:3891:TRP:CB	2.66	0.73
2:B:4857:VAL:HG13	2:D:4863:ILE:HB	1.69	0.73
2:F:4848:ASP:HB3	2:H:4819:TYR:HE1	1.53	0.73
2:F:4902:VAL:HG12	2:F:4903:PRO:HD3	1.67	0.73
2:D:4046:LYS:H	2:D:4077:GLU:HB3	1.54	0.73
2:F:207:PHE:CD1	2:H:2326:ILE:CG2	2.70	0.73
2:B:4515:ASN:ND2	2:H:4780:TYR:CE2	2.56	0.73
2:D:190:ARG:NH1	2:F:2423:ILE:HG23	2.04	0.73
2:F:4857:VAL:HG13	2:H:4863:ILE:CB	2.19	0.73
2:B:4902:VAL:HG12	2:B:4903:PRO:HD3	1.68	0.73
2:B:4780:TYR:CE2	2:D:4515:ASN:ND2	2.56	0.73
2:D:76:ARG:CB	2:F:3891:TRP:CB	2.66	0.72
2:F:4046:LYS:H	2:F:4077:GLU:HB3	1.54	0.72
2:D:4857:VAL:HG13	2:F:4863:ILE:HB	1.71	0.72
2:F:190:ARG:NH1	2:H:2423:ILE:HG23	2.04	0.72
2:H:4046:LYS:H	2:H:4077:GLU:HB3	1.54	0.72
2:D:4848:ASP:HB3	2:F:4819:TYR:HE1	1.55	0.72
2:B:3891:TRP:CB	2:H:76:ARG:CB	2.68	0.71
2:B:207:PHE:CD1	2:D:2326:ILE:CG2	2.72	0.71
2:B:4046:LYS:H	2:B:4077:GLU:HB3	1.54	0.71
2:B:4848:ASP:HB3	2:D:4819:TYR:HE1	1.56	0.71
2:D:4851:PHE:O	2:D:4855:VAL:HB	1.91	0.71
2:F:77:ALA:HB2	2:H:3891:TRP:CZ2	2.26	0.71
2:D:77:ALA:HB2	2:F:3891:TRP:CZ2	2.25	0.71
2:F:4851:PHE:O	2:F:4855:VAL:HB	1.91	0.71
2:D:1111:GLY:HA3	2:D:1211:GLN:HE21	1.56	0.71
2:B:76:ARG:CB	2:D:3891:TRP:CB	2.69	0.71
2:D:4865:GLY:HA2	2:F:4868:ILE:CG1	2.20	0.71
2:F:1138:ASP:HB2	2:F:1145:TRP:HE1	1.56	0.71
2:B:2344:LEU:O	2:B:2348:MET:HB2	1.91	0.70
2:B:1111:GLY:HA3	2:B:1211:GLN:HE21	1.56	0.70
2:F:4814:TYR:HE2	2:F:4815:MET:HE1	1.56	0.70
2:B:4851:PHE:O	2:B:4855:VAL:HB	1.91	0.70
2:H:1138:ASP:HB2	2:H:1145:TRP:HE1	1.56	0.70
2:B:2423:ILE:HG23	2:H:190:ARG:NH1	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:4857:VAL:HG13	2:F:4863:ILE:CB	2.22	0.70
2:H:4851:PHE:O	2:H:4855:VAL:HB	1.91	0.70
2:B:4857:VAL:HG13	2:D:4863:ILE:CB	2.21	0.70
2:H:1111:GLY:HA3	2:H:1211:GLN:HE21	1.56	0.70
2:F:4865:GLY:HA2	2:H:4868:ILE:CG1	2.21	0.70
2:B:4863:ILE:CB	2:H:4857:VAL:HG13	2.22	0.70
2:F:4780:TYR:CE2	2:H:4515:ASN:ND2	2.59	0.70
2:B:190:ARG:NH1	2:D:2423:ILE:HG23	2.06	0.70
2:D:4780:TYR:CE2	2:F:4515:ASN:ND2	2.58	0.70
2:F:2344:LEU:O	2:F:2348:MET:HB2	1.91	0.70
2:B:3891:TRP:CZ2	2:H:77:ALA:HB2	2.27	0.69
2:F:1242:ASN:HB3	2:F:1807:ARG:HB2	1.75	0.69
2:D:1138:ASP:HB2	2:D:1145:TRP:HE1	1.56	0.69
2:D:2344:LEU:O	2:D:2348:MET:HB2	1.91	0.69
2:B:1138:ASP:HB2	2:B:1145:TRP:HE1	1.56	0.69
2:H:1242:ASN:HB3	2:H:1807:ARG:HB2	1.74	0.69
2:H:2344:LEU:O	2:H:2348:MET:HB2	1.91	0.69
2:B:4819:TYR:HE1	2:H:4848:ASP:HB3	1.57	0.69
2:B:4861:ALA:HB1	2:D:4867:ILE:HG21	1.75	0.69
2:B:4868:ILE:CG1	2:H:4865:GLY:HA2	2.23	0.69
2:B:77:ALA:HB2	2:D:3891:TRP:CZ2	2.28	0.69
2:F:1111:GLY:HA3	2:F:1211:GLN:HE21	1.56	0.68
2:D:1242:ASN:HB3	2:D:1807:ARG:HB2	1.74	0.68
2:B:1242:ASN:HB3	2:B:1807:ARG:HB2	1.74	0.68
2:F:4857:VAL:CG1	2:H:4863:ILE:CG2	2.70	0.68
2:F:4861:ALA:HB1	2:H:4867:ILE:HG21	1.75	0.68
2:B:4865:GLY:HA2	2:D:4868:ILE:CG1	2.22	0.68
2:B:545:ARG:HH21	2:B:583:PRO:HG3	1.60	0.67
2:D:4857:VAL:CG1	2:F:4863:ILE:CG2	2.72	0.67
2:F:394:HIS:HD2	2:F:397:GLY:H	1.43	0.67
2:B:4867:ILE:HG21	2:H:4861:ALA:HB1	1.77	0.67
2:D:207:PHE:CD2	2:F:2326:ILE:HG23	2.30	0.67
2:D:545:ARG:HH21	2:D:583:PRO:HG3	1.60	0.67
2:B:4857:VAL:CG1	2:D:4863:ILE:CG2	2.73	0.67
2:D:4861:ALA:HB1	2:F:4867:ILE:HG21	1.76	0.67
2:B:262:TYR:HB2	2:B:389:ARG:HB3	1.77	0.67
2:D:394:HIS:HD2	2:D:397:GLY:H	1.43	0.67
2:D:4767:GLN:HG2	2:F:4753:THR:OG1	1.95	0.66
2:H:545:ARG:HH21	2:H:583:PRO:HG3	1.60	0.66
2:B:4863:ILE:CG2	2:H:4857:VAL:CG1	2.73	0.66
2:B:244:CYS:SG	2:B:245:LEU:N	2.69	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4865:GLY:CA	2:D:4868:ILE:HG12	2.26	0.66
2:D:244:CYS:SG	2:D:245:LEU:N	2.69	0.66
2:D:4902:VAL:HG12	2:D:4903:PRO:HD3	1.75	0.66
2:H:748:LEU:HD13	2:H:750:ARG:HE	1.61	0.66
2:F:545:ARG:HH21	2:F:583:PRO:HG3	1.60	0.66
2:D:4518:LEU:HD13	2:D:4521:TYR:CE2	2.31	0.66
2:F:207:PHE:CD2	2:H:2326:ILE:HG23	2.30	0.66
2:B:1431:ARG:HE	2:B:1505:LEU:HD21	1.60	0.66
2:D:1431:ARG:HE	2:D:1505:LEU:HD21	1.60	0.66
2:F:4518:LEU:HD13	2:F:4521:TYR:CE2	2.31	0.66
2:B:394:HIS:HD2	2:B:397:GLY:H	1.43	0.66
2:B:748:LEU:HD13	2:B:750:ARG:HE	1.61	0.66
2:D:262:TYR:HB2	2:D:389:ARG:HB3	1.77	0.66
2:H:244:CYS:SG	2:H:245:LEU:N	2.69	0.66
2:F:1431:ARG:HE	2:F:1505:LEU:HD21	1.60	0.66
2:F:244:CYS:SG	2:F:245:LEU:N	2.69	0.65
2:B:4767:GLN:HG2	2:D:4753:THR:OG1	1.96	0.65
2:H:262:TYR:HB2	2:H:389:ARG:HB3	1.77	0.65
2:H:1445:TRP:H	2:H:1487:MET:HB2	1.62	0.65
2:B:1445:TRP:H	2:B:1487:MET:HB2	1.62	0.65
2:D:144:ALA:HB1	2:D:206:ALA:HA	1.78	0.65
2:H:1431:ARG:HE	2:H:1505:LEU:HD21	1.60	0.65
2:D:1445:TRP:H	2:D:1487:MET:HB2	1.61	0.65
2:D:1482:ARG:HH11	2:D:1531:TYR:HA	1.61	0.65
2:F:1482:ARG:HH11	2:F:1531:TYR:HA	1.61	0.65
2:H:1117:TRP:HE1	2:H:1164:CYS:HB3	1.62	0.65
2:B:144:ALA:HB1	2:B:206:ALA:HA	1.78	0.65
2:F:1445:TRP:H	2:F:1487:MET:HB2	1.62	0.65
2:D:2891:GLN:HB3	2:D:2895:LYS:HE2	1.79	0.65
2:F:262:TYR:HB2	2:F:389:ARG:HB3	1.77	0.65
2:F:748:LEU:HD13	2:F:750:ARG:HE	1.61	0.65
2:F:144:ALA:HB1	2:F:206:ALA:HA	1.78	0.64
2:D:4810:MET:CG	2:F:4521:TYR:HB2	2.26	0.64
2:H:1703:TYR:HD2	2:H:1820:PRO:HB2	1.63	0.64
2:H:4518:LEU:HD13	2:H:4521:TYR:CE2	2.31	0.64
2:B:4518:LEU:HD13	2:B:4521:TYR:CE2	2.31	0.64
2:B:4753:THR:OG1	2:H:4767:GLN:HG2	1.98	0.64
2:F:4767:GLN:HG2	2:H:4753:THR:OG1	1.98	0.64
2:B:2891:GLN:HB3	2:B:2895:LYS:HE2	1.79	0.64
2:F:1117:TRP:HE1	2:F:1164:CYS:HB3	1.62	0.64
1:G:40:ARG:HH12	2:H:685:PHE:HB3	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:4511:ALA:HA	2:D:4514:ILE:HD12	1.80	0.64
2:H:1482:ARG:HH11	2:H:1531:TYR:HA	1.61	0.64
2:D:1117:TRP:HE1	2:D:1164:CYS:HB3	1.62	0.64
1:E:40:ARG:HH12	2:F:685:PHE:HB3	1.63	0.64
2:F:374:TYR:HA	2:F:391:ALA:HA	1.80	0.64
2:B:2770:GLU:HA	2:B:2773:ARG:HB2	1.80	0.64
2:D:748:LEU:HD13	2:D:750:ARG:HE	1.61	0.64
2:F:4511:ALA:HA	2:F:4514:ILE:HD12	1.80	0.64
2:H:144:ALA:HB1	2:H:206:ALA:HA	1.78	0.64
2:D:300:VAL:O	2:D:420:ARG:NH1	2.31	0.64
2:D:2770:GLU:HA	2:D:2773:ARG:HB2	1.80	0.64
2:H:374:TYR:HA	2:H:391:ALA:HA	1.80	0.64
2:B:2326:ILE:HG23	2:H:207:PHE:CD2	2.32	0.63
2:B:4511:ALA:HA	2:B:4514:ILE:HD12	1.80	0.63
2:B:4810:MET:CG	2:D:4521:TYR:HB2	2.28	0.63
2:H:394:HIS:HD2	2:H:397:GLY:H	1.43	0.63
2:B:1165:MET:HB2	2:B:1174:MET:HB2	1.81	0.63
2:B:1482:ARG:HH11	2:B:1531:TYR:HA	1.61	0.63
2:B:1703:TYR:HD2	2:B:1820:PRO:HB2	1.63	0.63
2:F:207:PHE:CD1	2:H:2326:ILE:HG23	2.32	0.63
2:B:4868:ILE:HG12	2:H:4865:GLY:CA	2.27	0.63
2:F:2891:GLN:HB3	2:F:2895:LYS:HE2	1.79	0.63
2:H:1165:MET:HB2	2:H:1174:MET:HB2	1.81	0.63
2:F:1114:ARG:HB2	2:F:1206:SER:HB3	1.81	0.63
2:H:2891:GLN:HB3	2:H:2895:LYS:HE2	1.79	0.63
2:F:1703:TYR:HD2	2:F:1820:PRO:HB2	1.63	0.63
2:H:2770:GLU:HA	2:H:2773:ARG:HB2	1.80	0.63
2:H:4511:ALA:HA	2:H:4514:ILE:HD12	1.80	0.63
1:A:40:ARG:HH12	2:B:685:PHE:HB3	1.63	0.63
1:C:87:HIS:H	1:C:91:ILE:HB	1.64	0.63
2:D:207:PHE:CD1	2:F:2326:ILE:HG23	2.30	0.63
1:G:31:GLN:HB2	1:G:96:THR:HB	1.81	0.63
2:H:4520:PHE:CB	2:H:4562:LEU:CD2	2.77	0.63
2:D:1165:MET:HB2	2:D:1174:MET:HB2	1.81	0.63
2:B:207:PHE:CD2	2:D:2326:ILE:HG23	2.34	0.63
2:B:1117:TRP:HE1	2:B:1164:CYS:HB3	1.62	0.63
1:C:40:ARG:HH12	2:D:685:PHE:HB3	1.63	0.63
2:F:2770:GLU:HA	2:F:2773:ARG:HB2	1.80	0.63
2:F:4520:PHE:CB	2:F:4562:LEU:CD2	2.77	0.63
2:H:300:VAL:O	2:H:420:ARG:NH1	2.31	0.63
2:H:1610:ARG:NH1	2:H:1612:SER:OG	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:GLN:HB2	1:A:96:THR:HB	1.81	0.62
2:B:374:TYR:HA	2:B:391:ALA:HA	1.80	0.62
2:B:1114:ARG:HB2	2:B:1206:SER:HB3	1.81	0.62
2:D:4848:ASP:OD2	2:F:4819:TYR:CE1	2.52	0.62
2:F:4865:GLY:CA	2:H:4868:ILE:HG12	2.25	0.62
1:A:87:HIS:H	1:A:91:ILE:HB	1.64	0.62
2:F:4047:ARG:NH1	2:F:4077:GLU:OE2	2.33	0.62
2:B:300:VAL:O	2:B:420:ARG:NH1	2.31	0.62
2:B:4047:ARG:NH1	2:B:4077:GLU:OE2	2.33	0.62
2:D:374:TYR:HA	2:D:391:ALA:HA	1.80	0.62
2:B:1610:ARG:NH1	2:B:1612:SER:OG	2.32	0.62
1:E:87:HIS:H	1:E:91:ILE:HB	1.64	0.62
2:F:1165:MET:HB2	2:F:1174:MET:HB2	1.81	0.62
2:D:4865:GLY:CA	2:F:4868:ILE:HG12	2.25	0.62
2:F:1137:PHE:HA	2:F:1144:ARG:HA	1.82	0.62
2:D:1137:PHE:HA	2:D:1144:ARG:HA	1.82	0.62
2:H:4047:ARG:NH1	2:H:4077:GLU:OE2	2.33	0.62
2:D:1114:ARG:HB2	2:D:1206:SER:HB3	1.81	0.62
2:B:4521:TYR:HB2	2:H:4810:MET:CG	2.29	0.62
1:C:31:GLN:HB2	1:C:96:THR:HB	1.81	0.62
2:D:1703:TYR:HD2	2:D:1820:PRO:HB2	1.63	0.62
1:E:31:GLN:HB2	1:E:96:THR:HB	1.81	0.62
2:H:1114:ARG:HB2	2:H:1206:SER:HB3	1.81	0.62
2:H:1137:PHE:HA	2:H:1144:ARG:HA	1.82	0.62
2:D:1153:GLY:HA3	2:D:1182:LEU:HB3	1.82	0.62
2:D:4520:PHE:CB	2:D:4562:LEU:CD2	2.77	0.62
2:F:677:LEU:HB2	2:F:755:ILE:HB	1.82	0.62
2:F:1610:ARG:NH1	2:F:1612:SER:OG	2.32	0.62
2:F:4810:MET:CG	2:H:4521:TYR:HB2	2.30	0.62
2:F:1153:GLY:HA3	2:F:1182:LEU:HB3	1.82	0.61
2:D:677:LEU:HB2	2:D:755:ILE:HB	1.82	0.61
2:D:4047:ARG:NH1	2:D:4077:GLU:OE2	2.33	0.61
2:D:4874:LEU:O	2:D:4878:GLN:NE2	2.33	0.61
2:B:1153:GLY:HA3	2:B:1182:LEU:HB3	1.82	0.61
2:D:1250:TRP:HE1	2:D:1643:GLU:HG3	1.65	0.61
2:F:1670:HIS:ND1	2:F:1778:TYR:O	2.34	0.61
2:F:4148:ARG:NH2	2:F:4150:TYR:OH	2.33	0.61
2:F:4874:LEU:O	2:F:4878:GLN:NE2	2.33	0.61
2:H:1153:GLY:HA3	2:H:1182:LEU:HB3	1.82	0.61
2:D:4148:ARG:NH2	2:D:4150:TYR:OH	2.33	0.61
2:B:1101:TRP:HA	2:B:1237:GLU:HB2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1670:HIS:ND1	2:D:1778:TYR:O	2.33	0.61
2:H:2127:ILE:HD11	2:H:2143:MET:HG3	1.83	0.61
2:B:1137:PHE:HA	2:B:1144:ARG:HA	1.82	0.61
2:B:2326:ILE:HG23	2:H:207:PHE:CD1	2.32	0.61
1:G:87:HIS:H	1:G:91:ILE:HB	1.64	0.61
2:B:1761:MET:SD	2:B:1761:MET:N	2.73	0.61
2:B:4520:PHE:CB	2:B:4562:LEU:CD2	2.77	0.61
2:D:1610:ARG:NH1	2:D:1612:SER:OG	2.32	0.61
2:F:300:VAL:O	2:F:420:ARG:NH1	2.31	0.61
2:B:4874:LEU:O	2:B:4878:GLN:NE2	2.33	0.61
2:H:677:LEU:HB2	2:H:755:ILE:HB	1.82	0.61
2:H:1250:TRP:HE1	2:H:1643:GLU:HG3	1.65	0.61
2:B:2127:ILE:HD11	2:B:2143:MET:HG3	1.83	0.61
2:F:4848:ASP:OD2	2:H:4819:TYR:CE1	2.54	0.61
2:B:1427:TYR:HA	2:B:1509:CYS:HA	1.83	0.61
2:H:4874:LEU:O	2:H:4878:GLN:NE2	2.33	0.61
2:D:1427:TYR:HA	2:D:1509:CYS:HA	1.83	0.60
2:F:1250:TRP:HE1	2:F:1643:GLU:HG3	1.65	0.60
2:B:1250:TRP:HE1	2:B:1643:GLU:HG3	1.65	0.60
2:B:4517:ILE:O	2:B:4519:LEU:N	2.32	0.60
2:F:1427:TYR:HA	2:F:1509:CYS:HA	1.83	0.60
2:B:1670:HIS:ND1	2:B:1778:TYR:O	2.34	0.60
2:D:1258:PHE:HB2	2:D:1593:HIS:HB3	1.83	0.60
2:H:1116:GLY:HA3	2:H:1136:ALA:HA	1.84	0.60
2:D:1101:TRP:HA	2:D:1237:GLU:HB2	1.83	0.60
2:B:1116:GLY:HA3	2:B:1136:ALA:HA	1.84	0.60
2:D:188:SER:HB2	2:D:190:ARG:HH21	1.67	0.60
2:F:1258:PHE:HB2	2:F:1593:HIS:HB3	1.83	0.60
2:H:1670:HIS:ND1	2:H:1778:TYR:O	2.34	0.60
2:B:677:LEU:HB2	2:B:755:ILE:HB	1.82	0.60
2:B:4148:ARG:NH2	2:B:4150:TYR:OH	2.33	0.60
2:D:1116:GLY:HA3	2:D:1136:ALA:HA	1.84	0.60
2:D:1726:ILE:HD11	2:D:2121:LEU:HD11	1.84	0.60
2:F:1124:PRO:HB2	2:F:1252:SER:HB3	1.83	0.60
2:H:1258:PHE:HB2	2:H:1593:HIS:HB3	1.83	0.60
2:H:1427:TYR:HA	2:H:1509:CYS:HA	1.83	0.60
2:H:1761:MET:SD	2:H:1761:MET:N	2.73	0.60
1:E:21:THR:H	1:E:107:GLU:HB2	1.67	0.60
2:F:2127:ILE:HD11	2:F:2143:MET:HG3	1.83	0.60
2:B:4848:ASP:OD2	2:D:4819:TYR:CE1	2.55	0.60
2:D:629:GLN:OE1	2:D:1669:ASN:ND2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1124:PRO:HB2	2:D:1252:SER:HB3	1.83	0.60
2:H:1101:TRP:HA	2:H:1237:GLU:HB2	1.82	0.60
2:B:1726:ILE:HD11	2:B:2121:LEU:HD11	1.84	0.60
2:B:188:SER:HB2	2:B:190:ARG:HH21	1.67	0.59
2:D:2470:VAL:HG11	2:D:2523:THR:HG23	1.84	0.59
2:F:1116:GLY:HA3	2:F:1136:ALA:HA	1.84	0.59
1:G:21:THR:H	1:G:107:GLU:HB2	1.67	0.59
2:B:1258:PHE:HB2	2:B:1593:HIS:HB3	1.83	0.59
2:F:756:SER:HB3	2:F:769:ARG:HB2	1.84	0.59
2:D:2127:ILE:HD11	2:D:2143:MET:HG3	1.83	0.59
2:F:298:ARG:HE	2:F:303:GLY:HA2	1.68	0.59
2:F:1809:PRO:HB3	2:F:1817:LEU:HB2	1.84	0.59
2:F:2470:VAL:HG11	2:F:2523:THR:HG23	1.85	0.59
2:H:4517:ILE:O	2:H:4519:LEU:N	2.32	0.59
2:B:2470:VAL:HG11	2:B:2523:THR:HG23	1.85	0.59
2:F:636:LEU:HD21	2:F:643:LEU:HD21	1.85	0.59
2:F:4517:ILE:O	2:F:4519:LEU:N	2.32	0.59
2:H:4148:ARG:NH2	2:H:4150:TYR:OH	2.33	0.59
2:D:4608:ALA:HB1	2:D:4650:VAL:HG11	1.84	0.59
2:H:629:GLN:OE1	2:H:1669:ASN:ND2	2.35	0.59
2:H:2470:VAL:HG11	2:H:2523:THR:HG23	1.84	0.59
2:H:4608:ALA:HB1	2:H:4650:VAL:HG11	1.84	0.59
2:B:4608:ALA:HB1	2:B:4650:VAL:HG11	1.84	0.59
2:F:4751:PHE:O	2:F:4755:ARG:NH1	2.36	0.59
2:D:4814:TYR:HE2	2:D:4815:MET:HE1	1.67	0.59
2:F:247:VAL:O	2:F:272:ARG:NH1	2.36	0.59
2:F:1726:ILE:HD11	2:F:2121:LEU:HD11	1.84	0.59
2:H:247:VAL:O	2:H:272:ARG:NH1	2.36	0.59
2:H:1124:PRO:HB2	2:H:1252:SER:HB3	1.83	0.59
2:D:4866:LEU:HD12	2:F:4871:PHE:HE2	1.68	0.59
2:F:629:GLN:OE1	2:F:1669:ASN:ND2	2.35	0.59
2:F:1101:TRP:HA	2:F:1237:GLU:HB2	1.83	0.59
2:B:247:VAL:O	2:B:272:ARG:NH1	2.36	0.59
2:B:4819:TYR:CE1	2:H:4848:ASP:OD2	2.56	0.59
2:D:832:LEU:O	2:D:1614:ARG:NH1	2.36	0.59
2:D:1809:PRO:HB3	2:D:1817:LEU:HB2	1.84	0.59
2:F:4608:ALA:HB1	2:F:4650:VAL:HG11	1.84	0.59
2:F:4845:ILE:HG23	2:H:4819:TYR:CD1	2.38	0.59
2:H:756:SER:HB3	2:H:769:ARG:HB2	1.84	0.59
2:H:1726:ILE:HD11	2:H:2121:LEU:HD11	1.84	0.59
2:B:1124:PRO:HB2	2:B:1252:SER:HB3	1.83	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:247:VAL:O	2:D:272:ARG:NH1	2.36	0.58
2:D:636:LEU:HD21	2:D:643:LEU:HD21	1.85	0.58
2:H:188:SER:HB2	2:H:190:ARG:HH21	1.67	0.58
2:H:298:ARG:HE	2:H:303:GLY:HA2	1.67	0.58
2:H:636:LEU:HD21	2:H:643:LEU:HD21	1.85	0.58
2:H:1809:PRO:HB3	2:H:1817:LEU:HB2	1.84	0.58
2:B:832:LEU:O	2:B:1614:ARG:NH1	2.36	0.58
1:C:21:THR:H	1:C:107:GLU:HB2	1.67	0.58
2:D:4751:PHE:O	2:D:4755:ARG:NH1	2.36	0.58
2:F:188:SER:HB2	2:F:190:ARG:HH21	1.67	0.58
2:H:4751:PHE:O	2:H:4755:ARG:NH1	2.36	0.58
2:B:150:GLN:NE2	2:B:158:CYS:SG	2.76	0.58
2:D:298:ARG:HE	2:D:303:GLY:HA2	1.68	0.58
2:F:832:LEU:O	2:F:1614:ARG:NH1	2.36	0.58
2:B:693:LEU:HD21	2:B:798:ILE:HG21	1.86	0.58
2:F:1121:GLY:O	2:F:1133:ARG:NH1	2.36	0.58
2:H:1589:GLN:NE2	2:H:1634:GLU:OE1	2.37	0.58
2:B:298:ARG:HE	2:B:303:GLY:HA2	1.68	0.58
2:B:629:GLN:OE1	2:B:1669:ASN:ND2	2.35	0.58
2:F:1589:GLN:NE2	2:F:1634:GLU:OE1	2.37	0.58
2:H:832:LEU:O	2:H:1614:ARG:NH1	2.36	0.58
2:H:248:PRO:O	2:H:257:ARG:NH2	2.37	0.58
1:A:21:THR:H	1:A:107:GLU:HB2	1.67	0.58
2:B:1809:PRO:HB3	2:B:1817:LEU:HB2	1.84	0.58
2:B:4751:PHE:O	2:B:4755:ARG:NH1	2.36	0.58
2:D:758:CYS:SG	2:D:759:LEU:N	2.77	0.58
2:F:4866:LEU:HD12	2:H:4871:PHE:HE2	1.69	0.58
2:B:248:PRO:O	2:B:257:ARG:NH2	2.37	0.58
2:H:693:LEU:HD21	2:H:798:ILE:HG21	1.86	0.58
2:F:802:PHE:HB2	2:F:1617:TRP:HB2	1.85	0.58
2:F:2142:LEU:HD23	2:F:2145:ARG:HD2	1.86	0.58
2:H:2142:LEU:HD23	2:H:2145:ARG:HD2	1.86	0.58
2:B:476:GLN:NE2	2:B:3679:GLU:OE1	2.37	0.58
2:B:2718:LEU:HD13	2:B:2780:LEU:HB3	1.86	0.58
2:B:4866:LEU:HD12	2:D:4871:PHE:HE2	1.69	0.58
2:D:2535:LEU:HD12	2:D:2537:ALA:H	1.69	0.58
2:F:2535:LEU:HD12	2:F:2537:ALA:H	1.69	0.58
2:B:4819:TYR:CD1	2:H:4845:ILE:HG23	2.39	0.57
2:D:248:PRO:O	2:D:257:ARG:NH2	2.37	0.57
2:D:756:SER:HB3	2:D:769:ARG:HB2	1.84	0.57
2:F:758:CYS:SG	2:F:759:LEU:N	2.77	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1589:GLN:NE2	2:D:1634:GLU:OE1	2.37	0.57
2:B:636:LEU:HD21	2:B:643:LEU:HD21	1.85	0.57
2:H:4640:SER:O	2:H:4643:ASN:ND2	2.38	0.57
2:B:758:CYS:SG	2:B:759:LEU:N	2.77	0.57
2:B:1089:ARG:HH21	2:B:1600:PRO:HG3	1.70	0.57
2:D:476:GLN:NE2	2:D:3679:GLU:OE1	2.37	0.57
2:D:2142:LEU:HD23	2:D:2145:ARG:HD2	1.86	0.57
2:D:2718:LEU:HD13	2:D:2780:LEU:HB3	1.86	0.57
2:D:4640:SER:O	2:D:4643:ASN:ND2	2.38	0.57
2:F:4865:GLY:HA2	2:H:4868:ILE:CD1	2.34	0.57
2:H:1089:ARG:HH21	2:H:1600:PRO:HG3	1.70	0.57
2:H:2718:LEU:HD13	2:H:2780:LEU:HB3	1.86	0.57
2:B:756:SER:HB3	2:B:769:ARG:HB2	1.84	0.57
2:B:1589:GLN:NE2	2:B:1634:GLU:OE1	2.37	0.57
2:D:693:LEU:HD21	2:D:798:ILE:HG21	1.86	0.57
2:H:758:CYS:SG	2:H:759:LEU:N	2.77	0.57
2:B:1631:HIS:HA	2:B:1638:SER:HA	1.87	0.57
2:B:2060:GLN:NE2	2:B:2092:GLN:O	2.38	0.57
2:B:2535:LEU:HD12	2:B:2537:ALA:H	1.69	0.57
2:F:4838:ASP:HB3	2:F:4841:GLU:HB2	1.87	0.57
2:H:476:GLN:NE2	2:H:3679:GLU:OE1	2.37	0.57
2:H:1121:GLY:O	2:H:1133:ARG:NH1	2.36	0.57
2:H:3808:ALA:HA	2:H:3811:ARG:HD3	1.87	0.57
2:B:3808:ALA:HA	2:B:3811:ARG:HD3	1.87	0.57
2:D:1631:HIS:HA	2:D:1638:SER:HA	1.87	0.57
2:D:1761:MET:N	2:D:1761:MET:SD	2.73	0.57
2:F:1089:ARG:HH21	2:F:1600:PRO:HG3	1.70	0.57
2:H:1043:LYS:HD3	2:H:1047:LYS:HE3	1.87	0.57
2:B:1121:GLY:O	2:B:1133:ARG:NH1	2.36	0.57
2:D:207:PHE:CE2	2:F:2326:ILE:CD1	2.88	0.57
2:F:248:PRO:O	2:F:257:ARG:NH2	2.37	0.57
2:F:476:GLN:NE2	2:F:3679:GLU:OE1	2.37	0.57
2:B:4814:TYR:HE2	2:B:4815:MET:HE1	1.70	0.57
2:B:4838:ASP:HB3	2:B:4841:GLU:HB2	1.87	0.57
2:B:2142:LEU:HD23	2:B:2145:ARG:HD2	1.86	0.57
2:D:1089:ARG:HH21	2:D:1600:PRO:HG3	1.70	0.57
2:D:4517:ILE:O	2:D:4519:LEU:N	2.32	0.57
1:E:87:HIS:NE2	2:F:1774:GLU:OE2	2.38	0.57
2:F:693:LEU:HD21	2:F:798:ILE:HG21	1.86	0.57
2:F:2060:GLN:NE2	2:F:2092:GLN:O	2.38	0.57
2:F:4857:VAL:CG1	2:H:4863:ILE:HG22	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:87:HIS:NE2	2:H:1774:GLU:OE2	2.38	0.57
2:H:150:GLN:NE2	2:H:158:CYS:SG	2.76	0.57
2:H:4814:TYR:HE2	2:H:4815:MET:HE1	1.70	0.57
2:H:4838:ASP:HB3	2:H:4841:GLU:HB2	1.87	0.57
2:B:657:PRO:HB3	2:B:834:VAL:HG22	1.87	0.56
2:B:4640:SER:O	2:B:4643:ASN:ND2	2.38	0.56
2:D:655:MET:HG2	2:D:836:HIS:HA	1.87	0.56
2:D:657:PRO:HB3	2:D:834:VAL:HG22	1.87	0.56
2:F:4138:GLU:OE2	2:F:4148:ARG:NH1	2.38	0.56
2:H:2535:LEU:HD12	2:H:2537:ALA:H	1.69	0.56
2:B:4138:GLU:OE2	2:B:4148:ARG:NH1	2.38	0.56
2:D:802:PHE:HB2	2:D:1617:TRP:HB2	1.85	0.56
2:F:2296:GLY:HA2	2:F:2299:TYR:HD2	1.70	0.56
2:H:802:PHE:HB2	2:H:1617:TRP:HB2	1.85	0.56
2:H:1631:HIS:HA	2:H:1638:SER:HA	1.87	0.56
1:A:87:HIS:NE2	2:B:1774:GLU:OE2	2.38	0.56
2:B:797:GLY:HA2	2:B:1622:LEU:HA	1.87	0.56
2:B:4871:PHE:HE2	2:H:4866:LEU:HD12	1.70	0.56
2:B:4888:LYS:HB3	2:B:4893:GLY:HA2	1.86	0.56
2:D:1043:LYS:HD3	2:D:1047:LYS:HE3	1.87	0.56
2:D:2060:GLN:NE2	2:D:2092:GLN:O	2.38	0.56
2:F:76:ARG:CB	2:H:3891:TRP:CG	2.88	0.56
2:F:1631:HIS:HA	2:F:1638:SER:HA	1.87	0.56
2:F:2421:ARG:NH2	2:F:2476:VAL:O	2.39	0.56
2:F:4520:PHE:HD1	2:F:4562:LEU:HD21	0.84	0.56
2:H:797:GLY:HA2	2:H:1622:LEU:HA	1.87	0.56
2:H:2060:GLN:NE2	2:H:2092:GLN:O	2.38	0.56
2:H:4138:GLU:OE2	2:H:4148:ARG:NH1	2.39	0.56
2:B:207:PHE:CD1	2:D:2326:ILE:HG23	2.33	0.56
2:B:802:PHE:HB2	2:B:1617:TRP:HB2	1.85	0.56
2:B:4845:ILE:HG23	2:D:4819:TYR:CD1	2.39	0.56
2:D:3808:ALA:HA	2:D:3811:ARG:HD3	1.87	0.56
2:D:4888:LYS:HB3	2:D:4893:GLY:HA2	1.86	0.56
2:F:2718:LEU:HD13	2:F:2780:LEU:HB3	1.86	0.56
2:H:655:MET:HG2	2:H:836:HIS:HA	1.87	0.56
2:H:4722:TYR:OH	2:H:4745:LEU:O	2.24	0.56
2:H:4888:LYS:HB3	2:H:4893:GLY:HA2	1.86	0.56
2:B:1043:LYS:HD3	2:B:1047:LYS:HE3	1.87	0.56
2:B:4520:PHE:HD1	2:B:4562:LEU:HD21	0.84	0.56
2:D:2296:GLY:HA2	2:D:2299:TYR:HD2	1.70	0.56
2:D:2421:ARG:NH2	2:D:2476:VAL:O	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:4865:GLY:HA2	2:F:4868:ILE:CD1	2.35	0.56
2:F:150:GLN:NE2	2:F:158:CYS:SG	2.76	0.56
2:F:655:MET:HG2	2:F:836:HIS:HA	1.87	0.56
2:F:4888:LYS:HB3	2:F:4893:GLY:HA2	1.86	0.56
2:H:4136:ARG:NH2	2:H:4150:TYR:OH	2.38	0.56
2:D:15:ARG:HB3	2:D:110:HIS:HB3	1.88	0.56
2:F:15:ARG:HB3	2:F:110:HIS:HB3	1.88	0.56
2:F:1043:LYS:HD3	2:F:1047:LYS:HE3	1.87	0.56
2:F:4640:SER:O	2:F:4643:ASN:ND2	2.38	0.56
2:F:4722:TYR:OH	2:F:4745:LEU:O	2.24	0.56
2:D:4138:GLU:OE2	2:D:4148:ARG:NH1	2.38	0.56
2:H:15:ARG:HB3	2:H:110:HIS:HB3	1.88	0.56
2:B:4865:GLY:HA2	2:D:4868:ILE:CD1	2.36	0.56
2:D:4838:ASP:HB3	2:D:4841:GLU:HB2	1.87	0.56
2:B:15:ARG:HB3	2:B:110:HIS:HB3	1.88	0.56
2:B:2421:ARG:NH2	2:B:2476:VAL:O	2.39	0.56
2:D:4056:HIS:O	2:D:4058:HIS:ND1	2.39	0.56
2:F:3808:ALA:HA	2:F:3811:ARG:HD3	1.87	0.56
1:C:87:HIS:NE2	2:D:1774:GLU:OE2	2.38	0.56
2:D:2157:TYR:HH	2:D:2203:TYR:HH	1.54	0.56
2:F:2728:HIS:NE2	2:F:2829:MET:SD	2.79	0.56
2:H:2421:ARG:NH2	2:H:2476:VAL:O	2.39	0.56
2:B:2296:GLY:HA2	2:B:2299:TYR:HD2	1.70	0.55
2:B:4622:PRO:O	2:B:4630:GLN:NE2	2.39	0.55
2:F:657:PRO:HB3	2:F:834:VAL:HG22	1.87	0.55
2:B:4912:GLN:O	2:B:4915:ASN:ND2	2.40	0.55
2:D:517:VAL:HG23	2:D:520:ARG:HE	1.71	0.55
2:H:2296:GLY:HA2	2:H:2299:TYR:HD2	1.70	0.55
2:H:2728:HIS:NE2	2:H:2829:MET:SD	2.79	0.55
2:B:243:GLU:HA	2:B:264:GLY:HA2	1.88	0.55
2:F:207:PHE:CE2	2:H:2326:ILE:CD1	2.89	0.55
2:H:4056:HIS:O	2:H:4058:HIS:ND1	2.39	0.55
2:B:1128:LEU:HD13	2:B:1206:SER:HB2	1.89	0.55
2:B:1304:LEU:HG	2:B:1591:LEU:H	1.72	0.55
2:B:4056:HIS:O	2:B:4058:HIS:ND1	2.39	0.55
2:B:4868:ILE:CD1	2:H:4865:GLY:HA2	2.37	0.55
2:D:150:GLN:NE2	2:D:158:CYS:SG	2.76	0.55
2:H:243:GLU:HA	2:H:264:GLY:HA2	1.88	0.55
2:H:1827:THR:HA	2:H:1830:ILE:HD12	1.89	0.55
2:H:4912:GLN:O	2:H:4915:ASN:ND2	2.40	0.55
2:B:655:MET:HG2	2:B:836:HIS:HA	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:76:ARG:CB	2:F:3891:TRP:CG	2.89	0.55
2:D:1827:THR:HA	2:D:1830:ILE:HD12	1.89	0.55
2:D:2718:LEU:HB3	2:D:2780:LEU:HD13	1.89	0.55
2:F:1304:LEU:HG	2:F:1591:LEU:H	1.72	0.55
2:F:4622:PRO:O	2:F:4630:GLN:NE2	2.39	0.55
2:H:4622:PRO:O	2:H:4630:GLN:NE2	2.39	0.55
2:B:1827:THR:HA	2:B:1830:ILE:HD12	1.89	0.55
2:F:1827:THR:HA	2:F:1830:ILE:HD12	1.89	0.55
2:F:2718:LEU:HB3	2:F:2780:LEU:HD13	1.89	0.55
2:B:517:VAL:HG23	2:B:520:ARG:HE	1.71	0.55
2:D:1128:LEU:HD13	2:D:1206:SER:HB2	1.89	0.55
2:D:4845:ILE:HG23	2:F:4819:TYR:CD1	2.41	0.55
2:F:4056:HIS:O	2:F:4058:HIS:ND1	2.39	0.55
2:H:1257:GLN:O	2:H:1596:TRP:N	2.40	0.55
2:B:4722:TYR:OH	2:B:4745:LEU:O	2.24	0.55
2:D:797:GLY:HA2	2:D:1622:LEU:HA	1.87	0.55
2:D:1121:GLY:O	2:D:1133:ARG:NH1	2.36	0.55
2:D:1304:LEU:HG	2:D:1591:LEU:H	1.72	0.55
2:D:3917:VAL:O	2:D:3920:THR:OG1	2.24	0.55
2:D:4857:VAL:CG1	2:F:4863:ILE:HG22	2.36	0.55
2:F:4912:GLN:O	2:F:4915:ASN:ND2	2.40	0.55
2:H:299:HIS:HD2	2:H:302:THR:H	1.55	0.55
2:B:4002:ASP:OD1	2:B:4115:ARG:NH1	2.40	0.55
2:B:4857:VAL:CG1	2:D:4863:ILE:HG22	2.37	0.55
2:D:1014:GLN:HB3	2:D:1032:LEU:HD21	1.89	0.55
2:D:2072:GLN:NE2	2:D:3647:LYS:O	2.40	0.55
2:D:3771:ASN:ND2	2:D:3773:THR:OG1	2.40	0.55
2:D:4622:PRO:O	2:D:4630:GLN:NE2	2.39	0.55
2:D:4627:ILE:O	2:D:4631:TRP:CB	2.55	0.55
2:D:4722:TYR:OH	2:D:4745:LEU:O	2.23	0.55
2:F:797:GLY:HA2	2:F:1622:LEU:HA	1.87	0.55
2:H:657:PRO:HB3	2:H:834:VAL:HG22	1.87	0.55
2:H:1304:LEU:HG	2:H:1591:LEU:H	1.72	0.55
2:H:4002:ASP:OD1	2:H:4115:ARG:NH1	2.40	0.55
2:B:2072:GLN:NE2	2:B:3647:LYS:O	2.40	0.54
2:D:1160:ASP:OD1	2:D:1178:ASN:ND2	2.40	0.54
2:D:1257:GLN:O	2:D:1596:TRP:N	2.40	0.54
2:D:4912:GLN:O	2:D:4915:ASN:ND2	2.40	0.54
2:F:299:HIS:HD2	2:F:302:THR:H	1.55	0.54
2:F:687:THR:HG22	2:F:689:GLU:H	1.72	0.54
2:F:3771:ASN:ND2	2:F:3773:THR:OG1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:4524:SER:HG	2:F:4558:VAL:N	2.05	0.54
2:H:2024:LEU:HD23	2:H:2026:ILE:H	1.73	0.54
2:H:2718:LEU:HB3	2:H:2780:LEU:HD13	1.89	0.54
2:B:2157:TYR:HH	2:B:2203:TYR:HH	1.50	0.54
2:D:556:ASP:HA	2:D:559:ILE:HD12	1.90	0.54
2:D:4002:ASP:OD1	2:D:4115:ARG:NH1	2.40	0.54
2:F:28:ILE:HD12	2:F:33:GLN:HG2	1.90	0.54
2:F:444:THR:OG1	2:F:445:VAL:N	2.40	0.54
2:F:4655:MET:HA	2:F:4667:ILE:HD12	1.90	0.54
2:F:1128:LEU:HD13	2:F:1206:SER:HB2	1.89	0.54
2:F:1154:ARG:NH2	2:F:1180:GLU:OE1	2.41	0.54
2:H:2072:GLN:NE2	2:H:3647:LYS:O	2.40	0.54
2:H:4520:PHE:HD1	2:H:4562:LEU:HD21	0.84	0.54
2:H:4524:SER:HG	2:H:4558:VAL:N	2.05	0.54
2:B:2718:LEU:HB3	2:B:2780:LEU:HD13	1.89	0.54
2:F:1160:ASP:OD1	2:F:1178:ASN:ND2	2.40	0.54
2:H:115:TYR:OH	2:H:179:ASP:OD2	2.26	0.54
2:H:3771:ASN:ND2	2:H:3773:THR:OG1	2.40	0.54
2:B:115:TYR:OH	2:B:179:ASP:OD2	2.26	0.54
2:B:3891:TRP:CG	2:H:76:ARG:CB	2.91	0.54
2:D:115:TYR:OH	2:D:179:ASP:OD2	2.26	0.54
2:H:1014:GLN:HB3	2:H:1032:LEU:HD21	1.89	0.54
2:H:1907:MET:HA	2:H:1910:LEU:HD23	1.90	0.54
2:H:4655:MET:HA	2:H:4667:ILE:HD12	1.90	0.54
2:B:1014:GLN:HB3	2:B:1032:LEU:HD21	1.89	0.54
2:B:1160:ASP:OD1	2:B:1178:ASN:ND2	2.40	0.54
2:B:2024:LEU:HD23	2:B:2026:ILE:H	1.72	0.54
1:C:7:ILE:H	1:C:72:ALA:HA	1.73	0.54
2:D:2024:LEU:HD23	2:D:2026:ILE:H	1.72	0.54
2:F:115:TYR:OH	2:F:179:ASP:OD2	2.26	0.54
2:F:681:HIS:HB2	2:F:799:LYS:HG2	1.90	0.54
2:F:3767:LEU:HD21	2:F:3774:VAL:HB	1.90	0.54
2:H:1086:ARG:HH22	2:H:1254:ARG:HD3	1.73	0.54
2:H:3767:LEU:HD21	2:H:3774:VAL:HB	1.90	0.54
2:B:1272:ARG:NH2	2:B:1590:PHE:O	2.41	0.54
2:D:444:THR:OG1	2:D:445:VAL:N	2.40	0.54
2:D:1154:ARG:NH2	2:D:1180:GLU:OE1	2.41	0.54
2:F:517:VAL:HG23	2:F:520:ARG:HE	1.71	0.54
2:F:1602:GLN:HE22	2:F:1642:LEU:HB3	1.73	0.54
2:H:28:ILE:HD12	2:H:33:GLN:HG2	1.90	0.54
2:H:517:VAL:HG23	2:H:520:ARG:HE	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:1160:ASP:OD1	2:H:1178:ASN:ND2	2.40	0.54
2:H:1272:ARG:NH2	2:H:1590:PHE:O	2.41	0.54
2:H:1922:ARG:NH1	2:H:2038:THR:O	2.39	0.54
1:A:7:ILE:H	1:A:72:ALA:HA	1.73	0.54
2:B:1257:GLN:O	2:B:1596:TRP:N	2.40	0.54
2:B:1907:MET:HA	2:B:1910:LEU:HD23	1.90	0.54
2:B:3771:ASN:ND2	2:B:3773:THR:OG1	2.40	0.54
2:D:28:ILE:HD12	2:D:33:GLN:HG2	1.90	0.54
2:D:243:GLU:HA	2:D:264:GLY:HA2	1.88	0.54
2:D:687:THR:HG22	2:D:689:GLU:H	1.72	0.54
2:F:243:GLU:HA	2:F:264:GLY:HA2	1.88	0.54
2:F:371:TRP:N	2:F:394:HIS:O	2.38	0.54
2:F:1257:GLN:O	2:F:1596:TRP:N	2.40	0.54
2:F:2072:GLN:NE2	2:F:3647:LYS:O	2.40	0.54
2:F:4002:ASP:OD1	2:F:4115:ARG:NH1	2.40	0.54
2:F:4627:ILE:O	2:F:4631:TRP:CB	2.55	0.54
2:H:444:THR:OG1	2:H:445:VAL:N	2.40	0.54
2:B:1154:ARG:NH2	2:B:1180:GLU:OE1	2.41	0.54
2:B:4627:ILE:O	2:B:4631:TRP:CB	2.55	0.54
2:D:371:TRP:N	2:D:394:HIS:O	2.38	0.54
2:F:1014:GLN:HB3	2:F:1032:LEU:HD21	1.89	0.54
2:H:1128:LEU:HD13	2:H:1206:SER:HB2	1.89	0.54
2:B:444:THR:OG1	2:B:445:VAL:N	2.40	0.54
2:B:4863:ILE:HG22	2:H:4857:VAL:CG1	2.38	0.54
2:D:480:ARG:NH2	2:D:3679:GLU:OE2	2.41	0.54
2:D:4655:MET:HA	2:D:4667:ILE:HD12	1.90	0.54
2:H:235:ARG:NH2	2:H:268:SER:O	2.41	0.54
2:H:506:HIS:NE2	2:H:534:TYR:OH	2.40	0.54
2:H:4627:ILE:O	2:H:4631:TRP:CB	2.55	0.54
2:B:25:THR:HG22	2:B:34:LYS:HG2	1.90	0.53
2:B:371:TRP:N	2:B:394:HIS:O	2.38	0.53
2:B:375:GLN:N	2:B:390:LYS:O	2.41	0.53
2:B:687:THR:HG22	2:B:689:GLU:H	1.72	0.53
2:D:1224:LEU:HD13	2:D:1227:PHE:HD2	1.74	0.53
2:D:1907:MET:HA	2:D:1910:LEU:HD23	1.90	0.53
2:D:4814:TYR:HE2	2:D:4815:MET:CE	2.21	0.53
2:F:2840:ALA:HB3	2:F:2906:ARG:HD3	1.91	0.53
2:H:646:THR:HA	2:H:1630:LEU:HA	1.91	0.53
2:B:4136:ARG:NH2	2:B:4150:TYR:OH	2.38	0.53
2:D:246:THR:OG1	2:D:272:ARG:NH1	2.42	0.53
2:D:1029:ASN:HB3	2:D:1032:LEU:HG	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1922:ARG:NH1	2:D:2038:THR:O	2.39	0.53
2:D:2728:HIS:NE2	2:D:2829:MET:SD	2.79	0.53
2:D:4037:ASP:OD2	2:D:4042:GLY:N	2.41	0.53
2:F:15:ARG:N	2:F:18:ASP:OD2	2.40	0.53
2:F:1907:MET:HA	2:F:1910:LEU:HD23	1.90	0.53
2:F:2024:LEU:HD23	2:F:2026:ILE:H	1.72	0.53
2:H:681:HIS:HB2	2:H:799:LYS:HG2	1.90	0.53
2:B:207:PHE:CE2	2:D:2326:ILE:CD1	2.91	0.53
2:B:1245:ARG:NH2	2:B:1797:GLU:OE2	2.42	0.53
2:B:2326:ILE:CD1	2:H:207:PHE:CE2	2.90	0.53
2:D:235:ARG:NH2	2:D:268:SER:O	2.41	0.53
2:D:1245:ARG:NH2	2:D:1797:GLU:OE2	2.42	0.53
2:D:1272:ARG:NH2	2:D:1590:PHE:O	2.41	0.53
2:D:3805:ASP:OD2	2:D:3808:ALA:N	2.41	0.53
2:D:4136:ARG:NH2	2:D:4150:TYR:OH	2.38	0.53
2:F:506:HIS:NE2	2:F:534:TYR:OH	2.40	0.53
2:F:646:THR:HA	2:F:1630:LEU:HA	1.90	0.53
2:F:1224:LEU:HD13	2:F:1227:PHE:HD2	1.74	0.53
2:B:246:THR:OG1	2:B:272:ARG:NH1	2.42	0.53
2:B:1086:ARG:HH22	2:B:1254:ARG:HD3	1.73	0.53
2:D:207:PHE:CD1	2:F:2326:ILE:HG22	2.42	0.53
