



## Full wwPDB EM Validation Report ⓘ

Dec 19, 2022 – 08:54 am GMT

PDB ID : 7NFC  
EMDB ID : EMD-12299  
Title : Cryo-EM structure of NHEJ super-complex (dimer)  
Authors : Chaplin, A.K.; Hardwick, S.W.; Kefala Stavridi, A.; Chirgadze, D.Y.; Blundell, T.L.  
Deposited on : 2021-02-05  
Resolution : 4.14 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:

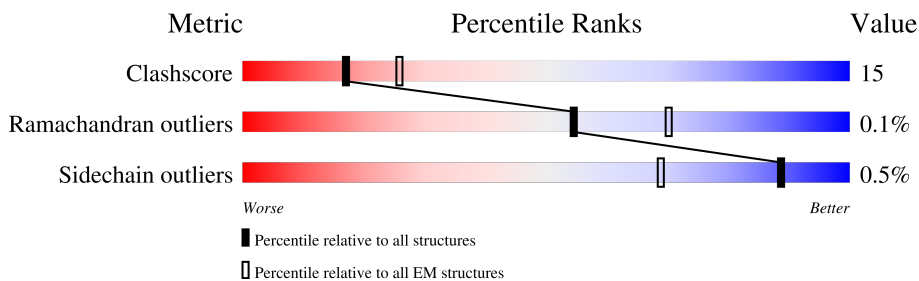
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 4.14 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	4148	
1	F	4148	
2	B	609	
2	G	609	
3	C	732	
3	H	732	
4	K	336	
4	L	336	

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Mol	Chain	Length	Quality of chain
4	N	336	<p>21% 47% 12% 40%</p>
4	O	336	<p>27% 45% 13% 42%</p>
5	M	911	<p>6% 22% 7% 72%</p>
5	P	911	<p>16% 10% 73%</p>
6	Q	299	<p>31% 51% 19% 29%</p>
6	R	299	<p>30% 51% 22% 27%</p>
7	D	27	<p>19% 81%</p>
8	E	28	<p>21% 79%</p>
8	I	28	<p>21% 79%</p>
9	J	27	<p>33% 67%</p>

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 89069 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 DNA-dependent protein kinase catalytic subunit,DNA-dependent protein kinase catalytic subunit,DNA-PKcs.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	3562	Total	C	N	O	S	0	0
			28076	18032	4728	5132	184		
1	F	3557	Total	C	N	O	S	0	0
			28060	18026	4720	5131	183		

- Molecule 2 is a protein called X-ray repair cross-complementing protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	476	Total	C	N	O	S	0	0
			3822	2452	648	705	17		
2	G	489	Total	C	N	O	S	0	0
			3948	2529	669	732	18		

- Molecule 3 is a protein called X-ray repair cross-complementing protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	477	Total	C	N	O	S	0	0
			3849	2466	646	714	23		
3	H	642	Total	C	N	O	S	0	0
			5150	3298	864	963	25		

- Molecule 4 is a protein called DNA repair protein XRCC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	K	201	Total	C	N	O	S	0	0
			1625	1028	278	312	7		
4	L	195	Total	C	N	O	S	0	0
			1592	1009	272	304	7		
4	N	201	Total	C	N	O	S	0	0
			1625	1028	278	312	7		
4	O	194	Total	C	N	O	S	0	0
			1579	1000	271	301	7		

- Molecule 5 is a protein called DNA ligase 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	258	Total	C	N	O	S	0	0
			2095	1333	353	396	13		
5	P	246	Total	C	N	O	S	0	0
			1965	1248	330	374	13		

- Molecule 6 is a protein called Non-homologous end-joining factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q	211	Total	C	N	O	S	0	0
			1690	1084	282	310	14		
6	R	218	Total	C	N	O	S	0	0
			1728	1105	288	320	15		

- Molecule 7 is a DNA chain called DNA (27-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	27	Total	C	N	O	P	0	0
			556	268	95	166	27		

- Molecule 8 is a DNA chain called DNA (28-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	28	Total	C	N	O	P	0	0
			576	277	107	164	28		
8	I	28	Total	C	N	O	P	0	0
			576	277	107	164	28		

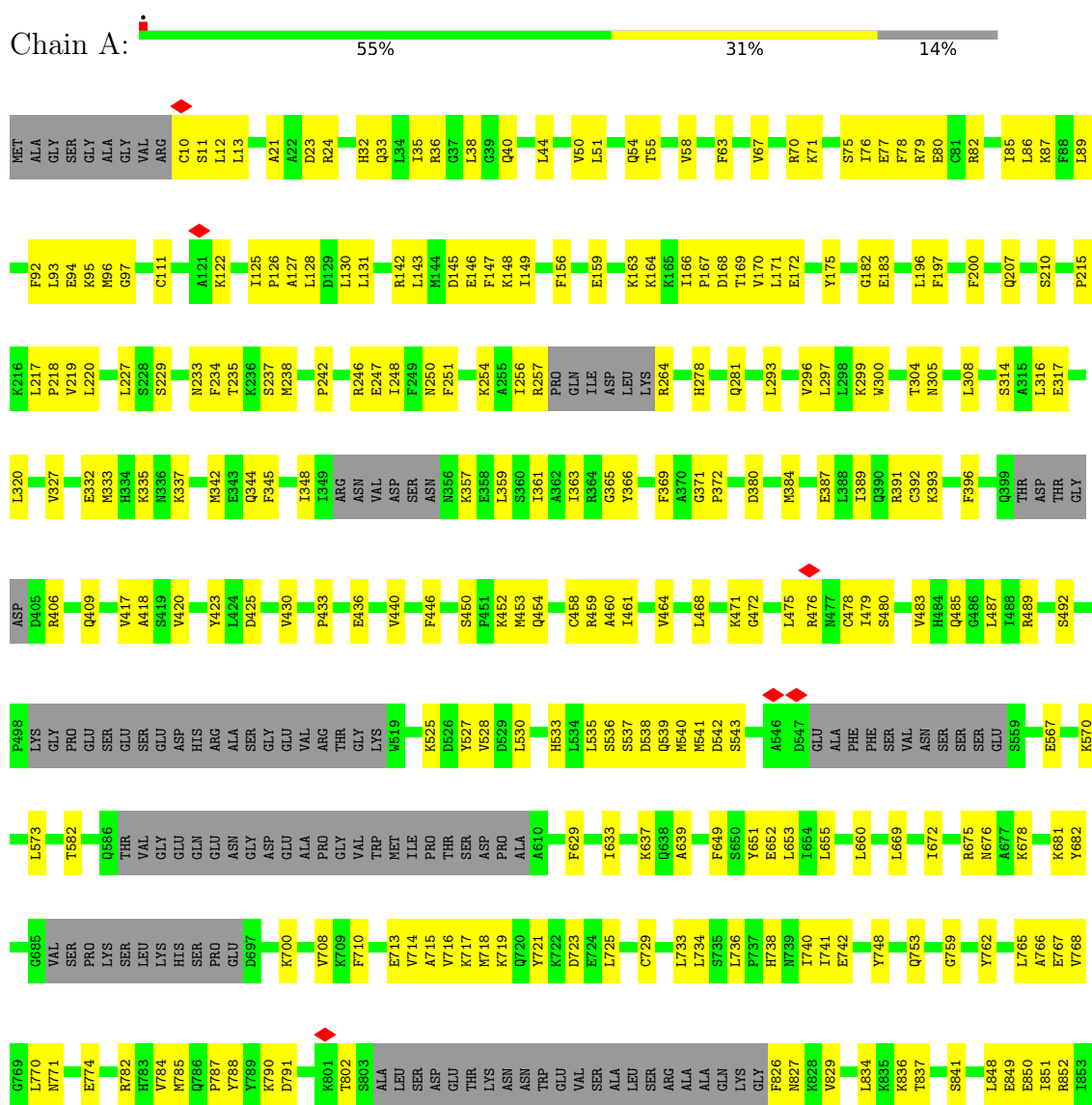
- Molecule 9 is a DNA chain called DNA (27-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	27	Total	C	N	O	P	0	0
			557	269	94	167	27		

### 3 Residue-property plots [i](#)

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

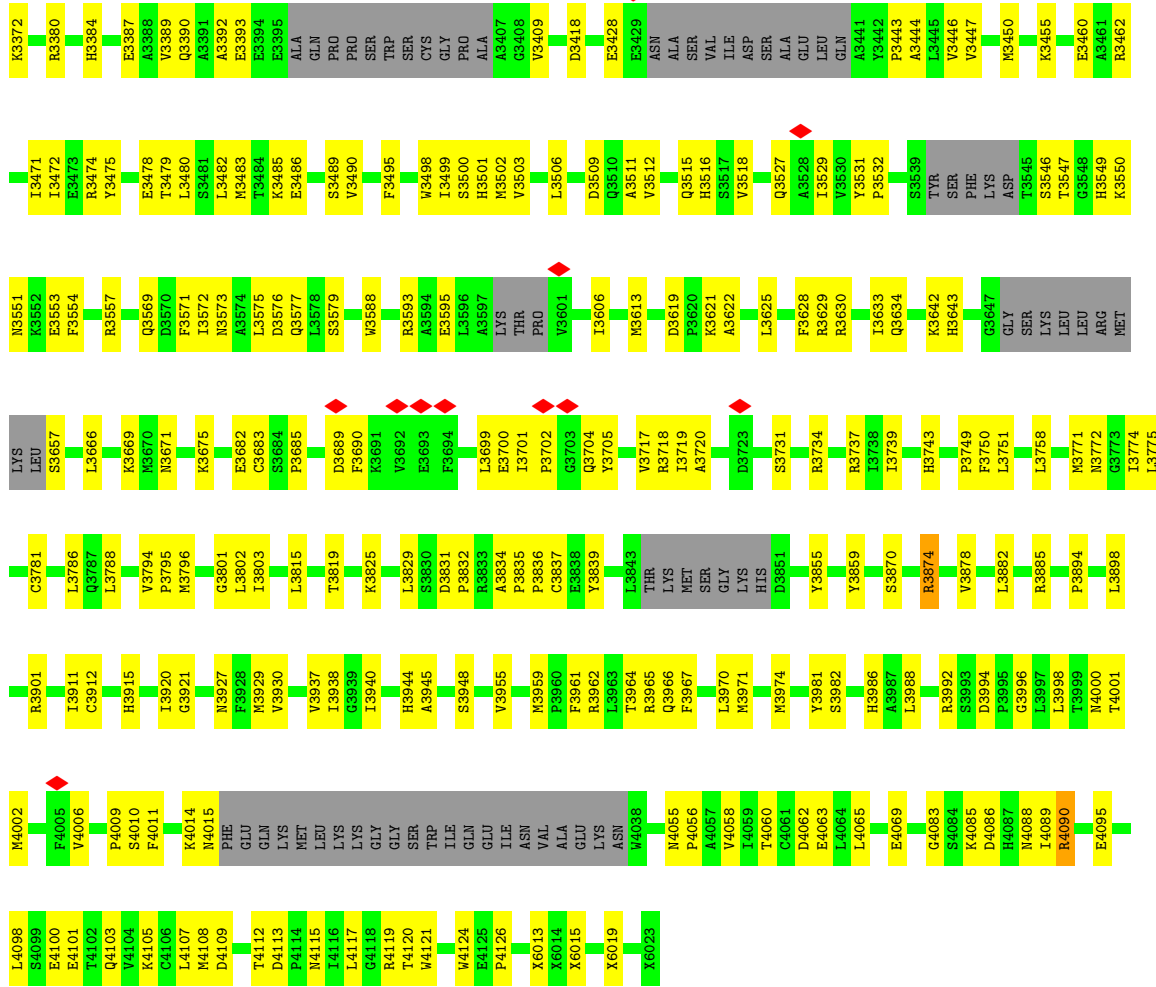
- Molecule 1: DNA-dependent protein kinase catalytic subunit,DNA-dependent protein kinase catalytic subunit,DNA-PKcs



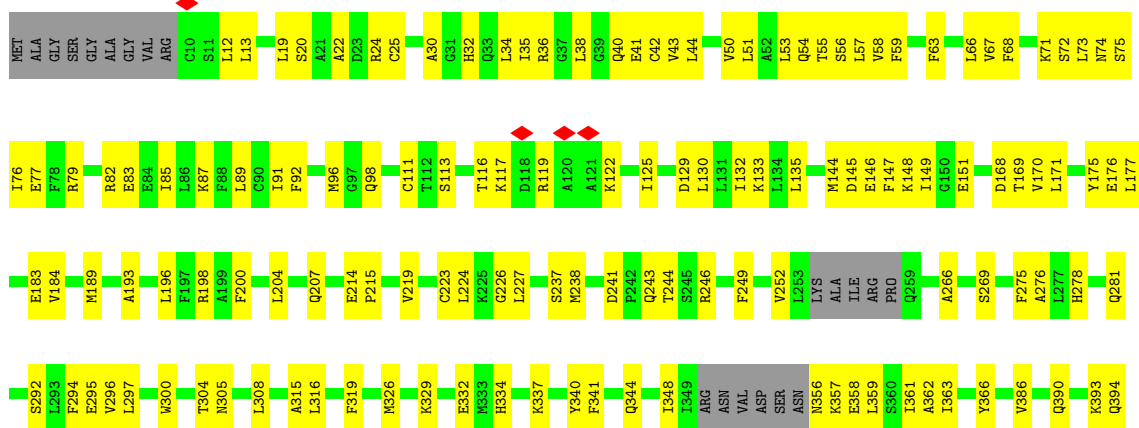
L1934	H935	L1009	F101	L1190	R1274	T1351	L1431	L1517	S1604	H1687	Q1771	SER	L1939
H936	S936	A1012	E102	F1191	A1278	S1352	L1435	F1521	F1605	L1688	H1772	T1862	L1957
S937	S861	I1013	I1106	K1193	L1279	P1353	M1435	F1521	R1606	K1689	H1773	F1863	E1958
V938	L862	D1014	A1112	Y1192	L1280	G1354	P1439	C1525	E1609	A1692	E1775	I1867	L1969
H941	G863	D1015	L1113	P1196	V1281	G1355	P1440	E1526	R1610	P1697	F1778	T1868	E1968
H944	G854	G1016	L1113	L1197	L1282	H1356	D1440	R1527	K1612	F1698	K1870	K1869	L1969
T946	Q866	I1017	A1114	L1198	G1283	K1357	A1442	L1528	Q1614	F1699	M1871	M1871	K1960
P949	H867	V1018	H1115	R1202	A1286	L1358	V1443	V1529	H1613	THR	R1788	Y1874	Y1962
P949	K868	R1026	A1116	R1203	Q1287	L1359	D1444	L1531	Q1614	SER	Q1794	L1877	Q1963
Q953	H870	D1027	K1119	M1204	Q1288	K1360	L1445	L1532	K1617	LEU	G1794	D1878	G1963
P956	L871	F1028	S1120	M1205	S1289	K1361	S1446	S1539	K1617	THR	E1799	D1878	Q1963
P957	THR	I1034	T1123	L1206	L1290	H1366	R1447	T1540	L1623	GLY	E1799	D1878	Q1963
P957	VAL	E1035	I1235	V1211	A1293	H1367	V1452	ALA	Q1624	GLY	S1800	D1878	Q1963
N958	THR	F1036	C1127	L1212	V1294	L1368	M1369	SER	H1625	SER	Y1801	M1880	Q1963
Y959	SER	Q1043	Y1295	L1212	R1370	L1368	A1461	LEU	W1626	LEU	Y1802	M1880	Q1963
Y962	SER	Q1043	F1296	G1216	V1371	L1372	H1465	GLY	K1627	SER	E1803	R1883	Q1963
K963	ASP	P1046	I1131	F1219	F1297	L1372	H1466	SER	K1628	SER	M1804	R1884	Q1963
H964	GLU	P1046	D1132	L1220	E1299	T1375	M1466	THR	W1633	GLY	F1805	L1884	Q1963
T965	M879	Q1048	H1133	L1220	E1299	L1467	I1467	GLY	W1633	GLY	R1806	L1884	Q1963
F966	M880	Q1048	I1137	F1224	S1300	L1468	P1469	V1560	K1635	I1718	ASP	L1884	Q1963
L969	K881	E1050	H1142	F1232	I1301	E1378	D1474	V1560	K1635	I1718	ASP	L1884	Q1963
L972	W886	K1051	V1143	P1232	H1303	I1382	L1475	Y1558	E1640	H1721	PRO	L1884	Q1963
D975	D887	S1058	S1144	I1235	D1305	T1382	L1475	F1559	K1642	F1723	ARG	L1884	Q1963
D977	R891	S1058	L1445	I1235	I1306	G1384	V1479	S1560	K1642	F1723	ARG	L1884	Q1963
T980	L892	K1061	K1149	Q1238	I1307	F1384	V1482	S1561	M1643	Q1725	PHE	L1884	Q1963
R981	S888	R1062	K1150	P1239	I1308	V1389	E1482	L1562	V1645	R1726	LYS	L1884	Q1963
L982	F894	L1066	R1151	LEU	A1309	V1391	L1483	E1565	L1646	R1727	ILE	L1884	Q1963
Y984	F898	L1066	R1152	LEU	E1310	M1392	L1484	E1568	A1647	E1728	ASN	L1884	Q1963
E985	R899	H1069	L1153	TVR	F1313	M1392	V1487	M1568	L1648	P1730	ARG	L1884	Q1963
P986	E900	P1070	L1165	LEU	GLY	M1392	Y1488	M1574	L1649	P1731	ARG	L1884	Q1963
L987	E901	N1071	L1169	TVR	THR	M1392	K1489	L1575	I1652	F1736	GLY	L1883	Q1963
V988	M901	A1072	K1170	LEU	GLY	M1392	G1490	L1576	S1658	Y1739	SER	L1836	Q1963
H989	K902	F1073	M1171	ARG	ALA	M1392	I1491	D1577	V1659	V1740	ILE	L1836	Q1963
Q990	P903	K1074	L1172	PHE	ALA	M1392	A1492	L1578	T1663	M1743	GLU	S1841	Q1963
L991	V904	R1075	L1165	ARG	GLY	M1392	PRO	V1579	S1664	K1744	GLY	T1843	Q1963
L992	F906	L1076	L1165	L1249	ASN	M1392	ASP	S1586	H1665	K1745	GLY	V1844	Q1963
H993	L911	A1081	V1169	L1254	ARG	M1392	ARG	V1587	H1666	F1746	V1845	V1844	Q1963
H993	L919	F1082	K1171	C1255	THR	M1392	ARG	D1588	S1667	L1747	D1846	D1846	Q1963
H994	T920	N1083	M1173	M1256	ASN	M1392	GLN	M1589	F1668	D1748	D1846	D1846	Q1963
F995	T920	M1084	L1173	W1264	ASN	M1392	LEU	K1591	P1669	D1748	D1846	D1846	Q1963
F996	S922	I1086	L1175	L1260	ARG	M1392	PRO	M1592	E1670	S1753	D1849	D1849	Q1963
K1000	D923	R1087	H1175	L1261	ARG	M1392	S1502	V1593	V1671	M1757	V1850	V1850	Q1963
F1001	R924	M1087	L1175	L1261	ARG	M1392	L1503	V1593	F1672	M1757	L1851	L1851	Q1963
E1002	Q925	R1090	Q1180	L1264	ARG	M1392	S1506	V1596	T1673	E1760	K1852	K1852	Q1963
S1003	Q926	R1090	C1183	L1264	ARG	M1392	S1506	V1596	T1673	E1760	K1852	K1852	Q1963
D1004	Q927	R1090	C1183	L1264	ARG	M1392	S1506	V1596	T1673	E1760	K1852	K1852	Q1963
D1005	V928	V1096	C1183	L1264	ARG	M1392	S1506	V1596	T1673	E1760	K1852	K1852	Q1963
V1006	V1007	V1096	C1183	L1264	ARG	M1392	S1506	V1596	T1673	E1760	K1852	K1852	Q1963
V1007	V1100	V1096	C1183	L1264	ARG	M1392	S1506	V1596	T1673	E1760	K1852	K1852	Q1963
V1100	V1100	V1096	C1183	L1264	ARG	M1392	S1506	V1596	T1673	E1760	K1852	K1852	Q1963







- Molecule 1: DNA-dependent protein kinase catalytic subunit, DNA-dependent protein kinase catalytic subunit, DNA-PKcs



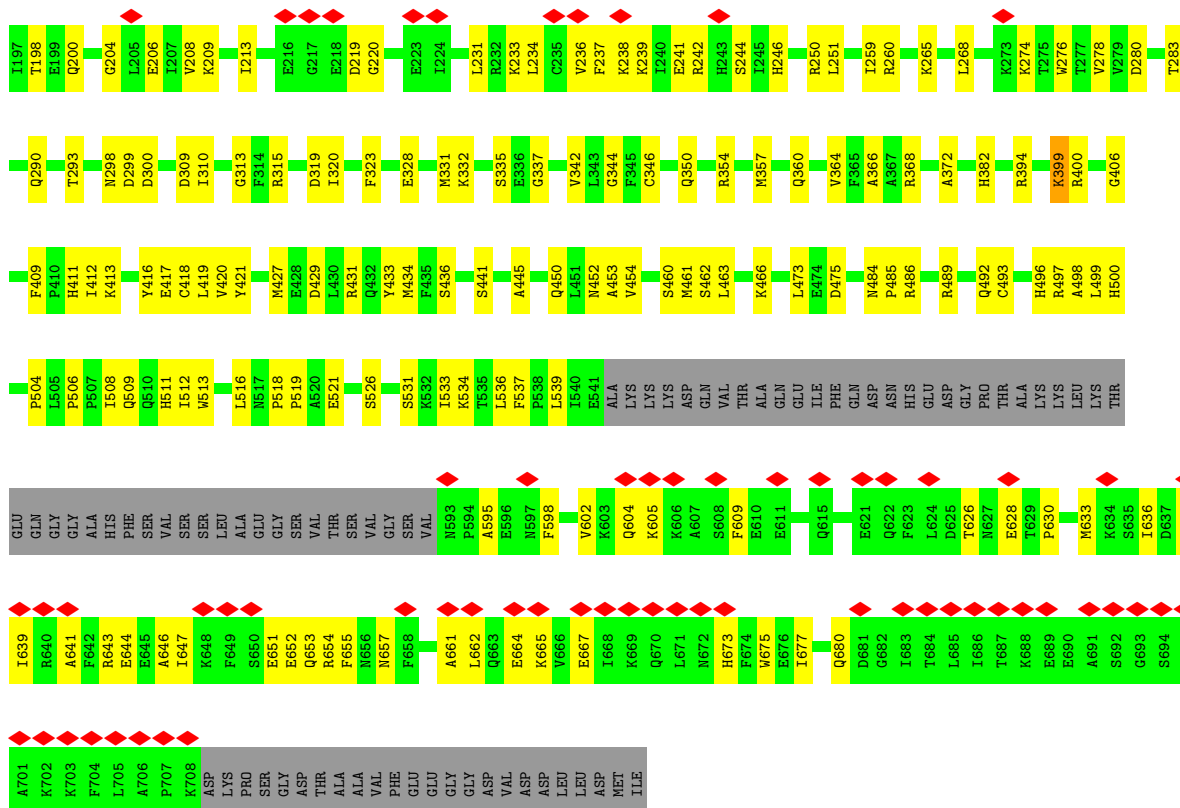




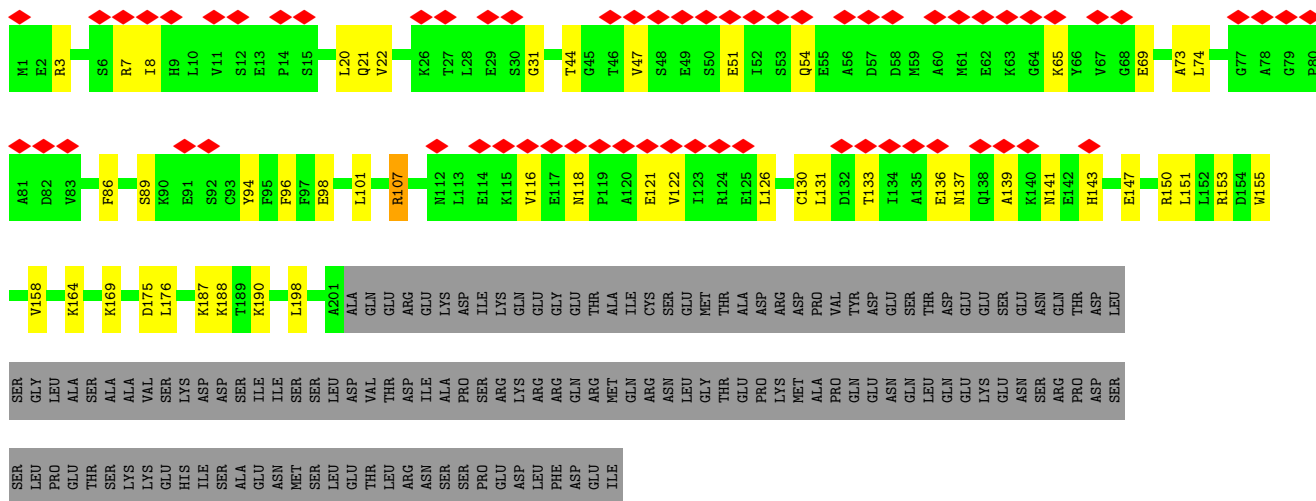




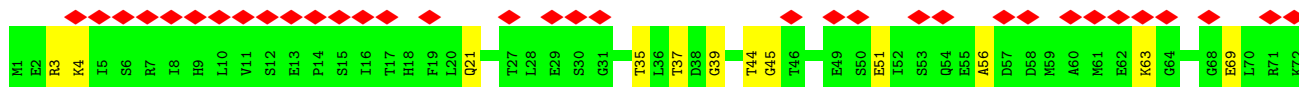
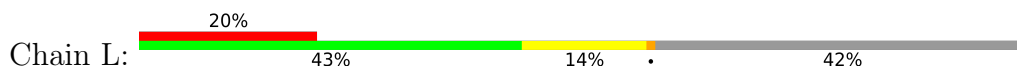


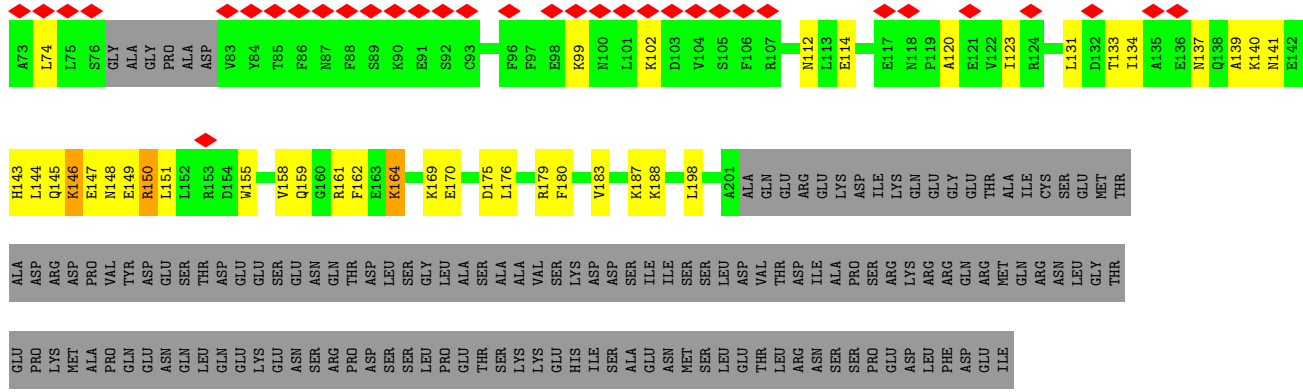


• Molecule 4: DNA repair protein XRCC4

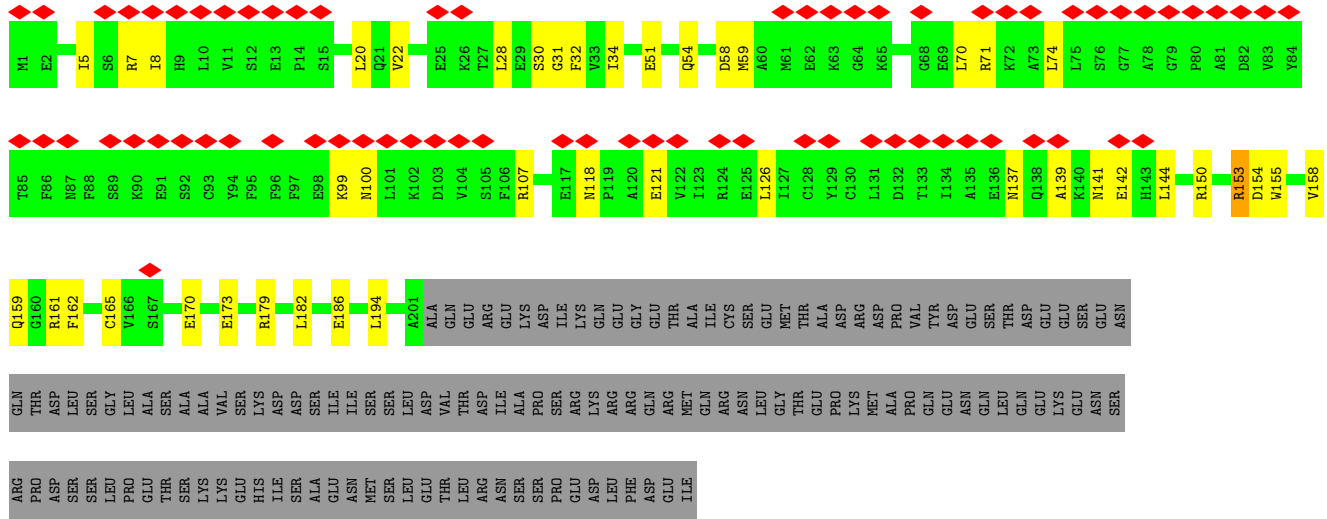


• Molecule 4: DNA repair protein XRCC4

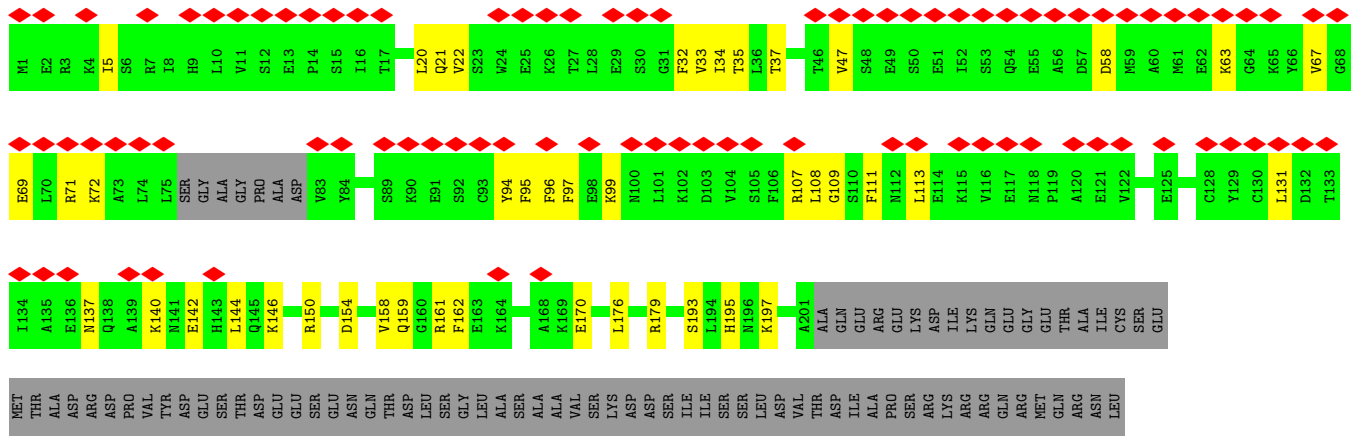




● Molecule 4: DNA repair protein XRCC4



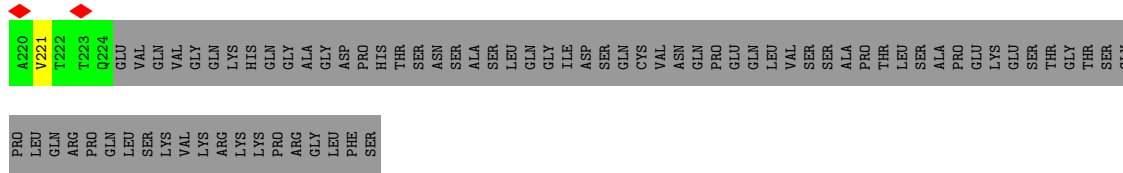
● Molecule 4: DNA repair protein XRCC4



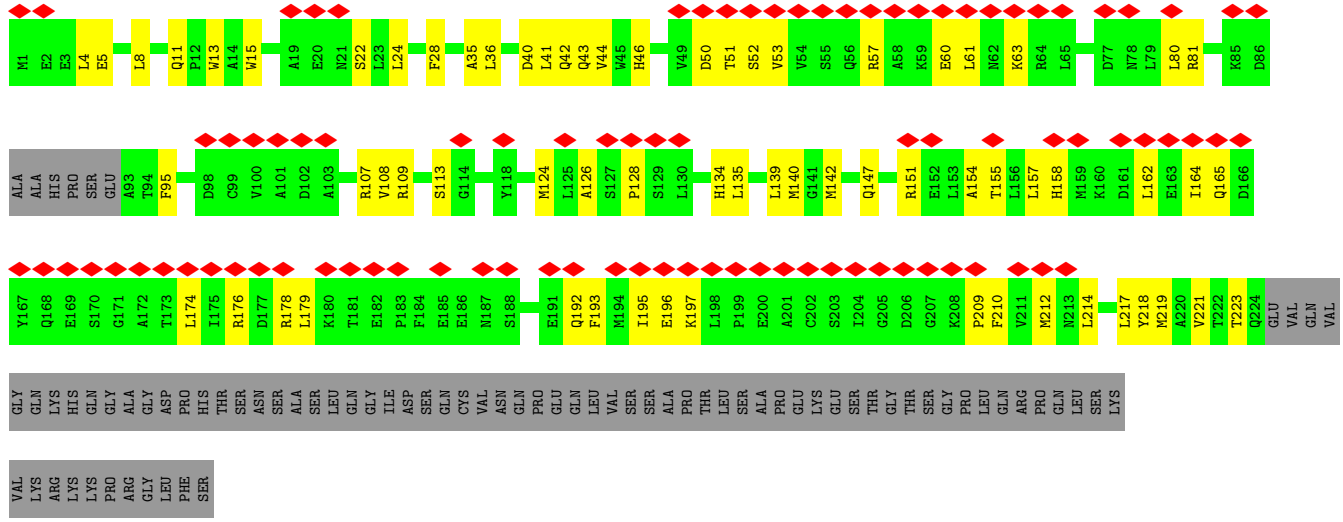




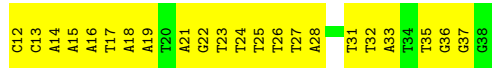




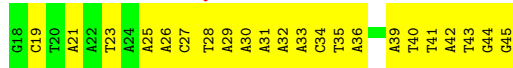
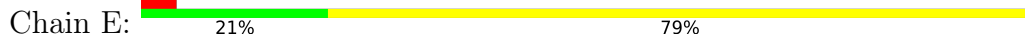
• Molecule 6: Non-homologous end-joining factor 1



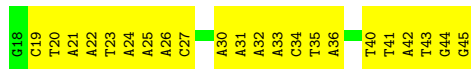
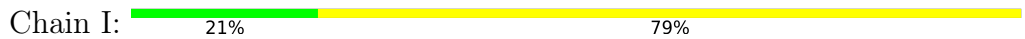
• Molecule 7: DNA (27-MER)



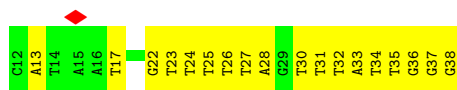
• Molecule 8: DNA (28-MER)



• Molecule 8: DNA (28-MER)



• Molecule 9: DNA (27-MER)



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	23421	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 ( $e^-/\text{\AA}^2$ )	46.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.695	Depositor
Minimum map value	-0.275	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.175	Depositor
Map size (Å)	704.16003, 704.16003, 704.16003	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.304, 1.304, 1.304	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.27	0/28527	0.47	0/38582
1	F	0.27	0/28510	0.47	1/38552 (0.0%)
2	B	0.26	0/3896	0.50	0/5248
2	G	0.27	0/4025	0.49	0/5421
3	C	0.25	0/3921	0.46	0/5282
3	H	0.26	0/5254	0.47	0/7085
4	K	0.24	0/1654	0.47	0/2224
4	L	0.24	0/1619	0.49	0/2174
4	N	0.24	0/1654	0.47	0/2224
4	O	0.24	0/1605	0.46	0/2155
5	M	0.25	0/2144	0.45	0/2895
5	P	0.28	0/2008	0.48	0/2712
6	Q	0.24	0/1722	0.53	0/2332
6	R	0.24	0/1762	0.51	0/2389
7	D	0.54	0/622	0.96	0/959
8	E	0.55	0/647	0.96	0/996
8	I	0.59	0/647	0.95	0/996
9	J	0.53	0/623	1.02	0/961
All	All	0.28	0/90840	0.50	1/123187 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	956	PRO	N-CA-CB	6.22	110.77	103.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	28076	0	28047	898	0
1	F	28060	0	28056	856	0
2	B	3822	0	3899	176	0
2	G	3948	0	4036	181	0
3	C	3849	0	3892	121	0
3	H	5150	0	5176	173	0
4	K	1625	0	1611	40	0
4	L	1592	0	1583	45	0
4	N	1625	0	1611	35	0
4	O	1579	0	1571	39	0
5	M	2095	0	2046	42	0
5	P	1965	0	1904	74	0
6	Q	1690	0	1699	51	0
6	R	1728	0	1728	62	0
7	D	556	0	310	35	0
8	E	576	0	318	28	0
8	I	576	0	318	34	0
9	J	557	0	311	29	0
All	All	89069	0	88116	2724	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 15.

All (2724) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1549:SER:O	1:A:1550:VAL:HG22	1.17	1.29
1:A:1549:SER:O	1:A:1550:VAL:CG2	2.04	1.05
3:H:56:LEU:H	3:H:81:ARG:HB2	1.39	0.88
1:A:327:VAL:HG13	1:A:333:MET:HB2	1.58	0.85
5:P:811:SER:HB2	5:P:849:GLY:HA3	1.57	0.84
1:A:2965:TYR:HB3	1:A:3001:CYS:HB2	1.58	0.83
4:L:179:ARG:HD3	5:M:778:PHE:HB3	1.60	0.83
2:B:352:PRO:HA	2:B:394:VAL:HA	1.61	0.83
1:F:1115:HIS:HA	1:F:1119:LYS:HD2	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:133:GLN:H	6:R:42:GLN:H	1.28	0.81
1:F:50:VAL:HG13	1:F:51:LEU:HG	1.62	0.81
1:A:168:ASP:H	1:A:171:LEU:HD12	1.45	0.81
1:F:1428:ILE:HA	1:F:1431:LEU:HB2	1.63	0.80
1:F:901:MET:HG2	1:F:903:PRO:HD3	1.63	0.79
7:D:24:DT:H3	8:E:34:DC:H42	1.26	0.79
5:P:812:MET:H	5:P:848:HIS:HB3	1.46	0.79
1:F:1104:LEU:HD22	1:F:1134:LEU:HD13	1.66	0.78
3:H:242:ARG:NH2	8:I:22:DA:N7	2.31	0.78
1:A:2433:LYS:HG3	1:A:2472:GLN:HE22	1.47	0.77
1:A:1611:GLN:HE21	1:A:1614:GLN:HE21	1.32	0.77
1:A:2594:ASP:HA	1:A:2768:GLN:HE22	1.47	0.77
1:A:2357:GLU:HA	1:A:2360:PHE:HB3	1.65	0.77
1:A:3255:ALA:HB1	1:A:3258:LEU:HB2	1.65	0.77
5:M:813:PHE:HB3	5:M:850:ALA:HB2	1.66	0.77
1:A:3750:PHE:HB3	1:A:3802:LEU:HD11	1.67	0.76
1:F:149:ILE:HD11	1:F:183:GLU:HB2	1.65	0.76
6:Q:132:SER:HB3	6:R:44:VAL:HA	1.67	0.76
1:F:12:LEU:HD21	1:F:44:LEU:HD22	1.68	0.76
6:R:15:TRP:HE1	6:R:22:SER:HA	1.50	0.76
1:A:1803:GLU:HA	1:A:1806:ARG:HH21	1.51	0.75
4:N:28:LEU:HD22	4:N:71:ARG:HH12	1.50	0.75
6:Q:135:LEU:HB2	6:R:41:LEU:HB2	1.66	0.75
1:A:1307:ILE:HG23	1:A:1309:ALA:H	1.50	0.75
2:B:322:TYR:HE1	3:C:274:LYS:HG3	1.52	0.74
1:F:2776:ARG:HH21	1:F:2782:ASP:HB2	1.50	0.74
4:L:45:GLY:HA3	4:L:114:GLU:H	1.51	0.74
6:Q:132:SER:HA	6:R:40:ASP:H	1.50	0.74
1:A:3321:LEU:HD13	1:A:3324:ARG:HH12	1.52	0.74
6:R:57:ARG:HG2	6:R:61:LEU:HD22	1.70	0.74
2:G:403:ARG:H	2:G:406:ILE:HD11	1.53	0.74
1:F:3142:ILE:O	1:F:3147:LYS:NZ	2.21	0.73
2:G:533:ASP:OD1	3:H:250:ARG:NH2	2.20	0.73
3:C:501:PRO:HB2	3:C:502:ARG:HH21	1.53	0.73
2:G:69:SER:HB3	2:G:245:LYS:HB3	1.69	0.73
1:F:3684:SER:HB3	1:F:3687:MET:HB2	1.70	0.73
1:A:3971:MET:SD	1:A:3974:MET:HG3	2.29	0.73
2:G:255:ALA:HB3	2:G:258:ARG:HH22	1.53	0.73
7:D:21:DA:H2''	8:E:33:DA:H62	1.54	0.72
1:F:2859:GLN:HE22	1:F:2880:CYS:HB3	1.54	0.72
2:B:173:ASP:HB2	2:B:214:SER:H	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3593:ARG:NH2	1:A:3657:SER:O	2.22	0.72
1:F:3982:SER:O	1:F:3986:HIS:ND1	2.21	0.72
3:H:647:ILE:HA	3:H:652:GLU:HG2	1.70	0.72
2:G:47:ALA:O	2:G:171:ASN:ND2	2.23	0.72
3:H:605:LYS:HB2	3:H:609:PHE:HZ	1.54	0.72
4:K:139:ALA:O	4:K:143:HIS:ND1	2.22	0.72
1:F:1268:ASN:ND2	1:F:1347:THR:OG1	2.23	0.72
8:I:21:DA:H4'	9:J:36:DG:H1'	1.71	0.72
1:A:197:PHE:O	1:A:246:ARG:NH2	2.23	0.72
2:B:303:PHE:HB3	3:C:290:GLN:HB3	1.72	0.72
1:F:1220:LEU:HD11	1:F:1287:GLN:HB2	1.70	0.72
1:F:1151:ARG:NH1	1:F:1163:LEU:O	2.23	0.71
5:P:860:VAL:O	5:P:884:ARG:NH2	2.23	0.71
1:A:901:MET:HG2	1:A:903:PRO:HD3	1.72	0.71
1:A:3137:GLU:OE2	1:A:3166:ASN:ND2	2.23	0.71
5:M:707:ILE:HA	5:M:710:LYS:HD2	1.72	0.71
1:F:833:HIS:O	1:F:838:LYS:NZ	2.21	0.71
1:F:2290:PRO:O	1:F:2292:CYS:N	2.23	0.71
2:G:261:LEU:HB2	2:G:269:ILE:HB	1.71	0.71
6:Q:134:HIS:H	6:R:42:GLN:HB2	1.56	0.71
1:A:4055:ASN:HB2	1:A:4095:GLU:HA	1.71	0.71
5:M:663:GLU:HB3	5:M:697:THR:HA	1.71	0.71
5:M:682:ILE:HG12	5:M:687:GLY:HA3	1.72	0.71
1:A:3349:ALA:O	1:A:3357:ARG:NH2	2.23	0.70
2:B:90:THR:HG21	2:B:103:TYR:HB2	1.73	0.70
3:H:662:LEU:HD23	3:H:665:LYS:HE2	1.74	0.70
1:A:3511:ALA:O	1:A:3515:GLN:NE2	2.25	0.70
6:R:11:GLN:HB2	6:R:28:PHE:HB2	1.73	0.70
1:A:1172:LEU:HD11	1:A:1187:SER:HB2	1.73	0.70
1:A:2408:MET:HA	1:A:2411:LEU:HD22	1.73	0.70
1:A:1151:ARG:NH1	1:A:1163:LEU:O	2.22	0.70
1:A:865:GLN:HB2	1:A:3168:TYR:HB3	1.73	0.70
5:P:814:ARG:H	5:P:850:ALA:N	1.90	0.70
2:G:366:LEU:H	2:G:434:LEU:HB2	1.57	0.69
4:K:22:VAL:HG21	4:K:74:LEU:HB3	1.74	0.69
3:H:65:ASP:H	3:H:78:THR:HG22	1.57	0.69
1:A:2959:ALA:HA	1:A:2962:ARG:HD3	1.74	0.69
1:A:3622:ALA:HB3	1:A:3630:ARG:HD2	1.74	0.69
4:N:153:ARG:NH1	4:N:154:ASP:OD1	2.25	0.69
1:A:2225:HIS:HB2	1:A:2231:PHE:HB2	1.72	0.69
2:B:366:LEU:HB2	2:B:434:LEU:HD12	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1171:TRP:O	1:A:1175:HIS:ND1	2.25	0.69
1:A:2331:MET:O	1:A:2334:LYS:NZ	2.26	0.69
1:F:827:ASN:HB3	1:F:836:LYS:HE2	1.74	0.69
1:A:248:ILE:HA	1:A:251:PHE:HD2	1.57	0.69
1:F:3593:ARG:NH2	1:F:3661:ASP:OD1	2.26	0.69
1:F:3679:ASN:HA	1:F:3726:VAL:HG22	1.74	0.69
4:O:5:ILE:HA	4:O:21:GLN:HA	1.74	0.69
7:D:27:DT:H2''	7:D:28:DA:C5	2.28	0.69
1:A:71:LYS:HB3	1:A:82:ARG:HH22	1.57	0.69
1:A:78:PHE:HB3	1:A:82:ARG:HH21	1.57	0.69
1:A:4086:ASP:HA	1:A:4089:ILE:HG12	1.73	0.68
5:P:746:MET:O	5:P:751:LYS:NZ	2.25	0.68
6:Q:134:HIS:HB3	6:R:42:GLN:HG3	1.75	0.68
1:A:2353:GLN:HA	1:A:2356:MET:HG3	1.75	0.68
1:F:2295:GLN:HG3	1:F:2298:GLU:HB3	1.75	0.68
1:F:3151:LEU:HA	1:F:3197:LEU:HD22	1.74	0.68
3:H:337:GLY:H	3:H:399:LYS:HB3	1.58	0.68
1:A:3266:SER:HB3	1:A:3273:LEU:HA	1.73	0.68
5:P:861:SER:O	5:P:887:LYS:NZ	2.25	0.68
1:F:207:GLN:NE2	1:F:215:PRO:O	2.26	0.68
1:F:1354:GLU:HA	1:F:1357:LYS:HB3	1.76	0.68
1:F:4055:ASN:HD22	1:F:4058:VAL:HG23	1.58	0.68
1:A:3266:SER:HA	1:A:3272:TRP:CD1	2.28	0.68
2:G:468:LYS:NZ	2:G:517:ARG:O	2.27	0.68
1:A:1238:GLN:HA	1:A:1296:PHE:HZ	1.59	0.68
1:A:2987:THR:HG23	1:A:2990:GLU:H	1.59	0.68
1:F:867:ASN:HB3	1:F:3129:LEU:HD11	1.75	0.68
4:N:118:ASN:ND2	4:N:121:GLU:OE1	2.25	0.68
1:F:2572:TYR:HE1	1:F:2791:ILE:HD11	1.59	0.68
2:G:339:ARG:O	3:H:489:ARG:NH1	2.26	0.68
5:P:663:GLU:HA	5:P:688:TYR:HB2	1.75	0.68
5:P:868:ASP:HB3	5:P:871:ARG:HE	1.58	0.68
1:A:304:THR:HG22	1:A:305:ASN:H	1.58	0.68
1:A:3443:PRO:HB3	1:A:3471:ILE:HD11	1.76	0.68
1:F:3493:TRP:HD1	1:F:3521:ILE:HG12	1.58	0.68
1:F:3659:PHE:HA	1:F:3662:ILE:HD12	1.76	0.68
1:A:919:LEU:HG	1:A:920:THR:HG23	1.74	0.67
1:A:3998:LEU:HB3	1:A:4002:MET:HE1	1.74	0.67
3:H:138:LEU:HD12	3:H:204:GLY:HA2	1.77	0.67
2:B:348:MET:HB2	2:B:397:LEU:HB3	1.76	0.67
1:F:40:GLN:OE1	1:F:2427:ARG:NH1	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:489:ARG:HD2	3:H:508:ILE:HG13	1.76	0.67
1:A:1304:HIS:HE1	1:A:1307:ILE:HG22	1.59	0.67
1:A:1420:ARG:NH2	1:A:1466:ASN:O	2.28	0.67
1:A:715:ALA:O	1:A:719:LYS:NZ	2.27	0.67
1:A:2791:ILE:HA	1:A:2794:LEU:HD12	1.76	0.67
1:F:304:THR:HG22	1:F:305:ASN:H	1.58	0.67
2:G:287:LYS:HB3	3:H:310:ILE:HD11	1.75	0.67
8:E:39:DA:N6	8:E:40:DT:O4	2.27	0.67
1:F:2959:ALA:HA	1:F:2962:ARG:HD3	1.75	0.67
2:G:193:LEU:HB2	2:G:198:ILE:HB	1.76	0.67
1:A:1442:GLN:OE1	1:A:1445:ARG:NH2	2.27	0.67
1:A:3837:CYS:SG	1:A:3874:ARG:NH1	2.68	0.67
2:G:94:LYS:NZ	2:G:104:VAL:O	2.28	0.67
5:M:692:ASN:OD1	5:M:708:ARG:NH2	2.28	0.67
8:I:21:DA:N3	9:J:35:DT:N3	2.35	0.67
1:F:2965:TYR:HB3	1:F:3001:CYS:HB2	1.77	0.67
8:I:35:DT:H3	9:J:22:DG:H22	1.41	0.67
1:A:672:ILE:O	1:A:676:ASN:ND2	2.29	0.66
2:B:95:ASN:HD21	2:B:99:PHE:H	1.43	0.66
1:A:3911:ILE:HD12	1:A:3937:VAL:HG23	1.77	0.66
1:F:1015:ASP:OD1	1:F:1016:GLY:N	2.28	0.66
1:F:2511:ILE:HD12	1:F:2550:ILE:HD12	1.76	0.66
1:F:767:GLU:OE2	1:F:854:ARG:NH1	2.29	0.66
5:P:665:CYS:HB2	5:P:697:THR:HG21	1.76	0.66
1:A:3944:HIS:ND1	1:A:3948:SER:O	2.28	0.66
1:A:170:VAL:HA	1:A:219:VAL:HG11	1.78	0.66
1:A:468:LEU:HD21	1:A:478:CYS:HB2	1.78	0.66
1:A:2181:GLY:H	1:A:2185:MET:HE1	1.59	0.66
1:F:24:ARG:HG3	1:F:25:CYS:H	1.60	0.66
1:F:3554:PHE:HD1	1:F:3557:ARG:HH21	1.42	0.66
1:A:111:CYS:HB2	1:A:130:LEU:HD22	1.76	0.66
6:Q:175:ILE:HG22	6:Q:177:ASP:H	1.60	0.66
1:A:23:ASP:O	1:A:70:ARG:NH2	2.29	0.66
1:A:996:THR:HG23	1:A:1043:GLN:HE21	1.61	0.66
5:P:654:LYS:N	5:P:684:GLU:O	2.29	0.66
7:D:37:DG:OP1	8:E:21:DA:N6	2.21	0.66
1:A:58:VAL:HG21	1:A:3098:ARG:HD2	1.79	0.65
1:A:1305:ASP:OD1	1:A:1334:LYS:NZ	2.27	0.65
1:F:1171:TRP:O	1:F:1175:HIS:ND1	2.27	0.65
1:F:3751:LEU:HD22	1:F:3803:ILE:HD11	1.79	0.65
2:G:90:THR:HB	2:G:101:ASN:HA	1.75	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:LYS:NZ	1:A:829:VAL:O	2.30	0.65
2:G:50:GLU:OE2	2:G:52:GLN:NE2	2.30	0.65
4:K:3:ARG:NH2	4:K:21:GLN:OE1	2.27	0.65
1:A:2869:LEU:HD13	1:A:2896:ALA:HA	1.78	0.65
1:F:672:ILE:O	1:F:676:ASN:ND2	2.30	0.65
9:J:26:DT:H2 <sup>''</sup>	9:J:27:DT:H3	1.60	0.65
1:A:125:ILE:HG13	1:A:126:PRO:HD3	1.77	0.65
3:H:496:HIS:CD2	3:H:500:HIS:HE1	2.15	0.65
1:F:2213:ASN:ND2	1:F:2248:CYS:O	2.29	0.65
1:F:2415:LEU:HB2	1:F:2420:PHE:HB2	1.78	0.65
1:F:2986:PRO:O	1:F:2991:LYS:NZ	2.30	0.65
1:F:2987:THR:HG23	1:F:2990:GLU:H	1.61	0.65
2:G:414:VAL:HB	2:G:433:GLN:HB2	1.79	0.65
6:Q:129:SER:HA	6:R:44:VAL:HB	1.78	0.65
1:A:2322:VAL:HA	1:A:2325:LEU:HD12	1.79	0.65
1:F:1663:THR:HG22	1:F:1664:SER:H	1.62	0.65
1:F:3062:LEU:HD13	1:F:3089:LEU:HD21	1.77	0.65
2:G:200:LEU:HD21	2:G:221:ILE:HG12	1.79	0.65
1:A:418:ALA:HB2	1:A:464:VAL:HG12	1.77	0.65
1:A:1397:ASP:OD1	1:A:1398:VAL:N	2.30	0.65
1:A:2263:LYS:HE3	1:A:2265:PRO:HB3	1.77	0.65
1:A:3428:GLU:OE1	1:A:3474:ARG:NH1	2.30	0.65
1:F:3700:GLU:HG3	1:F:3718:ARG:HA	1.79	0.65
2:G:157:VAL:HG22	2:G:159:PHE:H	1.61	0.65
3:H:43:GLN:HB3	3:H:91:LEU:HD21	1.78	0.65
4:K:65:LYS:NZ	4:K:69:GLU:OE2	2.29	0.65
5:M:663:GLU:HA	5:M:688:TYR:HB2	1.79	0.65
1:A:3126:LEU:O	1:A:3130:GLN:NE2	2.29	0.65
1:A:1264:LEU:HD23	1:A:1340:ARG:HG3	1.78	0.65
2:B:357:LYS:HE2	2:B:359:HIS:HE1	1.61	0.65
1:F:2196:TRP:HB2	1:F:2199:LEU:HB2	1.77	0.65
1:F:2894:GLU:HG3	1:F:3973:PRO:HG2	1.77	0.65
1:F:3444:ALA:HB2	1:F:3478:GLU:HG3	1.79	0.65
1:F:3511:ALA:O	1:F:3515:GLN:NE2	2.30	0.64
1:A:2295:GLN:HG3	1:A:2298:GLU:HB3	1.79	0.64
2:B:156:ASP:O	2:B:158:GLN:NE2	2.30	0.64
2:B:458:GLN:HE22	2:B:527:GLU:HG3	1.62	0.64
1:A:2312:TYR:HD2	1:A:2315:VAL:HG23	1.62	0.64
1:F:3796:MET:H	1:F:3801:GLY:HA2	1.62	0.64
1:F:3882:LEU:HA	1:F:3885:ARG:HE	1.63	0.64
1:F:3998:LEU:HA	1:F:4001:THR:HG22	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:453:ALA:HB1	3:C:533:ILE:HG12	1.79	0.64
1:F:2356:MET:HE1	1:F:2358:ASP:HB3	1.79	0.64
2:B:261:LEU:HB3	2:B:269:ILE:HB	1.78	0.64
2:B:428:THR:OG1	3:C:354:ARG:NH1	2.31	0.64
1:F:3444:ALA:HA	1:F:3482:LEU:HD11	1.80	0.64
1:F:1442:GLN:OE1	1:F:1445:ARG:NH2	2.31	0.64
1:F:2830:ASN:O	1:F:2834:GLN:NE2	2.30	0.64
1:A:2943:PHE:HB3	1:A:2954:GLN:HG2	1.80	0.64
2:B:300:THR:OG1	3:C:291:LYS:NZ	2.29	0.64
1:F:418:ALA:HB2	1:F:464:VAL:HG12	1.80	0.64
1:F:3138:ILE:HG22	1:F:3189:PHE:HZ	1.62	0.64
1:F:3258:LEU:O	1:F:3262:LEU:HG	1.97	0.64
1:F:3467:ARG:NH1	1:F:4000:ASN:OD1	2.31	0.64
3:H:44:ARG:HB2	3:H:237:PHE:HB2	1.80	0.64
1:A:1788:ARG:O	1:A:1794:GLN:NE2	2.31	0.64
1:A:3142:ILE:O	1:A:3147:LYS:NZ	2.28	0.64
1:A:256:ILE:HG23	1:A:257:ARG:HG2	1.78	0.63
1:A:3758:LEU:HB2	1:A:3795:PRO:HB3	1.81	0.63
1:F:2891:ARG:HG2	1:F:3894:PRO:HB3	1.81	0.63
1:F:3739:ILE:HA	1:F:3749:PRO:HA	1.78	0.63
4:L:139:ALA:O	4:L:143:HIS:ND1	2.25	0.63
4:N:51:GLU:HB3	4:N:54:GLN:HE22	1.63	0.63
1:A:278:HIS:HB3	1:A:281:GLN:HB2	1.79	0.63
1:A:865:GLN:NE2	1:A:3171:ALA:O	2.30	0.63
1:A:1625:HIS:HA	1:A:1628:LYS:HD3	1.80	0.63
1:A:2507:ILE:HA	1:A:2510:LEU:HD23	1.80	0.63
1:F:3512:VAL:HA	1:F:3515:GLN:HE21	1.62	0.63
1:F:3874:ARG:NH2	1:F:4117:LEU:O	2.32	0.63
4:K:198:LEU:HD13	4:L:198:LEU:HA	1.80	0.63
1:A:953:GLN:H	1:A:956:PRO:HG3	1.63	0.63
1:A:3483:MET:HA	1:A:3486:GLU:HB2	1.80	0.63
1:A:3718:ARG:H	1:A:3743:HIS:CE1	2.16	0.63
1:A:975:ASP:O	1:A:981:ARG:NH2	2.27	0.63
1:A:1283:GLY:H	1:A:1286:ALA:HB2	1.63	0.63
1:F:340:TYR:O	1:F:344:GLN:NE2	2.31	0.63
1:A:864:GLY:N	1:A:3168:TYR:O	2.32	0.63
5:M:746:MET:O	5:M:751:LYS:NZ	2.24	0.63
6:Q:136:ILE:HB	6:R:40:ASP:HA	1.81	0.63
1:A:1112:ALA:HA	1:A:1180:GLN:HG2	1.79	0.63
1:F:3369:ASP:HB3	1:F:3372:LYS:HG2	1.80	0.63
1:F:3835:PRO:HA	1:F:3839:TYR:HB2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:303:PHE:HB3	3:H:290:GLN:HB2	1.78	0.63
6:Q:142:MET:HG2	6:Q:221:VAL:HB	1.80	0.63
1:A:1009:LEU:O	1:A:1013:ILE:HD12	1.98	0.63
2:G:404:ARG:NH2	8:I:32:DA:OP1	2.32	0.63
6:Q:131:VAL:HG13	6:R:135:LEU:HD23	1.81	0.63
1:A:82:ARG:HA	1:A:85:ILE:HD12	1.80	0.62
1:A:2380:ASN:OD1	1:A:2381:ALA:N	2.32	0.62
1:F:396:PHE:HE1	1:F:441:MET:HG3	1.64	0.62
1:F:4086:ASP:HA	1:F:4089:ILE:HG12	1.80	0.62
2:G:194:ARG:HH22	2:G:221:ILE:HA	1.63	0.62
2:G:352:PRO:HA	2:G:394:VAL:HA	1.81	0.62
5:M:711:ASN:O	5:M:715:SER:N	2.29	0.62
1:A:2891:ARG:HG2	1:A:3894:PRO:HB3	1.81	0.62
1:A:3982:SER:O	1:A:3986:HIS:ND1	2.21	0.62
2:B:304:ASN:HB3	2:B:311:LEU:HD21	1.79	0.62
2:G:291:GLU:HA	5:P:690:VAL:HG23	1.81	0.62
2:G:521:LEU:HA	2:G:524:GLU:HB2	1.81	0.62
6:R:60:GLU:HG2	6:R:61:LEU:HD12	1.82	0.62
1:A:1502:SER:OG	1:A:1503:LEU:N	2.31	0.62
1:A:3278:GLN:HB3	1:A:3282:ARG:HH12	1.64	0.62
2:B:347:LEU:HD11	2:B:396:ALA:HB1	1.80	0.62
1:A:1589:ASN:HD21	1:A:1592:MET:HG2	1.64	0.62
2:B:141:TYR:O	2:B:182:LYS:NZ	2.33	0.62
1:F:2375:ALA:HB3	1:F:2404:ARG:HD3	1.80	0.62
1:F:3929:MET:O	1:F:3938:ILE:N	2.27	0.62
3:H:499:LEU:HD22	3:H:500:HIS:HD2	1.63	0.62
2:G:277:VAL:HG23	3:H:429:ASP:HB3	1.81	0.62
2:G:528:LEU:HD21	3:H:372:ALA:HB1	1.81	0.62
3:H:66:ASN:ND2	3:H:74:TYR:O	2.33	0.62
1:F:736:LEU:HD12	1:F:740:ILE:HG21	1.82	0.62
1:A:1568:ASN:HD22	1:A:1603:GLN:HB2	1.63	0.62
1:A:2196:TRP:HB2	1:A:2199:LEU:HB2	1.82	0.62
1:A:3720:ALA:HB3	1:A:3743:HIS:HB3	1.80	0.62
1:F:835:LYS:HD3	1:F:838:LYS:HD2	1.81	0.62
8:I:35:DT:H3	9:J:22:DG:N2	1.98	0.62
1:F:759:GLY:HA3	1:F:766:ALA:HB2	1.81	0.62
1:F:3809:THR:OG1	1:F:3929:MET:SD	2.51	0.62
1:F:785:MET:HA	1:F:788:TYR:CZ	2.35	0.62
1:F:1685:ASP:HB3	1:F:1688:LEU:HG	1.81	0.62
2:G:95:ASN:OD1	2:G:98:ASN:N	2.33	0.62
2:G:348:MET:HG3	2:G:410:PHE:HE1	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:3681:LYS:HB2	1:F:3687:MET:HG2	1.82	0.62
8:E:41:DT:H2''	8:E:42:DA:H5'	1.81	0.62
1:F:1367:HIS:HB2	1:F:1370:ARG:HH12	1.63	0.61
2:G:132:GLN:OE1	2:G:137:HIS:ND1	2.33	0.61
5:M:739:GLN:OE1	5:M:741:ARG:NH1	2.33	0.61
2:B:410:PHE:HB3	2:B:437:LEU:HD12	1.80	0.61
1:F:3443:PRO:HB3	1:F:3471:ILE:HD11	1.82	0.61
1:A:166:ILE:HG13	1:A:167:PRO:HD3	1.82	0.61
3:H:653:GLN:O	3:H:657:ASN:ND2	2.33	0.61
1:F:866:ILE:HG13	1:F:3168:TYR:HD2	1.64	0.61
1:F:2218:PHE:O	1:F:2222:HIS:ND1	2.33	0.61
2:G:67:ILE:HG13	2:G:119:LEU:HD21	1.82	0.61
5:M:822:SER:HB3	5:M:838:LEU:HD13	1.82	0.61
4:N:58:ASP:O	6:Q:75:HIS:NE2	2.34	0.61
5:P:666:VAL:HG11	5:P:679:GLU:HG2	1.81	0.61
1:A:1302:ALA:H	1:A:1334:LYS:HZ1	1.47	0.61
1:F:3620:PRO:O	1:F:3630:ARG:NH1	2.31	0.61
1:F:2742:MET:HE1	8:I:44:DG:H1	1.65	0.61
1:F:3035:PHE:HA	1:F:3038:GLU:HB2	1.82	0.61
4:L:69:GLU:OE1	4:L:99:LYS:NZ	2.33	0.61
4:L:158:VAL:HA	4:L:161:ARG:HG2	1.82	0.61
1:F:2514:ASN:HD22	1:F:2517:LEU:HG	1.64	0.61
6:Q:139:LEU:HA	6:Q:142:MET:HE3	1.82	0.61
1:F:1016:GLY:HA3	1:F:1029:CYS:SG	2.41	0.61
1:F:2151:ILE:HG12	1:F:2192:THR:HG21	1.83	0.61
1:F:2268:LYS:HE3	1:F:2312:TYR:HB2	1.81	0.61
3:H:598:PHE:HZ	3:H:638:CYS:HB2	1.65	0.61
1:F:996:THR:HG23	1:F:1043:GLN:HE21	1.66	0.61
1:A:149:ILE:HD11	1:A:183:GLU:HB2	1.81	0.61
1:A:1082:PHE:HA	1:A:1085:ILE:HG12	1.83	0.61
1:A:3700:GLU:HA	1:A:3719:ILE:H	1.65	0.61
1:F:2967:GLU:O	1:F:2971:GLN:HG2	2.01	0.61
3:H:508:ILE:HG23	3:H:509:GLN:H	1.64	0.61
1:A:2213:ASN:ND2	1:A:2248:CYS:O	2.33	0.60
3:C:238:LYS:HE2	3:C:483:PRO:HB3	1.82	0.60
1:F:1626:TRP:HZ2	1:F:1674:THR:HG21	1.65	0.60
1:F:2723:THR:HA	1:F:2726:LEU:HD13	1.81	0.60
2:G:493:LEU:HD11	5:P:708:ARG:HE	1.66	0.60
1:A:320:LEU:HD21	1:A:365:GLY:HA2	1.83	0.60
1:A:1375:THR:HG22	1:A:1382:ILE:HG21	1.82	0.60
1:A:2313:LYS:HA	1:A:2316:TYR:CZ	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:20:SER:HB2	1:F:66:LEU:HD23	1.83	0.60
7:D:18:DA:H2"	7:D:19:DA:C8	2.36	0.60
1:F:326:MET:HA	1:F:329:LYS:HE3	1.83	0.60
1:F:1172:LEU:HD11	1:F:1187:SER:HB2	1.83	0.60
1:F:3666:LEU:HA	1:F:3669:LYS:HZ2	1.66	0.60
4:N:155:TRP:HE1	4:O:158:VAL:HG21	1.66	0.60
1:A:3512:VAL:HA	1:A:3515:GLN:HE21	1.66	0.60
3:C:93:ASP:HB3	3:C:97:LYS:HE2	1.83	0.60
1:F:3789:ARG:HD3	1:F:3938:ILE:HD11	1.83	0.60
2:G:329:LEU:HA	3:H:497:ARG:HH21	1.66	0.60
4:L:170:GLU:OE2	5:M:851:LYS:NZ	2.35	0.60
1:A:40:GLN:HB3	1:A:2427:ARG:HH21	1.66	0.60
1:A:771:ASN:OD1	1:A:854:ARG:NH2	2.34	0.60
1:A:1491:ILE:HG21	1:A:1558:TYR:HE2	1.67	0.60
1:A:3335:ARG:NH2	1:A:3418:ASP:OD2	2.33	0.60
1:F:919:LEU:HG	1:F:920:THR:HG23	1.82	0.60
1:A:264:ARG:N	8:E:40:DT:OP1	2.35	0.60
1:A:1145:LEU:HB3	1:A:1165:LEU:HB2	1.82	0.60
1:A:3628:PHE:HB2	1:A:3675:LYS:HB3	1.83	0.60
1:F:935:HIS:HB2	1:F:984:TYR:HE1	1.67	0.60
2:G:48:MET:HE3	2:G:60:PHE:HA	1.84	0.60
1:A:2425:ARG:NH1	1:A:2460:GLU:OE1	2.34	0.60
1:A:2808:LEU:HD23	1:A:2812:LEU:HD23	1.82	0.60
1:A:3506:LEU:O	1:A:3551:ASN:ND2	2.35	0.60
1:F:716:VAL:HG11	1:F:1120:SER:HB2	1.84	0.60
1:F:3380:ARG:O	1:F:3384:HIS:ND1	2.35	0.60
6:R:193:PHE:HA	6:R:197:LYS:HG2	1.84	0.60
1:A:3079:GLU:OE2	1:A:3105:ASN:ND2	2.35	0.60
3:C:339:CYS:H	3:C:396:ALA:HB3	1.66	0.60
1:F:477:ASN:OD1	1:F:478:CYS:N	2.35	0.60
1:F:1112:ALA:HA	1:F:1180:GLN:HG2	1.83	0.60
1:F:2742:MET:SD	9:J:13:DA:N6	2.65	0.60
1:F:3771:MET:HA	1:F:3774:ILE:HD12	1.83	0.60
1:A:1532:LEU:HD11	1:A:1560:TYR:HB2	1.83	0.60
3:C:497:ARG:NH1	3:C:503:GLU:O	2.35	0.60
1:F:1576:ASP:HA	1:F:1579:VAL:HB	1.84	0.60
1:F:3921:GLY:H	1:F:3944:HIS:HB2	1.66	0.60
4:N:159:GLN:OE1	4:O:161:ARG:NH2	2.34	0.60
1:A:785:MET:HA	1:A:788:TYR:CZ	2.37	0.59
1:F:1204:PRO:HB2	1:F:1206:LEU:H	1.67	0.59
1:F:2825:THR:HG22	1:F:2828:GLU:HG2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:3103:ILE:HD13	1:F:3138:ILE:HD11	1.83	0.59
1:F:3392:ALA:HB1	1:F:3409:VAL:HG22	1.84	0.59
2:G:264:ASN:OD1	2:G:267:ILE:N	2.31	0.59
1:A:54:GLN:OE1	1:A:54:GLN:N	2.35	0.59
1:A:1211:VAL:HG13	1:A:1219:PHE:HZ	1.67	0.59
1:A:2291:GLN:CD	1:A:2292:CYS:H	2.05	0.59
1:F:71:LYS:HB2	1:F:82:ARG:CZ	2.32	0.59
6:Q:131:VAL:H	6:R:44:VAL:HG23	1.68	0.59
1:A:1645:VAL:HA	1:A:1648:LEU:HD12	1.84	0.59
1:A:2569:SER:OG	1:A:2571:ASP:OD1	2.20	0.59
1:A:2825:THR:HG22	1:A:2828:GLU:HG2	1.84	0.59
1:A:3007:GLU:O	1:A:3011:LEU:N	2.35	0.59
1:F:1820:VAL:HA	1:F:1824:LEU:HD23	1.83	0.59
1:F:2372:PRO:O	1:F:2404:ARG:NH1	2.36	0.59
5:P:743:MET:SD	5:P:746:MET:HB3	2.42	0.59
1:A:2514:ASN:HD22	1:A:2517:LEU:HG	1.66	0.59
2:B:94:LYS:HE2	2:B:103:TYR:HE1	1.67	0.59
2:B:372:GLU:HG2	2:B:378:SER:HB2	1.83	0.59
3:C:210:MET:HA	3:C:213:ILE:HG12	1.85	0.59
4:O:159:GLN:HG3	5:P:843:LEU:HD11	1.84	0.59
1:A:1015:ASP:OD1	1:A:1016:GLY:N	2.36	0.59
1:A:1389:VAL:N	1:A:1392:MET:SD	2.70	0.59
1:A:2298:GLU:HG2	1:A:2301:GLN:HB3	1.84	0.59
1:A:3666:LEU:HA	1:A:3669:LYS:HZ3	1.67	0.59
1:F:1765:VAL:O	1:F:1768:ARG:NE	2.36	0.59
1:F:3758:LEU:HB2	1:F:3795:PRO:HB3	1.85	0.59
3:H:431:ARG:HB3	3:H:433:TYR:CE1	2.38	0.59
3:H:509:GLN:HG3	3:H:511:HIS:H	1.67	0.59
1:A:483:VAL:HG21	1:A:567:GLU:HG3	1.84	0.59
1:A:675:ARG:HA	1:A:678:LYS:HE2	1.84	0.59
1:A:1465:HIS:HA	1:A:1468:LEU:HB3	1.84	0.59
1:A:3103:ILE:HD13	1:A:3138:ILE:HD11	1.85	0.59
2:B:217:TYR:HB3	2:B:221:ILE:HD12	1.85	0.59
2:G:399:ARG:HA	2:G:410:PHE:HA	1.82	0.59
1:A:1144:SER:O	1:A:1151:ARG:NH2	2.34	0.59
4:K:133:THR:O	4:K:137:ASN:ND2	2.33	0.59
1:A:1002:GLU:O	1:A:1004:GLN:NE2	2.36	0.59
1:A:2388:LYS:NZ	2:B:157:VAL:O	2.36	0.59
1:A:3392:ALA:HB1	1:A:3409:VAL:HG22	1.84	0.59
1:A:3625:LEU:H	1:A:3683:CYS:HA	1.68	0.59
3:C:349:SER:O	3:C:352:GLN:NE2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:715:ALA:O	1:F:719:LYS:NZ	2.35	0.59
3:H:636:ILE:HA	3:H:639:ILE:HG12	1.85	0.59
6:R:210:PHE:HA	6:R:214:LEU:HB2	1.85	0.59
1:A:229:SER:O	1:A:233:ASN:ND2	2.35	0.59
1:A:3855:TYR:OH	1:A:4120:THR:O	2.21	0.59
1:A:12:LEU:HD21	1:A:44:LEU:HD22	1.85	0.59
1:A:2824:LYS:O	1:A:2829:LYS:NZ	2.36	0.59
1:F:1115:HIS:CE1	1:F:1183:CYS:H	2.20	0.59
1:F:2313:LYS:HA	1:F:2316:TYR:CZ	2.37	0.59
8:I:45:DG:H5'	8:I:45:DG:H8	1.68	0.59
1:A:210:SER:OG	1:A:257:ARG:NH1	2.35	0.58
1:A:1640:GLU:HA	1:A:1643:MET:SD	2.43	0.58
1:A:2243:GLU:HG2	1:A:2283:ASN:HD21	1.67	0.58
1:A:2414:GLN:OE1	1:A:2414:GLN:N	2.34	0.58
1:A:2534:ASN:HB3	1:A:2537:ASP:HB2	1.84	0.58
1:F:305:ASN:ND2	8:I:41:DT:OP2	2.36	0.58
1:F:1717:LEU:O	1:F:1721:HIS:ND1	2.35	0.58
1:F:2327:LEU:O	1:F:2333:ARG:NH2	2.36	0.58
1:F:2388:LYS:NZ	2:G:154:PHE:O	2.33	0.58
2:G:39:ILE:HD12	2:G:84:ALA:HB3	1.85	0.58
2:B:362:LEU:HD23	2:B:436:PHE:HB3	1.84	0.58
1:F:933:LEU:HD22	1:F:2797:VAL:HG11	1.83	0.58
6:R:36:LEU:O	6:R:46:HIS:ND1	2.36	0.58
1:A:207:GLN:NE2	1:A:215:PRO:O	2.36	0.58
1:A:908:ASP:HA	1:A:911:LEU:HD23	1.84	0.58
1:A:2925:GLU:HA	1:A:2928:LYS:HD2	1.84	0.58
1:F:1190:LEU:HD12	1:F:1193:LYS:HD3	1.86	0.58
1:F:1297:PHE:HA	1:F:1301:ILE:HG12	1.85	0.58
1:F:3750:PHE:HB3	1:F:3802:LEU:HD11	1.86	0.58
2:G:254:ARG:NH1	8:I:33:DA:O3'	2.36	0.58
1:A:38:LEU:HD21	1:A:85:ILE:HG13	1.84	0.58
1:A:3380:ARG:O	1:A:3384:HIS:ND1	2.36	0.58