2:D:646:THR:HA	2:D:1630:LEU:HA	1.90	0.53
2:D:1602:GLN:HE22	2:D:1642:LEU:HB3	1.72	0.53
2:D:2760:PRO:HD2	2:D:2763:LEU:HD12	1.91	0.53
2:D:2840:ALA:HB3	2:D:2906:ARG:HD3	1.91	0.53
2:D:4524:SER:HG	2:D:4558:VAL:N	2.05	0.53
2:F:1272:ARG:NH2	2:F:1590:PHE:O	2.41	0.53
2:F:4037:ASP:OD2	2:F:4042:GLY:N	2.41	0.53
2:H:1245:ARG:NH2	2:H:1797:GLU:OE2	2.42	0.53
2:H:3805:ASP:OD2	2:H:3808:ALA:N	2.40	0.53
2:H:4782:TYR:OH	2:H:4847:PHE:O	2.27	0.53
2:B:28:ILE:HD12	2:B:33:GLN:HG2	1.90	0.53
2:B:299:HIS:HD2	2:B:302:THR:H	1.55	0.53
2:B:556:ASP:HA	2:B:559:ILE:HD12	1.90	0.53
2:D:299:HIS:HD2	2:D:302:THR:H	1.55	0.53
2:D:565:LEU:HD11	2:D:603:LYS:HG2	1.91	0.53
2:D:1938:GLN:OE1	2:D:1942:ARG:NH1	2.42	0.53
2:F:556:ASP:HA	2:F:559:ILE:HD12	1.90	0.53
2:F:1938:GLN:OE1	2:F:1942:ARG:NH1	2.42	0.53
2:F:3919:ASN:O	2:F:3922:THR:OG1	2.27	0.53
2:H:480:ARG:NH2	2:H:3679:GLU:OE2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:1154:ARG:NH2	2:H:1180:GLU:OE1	2.41	0.53
2:H:1308:ILE:HD12	2:H:1539:LEU:HB2	1.90	0.53
2:H:1912:GLN:OE1	2:H:2091:ARG:NH1	2.42	0.53
2:B:196:TYR:O	2:B:201:LEU:N	2.42	0.53
2:B:1602:GLN:HE22	2:B:1642:LEU:HB3	1.73	0.53
2:B:4655:MET:HA	2:B:4667:ILE:HD12	1.90	0.53
2:D:25:THR:HG22	2:D:34:LYS:HG2	1.90	0.53
2:D:1912:GLN:OE1	2:D:2091:ARG:NH1	2.42	0.53
2:D:3904:GLN:NE2	2:D:3965:GLN:OE1	2.41	0.53
2:F:4782:TYR:OH	2:F:4847:PHE:O	2.27	0.53
1:G:7:ILE:H	1:G:72:ALA:HA	1.73	0.53
2:H:3904:GLN:NE2	2:H:3965:GLN:OE1	2.41	0.53
2:B:235:ARG:NH2	2:B:268:SER:O	2.41	0.53
2:B:4524:SER:HG	2:B:4558:VAL:N	2.05	0.53
2:D:681:HIS:HB2	2:D:799:LYS:HG2	1.90	0.53
2:D:3767:LEU:HD21	2:D:3774:VAL:HB	1.90	0.53
2:D:4866:LEU:HD12	2:F:4871:PHE:CE2	2.44	0.53
2:F:196:TYR:O	2:F:201:LEU:N	2.42	0.53
2:F:1086:ARG:HH22	2:F:1254:ARG:HD3	1.73	0.53
2:F:1640:ASP:OD1	2:F:1640:ASP:N	2.41	0.53
2:F:1908:CYS:HB2	2:F:2088:LEU:HD11	1.91	0.53
2:F:2157:TYR:HH	2:F:2203:TYR:HH	1.55	0.53
2:H:196:TYR:O	2:H:201:LEU:N	2.42	0.53
2:B:678:MET:HG3	2:B:754:VAL:HG22	1.91	0.53
2:B:1092:LYS:H	2:B:1250:TRP:HZ3	1.56	0.53
2:B:2728:HIS:NE2	2:B:2829:MET:SD	2.79	0.53
2:B:2760:PRO:HD2	2:B:2763:LEU:HD12	1.91	0.53
2:B:3919:ASN:O	2:B:3922:THR:OG1	2.27	0.53
2:D:1092:LYS:H	2:D:1250:TRP:HZ3	1.56	0.53
2:F:246:THR:OG1	2:F:272:ARG:NH1	2.42	0.53
2:H:556:ASP:HA	2:H:559:ILE:HD12	1.90	0.53
2:H:678:MET:HG3	2:H:754:VAL:HG22	1.91	0.53
2:H:1640:ASP:N	2:H:1640:ASP:OD1	2.41	0.53
2:B:480:ARG:NH2	2:B:3679:GLU:OE2	2.41	0.53
2:B:601:LEU:HB3	2:B:642:LEU:HD21	1.91	0.53
2:B:1029:ASN:HB3	2:B:1032:LEU:HG	1.91	0.53
2:B:4782:TYR:OH	2:B:4847:PHE:O	2.27	0.53
2:B:4814:TYR:HE2	2:B:4815:MET:CE	2.21	0.53
2:D:15:ARG:N	2:D:18:ASP:OD2	2.40	0.53
2:D:196:TYR:O	2:D:201:LEU:N	2.42	0.53
2:D:4640:SER:HB3	2:D:4643:ASN:HD21	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:207:PHE:CE1	2:H:2326:ILE:HG21	2.40	0.53
2:F:480:ARG:NH2	2:F:3679:GLU:OE2	2.41	0.53
2:F:601:LEU:HB3	2:F:642:LEU:HD21	1.91	0.53
2:F:3805:ASP:OD2	2:F:3808:ALA:N	2.40	0.53
2:H:1173:MET:HB3	2:H:1192:PHE:HB2	1.91	0.53
2:H:2840:ALA:HB3	2:H:2906:ARG:HD3	1.91	0.53
2:B:76:ARG:CB	2:D:3891:TRP:CG	2.91	0.53
2:B:3805:ASP:OD2	2:B:3808:ALA:N	2.40	0.53
2:B:3904:GLN:NE2	2:B:3965:GLN:OE1	2.41	0.53
2:B:3983:LEU:O	2:B:3987:LEU:HB2	2.10	0.53
2:D:601:LEU:HB3	2:D:642:LEU:HD21	1.91	0.53
2:F:1308:ILE:HD12	2:F:1539:LEU:HB2	1.90	0.53
2:F:1761:MET:SD	2:F:1761:MET:N	2.73	0.53
2:F:3904:GLN:NE2	2:F:3965:GLN:OE1	2.41	0.53
2:F:4640:SER:HB3	2:F:4643:ASN:HD21	1.74	0.53
2:H:687:THR:HG22	2:H:689:GLU:H	1.72	0.53
2:H:4037:ASP:OD2	2:H:4042:GLY:N	2.41	0.53
2:B:1938:GLN:OE1	2:B:1942:ARG:NH1	2.42	0.52
2:B:2840:ALA:HB3	2:B:2906:ARG:HD3	1.91	0.52
2:B:4640:SER:HB3	2:B:4643:ASN:HD21	1.74	0.52
2:D:1086:ARG:HH22	2:D:1254:ARG:HD3	1.73	0.52
2:D:2204:PHE:O	2:D:2211:ASN:ND2	2.42	0.52
2:F:207:PHE:CD1	2:H:2326:ILE:HG22	2.43	0.52
2:F:235:ARG:NH2	2:F:268:SER:O	2.41	0.52
2:F:1029:ASN:HB3	2:F:1032:LEU:HG	1.91	0.52
2:F:2204:PHE:O	2:F:2211:ASN:ND2	2.42	0.52
2:F:2760:PRO:HD2	2:F:2763:LEU:HD12	1.91	0.52
2:F:3960:SER:HG	2:F:4070:CYS:HG	1.56	0.52
2:H:4640:SER:HB3	2:H:4643:ASN:HD21	1.74	0.52
2:H:4655:MET:O	2:H:4664:ARG:NH2	2.39	0.52
2:H:4814:TYR:HE2	2:H:4815:MET:CE	2.21	0.52
2:B:679:VAL:HA	2:B:800:VAL:HG12	1.92	0.52
2:B:681:HIS:HB2	2:B:799:LYS:HG2	1.90	0.52
2:B:1224:LEU:HD13	2:B:1227:PHE:HD2	1.74	0.52
2:B:1912:GLN:OE1	2:B:2091:ARG:NH1	2.42	0.52
2:B:3767:LEU:HD21	2:B:3774:VAL:HB	1.90	0.52
2:D:375:GLN:N	2:D:390:LYS:O	2.41	0.52
2:F:25:THR:HG22	2:F:34:LYS:HG2	1.90	0.52
2:F:565:LEU:HD11	2:F:603:LYS:HG2	1.91	0.52
2:F:4028:THR:HA	2:F:4033:PHE:HD2	1.75	0.52
2:F:4148:ARG:HH11	2:F:4959:PHE:HB3	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:4655:MET:O	2:F:4664:ARG:NH2	2.39	0.52
2:H:601:LEU:HB3	2:H:642:LEU:HD21	1.91	0.52
2:H:1938:GLN:OE1	2:H:1942:ARG:NH1	2.42	0.52
2:H:3983:LEU:O	2:H:3987:LEU:HB2	2.10	0.52
2:H:4597:PRO:HA	2:H:4600:ILE:HG22	1.91	0.52
2:B:1308:ILE:HD12	2:B:1539:LEU:HB2	1.90	0.52
2:B:1996:GLN:HA	2:B:1997:LEU:HD23	1.92	0.52
2:D:678:MET:HG3	2:D:754:VAL:HG22	1.91	0.52
2:D:1640:ASP:OD1	2:D:1640:ASP:N	2.41	0.52
1:E:7:ILE:H	1:E:72:ALA:HA	1.73	0.52
2:F:1132:GLU:HB3	2:F:1147:GLN:HE21	1.74	0.52
2:F:1245:ARG:NH2	2:F:1797:GLU:OE2	2.42	0.52
2:H:371:TRP:N	2:H:394:HIS:O	2.38	0.52
2:H:1132:GLU:HB3	2:H:1147:GLN:HE21	1.74	0.52
2:H:1908:CYS:HB2	2:H:2088:LEU:HD11	1.91	0.52
2:H:4028:THR:HA	2:H:4033:PHE:HD2	1.75	0.52
2:B:646:THR:HA	2:B:1630:LEU:HA	1.90	0.52
2:B:1119:ARG:NH2	2:B:1196:ASP:O	2.39	0.52
2:B:2204:PHE:O	2:B:2211:ASN:ND2	2.42	0.52
2:D:4655:MET:O	2:D:4664:ARG:NH2	2.39	0.52
2:F:246:THR:N	2:F:261:HIS:O	2.42	0.52
2:F:1092:LYS:H	2:F:1250:TRP:HZ3	1.56	0.52
2:B:1640:ASP:N	2:B:1640:ASP:OD1	2.41	0.52
2:B:2326:ILE:HG22	2:H:207:PHE:CD1	2.44	0.52
2:B:4037:ASP:OD2	2:B:4042:GLY:N	2.41	0.52
2:D:1301:PHE:HE2	2:D:1453:TYR:HA	1.75	0.52
2:F:805:GLY:O	2:F:810:GLU:N	2.43	0.52
2:F:1173:MET:HB3	2:F:1192:PHE:HB2	1.91	0.52
2:F:1301:PHE:HE2	2:F:1453:TYR:HA	1.75	0.52
2:F:2857:LYS:HE3	2:F:2861:LEU:HD11	1.92	0.52
2:F:3983:LEU:O	2:F:3987:LEU:HB2	2.10	0.52
2:F:4136:ARG:NH2	2:F:4150:TYR:OH	2.38	0.52
2:F:4722:TYR:HD2	2:F:4723:LEU:HD12	1.75	0.52
2:F:4848:ASP:HB3	2:H:4819:TYR:CE1	2.39	0.52
2:H:679:VAL:HA	2:H:800:VAL:HG12	1.92	0.52
2:B:15:ARG:N	2:B:18:ASP:OD2	2.40	0.52
2:B:233:VAL:HG13	2:B:300:VAL:HG21	1.92	0.52
2:B:1922:ARG:NH1	2:B:2038:THR:O	2.39	0.52
2:B:3683:LEU:HD22	2:B:3748:SER:HB3	1.92	0.52
2:D:1173:MET:HB3	2:D:1192:PHE:HB2	1.91	0.52
2:D:4148:ARG:HH11	2:D:4959:PHE:HB3	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:375:GLN:N	2:F:390:LYS:O	2.41	0.52
2:F:1094:TYR:OH	2:F:1808:ASP:OD1	2.27	0.52
2:F:4597:PRO:HA	2:F:4600:ILE:HG22	1.91	0.52
2:H:15:ARG:N	2:H:18:ASP:OD2	2.40	0.52
2:H:25:THR:HG22	2:H:34:LYS:HG2	1.90	0.52
2:H:246:THR:N	2:H:261:HIS:O	2.42	0.52
2:H:1092:LYS:H	2:H:1250:TRP:HZ3	1.56	0.52
2:H:1301:PHE:HE2	2:H:1453:TYR:HA	1.75	0.52
2:H:2760:PRO:HD2	2:H:2763:LEU:HD12	1.91	0.52
2:D:805:GLY:O	2:D:810:GLU:N	2.43	0.52
2:D:1251:LEU:O	2:D:1601:ASN:N	2.43	0.52
2:D:1996:GLN:HA	2:D:1997:LEU:HD23	1.92	0.52
2:D:4782:TYR:OH	2:D:4847:PHE:O	2.27	0.52
2:F:748:LEU:HB2	2:F:750:ARG:HG3	1.92	0.52
2:F:1922:ARG:NH1	2:F:2038:THR:O	2.39	0.52
2:F:3683:LEU:HD22	2:F:3748:SER:HB3	1.92	0.52
2:F:3803:VAL:HG21	2:F:3881:ARG:HD2	1.92	0.52
2:H:246:THR:OG1	2:H:272:ARG:NH1	2.42	0.52
2:H:565:LEU:HD11	2:H:603:LYS:HG2	1.91	0.52
1:A:16:PRO:HD2	1:A:64:ALA:HA	1.92	0.52
2:B:207:PHE:CD1	2:D:2326:ILE:HG22	2.45	0.52
2:B:1301:PHE:HE2	2:B:1453:TYR:HA	1.75	0.52
2:B:3803:VAL:HG21	2:B:3881:ARG:HD2	1.92	0.52
2:B:4028:THR:HA	2:B:4033:PHE:HD2	1.75	0.52
2:B:4082:GLU:HA	2:B:4086:LYS:HD2	1.92	0.52
2:B:4617:TYR:OH	2:B:4629:GLY:O	2.28	0.52
2:D:1908:CYS:HB2	2:D:2088:LEU:HD11	1.91	0.52
2:D:2116:ASP:OD1	2:D:2153:ASN:ND2	2.43	0.52
2:D:3983:LEU:O	2:D:3987:LEU:HB2	2.10	0.52
2:D:4722:TYR:HD2	2:D:4723:LEU:HD12	1.75	0.52
2:F:2116:ASP:OD1	2:F:2153:ASN:ND2	2.43	0.52
2:F:4617:TYR:OH	2:F:4629:GLY:O	2.28	0.52
2:H:1224:LEU:HD13	2:H:1227:PHE:HD2	1.74	0.52
2:H:3683:LEU:HD22	2:H:3748:SER:HB3	1.92	0.52
2:B:1094:TYR:OH	2:B:1808:ASP:OD1	2.27	0.52
2:B:4597:PRO:HA	2:B:4600:ILE:HG22	1.91	0.52
2:D:486:GLN:NE2	2:D:539:ALA:O	2.43	0.52
2:D:1132:GLU:HB3	2:D:1147:GLN:HE21	1.74	0.52
2:D:3683:LEU:HD22	2:D:3748:SER:HB3	1.92	0.52
2:D:4597:PRO:HA	2:D:4600:ILE:HG22	1.91	0.52
1:E:16:PRO:HD2	1:E:64:ALA:HA	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:679:VAL:HA	2:F:800:VAL:HG12	1.92	0.52
2:F:4866:LEU:HD12	2:H:4871:PHE:CE2	2.45	0.52
2:H:375:GLN:N	2:H:390:LYS:O	2.41	0.52
2:H:1602:GLN:HE22	2:H:1642:LEU:HB3	1.73	0.52
2:B:565:LEU:HD11	2:B:603:LYS:HG2	1.91	0.52
2:B:909:ASP:HB2	2:B:914:GLN:HB2	1.91	0.52
2:B:1098:ALA:O	2:B:1101:TRP:NE1	2.42	0.52
2:B:4568:TYR:O	2:B:4572:THR:OG1	2.22	0.52
1:C:16:PRO:HD2	1:C:64:ALA:HA	1.92	0.52
2:D:748:LEU:HB2	2:D:750:ARG:HG3	1.92	0.52
2:D:4518:LEU:N	2:D:4518:LEU:CD2	2.73	0.52
2:F:909:ASP:HB2	2:F:914:GLN:HB2	1.91	0.52
2:F:1912:GLN:OE1	2:F:2091:ARG:NH1	2.42	0.52
2:H:486:GLN:NE2	2:H:539:ALA:O	2.43	0.52
2:H:725:TYR:HA	2:H:732:LEU:HA	1.92	0.52
2:H:4617:TYR:OH	2:H:4629:GLY:O	2.28	0.52
2:B:1132:GLU:HB3	2:B:1147:GLN:HE21	1.74	0.51
2:B:2160:PRO:HB3	2:B:2207:ILE:HD12	1.91	0.51
2:B:2857:LYS:HE3	2:B:2861:LEU:HD11	1.92	0.51
2:B:4572:THR:O	2:B:4576:LEU:HB2	2.10	0.51
2:D:3803:VAL:HG21	2:D:3881:ARG:HD2	1.92	0.51
2:F:657:PRO:HA	2:F:834:VAL:HA	1.92	0.51
2:F:678:MET:HG3	2:F:754:VAL:HG22	1.91	0.51
2:F:3848:CYS:HB3	2:F:3856:GLN:HE21	1.76	0.51
2:H:162:ILE:HG23	2:H:181:LEU:HD13	1.92	0.51
2:H:657:PRO:HA	2:H:834:VAL:HA	1.92	0.51
2:H:805:GLY:O	2:H:810:GLU:N	2.43	0.51
2:H:1098:ALA:O	2:H:1101:TRP:NE1	2.42	0.51
2:B:748:LEU:HB2	2:B:750:ARG:HG3	1.92	0.51
2:B:2221:TYR:O	2:B:2225:ASN:ND2	2.44	0.51
2:B:4148:ARG:HH11	2:B:4959:PHE:HB3	1.75	0.51
2:B:4655:MET:O	2:B:4664:ARG:NH2	2.39	0.51
2:D:1308:ILE:HD12	2:D:1539:LEU:HB2	1.90	0.51
2:D:4572:THR:O	2:D:4576:LEU:HB2	2.10	0.51
2:D:4617:TYR:OH	2:D:4629:GLY:O	2.28	0.51
1:G:16:PRO:HD2	1:G:64:ALA:HA	1.92	0.51
2:H:233:VAL:HG13	2:H:300:VAL:HG21	1.92	0.51
2:H:1029:ASN:HB3	2:H:1032:LEU:HG	1.91	0.51
2:H:2160:PRO:HB3	2:H:2207:ILE:HD12	1.91	0.51
2:D:909:ASP:HB2	2:D:914:GLN:HB2	1.91	0.51
2:D:1094:TYR:OH	2:D:1808:ASP:OD1	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:2096:ILE:O	2:D:2100:VAL:N	2.43	0.51
2:D:2221:TYR:O	2:D:2225:ASN:ND2	2.44	0.51
2:D:3848:CYS:HB3	2:D:3856:GLN:HE21	1.76	0.51
2:F:162:ILE:HG23	2:F:181:LEU:HD13	1.93	0.51
2:F:725:TYR:HA	2:F:732:LEU:HA	1.92	0.51
2:F:2157:TYR:OH	2:F:2203:TYR:OH	2.26	0.51
2:H:483:LYS:O	2:H:544:ASN:ND2	2.38	0.51
2:H:3803:VAL:HG21	2:H:3881:ARG:HD2	1.92	0.51
2:B:506:HIS:NE2	2:B:534:TYR:OH	2.40	0.51
2:B:1251:LEU:O	2:B:1601:ASN:N	2.43	0.51
2:B:1908:CYS:HB2	2:B:2088:LEU:HD11	1.91	0.51
2:B:3848:CYS:HB3	2:B:3856:GLN:HE21	1.76	0.51
2:B:3917:VAL:O	2:B:3920:THR:OG1	2.24	0.51
2:B:4518:LEU:CD2	2:B:4518:LEU:N	2.73	0.51
2:B:4866:LEU:HD12	2:D:4871:PHE:CE2	2.44	0.51
2:D:1098:ALA:O	2:D:1101:TRP:NE1	2.42	0.51
2:D:4891:ILE:HD13	2:D:4914:HIS:HB3	1.92	0.51
2:H:2221:TYR:O	2:H:2225:ASN:ND2	2.44	0.51
2:H:2857:LYS:HE3	2:H:2861:LEU:HD11	1.92	0.51
2:B:1570:LEU:O	2:B:1573:SER:OG	2.27	0.51
2:B:1799:VAL:HG22	2:B:1894:LEU:HD13	1.93	0.51
1:C:42:ARG:NH2	2:D:1766:PRO:O	2.44	0.51
2:D:679:VAL:HA	2:D:800:VAL:HG12	1.92	0.51
2:D:1799:VAL:HG22	2:D:1894:LEU:HD13	1.93	0.51
1:E:28:GLY:N	1:E:37:ASP:O	2.37	0.51
2:F:1666:ALA:N	2:F:1669:ASN:OD1	2.41	0.51
2:F:4798:GLU:O	2:F:4802:THR:OG1	2.27	0.51
2:H:1996:GLN:HA	2:H:1997:LEU:HD23	1.92	0.51
2:H:3848:CYS:HB3	2:H:3856:GLN:HE21	1.76	0.51
2:H:4148:ARG:HH11	2:H:4959:PHE:HB3	1.75	0.51
2:B:486:GLN:NE2	2:B:539:ALA:O	2.43	0.51
2:B:776:GLN:HB3	2:B:1470:GLY:HA3	1.93	0.51
2:D:40:GLU:HB2	2:D:48:PHE:HE1	1.76	0.51
2:D:233:VAL:HG13	2:D:300:VAL:HG21	1.92	0.51
2:D:646:THR:OG1	2:D:1684:GLN:NE2	2.44	0.51
2:D:4118:THR:O	2:D:4122:LEU:HB2	2.11	0.51
2:F:1119:ARG:NH2	2:F:1196:ASP:O	2.39	0.51
2:F:1799:VAL:HG22	2:F:1894:LEU:HD13	1.93	0.51
2:F:4082:GLU:HA	2:F:4086:LYS:HD2	1.92	0.51
2:F:4118:THR:O	2:F:4122:LEU:HB2	2.11	0.51
2:F:4891:ILE:HD13	2:F:4914:HIS:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:40:GLU:HB2	2:H:48:PHE:HE1	1.76	0.51
2:H:2116:ASP:OD1	2:H:2153:ASN:ND2	2.43	0.51
2:B:805:GLY:O	2:B:810:GLU:N	2.43	0.51
2:D:4082:GLU:HA	2:D:4086:LYS:HD2	1.92	0.51
2:F:486:GLN:NE2	2:F:539:ALA:O	2.43	0.51
2:F:1300:MET:HB2	2:F:1545:ALA:HB3	1.93	0.51
2:F:4572:THR:O	2:F:4576:LEU:HB2	2.10	0.51
2:H:1300:MET:HB2	2:H:1545:ALA:HB3	1.93	0.51
2:H:2083:ARG:NH2	2:H:3686:ASP:OD1	2.43	0.51
2:H:4572:THR:O	2:H:4576:LEU:HB2	2.10	0.51
2:H:4794:TYR:HB2	2:H:4806:LYS:HD2	1.93	0.51
2:B:300:VAL:HG12	2:B:420:ARG:HH22	1.76	0.51
2:B:1173:MET:HB3	2:B:1192:PHE:HB2	1.91	0.51
2:B:2222:LEU:O	2:B:2226:SER:N	2.35	0.51
2:B:4085:VAL:O	2:B:4089:HIS:N	2.44	0.51
2:B:4871:PHE:CE2	2:H:4866:LEU:HD12	2.46	0.51
2:B:4891:ILE:HD13	2:B:4914:HIS:HB3	1.92	0.51
2:D:510:SER:O	2:D:520:ARG:NH2	2.44	0.51
2:D:2160:PRO:HB3	2:D:2207:ILE:HD12	1.91	0.51
2:F:290:ARG:HG2	2:F:353:GLU:HB2	1.93	0.51
2:F:510:SER:O	2:F:520:ARG:NH2	2.44	0.51
2:F:4124:GLU:HG3	2:F:4128:ASN:HD21	1.76	0.51
2:H:165:ALA:HB2	2:H:182:ILE:HG12	1.93	0.51
2:H:2558:LYS:O	2:H:2562:LEU:N	2.44	0.51
2:H:4085:VAL:O	2:H:4089:HIS:N	2.44	0.51
2:H:4722:TYR:HD2	2:H:4723:LEU:HD12	1.75	0.51
2:B:246:THR:N	2:B:261:HIS:O	2.42	0.51
2:B:646:THR:OG1	2:B:1684:GLN:NE2	2.44	0.51
2:D:2083:ARG:NH2	2:D:3686:ASP:OD1	2.43	0.51
2:D:4028:THR:HA	2:D:4033:PHE:HD2	1.75	0.51
2:F:1098:ALA:O	2:F:1101:TRP:NE1	2.42	0.51
2:F:1996:GLN:HA	2:F:1997:LEU:HD23	1.92	0.51
1:G:42:ARG:NH2	2:H:1766:PRO:O	2.44	0.51
2:H:646:THR:OG1	2:H:1684:GLN:NE2	2.44	0.51
2:H:776:GLN:HB3	2:H:1470:GLY:HA3	1.93	0.51
2:H:909:ASP:HB2	2:H:914:GLN:HB2	1.91	0.51
2:H:3919:ASN:O	2:H:3922:THR:OG1	2.27	0.51
2:H:4518:LEU:CD2	2:H:4518:LEU:N	2.73	0.51
2:D:1252:SER:HB2	2:D:1598:ARG:HB2	1.93	0.51
1:E:42:ARG:NH2	2:F:1766:PRO:O	2.44	0.51
2:F:40:GLU:HB2	2:F:48:PHE:HE1	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:2096:ILE:O	2:F:2100:VAL:N	2.43	0.51
2:F:2193:MET:HA	2:F:2196:ASN:HD22	1.76	0.51
2:H:694:ARG:O	2:H:793:SER:N	2.42	0.51
2:H:2204:PHE:O	2:H:2211:ASN:ND2	2.42	0.51
2:H:3806:LEU:O	2:H:3810:GLU:N	2.43	0.51
2:B:40:GLU:HB2	2:B:48:PHE:HE1	1.76	0.50
2:B:694:ARG:O	2:B:793:SER:N	2.42	0.50
2:B:2773:ARG:HA	2:B:2776:ILE:HD12	1.93	0.50
2:B:4124:GLU:HG3	2:B:4128:ASN:HD21	1.76	0.50
2:B:4722:TYR:HD2	2:B:4723:LEU:HD12	1.75	0.50
2:D:1119:ARG:NH2	2:D:1196:ASP:O	2.39	0.50
2:D:1171:HIS:O	2:D:1194:ASP:N	2.44	0.50
2:D:4848:ASP:HB3	2:F:4819:TYR:CE1	2.41	0.50
2:F:233:VAL:HG13	2:F:300:VAL:HG21	1.92	0.50
2:F:2221:TYR:O	2:F:2225:ASN:ND2	2.44	0.50
2:F:4018:PHE:O	2:F:4022:LEU:HB2	2.11	0.50
2:F:4794:TYR:HB2	2:F:4806:LYS:HD2	1.93	0.50
2:H:4568:TYR:O	2:H:4572:THR:OG1	2.22	0.50
2:H:4651:LYS:NZ	2:H:4670:LEU:O	2.45	0.50
1:A:42:ARG:NH2	2:B:1766:PRO:O	2.44	0.50
2:B:207:PHE:CE1	2:D:2326:ILE:HG21	2.42	0.50
2:B:2083:ARG:NH2	2:B:3686:ASP:OD1	2.43	0.50
2:B:4591:TYR:OH	2:B:4717:ASP:OD2	2.29	0.50
2:B:4798:GLU:O	2:B:4802:THR:OG1	2.27	0.50
2:D:2193:MET:HA	2:D:2196:ASN:HD22	1.76	0.50
2:D:4590:GLY:O	2:D:4594:LEU:N	2.44	0.50
2:D:4794:TYR:HB2	2:D:4806:LYS:HD2	1.93	0.50
2:F:1171:HIS:O	2:F:1194:ASP:N	2.44	0.50
2:F:2160:PRO:HB3	2:F:2207:ILE:HD12	1.91	0.50
2:F:3810:GLU:O	2:F:3814:LYS:HB2	2.12	0.50
2:F:4518:LEU:N	2:F:4518:LEU:CD2	2.74	0.50
2:H:748:LEU:HB2	2:H:750:ARG:HG3	1.92	0.50
2:H:1094:TYR:OH	2:H:1808:ASP:OD1	2.27	0.50
2:H:1666:ALA:N	2:H:1669:ASN:OD1	2.41	0.50
2:B:2116:ASP:OD1	2:B:2153:ASN:ND2	2.43	0.50
2:D:2773:ARG:HA	2:D:2776:ILE:HD12	1.93	0.50
2:F:165:ALA:HB2	2:F:182:ILE:HG12	1.93	0.50
2:F:2083:ARG:NH2	2:F:3686:ASP:OD1	2.44	0.50
2:F:4085:VAL:O	2:F:4089:HIS:N	2.44	0.50
2:F:4651:LYS:NZ	2:F:4670:LEU:O	2.45	0.50
2:H:300:VAL:HG12	2:H:420:ARG:HH22	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:657:PRO:HA	2:B:834:VAL:HA	1.92	0.50
2:B:1799:VAL:O	2:B:1803:SER:CB	2.60	0.50
2:D:162:ILE:HG23	2:D:181:LEU:HD13	1.93	0.50
2:D:657:PRO:HA	2:D:834:VAL:HA	1.92	0.50
2:D:4085:VAL:O	2:D:4089:HIS:N	2.44	0.50
2:D:4520:PHE:HD1	2:D:4562:LEU:HD21	0.84	0.50
1:E:89:GLY:HA3	2:F:1671:ARG:HH12	1.76	0.50
2:F:646:THR:OG1	2:F:1684:GLN:NE2	2.44	0.50
2:H:290:ARG:HG2	2:H:353:GLU:HB2	1.93	0.50
2:H:904:TYR:HB2	2:H:918:LEU:HB2	1.93	0.50
2:H:2193:MET:HA	2:H:2196:ASN:HD22	1.76	0.50
2:H:4082:GLU:HA	2:H:4086:LYS:HD2	1.92	0.50
2:H:4891:ILE:HD13	2:H:4914:HIS:HB3	1.92	0.50
2:B:165:ALA:HB2	2:B:182:ILE:HG12	1.93	0.50
2:B:1611:ILE:HB	2:B:1620:GLN:HB3	1.94	0.50
2:B:2193:MET:HA	2:B:2196:ASN:HD22	1.76	0.50
2:B:4118:THR:O	2:B:4122:LEU:HB2	2.11	0.50
2:D:776:GLN:HB3	2:D:1470:GLY:HA3	1.93	0.50
2:F:300:VAL:HG12	2:F:420:ARG:HH22	1.76	0.50
2:F:802:PHE:N	2:F:1616:GLY:O	2.45	0.50
2:H:802:PHE:N	2:H:1616:GLY:O	2.45	0.50
1:A:89:GLY:HA3	2:B:1671:ARG:HH12	1.76	0.50
2:B:620:CYS:N	2:B:623:VAL:O	2.39	0.50
2:D:207:PHE:CD2	2:F:2326:ILE:O	2.65	0.50
2:D:290:ARG:HG2	2:D:353:GLU:HB2	1.93	0.50
2:H:4118:THR:O	2:H:4122:LEU:HB2	2.11	0.50
2:B:1666:ALA:N	2:B:1669:ASN:OD1	2.41	0.50
2:B:4794:TYR:HB2	2:B:4806:LYS:HD2	1.93	0.50
2:D:300:VAL:HG12	2:D:420:ARG:HH22	1.76	0.50
2:F:1184:ASP:OD2	2:F:1188:SER:OG	2.30	0.50
2:F:1252:SER:HB2	2:F:1598:ARG:HB2	1.93	0.50
2:F:2773:ARG:HA	2:F:2776:ILE:HD12	1.93	0.50
2:F:4568:TYR:O	2:F:4572:THR:OG1	2.22	0.50
2:H:559:ILE:HD13	2:H:593:HIS:HB3	1.94	0.50
2:H:1611:ILE:HB	2:H:1620:GLN:HB3	1.94	0.50
2:B:289:ILE:HA	2:B:293:GLN:HE22	1.77	0.50
2:B:652:VAL:HA	2:B:795:SER:HB2	1.94	0.50
2:B:694:ARG:HB2	2:B:793:SER:HB2	1.94	0.50
2:B:725:TYR:HA	2:B:732:LEU:HA	1.92	0.50
2:B:3810:GLU:O	2:B:3814:LYS:HB2	2.12	0.50
2:D:289:ILE:HA	2:D:293:GLN:HE22	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:2857:LYS:HE3	2:D:2861:LEU:HD11	1.92	0.50
2:D:4651:LYS:NZ	2:D:4670:LEU:O	2.45	0.50
1:E:75:THR:HG23	1:E:98:ILE:HG12	1.94	0.50
2:H:1682:GLU:HA	2:H:1685:LEU:HD13	1.93	0.50
2:H:3810:GLU:O	2:H:3814:LYS:HB2	2.12	0.50
2:B:510:SER:O	2:B:520:ARG:NH2	2.44	0.50
2:B:559:ILE:HD13	2:B:593:HIS:HB3	1.94	0.50
2:B:2071:ALA:HA	2:B:2076:ILE:HD11	1.94	0.50
2:B:4651:LYS:NZ	2:B:4670:LEU:O	2.45	0.50
2:B:4814:TYR:CE2	2:B:4815:MET:CE	2.95	0.50
1:C:75:THR:HG23	1:C:98:ILE:HG12	1.94	0.50
2:D:904:TYR:HB2	2:D:918:LEU:HB2	1.93	0.50
2:D:3810:GLU:O	2:D:3814:LYS:HB2	2.12	0.50
2:D:4931:GLU:OE2	2:D:4942:TRP:NE1	2.45	0.50
2:H:510:SER:O	2:H:520:ARG:NH2	2.44	0.50
2:H:1799:VAL:O	2:H:1803:SER:CB	2.60	0.50
2:H:4018:PHE:O	2:H:4022:LEU:HB2	2.11	0.50
2:B:802:PHE:N	2:B:1616:GLY:O	2.45	0.49
2:B:1682:GLU:HA	2:B:1685:LEU:HD13	1.94	0.49
2:B:4515:ASN:HA	2:H:4780:TYR:OH	2.12	0.49
2:B:4931:GLU:OE2	2:B:4942:TRP:NE1	2.45	0.49
2:D:694:ARG:O	2:D:793:SER:N	2.42	0.49
2:D:725:TYR:HA	2:D:732:LEU:HA	1.92	0.49
2:D:1611:ILE:HB	2:D:1620:GLN:HB3	1.94	0.49
2:D:4018:PHE:O	2:D:4022:LEU:HB2	2.11	0.49
2:F:776:GLN:HB3	2:F:1470:GLY:HA3	1.93	0.49
2:F:4931:GLU:OE2	2:F:4942:TRP:NE1	2.45	0.49
2:H:652:VAL:HA	2:H:795:SER:HB2	1.94	0.49
2:H:1171:HIS:O	2:H:1194:ASP:N	2.44	0.49
2:H:1799:VAL:HG22	2:H:1894:LEU:HD13	1.93	0.49
2:H:4931:GLU:OE2	2:H:4942:TRP:NE1	2.45	0.49
2:B:162:ILE:HG23	2:B:181:LEU:HD13	1.92	0.49
2:B:1252:SER:HB2	2:B:1598:ARG:HB2	1.93	0.49
2:D:375:GLN:HE21	2:D:392:ILE:HD13	1.77	0.49
2:D:3810:GLU:O	2:D:3814:LYS:CB	2.60	0.49
1:E:54:GLU:OE1	2:F:1772:ASN:ND2	2.45	0.49
2:F:904:TYR:HB2	2:F:918:LEU:HB2	1.93	0.49
2:F:1251:LEU:O	2:F:1601:ASN:N	2.43	0.49
2:F:4814:TYR:HE2	2:F:4815:MET:CE	2.21	0.49
2:H:3763:GLY:HA2	2:H:3766:ILE:HD12	1.94	0.49
2:H:4590:GLY:O	2:H:4594:LEU:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:4814:TYR:CE2	2:H:4815:MET:CE	2.95	0.49
2:B:3856:GLN:NE2	2:B:3923:GLU:O	2.45	0.49
2:D:1682:GLU:HA	2:D:1685:LEU:HD13	1.93	0.49
2:D:2026:ILE:HG23	2:D:2030:LEU:HD12	1.94	0.49
2:D:2301:ASP:OD1	2:D:2304:ARG:NH2	2.46	0.49
2:D:3806:LEU:O	2:D:3810:GLU:N	2.43	0.49
2:D:4124:GLU:HG3	2:D:4128:ASN:HD21	1.76	0.49
2:F:2558:LYS:O	2:F:2562:LEU:N	2.44	0.49
2:F:3810:GLU:O	2:F:3814:LYS:CB	2.60	0.49
2:H:707:PRO:HD3	2:H:840:TYR:HE1	1.78	0.49
2:H:1443:VAL:O	2:H:1489:CYS:N	2.43	0.49
2:H:2773:ARG:HA	2:H:2776:ILE:HD12	1.93	0.49
2:H:4124:GLU:HG3	2:H:4128:ASN:HD21	1.76	0.49
2:B:1041:ARG:HA	2:B:1044:LYS:HG3	1.94	0.49
2:B:3763:GLY:HA2	2:B:3766:ILE:HD12	1.94	0.49
2:B:3810:GLU:O	2:B:3814:LYS:CB	2.60	0.49
2:B:4523:VAL:HG22	2:B:4559:HIS:HE1	1.78	0.49
1:C:89:GLY:HA3	2:D:1671:ARG:HH12	1.76	0.49
2:D:165:ALA:HB2	2:D:182:ILE:HG12	1.93	0.49
2:D:1300:MET:HB2	2:D:1545:ALA:HB3	1.93	0.49
2:D:4523:VAL:HG22	2:D:4559:HIS:HE1	1.78	0.49
2:F:375:GLN:HE21	2:F:392:ILE:HD13	1.77	0.49
2:F:559:ILE:HD13	2:F:593:HIS:HB3	1.94	0.49
2:F:1041:ARG:HA	2:F:1044:LYS:HG3	1.94	0.49
2:F:3806:LEU:O	2:F:3810:GLU:N	2.43	0.49
1:G:75:THR:HG23	1:G:98:ILE:HG12	1.94	0.49
1:G:89:GLY:HA3	2:H:1671:ARG:HH12	1.76	0.49
2:H:4176:ASP:HA	2:H:4180:GLU:HB3	1.95	0.49
1:A:54:GLU:OE1	2:B:1772:ASN:ND2	2.45	0.49
1:A:75:THR:HG23	1:A:98:ILE:HG12	1.94	0.49
2:B:904:TYR:HB2	2:B:918:LEU:HB2	1.93	0.49
2:B:2026:ILE:HG23	2:B:2030:LEU:HD12	1.94	0.49
2:B:2301:ASP:OD1	2:B:2304:ARG:NH2	2.46	0.49
1:C:54:GLU:OE1	2:D:1772:ASN:ND2	2.46	0.49
2:D:1666:ALA:N	2:D:1669:ASN:OD1	2.41	0.49
2:D:4796:LYS:HD2	2:D:4805:MET:HB3	1.95	0.49
2:H:1252:SER:HB2	2:H:1598:ARG:HB2	1.93	0.49
2:B:290:ARG:HG2	2:B:353:GLU:HB2	1.93	0.49
2:B:542:ARG:NE	2:B:577:CYS:SG	2.85	0.49
2:B:4176:ASP:HA	2:B:4180:GLU:HB3	1.95	0.49
2:D:4176:ASP:HA	2:D:4180:GLU:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:1682:GLU:HA	2:F:1685:LEU:HD13	1.94	0.49
2:F:1799:VAL:O	2:F:1803:SER:CB	2.60	0.49
2:F:3763:GLY:HA2	2:F:3766:ILE:HD12	1.94	0.49
2:F:4523:VAL:HG22	2:F:4559:HIS:HE1	1.78	0.49
2:F:4713:VAL:O	2:F:4716:THR:OG1	2.27	0.49
2:H:289:ILE:HA	2:H:293:GLN:HE22	1.77	0.49
2:B:207:PHE:CD2	2:D:2326:ILE:O	2.66	0.49
2:B:4018:PHE:O	2:B:4022:LEU:HB2	2.12	0.49
2:D:207:PHE:CE1	2:F:2326:ILE:HG21	2.39	0.49
2:D:4520:PHE:CB	2:D:4562:LEU:HD21	2.43	0.49
2:F:1611:ILE:HB	2:F:1620:GLN:HB3	1.94	0.49
2:F:4759:SER:HA	2:F:4762:THR:HG22	1.95	0.49
2:H:620:CYS:N	2:H:623:VAL:O	2.39	0.49
2:H:2096:ILE:O	2:H:2100:VAL:N	2.43	0.49
2:H:2301:ASP:OD1	2:H:2304:ARG:NH2	2.46	0.49
2:H:3921:LEU:HD23	2:H:3924:TYR:HD2	1.78	0.49
2:H:4798:GLU:O	2:H:4802:THR:OG1	2.27	0.49
2:B:2096:ILE:O	2:B:2100:VAL:N	2.43	0.49
2:B:2326:ILE:O	2:H:207:PHE:CD2	2.66	0.49
2:B:3806:LEU:O	2:B:3810:GLU:N	2.43	0.49
1:C:28:GLY:N	1:C:37:ASP:O	2.37	0.49
2:D:506:HIS:NE2	2:D:534:TYR:OH	2.40	0.49
2:D:559:ILE:HD13	2:D:593:HIS:HB3	1.94	0.49
2:D:802:PHE:N	2:D:1616:GLY:O	2.45	0.49
2:D:1799:VAL:O	2:D:1803:SER:CB	2.60	0.49
2:D:3763:GLY:HA2	2:D:3766:ILE:HD12	1.94	0.49
2:D:4798:GLU:O	2:D:4802:THR:OG1	2.27	0.49
2:D:4857:VAL:HG13	2:F:4863:ILE:HG21	1.93	0.49
2:F:207:PHE:CD2	2:H:2326:ILE:O	2.65	0.49
2:F:289:ILE:HA	2:F:293:GLN:HE22	1.77	0.49
2:F:694:ARG:HB2	2:F:793:SER:HB2	1.94	0.49
2:F:4590:GLY:O	2:F:4594:LEU:N	2.44	0.49
2:F:4796:LYS:HD2	2:F:4805:MET:HB3	1.95	0.49
2:B:694:ARG:HB3	2:B:716:ASN:HB3	1.94	0.49
2:B:4193:PHE:O	2:B:4197:THR:OG1	2.25	0.49
2:B:4796:LYS:HD2	2:B:4805:MET:HB3	1.95	0.49
2:B:4819:TYR:CE1	2:H:4848:ASP:HB3	2.42	0.49
2:B:4848:ASP:HB3	2:D:4819:TYR:CE1	2.42	0.49
2:D:694:ARG:HB2	2:D:793:SER:HB2	1.94	0.49
2:D:1041:ARG:HA	2:D:1044:LYS:HG3	1.94	0.49
2:F:2738:LEU:HD13	2:F:2819:ALA:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:2835:SER:H	2:F:2838:LEU:HB2	1.78	0.49
1:G:54:GLU:OE1	2:H:1772:ASN:ND2	2.45	0.49
2:H:375:GLN:HE21	2:H:392:ILE:HD13	1.77	0.49
2:H:750:ARG:N	2:H:753:ASP:OD2	2.46	0.49
2:H:1926:ILE:HD11	2:H:2034:VAL:HG22	1.95	0.49
2:B:1300:MET:HB2	2:B:1545:ALA:HB3	1.93	0.49
2:B:2326:ILE:HG21	2:H:207:PHE:CE1	2.41	0.49
2:B:2835:SER:H	2:B:2838:LEU:HB2	1.78	0.49
2:D:4814:TYR:CE2	2:D:4815:MET:CE	2.95	0.49
2:F:228:LEU:HB3	2:F:289:ILE:HB	1.95	0.49
2:F:1926:ILE:HD11	2:F:2034:VAL:HG22	1.95	0.49
2:F:2071:ALA:HA	2:F:2076:ILE:HD11	1.94	0.49
2:F:3856:GLN:NE2	2:F:3923:GLU:O	2.45	0.49
2:F:4569:MET:O	2:F:4573:LEU:HB2	2.13	0.49
2:F:4591:TYR:OH	2:F:4717:ASP:OD2	2.29	0.49
2:H:1041:ARG:HA	2:H:1044:LYS:HG3	1.94	0.49
2:H:2738:LEU:HD13	2:H:2819:ALA:HB3	1.95	0.49
2:B:483:LYS:O	2:B:544:ASN:ND2	2.38	0.48
2:B:2558:LYS:O	2:B:2562:LEU:N	2.44	0.48
2:B:4780:TYR:OH	2:D:4515:ASN:HA	2.12	0.48
2:D:207:PHE:HB3	2:F:2326:ILE:O	2.13	0.48
2:D:246:THR:N	2:D:261:HIS:O	2.42	0.48
2:D:483:LYS:O	2:D:544:ASN:ND2	2.38	0.48
2:D:707:PRO:HD3	2:D:840:TYR:HE1	1.78	0.48
2:D:2835:SER:H	2:D:2838:LEU:HB2	1.78	0.48
2:D:3856:GLN:NE2	2:D:3923:GLU:O	2.45	0.48
2:F:556:ASP:OD1	2:F:556:ASP:N	2.46	0.48
2:F:1570:LEU:O	2:F:1573:SER:OG	2.27	0.48
2:F:4176:ASP:HA	2:F:4180:GLU:HB3	1.95	0.48
2:H:556:ASP:OD1	2:H:556:ASP:N	2.46	0.48
2:H:1184:ASP:OD2	2:H:1188:SER:OG	2.30	0.48
2:H:2835:SER:H	2:H:2838:LEU:HB2	1.78	0.48
2:H:4759:SER:HA	2:H:4762:THR:HG22	1.95	0.48
2:B:707:PRO:HD3	2:B:840:TYR:HE1	1.78	0.48
2:B:803:LEU:HD13	2:B:813:PHE:H	1.78	0.48
2:B:4520:PHE:CB	2:B:4562:LEU:HD21	2.43	0.48
2:D:228:LEU:HB3	2:D:289:ILE:HB	1.95	0.48
2:F:542:ARG:NE	2:F:577:CYS:SG	2.85	0.48
2:F:3921:LEU:HD23	2:F:3924:TYR:HD2	1.78	0.48
2:F:4899:PHE:HB2	2:F:4906:PHE:HD1	1.78	0.48
2:H:3810:GLU:O	2:H:3814:LYS:CB	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:3917:VAL:O	2:H:3920:THR:OG1	2.24	0.48
2:B:375:GLN:HE21	2:B:392:ILE:HD13	1.77	0.48
2:B:556:ASP:N	2:B:556:ASP:OD1	2.46	0.48
2:D:652:VAL:HA	2:D:795:SER:HB2	1.94	0.48
2:D:694:ARG:HB3	2:D:716:ASN:HB3	1.94	0.48
2:D:2837:ASP:OD1	2:D:2906:ARG:NE	2.42	0.48
2:F:707:PRO:HD3	2:F:840:TYR:HE1	1.78	0.48
1:A:42:ARG:HG3	1:A:44:LYS:HB3	1.95	0.48
2:B:750:ARG:N	2:B:753:ASP:OD2	2.46	0.48
2:B:2425:ARG:HG3	2:B:2477:TYR:CE1	2.48	0.48
2:B:2738:LEU:HD13	2:B:2819:ALA:HB3	1.95	0.48
2:B:4759:SER:HA	2:B:4762:THR:HG22	1.95	0.48
2:B:4899:PHE:HB2	2:B:4906:PHE:HD1	1.78	0.48
2:D:803:LEU:HD13	2:D:813:PHE:H	1.78	0.48
2:D:4569:MET:O	2:D:4573:LEU:HB2	2.13	0.48
2:F:652:VAL:HA	2:F:795:SER:HB2	1.94	0.48
2:H:457:GLN:HA	2:H:460:ILE:HD12	1.95	0.48
2:H:694:ARG:HB3	2:H:716:ASN:HB3	1.94	0.48
2:H:4523:VAL:HG22	2:H:4559:HIS:HE1	1.78	0.48
2:B:122:ARG:HE	2:B:127:GLY:HA2	1.79	0.48
2:B:434:ASP:O	2:B:438:LYS:NZ	2.43	0.48
2:B:457:GLN:HA	2:B:460:ILE:HD12	1.95	0.48
2:D:207:PHE:HZ	2:F:2326:ILE:HD12	1.70	0.48
2:D:556:ASP:N	2:D:556:ASP:OD1	2.46	0.48
2:F:434:ASP:O	2:F:438:LYS:NZ	2.43	0.48
2:F:1443:VAL:O	2:F:1489:CYS:N	2.43	0.48
2:F:4520:PHE:CB	2:F:4562:LEU:HD21	2.43	0.48
1:G:74:LEU:HB2	1:G:99:PHE:HB2	1.95	0.48
2:H:542:ARG:NE	2:H:577:CYS:SG	2.85	0.48
2:H:694:ARG:HB2	2:H:793:SER:HB2	1.94	0.48
2:H:2026:ILE:HG23	2:H:2030:LEU:HD12	1.94	0.48
2:H:2071:ALA:HA	2:H:2076:ILE:HD11	1.94	0.48
2:H:2731:ASP:OD1	2:H:2822:TYR:OH	2.30	0.48
2:H:4569:MET:O	2:H:4573:LEU:HB2	2.13	0.48
2:H:4649:PHE:HB3	2:H:4653:LYS:HE3	1.96	0.48
2:H:4796:LYS:HD2	2:H:4805:MET:HB3	1.95	0.48
1:C:23:VAL:HB	1:C:105:ASN:H	1.79	0.48
2:D:2071:ALA:HA	2:D:2076:ILE:HD11	1.94	0.48
2:D:2222:LEU:O	2:D:2226:SER:N	2.35	0.48
2:D:4568:TYR:O	2:D:4572:THR:OG1	2.22	0.48
2:D:4649:PHE:HB3	2:D:4653:LYS:HE3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:122:ARG:HE	2:F:127:GLY:HA2	1.79	0.48
2:F:750:ARG:N	2:F:753:ASP:OD2	2.46	0.48
2:F:2026:ILE:HG23	2:F:2030:LEU:HD12	1.94	0.48
2:F:2301:ASP:OD1	2:F:2304:ARG:NH2	2.46	0.48
2:F:4814:TYR:CE2	2:F:4815:MET:CE	2.95	0.48
2:H:122:ARG:HE	2:H:127:GLY:HA2	1.79	0.48
2:H:1119:ARG:NH2	2:H:1196:ASP:O	2.39	0.48
2:B:4089:HIS:O	2:B:4093:LYS:N	2.44	0.48
2:D:4759:SER:HA	2:D:4762:THR:HG22	1.95	0.48
2:H:3856:GLN:NE2	2:H:3923:GLU:O	2.45	0.48
2:B:4569:MET:O	2:B:4573:LEU:HB2	2.13	0.48
2:D:2738:LEU:HD13	2:D:2819:ALA:HB3	1.95	0.48
2:F:803:LEU:HD13	2:F:813:PHE:H	1.78	0.48
2:H:4089:HIS:O	2:H:4093:LYS:N	2.44	0.48
2:B:4668:SER:HA	2:B:4671:LEU:HD12	1.96	0.48
2:D:185:SER:OG	2:D:186:VAL:N	2.47	0.48
2:D:1197:VAL:HA	2:D:1201:PHE:HE2	1.79	0.48
2:D:1209:VAL:N	2:D:1211:GLN:OE1	2.47	0.48
1:E:42:ARG:HG3	1:E:44:LYS:HB3	1.95	0.48
2:F:694:ARG:O	2:F:793:SER:N	2.42	0.48
2:F:1209:VAL:N	2:F:1211:GLN:OE1	2.47	0.48
2:H:803:LEU:HD13	2:H:813:PHE:H	1.78	0.48
1:C:74:LEU:HB2	1:C:99:PHE:HB2	1.95	0.48
2:D:122:ARG:HE	2:D:127:GLY:HA2	1.79	0.48
2:D:1310:CYS:HB2	2:D:1536:SER:HA	1.95	0.48
2:D:1799:VAL:O	2:D:1803:SER:OG	2.30	0.48
2:D:2558:LYS:O	2:D:2562:LEU:N	2.44	0.48
2:D:3748:SER:O	2:D:3793:SER:OG	2.30	0.48
2:F:185:SER:OG	2:F:186:VAL:N	2.47	0.48
2:F:1197:VAL:HA	2:F:1201:PHE:HE2	1.79	0.48
2:H:434:ASP:O	2:H:438:LYS:NZ	2.43	0.48
2:H:656:ARG:HH12	2:H:700:THR:HG22	1.79	0.48
2:H:1799:VAL:O	2:H:1803:SER:OG	2.30	0.48
2:H:2135:MET:HA	2:H:2136:GLY:HA3	1.68	0.48
2:H:4520:PHE:CB	2:H:4562:LEU:HD21	2.43	0.48
2:B:1184:ASP:OD2	2:B:1188:SER:OG	2.30	0.47
2:B:1926:ILE:HD11	2:B:2034:VAL:HG22	1.95	0.47
2:D:750:ARG:N	2:D:753:ASP:OD2	2.46	0.47
2:D:1443:VAL:O	2:D:1489:CYS:N	2.43	0.47
2:D:1926:ILE:HD11	2:D:2034:VAL:HG22	1.95	0.47
2:D:4642:PRO:HG2	2:D:4648:LYS:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:228:LEU:HB3	2:F:289:ILE:HD12	1.96	0.47
2:F:457:GLN:HA	2:F:460:ILE:HD12	1.95	0.47
2:F:694:ARG:HB3	2:F:716:ASN:HB3	1.94	0.47
2:F:2835:SER:O	2:F:2839:HIS:N	2.38	0.47
2:F:4594:LEU:O	2:F:4596:VAL:N	2.47	0.47
2:B:656:ARG:HH12	2:B:700:THR:HG22	1.79	0.47
2:B:4594:LEU:O	2:B:4596:VAL:N	2.47	0.47
2:D:457:GLN:HA	2:D:460:ILE:HD12	1.95	0.47
2:D:1302:TYR:HB2	2:D:1543:VAL:HB	1.96	0.47
2:D:4193:PHE:O	2:D:4197:THR:OG1	2.25	0.47
2:D:4627:ILE:HA	2:D:4630:GLN:HB2	1.96	0.47
1:E:74:LEU:HB2	1:E:99:PHE:HB2	1.95	0.47
2:F:4857:VAL:HG13	2:H:4863:ILE:HG21	1.93	0.47
2:B:443:SER:HA	2:B:444:THR:HA	1.64	0.47
2:B:1171:HIS:O	2:B:1194:ASP:N	2.44	0.47
2:B:1310:CYS:HB2	2:B:1536:SER:HA	1.96	0.47
2:B:1648:GLU:HA	2:B:1651:LEU:HB3	1.97	0.47
2:D:2038:THR:OG1	2:D:2039:TYR:N	2.47	0.47
1:E:23:VAL:HB	1:E:105:ASN:H	1.79	0.47
2:F:443:SER:HA	2:F:444:THR:HA	1.64	0.47
2:H:228:LEU:HB3	2:H:289:ILE:HB	1.95	0.47
2:H:443:SER:HA	2:H:444:THR:HA	1.64	0.47
2:H:4804:ASP:N	2:H:4804:ASP:OD1	2.47	0.47
1:A:74:LEU:HB2	1:A:99:PHE:HB2	1.95	0.47
2:B:228:LEU:HB3	2:B:289:ILE:HB	1.95	0.47
2:B:420:ARG:HE	2:B:420:ARG:H	1.63	0.47
2:B:2038:THR:OG1	2:B:2039:TYR:N	2.47	0.47
2:B:3921:LEU:HD23	2:B:3924:TYR:HD2	1.78	0.47
2:D:542:ARG:NE	2:D:577:CYS:SG	2.85	0.47
2:D:2256:LEU:HD11	2:D:3815:ALA:HB3	1.97	0.47
2:D:3919:ASN:O	2:D:3922:THR:OG1	2.27	0.47
2:D:4899:PHE:HB2	2:D:4906:PHE:HD1	1.78	0.47
2:F:1043:LYS:HA	2:F:1046:ASN:HB2	1.97	0.47
2:F:4804:ASP:OD1	2:F:4804:ASP:N	2.47	0.47
2:H:125:TYR:CZ	2:H:417:ARG:HB3	2.50	0.47
2:B:2256:LEU:HD11	2:B:3815:ALA:HB3	1.97	0.47
2:B:4627:ILE:HA	2:B:4630:GLN:HB2	1.96	0.47
2:D:1689:ILE:HG12	2:D:1703:TYR:HE1	1.80	0.47
2:D:4594:LEU:O	2:D:4596:VAL:N	2.47	0.47
2:F:218:SER:HB3	2:F:286:GLY:HA3	1.96	0.47
2:H:185:SER:OG	2:H:186:VAL:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:1043:LYS:HA	2:H:1046:ASN:HB2	1.97	0.47
2:H:1209:VAL:N	2:H:1211:GLN:OE1	2.47	0.47
2:H:1251:LEU:O	2:H:1601:ASN:N	2.43	0.47
2:H:4899:PHE:HB2	2:H:4906:PHE:HD1	1.78	0.47
2:B:228:LEU:HB3	2:B:289:ILE:HD12	1.96	0.47
2:B:1197:VAL:HA	2:B:1201:PHE:HE2	1.79	0.47
2:B:1209:VAL:N	2:B:1211:GLN:OE1	2.47	0.47
2:B:1302:TYR:HB2	2:B:1543:VAL:HB	1.96	0.47
2:B:1689:ILE:HG12	2:B:1703:TYR:HE1	1.80	0.47
2:B:2425:ARG:HG3	2:B:2477:TYR:HE1	1.79	0.47
2:D:228:LEU:HB3	2:D:289:ILE:HD12	1.96	0.47
2:D:656:ARG:HH12	2:D:700:THR:HG22	1.79	0.47
2:D:3956:GLN:HE21	2:D:3976:GLN:HE22	1.63	0.47
2:D:4780:TYR:OH	2:F:4515:ASN:HA	2.15	0.47
2:F:2256:LEU:HD11	2:F:3815:ALA:HB3	1.97	0.47
2:F:2858:LYS:HG2	2:F:2872:LEU:HD22	1.97	0.47
1:G:28:GLY:N	1:G:37:ASP:O	2.37	0.47
2:H:1310:CYS:HB2	2:H:1536:SER:HA	1.96	0.47
2:H:2488:LEU:O	2:H:2492:GLY:N	2.48	0.47
2:H:4642:PRO:HG2	2:H:4648:LYS:HD2	1.96	0.47
1:A:68:LEU:HA	1:A:103:LEU:HD23	1.97	0.47
2:B:218:SER:HB3	2:B:286:GLY:HA3	1.96	0.47
2:B:1043:LYS:HA	2:B:1046:ASN:HB2	1.97	0.47
1:C:42:ARG:HG3	1:C:44:LYS:HB3	1.95	0.47
2:D:1748:LEU:HD22	2:D:1749:PRO:HD2	1.95	0.47
2:D:4591:TYR:OH	2:D:4717:ASP:OD2	2.29	0.47
2:D:4668:SER:HA	2:D:4671:LEU:HD12	1.96	0.47
2:F:125:TYR:CZ	2:F:417:ARG:HB3	2.50	0.47
2:F:656:ARG:HH12	2:F:700:THR:HG22	1.79	0.47
2:F:672:LYS:HA	2:F:760:ASP:HA	1.97	0.47
2:F:1302:TYR:HB2	2:F:1543:VAL:HB	1.96	0.47
2:F:4089:HIS:O	2:F:4093:LYS:N	2.44	0.47
2:F:4857:VAL:CG1	2:H:4863:ILE:HG21	2.43	0.47
1:G:42:ARG:HG3	1:G:44:LYS:HB3	1.95	0.47
2:H:64:ILE:HA	2:H:123:HIS:HE1	1.80	0.47
2:H:218:SER:HB3	2:H:286:GLY:HA3	1.96	0.47
2:H:228:LEU:HB3	2:H:289:ILE:HD12	1.96	0.47
2:H:420:ARG:H	2:H:420:ARG:HE	1.63	0.47
2:H:1115:VAL:O	2:H:1137:PHE:N	2.48	0.47
2:H:1648:GLU:HA	2:H:1651:LEU:HB3	1.96	0.47
2:H:1748:LEU:HD22	2:H:1749:PRO:HD2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:2256:LEU:HD11	2:H:3815:ALA:HB3	1.96	0.47
2:H:3960:SER:HG	2:H:4070:CYS:HG	1.62	0.47
2:B:185:SER:OG	2:B:186:VAL:N	2.47	0.47
2:B:673:TRP:HB2	2:B:759:LEU:HB3	1.97	0.47
2:B:4648:LYS:O	2:B:4652:ARG:NE	2.48	0.47
2:D:653:SER:OG	2:D:794:PHE:O	2.31	0.47
2:D:673:TRP:HB2	2:D:759:LEU:HB3	1.96	0.47
1:E:40:ARG:HB3	2:F:688:ALA:HB1	1.97	0.47
2:F:64:ILE:HA	2:F:123:HIS:HE1	1.79	0.47
2:F:420:ARG:H	2:F:420:ARG:HE	1.63	0.47
2:F:483:LYS:O	2:F:544:ASN:ND2	2.38	0.47
2:F:1310:CYS:HB2	2:F:1536:SER:HA	1.96	0.47
2:F:2135:MET:HA	2:F:2136:GLY:HA3	1.68	0.47
2:F:2837:ASP:OD1	2:F:2906:ARG:NE	2.42	0.47
2:F:4648:LYS:O	2:F:4652:ARG:NE	2.48	0.47
2:H:4100:ALA:O	2:H:4104:THR:OG1	2.30	0.47
2:B:3956:GLN:HE21	2:B:3976:GLN:HE22	1.63	0.47
2:B:4052:ALA:O	2:B:4056:HIS:ND1	2.47	0.47
2:D:218:SER:HB3	2:D:286:GLY:HA3	1.96	0.47
2:D:420:ARG:HE	2:D:420:ARG:H	1.63	0.47
2:D:4857:VAL:CG1	2:F:4863:ILE:HG21	2.45	0.47
2:F:1934:VAL:HG21	2:F:3618:VAL:HA	1.97	0.47
2:F:2102:ALA:O	2:F:2106:THR:N	2.46	0.47
2:F:4717:ASP:HB3	2:F:4720:PHE:HB3	1.97	0.47
2:H:394:HIS:NE2	2:H:396:GLU:OE1	2.48	0.47
2:H:2148:GLY:O	2:H:2152:ASN:ND2	2.48	0.47
2:H:4594:LEU:O	2:H:4596:VAL:N	2.47	0.47
2:H:4668:SER:HA	2:H:4671:LEU:HD12	1.96	0.47
1:A:40:ARG:HB3	2:B:688:ALA:HB1	1.97	0.47
2:B:64:ILE:HA	2:B:123:HIS:HE1	1.79	0.47
2:B:394:HIS:NE2	2:B:396:GLU:OE1	2.48	0.47
2:B:653:SER:OG	2:B:794:PHE:O	2.31	0.47
2:B:2148:GLY:O	2:B:2152:ASN:ND2	2.48	0.47
2:B:4642:PRO:HG2	2:B:4648:LYS:HD2	1.96	0.47
2:B:4804:ASP:N	2:B:4804:ASP:OD1	2.47	0.47
1:C:68:LEU:HA	1:C:103:LEU:HD23	1.97	0.47
2:D:1115:VAL:O	2:D:1137:PHE:N	2.48	0.47
2:D:2858:LYS:HG2	2:D:2872:LEU:HD22	1.97	0.47
2:D:4804:ASP:OD1	2:D:4804:ASP:N	2.47	0.47
2:F:1306:MET:HB3	2:F:1575:HIS:CE1	2.50	0.47
2:F:1748:LEU:HD22	2:F:1749:PRO:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:4649:PHE:HB3	2:F:4653:LYS:HE3	1.96	0.47
2:F:4668:SER:HA	2:F:4671:LEU:HD12	1.96	0.47
1:G:23:VAL:HB	1:G:105:ASN:H	1.79	0.47
2:H:190:ARG:HG2	2:H:207:PHE:HE1	1.80	0.47
2:H:1306:MET:HB3	2:H:1575:HIS:CE1	2.49	0.47
2:B:681:HIS:HD2	2:B:799:LYS:HD3	1.80	0.46
2:B:848:ARG:NH1	2:B:1605:LYS:O	2.48	0.46
2:B:1115:VAL:O	2:B:1137:PHE:N	2.48	0.46
2:B:1748:LEU:HD22	2:B:1749:PRO:HD2	1.96	0.46
2:B:1929:PHE:HZ	2:B:2030:LEU:HB3	1.80	0.46
2:B:3925:ILE:HD11	2:B:3936:LEU:HD13	1.97	0.46
2:B:4100:ALA:O	2:B:4104:THR:OG1	2.30	0.46
1:C:49:ARG:HB3	1:C:52:LYS:HE2	1.97	0.46
2:D:1306:MET:HB3	2:D:1575:HIS:CE1	2.49	0.46
2:D:1570:LEU:O	2:D:1573:SER:OG	2.27	0.46
2:D:1648:GLU:HA	2:D:1651:LEU:HB3	1.97	0.46
2:D:1929:PHE:HZ	2:D:2030:LEU:HB3	1.80	0.46
2:D:3925:ILE:HD11	2:D:3936:LEU:HD13	1.97	0.46
2:F:4518:LEU:HD13	2:F:4521:TYR:HE2	1.80	0.46
2:F:4780:TYR:OH	2:H:4515:ASN:HA	2.15	0.46
2:H:1197:VAL:HA	2:H:1201:PHE:HE2	1.79	0.46
2:H:1302:TYR:HB2	2:H:1543:VAL:HB	1.96	0.46
2:H:4627:ILE:HA	2:H:4630:GLN:HB2	1.96	0.46
2:B:190:ARG:HG2	2:B:207:PHE:HE1	1.80	0.46
2:B:2326:ILE:O	2:H:207:PHE:HB3	2.15	0.46
2:D:64:ILE:HA	2:D:123:HIS:HE1	1.80	0.46
2:D:2102:ALA:O	2:D:2106:THR:N	2.46	0.46
2:D:2488:LEU:O	2:D:2492:GLY:N	2.48	0.46
2:D:3921:LEU:HD23	2:D:3924:TYR:HD2	1.78	0.46
2:D:4648:LYS:O	2:D:4652:ARG:NE	2.48	0.46
2:F:207:PHE:HB3	2:H:2326:ILE:O	2.15	0.46
2:F:673:TRP:HB2	2:F:759:LEU:HB3	1.97	0.46
2:F:1699:ARG:HH22	2:F:1821:LEU:HD11	1.80	0.46
2:F:1738:LEU:HD22	2:F:1739:PHE:H	1.79	0.46
2:F:3925:ILE:HD11	2:F:3936:LEU:HD13	1.97	0.46
2:F:4627:ILE:HA	2:F:4630:GLN:HB2	1.96	0.46
2:F:4642:PRO:HG2	2:F:4648:LYS:HD2	1.96	0.46
2:F:4733:GLY:HA3	2:F:4740:PHE:HD1	1.80	0.46
2:H:506:HIS:HE2	2:H:534:TYR:HH	1.61	0.46
2:H:673:TRP:HB2	2:H:759:LEU:HB3	1.97	0.46
2:H:1934:VAL:HG21	2:H:3618:VAL:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:3925:ILE:HD11	2:H:3936:LEU:HD13	1.97	0.46
2:B:672:LYS:HA	2:B:760:ASP:HA	1.97	0.46
2:B:1699:ARG:HH22	2:B:1821:LEU:HD11	1.80	0.46
2:B:1738:LEU:HD22	2:B:1739:PHE:H	1.80	0.46
2:B:4013:MET:N	2:B:4013:MET:SD	2.89	0.46
2:B:4649:PHE:HB3	2:B:4653:LYS:HE3	1.96	0.46
2:D:190:ARG:HG2	2:D:207:PHE:HE1	1.80	0.46
2:F:137:ARG:N	2:F:146:ASP:OD2	2.49	0.46
2:F:4052:ALA:O	2:F:4056:HIS:ND1	2.47	0.46
2:H:1484:ASN:H	2:H:1486:TYR:HA	1.80	0.46
2:H:4591:TYR:OH	2:H:4717:ASP:OD2	2.29	0.46
2:H:4623:SER:O	2:H:4630:GLN:NE2	2.48	0.46
2:B:3860:ARG:HH21	2:B:3932:ASN:HB2	1.80	0.46
2:D:707:PRO:HD2	2:D:1604:LEU:HD22	1.98	0.46
2:D:848:ARG:NH1	2:D:1605:LYS:O	2.48	0.46
2:D:4138:GLU:HG2	2:D:4148:ARG:HB3	1.98	0.46
2:D:4733:GLY:HA3	2:D:4740:PHE:HD1	1.80	0.46
1:E:68:LEU:HA	1:E:103:LEU:HD23	1.97	0.46
2:F:2488:LEU:O	2:F:2492:GLY:N	2.48	0.46
2:F:4046:LYS:N	2:F:4077:GLU:OE1	2.49	0.46
2:H:137:ARG:N	2:H:146:ASP:OD2	2.49	0.46
2:H:419:ILE:HG12	2:H:489:PHE:HE1	1.81	0.46
2:H:506:HIS:HB3	2:H:564:ARG:HH22	1.81	0.46
2:H:848:ARG:NH1	2:H:1605:LYS:O	2.48	0.46
2:H:4113:ASP:O	2:H:4117:GLN:N	2.46	0.46
2:H:4648:LYS:O	2:H:4652:ARG:NE	2.48	0.46
1:A:23:VAL:HB	1:A:105:ASN:H	1.79	0.46
2:B:707:PRO:HD2	2:B:1604:LEU:HD22	1.98	0.46
2:B:1306:MET:HB3	2:B:1575:HIS:CE1	2.49	0.46
2:B:4713:VAL:O	2:B:4716:THR:OG1	2.27	0.46
2:B:4733:GLY:HA3	2:B:4740:PHE:HD1	1.80	0.46
2:D:394:HIS:NE2	2:D:396:GLU:OE1	2.48	0.46
2:D:4013:MET:N	2:D:4013:MET:SD	2.89	0.46
2:F:190:ARG:HG2	2:F:207:PHE:HE1	1.80	0.46
2:F:3860:ARG:HH21	2:F:3932:ASN:HB2	1.80	0.46
2:F:4138:GLU:HG2	2:F:4148:ARG:HB3	1.98	0.46
2:H:1570:LEU:O	2:H:1573:SER:OG	2.27	0.46
2:H:1689:ILE:HG12	2:H:1703:TYR:HE1	1.80	0.46
2:B:1716:THR:HA	2:B:1719:LEU:HD12	1.98	0.46
2:B:4138:GLU:HG2	2:B:4148:ARG:HB3	1.98	0.46
1:C:40:ARG:HB3	2:D:688:ALA:HB1	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1184:ASP:OD2	2:D:1188:SER:OG	2.30	0.46
2:D:3924:TYR:O	2:D:3932:ASN:ND2	2.48	0.46
2:D:4717:ASP:HB3	2:D:4720:PHE:HB3	1.97	0.46
2:F:228:LEU:HD23	2:F:228:LEU:HA	1.82	0.46
2:F:394:HIS:NE2	2:F:396:GLU:OE1	2.48	0.46
2:F:1686:LEU:HA	2:F:1689:ILE:HD12	1.98	0.46
2:F:1689:ILE:HG12	2:F:1703:TYR:HE1	1.80	0.46
2:F:3917:VAL:O	2:F:3920:THR:OG1	2.24	0.46
2:F:3956:GLN:HE21	2:F:3976:GLN:HE22	1.63	0.46
2:H:1716:THR:HA	2:H:1719:LEU:HD12	1.98	0.46
2:H:1738:LEU:HD22	2:H:1739:PHE:H	1.79	0.46
2:H:2858:LYS:HG2	2:H:2872:LEU:HD22	1.97	0.46
2:H:3859:LEU:HD22	2:H:3871:ILE:HG21	1.98	0.46
2:H:4046:LYS:N	2:H:4077:GLU:OE1	2.49	0.46
2:B:207:PHE:HB3	2:D:2326:ILE:O	2.16	0.46
2:B:1611:ILE:N	2:B:1620:GLN:O	2.44	0.46
2:B:4523:VAL:CG2	2:H:4808:ASP:CG	2.62	0.46
2:D:1043:LYS:HA	2:D:1046:ASN:HB2	1.97	0.46
2:D:4623:SER:O	2:D:4630:GLN:NE2	2.49	0.46
2:F:419:ILE:HG12	2:F:489:PHE:HE1	1.81	0.46
2:F:848:ARG:NH1	2:F:1605:LYS:O	2.48	0.46
2:F:1648:GLU:HA	2:F:1651:LEU:HB3	1.97	0.46
2:F:2148:GLY:O	2:F:2152:ASN:ND2	2.48	0.46
1:G:68:LEU:HA	1:G:103:LEU:HD23	1.97	0.46
2:H:681:HIS:HD2	2:H:799:LYS:HD3	1.80	0.46
2:H:1686:LEU:HA	2:H:1689:ILE:HD12	1.98	0.46
2:H:3956:GLN:HE21	2:H:3976:GLN:HE22	1.63	0.46
2:H:4138:GLU:HG2	2:H:4148:ARG:HB3	1.98	0.46
2:B:137:ARG:N	2:B:146:ASP:OD2	2.49	0.46
2:B:1686:LEU:HA	2:B:1689:ILE:HD12	1.98	0.46
2:B:2791:GLU:H	2:B:2903:ALA:HB3	1.81	0.46
2:B:4113:ASP:O	2:B:4117:GLN:N	2.46	0.46
2:D:137:ARG:N	2:D:146:ASP:OD2	2.49	0.46
2:D:681:HIS:HD2	2:D:799:LYS:HD3	1.80	0.46
2:D:1738:LEU:HD22	2:D:1739:PHE:H	1.79	0.46
2:D:1934:VAL:HG21	2:D:3618:VAL:HA	1.97	0.46
2:D:2116:ASP:OD2	2:D:2154:LYS:N	2.49	0.46
2:D:4046:LYS:N	2:D:4077:GLU:OE1	2.49	0.46
2:F:1736:ILE:HG12	2:F:1753:LEU:HD12	1.98	0.46
2:F:3924:TYR:O	2:F:3932:ASN:ND2	2.49	0.46
1:G:40:ARG:HB3	2:H:688:ALA:HB1	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:672:LYS:HA	2:H:760:ASP:HA	1.97	0.46
2:H:4002:ASP:HA	2:H:4115:ARG:HH22	1.81	0.46
2:B:506:HIS:HB3	2:B:564:ARG:HH22	1.81	0.46
2:B:2488:LEU:O	2:B:2492:GLY:N	2.48	0.46
2:B:4160:GLN:HG3	2:B:4205:ALA:HB2	1.98	0.46
2:B:4857:VAL:HG13	2:D:4863:ILE:HG21	1.96	0.46
2:D:125:TYR:CZ	2:D:417:ARG:HB3	2.50	0.46
2:D:2040:LEU:HD11	2:D:3634:GLU:HG2	1.98	0.46
2:D:2148:GLY:O	2:D:2152:ASN:ND2	2.48	0.46
2:D:3860:ARG:HH21	2:D:3932:ASN:HB2	1.80	0.46
2:F:21:VAL:HG13	2:F:217:ILE:HG13	1.98	0.46
2:F:3859:LEU:HD22	2:F:3871:ILE:HG21	1.98	0.46
2:F:4013:MET:N	2:F:4013:MET:SD	2.89	0.46
2:H:115:TYR:HB2	2:H:171:GLU:HA	1.98	0.46
2:H:3924:TYR:O	2:H:3932:ASN:ND2	2.49	0.46
1:A:28:GLY:N	1:A:37:ASP:O	2.37	0.46
2:B:21:VAL:HG13	2:B:217:ILE:HG13	1.98	0.46
2:B:125:TYR:CZ	2:B:417:ARG:HB3	2.50	0.46
2:B:2835:SER:O	2:B:2839:HIS:N	2.38	0.46
2:D:699:SER:OG	2:D:701:GLU:O	2.31	0.46
2:D:1143:GLN:HA	2:D:1151:HIS:HA	1.98	0.46
2:D:1716:THR:HA	2:D:1719:LEU:HD12	1.98	0.46
2:F:506:HIS:HB3	2:F:564:ARG:HH22	1.81	0.46
2:F:2040:LEU:HD11	2:F:3634:GLU:HG2	1.98	0.46
2:F:4160:GLN:HG3	2:F:4205:ALA:HB2	1.98	0.46
2:H:565:LEU:HG	2:H:604:HIS:CE1	2.51	0.46
2:H:4013:MET:SD	2:H:4013:MET:N	2.89	0.46
2:H:4160:GLN:HG3	2:H:4205:ALA:HB2	1.98	0.46
2:B:1443:VAL:O	2:B:1489:CYS:N	2.43	0.45
2:B:3924:TYR:O	2:B:3932:ASN:ND2	2.49	0.45
2:B:4857:VAL:CG1	2:D:4863:ILE:HG21	2.46	0.45
2:D:20:VAL:HG12	2:D:216:PRO:HA	1.99	0.45
2:D:506:HIS:HB3	2:D:564:ARG:HH22	1.81	0.45
2:D:1699:ARG:HH22	2:D:1821:LEU:HD11	1.80	0.45
2:D:3845:GLN:HB2	2:D:3920:THR:HG22	1.98	0.45
1:E:49:ARG:HB3	1:E:52:LYS:HE2	1.97	0.45
2:F:1210:ALA:N	2:F:1211:GLN:OE1	2.50	0.45
2:F:1484:ASN:H	2:F:1486:TYR:HA	1.80	0.45
2:F:3845:GLN:HB2	2:F:3920:THR:HG22	1.98	0.45
2:H:699:SER:OG	2:H:701:GLU:O	2.31	0.45
2:H:2837:ASP:OD1	2:H:2906:ARG:NE	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:115:TYR:HB2	2:B:171:GLU:HA	1.98	0.45
2:B:2102:ALA:O	2:B:2106:THR:N	2.46	0.45
2:B:4519:LEU:HA	2:H:4810:MET:HB3	1.97	0.45
2:D:101:MET:HE2	2:D:104:THR:HG22	1.98	0.45
2:D:115:TYR:HB2	2:D:171:GLU:HA	1.98	0.45
2:D:207:PHE:CG	2:F:2326:ILE:HG23	2.51	0.45
2:D:456:LEU:HD12	2:D:536:LEU:HD13	1.99	0.45
2:D:1736:ILE:HG12	2:D:1753:LEU:HD12	1.98	0.45
2:D:3779:LEU:HD13	2:D:3855:PHE:HD1	1.81	0.45
2:F:565:LEU:HG	2:F:604:HIS:CE1	2.51	0.45
2:H:195:SER:OG	2:H:196:TYR:N	2.49	0.45
2:H:731:HIS:ND1	2:H:739:ARG:O	2.50	0.45
2:H:1210:ALA:N	2:H:1211:GLN:OE1	2.50	0.45
2:H:1699:ARG:HH22	2:H:1821:LEU:HD11	1.80	0.45
2:H:2038:THR:OG1	2:H:2039:TYR:N	2.47	0.45
2:H:3682:LYS:HZ3	2:H:3684:GLU:HG2	1.81	0.45
1:A:14:THR:HB	1:A:68:LEU:HB2	1.99	0.45
1:A:49:ARG:HB3	1:A:52:LYS:HE2	1.97	0.45
2:B:456:LEU:HD12	2:B:536:LEU:HD13	1.99	0.45
2:B:2040:LEU:HD11	2:B:3634:GLU:HG2	1.98	0.45
2:B:2116:ASP:OD2	2:B:2154:LYS:N	2.49	0.45
2:B:2858:LYS:HG2	2:B:2872:LEU:HD22	1.97	0.45
2:D:1686:LEU:HA	2:D:1689:ILE:HD12	1.98	0.45
2:D:2791:GLU:H	2:D:2903:ALA:HB3	1.81	0.45
2:D:4160:GLN:HG3	2:D:4205:ALA:HB2	1.98	0.45
2:F:1143:GLN:HA	2:F:1151:HIS:HA	1.98	0.45
2:F:1929:PHE:HZ	2:F:2030:LEU:HB3	1.80	0.45
2:F:3897:ASP:OD1	2:F:3958:LYS:NZ	2.40	0.45
2:F:4623:SER:O	2:F:4630:GLN:NE2	2.49	0.45
2:H:935:MET:O	2:H:939:THR:OG1	2.34	0.45
2:H:1736:ILE:HG12	2:H:1753:LEU:HD12	1.98	0.45
2:H:2116:ASP:OD2	2:H:2154:LYS:N	2.49	0.45
2:H:3860:ARG:HH21	2:H:3932:ASN:HB2	1.81	0.45
2:B:1934:VAL:HG21	2:B:3618:VAL:HA	1.97	0.45
2:B:3831:LEU:HA	2:B:3832:GLN:HA	1.57	0.45
2:D:21:VAL:HG13	2:D:217:ILE:HG13	1.98	0.45
2:D:626:ARG:NH2	2:D:1668:GLY:O	2.36	0.45
2:D:672:LYS:HA	2:D:760:ASP:HA	1.97	0.45
2:D:1210:ALA:N	2:D:1211:GLN:OE1	2.50	0.45
2:H:4518:LEU:HD13	2:H:4521:TYR:HE2	1.79	0.45
2:B:1210:ALA:N	2:B:1211:GLN:OE1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3779:LEU:HD13	2:B:3855:PHE:HD1	1.82	0.45
2:B:4590:GLY:O	2:B:4594:LEU:N	2.44	0.45
2:B:4717:ASP:HB3	2:B:4720:PHE:HB3	1.97	0.45
2:D:565:LEU:HG	2:D:604:HIS:CE1	2.51	0.45
2:D:2135:MET:HA	2:D:2136:GLY:HA3	1.68	0.45
2:D:4002:ASP:HA	2:D:4115:ARG:HH22	1.81	0.45
2:F:835:GLU:HG3	2:F:837:SER:H	1.82	0.45
2:F:2116:ASP:OD2	2:F:2154:LYS:N	2.49	0.45
1:G:14:THR:HB	1:G:68:LEU:HB2	1.99	0.45
2:H:713:TRP:CZ3	2:H:1627:PHE:HB2	2.52	0.45
2:H:1143:GLN:HA	2:H:1151:HIS:HA	1.98	0.45
2:H:1929:PHE:HZ	2:H:2030:LEU:HB3	1.80	0.45
2:H:4052:ALA:O	2:H:4056:HIS:ND1	2.47	0.45
2:B:20:VAL:HG12	2:B:216:PRO:HA	1.99	0.45
2:B:4623:SER:O	2:B:4630:GLN:NE2	2.48	0.45
2:D:713:TRP:CZ3	2:D:1627:PHE:HB2	2.52	0.45
2:D:731:HIS:ND1	2:D:739:ARG:O	2.50	0.45
2:D:1846:ILE:HG12	2:D:1894:LEU:HB3	1.99	0.45
2:F:681:HIS:HD2	2:F:799:LYS:HD3	1.80	0.45
2:F:707:PRO:HD2	2:F:1604:LEU:HD22	1.98	0.45
2:H:835:GLU:HG3	2:H:837:SER:H	1.82	0.45
1:A:67:SER:H	1:A:70:GLN:HB3	1.82	0.45
2:B:180:ASP:HB3	2:B:211:LEU:HD22	1.99	0.45
2:B:4518:LEU:HD13	2:B:4521:TYR:HE2	1.80	0.45
2:D:3859:LEU:HD22	2:D:3871:ILE:HG21	1.98	0.45
2:F:2791:GLU:H	2:F:2903:ALA:HB3	1.81	0.45
2:F:3907:PHE:HD2	2:F:3968:LEU:HD11	1.82	0.45
1:G:49:ARG:HB3	1:G:52:LYS:HE2	1.97	0.45
2:H:614:LEU:HD23	2:H:617:LEU:HD12	1.99	0.45
2:H:1846:ILE:HG12	2:H:1894:LEU:HB3	1.99	0.45
2:B:18:ASP:HB2	2:B:69:LEU:HD12	1.99	0.45
2:B:419:ILE:HG12	2:B:489:PHE:HE1	1.81	0.45
2:B:680:ASP:HB2	2:B:799:LYS:HG3	1.98	0.45
2:B:4002:ASP:HA	2:B:4115:ARG:HH22	1.81	0.45
2:B:4046:LYS:N	2:B:4077:GLU:OE1	2.49	0.45
2:B:4131:GLN:HA	2:B:4134:LEU:HD23	1.99	0.45
2:B:4138:GLU:HA	2:B:4148:ARG:HA	1.99	0.45
2:D:835:GLU:HG3	2:D:837:SER:H	1.82	0.45
2:D:1433:PHE:HB2	2:D:1552:VAL:HA	1.99	0.45
2:D:1484:ASN:H	2:D:1486:TYR:HA	1.80	0.45
2:D:1620:GLN:HE21	2:D:1622:LEU:HD21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:3907:PHE:HD2	2:D:3968:LEU:HD11	1.82	0.45
2:D:4869:ASP:OD1	2:F:4875:ARG:HD3	2.17	0.45
2:F:180:ASP:HB3	2:F:211:LEU:HD22	1.99	0.45
2:F:195:SER:OG	2:F:196:TYR:N	2.49	0.45
2:F:207:PHE:CG	2:H:2326:ILE:HG23	2.52	0.45
2:F:1620:GLN:HE21	2:F:1622:LEU:HD21	1.81	0.45
2:F:1846:ILE:HG12	2:F:1894:LEU:HB3	1.99	0.45
2:F:2196:ASN:OD1	2:F:2199:ARG:NH1	2.50	0.45
2:F:4002:ASP:HA	2:F:4115:ARG:HH22	1.81	0.45
1:G:67:SER:H	1:G:70:GLN:HB3	1.82	0.45
2:H:180:ASP:HB3	2:H:211:LEU:HD22	1.99	0.45
2:H:2040:LEU:HD11	2:H:3634:GLU:HG2	1.98	0.45
2:H:2988:SER:O	2:H:2992:CYS:N	2.47	0.45
2:H:4138:GLU:HA	2:H:4148:ARG:HA	1.99	0.45
2:H:4717:ASP:HB3	2:H:4720:PHE:HB3	1.97	0.45
2:B:993:GLU:HG2	2:B:1051:ARG:HG2	1.99	0.45
2:B:1040:ASP:HA	2:B:1043:LYS:HB2	1.99	0.45
2:B:1484:ASN:H	2:B:1486:TYR:HA	1.80	0.45
2:B:2837:ASP:OD1	2:B:2906:ARG:NE	2.42	0.45
2:B:3892:TYR:O	2:B:3896:LYS:NZ	2.50	0.45
2:B:3907:PHE:HD2	2:B:3968:LEU:HD11	1.82	0.45
2:D:18:ASP:HB2	2:D:69:LEU:HD12	1.99	0.45
2:D:180:ASP:HB3	2:D:211:LEU:HD22	1.99	0.45
2:D:238:HIS:HB3	2:D:243:GLU:HB3	1.99	0.45
2:D:419:ILE:HG12	2:D:489:PHE:HE1	1.81	0.45
2:D:614:LEU:HD23	2:D:617:LEU:HD12	1.99	0.45
2:D:2464:ASP:OD1	2:D:2464:ASP:N	2.50	0.45
2:D:4131:GLN:HA	2:D:4134:LEU:HD23	1.99	0.45
2:F:49:LEU:HD12	2:F:201:LEU:HB3	1.99	0.45
2:F:935:MET:O	2:F:939:THR:OG1	2.34	0.45
2:F:1716:THR:HA	2:F:1719:LEU:HD12	1.98	0.45
2:F:4083:GLU:HA	2:F:4087:ARG:HD2	1.98	0.45
2:H:49:LEU:HD12	2:H:201:LEU:HB3	1.99	0.45
2:H:707:PRO:HD2	2:H:1604:LEU:HD22	1.98	0.45
2:B:565:LEU:HG	2:B:604:HIS:CE1	2.51	0.45
2:B:674:TYR:OH	2:B:676:GLU:OE2	2.24	0.45
2:B:731:HIS:ND1	2:B:739:ARG:O	2.50	0.45
2:B:1736:ILE:HG12	2:B:1753:LEU:HD12	1.98	0.45
2:B:1846:ILE:HG12	2:B:1894:LEU:HB3	1.99	0.45
2:B:3859:LEU:HD22	2:B:3871:ILE:HG21	1.98	0.45
1:C:67:SER:H	1:C:70:GLN:HB3	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1221:VAL:HG13	2:D:1224:LEU:HD12	1.99	0.45
2:D:2835:SER:O	2:D:2839:HIS:N	2.38	0.45
2:F:680:ASP:HB2	2:F:799:LYS:HG3	1.98	0.45
2:F:713:TRP:CZ3	2:F:1627:PHE:HB2	2.52	0.45
2:F:745:ASN:HB3	2:F:747:HIS:HB2	1.99	0.45
2:F:1799:VAL:O	2:F:1803:SER:HB3	2.17	0.45
2:H:1261:VAL:HA	2:H:1596:TRP:HH2	1.82	0.45
2:H:3779:LEU:HD13	2:H:3855:PHE:HD1	1.82	0.45
2:H:3845:GLN:HB2	2:H:3920:THR:HG22	1.98	0.45
2:B:195:SER:OG	2:B:196:TYR:N	2.50	0.44
2:B:835:GLU:HG3	2:B:837:SER:H	1.82	0.44
2:B:1799:VAL:O	2:B:1803:SER:HB3	2.17	0.44
2:B:3845:GLN:HB2	2:B:3920:THR:HG22	1.98	0.44
2:B:4875:ARG:HD3	2:H:4869:ASP:OD1	2.18	0.44
1:C:14:THR:HB	1:C:68:LEU:HB2	1.99	0.44
2:D:195:SER:OG	2:D:196:TYR:N	2.49	0.44
2:D:207:PHE:CG	2:F:2326:ILE:CG2	3.00	0.44
2:D:4089:HIS:O	2:D:4093:LYS:N	2.44	0.44
2:F:456:LEU:HD12	2:F:536:LEU:HD13	1.99	0.44
2:F:1115:VAL:O	2:F:1137:PHE:N	2.48	0.44
2:F:1170:GLU:O	2:F:1172:THR:N	2.49	0.44
2:F:1261:VAL:HA	2:F:1596:TRP:HH2	1.82	0.44
2:F:1433:PHE:HB2	2:F:1552:VAL:HA	1.99	0.44
2:H:456:LEU:HD12	2:H:536:LEU:HD13	1.99	0.44
2:H:680:ASP:HB2	2:H:799:LYS:HG3	1.98	0.44
2:H:993:GLU:HG2	2:H:1051:ARG:HG2	1.99	0.44
2:H:2157:TYR:HH	2:H:2203:TYR:HH	1.54	0.44
2:H:4733:GLY:HA3	2:H:4740:PHE:HD1	1.80	0.44
2:B:2212:GLN:HE22	2:B:2250:ASP:H	1.65	0.44
1:C:75:THR:HA	1:C:98:ILE:HA	1.99	0.44
2:D:4767:GLN:O	2:D:4771:THR:OG1	2.28	0.44
2:D:4832:ILE:HD11	2:D:4844:ARG:HG3	2.00	0.44
1:E:14:THR:HB	1:E:68:LEU:HB2	1.99	0.44
2:F:115:TYR:HB2	2:F:171:GLU:HA	1.98	0.44
2:F:731:HIS:ND1	2:F:739:ARG:O	2.50	0.44
2:H:1926:ILE:HD12	2:H:1926:ILE:HA	1.89	0.44
2:H:2127:ILE:HD12	2:H:2127:ILE:HA	1.89	0.44
2:H:2791:GLU:H	2:H:2903:ALA:HB3	1.81	0.44
2:H:3892:TYR:O	2:H:3896:LYS:NZ	2.50	0.44
2:B:713:TRP:CZ3	2:B:1627:PHE:HB2	2.52	0.44
2:D:49:LEU:HD12	2:D:201:LEU:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:680:ASP:HB2	2:D:799:LYS:HG3	1.98	0.44
2:D:1799:VAL:O	2:D:1803:SER:HB3	2.17	0.44
2:D:3831:LEU:HA	2:D:3832:GLN:HA	1.57	0.44
2:F:644:LEU:HD22	2:F:1632:ILE:HG22	1.99	0.44
2:F:1221:VAL:HG13	2:F:1224:LEU:HD12	1.99	0.44
2:F:3831:LEU:HA	2:F:3832:GLN:HA	1.57	0.44
2:H:21:VAL:HG13	2:H:217:ILE:HG13	1.98	0.44
2:H:644:LEU:HD22	2:H:1632:ILE:HG22	1.99	0.44
2:H:1602:GLN:HB3	2:H:1604:LEU:HD12	2.00	0.44
2:H:2196:ASN:OD1	2:H:2199:ARG:NH1	2.50	0.44
2:B:207:PHE:HZ	2:D:2326:ILE:HD12	1.72	0.44
2:B:1143:GLN:HA	2:B:1151:HIS:HA	1.98	0.44
2:B:1253:LYS:HE2	2:B:1257:GLN:HE21	1.82	0.44
2:B:2103:LEU:HA	2:B:2106:THR:HG22	2.00	0.44
2:D:434:ASP:O	2:D:438:LYS:NZ	2.43	0.44
2:D:745:ASN:HB3	2:D:747:HIS:HB2	1.99	0.44
2:D:935:MET:O	2:D:939:THR:OG1	2.34	0.44
2:D:1040:ASP:HA	2:D:1043:LYS:HB2	1.99	0.44
2:D:3682:LYS:HZ3	2:D:3684:GLU:HG2	1.82	0.44
2:D:4093:LYS:HE2	2:D:4093:LYS:HB3	1.84	0.44
2:F:20:VAL:HG12	2:F:216:PRO:HA	1.99	0.44
2:F:77:ALA:HA	2:H:3891:TRP:CZ3	2.53	0.44
2:F:1253:LYS:HE2	2:F:1257:GLN:HE21	1.82	0.44
2:F:1926:ILE:HD12	2:F:1926:ILE:HA	1.89	0.44
2:F:2464:ASP:N	2:F:2464:ASP:OD1	2.50	0.44
2:F:3779:LEU:HD13	2:F:3855:PHE:HD1	1.82	0.44
2:H:1245:ARG:HE	2:H:1692:LYS:HD2	1.83	0.44
2:B:49:LEU:HD12	2:B:201:LEU:HB3	1.99	0.44
2:B:1620:GLN:HE21	2:B:1622:LEU:HD21	1.81	0.44
2:B:1699:ARG:NH1	2:B:1816:PHE:O	2.51	0.44
2:B:1799:VAL:O	2:B:1803:SER:OG	2.30	0.44
2:B:2135:MET:HA	2:B:2136:GLY:HA3	1.68	0.44
2:B:4863:ILE:HG21	2:H:4857:VAL:CG1	2.47	0.44
2:B:4869:ASP:OD1	2:D:4875:ARG:HD3	2.16	0.44
2:D:234:LEU:HD21	2:D:277:LEU:HD12	2.00	0.44
2:D:434:ASP:OD1	2:D:504:ARG:NE	2.41	0.44
2:D:4138:GLU:HA	2:D:4148:ARG:HA	1.99	0.44
2:F:238:HIS:HB3	2:F:243:GLU:HB3	2.00	0.44
2:F:1245:ARG:HE	2:F:1692:LYS:HD2	1.83	0.44
2:H:20:VAL:HG12	2:H:216:PRO:HA	1.99	0.44
2:H:1253:LYS:HE2	2:H:1257:GLN:HE21	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:1699:ARG:NH1	2:H:1816:PHE:O	2.51	0.44
2:H:2103:LEU:HA	2:H:2106:THR:HG22	2.00	0.44
2:H:4173:PHE:HZ	2:H:4190:PHE:HA	1.83	0.44
2:B:2196:ASN:OD1	2:B:2199:ARG:NH1	2.50	0.44
2:B:4810:MET:HB3	2:D:4519:LEU:HA	1.98	0.44
2:D:993:GLU:HG2	2:D:1051:ARG:HG2	1.99	0.44
2:D:1114:ARG:HH12	2:D:1127:GLU:HB3	1.82	0.44
2:D:1245:ARG:HE	2:D:1692:LYS:HD2	1.83	0.44
2:D:3983:LEU:HD12	2:D:3983:LEU:HA	1.87	0.44
2:D:4083:GLU:HA	2:D:4087:ARG:HD2	1.98	0.44
1:E:67:SER:H	1:E:70:GLN:HB3	1.82	0.44
2:F:234:LEU:HD21	2:F:277:LEU:HD12	2.00	0.44
2:F:614:LEU:HD23	2:F:617:LEU:HD12	1.99	0.44
1:G:75:THR:HA	1:G:98:ILE:HA	1.99	0.44
2:H:238:HIS:HB3	2:H:243:GLU:HB3	1.99	0.44
2:H:1620:GLN:HE21	2:H:1622:LEU:HD21	1.81	0.44
2:H:2212:GLN:HE22	2:H:2250:ASP:H	1.65	0.44
2:B:844:ARG:NH1	2:B:849:ASP:OD2	2.51	0.44
2:B:1114:ARG:HH12	2:B:1127:GLU:HB3	1.82	0.44
2:B:4173:PHE:HZ	2:B:4190:PHE:HA	1.83	0.44
2:D:77:ALA:HA	2:F:3891:TRP:CZ3	2.52	0.44
2:D:4173:PHE:HZ	2:D:4190:PHE:HA	1.83	0.44
1:E:75:THR:HA	1:E:98:ILE:HA	1.99	0.44
2:F:993:GLU:HG2	2:F:1051:ARG:HG2	2.00	0.44
2:F:4832:ILE:HD11	2:F:4844:ARG:HG3	2.00	0.44
2:F:4869:ASP:OD1	2:H:4875:ARG:HD3	2.17	0.44
2:H:4131:GLN:HA	2:H:4134:LEU:HD23	1.99	0.44
2:H:4832:ILE:HD11	2:H:4844:ARG:HG3	2.00	0.44
2:B:238:HIS:HB3	2:B:243:GLU:HB3	2.00	0.44
2:B:644:LEU:HD22	2:B:1632:ILE:HG22	1.99	0.44
2:B:745:ASN:HB3	2:B:747:HIS:HB2	1.99	0.44
2:B:1245:ARG:HE	2:B:1692:LYS:HD2	1.83	0.44
2:B:1602:GLN:HB3	2:B:1604:LEU:HD12	2.00	0.44
2:D:412:GLU:O	2:D:415:THR:OG1	2.33	0.44
2:D:644:LEU:HD22	2:D:1632:ILE:HG22	1.99	0.44
2:D:2212:GLN:HE22	2:D:2250:ASP:H	1.65	0.44
2:D:4750:GLY:H	2:D:4755:ARG:NE	2.16	0.44
2:F:1228:THR:HA	2:F:1232:LEU:HD12	1.99	0.44
2:F:4857:VAL:HG11	2:H:4863:ILE:HG22	1.98	0.44
2:H:1086:ARG:N	2:H:1207:LEU:O	2.48	0.44
2:H:3800:SER:OG	2:H:3801:CYS:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:4083:GLU:HA	2:H:4087:ARG:HD2	1.99	0.44
2:B:614:LEU:HD23	2:B:617:LEU:HD12	1.99	0.44
2:B:1221:VAL:HG13	2:B:1224:LEU:HD12	1.99	0.44
2:B:1433:PHE:HB2	2:B:1552:VAL:HA	1.99	0.44
2:B:2123:SER:O	2:B:2126:GLN:NE2	2.51	0.44
2:B:2793:THR:OG1	2:B:2901:GLY:O	2.30	0.44
2:D:2123:SER:O	2:D:2126:GLN:NE2	2.51	0.44
2:D:2196:ASN:OD1	2:D:2199:ARG:NH1	2.50	0.44
2:D:2832:VAL:O	2:D:2895:LYS:NZ	2.44	0.44
2:D:4113:ASP:O	2:D:4117:GLN:N	2.46	0.44
2:F:1570:LEU:HD23	2:F:1570:LEU:HA	1.84	0.44
2:F:2127:ILE:HD12	2:F:2127:ILE:HA	1.89	0.44
2:F:4657:LYS:HD2	2:F:4658:TYR:CZ	2.53	0.44
2:H:18:ASP:HB2	2:H:69:LEU:HD12	1.99	0.44
2:H:1104:GLU:HG2	2:H:1216:ASN:HB2	2.00	0.44
2:H:1272:ARG:NH1	2:H:1587:HIS:O	2.51	0.44
2:B:1104:GLU:HG2	2:B:1216:ASN:HB2	2.00	0.43