1:F:1304:HIS:HE1	1:F:1307:ILE:HG22	1.69	0.58
3:H:44:ARG:NH2	3:H:233:LYS:O	2.36	0.58
2:B:352:PRO:HB2	2:B:354:VAL:HG22	1.85	0.58
1:F:1502:SER:OG	1:F:1503:LEU:N	2.34	0.58
1:A:1487:VAL:HG23	1:A:1488:TYR:HD1	1.68	0.58
1:A:2372:PRO:O	1:A:2404:ARG:NH1	2.36	0.58
1:A:2404:ARG:NH2	1:A:2406:GLU:OE2	2.36	0.58
1:A:2464:HIS:CE1	1:A:2466:SER:HG	2.22	0.58
1:F:3455:LYS:O	1:F:3455:LYS:NZ	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1685:ASP:HB3	1:A:1688:LEU:HG	1.84	0.58
1:F:3288:SER:HA	1:F:3292:GLY:HA3	1.84	0.58
3:H:496:HIS:CD2	3:H:506:PRO:HD3	2.38	0.58
9:J:26:DT:H2''	9:J:27:DT:N3	2.19	0.58
2:B:480:ASN:OD1	2:B:483:LEU:N	2.30	0.58
2:B:522:VAL:HA	2:B:525:PHE:HB2	1.85	0.58
2:G:300:THR:HA	3:H:293:THR:HA	1.86	0.58
4:L:150:ARG:NH1	4:L:151:LEU:HG	2.18	0.58
1:A:2479:TRP:O	1:A:2483:ASN:ND2	2.29	0.58
1:A:3474:ARG:NH2	1:A:3475:TYR:OH	2.37	0.58
2:B:399:ARG:HA	2:B:410:PHE:HA	1.85	0.58
1:F:3048:LYS:HD2	1:F:3061:LEU:HB2	1.85	0.58
2:G:34:GLY:HA3	2:G:162:SER:HB3	1.83	0.58
5:P:660:GLU:HG2	5:P:686:GLY:HA3	1.84	0.58
1:A:1549:SER:C	1:A:1550:VAL:HG22	2.16	0.58
1:F:3733:ARG:NH2	1:F:3755:GLY:O	2.37	0.58
3:H:460:SER:OG	3:H:461:MET:SD	2.62	0.58
8:E:43:DT:H2''	8:E:44:DG:H5'	1.86	0.58
1:A:3546:SER:O	1:A:3550:LYS:NZ	2.37	0.57
1:A:4115:ASN:O	1:A:4119:ARG:N	2.36	0.57
1:F:802:THR:O	1:F:852:ARG:NH1	2.36	0.57
1:F:3389:VAL:HG13	1:F:3413:TYR:HE1	1.69	0.57
3:H:519:PRO:HB2	3:H:521:GLU:HG2	1.85	0.57
1:A:1304:HIS:ND1	1:A:1307:ILE:O	2.37	0.57
1:A:3148:GLN:NE2	1:A:3150:ASN:OD1	2.38	0.57
1:A:3151:LEU:HD21	1:A:3196:LYS:HE3	1.86	0.57
1:A:3313:SER:HB2	1:A:3316:LEU:HD22	1.87	0.57
2:B:247:ARG:NH2	2:B:491:GLU:OE2	2.36	0.57
1:F:469:ALA:HA	1:F:475:LEU:HD13	1.85	0.57
1:F:2348:GLN:OE1	1:F:2353:GLN:NE2	2.36	0.57
1:F:2380:ASN:OD1	1:F:2381:ALA:N	2.37	0.57
2:G:253:LYS:HD2	2:G:254:ARG:HB2	1.86	0.57
1:A:471:LYS:O	1:A:475:LEU:N	2.28	0.57
3:C:250:ARG:HA	3:C:260:ARG:HA	1.86	0.57
1:F:297:LEU:HD23	1:F:316:LEU:HA	1.86	0.57
1:A:3117:ILE:O	1:A:3125:ARG:NH2	2.37	0.57
2:B:252:ARG:NH1	2:B:254:ARG:O	2.31	0.57
2:B:413:LEU:HB2	2:B:432:PHE:HB3	1.86	0.57
1:F:113:SER:O	1:F:117:LYS:HB2	2.04	0.57
1:F:1151:ARG:HB2	1:F:1163:LEU:HD12	1.86	0.57
1:F:1195:VAL:HA	1:F:1198:LEU:HD12	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1685:ASP:H	1:F:1688:LEU:HD12	1.69	0.57
1:F:2388:LYS:NZ	2:G:157:VAL:O	2.38	0.57
1:F:3464:LYS:HD3	1:F:3997:LEU:HD21	1.85	0.57
1:A:3142:ILE:HA	1:A:3145:ILE:HG12	1.86	0.57
3:C:335:SER:OG	3:C:339:CYS:SG	2.58	0.57
1:F:2257:PHE:HB2	1:F:2299:TYR:HE1	1.69	0.57
1:F:2271:SER:HA	1:F:2274:ILE:HD12	1.87	0.57
1:F:2291:GLN:NE2	1:F:2292:CYS:SG	2.78	0.57
1:A:984:TYR:HA	1:A:987:LEU:HB3	1.86	0.57
1:A:2123:PRO:HA	1:A:2127:LYS:HG2	1.86	0.57
1:F:639:ALA:O	1:F:643:GLU:N	2.37	0.57
1:F:1305:ASP:OD1	1:F:1334:LYS:NZ	2.37	0.57
2:G:305:THR:HG23	3:H:290:GLN:HG3	1.85	0.57
1:A:89:LEU:O	1:A:93:LEU:N	2.36	0.57
1:A:2120:ARG:HE	1:A:2159:PRO:HG2	1.70	0.57
1:A:3553:GLU:HG3	1:A:3557:ARG:HH22	1.69	0.57
3:H:9:ALA:HB3	3:H:130:ARG:HG3	1.85	0.57
6:Q:27:VAL:HG11	6:Q:80:LEU:HD12	1.85	0.57
1:A:753:GLN:NE2	1:A:791:ASP:O	2.32	0.57
1:A:993:HIS:ND1	1:A:2779:ASP:OD1	2.32	0.57
1:A:1096:VAL:O	1:A:1100:VAL:HG13	2.04	0.57
2:B:485:GLN:NE2	3:C:333:TYR:O	2.38	0.57
1:F:3155:VAL:H	1:F:3159:ARG:HH22	1.51	0.57
7:D:25:DT:H3'	7:D:26:DT:H72	1.86	0.57
1:A:128:LEU:HD21	1:A:170:VAL:HB	1.86	0.57
2:B:468:LYS:NZ	2:B:517:ARG:O	2.32	0.57
1:F:2342:CYS:HB3	1:F:2377:ARG:HH22	1.70	0.57
1:F:2815:GLY:HA2	1:F:2818:LYS:HZ2	1.70	0.57
1:F:2824:LYS:O	1:F:2829:LYS:NZ	2.38	0.57
2:G:131:PHE:CZ	2:G:135:MET:HG2	2.39	0.57
1:A:1717:LEU:O	1:A:1721:HIS:ND1	2.38	0.57
1:A:1843:ILE:HA	1:A:1846:ASP:HB3	1.85	0.57
2:B:350:PHE:HD2	3:C:461:MET:HB2	1.70	0.57
5:P:746:MET:HE3	5:P:751:LYS:HG2	1.86	0.57
1:F:476:ARG:HH22	1:F:1558:TYR:HE1	1.52	0.56
1:F:1023:SER:OG	1:F:1026:ARG:NH2	2.38	0.56
2:G:246:VAL:HB	2:G:249:LYS:HZ1	1.70	0.56
1:A:1849:ASP:OD1	1:A:1850:VAL:N	2.38	0.56
2:B:362:LEU:HB3	2:B:436:PHE:HB2	1.86	0.56
1:F:538:ASP:HA	1:F:541:MET:HG3	1.87	0.56
1:F:2365:ASN:HD22	1:F:2396:LEU:HG	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:31:GLY:HA3	4:K:47:VAL:HG21	1.87	0.56
1:A:40:GLN:HG3	1:A:2427:ARG:HE	1.70	0.56
1:A:1576:ASP:HA	1:A:1579:VAL:HB	1.86	0.56
1:A:2732:PHE:HA	1:A:2734:ARG:HH11	1.70	0.56
1:A:3554:PHE:HD1	1:A:3557:ARG:HH21	1.54	0.56
2:B:276:LEU:HA	3:C:433:TYR:HE2	1.69	0.56
1:F:68:PHE:O	1:F:82:ARG:NH2	2.38	0.56
1:F:117:LYS:NZ	3:H:298:ASN:O	2.29	0.56
1:F:1048:GLN:HA	1:F:1051:LYS:HG2	1.86	0.56
1:F:1377:CYS:SG	1:F:1378:GLU:N	2.78	0.56
1:F:1608:ARG:HE	1:F:1612:LYS:HZ2	1.51	0.56
1:F:2534:ASN:HB3	1:F:2537:ASP:HB2	1.87	0.56
1:F:3639:GLU:O	1:F:3643:HIS:ND1	2.34	0.56
1:F:3702:PRO:HB2	1:F:3794:VAL:HG21	1.87	0.56
2:G:271:VAL:HG12	2:G:370:PRO:HA	1.85	0.56
2:G:318:ARG:HH21	3:H:278:VAL:HG13	1.70	0.56
3:H:409:PHE:HB3	3:H:420:VAL:HG23	1.87	0.56
5:P:813:PHE:HA	5:P:850:ALA:O	2.05	0.56
5:P:845:LEU:HD22	5:P:852:VAL:HG13	1.87	0.56
1:A:1820:VAL:HA	1:A:1824:LEU:HD13	1.85	0.56
2:B:470:ARG:HH21	3:C:346:CYS:HA	1.70	0.56
1:F:938:VAL:HA	1:F:941:MET:HG3	1.86	0.56
2:G:476:ASP:HB2	3:H:427:MET:HG3	1.87	0.56
1:A:2232:ARG:NH1	1:A:2275:GLN:OE1	2.39	0.56
1:A:2522:ARG:HH21	1:A:2564:GLU:HG3	1.70	0.56
1:F:2330:VAL:HG22	1:F:2331:MET:SD	2.46	0.56
5:P:694:GLY:O	5:P:718:HIS:NE2	2.33	0.56
1:A:1354:GLU:HA	1:A:1357:LYS:HB3	1.88	0.56
1:A:3151:LEU:HD22	1:A:3197:LEU:HA	1.87	0.56
1:A:3737:ARG:HA	1:A:3751:LEU:HA	1.88	0.56
1:F:672:ILE:HG13	1:F:676:ASN:HD21	1.70	0.56
1:F:865:GLN:HE22	1:F:3171:ALA:N	2.04	0.56
1:F:2131:GLY:O	1:F:2135:ASN:ND2	2.38	0.56
1:A:852:ARG:NH2	1:A:922:SER:OG	2.38	0.56
1:A:1354:GLU:HB3	1:A:1357:LYS:HD3	1.87	0.56
1:A:3110:PHE:CE1	1:A:3128:LYS:HG3	2.40	0.56
2:B:275:ASN:O	2:B:278:GLN:NE2	2.38	0.56
1:F:529:ASP:HA	1:F:532:ARG:HH11	1.70	0.56
1:F:1307:ILE:HG23	1:F:1309:ALA:H	1.70	0.56
1:F:1605:PHE:O	1:F:1608:ARG:NH2	2.39	0.56
1:F:2555:LEU:HD11	1:F:2854:PHE:HA	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:44:VAL:HG12	6:Q:130:LEU:HD21	1.87	0.56
1:F:116:THR:O	2:G:297:LYS:NZ	2.38	0.56
1:F:1238:GLN:HB2	1:F:1239:PRO:HD3	1.88	0.56
3:H:153:SER:HA	3:H:156:LYS:HE2	1.87	0.56
3:H:315:ARG:HH11	3:H:320:ILE:HG13	1.70	0.56
1:A:2511:ILE:HD12	1:A:2550:ILE:HD12	1.87	0.56
3:C:514:ASN:OD1	3:C:515:MET:N	2.39	0.56
1:F:584:GLU:O	1:F:613:HIS:N	2.38	0.56
1:F:3736:LYS:HB2	1:F:3752:VAL:HB	1.87	0.56
1:F:3828:TYR:OH	1:F:3876:SER:O	2.24	0.56
4:K:169:LYS:HB2	4:L:169:LYS:HG3	1.87	0.56
5:M:710:LYS:HA	5:M:713:ILE:HD12	1.86	0.56
1:A:168:ASP:OD1	1:A:169:THR:N	2.35	0.55
1:A:1261:LEU:HG	1:A:1340:ARG:HG2	1.89	0.55
1:A:2221:LYS:HZ2	1:A:2255:LEU:HD22	1.70	0.55
2:B:71:TYR:HB2	2:B:116:ILE:HD11	1.87	0.55
1:F:3826:ALA:O	1:F:3830:SER:HB3	2.06	0.55
3:H:412:ILE:HA	3:H:417:GLU:HG3	1.87	0.55
8:E:23:DT:H2''	8:E:25:DA:N1	2.21	0.55
1:A:996:THR:HG23	1:A:1043:GLN:NE2	2.20	0.55
1:A:3447:VAL:HA	1:A:3450:MET:HG3	1.88	0.55
1:F:1070:PRO:HA	1:F:1113:LEU:HD21	1.88	0.55
1:F:1134:LEU:HD23	1:F:1137:ILE:HD11	1.89	0.55
5:M:666:VAL:HA	5:M:701:ILE:HB	1.88	0.55
1:A:3050:LYS:NZ	1:A:3180:ASP:OD1	2.31	0.55
1:A:3294:SER:O	1:A:3298:LEU:HG	2.07	0.55
3:C:242:ARG:HD2	3:C:273:LYS:HE3	1.88	0.55
3:H:453:ALA:HB2	3:H:536:LEU:HD23	1.87	0.55
4:O:142:GLU:HB3	4:O:146:LYS:NZ	2.22	0.55
7:D:18:DA:H2'	7:D:18:DA:N3	2.20	0.55
1:A:200:PHE:CE2	1:A:227:LEU:HD21	2.41	0.55
1:A:2290:PRO:O	1:A:2292:CYS:N	2.39	0.55
1:A:3569:GLN:HA	1:A:3572:ILE:HD12	1.88	0.55
1:A:3576:ASP:O	1:A:3629:ARG:NH1	2.40	0.55
1:A:3717:VAL:HA	1:A:3743:HIS:HE1	1.72	0.55
1:F:782:ARG:NH1	1:F:3168:TYR:OH	2.40	0.55
4:K:187:LYS:HZ1	4:L:188:LYS:HG3	1.72	0.55
5:M:725:TRP:HE3	5:M:726:LEU:HD22	1.71	0.55
5:P:764:SER:OG	5:P:767:ILE:O	2.24	0.55
1:A:63:PHE:HE2	1:A:85:ILE:HG12	1.70	0.55
1:A:2205:VAL:HG22	1:A:2207:LYS:H	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:457:GLU:OE2	2:B:458:GLN:NE2	2.30	0.55
2:B:481:PRO:HA	2:B:484:GLN:HE21	1.70	0.55
5:P:813:PHE:H	5:P:848:HIS:HB2	1.70	0.55
1:A:71:LYS:CB	1:A:82:ARG:HH22	2.20	0.55
1:A:1610:ASN:OD1	1:A:1611:GLN:N	2.38	0.55
1:A:1614:GLN:HA	1:A:1617:LYS:HE2	1.89	0.55
1:A:2737:GLU:HG2	1:A:2740:SER:HB2	1.88	0.55
3:H:86:PRO:HA	3:H:90:LEU:HD12	1.88	0.55
8:I:34:DC:H42	9:J:23:DT:H3	1.53	0.55
1:A:983:LEU:HD22	1:A:2775:TYR:HE2	1.71	0.55
1:A:1841:SER:HA	1:A:1844:VAL:HG23	1.89	0.55
1:F:538:ASP:OD1	1:F:539:GLN:N	2.40	0.55
1:F:2331:MET:O	1:F:2334:LYS:NZ	2.32	0.55
1:F:2439:ILE:HD12	1:F:2454:LEU:HD21	1.89	0.55
1:F:3527:GLN:HB2	1:F:3705:TYR:HE2	1.72	0.55
1:F:4113:ASP:O	1:F:4117:LEU:HG	2.06	0.55
2:G:381:LEU:O	2:G:385:LEU:HG	2.05	0.55
1:A:3263:HIS:HB2	1:A:3276:TRP:CZ2	2.42	0.55
2:B:264:ASN:HD22	3:C:530:LEU:HD13	1.72	0.55
1:F:87:LYS:HE2	1:F:831:LEU:HD13	1.87	0.55
2:G:336:GLU:O	3:H:489:ARG:NH2	2.40	0.55
7:D:37:DG:C8	8:E:19:DC:H2"	2.42	0.55
1:A:1151:ARG:HB2	1:A:1163:LEU:HD12	1.89	0.55
1:F:2479:TRP:O	1:F:2483:ASN:ND2	2.26	0.55
1:F:3255:ALA:HB1	1:F:3258:LEU:HB2	1.89	0.55
3:H:453:ALA:HB1	3:H:533:ILE:HG12	1.88	0.55
4:K:101:LEU:HD21	6:R:113:SER:HB3	1.89	0.55
5:P:665:CYS:HB3	5:P:700:VAL:HA	1.88	0.55
1:A:3576:ASP:O	1:A:3579:SER:OG	2.21	0.55
3:C:253:ILE:HB	3:C:257:LEU:HB3	1.88	0.55
1:F:3118:ASP:HB3	1:F:3121:LEU:HD13	1.88	0.55
1:F:3226:ASP:N	1:F:3229:SER:HG	2.05	0.55
1:A:3512:VAL:O	1:A:3516:HIS:ND1	2.34	0.54
1:F:1452:VAL:HA	1:F:1517:LEU:HD11	1.89	0.54
2:G:35:ARG:HH21	2:G:80:ARG:HB3	1.72	0.54
2:G:166:ILE:HB	2:G:200:LEU:HA	1.89	0.54
6:R:195:ILE:HG23	6:R:196:GLU:HG3	1.88	0.54
1:A:2220:MET:HA	1:A:2223:VAL:HG12	1.89	0.54
1:A:3878:VAL:O	1:A:3965:ARG:NH1	2.39	0.54
1:F:1070:PRO:HG2	1:F:3715:TYR:HB2	1.88	0.54
1:A:2943:PHE:O	1:A:2954:GLN:NE2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2986:PRO:O	1:A:2991:LYS:NZ	2.40	0.54
2:B:484:GLN:O	2:B:488:ARG:HG2	2.08	0.54
1:F:79:ARG:NH1	1:F:119:ARG:HD2	2.23	0.54
1:F:1551:ILE:HG13	1:F:1552:HIS:H	1.73	0.54
1:F:1686:LEU:HA	1:F:1689:LYS:HD2	1.90	0.54
2:G:328:ILE:O	3:H:497:ARG:NE	2.41	0.54
3:H:641:ALA:O	3:H:644:GLU:HG3	2.06	0.54
5:P:856:LEU:HD11	5:P:882:PHE:HZ	1.72	0.54
1:A:1358:LEU:HA	1:A:1361:LYS:HE2	1.89	0.54
1:A:1878:ASP:OD1	1:A:1879:VAL:N	2.40	0.54
1:A:2402:LEU:HD11	1:A:2437:ASP:HB2	1.88	0.54
1:A:95:LYS:HD3	1:A:97:GLY:H	1.73	0.54
1:A:1958:GLU:HG2	1:A:1959:LEU:H	1.72	0.54
1:F:863:GLY:HA3	1:F:3167:ARG:O	2.07	0.54
1:F:1268:ASN:HD21	1:F:1344:PHE:HA	1.72	0.54
1:F:1766:LEU:HD23	1:F:1822:ARG:HH11	1.71	0.54
1:F:2466:SER:OG	1:F:2469:CYS:SG	2.65	0.54
1:F:3808:ASN:ND2	1:F:3933:GLU:OE1	2.40	0.54
1:F:3831:ASP:HB3	1:F:3832:PRO:HD3	1.90	0.54
1:A:542:ASP:OD1	1:A:543:SER:N	2.41	0.54
1:A:2290:PRO:O	1:A:2293:GLY:N	2.36	0.54
1:A:3035:PHE:HA	1:A:3038:GLU:HB2	1.90	0.54
1:A:3701:ILE:HB	1:A:3704:GLN:NE2	2.23	0.54
1:F:762:TYR:HD2	1:F:765:LEU:HB2	1.71	0.54
1:F:3142:ILE:HA	1:F:3145:ILE:HG12	1.89	0.54
1:F:3183:ILE:HD12	1:F:3238:MET:HB3	1.89	0.54
6:R:41:LEU:HD11	6:R:139:LEU:HD21	1.89	0.54
1:A:582:THR:HA	1:A:660:LEU:HD21	1.90	0.54
1:A:1420:ARG:NH1	1:A:1467:ILE:O	2.39	0.54
1:A:1675:TYR:OH	1:A:1692:ALA:O	2.22	0.54
1:A:1686:LEU:HA	1:A:1689:LYS:HD2	1.90	0.54
1:F:862:LEU:HD23	1:F:866:ILE:HG21	1.90	0.54
1:F:2940:ARG:O	1:F:2944:THR:HB	2.08	0.54
1:F:3126:LEU:O	1:F:3130:GLN:NE2	2.41	0.54
1:F:3639:GLU:HG3	1:F:3643:HIS:HE1	1.72	0.54
2:G:85:VAL:HG23	2:G:105:LEU:HB3	1.90	0.54
4:N:5:ILE:HG13	4:N:126:LEU:HD21	1.90	0.54
1:A:172:GLU:HG3	1:A:220:LEU:HD13	1.89	0.54
1:A:759:GLY:HA3	1:A:766:ALA:HB2	1.90	0.54
1:A:1204:PRO:HB2	1:A:1206:LEU:H	1.72	0.54
1:A:1389:VAL:HG23	1:A:1391:VAL:HG22	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2587:GLN:O	1:A:2777:HIS:N	2.38	0.54
1:A:3008:TRP:HA	1:A:3011:LEU:HD12	1.90	0.54
1:A:3882:LEU:HA	1:A:3885:ARG:HE	1.72	0.54
1:A:3981:TYR:HE1	1:A:4105:LYS:HB2	1.73	0.54
1:F:3112:GLN:O	1:F:3115:SER:OG	2.23	0.54
1:F:3269:ARG:HE	1:F:3272:TRP:HB2	1.73	0.54
1:F:3385:LEU:HB3	1:F:3416:LEU:HD12	1.89	0.54
4:L:162:PHE:HE2	5:M:843:LEU:HB3	1.72	0.54
5:M:713:ILE:HG12	5:M:745:HIS:HB2	1.90	0.54
1:F:305:ASN:O	1:F:308:LEU:N	2.40	0.54
1:F:2414:GLN:OE1	1:F:2414:GLN:N	2.40	0.54
1:F:3065:ILE:O	1:F:3069:MET:N	2.40	0.54
2:G:163:HIS:HE1	2:G:165:ARG:HB2	1.72	0.54
1:A:2589:TYR:H	1:A:2776:ARG:HA	1.73	0.54
5:P:747:CYS:SG	5:P:749:SER:OG	2.62	0.54
1:A:1115:HIS:CE1	1:A:1183:CYS:H	2.26	0.53
1:A:1406:LEU:HA	1:A:1409:SER:HB3	1.90	0.53
2:B:515:ASN:O	2:B:519:GLY:N	2.41	0.53
1:F:348:ILE:HG21	1:F:362:ALA:HB2	1.90	0.53
1:F:3700:GLU:OE1	1:F:3705:TYR:OH	2.24	0.53
5:P:725:TRP:HB2	5:P:742:PHE:CD2	2.44	0.53
1:A:175:TYR:O	1:A:227:LEU:HD12	2.08	0.53
1:A:977:ASP:OD1	1:A:980:THR:N	2.37	0.53
1:A:1605:PHE:HE2	1:A:6013:UNK:HA	1.73	0.53
1:A:3485:LYS:O	1:A:3489:SER:OG	2.25	0.53
2:B:40:PHE:HB2	2:B:85:VAL:HG12	1.90	0.53
1:F:135:LEU:HD21	1:F:177:LEU:HA	1.90	0.53
1:F:1849:ASP:OD1	1:F:1850:VAL:N	2.42	0.53
1:F:3506:LEU:HG	1:F:3515:GLN:HG3	1.88	0.53
3:H:81:ARG:HD2	3:H:90:LEU:HD22	1.90	0.53
1:A:1169:VAL:HG11	1:A:1198:LEU:HD11	1.91	0.53
1:A:3901:ARG:NH1	1:A:3971:MET:HG2	2.24	0.53
2:B:74:LYS:HG3	2:B:83:LEU:HD11	1.91	0.53
2:B:426:GLN:NE2	2:B:427:VAL:O	2.42	0.53
1:F:266:ALA:O	1:F:269:SER:OG	2.21	0.53
1:F:3179:TRP:HE3	1:F:3242:MET:SD	2.31	0.53
1:F:3278:GLN:HB3	1:F:3282:ARG:HH12	1.72	0.53
5:P:813:PHE:H	5:P:848:HIS:CB	2.21	0.53
6:Q:159:MET:SD	6:Q:160:LYS:HG3	2.48	0.53
8:I:27:DC:H2'	9:J:30:DT:C2	2.43	0.53
1:A:938:VAL:HA	1:A:941:MET:HG3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1833:LEU:HD11	1:A:1883:ARG:HD2	1.90	0.53
1:A:2271:SER:HA	1:A:2274:ILE:HD12	1.91	0.53
1:A:3502:MET:HG3	1:A:3518:VAL:HG11	1.89	0.53
3:C:497:ARG:HH22	3:C:504:PRO:HA	1.73	0.53
1:F:67:VAL:HA	1:F:71:LYS:HE2	1.90	0.53
1:F:651:TYR:CZ	1:F:655:LEU:HD11	2.44	0.53
1:F:959:TYR:CZ	1:F:963:LYS:HD2	2.43	0.53
1:F:3820:MET:HB3	1:F:3885:ARG:HH22	1.72	0.53
2:G:348:MET:HG3	2:G:410:PHE:CE1	2.44	0.53
4:L:51:GLU:OE1	4:L:112:ASN:ND2	2.33	0.53
1:A:886:TRP:O	1:A:888:ARG:NH1	2.41	0.53
1:A:1238:GLN:HA	1:A:1296:PHE:CZ	2.43	0.53
1:A:2244:CYS:SG	1:A:2245:TRP:N	2.82	0.53
1:F:993:HIS:NE2	1:F:1035:GLU:OE2	2.32	0.53
1:F:1058:SER:O	1:F:1062:ARG:HG2	2.08	0.53
2:G:318:ARG:HB3	3:H:276:TRP:HB3	1.90	0.53
4:K:187:LYS:HA	4:K:190:LYS:HD2	1.90	0.53
4:L:56:ALA:HB1	4:L:63:LYS:HG2	1.90	0.53
1:F:36:ARG:HD3	1:F:2426:HIS:CG	2.44	0.53
1:F:880:MET:O	1:F:881:LYS:HG2	2.08	0.53
1:F:2346:ALA:HB2	1:F:2377:ARG:HH11	1.74	0.53
2:G:329:LEU:HD12	3:H:497:ARG:HH21	1.73	0.53
3:H:33:GLN:HA	3:H:36:LYS:HG2	1.90	0.53
4:N:28:LEU:HD23	4:N:70:LEU:HD13	1.90	0.53
8:I:27:DC:H1'	9:J:31:DT:C2	2.43	0.53
1:A:10:CYS:SG	1:A:11:SER:N	2.81	0.53
1:A:992:ILE:HG23	1:A:1036:PHE:HD1	1.72	0.53
1:A:1864:ASP:OD1	1:A:1864:ASP:N	2.42	0.53
1:A:2283:ASN:HB2	1:A:2285:LEU:HG	1.91	0.53
1:A:3994:ASP:HB3	1:A:3998:LEU:HG	1.91	0.53
2:B:88:TYR:HB3	2:B:146:VAL:HG11	1.90	0.53
1:F:1238:GLN:HA	1:F:1296:PHE:CZ	2.43	0.53
3:H:44:ARG:CZ	3:H:234:LEU:HA	2.38	0.53
8:I:30:DA:H3'	8:I:32:DA:N6	2.24	0.53
1:A:1633:TRP:HA	1:A:1678:LEU:HD21	1.90	0.53
3:C:199:GLU:OE2	3:C:202:LYS:NZ	2.42	0.53
3:H:76:ASN:ND2	3:H:104:GLN:O	2.35	0.53
6:R:95:PHE:HE2	6:R:108:VAL:HG13	1.74	0.53
1:A:651:TYR:CZ	1:A:655:LEU:HD11	2.44	0.53
1:A:1475:LEU:HD23	1:A:1527:ARG:HD2	1.91	0.53
1:A:2439:ILE:HD12	1:A:2454:LEU:HD21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3479:THR:HA	1:A:3482:LEU:HB2	1.91	0.53
2:G:178:ASN:HD21	2:G:182:LYS:HD2	1.74	0.53
4:N:99:LYS:NZ	4:N:100:ASN:O	2.42	0.53
1:A:1418:HIS:O	1:A:1422:LYS:HG2	2.09	0.53
1:A:3172:LYS:HD3	1:A:3248:LYS:HB3	1.89	0.53
1:A:3915:HIS:HB2	1:A:3920:ILE:HB	1.91	0.53
2:B:400:TYR:N	2:B:409:TYR:O	2.30	0.53
1:F:1601:LEU:HD13	1:F:1651:LYS:HB3	1.91	0.53
1:F:2160:TYR:HD2	1:F:2164:TRP:CD1	2.26	0.53
1:F:2287:PRO:HG3	1:F:2330:VAL:HA	1.90	0.53
1:F:3566:GLY:O	1:F:3570:ASP:N	2.37	0.53
1:F:3974:MET:SD	1:F:3976:GLU:N	2.82	0.53
2:G:327:ILE:HG23	3:H:497:ARG:HG2	1.90	0.53
5:P:826:ILE:HG13	5:P:856:LEU:HD22	1.90	0.53
1:A:880:MET:O	1:A:881:LYS:HG2	2.09	0.52
1:A:1805:PHE:HZ	1:A:1869:LYS:HA	1.73	0.52
1:A:2271:SER:HB3	1:A:2315:VAL:HG22	1.91	0.52
1:A:3930:VAL:HB	1:A:3937:VAL:HG12	1.90	0.52
1:F:175:TYR:O	1:F:227:LEU:HD12	2.08	0.52
1:F:2157:PHE:HB2	1:F:2160:TYR:HB3	1.92	0.52
1:F:3428:GLU:OE1	1:F:3474:ARG:NH2	2.42	0.52
1:F:4115:ASN:O	1:F:4119:ARG:N	2.40	0.52
1:A:4055:ASN:HD22	1:A:4058:VAL:HG23	1.74	0.52
2:B:357:LYS:HE2	2:B:359:HIS:CE1	2.43	0.52
3:C:529:PRO:HA	3:C:532:LYS:HG2	1.91	0.52
1:F:440:VAL:HG21	1:F:485:GLN:HG3	1.91	0.52
1:F:1058:SER:HA	1:F:1061:LYS:HE2	1.92	0.52
1:F:1082:PHE:HA	1:F:1085:ILE:HG12	1.91	0.52
1:F:1790:SER:HG	1:F:1793:THR:HG1	1.55	0.52
1:F:3354:ASP:O	1:F:3358:ARG:NH1	2.42	0.52
1:F:3364:GLY:HA3	1:F:3373:VAL:HA	1.91	0.52
2:G:59:PRO:HA	2:G:62:MET:SD	2.49	0.52
2:G:203:MET:HE1	2:G:237:SER:HB2	1.91	0.52
4:L:4:LYS:HG3	4:L:74:LEU:HD22	1.92	0.52
5:P:737:PRO:O	5:P:739:GLN:NE2	2.42	0.52
5:P:754:PHE:O	5:P:758:TYR:N	2.39	0.52
1:A:79:ARG:HE	1:A:82:ARG:HD2	1.73	0.52
1:A:1086:TYR:CE1	1:A:1133:HIS:HB3	2.43	0.52
1:A:1590:THR:HG21	1:A:1641:THR:HG23	1.89	0.52
1:A:4108:MET:O	1:A:4112:THR:OG1	2.25	0.52
2:B:414:VAL:HB	2:B:433:GLN:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1779:GLN:O	1:F:1783:ARG:HG2	2.10	0.52
2:G:444:ARG:HH11	3:H:244:SER:HB2	1.74	0.52
7:D:23:DT:H2'	7:D:24:DT:N3	2.24	0.52
1:A:4113:ASP:O	1:A:4117:LEU:HG	2.09	0.52
2:B:259:LEU:HD11	2:B:400:TYR:HE1	1.74	0.52
1:F:56:SER:HA	1:F:59:PHE:HD2	1.74	0.52
1:F:1153:LEU:HD12	1:F:1154:PRO:HD2	1.92	0.52
1:F:1568:ASN:HD22	1:F:1603:GLN:HB2	1.74	0.52
1:F:3472:ILE:HA	1:F:3479:THR:HG21	1.91	0.52
1:F:3493:TRP:CD1	1:F:3521:ILE:HG12	2.42	0.52
2:G:194:ARG:NH1	2:G:220:ILE:O	2.43	0.52
2:G:474:ARG:HB3	2:G:477:SER:HB2	1.90	0.52
4:L:37:THR:HG22	4:L:39:GLY:H	1.74	0.52
1:A:672:ILE:HG13	1:A:676:ASN:HD21	1.74	0.52
2:G:348:MET:HG2	2:G:398:CYS:HA	1.90	0.52
5:M:659:PHE:HD2	5:M:685:PHE:HB3	1.73	0.52
1:A:450:SER:O	1:A:454:GLN:HG3	2.10	0.52
1:A:1867:ILE:HD13	1:A:1936:ARG:HB3	1.92	0.52
1:A:2948:GLY:HA3	1:A:2954:GLN:HE21	1.73	0.52
3:C:327:ASP:O	3:C:331:MET:HG3	2.10	0.52
1:F:639:ALA:HA	1:F:642:PHE:HB3	1.91	0.52
2:G:419:GLU:OE1	2:G:428:THR:OG1	2.26	0.52
1:A:36:ARG:HD3	1:A:2426:HIS:HB2	1.90	0.52
1:A:1153:LEU:HD12	1:A:1154:PRO:HD2	1.90	0.52
2:B:85:VAL:HG22	2:B:106:GLN:HB3	1.92	0.52
1:F:891:ARG:NH1	1:F:956:PRO:O	2.43	0.52
1:F:1348:LEU:O	1:F:1352:SER:OG	2.22	0.52
1:F:2312:TYR:CE2	1:F:2314:GLU:HB3	2.45	0.52
1:F:3011:LEU:HD22	1:F:3047:SER:HA	1.91	0.52
1:F:3781:CYS:HB3	1:F:3786:LEU:HB2	1.92	0.52
1:A:314:SER:O	1:A:317:GLU:HG3	2.10	0.52
1:A:1727:ARG:HD2	1:A:1772:HIS:HB2	1.91	0.52
1:A:3503:VAL:HG11	1:A:3532:PRO:HB3	1.92	0.52
1:A:3921:GLY:H	1:A:3944:HIS:HB2	1.73	0.52
3:C:266:SER:N	3:C:361:VAL:O	2.41	0.52
1:F:2847:THR:OG1	1:F:2849:SER:O	2.25	0.52
4:K:150:ARG:O	4:K:153:ARG:HG3	2.10	0.52
4:O:69:GLU:HA	4:O:72:LYS:HG2	1.91	0.52
1:A:1279:LEU:HD22	1:A:1356:TRP:HE1	1.74	0.52
1:A:3169:PRO:HG2	1:A:3179:TRP:CZ2	2.45	0.52
1:A:3771:MET:HA	1:A:3774:ILE:HD12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:92:LYS:HE2	2:B:135:MET:HA	1.92	0.52
3:C:86:PRO:HA	3:C:90:LEU:HD12	1.92	0.52
3:C:326:VAL:O	3:C:330:GLN:HG2	2.10	0.52
1:F:1438:GLY:O	1:F:1445:ARG:NH2	2.37	0.52
1:F:2201:THR:HG23	1:F:2203:THR:HG22	1.92	0.52
1:F:2753:ARG:O	1:F:2757:ILE:HG12	2.10	0.52
8:I:24:DA:H5'	8:I:25:DA:N7	2.25	0.52
1:F:98:GLN:NE2	1:F:98:GLN:O	2.42	0.52
1:F:1268:ASN:ND2	1:F:1344:PHE:HA	2.25	0.52
1:F:3575:LEU:HD13	1:F:3578:LEU:HD12	1.92	0.52
1:A:1016:GLY:O	1:A:1026:ARG:HG2	2.10	0.51
1:A:1281:VAL:HG23	1:A:1282:LEU:HG	1.91	0.51
1:A:1725:GLN:HG3	1:A:1728:GLU:H	1.75	0.51
1:A:1957:ASN:HB2	1:A:2103:HIS:NE2	2.25	0.51
1:F:214:GLU:OE2	8:I:31:DA:N6	2.36	0.51
1:F:996:THR:HG23	1:F:1043:GLN:NE2	2.24	0.51
1:F:1367:HIS:HB2	1:F:1370:ARG:NH1	2.25	0.51
1:F:3305:SER:OG	1:F:3308:ASP:OD1	2.28	0.51
2:G:515:ASN:O	2:G:519:GLY:N	2.42	0.51
1:A:708:VAL:HG22	1:A:740:ILE:HG13	1.92	0.51
1:A:1452:VAL:HA	1:A:1517:LEU:HD11	1.91	0.51
1:F:72:SER:H	1:F:82:ARG:NH2	2.08	0.51
1:F:860:GLY:HA3	1:F:3136:THR:HG21	1.91	0.51
1:F:3155:VAL:HG23	1:F:3159:ARG:HH12	1.75	0.51
2:G:484:GLN:O	2:G:488:ARG:HG2	2.10	0.51
3:H:246:HIS:NE2	9:J:36:DG:OP1	2.42	0.51
3:H:633:MET:HA	3:H:636:ILE:HG12	1.92	0.51
4:O:34:ILE:HD13	4:O:95:PHE:HE2	1.75	0.51
8:E:26:DA:C2	8:E:27:DC:H2'	2.44	0.51
1:A:196:LEU:HB3	1:A:200:PHE:CZ	2.45	0.51
1:A:1294:VAL:HA	1:A:1297:PHE:CD2	2.45	0.51
1:A:1649:LEU:HA	1:A:1652:ILE:HD12	1.93	0.51
1:A:1878:ASP:HB3	1:A:1947:CYS:HA	1.92	0.51
1:A:2174:SER:OG	1:A:2214:ARG:NH1	2.43	0.51
2:B:251:THR:O	3:C:431:ARG:NH1	2.42	0.51
1:F:938:VAL:HG21	1:F:969:LEU:HD11	1.93	0.51
1:F:1010:LEU:HG	1:F:1014:LEU:HD23	1.91	0.51
1:F:1958:GLU:HG2	1:F:1959:LEU:N	2.25	0.51
1:F:3110:PHE:CD2	1:F:3135:LEU:HD11	2.45	0.51
1:F:3244:ASP:OD1	1:F:3247:ARG:NH2	2.32	0.51
2:G:407:PRO:HG3	3:H:486:ARG:HD3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:44:ARG:HH11	3:H:236:VAL:H	1.57	0.51
4:N:165:CYS:HG	4:O:162:PHE:HZ	1.59	0.51
1:A:762:TYR:HD2	1:A:765:LEU:HD23	1.75	0.51
1:A:959:TYR:CE2	1:A:963:LYS:HD2	2.45	0.51
1:A:2834:GLN:HG3	1:A:2838:GLN:HE21	1.75	0.51
1:A:3269:ARG:CZ	1:A:3272:TRP:HB2	2.41	0.51
1:A:3619:ASP:OD1	1:A:3619:ASP:N	2.44	0.51
1:F:770:LEU:HD11	1:F:858:MET:HG2	1.92	0.51
1:F:982:GLN:HE21	1:F:2591:ILE:HG23	1.75	0.51
1:F:1069:HIS:NE2	1:F:3743:HIS:O	2.44	0.51
1:F:1086:TYR:CE1	1:F:1133:HIS:HB3	2.45	0.51
2:G:444:ARG:NH2	3:H:241:GLU:OE1	2.40	0.51
3:H:357:MET:N	3:H:357:MET:SD	2.84	0.51
1:A:3263:HIS:HB2	1:A:3276:TRP:CE2	2.45	0.51
1:A:3965:ARG:HD3	1:A:3966:GLN:HE22	1.75	0.51
2:B:48:MET:HG3	2:B:128:GLN:HE21	1.76	0.51
2:B:146:VAL:HA	2:B:149:VAL:HG12	1.93	0.51
2:B:255:ALA:O	8:E:32:DA:N6	2.43	0.51
1:F:1372:LEU:O	1:F:1376:LEU:HG	2.11	0.51
1:F:3506:LEU:HD21	1:F:3554:PHE:HD2	1.76	0.51
1:F:4055:ASN:HB2	1:F:4095:GLU:HA	1.92	0.51
1:F:4107:LEU:O	1:F:4111:ALA:HB3	2.09	0.51
4:N:20:LEU:HD21	4:N:74:LEU:HD13	1.92	0.51
6:Q:210:PHE:HB2	6:R:140:MET:HG3	1.93	0.51
1:A:923:ASP:O	1:A:926:THR:N	2.44	0.51
2:B:407:PRO:HB3	3:C:486:ARG:HG3	1.92	0.51
1:F:542:ASP:OD1	1:F:543:SER:N	2.42	0.51
1:F:1086:TYR:CD1	1:F:1133:HIS:HB3	2.46	0.51
1:F:2746:LYS:O	1:F:2750:GLU:HG2	2.10	0.51
4:L:146:LYS:O	4:L:149:GLU:HG3	2.10	0.51
5:P:812:MET:O	5:P:850:ALA:HB3	2.11	0.51
1:A:1375:THR:HG22	1:A:1382:ILE:HD13	1.91	0.51
1:A:3295:GLU:O	1:A:3299:THR:HG22	2.11	0.51
2:B:77:SER:HB2	2:B:249:LYS:HB3	1.92	0.51
1:F:2225:HIS:HB2	1:F:2231:PHE:HB2	1.93	0.51
1:F:3811:THR:HG23	1:F:3814:ASP:H	1.76	0.51
1:F:3970:LEU:HG	1:F:3971:MET:HG3	1.93	0.51
2:G:101:ASN:ND2	2:G:140:ASP:O	2.43	0.51
3:H:7:LYS:HE2	3:H:128:GLU:HG3	1.92	0.51
7:D:33:DA:H5''	7:D:33:DA:C8	2.46	0.51
1:A:250:ASN:OD1	1:A:254:LYS:NZ	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1611:GLN:HB2	1:A:1613:HIS:ND1	2.26	0.51
1:A:3500:SER:HA	1:A:3503:VAL:HG12	1.93	0.51
1:A:3992:ARG:NH2	1:A:4100:GLU:HG3	2.25	0.51
2:B:396:ALA:HB3	2:B:413:LEU:HD21	1.92	0.51
1:F:1780:SER:HA	1:F:1783:ARG:HG2	1.91	0.51
1:F:2410:GLU:O	1:F:2414:GLN:NE2	2.44	0.51
4:O:150:ARG:NH2	4:O:154:ASP:OD2	2.44	0.51
6:Q:11:GLN:HG3	6:Q:28:PHE:HB2	1.92	0.51
7:D:31:DT:H2'	7:D:32:DT:C2	2.45	0.51
1:A:1046:PRO:O	1:A:1049:GLN:N	2.43	0.51
1:A:3751:LEU:HD22	1:A:3803:ILE:HD11	1.92	0.51
1:F:125:ILE:HD12	1:F:125:ILE:H	1.75	0.51
1:F:1746:PHE:HB3	1:F:1762:MET:SD	2.50	0.51
1:F:2357:GLU:HA	1:F:2360:PHE:HB3	1.93	0.51
1:F:2964:ASP:HB2	1:F:3252:PHE:HD2	1.76	0.51
1:F:4086:ASP:OD1	1:F:4087:HIS:N	2.43	0.51
2:G:317:LYS:NZ	2:G:330:GLU:OE1	2.43	0.51
4:O:67:VAL:HB	4:O:71:ARG:HH12	1.76	0.51
6:Q:128:PRO:HB3	6:R:128:PRO:HA	1.93	0.51
6:R:193:PHE:HD1	6:R:197:LYS:HG3	1.76	0.51
1:A:2963:SER:OG	1:A:3250:ASN:O	2.22	0.51
1:A:3796:MET:H	1:A:3801:GLY:HA2	1.76	0.51
1:F:146:GLU:N	1:F:146:GLU:OE1	2.44	0.51
1:F:1601:LEU:HB3	1:F:1655:ILE:HD11	1.93	0.51
2:G:355:LEU:HD11	3:H:475:ASP:HB2	1.92	0.51
4:K:187:LYS:NZ	4:L:188:LYS:HG3	2.26	0.51
6:R:154:ALA:O	6:R:158:HIS:ND1	2.44	0.51
1:A:425:ASP:OD1	1:A:425:ASP:N	2.44	0.50
1:A:1071:ASN:OD1	1:A:1073:PHE:N	2.43	0.50
1:A:1474:ASP:OD1	1:A:1474:ASP:N	2.43	0.50
1:A:1560:TYR:OH	1:A:1599:GLY:HA3	2.11	0.50
1:A:2151:ILE:HG12	1:A:2192:THR:HG21	1.93	0.50
1:F:2844:LEU:HB3	1:F:2875:ALA:HB1	1.93	0.50
1:F:2929:LEU:O	1:F:2932:SER:OG	2.22	0.50
1:A:440:VAL:HG21	1:A:485:GLN:HG3	1.94	0.50
1:A:1302:ALA:H	1:A:1334:LYS:NZ	2.07	0.50
1:A:1357:LYS:HG3	1:A:1361:LYS:HZ3	1.76	0.50
1:A:1369:MET:HA	1:A:1372:LEU:HG	1.93	0.50
1:A:2571:ASP:O	1:A:2787:HIS:ND1	2.43	0.50
1:A:2833:THR:HG21	1:A:2867:ALA:HB1	1.91	0.50
1:A:2980:ASP:N	1:A:2980:ASP:OD1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3283:LEU:O	1:A:3287:ARG:HG3	2.11	0.50
1:A:4006:VAL:HG11	1:A:4009:PRO:HB3	1.91	0.50
2:B:261:LEU:HA	2:B:345:LEU:HB2	1.93	0.50
1:F:169:THR:OG1	9:J:22:DG:OP1	2.22	0.50
1:F:1164:CYS:SG	1:F:1165:LEU:N	2.84	0.50
2:G:500:PRO:HD3	5:P:707:ILE:HG12	1.94	0.50
6:Q:134:HIS:N	6:R:42:GLN:HB2	2.23	0.50
1:A:879:MET:HG2	1:A:881:LYS:H	1.75	0.50
1:A:1058:SER:HA	1:A:1061:LYS:HE2	1.93	0.50
1:A:1261:LEU:HD11	1:A:1337:VAL:HA	1.93	0.50
1:A:3138:ILE:HG22	1:A:3189:PHE:HZ	1.75	0.50
1:A:3831:ASP:HB3	1:A:3832:PRO:HD3	1.94	0.50
3:C:157:CYS:SG	3:C:158:ASP:N	2.84	0.50
3:C:489:ARG:NH1	3:C:507:PRO:O	2.45	0.50
1:F:483:VAL:HG21	1:F:567:GLU:HG3	1.93	0.50
1:F:2935:GLU:OE2	1:F:2938:VAL:N	2.33	0.50
2:G:163:HIS:CE1	2:G:165:ARG:HB2	2.46	0.50
4:L:143:HIS:O	4:L:146:LYS:HG3	2.11	0.50
1:A:433:PRO:HA	1:A:436:GLU:HG2	1.93	0.50
1:A:1164:CYS:SG	1:A:1165:LEU:N	2.84	0.50
1:A:2353:GLN:HB3	1:A:2360:PHE:HB2	1.93	0.50
3:C:299:ASP:OD1	3:C:303:THR:OG1	2.24	0.50
1:F:189:MET:O	1:F:193:ALA:N	2.44	0.50
1:F:655:LEU:O	1:F:659:ARG:HG2	2.11	0.50
1:F:1407:LYS:HA	1:F:1412:LYS:HB3	1.93	0.50
1:F:1419:LEU:HG	1:F:1467:ILE:HD13	1.93	0.50
4:N:161:ARG:HH22	5:P:837:ARG:HD2	1.75	0.50
7:D:15:DA:N6	8:E:43:DT:O4	2.44	0.50
1:A:237:SER:OG	1:A:238:MET:N	2.43	0.50
1:A:2161:ALA:HA	1:A:2164:TRP:HB2	1.94	0.50
1:A:3702:PRO:HB2	1:A:3794:VAL:HG11	1.94	0.50
1:F:535:LEU:HD23	1:F:565:TYR:HD1	1.76	0.50
1:F:2921:LEU:O	1:F:2925:GLU:HG3	2.12	0.50
1:F:3294:SER:O	1:F:3298:LEU:HG	2.12	0.50
3:H:654:ARG:HA	3:H:657:ASN:HD21	1.75	0.50
4:N:144:LEU:HB3	4:O:144:LEU:HB3	1.93	0.50
1:A:2428:ASP:HB2	1:A:2431:ARG:HB2	1.93	0.50
3:C:509:GLN:OE1	3:C:511:HIS:ND1	2.39	0.50
1:F:19:LEU:HA	1:F:34:LEU:HD22	1.94	0.50
1:F:1373:VAL:HG11	1:F:1422:LYS:HG3	1.94	0.50
1:F:1583:MET:HG3	1:F:1628:LYS:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1597:LEU:O	1:F:1601:LEU:HG	2.12	0.50
1:F:3191:SER:O	1:F:3194:GLU:N	2.44	0.50
2:G:364:PRO:HG3	3:H:357:MET:HA	1.94	0.50
2:G:369:TYR:CD1	2:G:370:PRO:HD2	2.45	0.50
3:H:184:ARG:HG2	3:H:519:PRO:HB3	1.94	0.50
1:A:1357:LYS:HG3	1:A:1361:LYS:NZ	2.27	0.50
1:A:2331:MET:HG2	1:A:2334:LYS:HG2	1.92	0.50
1:A:3998:LEU:O	1:A:4001:THR:HG22	2.11	0.50
1:F:1238:GLN:HA	1:F:1296:PHE:HZ	1.77	0.50
1:F:1333:SER:O	1:F:1337:VAL:HG23	2.12	0.50
1:F:3714:GLU:OE1	1:F:3714:GLU:N	2.45	0.50
3:H:441:SER:O	3:H:445:ALA:N	2.45	0.50
5:M:843:LEU:HA	5:M:846:ARG:HG2	1.92	0.50
4:N:161:ARG:CZ	5:P:840:ILE:HG21	2.42	0.50
4:O:22:VAL:HG23	4:O:35:THR:H	1.77	0.50
4:O:22:VAL:HA	4:O:35:THR:HB	1.94	0.50
1:A:406:ARG:HE	1:A:409:GLN:NE2	2.09	0.50
1:A:1018:VAL:HG22	1:A:1074:LYS:HG2	1.94	0.50
1:A:2847:THR:OG1	1:A:2849:SER:O	2.27	0.50
2:B:350:PHE:HB3	2:B:394:VAL:HG12	1.94	0.50
3:C:251:LEU:N	3:C:259:ILE:O	2.45	0.50
1:F:2101:VAL:HG13	1:F:2153:THR:HG22	1.93	0.50
6:R:107:ARG:HD3	6:R:109:ARG:HH21	1.77	0.50
1:A:92:PHE:CD1	1:A:96:MET:HG3	2.47	0.50
1:A:682:TYR:CZ	1:A:700:LYS:HD3	2.46	0.50
1:A:1626:TRP:HZ2	1:A:1674:THR:HG21	1.76	0.50
2:B:510:LYS:HG2	2:B:513:ALA:HB3	1.94	0.50
1:F:908:ASP:HA	1:F:911:LEU:HD23	1.92	0.50
1:F:1713:VAL:O	1:F:1716:GLN:HG2	2.12	0.50
3:H:44:ARG:NH1	3:H:236:VAL:H	2.10	0.50
3:H:250:ARG:NH1	3:H:260:ARG:HH21	2.10	0.50
4:N:141:ASN:HD21	4:O:140:LYS:HD3	1.77	0.50
4:O:33:VAL:HG22	4:O:47:VAL:H	1.76	0.50
5:P:743:MET:HE2	5:P:743:MET:HA	1.93	0.50
6:R:57:ARG:HA	6:R:61:LEU:HB2	1.93	0.50
9:J:33:DA:H2''	9:J:34:DT:C2	2.47	0.50
1:A:933:LEU:HD11	1:A:2794:LEU:HD23	1.93	0.49
1:A:2333:ARG:HH22	1:A:2371:PHE:HE1	1.60	0.49
1:A:2567:SER:HA	1:A:2572:TYR:CD2	2.47	0.49
1:A:3085:GLU:OE1	1:A:3085:GLU:N	2.38	0.49
1:A:3577:GLN:NE2	1:A:3629:ARG:HB3	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3588:TRP:CE2	1:A:3613:MET:HG2	2.47	0.49
1:F:76:ILE:HA	1:F:79:ARG:HB2	1.93	0.49
1:F:1096:VAL:O	1:F:1100:VAL:HG13	2.12	0.49
1:F:1211:VAL:HG13	1:F:1219:PHE:HZ	1.77	0.49
1:F:1444:ASP:N	1:F:1444:ASP:OD1	2.44	0.49
1:F:1691:GLN:O	1:F:1694:THR:OG1	2.22	0.49
1:F:3034:PRO:O	1:F:3038:GLU:N	2.45	0.49
1:F:3930:VAL:HB	1:F:3937:VAL:HG12	1.93	0.49
2:G:64:ILE:HD13	2:G:67:ILE:HD11	1.93	0.49
2:G:263:LEU:HD22	2:G:347:LEU:HD22	1.94	0.49
2:G:350:PHE:H	3:H:463:LEU:HD13	1.77	0.49
4:L:145:GLN:HA	4:L:148:ASN:HD21	1.77	0.49
4:O:193:SER:O	4:O:197:LYS:HG2	2.11	0.49
8:I:40:DT:H2''	8:I:41:DT:O4'	2.12	0.49
1:A:111:CYS:HB2	1:A:130:LEU:CD2	2.42	0.49
1:A:1102:GLU:O	1:A:1106:ILE:HG12	2.12	0.49
1:F:1840:PHE:O	1:F:1844:VAL:HG23	2.12	0.49
1:F:3643:HIS:HB3	1:F:3659:PHE:HE2	1.76	0.49
7:D:22:DG:H5''	7:D:23:DT:H73	1.93	0.49
1:A:898:PHE:HB2	1:A:901:MET:O	2.12	0.49
1:A:3369:ASP:HB3	1:A:3372:LYS:HG2	1.94	0.49
1:A:4120:THR:HG21	1:A:4126:PRO:HG3	1.94	0.49
1:F:4055:ASN:HD21	1:F:4057:ALA:HB3	1.77	0.49
2:G:469:LEU:HD11	2:G:514:MET:HB2	1.94	0.49
3:H:251:LEU:HB3	3:H:259:ILE:HB	1.94	0.49
1:A:1565:GLU:OE2	1:A:1603:GLN:NE2	2.45	0.49
1:A:1603:GLN:HA	1:A:1606:ARG:HH21	1.77	0.49
1:A:3155:VAL:H	1:A:3159:ARG:HH22	1.58	0.49
2:B:317:LYS:N	3:C:279:VAL:O	2.34	0.49
2:B:476:ASP:OD1	2:B:476:ASP:N	2.46	0.49
1:F:584:GLU:HB2	1:F:613:HIS:HB3	1.94	0.49
1:F:1287:GLN:HG3	1:F:1289:SER:H	1.77	0.49
1:F:1921:ASP:OD1	1:F:1922:ALA:N	2.45	0.49
1:F:1934:LEU:HD13	1:F:1937:ARG:HH21	1.77	0.49
1:F:3658:ASP:OD1	1:F:3658:ASP:N	2.43	0.49
5:P:748:PRO:HA	5:P:751:LYS:HD2	1.95	0.49
6:Q:133:GLN:N	6:R:43:GLN:H	2.11	0.49
8:E:40:DT:H4'	8:E:41:DT:OP1	2.11	0.49
1:A:305:ASN:O	1:A:308:LEU:N	2.45	0.49
1:A:1333:SER:O	1:A:1337:VAL:HG23	2.13	0.49
1:A:1921:ASP:OD1	1:A:1922:ALA:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:80:ARG:HH22	7:D:24:DT:H4'	1.78	0.49
2:B:173:ASP:HB2	2:B:214:SER:N	2.27	0.49
1:F:1448:LEU:HD11	1:F:1514:LEU:HD21	1.94	0.49
1:F:1465:HIS:HD2	1:F:1468:LEU:HD23	1.77	0.49
1:F:1715:GLU:HA	1:F:1718:ILE:HG12	1.94	0.49
3:H:466:LYS:HD2	3:H:473:LEU:H	1.77	0.49
1:A:767:GLU:OE2	1:A:771:ASN:ND2	2.32	0.49
1:A:3050:LYS:HZ1	1:A:3181:ASP:HA	1.78	0.49
2:B:145:GLU:OE1	2:B:145:GLU:N	2.46	0.49
1:F:73:LEU:O	1:F:79:ARG:NH2	2.45	0.49
1:F:1019:ASP:N	1:F:1019:ASP:OD1	2.46	0.49
1:F:3002:TYR:CD1	1:F:3010:SER:HB2	2.47	0.49
3:H:81:ARG:HB3	3:H:84:MET:SD	2.52	0.49
3:H:489:ARG:O	3:H:492:GLN:HG3	2.12	0.49
4:L:137:ASN:O	4:L:141:ASN:ND2	2.45	0.49
1:A:1663:THR:HG22	1:A:1664:SER:H	1.77	0.49
1:A:2188:GLU:HG2	1:A:2729:ARG:HH12	1.77	0.49
1:A:3998:LEU:O	1:A:4001:THR:N	2.42	0.49
1:F:3665:MET:HA	1:F:3668:LEU:HG	1.94	0.49
1:F:3855:TYR:OH	1:F:4120:THR:O	2.30	0.49
4:N:5:ILE:HD11	4:N:126:LEU:HD11	1.93	0.49
6:Q:15:TRP:HE1	6:Q:22:SER:HA	1.78	0.49
1:A:24:ARG:HH21	1:A:70:ARG:HH21	1.59	0.49
1:A:1489:LYS:HD2	1:A:1492:ALA:HB3	1.94	0.49
1:A:3301:LEU:HB3	1:A:3304:VAL:HA	1.94	0.49
1:A:3630:ARG:O	1:A:3634:GLN:NE2	2.40	0.49
3:C:64:THR:HG22	3:C:66:ASN:H	1.78	0.49
1:F:50:VAL:O	1:F:54:GLN:NE2	2.45	0.49
1:F:2138:VAL:HG13	1:F:2143:ARG:HE	1.76	0.49
1:F:3577:GLN:HB3	1:F:3683:CYS:SG	2.53	0.49
1:F:3717:VAL:HA	1:F:3743:HIS:CE1	2.48	0.49
3:H:280:ASP:HB3	3:H:283:THR:HG22	1.94	0.49
4:L:155:TRP:O	4:L:159:GLN:HG2	2.12	0.49
6:R:50:ASP:OD1	6:R:51:THR:N	2.45	0.49
8:E:28:DT:H6	8:E:28:DT:H5''	1.76	0.49
1:A:716:VAL:HG11	1:A:1120:SER:HB2	1.94	0.49
1:A:1715:GLU:HA	1:A:1718:ILE:HG12	1.95	0.49
1:A:2301:GLN:HA	1:A:2304:VAL:HG22	1.95	0.49
1:A:2402:LEU:HD12	1:A:2438:ILE:HG13	1.95	0.49
1:A:3549:HIS:ND1	1:A:3553:GLU:OE1	2.43	0.49
1:A:3689:ASP:CG	1:A:3690:PHE:H	2.16	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:86:VAL:HG22	2:B:104:VAL:HG22	1.95	0.49
2:B:125:GLN:HG3	2:B:129:LYS:HZ1	1.77	0.49
1:F:2373:PRO:HA	1:F:2404:ARG:HH12	1.77	0.49
2:G:428:THR:OG1	3:H:354:ARG:NH1	2.46	0.49
3:H:411:HIS:N	3:H:418:CYS:O	2.45	0.49
5:M:668:SER:OG	5:M:669:GLY:N	2.46	0.49
1:A:1435:ASN:ND2	1:A:1440:ASP:OD2	2.46	0.49
2:B:45:SER:HA	2:B:138:GLY:H	1.77	0.49
1:F:3169:PRO:HG2	1:F:3179:TRP:CH2	2.48	0.49
1:F:3266:SER:HA	1:F:3272:TRP:CD1	2.48	0.49
2:G:278:GLN:OE1	3:H:431:ARG:NH2	2.46	0.49
2:G:318:ARG:HE	3:H:278:VAL:HG22	1.78	0.49
3:H:153:SER:HA	3:H:156:LYS:HG2	1.95	0.49
3:H:413:LYS:NZ	3:H:416:TYR:O	2.34	0.49
5:M:654:LYS:N	5:M:684:GLU:O	2.46	0.49
4:N:30:SER:OG	4:N:31:GLY:N	2.46	0.49
7:D:22:DG:C8	7:D:23:DT:H72	2.48	0.49
1:A:1298:LEU:HG	1:A:1367:HIS:CD2	2.48	0.48
1:A:1407:LYS:HA	1:A:1412:LYS:HB3	1.95	0.48
1:A:1778:PHE:O	1:A:1781:SER:OG	2.25	0.48
1:A:3622:ALA:HB2	1:A:3633:ILE:HD11	1.93	0.48
2:B:141:TYR:HE2	2:B:176:HIS:HD1	1.59	0.48
2:B:459:VAL:HA	2:B:462:MET:SD	2.53	0.48
3:C:418:CYS:SG	3:C:419:LEU:N	2.86	0.48
1:F:430:VAL:HG21	1:F:1643:MET:HB3	1.94	0.48
1:F:2155:GLU:HA	1:F:2158:ARG:HG2	1.95	0.48
2:G:411:VAL:HG22	2:G:436:PHE:HA	1.94	0.48
3:H:234:LEU:HB3	3:H:237:PHE:HB3	1.95	0.48
8:I:30:DA:H3'	8:I:32:DA:H61	1.78	0.48
1:A:417:VAL:HA	1:A:420:VAL:HG12	1.94	0.48
1:A:1371:VAL:O	1:A:1375:THR:HG23	2.13	0.48
1:A:2817:LEU:HD23	1:A:2865:HIS:CE1	2.47	0.48
1:A:3387:GLU:O	1:A:3390:GLN:HG2	2.13	0.48
1:A:3515:GLN:HB3	1:A:3554:PHE:CE2	2.48	0.48
1:A:3547:THR:HA	1:A:3550:LYS:HD3	1.95	0.48
1:A:3981:TYR:OH	1:A:4101:GLU:HB2	2.13	0.48
2:B:319:SER:N	3:C:277:THR:O	2.45	0.48
2:B:351:LYS:O	2:B:395:ALA:N	2.46	0.48
3:C:523:THR:O	3:C:527:GLN:HG2	2.12	0.48
1:F:111:CYS:O	1:F:130:LEU:HD11	2.13	0.48
1:F:1196:PRO:HA	1:F:1202:ARG:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:2133:LEU:HD11	1:F:2171:LEU:HD13	1.94	0.48
1:F:2481:HIS:NE2	1:F:2530:ARG:HG2	2.27	0.48
1:F:3097:ASP:N	1:F:3097:ASP:OD1	2.45	0.48
1:F:3269:ARG:HG3	1:F:3272:TRP:H	1.77	0.48
1:F:3533:PHE:O	1:F:3537:SER:N	2.46	0.48
1:F:3888:VAL:HA	1:F:3891:SER:HB3	1.95	0.48
3:H:319:ASP:OD1	3:H:320:ILE:N	2.43	0.48
3:H:450:GLN:HA	3:H:537:PHE:HZ	1.78	0.48
1:A:1058:SER:O	1:A:1062:ARG:HG2	2.13	0.48
1:A:2349:LEU:HB3	1:A:2360:PHE:HE1	1.77	0.48
1:A:3625:LEU:HB2	1:A:3682:GLU:O	2.13	0.48
1:A:3739:ILE:HA	1:A:3749:PRO:HA	1.96	0.48
2:B:299:LYS:HD3	3:C:296:CYS:HB2	1.94	0.48
1:F:359:LEU:O	1:F:363:ILE:HG12	2.13	0.48
1:F:840:LEU:HD23	1:F:840:LEU:H	1.78	0.48
1:F:2348:GLN:OE1	1:F:2352:HIS:NE2	2.46	0.48
1:F:3326:GLN:NE2	1:F:3326:GLN:O	2.46	0.48
3:H:233:LYS:HE3	3:H:512:ILE:HD12	1.95	0.48
4:L:147:GLU:O	4:L:150:ARG:HD3	2.13	0.48
6:Q:57:ARG:HB3	6:Q:119:TRP:HH2	1.77	0.48
1:A:143:LEU:N	1:A:146:GLU:OE2	2.46	0.48
1:A:848:LEU:HD11	1:A:922:SER:HB2	1.95	0.48
1:A:1115:HIS:HA	1:A:1119:LYS:HD3	1.95	0.48
1:A:1528:LEU:HD23	1:A:1531:LEU:HD12	1.96	0.48
1:A:3072:GLU:OE1	1:A:3072:GLU:N	2.44	0.48
1:A:3443:PRO:HA	1:A:3446:VAL:HG22	1.94	0.48
1:A:3927:ASN:O	1:A:3940:ILE:N	2.36	0.48
1:F:1354:GLU:HB3	1:F:1357:LYS:HD3	1.94	0.48
1:F:1881:TYR:CE1	1:F:1951:VAL:HA	2.48	0.48
1:F:3358:ARG:H	1:F:3358:ARG:HD2	1.78	0.48
2:G:262:LYS:HG3	2:G:346:MET:HA	1.96	0.48
2:G:278:GLN:NE2	3:H:433:TYR:OH	2.36	0.48
3:H:484:ASN:HD21	3:H:486:ARG:HB3	1.76	0.48
3:H:595:ALA:HA	3:H:598:PHE:CE2	2.48	0.48
3:H:605:LYS:HB2	3:H:609:PHE:CZ	2.43	0.48
4:N:155:TRP:HZ3	4:O:150:ARG:HH22	1.62	0.48
5:P:659:PHE:HB2	5:P:685:PHE:O	2.13	0.48
1:F:175:TYR:HB2	1:F:223:CYS:HB3	1.94	0.48
1:F:417:VAL:HA	1:F:420:VAL:HG12	1.96	0.48
1:F:2241:LEU:HA	1:F:2244:CYS:SG	2.53	0.48
1:F:3007:GLU:O	1:F:3011:LEU:HG	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:39:ILE:HD11	2:G:108:LEU:HD21	1.96	0.48
3:H:209:LYS:O	3:H:213:ILE:HG23	2.14	0.48
1:A:460:ALA:O	1:A:464:VAL:HG13	2.14	0.48
1:A:729:CYS:O	1:A:733:LEU:HD23	2.14	0.48
1:A:741:ILE:HA	1:A:748:TYR:HE2	1.79	0.48
1:A:768:VAL:HA	1:A:771:ASN:HD22	1.79	0.48
1:A:2215:LEU:HD23	1:A:2219:LEU:HD23	1.96	0.48
1:A:3527:GLN:HB2	1:A:3705:TYR:CE2	2.49	0.48
1:A:3815:LEU:O	1:A:3819:THR:HG23	2.14	0.48
1:A:3930:VAL:HA	1:A:3937:VAL:HA	1.95	0.48
2:B:325:ARG:HH12	3:C:89:ASP:HB3	1.77	0.48
3:C:253:ILE:HG23	3:C:342:VAL:HG11	1.95	0.48
3:C:363:LYS:HB2	3:C:418:CYS:SG	2.54	0.48
1:F:900:GLU:OE1	1:F:900:GLU:N	2.46	0.48
1:F:2362:VAL:O	1:F:2366:LYS:HG2	2.13	0.48
1:F:2522:ARG:HH22	1:F:2564:GLU:HG3	1.78	0.48
3:H:531:SER:HA	3:H:534:LYS:HG2	1.96	0.48
4:K:175:ASP:OD1	4:K:176:LEU:N	2.47	0.48
5:M:665:CYS:HB2	5:M:697:THR:HG21	1.95	0.48
5:P:842:ALA:HA	5:P:845:LEU:HD12	1.94	0.48
1:A:217:LEU:HD23	1:A:218:PRO:HD3	1.95	0.48
1:A:1444:ASP:HA	1:A:1447:ARG:HH21	1.79	0.48
1:A:1740:VAL:HA	1:A:1743:MET:HG3	1.96	0.48
1:A:3301:LEU:HD23	1:A:3304:VAL:HA	1.95	0.48
1:A:3825:LYS:O	1:A:3829:LEU:HB2	2.14	0.48
2:B:429:PRO:HG2	3:C:435:PHE:HD2	1.79	0.48
1:F:573:LEU:HD22	1:F:649:PHE:HD1	1.78	0.48
1:F:758:LEU:HD13	1:F:976:VAL:HG21	1.96	0.48
1:F:898:PHE:HB2	1:F:901:MET:O	2.14	0.48
1:F:1135:CYS:HB3	1:F:1190:LEU:HD11	1.95	0.48
1:F:1687:HIS:ND1	1:F:1741:ASP:OD2	2.46	0.48
1:F:3735:PRO:HB3	1:F:3751:LEU:HD21	1.95	0.48
1:F:3738:ILE:HD12	1:F:3740:ILE:HD11	1.96	0.48
1:F:3775:LEU:HD13	1:F:3786:LEU:HB3	1.96	0.48
3:H:300:ASP:OD1	3:H:300:ASP:N	2.46	0.48
4:L:35:THR:HG22	4:L:44:THR:HG23	1.94	0.48
1:A:459:ARG:HG2	1:A:540:MET:HE2	1.96	0.48
1:A:1322:THR:O	1:A:1326:GLU:N	2.47	0.48
1:A:1697:PRO:HA	1:A:1753:SER:HB3	1.96	0.48
1:A:3301:LEU:HB2	1:A:3333:THR:HG21	1.96	0.48
1:A:3700:GLU:HG3	1:A:3718:ARG:HA	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:251:LEU:HB3	3:C:259:ILE:HG13	1.96	0.48
1:F:1803:GLU:HA	1:F:1806:ARG:HH21	1.79	0.48
1:F:3050:LYS:NZ	1:F:3180:ASP:OD1	2.36	0.48
2:G:386:LEU:HD13	2:G:430:PRO:HB2	1.94	0.48
4:K:7:ARG:HG2	4:L:131:LEU:HD13	1.95	0.48
1:A:13:LEU:HD21	1:A:3069:MET:HB3	1.95	0.48
1:A:458:CYS:HG	1:A:533:HIS:CD2	2.32	0.48
1:A:1428:ILE:HA	1:A:1431:LEU:HB2	1.96	0.48
1:A:3262:LEU:HD22	1:A:3272:TRP:HZ2	1.77	0.48
2:B:249:LYS:NZ	2:B:250:GLU:O	2.44	0.48
1:F:866:ILE:HG13	1:F:3168:TYR:CD2	2.46	0.48
1:F:1069:HIS:ND1	1:F:3743:HIS:HD2	2.11	0.48
8:E:28:DT:H1'	8:E:29:DA:H5''	1.96	0.48
8:I:34:DC:N4	9:J:23:DT:H3	2.11	0.48
1:A:94:GLU:CD	1:A:95:LYS:H	2.16	0.48
1:A:713:GLU:O	1:A:717:LYS:HG2	2.14	0.48
1:A:902:LYS:HG2	1:F:2570:PRO:HB2	1.96	0.48
1:A:2745:ARG:HH21	8:E:45:DG:H2'	1.78	0.48
1:A:3149:GLY:O	1:A:3152:SER:OG	2.31	0.48
2:B:80:ARG:NH2	7:D:25:DT:OP1	2.47	0.48
1:F:923:ASP:O	1:F:926:THR:N	2.47	0.48
1:F:1565:GLU:OE1	1:F:1606:ARG:NH1	2.47	0.48
1:F:1864:ASP:OD1	1:F:1864:ASP:N	2.47	0.48
1:F:3509:ASP:N	1:F:3509:ASP:OD1	2.46	0.48
3:H:342:VAL:HG12	3:H:344:GLY:H	1.78	0.48
6:R:219:MET:O	6:R:223:THR:OG1	2.31	0.48
9:J:37:DG:H1'	9:J:38:DG:C2	2.48	0.48
1:A:2751:GLN:NE2	1:A:2752:LYS:HG2	2.29	0.47
1:A:4011:PHE:O	1:A:4015:ASN:ND2	2.46	0.47
3:C:36:LYS:NZ	3:C:231:LEU:HD11	2.29	0.47
1:F:74:ASN:HD21	1:F:122:LYS:HB2	1.78	0.47
1:F:1249:SER:OG	1:F:1310:GLU:OE1	2.25	0.47
1:F:3679:ASN:HB3	1:F:3725:ARG:HA	1.96	0.47
5:M:716:ASN:ND2	5:M:748:PRO:HD3	2.29	0.47
6:Q:133:GLN:H	6:R:42:GLN:N	2.04	0.47
7:D:15:DA:H2''	7:D:16:DA:C8	2.49	0.47
8:I:27:DC:H2'	9:J:30:DT:H1'	1.94	0.47
1:A:734:LEU:HD11	1:A:768:VAL:HG13	1.96	0.47
1:A:2486:ASP:OD1	1:A:2486:ASP:N	2.45	0.47
3:C:528:ILE:HG22	3:C:532:LYS:HZ1	1.79	0.47
1:F:144:MET:N	1:F:146:GLU:OE1	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:865:GLN:HB2	1:F:3168:TYR:CG	2.49	0.47
1:F:894:PHE:O	1:F:905:ILE:N	2.31	0.47
1:F:994:TRP:CG	1:F:2581:LEU:HD21	2.48	0.47
1:F:1725:GLN:NE2	1:F:1769:GLU:HG3	2.29	0.47
1:F:2428:ASP:O	1:F:2432:GLN:HG2	2.14	0.47
1:F:3088:LEU:HD21	1:F:3138:ILE:HG21	1.96	0.47
7:D:28:DA:H2	8:E:30:DA:N1	2.12	0.47
9:J:25:DT:H2'	9:J:26:DT:C4	2.49	0.47
1:A:736:LEU:HB3	1:A:740:ILE:HG21	1.96	0.47
1:A:4098:LEU:HD11	1:A:4103:GLN:HA	1.96	0.47
2:B:333:GLU:O	2:B:337:LEU:HG	2.15	0.47
3:C:165:LEU:HD21	3:C:205:LEU:HD11	1.95	0.47
1:F:145:ASP:HA	1:F:147:PHE:CE2	2.48	0.47
1:F:396:PHE:CE1	1:F:441:MET:HG3	2.47	0.47
1:F:425:ASP:OD1	1:F:425:ASP:N	2.48	0.47
1:F:2322:VAL:HA	1:F:2325:LEU:HD12	1.95	0.47
1:F:2335:ASN:ND2	1:F:2337:LEU:HD23	2.29	0.47
1:F:3669:LYS:HG3	1:F:3670:MET:SD	2.54	0.47
1:F:3680:LEU:HD21	1:F:3688:SER:HA	1.96	0.47
2:G:465:ILE:HG23	2:G:518:LEU:HD21	1.97	0.47
5:M:708:ARG:O	5:M:712:ILE:HG12	2.14	0.47
1:A:369:PHE:O	1:A:372:PRO:HD2	2.14	0.47
1:A:790:LYS:HA	1:A:869:ASN:HB3	1.96	0.47
1:A:901:MET:N	1:A:901:MET:SD	2.87	0.47
1:A:908:ASP:OD1	1:A:908:ASP:N	2.47	0.47
1:A:1099:PHE:CE1	1:A:1152:ARG:HD3	2.50	0.47
1:A:2548:PRO:HB2	1:A:2848:PHE:CD1	2.49	0.47
3:C:357:MET:HG2	3:C:425:PRO:HB3	1.96	0.47
1:F:92:PHE:O	1:F:96:MET:HG2	2.15	0.47
1:F:1474:ASP:OD1	1:F:1474:ASP:N	2.47	0.47
1:F:3569:GLN:HA	1:F:3572:ILE:HD12	1.95	0.47
1:F:4054:ALA:H	1:F:4103:GLN:NE2	2.12	0.47
4:L:134:ILE:HA	4:L:137:ASN:HD21	1.79	0.47
1:A:1424:THR:HA	1:A:1467:ILE:HD11	1.97	0.47
1:A:2205:VAL:HG13	1:A:2208:ASP:H	1.79	0.47
1:A:3825:LYS:HA	1:A:3829:LEU:HD23	1.96	0.47
1:F:168:ASP:H	1:F:171:LEU:HD12	1.79	0.47
1:F:899:ARG:HD3	1:F:2568:MET:HB3	1.95	0.47