2:B:1228:THR:HA	2:B:1232:LEU:HD12	1.99	0.43
2:B:1261:VAL:HA	2:B:1596:TRP:HH2	1.82	0.43
2:D:459:LEU:HD23	2:D:459:LEU:HA	1.86	0.43
2:D:1445:TRP:HB3	2:D:1539:LEU:HD13	2.00	0.43
2:D:3892:TYR:O	2:D:3896:LYS:NZ	2.50	0.43
2:D:4052:ALA:O	2:D:4056:HIS:ND1	2.47	0.43
2:F:18:ASP:HB2	2:F:69:LEU:HD12	1.99	0.43
2:F:766:ILE:HB	2:F:779:PHE:HB2	2.00	0.43
2:F:1434:PRO:HD2	2:F:1552:VAL:HG23	2.00	0.43
2:F:1445:TRP:HB3	2:F:1539:LEU:HD13	2.00	0.43
2:F:1699:ARG:NH1	2:F:1816:PHE:O	2.51	0.43
2:F:3892:TYR:O	2:F:3896:LYS:NZ	2.50	0.43
1:G:21:THR:OG1	1:G:49:ARG:NE	2.50	0.43
2:H:1221:VAL:HG13	2:H:1224:LEU:HD12	1.99	0.43
2:H:1799:VAL:O	2:H:1803:SER:HB3	2.17	0.43
2:B:3767:LEU:HA	2:B:3767:LEU:HD23	1.84	0.43
2:D:1261:VAL:HA	2:D:1596:TRP:HH2	1.82	0.43
2:D:4576:LEU:HD13	2:D:4579:LEU:HD22	2.01	0.43
2:F:4138:GLU:HA	2:F:4148:ARG:HA	1.99	0.43
2:F:4750:GLY:H	2:F:4755:ARG:NE	2.16	0.43
2:H:745:ASN:HB3	2:H:747:HIS:HB2	1.99	0.43
2:H:766:ILE:HB	2:H:779:PHE:HB2	2.00	0.43
2:H:1433:PHE:HB2	2:H:1552:VAL:HA	1.99	0.43
2:B:234:LEU:HD21	2:B:277:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2473:LEU:HD12	2:B:2477:TYR:HD2	1.83	0.43
2:B:4832:ILE:HD11	2:B:4844:ARG:HG3	2.00	0.43
2:B:4857:VAL:HG11	2:D:4863:ILE:HG22	2.01	0.43
2:D:1253:LYS:HE2	2:D:1257:GLN:HE21	1.82	0.43
2:D:1272:ARG:NH1	2:D:1587:HIS:O	2.51	0.43
2:D:4657:LYS:HD2	2:D:4658:TYR:CZ	2.53	0.43
2:F:1272:ARG:NH1	2:F:1587:HIS:O	2.51	0.43
2:F:4131:GLN:HA	2:F:4134:LEU:HD23	1.99	0.43
2:H:234:LEU:HD21	2:H:277:LEU:HD12	2.00	0.43
2:H:2835:SER:O	2:H:2839:HIS:N	2.38	0.43
2:H:4766:LYS:HE3	2:H:4770:LEU:HD11	2.00	0.43
2:B:1272:ARG:NH1	2:B:1587:HIS:O	2.51	0.43
2:B:4657:LYS:HD2	2:B:4658:TYR:CZ	2.53	0.43
1:C:44:LYS:HA	1:C:45:PRO:HD3	1.90	0.43
2:D:2473:LEU:HD12	2:D:2477:TYR:HD2	1.83	0.43
2:D:4750:GLY:H	2:D:4755:ARG:HE	1.66	0.43
2:F:439:LYS:HD3	2:F:441:LYS:HB2	2.01	0.43
2:F:699:SER:OG	2:F:701:GLU:O	2.31	0.43
2:F:1086:ARG:N	2:F:1207:LEU:O	2.48	0.43
2:F:1602:GLN:HB3	2:F:1604:LEU:HD12	2.00	0.43
2:F:1696:GLY:HA2	2:F:1699:ARG:HB3	2.00	0.43
2:F:2222:LEU:O	2:F:2226:SER:N	2.35	0.43
2:F:2793:THR:OG1	2:F:2901:GLY:O	2.30	0.43
2:F:4173:PHE:HZ	2:F:4190:PHE:HA	1.83	0.43
2:H:844:ARG:NH1	2:H:849:ASP:OD2	2.51	0.43
2:H:4657:LYS:HD2	2:H:4658:TYR:CZ	2.53	0.43
2:B:935:MET:O	2:B:939:THR:OG1	2.34	0.43
2:B:4083:GLU:HA	2:B:4087:ARG:HD2	1.99	0.43
2:B:4750:GLY:H	2:B:4755:ARG:NE	2.16	0.43
2:D:620:CYS:N	2:D:623:VAL:O	2.39	0.43
2:D:836:HIS:CE1	2:D:1610:ARG:HB2	2.54	0.43
2:D:1699:ARG:NH1	2:D:1816:PHE:O	2.51	0.43
2:D:4857:VAL:HG11	2:F:4863:ILE:HG22	2.00	0.43
2:F:306:LEU:HG	2:F:314:LEU:HD11	2.00	0.43
2:F:1040:ASP:HA	2:F:1043:LYS:HB2	1.99	0.43
2:F:1114:ARG:HH12	2:F:1127:GLU:HB3	1.82	0.43
2:H:306:LEU:HG	2:H:314:LEU:HD11	2.00	0.43
2:H:1040:ASP:HA	2:H:1043:LYS:HB2	2.00	0.43
2:B:861:ALA:HB3	2:B:863:THR:HG23	2.01	0.43
2:B:1505:LEU:O	2:B:1523:ASN:N	2.52	0.43
1:C:29:MET:HB3	1:C:35:LYS:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:796:ALA:HB3	2:D:798:ILE:HG13	2.00	0.43
2:D:4611:LEU:HD21	2:D:4617:TYR:HD2	1.84	0.43
2:F:836:HIS:CE1	2:F:1610:ARG:HB2	2.54	0.43
2:F:2103:LEU:HA	2:F:2106:THR:HG22	2.00	0.43
2:F:2123:SER:O	2:F:2126:GLN:NE2	2.51	0.43
2:F:2212:GLN:HE22	2:F:2250:ASP:H	1.65	0.43
2:F:4750:GLY:H	2:F:4755:ARG:HE	1.67	0.43
2:H:1466:THR:HG22	2:H:1482:ARG:HA	2.01	0.43
2:H:2102:ALA:O	2:H:2106:THR:N	2.46	0.43
2:H:2123:SER:O	2:H:2126:GLN:NE2	2.51	0.43
2:B:3797:LEU:HD23	2:B:3797:LEU:HA	1.88	0.43
2:B:4766:LYS:HE3	2:B:4770:LEU:HD11	2.00	0.43
2:D:1104:GLU:HG2	2:D:1216:ASN:HB2	2.00	0.43
2:D:1449:ASP:OD1	2:D:1449:ASP:N	2.52	0.43
2:D:1696:GLY:HA2	2:D:1699:ARG:HB3	2.00	0.43
2:D:2198:CYS:HA	2:D:2201:LEU:HD12	2.01	0.43
2:D:3997:GLY:HA2	2:D:4000:MET:SD	2.59	0.43
2:D:4023:LYS:HA	2:D:4026:ASP:HB2	2.01	0.43
2:D:4713:VAL:O	2:D:4716:THR:OG1	2.27	0.43
2:F:1176:THR:HG22	2:F:1181:ILE:HG12	2.01	0.43
2:F:2038:THR:OG1	2:F:2039:TYR:N	2.47	0.43
2:H:1114:ARG:HH12	2:H:1127:GLU:HB3	1.82	0.43
2:H:1190:LEU:HD12	2:H:1193:LYS:HE2	2.00	0.43
2:H:1228:THR:HA	2:H:1232:LEU:HD12	1.99	0.43
2:H:1445:TRP:HB3	2:H:1539:LEU:HD13	2.00	0.43
2:H:1675:ALA:O	2:H:1679:HIS:ND1	2.48	0.43
2:H:3907:PHE:HD2	2:H:3968:LEU:HD11	1.82	0.43
1:A:75:THR:HA	1:A:98:ILE:HA	1.99	0.43
2:B:256:GLN:O	2:B:304:LYS:NZ	2.48	0.43
2:B:452:VAL:O	2:B:456:LEU:HB2	2.19	0.43
2:B:1466:THR:HG22	2:B:1482:ARG:HA	2.01	0.43
2:B:3800:SER:OG	2:B:3801:CYS:N	2.51	0.43
2:B:4521:TYR:H	2:H:4810:MET:CG	2.32	0.43
2:D:861:ALA:HB3	2:D:863:THR:HG23	2.01	0.43
2:D:1434:PRO:HD2	2:D:1552:VAL:HG23	2.00	0.43
2:F:35:LEU:HA	2:F:51:SER:HA	2.01	0.43
2:F:207:PHE:CG	2:H:2326:ILE:CG2	3.01	0.43
2:F:1449:ASP:OD1	2:F:1449:ASP:N	2.52	0.43
2:F:1466:THR:HG22	2:F:1482:ARG:HA	2.01	0.43
2:F:4632:ASP:OD1	2:F:4709:TRP:NE1	2.48	0.43
2:H:233:VAL:HG22	2:H:276:ARG:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:297:LEU:HD23	2:H:297:LEU:HA	1.87	0.43
2:H:836:HIS:CE1	2:H:1610:ARG:HB2	2.54	0.43
2:H:2731:ASP:HB3	2:H:2826:ALA:HB2	2.00	0.43
2:H:4778:VAL:O	2:H:4782:TYR:HB2	2.19	0.43
2:B:644:LEU:HB2	2:B:1654:HIS:HD2	1.84	0.43
2:B:796:ALA:HB3	2:B:798:ILE:HG13	2.00	0.43
2:D:1228:THR:HA	2:D:1232:LEU:HD12	1.99	0.43
2:D:2103:LEU:HA	2:D:2106:THR:HG22	2.00	0.43
1:E:29:MET:HB3	1:E:35:LYS:HG2	2.01	0.43
2:F:434:ASP:OD1	2:F:504:ARG:NE	2.40	0.43
2:F:452:VAL:O	2:F:456:LEU:HB2	2.19	0.43
2:F:626:ARG:NH2	2:F:1668:GLY:O	2.36	0.43
2:F:2731:ASP:HB3	2:F:2826:ALA:HB2	2.00	0.43
2:F:3997:GLY:HA2	2:F:4000:MET:SD	2.59	0.43
2:F:4737:ASN:HA	2:F:4740:PHE:HB2	2.01	0.43
2:H:794:PHE:HE2	2:H:1621:CYS:HB2	1.83	0.43
2:H:796:ALA:HB3	2:H:798:ILE:HG13	2.00	0.43
2:H:2198:CYS:HA	2:H:2201:LEU:HD12	2.01	0.43
2:H:2473:LEU:HD12	2:H:2477:TYR:HD2	1.83	0.43
2:H:3831:LEU:HA	2:H:3832:GLN:HA	1.57	0.43
2:H:4737:ASN:HA	2:H:4740:PHE:HB2	2.01	0.43
2:B:647:ARG:HA	2:B:647:ARG:HD2	1.84	0.43
2:B:1170:GLU:O	2:B:1172:THR:N	2.49	0.43
2:B:1190:LEU:HD12	2:B:1193:LYS:HE2	2.00	0.43
2:B:2326:ILE:HG23	2:H:207:PHE:CG	2.53	0.43
2:D:256:GLN:O	2:D:304:LYS:NZ	2.48	0.43
2:F:305:TYR:HE2	2:F:319:LYS:HG2	1.83	0.43
2:F:844:ARG:NH1	2:F:849:ASP:OD2	2.51	0.43
2:F:1190:LEU:HD12	2:F:1193:LYS:HE2	2.00	0.43
2:F:2834:LEU:HB2	2:F:2839:HIS:CE1	2.54	0.43
2:F:4652:ARG:HA	2:F:4655:MET:HB2	2.01	0.43
1:G:29:MET:HB3	1:G:35:LYS:HG2	2.01	0.43
2:H:439:LYS:HD3	2:H:441:LYS:HB2	2.01	0.43
2:H:551:PHE:HD1	2:H:551:PHE:HA	1.70	0.43
2:B:101:MET:HE2	2:B:104:THR:HG22	2.01	0.42
2:B:794:PHE:HE2	2:B:1621:CYS:HB2	1.83	0.42
2:B:836:HIS:CE1	2:B:1610:ARG:HB2	2.54	0.42
2:B:1033:VAL:HG23	2:B:1038:LEU:HB3	2.01	0.42
2:B:1250:TRP:HB3	2:B:1600:PRO:HB2	2.01	0.42
2:B:1809:PRO:HA	2:B:1817:LEU:HD13	2.01	0.42
2:B:4046:LYS:HA	2:B:4049:PHE:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4576:LEU:HD13	2:B:4579:LEU:HD22	2.01	0.42
2:D:644:LEU:HB2	2:D:1654:HIS:HD2	1.84	0.42
2:D:1789:ALA:HA	2:D:1792:ILE:HD12	2.01	0.42
2:D:4834:ASP:OD1	2:D:4834:ASP:N	2.52	0.42
2:F:763:ALA:O	2:F:765:SER:N	2.51	0.42
2:F:1104:GLU:HG2	2:F:1216:ASN:HB2	2.00	0.42
2:F:4576:LEU:HD13	2:F:4579:LEU:HD22	2.01	0.42
2:H:452:VAL:O	2:H:456:LEU:HB2	2.19	0.42
2:H:644:LEU:HB2	2:H:1654:HIS:HD2	1.84	0.42
2:H:1250:TRP:HB3	2:H:1600:PRO:HB2	2.01	0.42
2:H:1676:LEU:HD23	2:H:1676:LEU:HA	1.87	0.42
2:H:2832:VAL:O	2:H:2895:LYS:NZ	2.44	0.42
2:H:4046:LYS:HA	2:H:4049:PHE:HB3	2.01	0.42
2:H:4652:ARG:HA	2:H:4655:MET:HB2	2.01	0.42
2:H:4750:GLY:H	2:H:4755:ARG:HE	1.66	0.42
1:A:29:MET:HB3	1:A:35:LYS:HG2	2.01	0.42
2:B:3730:ALA:HA	2:B:3733:HIS:CE1	2.54	0.42
2:B:4778:VAL:O	2:B:4782:TYR:HB2	2.19	0.42
2:B:4863:ILE:HG21	2:H:4857:VAL:HG13	1.96	0.42
2:D:233:VAL:HG22	2:D:276:ARG:HB2	2.01	0.42
2:D:1170:GLU:O	2:D:1172:THR:N	2.49	0.42
2:D:1602:GLN:HB3	2:D:1604:LEU:HD12	2.00	0.42
2:D:1611:ILE:N	2:D:1620:GLN:O	2.44	0.42
2:F:1676:LEU:HD23	2:F:1676:LEU:HA	1.87	0.42
2:F:2473:LEU:HD12	2:F:2477:TYR:HD2	1.83	0.42
2:F:4023:LYS:HA	2:F:4026:ASP:HB2	2.01	0.42
2:H:861:ALA:HB3	2:H:863:THR:HG23	2.01	0.42
2:H:1434:PRO:HD2	2:H:1552:VAL:HG23	2.00	0.42
2:H:1757:LEU:HD13	2:H:1757:LEU:HA	1.83	0.42
2:H:1809:PRO:HA	2:H:1817:LEU:HD13	2.01	0.42
2:H:4750:GLY:H	2:H:4755:ARG:NE	2.16	0.42
2:B:1090:ALA:HA	2:B:1249:MET:HG2	2.02	0.42
2:B:1434:PRO:HD2	2:B:1552:VAL:HG23	2.00	0.42
2:B:1789:ALA:HA	2:B:1792:ILE:HD12	2.01	0.42
2:B:3997:GLY:HA2	2:B:4000:MET:SD	2.59	0.42
2:D:77:ALA:HB2	2:F:3891:TRP:CH2	2.54	0.42
2:D:439:LYS:HD3	2:D:441:LYS:HB2	2.01	0.42
2:D:794:PHE:HE2	2:D:1621:CYS:HB2	1.83	0.42
2:D:1086:ARG:N	2:D:1207:LEU:O	2.48	0.42
2:D:1190:LEU:HD12	2:D:1193:LYS:HE2	2.00	0.42
2:D:1809:PRO:HA	2:D:1817:LEU:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:4652:ARG:HA	2:D:4655:MET:HB2	2.01	0.42
2:F:794:PHE:HE2	2:F:1621:CYS:HB2	1.83	0.42
2:F:1033:VAL:HG23	2:F:1038:LEU:HB3	2.01	0.42
2:F:1505:LEU:O	2:F:1523:ASN:N	2.52	0.42
2:F:3730:ALA:HA	2:F:3733:HIS:CE1	2.54	0.42
2:F:4202:GLN:O	2:F:4206:GLN:HB3	2.20	0.42
2:H:256:GLN:O	2:H:304:LYS:NZ	2.47	0.42
2:H:1153:GLY:N	2:H:1183:LEU:O	2.53	0.42
2:H:4061:GLN:O	2:H:4064:THR:OG1	2.27	0.42
2:B:35:LEU:HA	2:B:51:SER:HA	2.01	0.42
2:B:1696:GLY:HA2	2:B:1699:ARG:HB3	2.00	0.42
2:B:2422:SER:O	2:B:2426:SER:N	2.48	0.42
2:B:4652:ARG:HA	2:B:4655:MET:HB2	2.01	0.42
2:B:4792:LYS:HE3	2:B:4792:LYS:HB3	1.92	0.42
2:D:766:ILE:HB	2:D:779:PHE:HB2	2.00	0.42
2:D:844:ARG:NH1	2:D:849:ASP:OD2	2.51	0.42
2:D:1466:THR:HG22	2:D:1482:ARG:HA	2.01	0.42
2:D:1926:ILE:HD12	2:D:1926:ILE:HA	1.89	0.42
1:E:44:LYS:HA	1:E:45:PRO:HD3	1.90	0.42
2:F:875:PRO:HG2	2:F:878:LEU:HD12	2.02	0.42
2:F:3800:SER:OG	2:F:3801:CYS:N	2.51	0.42
2:F:4766:LYS:HE3	2:F:4770:LEU:HD11	2.00	0.42
2:F:4778:VAL:O	2:F:4782:TYR:HB2	2.19	0.42
2:H:1090:ALA:HA	2:H:1249:MET:HG2	2.02	0.42
2:H:1764:SER:N	2:H:1779:SER:O	2.53	0.42
2:B:207:PHE:CG	2:D:2326:ILE:HG23	2.55	0.42
2:B:306:LEU:HG	2:B:314:LEU:HD11	2.00	0.42
2:B:766:ILE:HB	2:B:779:PHE:HB2	2.00	0.42
2:B:875:PRO:HG2	2:B:878:LEU:HD12	2.02	0.42
2:B:897:LYS:HE2	2:B:915:HIS:CG	2.55	0.42
2:B:4811:LEU:O	2:B:4814:TYR:HB3	2.19	0.42
2:D:2894:LEU:HA	2:D:2897:LEU:HD12	2.02	0.42
2:D:4202:GLN:O	2:D:4206:GLN:HB3	2.20	0.42
2:F:796:ALA:HB3	2:F:798:ILE:HG13	2.00	0.42
2:F:897:LYS:HE2	2:F:915:HIS:CG	2.55	0.42
2:F:1628:MET:HB2	2:F:1687:TYR:HE2	1.84	0.42
2:F:3797:LEU:HD23	2:F:3797:LEU:HA	1.88	0.42
2:F:4611:LEU:HD21	2:F:4617:TYR:HD2	1.84	0.42
2:H:682:THR:H	2:H:751:THR:HG22	1.85	0.42
2:H:763:ALA:O	2:H:765:SER:N	2.52	0.42
2:H:1628:MET:HB2	2:H:1687:TYR:HE2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:1696:GLY:HA2	2:H:1699:ARG:HB3	2.00	0.42
2:H:3997:GLY:HA2	2:H:4000:MET:SD	2.59	0.42
2:H:4811:LEU:O	2:H:4814:TYR:HB3	2.20	0.42
2:B:233:VAL:HG22	2:B:276:ARG:HB2	2.01	0.42
2:B:394:HIS:CD2	2:B:396:GLU:H	2.38	0.42
2:B:1176:THR:HG22	2:B:1181:ILE:HG12	2.01	0.42
2:B:1628:MET:HB2	2:B:1687:TYR:HE2	1.84	0.42
2:B:1764:SER:N	2:B:1779:SER:O	2.53	0.42
2:B:3834:ASP:OD1	2:B:3834:ASP:N	2.53	0.42
2:B:4037:ASP:OD2	2:B:4041:LYS:N	2.53	0.42
2:D:416:ALA:HA	2:D:419:ILE:HD12	2.01	0.42
2:D:661:LEU:O	2:D:788:PHE:N	2.53	0.42
2:D:763:ALA:O	2:D:765:SER:N	2.51	0.42
2:D:1176:THR:HG22	2:D:1181:ILE:HG12	2.01	0.42
2:D:3762:LEU:HD12	2:D:3762:LEU:HA	1.86	0.42
2:D:3800:SER:OG	2:D:3801:CYS:N	2.51	0.42
2:F:233:VAL:HG22	2:F:276:ARG:HB2	2.00	0.42
2:F:420:ARG:HA	2:F:423:VAL:HB	2.02	0.42
2:F:644:LEU:HB2	2:F:1654:HIS:HD2	1.84	0.42
2:F:1611:ILE:N	2:F:1620:GLN:O	2.43	0.42
2:F:2894:LEU:HA	2:F:2897:LEU:HD12	2.02	0.42
2:H:394:HIS:CD2	2:H:396:GLU:H	2.38	0.42
2:H:897:LYS:HE2	2:H:915:HIS:CG	2.55	0.42
2:H:1505:LEU:O	2:H:1523:ASN:N	2.52	0.42
2:H:2222:LEU:O	2:H:2226:SER:N	2.35	0.42
2:H:4202:GLN:O	2:H:4206:GLN:HB3	2.20	0.42
2:H:4611:LEU:HD21	2:H:4617:TYR:HD2	1.84	0.42
2:B:52:THR:HG22	2:B:60:PRO:HG3	2.02	0.42
2:B:682:THR:H	2:B:751:THR:HG22	1.85	0.42
2:B:2464:ASP:OD1	2:B:2464:ASP:N	2.50	0.42
2:B:4093:LYS:HE2	2:B:4093:LYS:HB3	1.84	0.42
2:B:4750:GLY:H	2:B:4755:ARG:HE	1.66	0.42
1:C:21:THR:OG1	1:C:49:ARG:NE	2.50	0.42
2:D:305:TYR:HE2	2:D:319:LYS:HG2	1.84	0.42
2:D:306:LEU:HG	2:D:314:LEU:HD11	2.00	0.42
2:D:678:MET:O	2:D:801:ARG:N	2.46	0.42
2:D:4518:LEU:HD13	2:D:4521:TYR:HE2	1.80	0.42
2:F:77:ALA:HB2	2:H:3891:TRP:CH2	2.54	0.42
2:F:121:LEU:HD23	2:F:121:LEU:HA	1.86	0.42
2:F:647:ARG:HD2	2:F:647:ARG:HA	1.84	0.42
2:F:861:ALA:HB3	2:F:863:THR:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:1153:GLY:N	2:F:1183:LEU:O	2.53	0.42
2:F:2198:CYS:HA	2:F:2201:LEU:HD12	2.01	0.42
2:H:35:LEU:HA	2:H:51:SER:HA	2.01	0.42
2:H:1170:GLU:O	2:H:1172:THR:N	2.49	0.42
1:A:82:TYR:OH	2:B:1768:PHE:O	2.28	0.42
2:B:305:TYR:HE2	2:B:319:LYS:HG2	1.84	0.42
2:B:439:LYS:HD3	2:B:441:LYS:HB2	2.01	0.42
2:B:1153:GLY:N	2:B:1183:LEU:O	2.53	0.42
2:B:1445:TRP:HB3	2:B:1539:LEU:HD13	2.00	0.42
2:B:2198:CYS:HA	2:B:2201:LEU:HD12	2.01	0.42
2:B:2731:ASP:HB3	2:B:2826:ALA:HB2	2.00	0.42
2:B:2988:SER:O	2:B:2992:CYS:N	2.47	0.42
2:D:52:THR:HG22	2:D:60:PRO:HG3	2.02	0.42
2:D:3834:ASP:N	2:D:3834:ASP:OD1	2.53	0.42
2:F:1250:TRP:HB3	2:F:1600:PRO:HB2	2.01	0.42
2:F:1572:LYS:HB3	2:F:1584:PRO:HA	2.01	0.42
2:F:1626:GLN:O	2:F:1687:TYR:OH	2.36	0.42
2:F:2843:GLU:OE2	2:F:2875:TYR:OH	2.34	0.42
2:F:2988:SER:O	2:F:2992:CYS:N	2.47	0.42
2:F:4635:VAL:O	2:F:4638:THR:OG1	2.31	0.42
2:H:52:THR:HG22	2:H:60:PRO:HG3	2.02	0.42
2:H:305:TYR:HE2	2:H:319:LYS:HG2	1.83	0.42
2:H:4036:TYR:HE2	2:H:4048:ASP:HB3	1.85	0.42
2:H:4093:LYS:HE2	2:H:4093:LYS:HB3	1.84	0.42
2:H:4576:LEU:HD13	2:H:4579:LEU:HD22	2.01	0.42
1:A:15:PHE:HA	1:A:67:SER:HA	2.01	0.42
2:B:661:LEU:O	2:B:788:PHE:N	2.53	0.42
2:B:3891:TRP:CZ3	2:H:77:ALA:HA	2.54	0.42
2:B:4737:ASN:HA	2:B:4740:PHE:HB2	2.01	0.42
2:D:1628:MET:HB2	2:D:1687:TYR:HE2	1.84	0.42
2:D:3730:ALA:HA	2:D:3733:HIS:CE1	2.54	0.42
2:D:4766:LYS:HE3	2:D:4770:LEU:HD11	2.00	0.42
1:E:15:PHE:HA	1:E:67:SER:HA	2.02	0.42
2:F:4808:ASP:CG	2:H:4523:VAL:CG2	2.66	0.42
2:B:554:SER:O	2:B:558:LEU:N	2.49	0.42
2:B:763:ALA:O	2:B:765:SER:N	2.51	0.42
2:B:2731:ASP:OD1	2:B:2822:TYR:OH	2.30	0.42
2:B:2834:LEU:HB2	2:B:2839:HIS:CE1	2.54	0.42
2:B:3897:ASP:OD1	2:B:3958:LYS:NZ	2.40	0.42
2:B:4808:ASP:OD2	2:D:4523:VAL:HG11	2.20	0.42
2:D:452:VAL:O	2:D:456:LEU:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1572:LYS:HB3	2:D:1584:PRO:HA	2.02	0.42
2:D:1607:ASP:HB3	2:D:1608:VAL:HG23	2.02	0.42
2:D:3854:ASP:OD1	2:D:3854:ASP:N	2.53	0.42
2:D:4036:TYR:HE2	2:D:4048:ASP:HB3	1.85	0.42
2:D:4037:ASP:OD2	2:D:4041:LYS:N	2.53	0.42
2:D:4737:ASN:HA	2:D:4740:PHE:HB2	2.01	0.42
2:D:4767:GLN:CG	2:F:4753:THR:OG1	2.67	0.42
2:D:4810:MET:HB3	2:F:4519:LEU:HA	2.01	0.42
2:F:119:ILE:HD13	2:F:162:ILE:HD11	2.02	0.42
2:F:195:SER:HB3	2:F:202:HIS:HB2	2.02	0.42
2:F:394:HIS:CD2	2:F:396:GLU:H	2.38	0.42
2:F:3696:MET:O	2:F:3699:SER:OG	2.28	0.42
2:H:1176:THR:HG22	2:H:1181:ILE:HG12	2.01	0.42
2:H:2834:LEU:HB2	2:H:2839:HIS:CE1	2.54	0.42
2:B:123:HIS:CD2	2:B:126:SER:H	2.38	0.41
2:B:626:ARG:NH2	2:B:1668:GLY:O	2.36	0.41
2:B:3677:LEU:HD23	2:B:3677:LEU:HA	1.91	0.41
2:B:4863:ILE:HG22	2:H:4857:VAL:HG13	1.98	0.41
2:D:394:HIS:CD2	2:D:396:GLU:H	2.38	0.41
2:D:682:THR:H	2:D:751:THR:HG22	1.85	0.41
2:D:897:LYS:HE2	2:D:915:HIS:CG	2.55	0.41
2:D:1090:ALA:HA	2:D:1249:MET:HG2	2.02	0.41
2:D:1250:TRP:HB3	2:D:1600:PRO:HB2	2.01	0.41
2:F:620:CYS:N	2:F:623:VAL:O	2.39	0.41
2:F:4036:TYR:HE2	2:F:4048:ASP:HB3	1.85	0.41
2:F:4046:LYS:HA	2:F:4049:PHE:HB3	2.01	0.41
2:F:4834:ASP:N	2:F:4834:ASP:OD1	2.52	0.41
2:H:1033:VAL:HG23	2:H:1038:LEU:HB3	2.01	0.41
2:H:2834:LEU:HD22	2:H:2838:LEU:HB3	2.02	0.41
2:H:4037:ASP:OD2	2:H:4041:LYS:N	2.53	0.41
2:B:1607:ASP:HB3	2:B:1608:VAL:HG23	2.02	0.41
2:B:2326:ILE:CG2	2:H:207:PHE:CG	3.02	0.41
2:B:2894:LEU:HA	2:B:2897:LEU:HD12	2.02	0.41
2:B:3983:LEU:HD12	2:B:3983:LEU:HA	1.88	0.41
2:D:35:LEU:HA	2:D:51:SER:HA	2.01	0.41
2:D:119:ILE:HD13	2:D:162:ILE:HD11	2.02	0.41
2:D:875:PRO:HG2	2:D:878:LEU:HD12	2.02	0.41
2:D:4808:ASP:OD2	2:F:4523:VAL:HG11	2.19	0.41
2:F:52:THR:HG22	2:F:60:PRO:HG3	2.02	0.41
2:F:290:ARG:HA	2:F:353:GLU:HG2	2.02	0.41
2:F:1809:PRO:HA	2:F:1817:LEU:HD13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:3993:ASN:HD22	2:F:4110:MET:HA	1.84	0.41
2:H:130:LEU:HA	2:H:149:LEU:HD23	2.03	0.41
2:H:195:SER:HB3	2:H:202:HIS:HB2	2.02	0.41
2:H:420:ARG:HA	2:H:423:VAL:HB	2.02	0.41
2:H:585:ALA:HA	2:H:588:ILE:HD12	2.02	0.41
2:H:647:ARG:HD2	2:H:647:ARG:HA	1.84	0.41
2:H:2730:HIS:CE1	2:H:2764:LEU:HD11	2.56	0.41
2:H:4023:LYS:HA	2:H:4026:ASP:HB2	2.01	0.41
2:B:551:PHE:HD1	2:B:551:PHE:HA	1.70	0.41
2:B:4810:MET:CG	2:D:4521:TYR:H	2.34	0.41
2:D:195:SER:HB3	2:D:202:HIS:HB2	2.02	0.41
2:D:2731:ASP:HB3	2:D:2826:ALA:HB2	2.00	0.41
2:D:3993:ASN:HD22	2:D:4110:MET:HA	1.84	0.41
2:D:4046:LYS:HA	2:D:4049:PHE:HB3	2.01	0.41
2:D:4778:VAL:O	2:D:4782:TYR:HB2	2.19	0.41
1:E:21:THR:OG1	1:E:49:ARG:NE	2.50	0.41
2:F:64:ILE:H	2:F:64:ILE:HG13	1.74	0.41
2:F:1090:ALA:HA	2:F:1249:MET:HG2	2.01	0.41
2:F:1607:ASP:HB3	2:F:1608:VAL:HG23	2.02	0.41
2:F:3760:LEU:HD23	2:F:3760:LEU:HA	1.89	0.41
2:F:3854:ASP:N	2:F:3854:ASP:OD1	2.53	0.41
2:F:4037:ASP:OD2	2:F:4041:LYS:N	2.53	0.41
2:F:4810:MET:HB3	2:H:4519:LEU:HA	2.01	0.41
2:H:412:GLU:O	2:H:415:THR:OG1	2.33	0.41
2:H:1253:LYS:HD2	2:H:1255:LEU:HB2	2.02	0.41
2:H:1607:ASP:HB3	2:H:1608:VAL:HG23	2.02	0.41
2:H:2464:ASP:N	2:H:2464:ASP:OD1	2.50	0.41
2:H:3730:ALA:HA	2:H:3733:HIS:CE1	2.54	0.41
2:B:77:ALA:HA	2:D:3891:TRP:CZ3	2.56	0.41
2:B:372:LEU:HD11	2:B:391:ALA:HB1	2.03	0.41
2:B:416:ALA:O	2:B:420:ARG:NH2	2.51	0.41
2:B:782:PHE:HZ	2:B:1467:VAL:HG22	1.86	0.41
2:B:2730:HIS:CE1	2:B:2764:LEU:HD11	2.56	0.41
2:D:1505:LEU:O	2:D:1523:ASN:N	2.52	0.41
2:D:2834:LEU:HB2	2:D:2839:HIS:CE1	2.54	0.41
2:D:4011:VAL:HA	2:D:4014:ILE:HG12	2.03	0.41
2:F:682:THR:H	2:F:751:THR:HG22	1.85	0.41
2:F:1843:LEU:O	2:F:1846:ILE:N	2.54	0.41
2:F:3682:LYS:HZ3	2:F:3684:GLU:HA	1.84	0.41
2:B:195:SER:HB3	2:B:202:HIS:HB2	2.02	0.41
2:B:416:ALA:HA	2:B:419:ILE:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2834:LEU:HD22	2:B:2838:LEU:HB3	2.02	0.41
2:B:3682:LYS:HZ3	2:B:3684:GLU:HG2	1.85	0.41
2:D:420:ARG:HA	2:D:423:VAL:HB	2.02	0.41
2:D:1843:LEU:O	2:D:1846:ILE:N	2.54	0.41
2:F:1764:SER:N	2:F:1779:SER:O	2.53	0.41
2:F:3983:LEU:HD12	2:F:3983:LEU:HA	1.87	0.41
2:F:4189:LEU:HA	2:F:4192:ASN:HD22	1.86	0.41
2:H:123:HIS:CD2	2:H:126:SER:H	2.38	0.41
2:H:1156:TRP:CZ3	2:H:1158:ALA:HA	2.56	0.41
2:H:1572:LYS:HB3	2:H:1584:PRO:HA	2.02	0.41
2:H:1738:LEU:HD21	2:H:2039:TYR:HE1	1.86	0.41
2:H:2843:GLU:OE2	2:H:2875:TYR:OH	2.34	0.41
2:H:3797:LEU:HA	2:H:3797:LEU:HD23	1.88	0.41
2:H:3834:ASP:OD1	2:H:3834:ASP:N	2.53	0.41
2:H:4189:LEU:HA	2:H:4192:ASN:HD22	1.86	0.41
2:B:585:ALA:HA	2:B:588:ILE:HD12	2.02	0.41
2:B:1169:THR:OG1	2:B:1170:GLU:N	2.54	0.41
2:B:1285:VAL:HG12	2:B:1286:THR:HG23	2.03	0.41
2:B:3854:ASP:OD1	2:B:3854:ASP:N	2.53	0.41
2:B:4863:ILE:HG22	2:H:4857:VAL:HG11	2.01	0.41
1:C:15:PHE:HA	1:C:67:SER:HA	2.02	0.41
2:D:554:SER:O	2:D:558:LEU:N	2.49	0.41
2:D:1033:VAL:HG23	2:D:1038:LEU:HB3	2.01	0.41
2:D:2063:ILE:O	2:D:2067:MET:HG2	2.21	0.41
2:D:3897:ASP:OD1	2:D:3958:LYS:NZ	2.40	0.41
2:D:4811:LEU:O	2:D:4814:TYR:HB3	2.19	0.41
2:F:1156:TRP:CZ3	2:F:1158:ALA:HA	2.56	0.41
2:F:1253:LYS:HD2	2:F:1255:LEU:HB2	2.02	0.41
2:F:1267:HIS:NE2	2:F:1293:GLN:OE1	2.53	0.41
2:F:1738:LEU:HD21	2:F:2039:TYR:HE1	1.86	0.41
2:F:2063:ILE:O	2:F:2067:MET:HG2	2.21	0.41
2:F:4811:LEU:O	2:F:4814:TYR:HB3	2.20	0.41
2:F:4889:CYS:HB2	2:F:4892:CYS:HB3	2.03	0.41
2:H:290:ARG:HA	2:H:353:GLU:HG2	2.02	0.41
2:H:875:PRO:HG2	2:H:878:LEU:HD12	2.02	0.41
2:H:1449:ASP:OD1	2:H:1449:ASP:N	2.52	0.41
2:B:290:ARG:HA	2:B:353:GLU:HG2	2.02	0.41
2:B:1156:TRP:CZ3	2:B:1158:ALA:HA	2.56	0.41
2:B:3993:ASN:HD22	2:B:4110:MET:HA	1.84	0.41
2:B:4189:LEU:HA	2:B:4192:ASN:HD22	1.86	0.41
2:D:123:HIS:CD2	2:D:126:SER:H	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:585:ALA:HA	2:D:588:ILE:HD12	2.02	0.41
2:D:782:PHE:HZ	2:D:1467:VAL:HG22	1.86	0.41
2:D:1153:GLY:N	2:D:1183:LEU:O	2.53	0.41
2:D:1156:TRP:CZ3	2:D:1158:ALA:HA	2.56	0.41
2:D:4810:MET:CG	2:F:4521:TYR:H	2.34	0.41
2:F:2730:HIS:CE1	2:F:2764:LEU:HD11	2.56	0.41
2:F:4865:GLY:HA2	2:H:4868:ILE:HD11	2.03	0.41
2:H:64:ILE:H	2:H:64:ILE:HG13	1.74	0.41
2:H:372:LEU:HD11	2:H:391:ALA:HB1	2.03	0.41
2:H:554:SER:O	2:H:558:LEU:N	2.49	0.41
2:H:1169:THR:OG1	2:H:1170:GLU:N	2.54	0.41
2:H:4834:ASP:OD1	2:H:4834:ASP:N	2.52	0.41
2:B:411:GLU:HA	2:B:414:ARG:HB2	2.03	0.41
2:B:1843:LEU:O	2:B:1846:ILE:N	2.54	0.41
2:B:2063:ILE:O	2:B:2067:MET:HG2	2.21	0.41
2:F:416:ALA:HA	2:F:419:ILE:HD12	2.02	0.41
2:F:1757:LEU:HA	2:F:1757:LEU:HD13	1.83	0.41
2:F:4125:SER:HA	2:F:4128:ASN:HD22	1.86	0.41
2:F:4857:VAL:HG13	2:H:4863:ILE:HG22	1.96	0.41
2:H:416:ALA:HA	2:H:419:ILE:HD12	2.02	0.41
2:H:1843:LEU:HD23	2:H:1843:LEU:HA	1.88	0.41
2:H:3993:ASN:HD22	2:H:4110:MET:HA	1.84	0.41
2:H:4011:VAL:HA	2:H:4014:ILE:HG12	2.03	0.41
2:H:4518:LEU:HD23	2:H:4518:LEU:H	1.86	0.41
1:A:21:THR:OG1	1:A:49:ARG:NE	2.50	0.41
2:B:26:ALA:O	2:B:33:GLN:N	2.49	0.41
2:B:130:LEU:HA	2:B:149:LEU:HD23	2.03	0.41
2:B:420:ARG:HA	2:B:423:VAL:HB	2.02	0.41
2:B:1676:LEU:HD23	2:B:1676:LEU:HA	1.87	0.41
2:B:1738:LEU:HD21	2:B:2039:TYR:HE1	1.86	0.41
2:B:3762:LEU:HD12	2:B:3762:LEU:HA	1.86	0.41
2:B:4202:GLN:O	2:B:4206:GLN:HB3	2.20	0.41
2:B:4611:LEU:HD21	2:B:4617:TYR:HD2	1.84	0.41
2:D:130:LEU:HA	2:D:149:LEU:HD23	2.03	0.41
2:D:150:GLN:NE2	2:D:152:ASP:O	2.54	0.41
2:D:486:GLN:OE1	2:D:547:ASN:ND2	2.54	0.41
2:D:3767:LEU:HD23	2:D:3767:LEU:HA	1.84	0.41
2:D:4780:TYR:OH	2:F:4518:LEU:HB2	2.21	0.41
2:D:4889:CYS:HB2	2:D:4892:CYS:HB3	2.03	0.41
2:F:123:HIS:CD2	2:F:126:SER:H	2.38	0.41
2:F:415:THR:O	2:F:419:ILE:HG13	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:1440:ASN:HB2	2:F:1548:THR:HG21	2.03	0.41
2:F:1789:ALA:HA	2:F:1792:ILE:HD12	2.01	0.41
2:F:1999:ASP:O	2:F:2003:ASP:N	2.54	0.41
1:G:15:PHE:HA	1:G:67:SER:HA	2.02	0.41
2:H:121:LEU:HD23	2:H:121:LEU:HA	1.86	0.41
2:H:1157:GLN:N	2:H:1160:ASP:OD2	2.54	0.41
2:H:1177:LEU:N	2:H:1180:GLU:O	2.54	0.41
2:H:1285:VAL:HG12	2:H:1286:THR:HG23	2.03	0.41
2:H:1999:ASP:O	2:H:2003:ASP:N	2.54	0.41
2:H:2011:GLU:O	2:H:2027:ARG:NH2	2.54	0.41
2:H:2063:ILE:O	2:H:2067:MET:HG2	2.21	0.41
2:H:2894:LEU:HA	2:H:2897:LEU:HD12	2.02	0.41
2:H:3831:LEU:HA	2:H:3831:LEU:HD23	1.85	0.41
2:B:486:GLN:OE1	2:B:547:ASN:ND2	2.54	0.41
2:B:1136:ALA:HB3	2:B:1145:TRP:HB2	2.03	0.41
2:B:2326:ILE:HD12	2:H:207:PHE:HZ	1.72	0.41
2:B:4834:ASP:N	2:B:4834:ASP:OD1	2.52	0.41
2:D:1440:ASN:HB2	2:D:1548:THR:HG21	2.03	0.41
2:D:1753:LEU:HD11	2:D:1921:HIS:CD2	2.56	0.41
2:D:1764:SER:N	2:D:1779:SER:O	2.53	0.41
2:D:2549:LEU:O	2:D:2553:VAL:N	2.54	0.41
2:D:4189:LEU:HA	2:D:4192:ASN:HD22	1.86	0.41
2:F:123:HIS:NE2	2:F:125:TYR:HB3	2.36	0.41
2:F:130:LEU:HA	2:F:149:LEU:HD23	2.03	0.41
2:F:486:GLN:OE1	2:F:547:ASN:ND2	2.54	0.41
2:F:2088:LEU:O	2:F:2092:GLN:HG2	2.21	0.41
2:F:2177:VAL:HG22	2:F:2221:TYR:CZ	2.56	0.41
2:F:4113:ASP:O	2:F:4117:GLN:N	2.46	0.41
2:H:486:GLN:OE1	2:H:547:ASN:ND2	2.54	0.41
2:H:1255:LEU:HA	2:H:1256:PRO:HD3	1.88	0.41
2:H:1611:ILE:N	2:H:1620:GLN:O	2.44	0.41
2:H:1789:ALA:HA	2:H:1792:ILE:HD12	2.01	0.41
2:H:2298:ARG:HD3	2:H:2298:ARG:HA	1.90	0.41
2:H:3767:LEU:HA	2:H:3767:LEU:HD23	1.84	0.41
2:B:123:HIS:NE2	2:B:125:TYR:HB3	2.36	0.40
2:B:699:SER:OG	2:B:701:GLU:O	2.31	0.40
2:B:1572:LYS:HB3	2:B:1584:PRO:HA	2.02	0.40
2:B:1655:TYR:OH	2:B:1659:ARG:NH2	2.51	0.40
2:B:3871:ILE:O	2:B:3874:SER:OG	2.40	0.40
2:B:4113:ASP:HB2	2:B:4116:LEU:HB3	2.03	0.40
2:D:1177:LEU:N	2:D:1180:GLU:O	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:4011:VAL:HA	2:F:4014:ILE:HG12	2.03	0.40
2:H:119:ILE:HD13	2:H:162:ILE:HD11	2.02	0.40
2:H:1136:ALA:HB3	2:H:1145:TRP:HB2	2.03	0.40
2:H:1843:LEU:O	2:H:1846:ILE:N	2.54	0.40
2:H:1940:ASN:O	2:H:1944:ARG:HG2	2.21	0.40
2:H:2177:VAL:HG22	2:H:2221:TYR:CZ	2.56	0.40
2:H:3663:ASP:HA	2:H:3664:PRO:HD3	1.95	0.40
2:B:1157:GLN:N	2:B:1160:ASP:OD2	2.54	0.40
2:B:1177:LEU:N	2:B:1180:GLU:O	2.54	0.40
2:B:1255:LEU:HA	2:B:1256:PRO:HD3	1.88	0.40
2:B:2177:VAL:HG22	2:B:2221:TYR:CZ	2.56	0.40
2:B:4011:VAL:HA	2:B:4014:ILE:HG12	2.03	0.40
2:B:4036:TYR:HE2	2:B:4048:ASP:HB3	1.85	0.40
2:B:4889:CYS:HB2	2:B:4892:CYS:HB3	2.03	0.40
2:D:411:GLU:HA	2:D:414:ARG:HB2	2.03	0.40
2:D:415:THR:O	2:D:419:ILE:HG13	2.21	0.40
2:D:1253:LYS:HD2	2:D:1255:LEU:HB2	2.02	0.40
2:D:1645:THR:H	2:D:1645:THR:HG23	1.68	0.40
2:D:4957:ASP:OD1	2:D:4957:ASP:N	2.54	0.40
2:F:191:TYR:N	2:F:206:ALA:O	2.54	0.40
2:H:411:GLU:HA	2:H:414:ARG:HB2	2.03	0.40
2:H:782:PHE:HZ	2:H:1467:VAL:HG22	1.86	0.40
2:H:2157:TYR:OH	2:H:2203:TYR:OH	2.26	0.40
2:H:3871:ILE:O	2:H:3874:SER:OG	2.40	0.40
2:H:3983:LEU:HD12	2:H:3983:LEU:HA	1.88	0.40
2:H:4713:VAL:O	2:H:4716:THR:OG1	2.27	0.40
2:B:119:ILE:HD13	2:B:162:ILE:HD11	2.02	0.40
2:B:717:GLY:H	2:B:722:LEU:HB3	1.86	0.40
2:B:1137:PHE:CE2	2:B:1139:GLY:HA2	2.57	0.40
2:B:1709:ILE:HD13	2:B:1709:ILE:HA	1.94	0.40
2:B:1753:LEU:HD11	2:B:1921:HIS:CD2	2.56	0.40
2:B:4023:LYS:HA	2:B:4026:ASP:HB2	2.01	0.40
2:B:4808:ASP:CG	2:D:4523:VAL:CG2	2.62	0.40
2:D:1157:GLN:N	2:D:1160:ASP:OD2	2.54	0.40
2:D:1999:ASP:O	2:D:2003:ASP:N	2.54	0.40
2:D:2157:TYR:OH	2:D:2203:TYR:OH	2.26	0.40
2:D:2834:LEU:HD22	2:D:2838:LEU:HB3	2.02	0.40
1:E:78:PRO:HA	1:E:81:ALA:HB3	2.04	0.40
2:F:297:LEU:HD23	2:F:297:LEU:HA	1.87	0.40
2:F:585:ALA:HA	2:F:588:ILE:HD12	2.02	0.40
2:F:653:SER:OG	2:F:794:PHE:O	2.31	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:2011:GLU:O	2:F:2027:ARG:NH2	2.54	0.40
2:H:415:THR:O	2:H:419:ILE:HG13	2.21	0.40
2:H:517:VAL:HG23	2:H:520:ARG:NE	2.35	0.40
2:H:678:MET:O	2:H:801:ARG:N	2.46	0.40
2:H:3762:LEU:HA	2:H:3762:LEU:HD12	1.86	0.40
2:H:4113:ASP:HB2	2:H:4116:LEU:HB3	2.03	0.40
2:B:3893:TYR:CE2	2:B:3899:ILE:HG23	2.57	0.40
2:D:123:HIS:NE2	2:D:125:TYR:HB3	2.36	0.40
2:D:228:LEU:HD23	2:D:228:LEU:HA	1.82	0.40
2:D:976:TYR:CZ	2:D:978:PRO:HG3	2.57	0.40
2:D:1136:ALA:HB3	2:D:1145:TRP:HB2	2.03	0.40
2:D:1505:LEU:HD23	2:D:1505:LEU:HA	1.97	0.40
2:D:2088:LEU:O	2:D:2092:GLN:HG2	2.21	0.40
2:D:4518:LEU:H	2:D:4518:LEU:HD23	1.86	0.40
2:F:459:LEU:HD23	2:F:459:LEU:HA	1.86	0.40
2:F:973:THR:HG23	2:F:977:LYS:HB3	2.04	0.40
2:F:976:TYR:CZ	2:F:978:PRO:HG3	2.57	0.40
2:F:1177:LEU:N	2:F:1180:GLU:O	2.54	0.40
2:F:1305:SER:HB2	2:F:1593:HIS:CD2	2.57	0.40
2:F:1707:ILE:HG22	2:F:1712:SER:HB3	2.04	0.40
2:F:4518:LEU:HD23	2:F:4518:LEU:H	1.86	0.40
2:H:626:ARG:NH2	2:H:1668:GLY:O	2.36	0.40
2:H:1902:PRO:HA	2:H:1905:LEU:HB3	2.04	0.40
2:H:4125:SER:HA	2:H:4128:ASN:HD22	1.86	0.40
2:B:1253:LYS:HD2	2:B:1255:LEU:HB2	2.02	0.40
2:B:2088:LEU:O	2:B:2092:GLN:HG2	2.21	0.40
2:B:4518:LEU:H	2:B:4518:LEU:HD23	1.86	0.40
2:D:517:VAL:HG23	2:D:520:ARG:NE	2.35	0.40
2:D:647:ARG:HD2	2:D:647:ARG:HA	1.84	0.40
2:D:4113:ASP:HB2	2:D:4116:LEU:HB3	2.03	0.40
2:F:36:CYS:O	2:F:50:GLU:N	2.55	0.40
2:F:412:GLU:O	2:F:415:THR:OG1	2.33	0.40
2:H:36:CYS:O	2:H:50:GLU:N	2.55	0.40
2:H:1753:LEU:HD11	2:H:1921:HIS:CD2	2.56	0.40
2:H:1833:ILE:HG22	2:H:1834:PHE:H	1.87	0.40
2:H:1905:LEU:HB2	2:H:2081:LEU:HD12	2.04	0.40
2:H:3893:TYR:CE2	2:H:3899:ILE:HG23	2.57	0.40