1:F:2938:VAL:O	1:F:2942:ILE:HG12	2.15	0.47
1:F:3443:PRO:HA	1:F:3446:VAL:HG22	1.97	0.47
2:G:166:ILE:O	2:G:201:ASP:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:366:LEU:HB2	2:G:434:LEU:HD12	1.97	0.47
3:H:309:ASP:OD1	3:H:309:ASP:N	2.46	0.47
4:O:107:ARG:NH1	4:O:108:LEU:O	2.48	0.47
6:R:176:ARG:NH1	6:R:179:LEU:HD23	2.29	0.47
1:A:653:LEU:HD21	1:A:669:LEU:HB3	1.95	0.47
1:A:2584:CYS:HB2	1:A:2780:LEU:HD12	1.97	0.47
1:A:2866:ALA:HA	1:A:2869:LEU:HG	1.97	0.47
2:B:176:HIS:CE1	2:B:178:ASN:HD21	2.32	0.47
2:B:304:ASN:ND2	2:B:307:THR:HB	2.30	0.47
1:F:3283:LEU:O	1:F:3287:ARG:HG3	2.15	0.47
2:G:206:LYS:HG2	2:G:207:LYS:HG3	1.96	0.47
4:K:89:SER:OG	4:K:94:TYR:O	2.29	0.47
5:P:813:PHE:N	5:P:850:ALA:H	2.12	0.47
6:Q:136:ILE:O	6:Q:140:MET:N	2.38	0.47
1:A:1833:LEU:HG	1:A:1836:LEU:HD23	1.96	0.47
1:A:4090:ARG:NH2	1:A:4109:ASP:OD2	2.47	0.47
2:B:100:LYS:HZ3	2:B:101:ASN:H	1.62	0.47
2:B:398:CYS:SG	2:B:399:ARG:N	2.87	0.47
2:B:422:ASP:N	2:B:422:ASP:OD1	2.44	0.47
2:B:468:LYS:HG3	2:B:518:LEU:HA	1.95	0.47
3:C:283:THR:HB	3:C:285:LYS:HE2	1.95	0.47
3:C:500:HIS:HB3	3:C:503:GLU:HB3	1.96	0.47
1:F:58:VAL:HG21	1:F:3098:ARG:HD2	1.96	0.47
1:F:196:LEU:HB3	1:F:200:PHE:CZ	2.50	0.47
1:F:778:ILE:HD12	1:F:3161:LEU:HD11	1.97	0.47
1:F:868:LYS:NZ	1:F:3170:ASP:OD1	2.48	0.47
1:F:1181:THR:OG1	1:F:1184:ARG:NH2	2.47	0.47
1:F:1504:ASP:O	1:F:1508:LYS:N	2.41	0.47
1:F:1575:LEU:HD11	1:F:1617:LYS:HD2	1.97	0.47
1:F:2147:ALA:HB2	1:F:2171:LEU:HD21	1.95	0.47
1:F:2312:TYR:HD2	1:F:2315:VAL:HG23	1.80	0.47
1:F:2511:ILE:HD11	1:F:2553:HIS:HB2	1.96	0.47
1:F:3151:LEU:HD22	1:F:3197:LEU:HB2	1.97	0.47
1:F:3455:LYS:HE2	1:F:3491:PRO:HG3	1.97	0.47
1:F:3720:ALA:HB3	1:F:3743:HIS:HA	1.95	0.47
3:H:10:VAL:HG22	3:H:131:HIS:HB3	1.96	0.47
3:H:662:LEU:HA	3:H:665:LYS:HG2	1.97	0.47
7:D:17:DT:H3	8:E:39:DA:H61	1.61	0.47
8:I:23:DT:H3'	8:I:24:DA:C8	2.50	0.47
1:A:33:GLN:OE1	1:A:2422:GLN:NE2	2.39	0.47
1:A:359:LEU:O	1:A:363:ILE:HG12	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:784:VAL:O	1:A:787:PRO:HD2	2.14	0.47
1:A:1722:PHE:HA	1:A:1729:PHE:HZ	1.79	0.47
1:A:2723:THR:HA	1:A:2726:LEU:HD13	1.97	0.47
2:B:348:MET:N	2:B:397:LEU:O	2.45	0.47
1:F:122:LYS:HD2	1:F:122:LYS:HA	1.79	0.47
1:F:1413:ASP:OD1	1:F:1414:ILE:N	2.48	0.47
1:F:2349:LEU:HB3	1:F:2360:PHE:HE1	1.79	0.47
1:F:3930:VAL:HA	1:F:3937:VAL:HA	1.96	0.47
2:G:36:ASP:OD1	2:G:163:HIS:ND1	2.35	0.47
3:H:32:GLU:HA	3:H:35:LYS:HZ3	1.79	0.47
5:P:666:VAL:HB	5:P:689:ILE:HG23	1.97	0.47
1:A:50:VAL:HG13	1:A:51:LEU:HG	1.97	0.47
1:A:1196:PRO:HA	1:A:1202:ARG:O	2.15	0.47
1:A:2750:GLU:O	1:A:2754:GLU:HG2	2.15	0.47
1:A:3097:ASP:OD1	1:A:3098:ARG:N	2.48	0.47
2:B:509:PRO:HD3	3:C:394:ARG:HD3	1.97	0.47
3:C:266:SER:HB3	3:C:361:VAL:HG12	1.95	0.47
1:F:40:GLN:CD	1:F:2427:ARG:HB2	2.35	0.47
1:F:79:ARG:HH22	1:F:82:ARG:HD2	1.79	0.47
1:F:486:GLY:O	1:F:490:ILE:HG12	2.15	0.47
1:F:1769:GLU:HB2	1:F:1772:HIS:CG	2.49	0.47
1:F:1948:ALA:HA	1:F:1951:VAL:HG22	1.95	0.47
1:F:2353:GLN:HA	1:F:2356:MET:HG3	1.96	0.47
1:F:2584:CYS:HB2	1:F:2780:LEU:HD12	1.97	0.47
1:F:2821:ASP:N	1:F:2821:ASP:OD1	2.48	0.47
1:F:3165:THR:HG21	1:F:3241:LYS:HE2	1.96	0.47
1:F:3619:ASP:N	1:F:3619:ASP:OD1	2.48	0.47
3:H:413:LYS:HG2	3:H:416:TYR:H	1.80	0.47
6:Q:135:LEU:N	6:R:40:ASP:O	2.47	0.47
6:Q:159:MET:HA	6:Q:162:LEU:HD12	1.97	0.47
8:I:35:DT:C4	8:I:36:DA:C6	3.03	0.47
1:A:1479:VAL:HG11	1:A:1521:PHE:HD2	1.79	0.47
1:A:2548:PRO:HB2	1:A:2848:PHE:HD1	1.80	0.47
2:B:42:VAL:HG12	2:B:169:PHE:HB2	1.97	0.47
2:B:367:PHE:CE1	2:B:431:GLY:HA3	2.50	0.47
3:C:9:ALA:HB3	3:C:130:ARG:HG3	1.97	0.47
3:C:49:GLU:O	3:C:51:LYS:NZ	2.48	0.47
3:C:297:LEU:HD13	3:C:305:VAL:HG21	1.97	0.47
1:F:176:GLU:OE2	1:F:226:GLY:HA3	2.15	0.47
1:F:2405:VAL:HA	1:F:2408:MET:HE1	1.97	0.47
1:F:3528:ALA:HB2	1:F:3705:TYR:HD2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:3915:HIS:HB2	1:F:3920:ILE:HB	1.96	0.47
4:K:94:TYR:CZ	4:K:96:PHE:HB3	2.50	0.47
4:L:145:GLN:HA	4:L:148:ASN:ND2	2.29	0.47
5:M:803:TYR:HB2	5:M:805:TRP:CE2	2.50	0.47
4:N:162:PHE:HD1	4:O:162:PHE:HD1	1.63	0.47
6:R:13:TRP:HB3	6:R:210:PHE:CZ	2.49	0.47
1:A:865:GLN:HE22	1:A:3171:ALA:N	2.12	0.46
1:A:1635:LYS:HD2	1:A:1635:LYS:HA	1.76	0.46
1:A:3269:ARG:HG3	1:A:3272:TRP:H	1.79	0.46
1:A:3480:LEU:HA	1:A:3483:MET:HE3	1.97	0.46
3:C:250:ARG:HB3	3:C:338:LYS:NZ	2.30	0.46
1:F:2492:ASP:O	1:F:2496:GLN:HG3	2.15	0.46
1:F:2990:GLU:HG2	1:F:2994:TRP:CE2	2.50	0.46
1:F:3012:GLU:O	1:F:3015:SER:OG	2.22	0.46
2:G:413:LEU:HB3	2:G:432:PHE:CD1	2.50	0.46
4:N:150:ARG:O	4:N:153:ARG:HD3	2.15	0.46
5:P:753:HIS:HA	5:P:756:ARG:HE	1.80	0.46
5:P:772:ASN:O	5:P:776:GLU:HG2	2.14	0.46
9:J:24:DT:H2"	9:J:25:DT:C6	2.50	0.46
1:A:38:LEU:CD2	1:A:85:ILE:HG13	2.45	0.46
1:A:2356:MET:HE1	1:A:2359:LYS:H	1.79	0.46
1:A:3642:LYS:HG3	1:A:3643:HIS:ND1	2.30	0.46
2:B:38:LEU:HD13	2:B:165:ARG:HG3	1.96	0.46
2:B:125:GLN:NE2	2:B:128:GLN:OE1	2.45	0.46
2:B:240:GLU:O	2:B:244:ARG:N	2.39	0.46
3:C:251:LEU:HB2	3:C:261:ILE:HD13	1.96	0.46
1:F:1304:HIS:ND1	1:F:1307:ILE:O	2.34	0.46
1:F:1504:ASP:HB3	1:F:1507:CYS:HB2	1.96	0.46
1:F:3505:LEU:HD12	1:F:3508:LYS:HD2	1.97	0.46
3:H:630:PRO:HA	3:H:633:MET:HG3	1.97	0.46
5:P:816:HIS:C	5:P:851:LYS:H	2.18	0.46
1:A:1960:LYS:O	1:A:1962:TYR:N	2.49	0.46
1:A:2732:PHE:HA	1:A:2734:ARG:NH1	2.31	0.46
1:A:3482:LEU:O	1:A:3486:GLU:HG3	2.16	0.46
2:B:312:LEU:N	2:B:315:ASP:OD2	2.39	0.46
1:F:32:HIS:O	1:F:35:ILE:HG22	2.16	0.46
1:F:406:ARG:HG3	1:F:409:GLN:NE2	2.31	0.46
1:F:718:MET:HA	1:F:721:TYR:CD2	2.50	0.46
1:F:1783:ARG:HH22	1:F:1830:HIS:HB2	1.79	0.46
1:F:1867:ILE:HD11	1:F:1940:TYR:HB2	1.97	0.46
1:F:2826:LEU:HA	1:F:2829:LYS:HE2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:3825:LYS:O	1:F:3829:LEU:HB2	2.16	0.46
1:F:3923:ARG:HA	1:F:3959:MET:CE	2.46	0.46
2:G:416:GLN:N	2:G:431:GLY:O	2.43	0.46
3:H:364:VAL:HB	3:H:419:LEU:HB2	1.97	0.46
4:O:58:ASP:OD1	4:O:58:ASP:N	2.45	0.46
5:P:690:VAL:HG22	5:P:692:ASN:H	1.79	0.46
1:A:639:ALA:HB2	1:A:676:ASN:HB3	1.97	0.46
1:A:1366:THR:O	1:A:1369:MET:HG3	2.15	0.46
1:A:1558:TYR:CZ	1:A:1562:LEU:HD11	2.51	0.46
1:A:1745:LYS:HA	1:A:1748:ASP:OD2	2.16	0.46
1:A:2392:VAL:O	1:A:2396:LEU:HG	2.14	0.46
1:A:3182:ILE:O	1:A:3186:ARG:HG2	2.15	0.46
1:F:196:LEU:HB3	1:F:200:PHE:CE2	2.50	0.46
1:F:1154:PRO:HD3	1:F:1163:LEU:HD11	1.98	0.46
1:F:3980:MET:SD	1:F:3980:MET:N	2.87	0.46
2:G:90:THR:HB	2:G:101:ASN:CA	2.46	0.46
2:G:244:ARG:HG2	2:G:246:VAL:HG13	1.98	0.46
2:G:262:LYS:NZ	2:G:344:GLY:HA3	2.31	0.46
3:H:37:VAL:HG12	3:H:231:LEU:HD21	1.97	0.46
5:P:696:ASP:OD1	5:P:696:ASP:N	2.48	0.46
1:A:787:PRO:O	1:A:790:LYS:NZ	2.29	0.46
1:A:1608:ARG:HH21	1:A:1612:LYS:NZ	2.14	0.46
1:A:3158:LYS:HZ3	1:A:3186:ARG:NH1	2.13	0.46
1:A:3455:LYS:O	1:A:3455:LYS:NZ	2.33	0.46
1:A:3835:PRO:HG2	1:A:3836:PRO:HD3	1.97	0.46
3:C:135:PHE:HD1	3:C:227:PHE:CE1	2.33	0.46
3:C:147:LEU:HD11	3:C:211:VAL:HG21	1.96	0.46
3:C:316:TYR:N	3:C:319:ASP:O	2.48	0.46
1:F:982:GLN:NE2	1:F:2591:ILE:HG23	2.30	0.46
1:F:1158:PRO:HG2	1:F:1159:PRO:HD3	1.96	0.46
1:F:1420:ARG:NE	1:F:1466:ASN:O	2.49	0.46
1:F:2731:ARG:O	1:F:2734:ARG:NH2	2.49	0.46
1:F:3267:LYS:H	1:F:3267:LYS:HG2	1.58	0.46
1:A:24:ARG:NH2	1:A:70:ARG:HH21	2.13	0.46
1:A:32:HIS:O	1:A:35:ILE:HG22	2.16	0.46
1:A:475:LEU:HD22	1:A:476:ARG:HD3	1.98	0.46
1:A:1101:PHE:HD2	1:A:1163:LEU:HD13	1.81	0.46
1:A:1663:THR:HG22	1:A:1664:SER:N	2.30	0.46
1:A:3146:SER:C	1:A:3147:LYS:HD2	2.36	0.46
3:C:148:ASP:OD1	3:C:148:ASP:N	2.49	0.46
3:C:297:LEU:HB3	3:C:303:THR:OG1	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1148:ALA:HB2	1:F:1164:CYS:HB2	1.98	0.46
1:F:2310:VAL:HA	1:F:2316:TYR:CE2	2.51	0.46
2:G:367:PHE:CE2	2:G:369:TYR:HB2	2.51	0.46
6:Q:44:VAL:HG12	6:Q:130:LEU:HD11	1.98	0.46
1:A:63:PHE:CE2	1:A:85:ILE:HG12	2.51	0.46
1:A:342:MET:HE3	1:A:366:TYR:HE1	1.81	0.46
1:A:1086:TYR:CZ	1:A:1133:HIS:HB3	2.51	0.46
1:A:1133:HIS:O	1:A:1137:ILE:HG12	2.15	0.46
1:A:1367:HIS:HB2	1:A:1370:ARG:HH12	1.79	0.46
1:A:2478:MET:HG2	1:A:2524:PHE:CE1	2.50	0.46
1:A:3265:GLU:O	1:A:3268:THR:OG1	2.26	0.46
2:B:290:ARG:HH11	5:M:690:VAL:HG21	1.81	0.46
1:F:3483:MET:HE3	1:F:3513:ALA:H	1.80	0.46
2:G:85:VAL:HG22	2:G:106:GLN:HB3	1.96	0.46
2:G:362:LEU:HG	2:G:438:PRO:HG3	1.98	0.46
3:H:40:MET:HA	3:H:43:GLN:HG3	1.96	0.46
1:A:1251:GLN:OE1	1:A:1251:GLN:N	2.39	0.46
1:A:1287:GLN:HB3	1:A:1290:LEU:HD12	1.97	0.46
1:A:1801:VAL:HA	1:A:1804:MET:HG2	1.98	0.46
1:A:3296:GLN:HG3	1:A:3337:ILE:HD11	1.97	0.46
2:B:89:GLY:HA2	2:B:101:ASN:HB3	1.98	0.46
2:B:416:GLN:N	2:B:431:GLY:O	2.38	0.46
2:B:481:PRO:HG2	3:C:403:PRO:HG2	1.98	0.46
3:C:265:LYS:NZ	8:E:23:DT:H5'	2.31	0.46
3:C:277:THR:HG22	3:C:286:LYS:HZ2	1.81	0.46
3:C:465:LYS:N	3:C:474:GLU:O	2.48	0.46
1:F:75:SER:HB2	1:F:77:GLU:HG2	1.98	0.46
1:F:2246:LYS:H	1:F:2249:LEU:HD11	1.81	0.46
1:F:2382:VAL:HA	1:F:2385:LEU:HG	1.98	0.46
1:F:3008:TRP:HA	1:F:3011:LEU:HD12	1.98	0.46
1:F:3369:ASP:OD1	1:F:3370:SER:N	2.49	0.46
1:F:3499:ILE:HA	1:F:3502:MET:SD	2.56	0.46
5:P:811:SER:CB	5:P:849:GLY:HA3	2.37	0.46
8:E:34:DC:H5	8:E:35:DT:C2	2.32	0.46
1:A:849:GLU:OE1	1:A:849:GLU:N	2.40	0.46
1:A:901:MET:HB2	1:A:2819:GLU:HG2	1.98	0.46
1:A:3959:MET:HG3	1:A:4124:TRP:NE1	2.31	0.46
2:B:60:PHE:O	2:B:63:SER:OG	2.26	0.46
1:F:935:HIS:CD2	1:F:2775:TYR:HE1	2.34	0.46
1:F:1046:PRO:HA	1:F:1049:GLN:HE21	1.81	0.46
1:F:1342:MET:O	1:F:1346:THR:HG23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1580:LEU:HD13	1:F:1625:HIS:CD2	2.50	0.46
1:F:3583:LEU:HA	1:F:3586:LYS:HE2	1.97	0.46
2:G:419:GLU:N	2:G:426:GLN:HE22	2.13	0.46
3:H:51:LYS:HB3	3:H:125:LYS:NZ	2.31	0.46
4:K:130:CYS:SG	4:K:131:LEU:N	2.89	0.46
1:A:163:LYS:NZ	3:C:291:LYS:HD3	2.31	0.46
1:A:459:ARG:HG2	1:A:540:MET:CE	2.46	0.46
1:A:3107:ILE:O	1:A:3111:MET:HG2	2.15	0.46
1:A:3704:GLN:HE22	1:A:3717:VAL:HG13	1.80	0.46
3:C:242:ARG:HE	3:C:243:HIS:H	1.64	0.46
1:F:1048:GLN:HA	1:F:1051:LYS:HZ2	1.81	0.46
1:F:1608:ARG:HE	1:F:1612:LYS:NZ	2.14	0.46
1:F:2161:ALA:HA	1:F:2164:TRP:HB2	1.96	0.46
1:F:2427:ARG:HH21	1:F:2465:PRO:HD2	1.81	0.46
1:F:2443:MET:HA	1:F:2446:LEU:HB2	1.98	0.46
1:F:2510:LEU:O	1:F:2518:GLN:NE2	2.42	0.46
1:F:4121:TRP:HB3	1:F:4124:TRP:HB2	1.97	0.46
4:N:137:ASN:HB3	4:O:137:ASN:HB3	1.97	0.46
6:Q:133:GLN:HB2	6:R:43:GLN:HB2	1.98	0.46
1:A:357:LYS:O	1:A:361:ILE:HG12	2.16	0.45
1:A:1150:LYS:HA	1:A:1150:LYS:HD2	1.79	0.45
1:A:1260:LEU:HD21	1:A:1293:ALA:HB1	1.97	0.45
1:A:2154:GLU:HA	1:A:2157:PHE:CZ	2.51	0.45
1:A:2589:TYR:HB2	1:A:2777:HIS:HB2	1.98	0.45
1:A:2921:LEU:O	1:A:2925:GLU:HG3	2.16	0.45
1:A:3772:ASN:ND2	1:A:3788:LEU:O	2.44	0.45
3:C:154:LEU:HA	3:C:159:ILE:HB	1.98	0.45
1:F:1048:GLN:OE1	1:F:1048:GLN:N	2.49	0.45
2:G:291:GLU:HG3	5:P:690:VAL:HG23	1.98	0.45
6:R:4:LEU:O	6:R:8:LEU:HB2	2.15	0.45
1:A:251:PHE:HE1	1:A:293:LEU:HD11	1.80	0.45
1:A:862:LEU:HD12	1:A:866:ILE:HG21	1.98	0.45
1:A:935:HIS:CE1	1:A:987:LEU:HD13	2.51	0.45
1:A:3509:ASP:N	1:A:3509:ASP:OD1	2.44	0.45
1:A:3550:LYS:O	1:A:3553:GLU:HG2	2.16	0.45
2:B:90:THR:OG1	2:B:135:MET:O	2.33	0.45
3:C:247:TRP:HD1	3:C:263:ALA:HB3	1.82	0.45
1:F:237:SER:OG	1:F:238:MET:N	2.49	0.45
1:F:913:ARG:O	1:F:916:GLU:HG3	2.16	0.45
1:F:2227:LYS:HB2	1:F:2230:VAL:HG22	1.98	0.45
1:F:3462:ARG:HG2	1:F:3498:TRP:HZ3	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:3911:ILE:HD12	1:F:3937:VAL:HG23	1.98	0.45
2:G:340:PHE:HE2	3:H:485:PRO:HB2	1.81	0.45
2:G:389:CYS:HA	2:G:392:LYS:HB3	1.98	0.45
2:G:473:TYR:HD2	3:H:350:GLN:HB3	1.82	0.45
4:K:188:LYS:HZ1	5:M:763:ASP:HB3	1.81	0.45
5:M:722:LYS:HG3	5:M:742:PHE:O	2.15	0.45
1:A:21:ALA:HA	1:A:24:ARG:HH12	1.81	0.45
1:A:710:PHE:O	1:A:714:VAL:HG23	2.16	0.45
1:A:1773:VAL:O	1:A:1773:VAL:HG12	2.16	0.45
1:A:2420:PHE:CE2	1:A:2439:ILE:HD11	2.51	0.45
1:A:3308:ASP:N	1:A:3308:ASP:OD1	2.48	0.45
1:A:3915:HIS:CE1	1:A:3961:PHE:HB3	2.51	0.45
2:B:416:GLN:NE2	2:B:433:GLN:OE1	2.41	0.45
3:C:363:LYS:HA	3:C:420:VAL:HA	1.99	0.45
1:F:642:PHE:HZ	1:F:673:THR:HG23	1.81	0.45
1:F:1217:VAL:HA	1:F:1285:GLU:OE1	2.17	0.45
1:F:2869:LEU:HB2	1:F:2899:ARG:NH1	2.31	0.45
1:F:3321:LEU:HD13	1:F:3324:ARG:HH12	1.81	0.45
3:H:626:THR:HG22	3:H:628:GLU:H	1.80	0.45
3:H:661:ALA:HA	3:H:664:GLU:CD	2.36	0.45
4:K:3:ARG:NH1	4:K:122:VAL:O	2.50	0.45
4:N:155:TRP:HA	4:N:158:VAL:HG22	1.98	0.45
1:A:145:ASP:HA	1:A:147:PHE:CE2	2.51	0.45
1:A:345:PHE:HB3	1:A:366:TYR:CE1	2.51	0.45
1:A:1672:PHE:CZ	1:A:1676:ILE:HD11	2.52	0.45
1:A:2257:PHE:O	1:A:2261:SER:OG	2.25	0.45
1:A:2430:GLU:OE1	1:A:2430:GLU:N	2.29	0.45
1:A:3988:LEU:HD12	1:A:3988:LEU:HA	1.82	0.45
3:C:247:TRP:CD1	3:C:263:ALA:HB3	2.52	0.45
1:F:168:ASP:OD1	1:F:169:THR:N	2.43	0.45
1:F:1095:LEU:O	1:F:1099:PHE:N	2.48	0.45
1:F:1580:LEU:O	1:F:1584:GLN:HG2	2.17	0.45
1:F:2522:ARG:HH21	1:F:2560:ASN:HB3	1.81	0.45
1:F:3146:SER:C	1:F:3147:LYS:HD2	2.37	0.45
1:F:3174:ASP:HB3	1:F:3178:ILE:HD13	1.98	0.45
1:F:3500:SER:HA	1:F:3503:VAL:HG12	1.97	0.45
2:G:480:ASN:OD1	2:G:483:LEU:N	2.33	0.45
3:H:115:MET:O	3:H:119:GLN:HG2	2.17	0.45
3:H:602:VAL:HA	3:H:609:PHE:CD2	2.52	0.45
5:M:843:LEU:HD23	5:M:846:ARG:HH11	1.82	0.45
7:D:35:DT:H2'	7:D:36:DG:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:THR:O	1:A:58:VAL:HG12	2.16	0.45
1:A:925:GLN:HA	1:A:2769:VAL:HG13	1.99	0.45
1:A:1145:LEU:HD23	1:A:1165:LEU:HD13	1.97	0.45
1:A:2405:VAL:O	1:A:2408:MET:HE2	2.15	0.45
1:A:3389:VAL:O	1:A:3393:GLU:HG3	2.17	0.45
1:A:3835:PRO:HA	1:A:3839:TYR:HB2	1.98	0.45
2:B:95:ASN:ND2	2:B:99:PHE:H	2.12	0.45
2:B:247:ARG:HG2	2:B:247:ARG:O	2.17	0.45
3:C:259:ILE:HD12	3:C:377:LEU:HD21	1.98	0.45
1:F:1379:PRO:HB2	1:F:1385:ASN:HD22	1.81	0.45
1:F:1773:VAL:O	1:F:1773:VAL:HG12	2.16	0.45
1:F:2745:ARG:HG3	8:I:45:DG:O4'	2.16	0.45
1:F:3959:MET:CE	1:F:4124:TRP:HE1	2.29	0.45
2:G:148:TRP:N	2:G:189:LYS:HZ1	2.15	0.45
4:L:144:LEU:O	4:L:148:ASN:ND2	2.50	0.45
4:N:155:TRP:NE1	4:O:158:VAL:HG21	2.31	0.45
5:P:670:THR:HG23	5:P:675:LYS:HB2	1.98	0.45
5:P:681:ARG:NH2	5:P:730:PHE:HB3	2.32	0.45
6:Q:100:VAL:HG12	6:Q:101:ALA:H	1.80	0.45
6:R:80:LEU:HD23	6:R:80:LEU:H	1.82	0.45
1:A:450:SER:N	1:A:453:MET:SD	2.89	0.45
1:A:1593:VAL:HA	1:A:1596:VAL:HG22	1.98	0.45
2:B:203:MET:SD	2:B:238:LYS:N	2.74	0.45
2:B:361:TYR:OH	3:C:356:PHE:O	2.22	0.45
1:F:117:LYS:NZ	3:H:299:ASP:HA	2.32	0.45
1:F:241:ASP:O	1:F:244:THR:HG22	2.17	0.45
1:F:1066:LEU:HD12	1:F:1074:LYS:HB3	1.98	0.45
1:F:2408:MET:HG3	1:F:2411:LEU:HD13	1.98	0.45
1:F:3128:LYS:HA	1:F:3128:LYS:HD3	1.78	0.45
2:G:200:LEU:HD23	2:G:200:LEU:H	1.82	0.45
3:H:9:ALA:O	3:H:131:HIS:N	2.32	0.45
3:H:237:PHE:CE2	3:H:239:LYS:HB2	2.51	0.45
4:N:179:ARG:O	4:N:182:LEU:HG	2.17	0.45
5:P:668:SER:HB3	5:P:703:GLY:H	1.82	0.45
6:Q:29:ILE:HD13	6:Q:76:LEU:HB3	1.97	0.45
6:R:214:LEU:O	6:R:218:TYR:HB2	2.17	0.45
1:A:371:GLY:HA2	1:A:423:TYR:CZ	2.51	0.45
1:A:525:LYS:HE2	1:A:525:LYS:HB2	1.71	0.45
1:A:1287:GLN:HG3	1:A:1289:SER:H	1.81	0.45
1:A:1525:CYS:O	1:A:1529:VAL:HG23	2.16	0.45
1:A:3577:GLN:HE21	1:A:3629:ARG:HB3	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:100:LYS:HA	2:B:100:LYS:HD2	1.77	0.45
3:C:213:ILE:HB	3:C:221:LEU:HD22	1.99	0.45
3:C:488:GLN:O	3:C:492:GLN:HG3	2.17	0.45
1:F:1101:PHE:HD2	1:F:1163:LEU:HD13	1.82	0.45
1:F:2264:ASP:N	1:F:2265:PRO:HD3	2.31	0.45
1:F:2404:ARG:HA	1:F:2404:ARG:HD2	1.75	0.45
2:G:171:ASN:HB3	2:G:206:LYS:HB2	1.98	0.45
2:G:350:PHE:HB3	2:G:394:VAL:HG12	1.98	0.45
2:G:459:VAL:HG11	3:H:382:HIS:ND1	2.31	0.45
3:H:496:HIS:NE2	3:H:504:PRO:O	2.48	0.45
1:A:332:GLU:HB2	1:A:335:LYS:NZ	2.32	0.45
1:A:994:TRP:HE1	1:A:1000:LYS:HZ3	1.62	0.45
1:A:2492:ASP:OD1	1:A:2493:ASN:N	2.50	0.45
2:B:94:LYS:N	2:B:102:ILE:O	2.41	0.45
1:F:730:LEU:HD11	1:F:765:LEU:HD11	1.99	0.45
1:F:1643:MET:SD	1:F:1688:LEU:HD22	2.57	0.45
1:F:3141:PHE:HA	1:F:3144:PHE:CE1	2.52	0.45
1:F:3588:TRP:CD1	1:F:3609:MET:SD	3.10	0.45
1:F:3959:MET:HE3	1:F:4124:TRP:HE1	1.80	0.45
2:G:254:ARG:NH1	8:I:34:DC:O4'	2.50	0.45
2:G:351:LYS:O	2:G:395:ALA:N	2.50	0.45
3:H:461:MET:HG3	3:H:526:SER:OG	2.17	0.45
4:K:73:ALA:HB1	4:K:86:PHE:HZ	1.81	0.45
4:O:20:LEU:HD21	4:O:35:THR:O	2.16	0.45
6:Q:53:VAL:O	6:Q:56:GLN:HG3	2.15	0.45
6:Q:154:ALA:O	6:Q:158:HIS:ND1	2.36	0.45
8:E:31:DA:H2'	8:E:31:DA:N3	2.31	0.45
8:I:33:DA:H2	9:J:25:DT:H3	1.63	0.45
8:I:41:DT:O3'	8:I:42:DA:H8	2.00	0.45
1:A:1065:SER:O	1:A:1069:HIS:N	2.50	0.45
1:A:1867:ILE:O	1:A:1871:MET:HG2	2.17	0.45
1:A:1963:GLN:HA	1:A:2125:TRP:CH2	2.52	0.45
1:A:2142:ILE:O	1:A:2146:LEU:HG	2.17	0.45
1:A:3490:VAL:HG21	1:A:3495:PHE:CE2	2.51	0.45
1:A:3962:ARG:HD2	1:A:4124:TRP:CZ2	2.52	0.45
3:C:129:LYS:NZ	3:C:131:HIS:HB2	2.32	0.45
1:F:82:ARG:HA	1:F:85:ILE:HD12	1.99	0.45
1:F:1218:SER:O	1:F:1222:ASN:N	2.48	0.45
1:F:1603:GLN:OE1	1:F:1606:ARG:NH2	2.50	0.45
5:P:749:SER:HG	5:P:750:THR:N	2.15	0.45
7:D:19:DA:H2	8:E:39:DA:C2	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:472:GLY:O	1:A:475:LEU:HB3	2.17	0.45
1:A:652:GLU:HA	1:A:655:LEU:HD12	1.99	0.45
1:A:675:ARG:HG2	1:A:678:LYS:HE2	1.98	0.45
1:A:1150:LYS:HD2	1:A:1162:SER:HA	1.99	0.45
1:A:2844:LEU:HD21	1:A:2858:ILE:HG21	1.99	0.45
1:A:3781:CYS:HB3	1:A:3786:LEU:HB2	1.99	0.45
2:B:85:VAL:HG23	2:B:105:LEU:HB3	1.99	0.45
2:B:429:PRO:HG2	3:C:435:PHE:CD2	2.52	0.45
1:F:1169:VAL:HG11	1:F:1198:LEU:HD11	1.98	0.45
1:F:3577:GLN:HA	1:F:3629:ARG:CZ	2.47	0.45
1:F:4125:GLU:HG3	1:F:4127:TRP:NE1	2.32	0.45
2:G:35:ARG:NH2	2:G:80:ARG:HB3	2.32	0.45
2:G:367:PHE:HE2	2:G:369:TYR:HB2	1.82	0.45
2:G:370:PRO:HD3	2:G:382:PHE:CD2	2.52	0.45
3:H:335:SER:HB3	3:H:394:ARG:HH12	1.82	0.45
6:R:81:ARG:HD2	6:R:81:ARG:O	2.17	0.45
1:A:242:PRO:O	1:A:246:ARG:HG2	2.16	0.44
1:A:1377:CYS:SG	1:A:1378:GLU:N	2.89	0.44
1:A:1667:SER:O	1:A:1670:GLU:HG2	2.16	0.44
1:A:1877:LEU:HA	1:A:1880:MET:HG2	1.98	0.44
1:A:2410:GLU:O	1:A:2414:GLN:NE2	2.50	0.44
1:A:3048:LYS:HD2	1:A:3061:LEU:HB2	1.99	0.44
1:A:3246:ALA:CB	1:A:3254:LEU:HD11	2.47	0.44
1:F:145:ASP:O	1:F:148:LYS:NZ	2.38	0.44
1:F:1069:HIS:CE1	1:F:3743:HIS:HD2	2.35	0.44
1:F:1353:PRO:HD2	1:F:1356:TRP:CE3	2.51	0.44
1:F:3387:GLU:O	1:F:3390:GLN:NE2	2.50	0.44
2:G:346:MET:HG2	2:G:399:ARG:HH21	1.82	0.44
2:G:493:LEU:HD23	3:H:323:PHE:CE1	2.53	0.44
4:L:175:ASP:OD1	4:L:176:LEU:N	2.50	0.44
5:M:833:ASN:HB3	5:M:836:THR:HG21	1.99	0.44
4:O:94:TYR:HD2	4:O:96:PHE:HB2	1.82	0.44
6:R:46:HIS:HB3	6:R:126:ALA:HB2	1.99	0.44
8:I:25:DA:N6	9:J:33:DA:N3	2.64	0.44
1:A:475:LEU:O	1:A:479:ILE:HG12	2.16	0.44
1:A:537:SER:O	1:A:541:MET:HG3	2.16	0.44
1:A:1153:LEU:HD11	1:A:1157:PHE:HB3	1.99	0.44
1:A:2216:LEU:HD13	1:A:2241:LEU:HD23	2.00	0.44
1:A:2411:LEU:O	1:A:2415:LEU:HG	2.16	0.44
1:A:2953:THR:HG1	1:A:2994:TRP:HE1	1.63	0.44
1:F:992:ILE:HG21	1:F:1036:PHE:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1343:GLU:HG2	1:F:1398:VAL:HG21	1.98	0.44
1:F:1551:ILE:HG13	1:F:1552:HIS:N	2.32	0.44
1:F:1690:GLY:O	1:F:1694:THR:HG23	2.17	0.44
1:F:1740:VAL:HA	1:F:1743:MET:HG3	1.98	0.44
1:F:2091:HIS:HB2	1:F:2094:MET:HG3	1.99	0.44
1:F:3007:GLU:O	1:F:3011:LEU:N	2.50	0.44
1:F:3052:LEU:HA	1:F:3056:GLU:O	2.17	0.44
1:F:3118:ASP:OD1	1:F:3119:VAL:N	2.50	0.44
2:G:45:SER:HA	2:G:138:GLY:H	1.80	0.44
4:K:96:PHE:HD2	4:K:98:GLU:HG3	1.83	0.44
4:L:133:THR:O	4:L:137:ASN:ND2	2.51	0.44
4:L:155:TRP:HA	4:L:158:VAL:HG12	1.99	0.44
1:A:122:LYS:HD2	1:A:122:LYS:HA	1.87	0.44
1:A:247:GLU:HG2	1:A:251:PHE:CE2	2.52	0.44
1:A:827:ASN:HB3	1:A:836:LYS:HZ3	1.81	0.44
1:A:827:ASN:HB3	1:A:836:LYS:NZ	2.33	0.44
1:A:1526:GLU:OE2	1:A:1574:ASN:ND2	2.51	0.44
3:C:528:ILE:HG22	3:C:532:LYS:NZ	2.33	0.44
1:F:40:GLN:HA	1:F:43:VAL:HG22	1.97	0.44
1:F:168:ASP:OD2	9:J:22:DG:H5 <sup>''</sup>	2.17	0.44
1:F:754:MET:O	1:F:758:LEU:HD23	2.17	0.44
1:F:1144:SER:O	1:F:1151:ARG:NH2	2.49	0.44
1:F:3686:TRP:CD1	1:F:3690:PHE:HD2	2.35	0.44
2:G:168:LEU:N	2:G:201:ASP:O	2.48	0.44
2:G:458:GLN:O	2:G:462:MET:HE2	2.17	0.44
4:K:51:GLU:O	4:K:54:GLN:HG3	2.17	0.44
1:A:3462:ARG:HG2	1:A:3498:TRP:HZ3	1.81	0.44
1:A:3775:LEU:HD13	1:A:3786:LEU:HB3	2.00	0.44
2:B:189:LYS:HE2	2:B:189:LYS:HB2	1.87	0.44
2:B:416:GLN:HB3	2:B:431:GLY:H	1.81	0.44
3:C:242:ARG:HD3	3:C:271:ARG:CZ	2.47	0.44
1:F:22:ALA:HB3	1:F:34:LEU:HD21	2.00	0.44
1:F:749:VAL:O	1:F:753:GLN:HG2	2.17	0.44
1:F:889:GLU:HB2	1:F:891:ARG:HH21	1.82	0.44
1:F:1626:TRP:CZ2	1:F:1674:THR:HG21	2.51	0.44
1:F:2371:PHE:HD2	1:F:2374:LEU:HB2	1.82	0.44
1:F:2548:PRO:HB2	1:F:2848:PHE:CD1	2.53	0.44
1:F:3577:GLN:OE1	1:F:3629:ARG:NE	2.49	0.44
5:M:900:LYS:HB3	5:M:900:LYS:HE2	1.85	0.44
8:I:33:DA:H2 <sup>''</sup>	8:I:34:DC:C6	2.53	0.44
1:A:1713:VAL:O	1:A:1716:GLN:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3137:GLU:OE1	1:A:3186:ARG:NH2	2.51	0.44
1:A:3498:TRP:HD1	1:A:3501:HIS:CE1	2.36	0.44
2:B:473:TYR:HD2	3:C:350:GLN:HB3	1.82	0.44
3:C:267:ILE:H	3:C:361:VAL:HB	1.83	0.44
1:F:2220:MET:HA	1:F:2223:VAL:HG12	1.99	0.44
1:F:2306:ASN:HA	1:F:2309:PHE:CD2	2.52	0.44
1:F:2331:MET:HG2	1:F:2334:LYS:HG2	1.98	0.44
1:F:2339:GLU:O	1:F:2343:GLU:HG2	2.17	0.44
2:G:72:ILE:O	2:G:76:ILE:HG12	2.17	0.44
2:G:173:ASP:HB2	2:G:215:LEU:HG	1.99	0.44
2:G:320:GLN:OE1	3:H:274:LYS:HE3	2.18	0.44
2:G:372:GLU:OE2	2:G:379:SER:N	2.44	0.44
4:K:176:LEU:HD23	4:K:176:LEU:HA	1.86	0.44
4:L:150:ARG:HH12	4:L:151:LEU:HG	1.81	0.44
6:Q:16:LEU:HB3	6:Q:23:LEU:HD12	1.99	0.44
6:R:50:ASP:HB3	6:R:53:VAL:HG12	1.99	0.44
6:R:192:GLN:HA	6:R:195:ILE:HG22	2.00	0.44
1:A:164:LYS:HB3	1:A:166:ILE:HG12	1.99	0.44
1:A:489:ARG:O	1:A:492:SER:OG	2.30	0.44
1:A:1186:LYS:HA	1:A:1186:LYS:HD2	1.76	0.44
1:A:2153:THR:O	1:A:2156:VAL:HG12	2.18	0.44
1:A:2306:ASN:HA	1:A:2309:PHE:CD2	2.53	0.44
1:A:3321:LEU:HD13	1:A:3324:ARG:NH1	2.28	0.44
2:B:350:PHE:HA	2:B:396:ALA:HA	1.98	0.44
1:F:278:HIS:HB3	1:F:281:GLN:HG3	1.98	0.44
1:F:669:LEU:O	1:F:673:THR:OG1	2.29	0.44
1:F:2260:PHE:HB3	1:F:2273:GLY:HA3	2.00	0.44
1:F:2304:VAL:O	1:F:2307:MET:HB2	2.17	0.44
1:F:3968:ILE:HD12	1:F:3976:GLU:HG3	1.99	0.44
1:F:3968:ILE:HG23	1:F:3976:GLU:HG3	2.00	0.44
1:A:1357:LYS:O	1:A:1360:LYS:HB3	2.17	0.44
1:A:2239:LYS:HB2	1:A:2279:ILE:HD12	2.00	0.44
1:A:3118:ASP:HB3	1:A:3121:LEU:HD13	2.00	0.44
1:A:4086:ASP:N	1:A:4086:ASP:OD1	2.50	0.44
2:B:288:LEU:HB2	3:C:311:ILE:HB	1.99	0.44
1:F:405:ASP:HB3	1:F:406:ARG:H	1.64	0.44
1:F:539:GLN:N	1:F:539:GLN:OE1	2.46	0.44
1:F:1757:MET:O	1:F:1760:GLU:HG2	2.17	0.44
1:F:1769:GLU:H	1:F:1772:HIS:CE1	2.36	0.44
1:F:2184:TYR:HE1	1:F:2734:ARG:HD2	1.82	0.44
1:F:2257:PHE:HA	1:F:2260:PHE:CE2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:2928:LYS:HZ2	1:F:2996:LEU:HD12	1.82	0.44
1:F:3048:LYS:HE2	1:F:3061:LEU:HD13	1.99	0.44
1:F:3772:ASN:HD21	1:F:3788:LEU:HB3	1.83	0.44
1:F:3792:SER:N	1:F:3804:GLU:OE1	2.51	0.44
1:F:3992:ARG:HA	1:F:3992:ARG:HD3	1.67	0.44
4:K:3:ARG:HB3	4:K:21:GLN:NE2	2.32	0.44
4:K:141:ASN:HD21	4:L:140:LYS:HE2	1.82	0.44
5:M:800:GLU:HG2	5:M:805:TRP:HB2	1.99	0.44
1:A:990:GLN:HB3	1:A:2781:PRO:HD3	1.99	0.44
1:A:1066:LEU:HA	1:A:1069:HIS:HD2	1.82	0.44
1:A:2854:PHE:O	1:A:2858:ILE:HG12	2.18	0.44
1:A:2880:CYS:HA	1:A:2885:GLN:HB2	1.99	0.44
1:A:3123:GLN:OE1	1:A:3123:GLN:N	2.40	0.44
1:A:3859:TYR:CE1	1:A:4119:ARG:HA	2.52	0.44
3:C:497:ARG:HA	3:C:497:ARG:HD3	1.79	0.44
1:F:433:PRO:O	1:F:436:GLU:HG2	2.17	0.44
1:F:910:PHE:HE1	1:F:2807:GLN:HB3	1.83	0.44
1:F:1294:VAL:HA	1:F:1297:PHE:CD2	2.53	0.44
1:F:1778:PHE:O	1:F:1781:SER:OG	2.25	0.44
1:F:3243:ILE:HD13	1:F:3262:LEU:HD11	1.98	0.44
1:F:3700:GLU:OE2	1:F:3716:HIS:ND1	2.32	0.44
2:G:241:ASP:HA	2:G:244:ARG:NH1	2.33	0.44
3:H:194:LEU:HG	3:H:195:LYS:HD2	1.99	0.44
3:H:667:GLU:HA	3:H:675:TRP:CZ3	2.53	0.44
4:N:170:GLU:O	4:N:173:GLU:HG2	2.17	0.44
8:I:45:DG:H5'	8:I:45:DG:C8	2.51	0.44
1:A:949:PRO:HD3	1:F:2579:HIS:HB3	1.99	0.44
1:A:1212:LEU:HD12	1:A:1216:GLY:HA2	1.99	0.44
1:A:1723:PRO:HB2	1:A:1724:MET:CE	2.48	0.44
1:A:1725:GLN:HE22	1:A:1727:ARG:HH21	1.65	0.44
1:A:2428:ASP:O	1:A:2432:GLN:HG2	2.17	0.44
1:A:2526:SER:O	1:A:2538:ARG:NH2	2.51	0.44
1:A:2919:ASP:OD1	1:A:2919:ASP:N	2.51	0.44
1:A:3019:ILE:HG13	1:A:3020:ASP:H	1.83	0.44
1:A:3967:PHE:O	1:A:3970:LEU:HD22	2.18	0.44
1:A:4065:LEU:HG	1:A:4069:GLU:HB3	1.99	0.44
2:B:93:ASP:OD1	2:B:93:ASP:N	2.51	0.44
2:B:400:TYR:CZ	2:B:402:PRO:HG3	2.53	0.44
2:B:474:ARG:HB3	2:B:477:SER:HB3	2.00	0.44
3:C:353:ARG:HA	3:C:356:PHE:CD1	2.53	0.44
1:F:1255:CYS:HA	1:F:1258:ASP:OD2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:2274:ILE:HD11	1:F:2306:ASN:ND2	2.33	0.44
1:F:3959:MET:HG3	1:F:4124:TRP:CZ2	2.53	0.44
3:H:452:ASN:OD1	3:H:453:ALA:N	2.50	0.44
4:O:32:PHE:HZ	4:O:109:GLY:HA2	1.81	0.44
5:P:708:ARG:O	5:P:712:ILE:HG12	2.18	0.44
5:P:771:LEU:HB3	5:P:775:LYS:NZ	2.33	0.44
7:D:17:DT:H6	7:D:17:DT:H2'	1.68	0.44
1:A:1220:LEU:HA	1:A:1224:PHE:HD2	1.83	0.43
1:A:1439:PRO:HA	1:A:1445:ARG:HH22	1.82	0.43
1:A:1646:LEU:O	1:A:1649:LEU:HG	2.18	0.43
1:A:2375:ALA:HB1	1:A:2379:MET:HE3	1.99	0.43
1:A:3133:GLN:HA	1:A:3136:THR:HG22	1.99	0.43
1:A:3512:VAL:HB	1:A:3516:HIS:CE1	2.53	0.43
1:A:3683:CYS:O	1:A:3685:PRO:HD3	2.17	0.43
3:C:251:LEU:H	3:C:261:ILE:HG12	1.81	0.43
1:F:198:ARG:NH1	2:G:315:ASP:OD2	2.51	0.43
1:F:393:LYS:HA	1:F:393:LYS:HD2	1.55	0.43
1:F:1133:HIS:O	1:F:1137:ILE:HG12	2.18	0.43
1:F:1725:GLN:OE1	1:F:1726:SER:N	2.51	0.43
1:F:2589:TYR:HB2	1:F:2777:HIS:HB2	2.00	0.43
1:F:2827:SER:OG	1:F:2828:GLU:OE2	2.36	0.43
1:F:2980:ASP:N	1:F:2980:ASP:OD1	2.50	0.43
2:G:145:GLU:OE1	2:G:145:GLU:N	2.51	0.43
4:K:44:THR:HG23	4:K:116:VAL:HG23	1.99	0.43
4:K:169:LYS:HE2	4:K:169:LYS:HB3	1.83	0.43
4:L:176:LEU:HD23	4:L:176:LEU:HA	1.84	0.43
5:P:813:PHE:C	5:P:849:GLY:H	2.21	0.43
1:A:899:ARG:HD3	1:A:2568:MET:HB3	2.00	0.43
1:A:2737:GLU:O	1:A:2741:LEU:N	2.41	0.43
1:A:3005:LEU:O	1:A:3010:SER:OG	2.28	0.43
2:B:470:ARG:HD2	3:C:389:MET:HE1	2.00	0.43
1:F:243:GLN:O	1:F:246:ARG:HG2	2.18	0.43
1:F:2184:TYR:CE1	1:F:2734:ARG:HD2	2.53	0.43
1:F:3823:GLU:HG2	1:F:3824:GLU:N	2.33	0.43
1:F:3919:GLY:HA3	1:F:3947:GLY:HA2	1.99	0.43
3:H:434:MET:SD	3:H:436:SER:OG	2.66	0.43
6:Q:50:ASP:OD1	6:Q:51:THR:N	2.37	0.43
7:D:13:DC:OP1	7:D:14:DA:N6	2.51	0.43
1:A:1643:MET:HA	1:A:1646:LEU:HD12	2.00	0.43
1:A:1760:GLU:O	1:A:1764:GLU:HG2	2.17	0.43
1:A:2844:LEU:HB3	1:A:2875:ALA:HB1	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3165:THR:HB	1:A:3169:PRO:HG3	1.99	0.43
1:A:3353:GLU:HG2	1:A:3357:ARG:HG3	1.99	0.43
2:B:170:THR:O	2:B:205:LEU:HD13	2.18	0.43
1:F:249:PHE:O	1:F:252:VAL:HG12	2.18	0.43
1:F:460:ALA:O	1:F:464:VAL:HG13	2.18	0.43
1:F:732:PHE:O	1:F:735:SER:OG	2.26	0.43
1:F:2162:LYS:HG3	1:F:2163:HIS:ND1	2.33	0.43
1:F:3419:PHE:O	1:F:3423:GLN:HG2	2.17	0.43
2:G:351:LYS:N	2:G:395:ALA:O	2.43	0.43
3:H:65:ASP:O	3:H:78:THR:HA	2.18	0.43
3:H:116:ASP:O	3:H:120:HIS:ND1	2.49	0.43
5:M:659:PHE:HB2	5:M:685:PHE:O	2.18	0.43
5:P:788:THR:HG23	5:P:791:GLU:H	1.82	0.43
1:A:1367:HIS:HB2	1:A:1370:ARG:NH1	2.34	0.43
1:A:3898:LEU:O	1:A:3901:ARG:HG3	2.17	0.43
2:B:360:HIS:HB2	2:B:438:PRO:HG2	2.00	0.43
1:F:13:LEU:HD21	1:F:3069:MET:HG3	2.00	0.43
2:G:262:LYS:HB3	2:G:268:VAL:HG12	1.99	0.43
2:G:276:LEU:HA	3:H:433:TYR:CE1	2.54	0.43
3:H:360:GLN:NE2	8:I:24:DA:N1	2.65	0.43
4:N:59:MET:SD	4:N:59:MET:N	2.87	0.43
6:Q:157:LEU:HD21	6:R:157:LEU:HA	1.99	0.43
1:A:765:LEU:HA	1:A:768:VAL:HG12	2.01	0.43
1:A:1071:ASN:HB3	1:A:1074:LYS:HG3	2.00	0.43
1:A:1158:PRO:HG2	1:A:1159:PRO:HD3	2.00	0.43
1:A:4056:PRO:O	1:A:4060:THR:OG1	2.26	0.43
2:B:37:SER:H	2:B:161:MET:HE1	1.84	0.43
2:B:204:HIS:O	2:B:205:LEU:HD12	2.18	0.43
3:C:242:ARG:NE	3:C:243:HIS:H	2.16	0.43
1:F:394:GLN:CD	1:F:1737:ASN:HB3	2.39	0.43
1:F:710:PHE:O	1:F:714:VAL:HG23	2.19	0.43
1:F:975:ASP:N	1:F:981:ARG:HH21	2.17	0.43
1:F:1769:GLU:HB2	1:F:1772:HIS:CD2	2.52	0.43
1:F:2349:LEU:HB3	1:F:2360:PHE:CE1	2.54	0.43
1:F:2899:ARG:HH21	1:F:2900:LEU:HG	1.84	0.43
1:F:2964:ASP:HB2	1:F:3252:PHE:CD2	2.54	0.43
1:F:3887:PHE:HA	1:F:3890:MET:SD	2.58	0.43
1:F:3962:ARG:HD2	1:F:4124:TRP:CZ2	2.54	0.43
2:G:325:ARG:HG3	3:H:88:PHE:CD2	2.54	0.43
3:H:163:PHE:HB3	3:H:208:VAL:HG21	2.00	0.43
5:P:659:PHE:HD2	5:P:685:PHE:HB3	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1300:SER:HA	1:A:1304:HIS:HB3	2.00	0.43
1:A:1372:LEU:O	1:A:1375:THR:OG1	2.25	0.43
1:A:2126:MET:SD	1:A:2126:MET:N	2.92	0.43
1:A:2482:ASP:HA	1:A:2485:ARG:HD2	1.99	0.43
1:A:2492:ASP:O	1:A:2496:GLN:HG3	2.19	0.43
1:A:2967:GLU:O	1:A:2971:GLN:HG2	2.18	0.43
1:A:3961:PHE:HE2	1:A:4107:LEU:HD21	1.83	0.43
2:B:193:LEU:HB2	2:B:198:ILE:HD12	2.01	0.43
2:B:203:MET:SD	2:B:237:SER:HB2	2.58	0.43
2:B:276:LEU:HD23	2:B:276:LEU:H	1.84	0.43
2:B:403:ARG:NH1	8:E:31:DA:O3'	2.51	0.43
1:F:528:VAL:HA	1:F:633:ILE:HD11	2.00	0.43
1:F:978:GLN:HG2	1:F:2597:PHE:HA	2.01	0.43
1:F:1419:LEU:HD21	1:F:1467:ILE:HB	2.01	0.43
1:F:2238:ILE:O	1:F:2241:LEU:HG	2.18	0.43
1:F:3383:GLN:HG3	1:F:3387:GLU:OE2	2.18	0.43
1:F:4090:ARG:HH22	1:F:4106:CYS:HA	1.82	0.43
3:H:33:GLN:HA	3:H:36:LYS:HE3	2.00	0.43
3:H:400:ARG:HH12	9:J:34:DT:P	2.41	0.43
4:O:95:PHE:HB2	4:O:113:LEU:HD13	1.98	0.43
6:Q:146:LEU:HD13	6:R:147:GLN:HE21	1.83	0.43
8:I:43:DT:H2''	8:I:44:DG:C2	2.53	0.43
1:A:168:ASP:OD2	7:D:22:DG:H5'	2.19	0.43
1:A:767:GLU:HB2	1:A:851:ILE:HD11	2.01	0.43
1:A:894:PHE:O	1:A:905:ILE:N	2.40	0.43
1:A:1046:PRO:O	1:A:1049:GLN:HB2	2.18	0.43
1:A:2450:GLU:O	1:A:2453:GLU:HG2	2.19	0.43
1:A:3527:GLN:O	1:A:3529:ILE:HD12	2.19	0.43
1:A:3571:PHE:CE2	1:A:3699:LEU:HD22	2.53	0.43
1:A:3595:GLU:HB2	1:A:3606:ILE:HD11	2.00	0.43
1:A:3878:VAL:HG13	1:A:3965:ARG:HH11	1.83	0.43
3:C:115:MET:O	3:C:119:GLN:HG2	2.18	0.43
3:C:315:ARG:HH11	3:C:320:ILE:HG13	1.84	0.43
1:F:475:LEU:O	1:F:479:ILE:HG12	2.18	0.43
1:F:1745:LYS:HA	1:F:1748:ASP:OD2	2.19	0.43
1:F:2153:THR:O	1:F:2156:VAL:HG12	2.19	0.43
1:F:2522:ARG:NH2	1:F:2564:GLU:HG3	2.34	0.43
2:G:388:LYS:HG3	3:H:454:VAL:HG11	2.00	0.43
2:G:489:ASN:ND2	3:H:331:MET:HB2	2.34	0.43
4:K:8:ILE:HG21	4:K:20:LEU:H	1.83	0.43
4:N:186:GLU:OE2	5:P:803:TYR:OH	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:19:DA:H2	8:E:39:DA:H2	1.65	0.43
1:A:264:ARG:HG3	8:E:39:DA:H2''	2.00	0.43
1:A:389:ILE:O	1:A:393:LYS:HG2	2.19	0.43
1:A:535:LEU:O	1:A:637:LYS:NZ	2.29	0.43
1:A:536:SER:HB3	1:A:637:LYS:HD3	2.01	0.43
1:A:1173:LEU:HD12	1:A:1191:PHE:CE1	2.54	0.43
1:A:2464:HIS:ND1	1:A:2466:SER:OG	2.52	0.43
1:A:2578:GLU:OE1	1:A:2578:GLU:N	2.42	0.43
1:A:2788:SER:HA	1:A:2791:ILE:HG12	2.00	0.43
3:C:497:ARG:NH2	3:C:504:PRO:HA	2.34	0.43
1:F:145:ASP:OD1	1:F:145:ASP:N	2.50	0.43
1:F:1379:PRO:O	1:F:1382:ILE:HG12	2.18	0.43
1:F:1596:VAL:O	1:F:1600:MET:HG2	2.19	0.43
1:F:1959:LEU:HA	1:F:2123:PRO:HG3	1.99	0.43
1:F:2510:LEU:HD12	1:F:2521:ILE:HG23	2.00	0.43
1:F:3420:CYS:SG	1:F:3421:ASP:N	2.92	0.43
2:G:418:GLU:HG2	2:G:426:GLN:OE1	2.18	0.43
2:G:426:GLN:HG3	2:G:429:PRO:HG3	2.01	0.43
4:K:107:ARG:O	4:K:107:ARG:HD3	2.19	0.43
5:P:757:GLU:HG3	5:P:758:TYR:CD2	2.52	0.43
5:P:819:TYR:HA	5:P:853:VAL:HB	2.01	0.43
6:Q:98:ASP:OD1	6:Q:98:ASP:N	2.52	0.43
6:R:50:ASP:OD1	6:R:52:SER:N	2.39	0.43
7:D:13:DC:H4'	7:D:14:DA:H2'	2.01	0.43
1:A:142:ARG:CZ	1:A:182:GLY:HA2	2.49	0.43
1:A:446:PHE:CD1	1:A:530:LEU:HD12	2.54	0.43
1:A:715:ALA:O	1:A:718:MET:HG3	2.19	0.43
1:A:935:HIS:HB2	1:A:984:TYR:HE1	1.83	0.43
1:A:1081:ALA:O	1:A:1085:ILE:HG23	2.19	0.43
1:A:1115:HIS:CD2	1:A:1119:LYS:HD3	2.53	0.43
1:A:2371:PHE:CD2	1:A:2374:LEU:HB2	2.53	0.43
1:A:2532:PRO:O	1:A:2538:ARG:NH1	2.50	0.43
2:B:35:ARG:NH2	2:B:80:ARG:HB3	2.34	0.43
2:B:81:ASP:N	2:B:81:ASP:OD1	2.52	0.43
2:B:126:GLN:O	2:B:130:ARG:HG2	2.17	0.43
2:B:130:ARG:NH1	2:B:133:ASP:OD2	2.51	0.43
2:B:357:LYS:H	2:B:360:HIS:CE1	2.36	0.43
2:B:488:ARG:O	2:B:491:GLU:HG2	2.19	0.43
3:C:36:LYS:HZ1	3:C:231:LEU:HD11	1.83	0.43
1:F:356:ASN:HB3	1:F:358:GLU:HG2	2.00	0.43
1:F:774:GLU:O	1:F:778:ILE:HG12	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1611:GLN:HB2	1:F:1613:HIS:ND1	2.34	0.43
1:F:1747:LEU:HD21	1:F:1778:PHE:HD1	1.82	0.43
1:F:3321:LEU:HD13	1:F:3324:ARG:NH1	2.34	0.43
3:H:18:PHE:HA	3:H:101:GLY:HA3	2.00	0.43
3:H:219:ASP:OD1	3:H:220:GLY:N	2.52	0.43
3:H:646:ALA:HA	3:H:651:GLU:HG3	2.00	0.43
4:K:187:LYS:HD3	4:L:187:LYS:HB3	2.01	0.43
4:O:142:GLU:HB3	4:O:146:LYS:HZ1	1.83	0.43
1:A:525:LYS:O	1:A:528:VAL:HG22	2.19	0.43
1:A:2746:LYS:HD2	7:D:12:DC:H3'	2.00	0.43
1:A:3244:ASP:O	1:A:3248:LYS:HG2	2.19	0.43
1:F:30:ALA:O	1:F:34:LEU:HG	2.19	0.43
1:F:275:PHE:CZ	1:F:319:PHE:HB2	2.54	0.43
1:F:294:PHE:CE2	1:F:344:GLN:HG2	2.54	0.43
1:F:2255:LEU:HA	1:F:2258:GLU:HG2	2.00	0.43
1:F:2486:ASP:N	1:F:2486:ASP:OD1	2.51	0.43
1:F:2869:LEU:HD13	1:F:2896:ALA:HA	1.99	0.43
1:F:3809:THR:OG1	1:F:3930:VAL:O	2.37	0.43
1:F:3912:CYS:HA	1:F:3915:HIS:CD2	2.54	0.43
2:G:330:GLU:HB3	2:G:333:GLU:HG2	2.01	0.43
3:H:84:MET:SD	3:H:84:MET:N	2.92	0.43
3:H:673:HIS:ND1	3:H:673:HIS:O	2.52	0.43
4:L:161:ARG:O	4:L:164:LYS:HG3	2.18	0.43
6:Q:157:LEU:HG	6:R:157:LEU:HD13	2.00	0.43
6:Q:211:VAL:HG23	6:Q:212:MET:SD	2.59	0.43
6:R:24:LEU:HD23	6:R:210:PHE:CE1	2.53	0.43
7:D:16:DA:H2''	7:D:17:DT:C5	2.53	0.43
1:A:1190:LEU:HD23	1:A:1193:LYS:HD3	2.01	0.42
1:A:3128:LYS:HD3	1:A:3128:LYS:HA	1.83	0.42
1:A:3981:TYR:CE1	1:A:4105:LYS:HB2	2.53	0.42
2:B:90:THR:O	2:B:100:LYS:NZ	2.52	0.42
2:B:293:ASN:HD21	5:M:692:ASN:ND2	2.17	0.42
2:B:446:MET:SD	2:B:446:MET:N	2.92	0.42
3:C:83:LEU:HD23	3:C:83:LEU:H	1.84	0.42
1:F:12:LEU:HA	1:F:41:GLU:OE2	2.19	0.42
1:F:635:PRO:HB3	1:F:672:ILE:HD11	2.01	0.42
1:F:1685:ASP:OD1	1:F:1686:LEU:N	2.52	0.42
1:F:3293:CYS:O	1:F:3297:VAL:HG23	2.19	0.42
1:F:4065:LEU:HD12	1:F:4069:GLU:HB3	2.01	0.42
2:G:154:PHE:CZ	2:G:166:ILE:HD11	2.53	0.42
2:G:353:LEU:O	2:G:353:LEU:HD23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:109:GLY:HA3	4:O:111:PHE:CZ	2.54	0.42
1:A:387:GLU:O	1:A:391:ARG:HG2	2.19	0.42
1:A:567:GLU:HA	1:A:570:LYS:HE2	2.01	0.42
1:A:770:LEU:O	1:A:774:GLU:HG3	2.19	0.42
1:A:2454:LEU:O	1:A:2458:VAL:HG23	2.18	0.42
1:A:3078:LEU:HA	1:A:3082:TYR:HD2	1.84	0.42
1:A:3197:LEU:HD22	1:A:3227:ILE:HG21	2.00	0.42
1:A:3474:ARG:HE	1:A:3474:ARG:HB3	1.69	0.42
1:A:3499:ILE:HA	1:A:3502:MET:SD	2.60	0.42
1:A:3553:GLU:HG3	1:A:3557:ARG:NH2	2.33	0.42
1:A:4085:LYS:O	1:A:4089:ILE:HG23	2.19	0.42
2:B:332:GLU:O	2:B:335:GLU:HG2	2.18	0.42
1:F:532:ARG:O	1:F:536:SER:OG	2.29	0.42
1:F:798:GLY:HA2	1:F:801:LYS:NZ	2.33	0.42
1:F:860:GLY:C	1:F:3136:THR:HG21	2.40	0.42
1:F:1020:PRO:HA	1:F:1073:PHE:CE1	2.54	0.42
1:F:1358:LEU:HA	1:F:1361:LYS:HE2	2.01	0.42
1:F:2365:ASN:ND2	1:F:2396:LEU:HG	2.34	0.42
1:F:3251:ASN:HB2	1:F:3254:LEU:HD13	2.01	0.42
1:F:3531:TYR:HB2	1:F:3532:PRO:HD3	2.01	0.42
1:F:4057:ALA:HB1	1:F:4082:ARG:HA	2.01	0.42
2:G:526:LYS:HE2	2:G:528:LEU:HB3	2.01	0.42
5:M:754:PHE:O	5:M:758:TYR:N	2.52	0.42
4:N:8:ILE:HG13	4:N:8:ILE:O	2.19	0.42
5:P:675:LYS:N	5:P:676:PRO:HD2	2.35	0.42
1:A:21:ALA:HA	1:A:24:ARG:NH1	2.35	0.42
1:A:164:LYS:HE3	1:A:166:ILE:HG23	2.01	0.42
1:A:344:GLN:O	1:A:348:ILE:HG12	2.19	0.42
1:A:959:TYR:CE1	1:A:1007:VAL:HG21	2.54	0.42
1:A:1006:THR:HG22	1:A:1054:VAL:HG21	2.01	0.42
1:A:1087:ARG:HA	1:A:1090:ARG:NH2	2.35	0.42
1:A:2295:GLN:HG3	1:A:2298:GLU:H	1.83	0.42
1:A:3569:GLN:NE2	1:A:3573:ASN:OD1	2.48	0.42
1:A:4083:GLY:HA3	1:A:4088:ASN:HB2	2.01	0.42
2:B:174:ASN:HB2	2:B:215:LEU:HB2	2.01	0.42
3:C:53:GLU:HB3	3:C:83:LEU:HB2	1.99	0.42
3:C:134:ILE:HG21	3:C:163:PHE:CE1	2.55	0.42
1:F:147:PHE:C	1:F:148:LYS:HD3	2.40	0.42
1:F:1004:GLN:HG2	1:F:1005:ASP:N	2.34	0.42
1:F:1075:ARG:HD3	1:F:1113:LEU:HD23	2.00	0.42
1:F:1388:ASP:HA	1:F:1392:MET:HG2	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:2173:ALA:HB1	1:F:2214:ARG:NH2	2.34	0.42
1:F:3148:GLN:NE2	1:F:3150:ASN:OD1	2.53	0.42
1:F:3285:HIS:NE2	1:F:3333:THR:HB	2.34	0.42
1:F:3506:LEU:HD21	1:F:3554:PHE:CD2	2.55	0.42
2:G:66:CYS:O	2:G:70:VAL:HG13	2.19	0.42
3:H:677:ILE:HA	3:H:680:GLN:HG2	2.00	0.42
4:L:3:ARG:NE	4:L:21:GLN:OE1	2.51	0.42
6:R:217:LEU:O	6:R:221:VAL:HG23	2.19	0.42
1:A:130:LEU:HA	1:A:130:LEU:HD23	1.73	0.42
1:A:234:PHE:CD2	1:A:235:THR:HG23	2.53	0.42
1:A:851:ILE:HD13	1:A:851:ILE:HA	1.92	0.42
1:A:1623:LEU:HD12	1:A:1623:LEU:HA	1.88	0.42
1:A:3625:LEU:N	1:A:3683:CYS:HA	2.33	0.42
3:C:83:LEU:HD22	3:C:121:GLU:HG2	2.01	0.42
1:F:36:ARG:HD3	1:F:2426:HIS:CD2	2.55	0.42
1:F:1296:PHE:HA	1:F:1299:GLU:HG2	2.01	0.42
1:F:1714:LEU:HB3	1:F:1761:LEU:HD21	2.00	0.42
1:F:2122:LEU:HB2	1:F:2126:MET:SD	2.59	0.42
1:F:2955:SER:O	1:F:2958:LEU:HG	2.20	0.42
1:F:3133:GLN:O	1:F:3136:THR:HG22	2.18	0.42
3:H:508:ILE:HG23	3:H:509:GLN:N	2.32	0.42
4:O:158:VAL:HG22	4:O:161:ARG:HE	1.85	0.42
5:P:666:VAL:HG12	5:P:675:LYS:HE3	2.00	0.42
1:A:156:PHE:HA	1:A:159:GLU:HG3	2.01	0.42
1:A:738:HIS:O	1:A:742:GLU:HG3	2.20	0.42
1:A:1482:GLU:OE1	1:A:1482:GLU:N	2.50	0.42
1:A:1815:THR:OG1	1:A:1816:ARG:N	2.53	0.42
1:A:2102:LYS:HD3	1:A:2102:LYS:HA	1.82	0.42
1:A:2576:MET:HE3	1:A:2787:HIS:HA	2.01	0.42
1:A:2584:CYS:SG	1:A:2585:GLU:N	2.93	0.42
1:A:3175:PRO:O	1:A:3177:ASN:N	2.53	0.42
1:A:3571:PHE:O	1:A:3575:LEU:HG	2.19	0.42
2:B:32:TYR:N	2:B:253:LYS:HZ2	2.17	0.42
2:B:66:CYS:SG	2:B:242:LEU:HB2	2.60	0.42
3:C:198:THR:OG1	3:C:199:GLU:N	2.50	0.42
3:C:200:GLN:HA	3:C:203:GLU:HG2	2.02	0.42
1:F:19:LEU:HD13	1:F:34:LEU:HD22	2.01	0.42
1:F:296:VAL:HG22	1:F:300:TRP:CD1	2.54	0.42
1:F:784:VAL:HG13	1:F:785:MET:SD	2.58	0.42
1:F:1018:VAL:HG22	1:F:1074:LYS:HG2	2.00	0.42
1:F:1403:MET:SD	1:F:1415:LEU:HD11	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1598:ASN:HA	1:F:1601:LEU:HD12	2.00	0.42
1:F:1716:GLN:HG3	1:F:1717:LEU:HD12	2.01	0.42
1:F:1816:ARG:HA	1:F:1819:PHE:CE2	2.54	0.42
1:F:1945:TYR:CE2	1:F:1949:ILE:HD11	2.54	0.42
1:F:2215:LEU:HD23	1:F:2219:LEU:HD23	2.00	0.42
1:F:2387:PRO:O	2:G:158:GLN:NE2	2.42	0.42
1:F:2724:ASP:N	1:F:2724:ASP:OD1	2.52	0.42
1:F:3037:GLN:HA	1:F:3040:TYR:CD2	2.54	0.42
2:G:131:PHE:O	2:G:135:MET:HB3	2.18	0.42
4:N:7:ARG:HD3	4:O:131:LEU:HD12	2.00	0.42
5:P:739:GLN:O	5:P:741:ARG:N	2.47	0.42
6:Q:13:TRP:CE3	6:Q:24:LEU:HG	2.55	0.42
6:R:5:GLU:HG3	6:R:134:HIS:CE1	2.54	0.42
6:R:13:TRP:HB3	6:R:210:PHE:CE1	2.55	0.42
1:A:380:ASP:O	1:A:384:MET:HG2	2.19	0.42
1:A:1586:SER:OG	1:A:1593:VAL:HG21	2.20	0.42
1:A:2413:PHE:HB3	2:B:148:TRP:CH2	2.54	0.42
1:A:3472:ILE:HA	1:A:3479:THR:HG21	2.01	0.42
1:A:3588:TRP:CZ2	1:A:3613:MET:HG2	2.55	0.42
2:B:204:HIS:NE2	2:B:237:SER:HB3	2.34	0.42
3:C:89:ASP:OD1	3:C:90:LEU:N	2.52	0.42
3:C:469:LYS:HA	3:C:469:LYS:HD3	1.88	0.42
1:F:129:ASP:HA	1:F:132:ILE:HG12	2.00	0.42
1:F:1800:SER:O	1:F:1803:GLU:HG3	2.19	0.42
1:F:3633:ILE:HG13	1:F:3634:GLN:N	2.35	0.42
2:G:204:HIS:CG	2:G:208:PRO:HA	2.55	0.42
2:G:321:ILE:H	3:H:274:LYS:HE2	1.85	0.42
3:H:44:ARG:NH2	3:H:234:LEU:HA	2.34	0.42
4:L:4:LYS:HE2	4:L:74:LEU:HB3	2.02	0.42
1:A:79:ARG:O	1:A:82:ARG:HG2	2.19	0.42
1:A:892:LEU:HD12	1:A:892:LEU:HA	1.83	0.42
1:A:985:GLU:HA	1:A:988:VAL:HG22	2.02	0.42
1:A:1047:GLN:O	1:A:1051:LYS:HD3	2.19	0.42
1:A:1076:LEU:HB3	1:A:1123:THR:HG23	2.01	0.42
1:F:357:LYS:O	1:F:361:ILE:HG12	2.20	0.42
1:F:1852:LYS:NZ	1:F:1918:LEU:HB3	2.35	0.42
1:F:2256:ILE:O	1:F:2260:PHE:HD2	2.02	0.42
1:F:3980:MET:O	1:F:3984:MET:HG2	2.19	0.42
2:G:204:HIS:ND1	2:G:208:PRO:HA	2.35	0.42
2:G:269:ILE:HG23	2:G:378:SER:HB3	2.01	0.42
3:H:9:ALA:HB2	3:H:127:PHE:CD1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:722:LYS:NZ	5:M:744:ILE:HD11	2.34	0.42
4:N:99:LYS:HD2	4:N:99:LYS:HA	1.82	0.42
4:N:194:LEU:HD11	4:O:195:HIS:CE1	2.55	0.42
1:A:681:LYS:HD3	1:A:681:LYS:HA	1.84	0.42
1:A:723:ASP:C	1:A:725:LEU:H	2.23	0.42
1:A:1102:GLU:H	1:A:1102:GLU:CD	2.21	0.42
1:A:1113:LEU:HD12	1:A:1113:LEU:HA	1.91	0.42
1:A:1757:MET:O	1:A:1760:GLU:HG2	2.20	0.42
1:A:1799:GLU:O	1:A:1802:TYR:HB3	2.20	0.42
1:A:2327:LEU:HB3	1:A:2371:PHE:CD1	2.55	0.42
2:B:76:ILE:HD11	2:B:487:PHE:CE1	2.55	0.42
2:B:200:LEU:H	2:B:200:LEU:HD23	1.85	0.42
2:B:272:GLY:O	2:B:369:TYR:N	2.40	0.42
2:B:488:ARG:HE	2:B:491:GLU:CD	2.23	0.42
3:C:132:ILE:HB	3:C:161:LEU:HB3	2.01	0.42
1:F:1729:PHE:HD1	1:F:1735:ARG:HH11	1.65	0.42
1:F:2335:ASN:OD1	1:F:2336:ILE:N	2.52	0.42
1:F:2578:GLU:HG2	1:F:2579:HIS:N	2.35	0.42
2:G:303:PHE:N	3:H:290:GLN:O	2.53	0.42
3:H:41:PHE:HE1	3:H:236:VAL:HG11	1.85	0.42
3:H:156:LYS:HG3	3:H:157:CYS:SG	2.59	0.42
4:O:131:LEU:HD23	4:O:131:LEU:HA	1.90	0.42
5:P:722:LYS:HG3	5:P:742:PHE:O	2.19	0.42
6:R:135:LEU:HD12	6:R:135:LEU:HA	1.91	0.42
7:D:23:DT:H2'	7:D:24:DT:C4	2.55	0.42
1:A:24:ARG:NH2	1:A:70:ARG:HE	2.18	0.42
1:A:296:VAL:HA	1:A:299:LYS:HG2	2.02	0.42
1:A:538:ASP:HA	1:A:541:MET:HG3	2.02	0.42
1:A:1149:LYS:O	1:A:1163:LEU:N	2.42	0.42
1:A:1666:GLY:O	1:A:1669:PRO:HD2	2.20	0.42
1:A:2348:GLN:OE1	1:A:2353:GLN:NE2	2.52	0.42
1:A:3133:GLN:NE2	1:A:3137:GLU:OE2	2.53	0.42
1:A:3258:LEU:HA	1:A:3261:GLU:OE1	2.20	0.42
1:A:3945:ALA:H	1:A:3948:SER:HG	1.64	0.42
1:A:4062:ASP:OD1	1:A:4063:GLU:N	2.52	0.42
2:B:264:ASN:OD1	2:B:265:LYS:N	2.47	0.42
1:F:433:PRO:HB3	1:F:6018:UNK:HA	2.01	0.42
1:F:1560:TYR:CZ	1:F:1596:VAL:HA	2.55	0.42
1:F:2130:HIS:NE2	1:F:2167:PRO:HG3	2.35	0.42
1:F:2938:VAL:HG12	1:F:2942:ILE:HG12	2.02	0.42
1:F:2978:LYS:HG2	1:F:2980:ASP:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:3030:ILE:HD12	1:F:3030:ILE:H	1.85	0.42
1:F:3100:LYS:HA	1:F:3103:ILE:HG22	2.02	0.42
1:F:3149:GLY:O	1:F:3152:SER:OG	2.30	0.42
1:F:3480:LEU:O	1:F:3483:MET:HG2	2.20	0.42
3:H:265:LYS:HD3	3:H:268:LEU:HD22	2.02	0.42