There are no symmetry-related clashes.



## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	105/108 (97%)	95 (90%)	10 (10%)	0	100	100
1	C	105/108 (97%)	95 (90%)	10 (10%)	0	100	100
1	E	105/108 (97%)	95 (90%)	10 (10%)	0	100	100
1	G	105/108 (97%)	95 (90%)	10 (10%)	0	100	100
2	B	3365/4968 (68%)	2969 (88%)	382 (11%)	14 (0%)	34	72
2	D	3365/4968 (68%)	2969 (88%)	382 (11%)	14 (0%)	34	72
2	F	3365/4968 (68%)	2968 (88%)	383 (11%)	14 (0%)	34	72
2	H	3365/4968 (68%)	2968 (88%)	383 (11%)	14 (0%)	34	72
All	All	13880/20304 (68%)	12254 (88%)	1570 (11%)	56 (0%)	38	72

All (56) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	143	LEU
2	B	4595	LYS
2	D	143	LEU
2	D	4595	LYS
2	F	143	LEU
2	F	4595	LYS
2	H	143	LEU
2	H	4595	LYS
2	B	730	LEU
2	B	4518	LEU
2	D	730	LEU
2	D	4518	LEU
2	F	730	LEU
2	F	4518	LEU
2	H	730	LEU
2	H	4518	LEU
2	B	142	LYS