3:H:328:GLU:HA	3:H:331:MET:HG2	2.01	0.42
6:Q:100:VAL:HG12	6:Q:101:ALA:N	2.34	0.42
6:R:95:PHE:CE2	6:R:108:VAL:HG13	2.53	0.42
1:A:966:PHE:HD1	1:A:969:LEU:HD12	1.84	0.42
1:A:1278:ALA:HB3	1:A:1356:TRP:CD1	2.55	0.42
1:A:1400:VAL:HG13	1:A:1461:ALA:HB2	2.02	0.42
1:A:2155:GLU:HA	1:A:2158:ARG:HD3	2.01	0.42
1:A:2260:PHE:HA	1:A:2270:ASN:HB2	2.01	0.42
1:A:2953:THR:OG1	1:A:2994:TRP:NE1	2.49	0.42
1:A:3460:GLU:OE1	1:A:3460:GLU:N	2.45	0.42
1:A:3859:TYR:OH	1:A:4120:THR:O	2.38	0.42
3:C:345:PHE:HB3	3:C:389:MET:SD	2.60	0.42
1:F:63:PHE:CE2	1:F:85:ILE:HG12	2.54	0.42
1:F:276:ALA:HB2	1:F:315:ALA:HA	2.01	0.42
1:F:718:MET:SD	1:F:719:LYS:HG3	2.60	0.42
1:F:753:GLN:NE2	1:F:791:ASP:O	2.42	0.42
1:F:1484:LEU:HA	1:F:1487:VAL:HG12	2.02	0.42
1:F:1625:HIS:HA	1:F:1628:LYS:NZ	2.35	0.42
1:F:1627:LYS:NZ	1:F:1670:GLU:HB2	2.35	0.42
1:F:2142:ILE:O	1:F:2146:LEU:HG	2.19	0.42
1:F:2201:THR:HA	1:F:2202:PRO:HD3	1.89	0.42
1:F:2208:ASP:OD1	1:F:2209:GLU:N	2.52	0.42
1:F:3175:PRO:O	1:F:3177:ASN:N	2.53	0.42
4:K:137:ASN:HB3	4:L:137:ASN:HB2	2.02	0.42
4:L:102:LYS:HE3	4:L:102:LYS:HB2	1.96	0.42
5:P:725:TRP:NE1	5:P:736:VAL:O	2.43	0.42
6:Q:40:ASP:OD1	6:Q:40:ASP:N	2.51	0.42
1:A:82:ARG:O	1:A:86:LEU:HG	2.20	0.41
1:A:461:ILE:O	1:A:464:VAL:HG22	2.19	0.41
1:A:1005:ASP:OD1	1:A:1005:ASP:N	2.54	0.41
1:A:1034:ARG:HD2	1:A:1084:ASN:O	2.20	0.41
1:A:1347:THR:O	1:A:1351:THR:OG1	2.31	0.41
1:A:1419:LEU:HG	1:A:1467:ILE:HD13	2.02	0.41
1:A:1506:SER:O	1:A:1509:GLN:HG3	2.19	0.41
1:A:2243:GLU:HA	1:A:2246:LYS:HE3	2.02	0.41
1:A:2312:TYR:CE2	1:A:2314:GLU:HB3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2411:LEU:HD21	1:A:2442:MET:HG2	2.00	0.41
1:F:889:GLU:OE2	1:F:3889:ARG:NH2	2.53	0.41
1:F:984:TYR:HA	1:F:987:LEU:HB3	2.02	0.41
1:F:1352:SER:HB2	1:F:1356:TRP:HB2	2.02	0.41
1:F:2216:LEU:O	1:F:2219:LEU:HG	2.19	0.41
2:G:90:THR:HG21	2:G:93:ASP:HA	2.02	0.41
2:G:416:GLN:HB2	2:G:431:GLY:N	2.35	0.41
4:L:134:ILE:HA	4:L:137:ASN:ND2	2.35	0.41
5:M:678:LEU:HD23	5:M:681:ARG:HH21	1.85	0.41
8:E:45:DG:H21	8:E:45:DG:P	2.43	0.41
8:I:26:DA:H2 <sup>7</sup>	8:I:27:DC:C6	2.55	0.41
1:A:962:TYR:HB3	1:A:966:PHE:CE2	2.55	0.41
1:A:1958:GLU:HG2	1:A:1959:LEU:N	2.35	0.41
1:A:2962:ARG:NH1	1:A:2967:GLU:OE2	2.32	0.41
1:A:3444:ALA:HB2	1:A:3478:GLU:HG3	2.02	0.41
2:B:100:LYS:NZ	2:B:101:ASN:OD1	2.40	0.41
2:B:462:MET:HA	2:B:465:ILE:HB	2.01	0.41
1:F:42:CYS:SG	1:F:91:ILE:HD11	2.60	0.41
1:F:72:SER:H	1:F:82:ARG:HH22	1.67	0.41
1:F:151:GLU:H	1:F:151:GLU:HG2	1.66	0.41
1:F:860:GLY:CA	1:F:3136:THR:HG21	2.50	0.41
1:F:983:LEU:HD12	1:F:984:TYR:CD1	2.56	0.41
1:F:2164:TRP:C	1:F:2167:PRO:HD2	2.41	0.41
1:F:3014:CYS:O	1:F:3016:THR:HG23	2.20	0.41
1:F:3281:CYS:HB2	1:F:3329:LEU:HD13	2.02	0.41
1:F:3462:ARG:HG2	1:F:3498:TRP:CZ3	2.55	0.41
2:G:67:ILE:HA	2:G:70:VAL:HG22	2.02	0.41
2:G:134:MET:SD	2:G:135:MET:HB2	2.60	0.41
2:G:362:LEU:HD23	2:G:362:LEU:HA	1.84	0.41
2:G:363:ARG:NH2	9:J:28:DA:OP2	2.33	0.41
4:K:133:THR:O	4:K:136:GLU:HG3	2.20	0.41
5:P:825:VAL:HG23	5:P:828:ASP:HB2	2.02	0.41
6:R:174:LEU:HB2	6:R:179:LEU:HD11	2.02	0.41
1:A:35:ILE:HD12	1:A:80:GLU:HG3	2.02	0.41
1:A:826:PHE:O	1:A:836:LYS:NZ	2.51	0.41
1:A:988:VAL:HG21	1:A:1028:PHE:HZ	1.84	0.41
1:A:1268:ASN:HD21	1:A:1344:PHE:HB2	1.86	0.41
1:A:3037:GLN:HA	1:A:3040:TYR:CD2	2.55	0.41
1:A:3259:LEU:O	1:A:3276:TRP:NE1	2.46	0.41
1:A:3531:TYR:HB2	1:A:3532:PRO:HD3	2.02	0.41
1:A:3834:ALA:N	1:A:3835:PRO:HD2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:338:LYS:HE3	2:B:407:PRO:HD3	2.01	0.41
1:F:337:LYS:HA	1:F:341:PHE:CD2	2.54	0.41
1:F:3231:ILE:HG13	1:F:3232:ARG:N	2.34	0.41
1:F:3856:MET:N	1:F:3856:MET:SD	2.93	0.41
1:F:3971:MET:HE1	1:F:3973:PRO:HD2	2.03	0.41
1:F:4054:ALA:HA	1:F:4097:GLY:H	1.85	0.41
2:G:348:MET:HE1	3:H:518:PRO:HD3	2.02	0.41
3:H:37:VAL:HA	3:H:40:MET:HG3	2.02	0.41
3:H:496:HIS:CG	3:H:506:PRO:HD3	2.55	0.41
4:N:22:VAL:HG23	4:N:32:PHE:HB2	2.02	0.41
5:P:837:ARG:HG2	5:P:840:ILE:HB	2.02	0.41
6:Q:164:ILE:HA	6:Q:167:TYR:CD2	2.56	0.41
6:R:142:MET:HA	6:R:221:VAL:HG11	2.02	0.41
9:J:17:DT:H6	9:J:17:DT:H2'	1.67	0.41
9:J:27:DT:H6	9:J:27:DT:H2'	1.59	0.41
1:A:392:CYS:O	1:A:396:PHE:HB3	2.20	0.41
1:A:850:GLU:HG3	1:A:851:ILE:N	2.35	0.41
1:A:891:ARG:HD3	1:A:957:PRO:HA	2.01	0.41
1:A:928:VAL:HB	1:A:2769:VAL:HG11	2.02	0.41
1:A:1255:CYS:HA	1:A:1258:ASP:OD2	2.20	0.41
1:A:2133:LEU:HD13	1:A:2146:LEU:HD12	2.03	0.41
1:A:2525:TRP:CH2	1:A:2545:LEU:HD11	2.55	0.41
1:A:3444:ALA:HA	1:A:3482:LEU:HD11	2.02	0.41
2:B:532:PRO:HG3	3:C:373:ALA:HB2	2.03	0.41
1:F:1023:SER:HG	1:F:1026:ARG:NH2	2.18	0.41
1:F:1101:PHE:CD1	1:F:1168:LEU:HG	2.55	0.41
1:F:1131:ILE:HD11	1:F:1186:LYS:HG2	2.01	0.41
1:F:1372:LEU:HD22	1:F:1402:LEU:HD21	2.02	0.41
1:F:2224:PHE:O	1:F:2225:HIS:ND1	2.53	0.41
1:F:2376:ASP:OD1	1:F:2377:ARG:N	2.54	0.41
1:F:2773:ARG:HG2	1:F:2789:SER:OG	2.21	0.41
1:F:2965:TYR:O	1:F:2969:ALA:N	2.38	0.41
1:F:3234:CYS:O	1:F:3238:MET:HG2	2.20	0.41
1:F:3243:ILE:CD1	1:F:3262:LEU:HD11	2.50	0.41
1:F:3781:CYS:O	1:F:3785:ALA:N	2.53	0.41
3:H:400:ARG:HH22	9:J:34:DT:P	2.42	0.41
6:Q:60:GLU:HG3	6:Q:61:LEU:HD12	2.02	0.41
6:R:176:ARG:HD2	6:R:178:ARG:HB3	2.03	0.41
7:D:37:DG:H21	8:E:21:DA:H5'	1.84	0.41
8:I:19:DC:H1'	8:I:20:DT:C4	2.55	0.41
1:A:452:LYS:HB3	7:D:12:DC:H41	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:479:ILE:HG13	1:A:480:SER:N	2.35	0.41
1:A:864:GLY:HA3	1:A:3170:ASP:CG	2.41	0.41
1:A:865:GLN:O	1:A:868:LYS:HG2	2.20	0.41
1:A:972:LEU:HB3	1:A:984:TYR:CD2	2.56	0.41
1:A:1235:ILE:HD12	1:A:1238:GLN:OE1	2.21	0.41
1:A:1264:LEU:O	1:A:1268:ASN:ND2	2.53	0.41
1:A:1346:THR:HG22	1:A:1402:LEU:HB2	2.02	0.41
1:A:2097:LEU:HD12	1:A:2149:LEU:HD21	2.02	0.41
1:A:2257:PHE:HA	1:A:2260:PHE:CE1	2.56	0.41
1:A:2412:TYR:OH	1:A:2453:GLU:OE2	2.29	0.41
1:A:2899:ARG:HH21	1:A:2900:LEU:HG	1.85	0.41
2:B:183:ALA:O	2:B:187:ARG:HG3	2.20	0.41
2:B:244:ARG:HG3	2:B:246:VAL:HG23	2.02	0.41
2:B:304:ASN:CG	2:B:307:THR:HB	2.41	0.41
3:C:41:PHE:O	3:C:45:GLN:HG2	2.21	0.41
3:C:155:LYS:HZ1	3:C:215:LEU:HB2	1.85	0.41
3:C:236:VAL:HG23	3:C:236:VAL:O	2.19	0.41
1:F:681:LYS:HA	1:F:681:LYS:HD3	1.78	0.41
1:F:1059:LEU:O	1:F:1063:LEU:HD23	2.20	0.41
1:F:1436:LEU:HD23	1:F:1436:LEU:H	1.84	0.41
1:F:1590:THR:HG21	1:F:1641:THR:HG23	2.02	0.41
1:F:1713:VAL:HA	1:F:1716:GLN:HG2	2.02	0.41
1:F:1878:ASP:OD1	1:F:1879:VAL:N	2.54	0.41
1:F:2154:GLU:HA	1:F:2157:PHE:CE1	2.55	0.41
1:F:2349:LEU:O	1:F:2353:GLN:HB2	2.20	0.41
1:F:2833:THR:HG21	1:F:2867:ALA:HB1	2.02	0.41
1:F:4012:ASP:HB2	1:F:4038:TRP:CE2	2.56	0.41
3:H:198:THR:HG22	3:H:200:GLN:H	1.86	0.41
3:H:366:ALA:O	3:H:368:ARG:NH1	2.46	0.41
6:Q:160:LYS:HB3	6:R:164:ILE:HD11	2.01	0.41
1:A:337:LYS:HE3	1:A:337:LYS:HB3	1.95	0.41
1:A:860:GLY:HA3	1:A:3136:THR:HG21	2.03	0.41
1:A:907:LEU:HD23	1:A:937:MET:HG3	2.02	0.41
1:A:1240:THR:HG22	1:A:1310:GLU:HA	2.01	0.41
1:A:1468:LEU:HD12	1:A:1469:PRO:HD2	2.02	0.41
1:A:1598:ASN:HA	1:A:1601:LEU:HD12	2.03	0.41
1:A:1935:GLU:O	1:A:1939:LEU:HG	2.21	0.41
1:A:2955:SER:O	1:A:2958:LEU:HG	2.20	0.41
1:A:3226:ASP:HB3	1:A:3227:ILE:H	1.75	0.41
3:C:463:LEU:O	3:C:476:LEU:N	2.25	0.41
1:F:332:GLU:HA	1:F:334:HIS:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1603:GLN:O	1:F:1603:GLN:NE2	2.54	0.41
1:F:1772:HIS:CD2	1:F:1773:VAL:HG23	2.55	0.41
1:F:2753:ARG:O	1:F:2756:GLU:HG3	2.20	0.41
1:F:3008:TRP:O	1:F:3011:LEU:HB2	2.20	0.41
1:F:3255:ALA:HB1	1:F:3258:LEU:HD23	2.03	0.41
1:F:3621:LYS:HA	1:F:3630:ARG:NH2	2.35	0.41
1:F:4090:ARG:NH1	1:F:4091:ALA:HB2	2.36	0.41
2:G:130:ARG:O	2:G:134:MET:HG3	2.21	0.41
2:G:367:PHE:CE1	2:G:431:GLY:HA3	2.55	0.41
3:H:125:LYS:HB2	3:H:125:LYS:HE3	1.89	0.41
3:H:513:TRP:HA	3:H:516:LEU:HD13	2.02	0.41
3:H:643:ARG:HD2	3:H:655:PHE:CD2	2.55	0.41
5:P:728:GLU:HB3	5:P:736:VAL:HG21	2.02	0.41
6:Q:158:HIS:O	6:Q:162:LEU:HG	2.21	0.41
6:Q:190:LEU:HD23	6:Q:190:LEU:HA	1.94	0.41
6:R:162:LEU:O	6:R:165:GLN:HG3	2.21	0.41
8:I:44:DG:H2'	8:I:45:DG:H2'	2.02	0.41
1:A:297:LEU:HD23	1:A:316:LEU:HA	2.03	0.41
1:A:1127:CYS:O	1:A:1131:ILE:HG12	2.20	0.41
1:A:1342:MET:O	1:A:1346:THR:HG23	2.20	0.41
1:A:1747:LEU:HD23	1:A:1747:LEU:HA	1.94	0.41
1:A:3068:ALA:HB1	1:A:3074:GLN:HG2	2.00	0.41
2:B:172:GLU:HB2	2:B:175:PRO:HB3	2.03	0.41
2:B:414:VAL:O	2:B:432:PHE:HA	2.20	0.41
3:C:324:SER:OG	3:C:327:ASP:HB2	2.20	0.41
1:F:170:VAL:HA	1:F:219:VAL:HG11	2.03	0.41
1:F:292:SER:O	1:F:295:GLU:HG2	2.21	0.41
1:F:2298:GLU:HG2	1:F:2301:GLN:HB3	2.02	0.41
1:F:2733:MET:SD	1:F:2733:MET:N	2.94	0.41
1:F:3244:ASP:HB3	1:F:3248:LYS:NZ	2.35	0.41
1:F:3665:MET:SD	1:F:3669:LYS:NZ	2.93	0.41
1:F:3955:VAL:HG11	1:F:4121:TRP:CZ3	2.56	0.41
2:G:35:ARG:HE	2:G:80:ARG:HB3	1.85	0.41
2:G:295:PRO:O	3:H:298:ASN:ND2	2.53	0.41
2:G:396:ALA:HB3	2:G:413:LEU:HB2	2.02	0.41
3:H:206:GLU:O	3:H:209:LYS:HG2	2.20	0.41
3:H:604:GLN:HG3	3:H:605:LYS:HG3	2.02	0.41
1:A:145:ASP:O	1:A:148:LYS:NZ	2.33	0.41
1:A:487:LEU:HD23	1:A:487:LEU:HA	1.93	0.41
1:A:762:TYR:CD2	1:A:765:LEU:HD23	2.55	0.41
1:A:767:GLU:O	1:A:771:ASN:ND2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:965:THR:HG22	1:A:969:LEU:HG	2.02	0.41
1:A:1220:LEU:HA	1:A:1224:PHE:HB2	2.03	0.41
1:A:1623:LEU:HD11	1:A:1671:VAL:HG11	2.02	0.41
1:A:1833:LEU:HA	1:A:1836:LEU:HB3	2.03	0.41
1:A:1851:LEU:HD11	1:A:1874:TYR:CE1	2.56	0.41
1:A:2382:VAL:HA	1:A:2385:LEU:HG	2.02	0.41
1:A:3718:ARG:H	1:A:3743:HIS:HE1	1.62	0.41
1:A:3962:ARG:HH21	1:A:3964:THR:HB	1.85	0.41
2:B:259:LEU:HD11	2:B:400:TYR:CE1	2.54	0.41
1:F:24:ARG:HG3	1:F:25:CYS:N	2.31	0.41
1:F:67:VAL:O	1:F:82:ARG:NH2	2.51	0.41
1:F:386:VAL:O	1:F:390:GLN:HG2	2.21	0.41
1:F:479:ILE:HG13	1:F:480:SER:N	2.36	0.41
1:F:1476:HIS:ND1	1:F:1521:PHE:HB3	2.35	0.41
1:F:3677:PRO:HG3	1:F:3683:CYS:HB2	2.02	0.41
1:F:3704:GLN:CD	1:F:3716:HIS:HE1	2.24	0.41
1:F:3994:ASP:O	1:F:3998:LEU:N	2.49	0.41
2:G:90:THR:HG23	2:G:135:MET:CE	2.50	0.41
2:G:100:LYS:NZ	2:G:101:ASN:H	2.18	0.41
2:G:174:ASN:HB2	2:G:215:LEU:HB2	2.03	0.41
4:N:20:LEU:HD13	4:N:34:ILE:HG13	2.02	0.41
4:O:158:VAL:HG22	4:O:161:ARG:HH21	1.84	0.41
5:P:713:ILE:HG23	5:P:745:HIS:HB2	2.01	0.41
6:R:4:LEU:O	6:R:8:LEU:CB	2.68	0.41
1:A:40:GLN:NE2	1:A:2427:ARG:H	2.19	0.41
1:A:67:VAL:HA	1:A:71:LYS:HE2	2.02	0.41
1:A:127:ALA:O	1:A:131:LEU:HG	2.21	0.41
1:A:296:VAL:HG22	1:A:300:TRP:CD1	2.56	0.41
1:A:430:VAL:HG21	1:A:1643:MET:HG2	2.02	0.41
1:A:538:ASP:OD1	1:A:539:GLN:N	2.51	0.41
1:A:573:LEU:HD13	1:A:649:PHE:HD1	1.86	0.41
1:A:834:LEU:HD12	1:A:837:THR:HG23	2.03	0.41
1:A:1071:ASN:H	1:A:1075:ARG:NH1	2.19	0.41
1:A:1086:TYR:CD1	1:A:1133:HIS:HB3	2.56	0.41
1:A:1203:SER:N	1:A:1204:PRO:HD3	2.35	0.41
1:A:1264:LEU:HD11	1:A:1344:PHE:CG	2.55	0.41
1:A:1511:ALA:HA	1:A:1514:LEU:HD12	2.03	0.41
1:A:1574:ASN:CG	1:A:1578:ALA:H	2.21	0.41
1:A:1588:ASP:OD1	1:A:1589:ASN:N	2.52	0.41
1:A:1731:PRO:HA	1:A:1736:PHE:CD2	2.56	0.41
1:A:1805:PHE:CZ	1:A:1869:LYS:HA	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2375:ALA:O	1:A:2379:MET:HG2	2.21	0.41
1:A:2478:MET:HG2	1:A:2524:PHE:CD1	2.56	0.41
1:A:2506:LEU:HD23	1:A:2506:LEU:HA	1.88	0.41
1:A:2567:SER:HA	1:A:2572:TYR:CE2	2.56	0.41
1:A:2773:ARG:NE	1:A:2775:TYR:HE1	2.18	0.41
1:A:3234:CYS:O	1:A:3238:MET:HG2	2.20	0.41
1:A:3912:CYS:HA	1:A:3915:HIS:NE2	2.36	0.41
1:A:3955:VAL:HG11	1:A:4121:TRP:CE3	2.56	0.41
1:A:4010:SER:O	1:A:4014:LYS:HG2	2.21	0.41
2:B:193:LEU:HB2	2:B:198:ILE:HB	2.03	0.41
2:B:203:MET:SD	2:B:238:LYS:HB2	2.61	0.41
2:B:253:LYS:HD2	2:B:253:LYS:HA	1.82	0.41
2:B:255:ALA:HB1	2:B:273:ILE:O	2.21	0.41
1:F:53:LEU:O	1:F:57:LEU:HG	2.21	0.41
1:F:55:THR:O	1:F:58:VAL:HG12	2.20	0.41
1:F:83:GLU:HG2	1:F:129:ASP:OD2	2.21	0.41
1:F:183:GLU:HG2	1:F:184:VAL:H	1.86	0.41
1:F:204:LEU:HD21	1:F:224:LEU:HD22	2.03	0.41
1:F:583:LEU:HB2	1:F:614:PRO:HA	2.02	0.41
1:F:1568:ASN:O	1:F:1572:LEU:HD23	2.21	0.41
1:F:1783:ARG:HH12	1:F:1830:HIS:HB2	1.86	0.41
1:F:2188:GLU:HG2	1:F:2728:LEU:HD21	2.01	0.41
1:F:2331:MET:O	1:F:2331:MET:HG2	2.20	0.41
1:F:2366:LYS:HA	1:F:2369:LYS:NZ	2.35	0.41
1:F:2418:LYS:HA	1:F:2418:LYS:HD3	1.81	0.41
1:F:2526:SER:O	1:F:2538:ARG:NH2	2.53	0.41
1:F:2531:LEU:HD23	1:F:2531:LEU:HA	1.81	0.41
1:F:2820:MET:SD	1:F:2821:ASP:N	2.94	0.41
1:F:3447:VAL:HG11	1:F:3471:ILE:HD13	2.03	0.41
1:F:3922:ASP:HB3	1:F:3928:PHE:CE1	2.56	0.41
2:G:91:GLU:OE1	2:G:136:GLY:HA3	2.20	0.41
2:G:286:ILE:N	3:H:313:GLY:O	2.37	0.41
2:G:290:ARG:HH12	5:P:695:PRO:HD2	1.86	0.41
2:G:351:LYS:C	2:G:394:VAL:HG13	2.41	0.41
3:H:406:GLY:HA3	3:H:421:TYR:CE1	2.55	0.41
4:K:21:GLN:HE22	4:K:126:LEU:HD12	1.86	0.41
4:L:120:ALA:HA	4:L:123:ILE:HG22	2.03	0.41
7:D:21:DA:H61	8:E:36:DA:H61	1.68	0.41
1:A:21:ALA:O	1:A:24:ARG:HG2	2.21	0.41
1:A:629:PHE:O	1:A:633:ILE:HG12	2.21	0.41
1:A:900:GLU:OE1	1:A:900:GLU:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1353:PRO:HD2	1:A:1356:TRP:CE3	2.56	0.41
1:A:1484:LEU:HD13	1:A:1531:LEU:HD13	2.03	0.41
1:A:2216:LEU:O	1:A:2219:LEU:HG	2.21	0.41
1:A:2295:GLN:HG3	1:A:2298:GLU:CB	2.49	0.41
1:A:2331:MET:O	1:A:2331:MET:HG2	2.21	0.41
1:A:2379:MET:SD	1:A:2404:ARG:HG3	2.61	0.41
1:A:3050:LYS:NZ	1:A:3184:THR:OG1	2.47	0.41
2:B:58:THR:N	2:B:59:PRO:HD2	2.36	0.41
1:F:1022:ASP:O	1:F:1025:LEU:HB3	2.20	0.41
1:F:1570:GLU:HA	1:F:1573:LYS:HE2	2.03	0.41
1:F:2797:VAL:HG13	1:F:2804:ILE:HD12	2.03	0.41
1:F:2963:SER:OG	1:F:3250:ASN:O	2.21	0.41
1:F:3175:PRO:HA	1:F:3249:GLN:HE22	1.85	0.41
1:F:3558:ILE:O	1:F:3562:LEU:HG	2.21	0.41
2:G:112:GLY:O	2:G:116:ILE:HG12	2.20	0.41
2:G:257:SER:OG	2:G:273:ILE:HB	2.20	0.41
2:G:327:ILE:HD11	3:H:498:ALA:HB2	2.03	0.41
4:K:118:ASN:HB3	4:K:121:GLU:HG3	2.01	0.41
4:K:164:LYS:HZ2	5:M:898:ILE:HG23	1.86	0.41
4:N:139:ALA:O	4:N:142:GLU:HG3	2.21	0.41
4:O:63:LYS:O	4:O:67:VAL:HG22	2.20	0.41
5:P:816:HIS:N	5:P:850:ALA:HA	2.36	0.41
1:A:2097:LEU:HB2	1:A:2149:LEU:HD11	2.03	0.40
1:A:2187:VAL:HA	1:A:2190:VAL:HG22	2.03	0.40
1:A:2574:ASN:O	1:A:2787:HIS:ND1	2.54	0.40
1:A:6015:UNK:O	1:A:6019:UNK:N	2.54	0.40
2:B:340:PHE:CD2	2:B:408:PRO:HG3	2.56	0.40
2:B:424:LYS:HA	2:B:424:LYS:HD3	1.80	0.40
2:B:493:LEU:HD12	2:B:493:LEU:HA	1.84	0.40
1:F:734:LEU:HD11	1:F:768:VAL:HG22	2.04	0.40
1:F:1105:VAL:HG21	1:F:1154:PRO:HB2	2.03	0.40
1:F:1304:HIS:CE1	1:F:1307:ILE:HG22	2.54	0.40
1:F:1639:LEU:HA	1:F:1642:LYS:HE3	2.02	0.40
1:F:1803:GLU:HA	1:F:1806:ARG:NH2	2.36	0.40
1:F:1818:SER:O	1:F:1822:ARG:HG3	2.21	0.40
1:F:2481:HIS:HD1	1:F:2499:PHE:HE1	1.68	0.40
1:F:2839:ASP:HA	1:F:2842:ARG:NH1	2.36	0.40
1:F:3445:LEU:O	1:F:3448:GLU:HG2	2.20	0.40
1:F:3534:ILE:HD13	1:F:3534:ILE:HA	1.89	0.40
2:G:143:LEU:O	2:G:147:LEU:HG	2.22	0.40
2:G:164:LYS:HE3	2:G:164:LYS:HB3	1.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:365:SER:OG	2:G:434:LEU:N	2.53	0.40
4:L:180:PHE:HA	4:L:183:VAL:HG12	2.02	0.40
5:M:659:PHE:CD2	5:M:685:PHE:HB3	2.55	0.40
5:M:764:SER:OG	5:M:767:ILE:O	2.36	0.40
4:O:97:PHE:HE2	4:O:99:LYS:HD3	1.85	0.40
4:O:170:GLU:OE2	5:P:847:PHE:HA	2.20	0.40
4:O:176:LEU:HD23	4:O:179:ARG:HH11	1.86	0.40
5:P:770:ASP:OD1	5:P:773:GLN:HG2	2.21	0.40
9:J:33:DA:H2''	9:J:34:DT:O2	2.21	0.40
1:A:238:MET:N	1:A:238:MET:SD	2.94	0.40
1:A:1012:ALA:HA	1:A:1015:ASP:OD2	2.21	0.40
1:A:1142:HIS:CG	1:A:1197:LEU:HD12	2.56	0.40
1:A:1771:GLN:H	1:A:1775:GLU:CD	2.24	0.40
1:A:2356:MET:SD	1:A:2357:GLU:N	2.94	0.40
1:A:2464:HIS:O	1:A:2466:SER:N	2.53	0.40
1:A:2735:ASP:N	1:A:2735:ASP:OD1	2.50	0.40
1:A:2752:LYS:HD3	1:A:2752:LYS:HA	1.96	0.40
1:A:3183:ILE:HD12	1:A:3238:MET:HB3	2.03	0.40
1:A:3701:ILE:HG13	1:A:3719:ILE:HG13	2.03	0.40
1:A:3731:SER:H	1:A:3734:ARG:HA	1.85	0.40
1:F:1071:ASN:OD1	1:F:1073:PHE:N	2.52	0.40
1:F:1771:GLN:HA	1:F:1775:GLU:HG3	2.02	0.40
1:F:2356:MET:SD	1:F:2357:GLU:N	2.95	0.40
1:F:2517:LEU:HA	1:F:2520:ILE:HG22	2.04	0.40
1:F:3015:SER:O	1:F:3016:THR:OG1	2.33	0.40
1:F:3186:ARG:O	1:F:3190:LEU:HG	2.21	0.40
2:G:205:LEU:HD12	2:G:205:LEU:HA	1.95	0.40
2:G:350:PHE:HB2	3:H:462:SER:HA	2.02	0.40
3:H:44:ARG:HD2	3:H:236:VAL:HB	2.04	0.40
3:H:74:TYR:CD2	3:H:109:ASP:HB3	2.56	0.40
3:H:539:LEU:HD23	3:H:539:LEU:HA	1.88	0.40
6:Q:67:ALA:HB3	6:Q:72:PHE:CE1	2.56	0.40
6:Q:211:VAL:O	6:Q:215:GLN:HG2	2.21	0.40
6:R:209:PRO:HA	6:R:212:MET:HG2	2.03	0.40
9:J:37:DG:H1'	9:J:38:DG:N2	2.36	0.40
1:A:75:SER:HB2	1:A:77:GLU:HG2	2.03	0.40
1:A:446:PHE:HB3	1:A:527:TYR:HE1	1.86	0.40
1:A:1271:ILE:O	1:A:1274:ARG:HD2	2.21	0.40
1:A:1297:PHE:HA	1:A:1301:ILE:HG12	2.03	0.40
1:A:2129:LEU:HD22	1:A:2146:LEU:HD21	2.02	0.40
1:A:2193:ILE:HA	1:A:2196:TRP:CH2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2724:ASP:N	1:A:2724:ASP:OD1	2.54	0.40
1:A:2749:ALA:O	1:A:2753:ARG:HG2	2.21	0.40
1:A:2837:LEU:HD21	1:A:2868:LEU:HA	2.03	0.40
1:A:3278:GLN:HB3	1:A:3282:ARG:NH1	2.31	0.40
1:A:3911:ILE:O	1:A:3915:HIS:CD2	2.75	0.40
2:B:73:SER:O	2:B:77:SER:HB3	2.22	0.40
2:B:367:PHE:HE1	2:B:431:GLY:HA3	1.86	0.40
2:B:444:ARG:HH21	3:C:268:LEU:HD23	1.86	0.40
3:C:31:PHE:CZ	3:C:100:PRO:HG3	2.57	0.40
3:C:335:SER:OG	3:C:394:ARG:NH2	2.55	0.40
1:F:38:LEU:CD2	1:F:85:ILE:HG13	2.51	0.40
1:F:89:LEU:O	1:F:133:LYS:NZ	2.54	0.40
1:F:1045:THR:HG22	1:F:1047:GLN:H	1.87	0.40
1:F:1087:ARG:H	1:F:1087:ARG:HG2	1.65	0.40
1:F:1203:SER:N	1:F:1204:PRO:HD3	2.36	0.40
1:F:1622:ILE:HD12	1:F:1622:ILE:HA	1.92	0.40
1:F:2130:HIS:CD2	1:F:2167:PRO:HG3	2.57	0.40
1:F:2288:TYR:CZ	1:F:2290:PRO:HA	2.56	0.40
1:F:2820:MET:HA	1:F:2823:PHE:CE1	2.56	0.40
1:F:2858:ILE:HD13	1:F:2858:ILE:HA	1.91	0.40
1:F:2964:ASP:OD1	1:F:2967:GLU:HB3	2.22	0.40
1:F:3700:GLU:HG2	1:F:3704:GLN:HE21	1.87	0.40
1:F:3736:LYS:O	1:F:3752:VAL:N	2.44	0.40
1:F:3886:ALA:O	1:F:3889:ARG:HB3	2.22	0.40
3:H:132:ILE:O	3:H:161:LEU:HA	2.21	0.40
3:H:236:VAL:O	3:H:238:LYS:HE3	2.22	0.40
4:K:147:GLU:O	4:K:151:LEU:HD23	2.21	0.40
4:K:155:TRP:HD1	4:L:158:VAL:HG11	1.86	0.40
4:K:158:VAL:HG11	4:L:159:GLN:OE1	2.21	0.40
6:R:35:ALA:HB1	6:R:46:HIS:CE1	2.56	0.40
6:R:151:ARG:O	6:R:155:THR:HG23	2.22	0.40
7:D:23:DT:H5''	7:D:24:DT:O4	2.22	0.40
1:A:332:GLU:HB2	1:A:335:LYS:HZ2	1.85	0.40
1:A:1253:THR:O	1:A:1257:LEU:HG	2.21	0.40
1:A:1721:HIS:HB3	1:A:1739:TYR:CE1	2.57	0.40
1:A:2335:ASN:OD1	1:A:2336:ILE:N	2.51	0.40
1:A:2427:ARG:HG3	1:A:2432:GLN:NE2	2.37	0.40
1:A:2957:LEU:HD23	1:A:2957:LEU:HA	1.82	0.40
1:A:3996:GLY:O	1:A:4000:ASN:ND2	2.54	0.40
2:B:220:ILE:HG23	2:B:221:ILE:HG13	2.04	0.40
2:B:300:THR:HB	3:C:293:THR:HG23	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:246:HIS:HB2	3:C:264:TYR:CE2	2.57	0.40
3:C:408:ALA:HA	3:C:421:TYR:HA	2.04	0.40
1:F:2952:ILE:HD11	1:F:2971:GLN:OE1	2.21	0.40
1:F:3997:LEU:HD23	1:F:3997:LEU:HA	1.96	0.40
1:F:4011:PHE:HA	1:F:4014:LYS:NZ	2.36	0.40
2:G:337:LEU:HD11	3:H:493:CYS:SG	2.61	0.40
3:H:6:ASN:HA	3:H:128:GLU:OE1	2.22	0.40
3:H:16:VAL:O	3:H:16:VAL:HG12	2.21	0.40
5:M:753:HIS:NE2	5:M:757:GLU:OE2	2.55	0.40
4:O:20:LEU:HD13	4:O:37:THR:HG22	2.03	0.40
5:P:741:ARG:NH1	5:P:742:PHE:HB3	2.37	0.40
5:P:878:PHE:O	5:P:881:THR:OG1	2.25	0.40
7:D:22:DG:H8	7:D:23:DT:H72	1.85	0.40
1:A:76:ILE:HD11	1:A:122:LYS:HE2	2.04	0.40
1:A:527:TYR:HB2	1:A:629:PHE:HE1	1.86	0.40
1:A:717:LYS:HB3	1:A:721:TYR:OH	2.22	0.40
1:A:718:MET:HA	1:A:721:TYR:CD2	2.57	0.40
1:A:1487:VAL:HG23	1:A:1488:TYR:CD1	2.52	0.40
1:A:1769:GLU:HB2	1:A:1772:HIS:CG	2.57	0.40
1:A:2333:ARG:NH2	1:A:2371:PHE:HE1	2.18	0.40
1:A:3870:SER:O	1:A:3874:ARG:NE	2.34	0.40
1:A:3929:MET:N	1:A:3938:ILE:O	2.51	0.40
2:B:33:SER:HB2	2:B:253:LYS:HZ3	1.86	0.40
2:B:102:ILE:HD11	2:B:145:GLU:HB3	2.04	0.40
2:B:299:LYS:HB3	2:B:299:LYS:HE2	1.73	0.40
2:B:350:PHE:HB2	3:C:461:MET:O	2.22	0.40
2:B:485:GLN:NE2	3:C:333:TYR:H	2.19	0.40
2:B:514:MET:SD	2:B:515:ASN:N	2.94	0.40
3:C:238:LYS:NZ	3:C:240:ILE:O	2.55	0.40
3:C:485:PRO:HG2	3:C:516:LEU:HD21	2.02	0.40
1:F:275:PHE:CE2	1:F:319:PHE:HB2	2.56	0.40
1:F:363:ILE:HD13	1:F:366:TYR:CE2	2.57	0.40
1:F:409:GLN:OE1	1:F:409:GLN:N	2.47	0.40
1:F:527:TYR:HB2	1:F:629:PHE:CE1	2.56	0.40
1:F:637:LYS:HD2	1:F:637:LYS:HA	1.86	0.40
1:F:977:ASP:OD1	1:F:978:GLN:N	2.54	0.40
1:F:1013:ILE:HA	1:F:1017:ILE:HD13	2.04	0.40
1:F:1429:GLU:HB3	1:F:1482:GLU:OE2	2.21	0.40
1:F:1697:PRO:HA	1:F:1753:SER:HB3	2.04	0.40
1:F:1723:PRO:O	1:F:1768:ARG:NH1	2.53	0.40
1:F:2253:TYR:HA	1:F:2256:ILE:HD12	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:2849:SER:HB3	1:F:3080:LEU:HD13	2.04	0.40
2:G:189:LYS:HE2	2:G:189:LYS:HB3	1.85	0.40
2:G:252:ARG:HB2	3:H:431:ARG:HD2	2.03	0.40
3:H:346:CYS:SG	3:H:350:GLN:HG3	2.61	0.40
4:K:187:LYS:HZ2	4:L:187:LYS:HB2	1.86	0.40
5:M:787:GLN:OE1	5:M:787:GLN:N	2.54	0.40
4:O:20:LEU:HB2	4:O:37:THR:HG22	2.02	0.40
7:D:26:DT:H2''	7:D:27:DT:C6	2.56	0.40
9:J:32:DT:H2''	9:J:33:DA:O4'	2.20	0.40