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Mol	Chain	Res	Type
2	B	1580	PRO
2	B	4071	ALA
2	D	142	LYS
2	D	1580	PRO
2	D	4071	ALA
2	F	142	LYS
2	F	1580	PRO
2	F	4071	ALA
2	H	142	LYS
2	H	1580	PRO
2	H	4071	ALA
2	B	4903	PRO
2	F	4903	PRO
2	H	4903	PRO
2	B	2233	PRO
2	D	2233	PRO
2	D	4903	PRO
2	F	2233	PRO
2	H	2233	PRO
2	B	1848	PRO
2	D	1848	PRO
2	F	1848	PRO
2	H	1848	PRO
2	B	3803	VAL
2	D	3803	VAL
2	F	3803	VAL
2	B	853	PRO
2	B	1535	PRO
2	D	853	PRO
2	F	853	PRO
2	H	853	PRO
2	H	1535	PRO
2	H	3803	VAL
2	B	828	PRO
2	D	828	PRO
2	D	1535	PRO
2	F	828	PRO
2	F	1535	PRO
2	H	828	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	88/89 (99%)	87 (99%)	1 (1%)	73	85
1	C	88/89 (99%)	87 (99%)	1 (1%)	73	85
1	E	88/89 (99%)	87 (99%)	1 (1%)	73	85
1	G	88/89 (99%)	87 (99%)	1 (1%)	73	85
2	B	2688/4355 (62%)	2655 (99%)	33 (1%)	71	84
2	D	2688/4355 (62%)	2655 (99%)	33 (1%)	71	84
2	F	2688/4355 (62%)	2655 (99%)	33 (1%)	71	84
2	H	2689/4355 (62%)	2655 (99%)	34 (1%)	69	82
All	All	11105/17776 (62%)	10968 (99%)	137 (1%)	72	84

All (137) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ARG
2	B	44	ASN
2	B	84	ASN
2	B	298	ARG
2	B	420	ARG
2	B	531	ASN
2	B	628	ASN
2	B	658	ASN
2	B	841	LYS
2	B	854	THR
2	B	925	PRO
2	B	990	PRO
2	B	1054	VAL
2	B	1089	ARG
2	B	2027	ARG
2	B	2118	ILE
2	B	2206	ARG
2	B	2211	ASN
2	B	2328	ARG

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Mol	Chain	Res	Type
2	B	3813	ASN
2	B	3870	ASN
2	B	3906	ASN
2	B	4087	ARG
2	B	4136	ARG
2	B	4171	ARG
2	B	4179	ASN
2	B	4499	ASN
2	B	4518	LEU
2	B	4519	LEU
2	B	4652	ARG
2	B	4792	LYS
2	B	4809	ASP
2	B	4900	ASP
2	B	4902	VAL
1	C	13	ARG
2	D	44	ASN
2	D	84	ASN
2	D	298	ARG
2	D	420	ARG
2	D	531	ASN
2	D	628	ASN
2	D	658	ASN
2	D	841	LYS
2	D	854	THR
2	D	925	PRO
2	D	950	VAL
2	D	990	PRO
2	D	1089	ARG
2	D	2027	ARG
2	D	2118	ILE
2	D	2206	ARG
2	D	2211	ASN
2	D	2328	ARG
2	D	3813	ASN
2	D	3870	ASN
2	D	3906	ASN
2	D	4087	ARG
2	D	4136	ARG
2	D	4171	ARG
2	D	4179	ASN
2	D	4499	ASN

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Mol	Chain	Res	Type
2	D	4518	LEU
2	D	4519	LEU
2	D	4652	ARG
2	D	4792	LYS
2	D	4809	ASP
2	D	4900	ASP
2	D	4902	VAL
1	E	13	ARG
2	F	44	ASN
2	F	84	ASN
2	F	298	ARG
2	F	420	ARG
2	F	531	ASN
2	F	628	ASN
2	F	658	ASN
2	F	841	LYS
2	F	854	THR
2	F	925	PRO
2	F	950	VAL
2	F	990	PRO
2	F	1089	ARG
2	F	2027	ARG
2	F	2118	ILE
2	F	2206	ARG
2	F	2211	ASN
2	F	2328	ARG
2	F	3813	ASN
2	F	3870	ASN
2	F	3906	ASN
2	F	4087	ARG
2	F	4136	ARG
2	F	4171	ARG
2	F	4179	ASN
2	F	4499	ASN
2	F	4518	LEU
2	F	4519	LEU
2	F	4652	ARG
2	F	4792	LYS
2	F	4809	ASP
2	F	4900	ASP
2	F	4902	VAL
1	G	13	ARG

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Mol	Chain	Res	Type
2	H	44	ASN
2	H	84	ASN
2	H	298	ARG
2	H	420	ARG
2	H	531	ASN
2	H	628	ASN
2	H	658	ASN
2	H	841	LYS
2	H	854	THR
2	H	925	PRO
2	H	950	VAL
2	H	990	PRO
2	H	1054	VAL
2	H	1089	ARG
2	H	2027	ARG
2	H	2118	ILE
2	H	2206	ARG
2	H	2211	ASN
2	H	2328	ARG
2	H	3813	ASN
2	H	3870	ASN
2	H	3906	ASN
2	H	4087	ARG
2	H	4136	ARG
2	H	4171	ARG
2	H	4179	ASN
2	H	4499	ASN
2	H	4518	LEU
2	H	4519	LEU
2	H	4652	ARG
2	H	4792	LYS
2	H	4809	ASP
2	H	4900	ASP
2	H	4902	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (198) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	23	GLN
2	B	44	ASN
2	B	57	ASN
2	B	123	HIS

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Mol	Chain	Res	Type
2	B	150	GLN
2	B	252	HIS
2	B	293	GLN
2	B	375	GLN
2	B	394	HIS
2	B	398	HIS
2	B	477	ASN
2	B	531	ASN
2	B	547	ASN
2	B	628	ASN
2	B	681	HIS
2	B	776	GLN
2	B	888	ASN
2	B	1147	GLN
2	B	1265	HIS
2	B	1620	GLN
2	B	1656	HIS
2	B	1691	ASN
2	B	1722	ASN
2	B	1772	ASN
2	B	1918	GLN
2	B	1940	ASN
2	B	2060	GLN
2	B	2152	ASN
2	B	2225	ASN
2	B	2317	ASN
2	B	2831	ASN
2	B	3813	ASN
2	B	3852	ASN
2	B	3856	GLN
2	B	3870	ASN
2	B	3904	GLN
2	B	3906	ASN
2	B	3919	ASN
2	B	3954	HIS
2	B	3956	GLN
2	B	3965	GLN
2	B	3993	ASN
2	B	3999	GLN
2	B	4128	ASN
2	B	4160	GLN
2	B	4499	ASN

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Mol	Chain	Res	Type
2	B	4643	ASN
2	B	4817	HIS
2	B	4878	GLN
2	B	4918	ASN
2	D	23	GLN
2	D	44	ASN
2	D	57	ASN
2	D	123	HIS
2	D	150	GLN
2	D	252	HIS
2	D	293	GLN
2	D	375	GLN
2	D	394	HIS
2	D	398	HIS
2	D	477	ASN
2	D	531	ASN
2	D	547	ASN
2	D	628	ASN
2	D	681	HIS
2	D	888	ASN
2	D	1147	GLN
2	D	1265	HIS
2	D	1620	GLN
2	D	1656	HIS
2	D	1691	ASN
2	D	1722	ASN
2	D	1772	ASN
2	D	1918	GLN
2	D	1921	HIS
2	D	1940	ASN
2	D	2060	GLN
2	D	2152	ASN
2	D	2225	ASN
2	D	2317	ASN
2	D	2831	ASN
2	D	3813	ASN
2	D	3852	ASN
2	D	3856	GLN
2	D	3870	ASN
2	D	3904	GLN
2	D	3906	ASN
2	D	3919	ASN

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Mol	Chain	Res	Type
2	D	3954	HIS
2	D	3956	GLN
2	D	3965	GLN
2	D	3993	ASN
2	D	3999	GLN
2	D	4128	ASN
2	D	4160	GLN
2	D	4179	ASN
2	D	4499	ASN
2	D	4643	ASN
2	D	4817	HIS
2	D	4878	GLN
2	D	4918	ASN
2	F	23	GLN
2	F	44	ASN
2	F	57	ASN
2	F	123	HIS
2	F	150	GLN
2	F	252	HIS
2	F	293	GLN
2	F	375	GLN
2	F	394	HIS
2	F	398	HIS
2	F	477	ASN
2	F	531	ASN
2	F	547	ASN
2	F	628	ASN
2	F	681	HIS
2	F	776	GLN
2	F	888	ASN
2	F	1147	GLN
2	F	1265	HIS
2	F	1620	GLN
2	F	1656	HIS
2	F	1691	ASN
2	F	1772	ASN
2	F	1918	GLN
2	F	1940	ASN
2	F	2152	ASN
2	F	2225	ASN
2	F	2317	ASN
2	F	2831	ASN

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Mol	Chain	Res	Type
2	F	3813	ASN
2	F	3852	ASN
2	F	3856	GLN
2	F	3870	ASN
2	F	3904	GLN
2	F	3906	ASN
2	F	3919	ASN
2	F	3954	HIS
2	F	3956	GLN
2	F	3965	GLN
2	F	3993	ASN
2	F	3999	GLN
2	F	4128	ASN
2	F	4160	GLN
2	F	4179	ASN
2	F	4499	ASN
2	F	4643	ASN
2	F	4817	HIS
2	F	4878	GLN
2	F	4918	ASN
2	H	23	GLN
2	H	44	ASN
2	H	57	ASN
2	H	123	HIS
2	H	150	GLN
2	H	252	HIS
2	H	293	GLN
2	H	375	GLN
2	H	394	HIS
2	H	398	HIS
2	H	477	ASN
2	H	531	ASN
2	H	547	ASN
2	H	628	ASN
2	H	681	HIS
2	H	888	ASN
2	H	1147	GLN
2	H	1265	HIS
2	H	1620	GLN
2	H	1656	HIS
2	H	1691	ASN
2	H	1772	ASN

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Mol	Chain	Res	Type
2	H	1918	GLN
2	H	1940	ASN
2	H	2152	ASN
2	H	2225	ASN
2	H	2317	ASN
2	H	2831	ASN
2	H	3813	ASN
2	H	3852	ASN
2	H	3856	GLN
2	H	3870	ASN
2	H	3904	GLN
2	H	3906	ASN
2	H	3919	ASN
2	H	3954	HIS
2	H	3956	GLN
2	H	3965	GLN
2	H	3993	ASN
2	H	3999	GLN
2	H	4128	ASN
2	H	4160	GLN
2	H	4179	ASN
2	H	4499	ASN
2	H	4643	ASN
2	H	4817	HIS
2	H	4878	GLN
2	H	4918	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

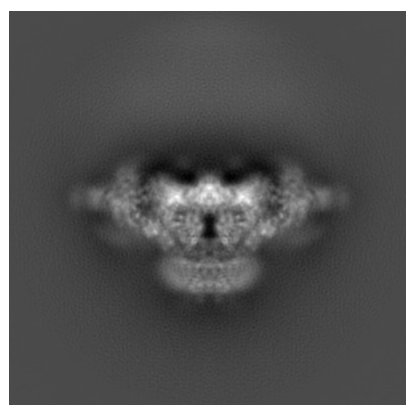
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9824. These allow visual inspection of the internal detail of the map and identification of artifacts.

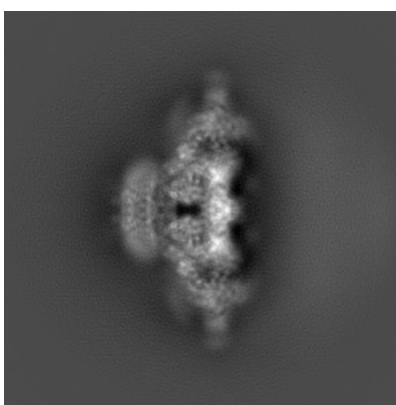
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

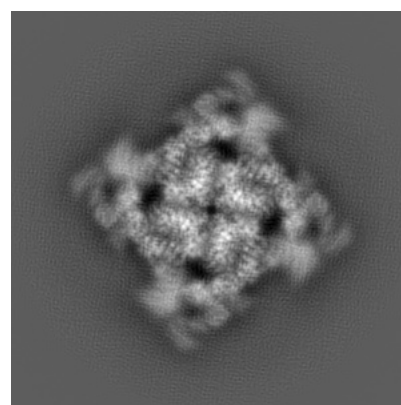
#### 6.1.1 Primary map



X



Y

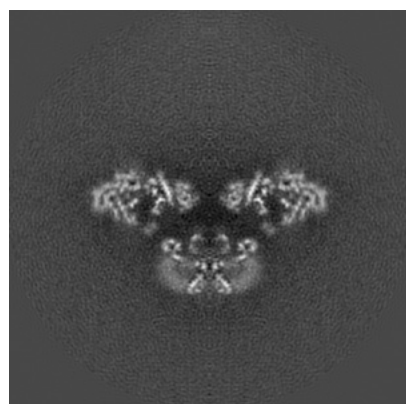


Z

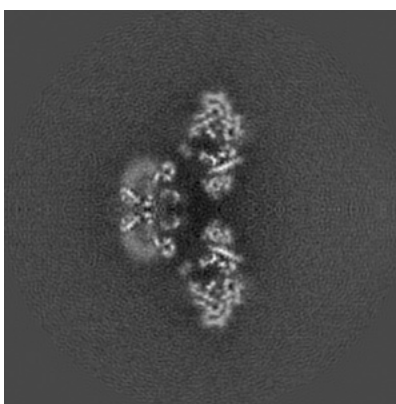
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

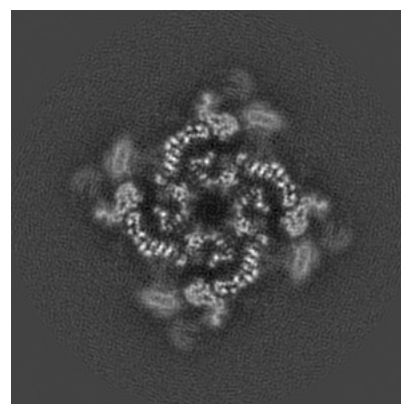
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

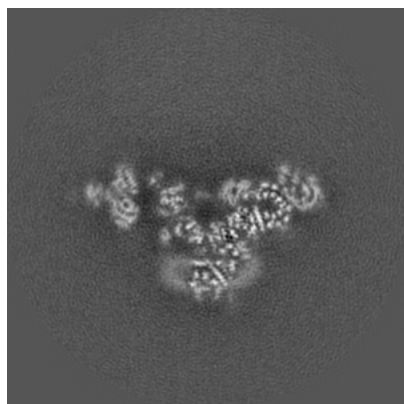


Z Index: 200

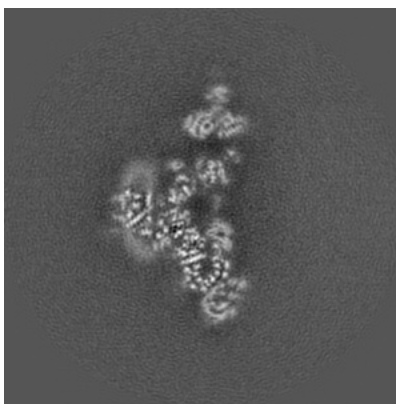
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

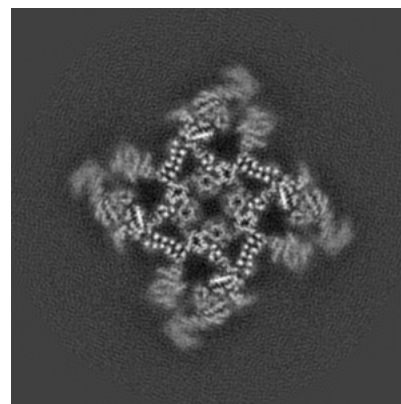
### 6.3.1 Primary map



X Index: 189



Y Index: 189

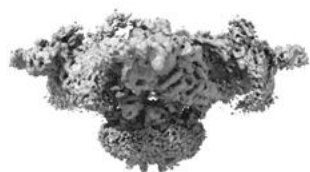


Z Index: 209

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

## 6.4 Orthogonal surface views [i](#)

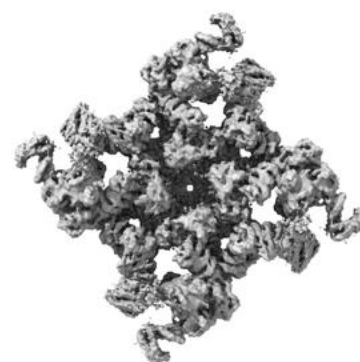
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

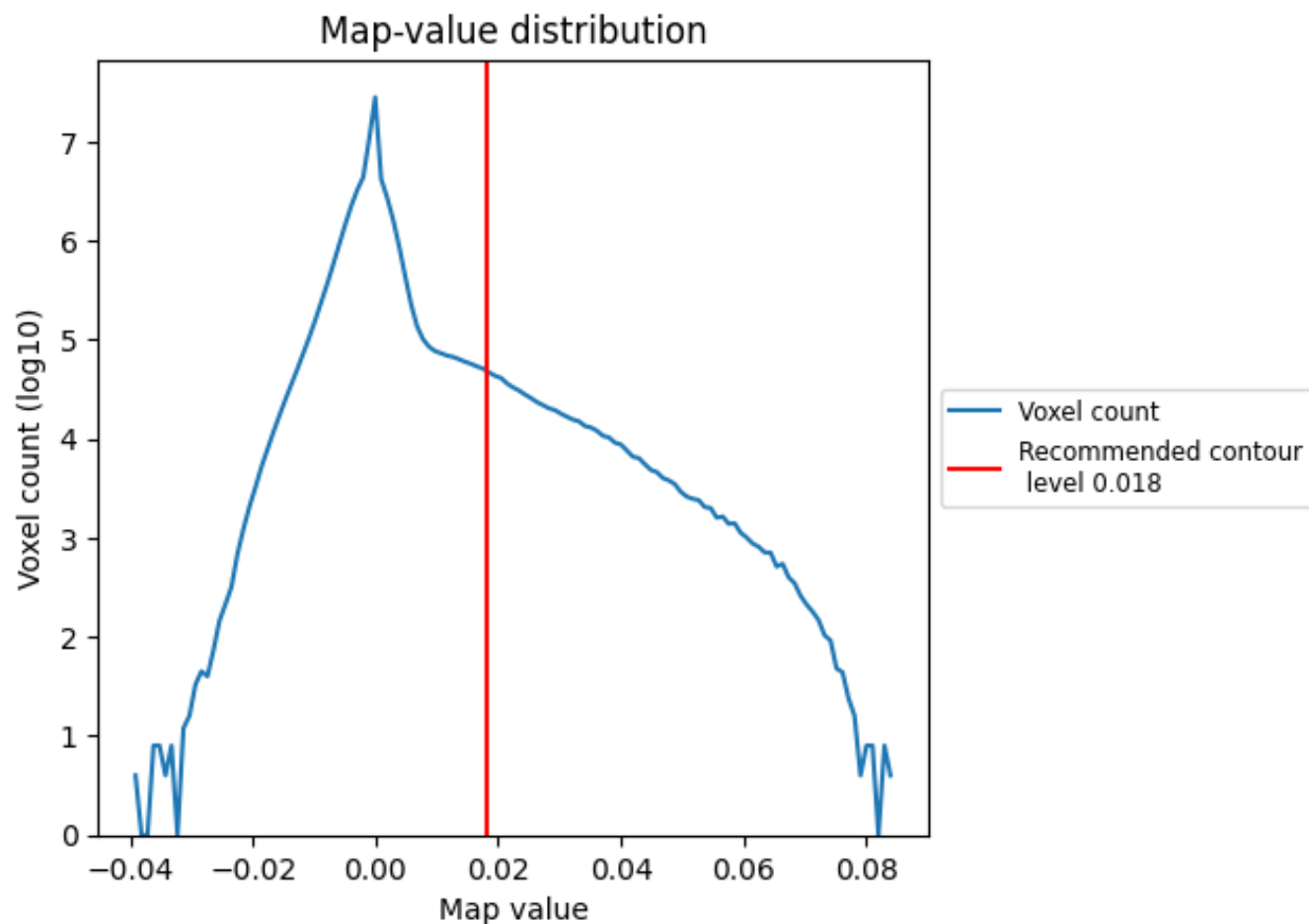
## 6.5 Mask visualisation

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.

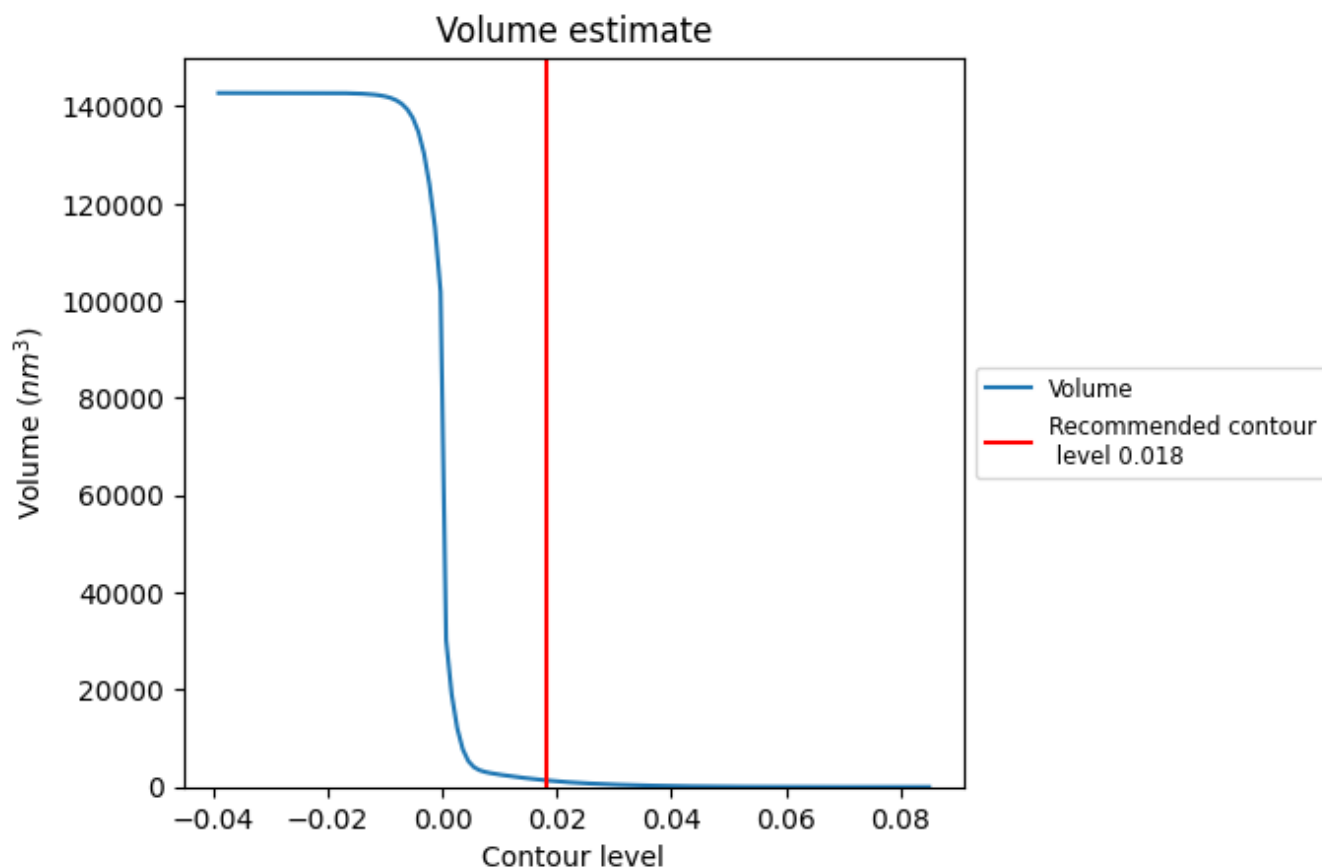
### 7.1 Map-value distribution [i](#)



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.



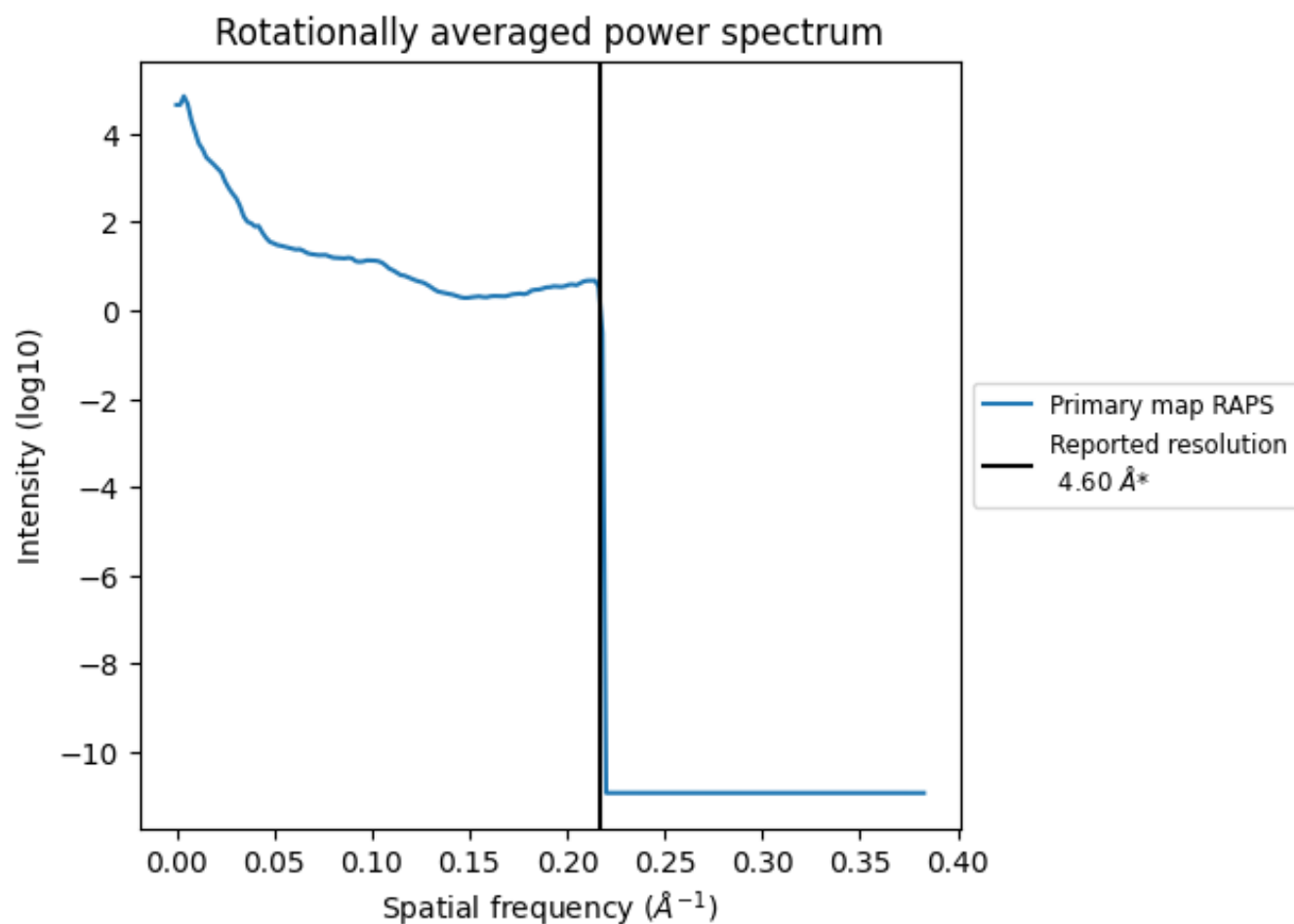
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1373 nm<sup>3</sup>; this corresponds to an approximate mass of 1240 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 ⓘ

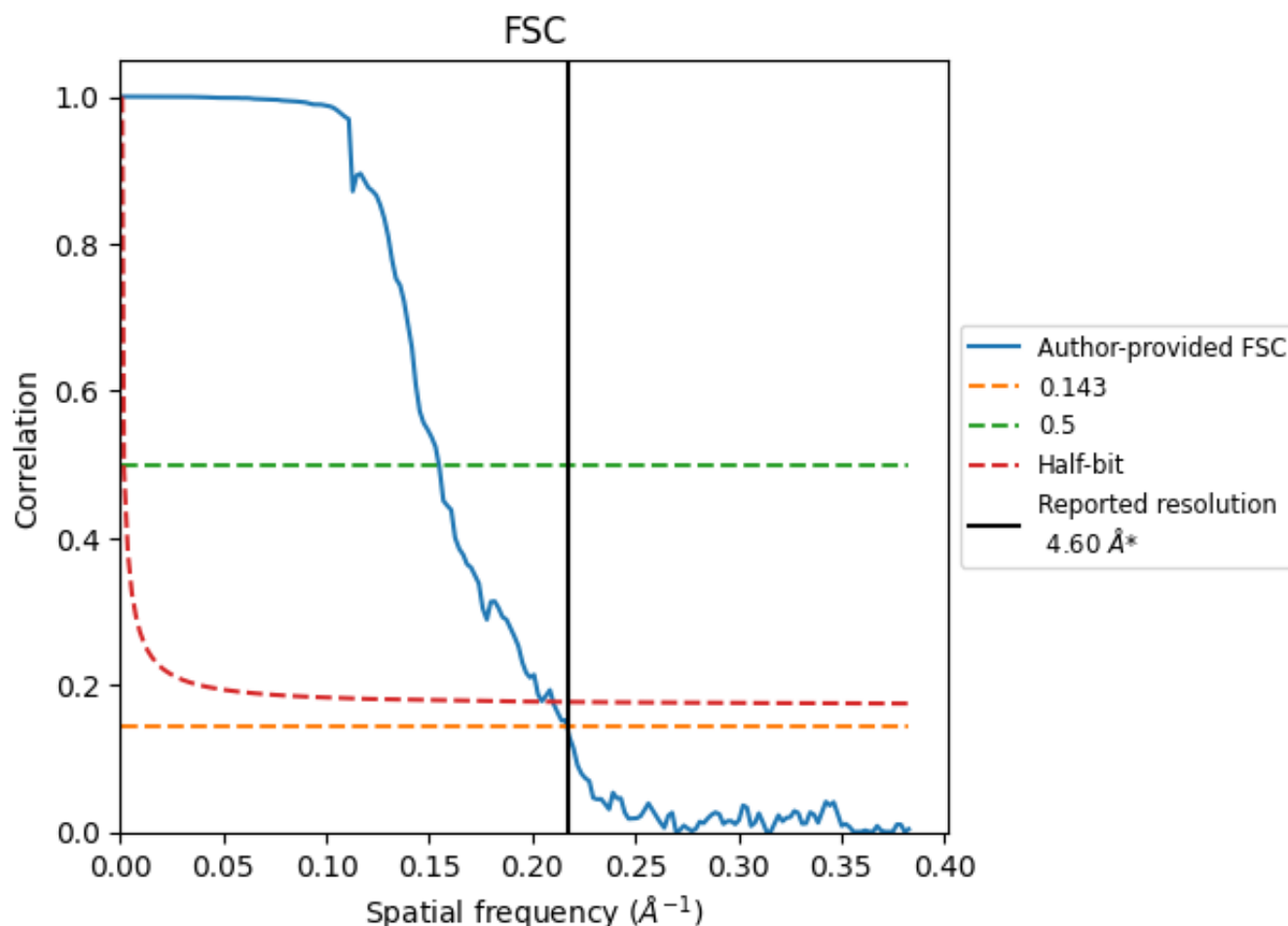


\*Reported resolution corresponds to spatial frequency of 0.217 Å<sup>-1</sup>

## 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 0.217  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

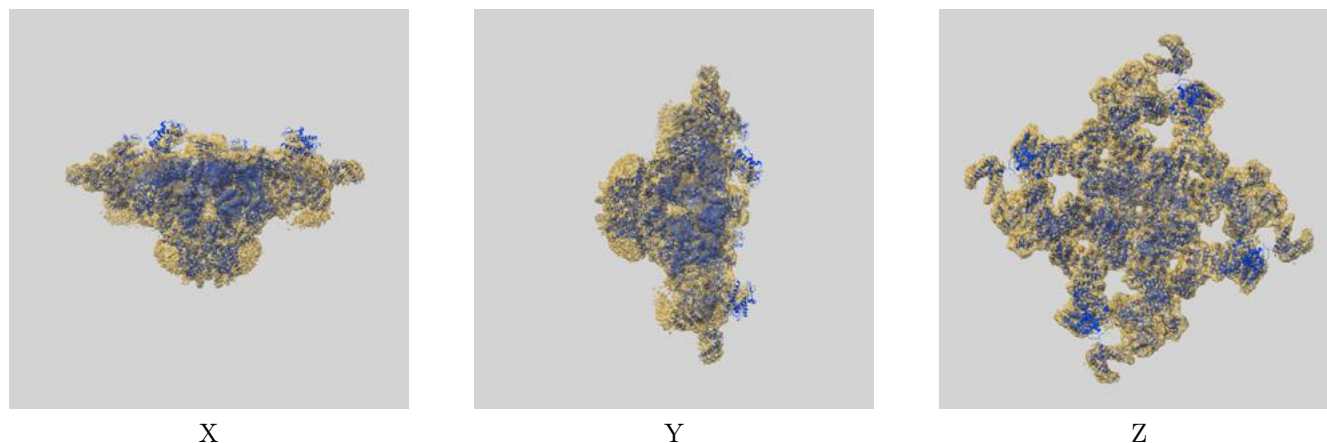
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.61	6.46	4.76
Unmasked-calculated*	-	-	-

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

## 9 Map-model fit [i](#)

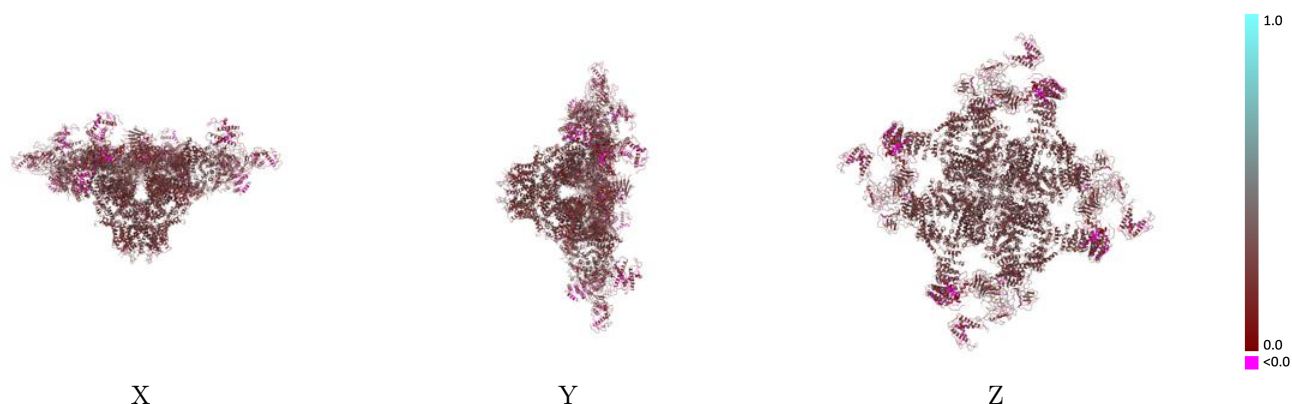
This section contains information regarding the fit between EMDB map EMD-9824 and PDB model 6JGZ. Per-residue inclusion information can be found in section [3](#) on page [4](#).

### 9.1 Map-model overlay [i](#)



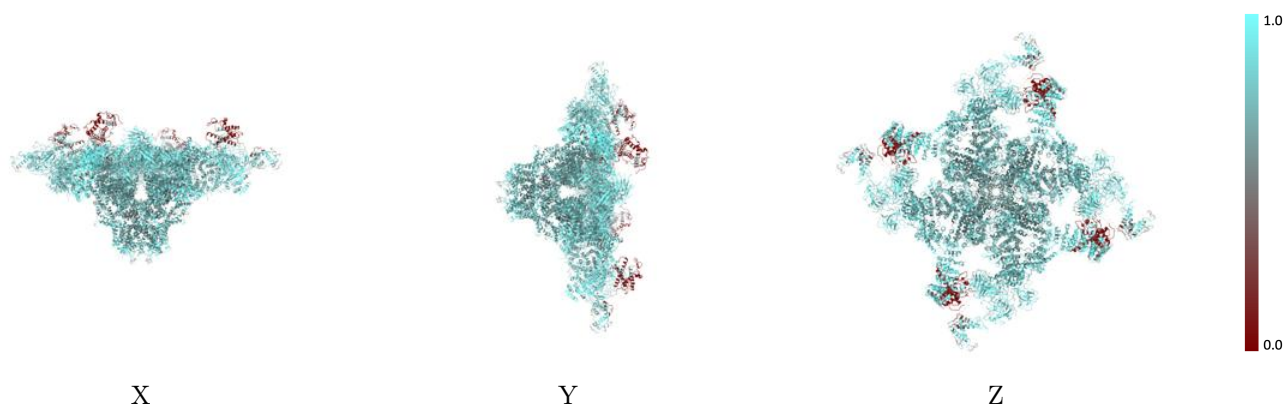
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



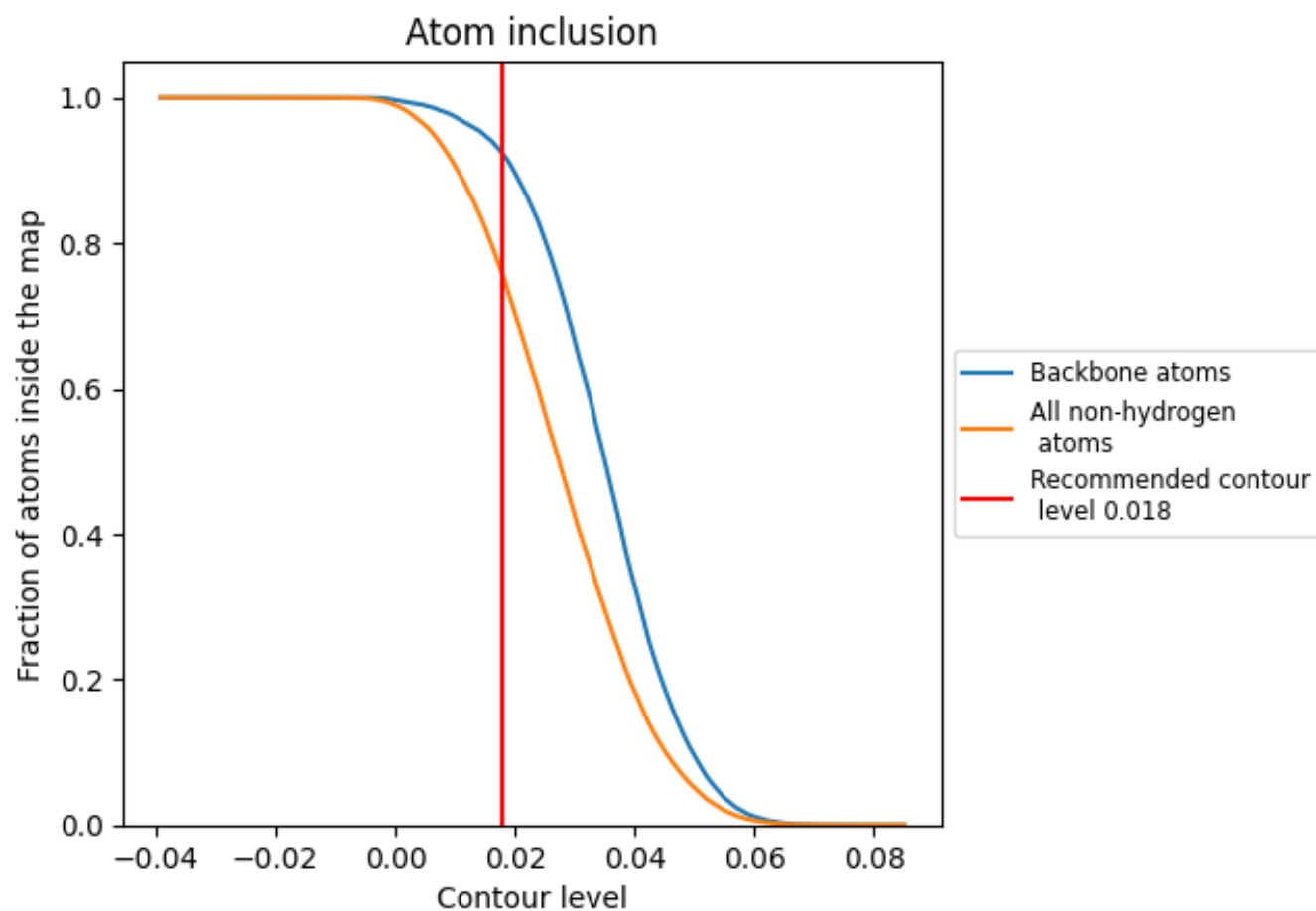
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.018).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7551	<div></div> 0.2490
A	<div></div> 0.8166	<div></div> 0.2650
B	<div></div> 0.7531	<div></div> 0.2480
C	<div></div> 0.8191	<div></div> 0.2650
D	<div></div> 0.7533	<div></div> 0.2490
E	<div></div> 0.8166	<div></div> 0.2650
F	<div></div> 0.7531	<div></div> 0.2480
G	<div></div> 0.8141	<div></div> 0.2650
H	<div></div> 0.7532	<div></div> 0.2480