There are no symmetry-related clashes.

### 5.3 Torsion angles [i](#)

#### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	3474/4148 (84%)	3222 (93%)	248 (7%)	4 (0%)	51	85
1	F	3467/4148 (84%)	3198 (92%)	265 (8%)	4 (0%)	51	85
2	B	468/609 (77%)	430 (92%)	37 (8%)	1 (0%)	47	80
2	G	485/609 (80%)	460 (95%)	25 (5%)	0	100	100
3	C	465/732 (64%)	445 (96%)	20 (4%)	0	100	100
3	H	636/732 (87%)	597 (94%)	39 (6%)	0	100	100
4	K	199/336 (59%)	195 (98%)	4 (2%)	0	100	100
4	L	191/336 (57%)	184 (96%)	7 (4%)	0	100	100
4	N	199/336 (59%)	191 (96%)	8 (4%)	0	100	100
4	O	190/336 (56%)	182 (96%)	8 (4%)	0	100	100
5	M	256/911 (28%)	239 (93%)	17 (7%)	0	100	100
5	P	242/911 (27%)	225 (93%)	16 (7%)	1 (0%)	34	71
6	Q	205/299 (69%)	185 (90%)	20 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	R	214/299 (72%)	200 (94%)	14 (6%)	0	100	100
All	All	10691/14742 (72%)	9953 (93%)	728 (7%)	10 (0%)	54	85

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2291	GLN
1	F	955	ALA
1	F	956	PRO
1	F	2291	GLN
1	A	1550	VAL
1	A	3671	ASN
2	B	213	ILE
1	F	3304	VAL
1	A	841	SER
5	P	849	GLY

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	3054/3671 (83%)	3040 (100%)	14 (0%)	88	93
1	F	3058/3671 (83%)	3048 (100%)	10 (0%)	92	95
2	B	427/548 (78%)	425 (100%)	2 (0%)	88	93
2	G	444/548 (81%)	444 (100%)	0	100	100
3	C	434/649 (67%)	432 (100%)	2 (0%)	88	93
3	H	575/649 (89%)	573 (100%)	2 (0%)	92	95
4	K	179/303 (59%)	178 (99%)	1 (1%)	86	92
4	L	177/303 (58%)	174 (98%)	3 (2%)	60	78
4	N	179/303 (59%)	177 (99%)	2 (1%)	73	84
4	O	175/303 (58%)	175 (100%)	0	100	100
5	M	234/808 (29%)	232 (99%)	2 (1%)	78	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	P	217/808 (27%)	214 (99%)	3 (1%)	67	80
6	Q	187/262 (71%)	186 (100%)	1 (0%)	88	93
6	R	191/262 (73%)	189 (99%)	2 (1%)	76	86
All	All	9531/13088 (73%)	9487 (100%)	44 (0%)	89	93

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	782	ARG
1	A	802	THR
1	A	946	THR
1	A	1426	GLN
1	A	1539	SER
1	A	1549	SER
1	A	1727	ARG
1	A	1768	ARG
1	A	2263	LYS
1	A	2311	ARG
1	A	2734	ARG
1	A	3621	LYS
1	A	3874	ARG
1	A	4090	ARG
2	B	247	ARG
2	B	252	ARG
3	C	232	ARG
3	C	338	LYS
1	F	442	GLN
1	F	453	MET
1	F	476	ARG
1	F	1727	ARG
1	F	1768	ARG
1	F	2311	ARG
1	F	3621	LYS
1	F	3664	ASN
1	F	3874	ARG
1	F	4090	ARG
3	H	332	LYS
3	H	399	LYS
4	K	107	ARG
4	L	146	LYS
4	L	150	ARG

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Mol	Chain	Res	Type
4	L	164	LYS
5	M	782	LYS
5	M	883	LYS
4	N	107	ARG
4	N	153	ARG
5	P	741	ARG
5	P	817	THR
5	P	890	LYS
6	Q	64	ARG
6	R	63	LYS
6	R	124	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	409	GLN
1	A	676	ASN
1	A	1043	GLN
1	A	1069	HIS
1	A	1201	ASN
1	A	1568	ASN
1	A	1611	GLN
1	A	2291	GLN
1	A	2348	GLN
1	A	2353	GLN
1	A	2751	GLN
1	A	2838	GLN
1	A	2954	GLN
1	A	3148	GLN
1	A	3150	ASN
1	A	3166	ASN
1	A	3515	GLN
1	A	3704	GLN
1	A	3915	HIS
1	A	3966	GLN
2	B	293	ASN
2	B	359	HIS
1	F	344	GLN
1	F	676	ASN
1	F	982	GLN
1	F	1043	GLN
1	F	1268	ASN

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Mol	Chain	Res	Type
1	F	1568	ASN
1	F	2217	ASN
1	F	2291	GLN
1	F	2348	GLN
1	F	2353	GLN
1	F	2365	ASN
1	F	2426	HIS
1	F	2587	GLN
1	F	2834	GLN
1	F	2859	GLN
1	F	3704	GLN
1	F	3743	HIS
1	F	3924	HIS
1	F	3927	ASN
1	F	4055	ASN
2	G	178	ASN
2	G	426	GLN
3	H	496	HIS
3	H	500	HIS
3	H	657	ASN
3	H	680	GLN
4	L	148	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	F	1
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F	4128:MET	C	6004:UNK	N	90.10
1	A	4128:MET	C	6004:UNK	N	89.52

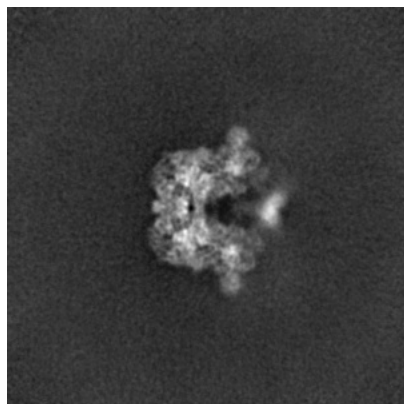
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12299. These allow visual inspection of the internal detail of the map and identification of artifacts.

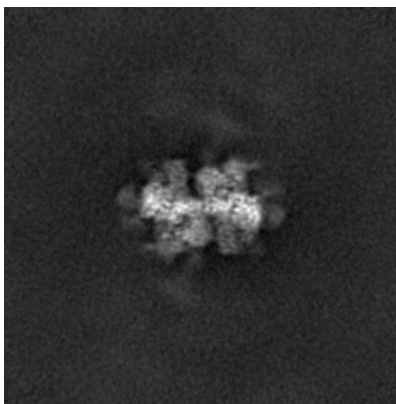
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

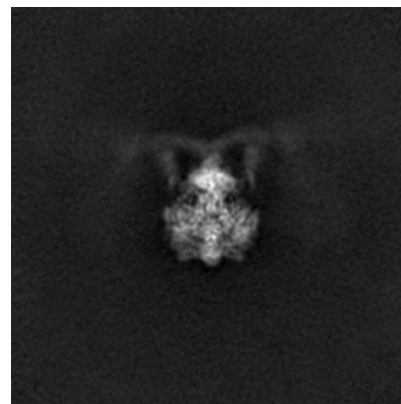
#### 6.1.1 Primary map



X

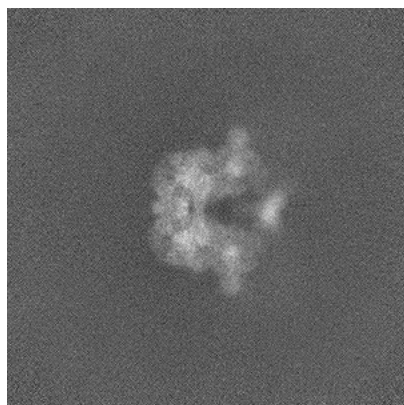


Y

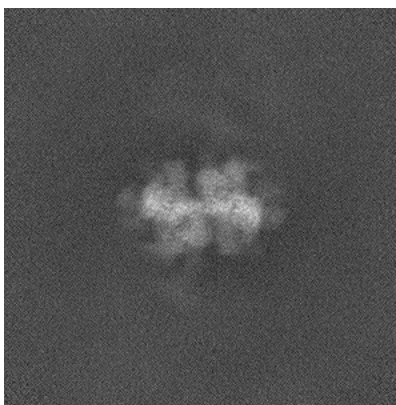


Z

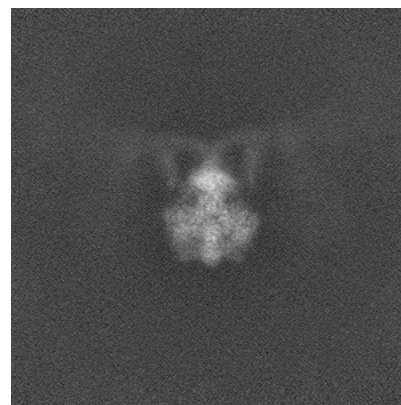
#### 6.1.2 Raw map



X



Y



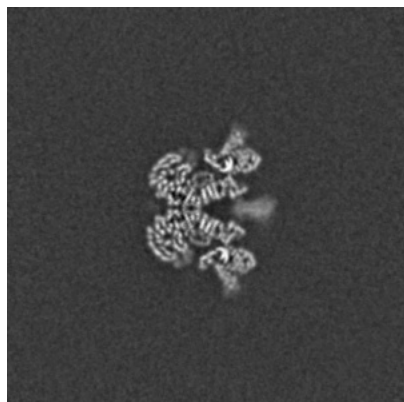
Z

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

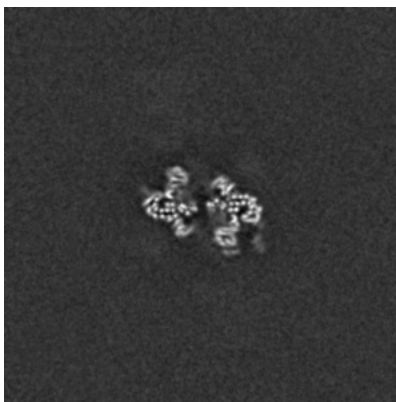


## 6.2 Central slices [i](#)

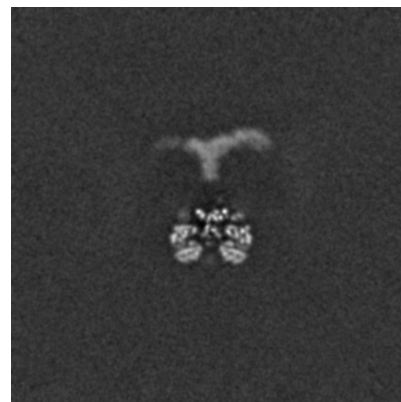
### 6.2.1 Primary map



X Index: 270

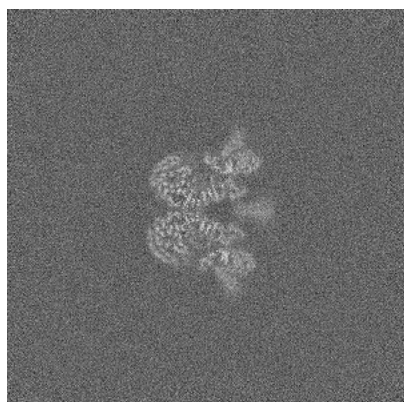


Y Index: 270



Z Index: 270

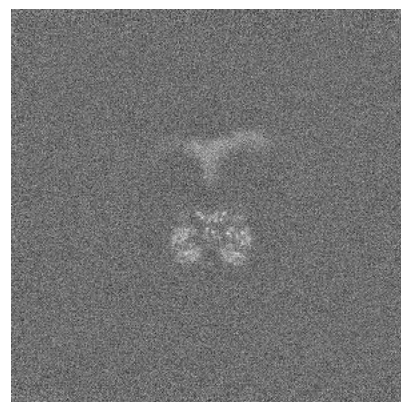
### 6.2.2 Raw map



X Index: 270



Y Index: 270

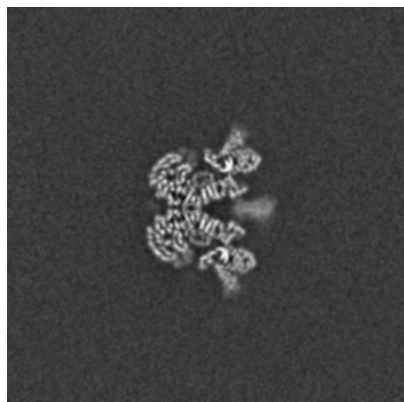


Z Index: 270

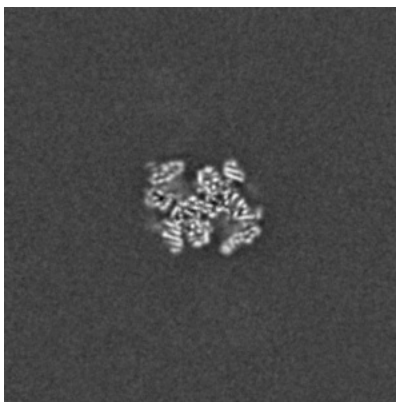
The images above show central slices of the map in three orthogonal directions.

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

### 6.3.1 Primary map



X Index: 270

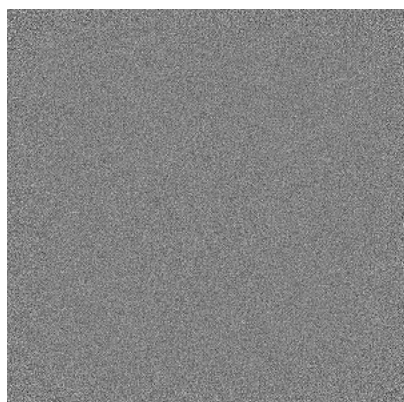


Y Index: 241

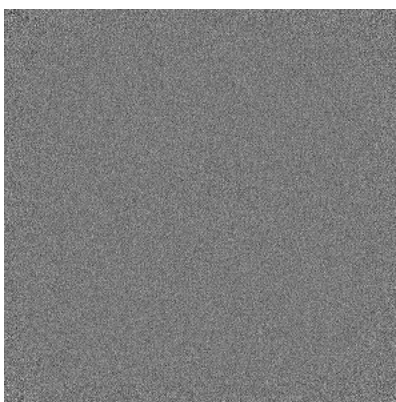


Z Index: 313

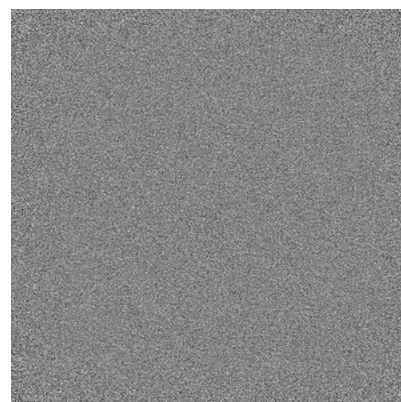
### 6.3.2 Raw map



X Index: 0



Y Index: 0



Z Index: 0

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

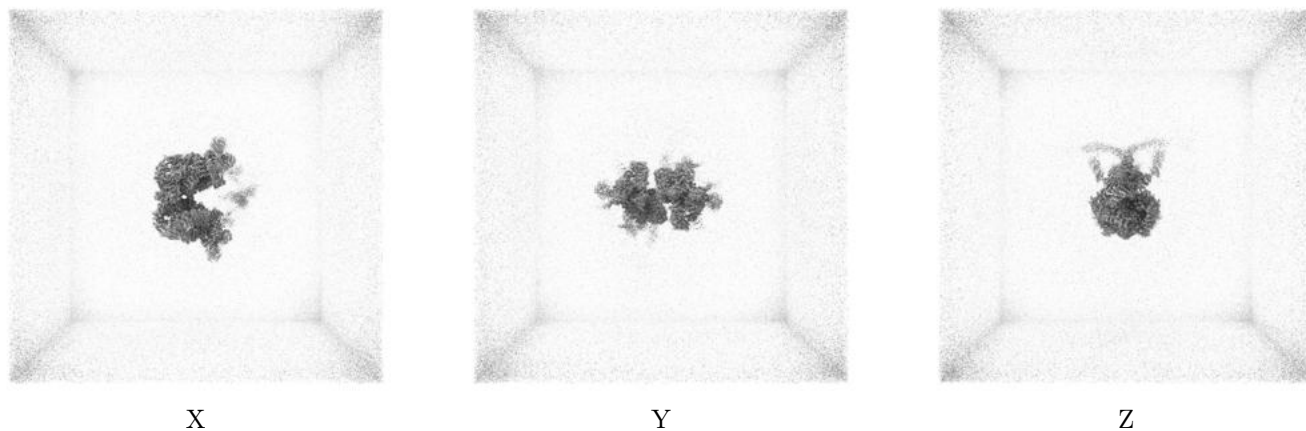
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.175. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map



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

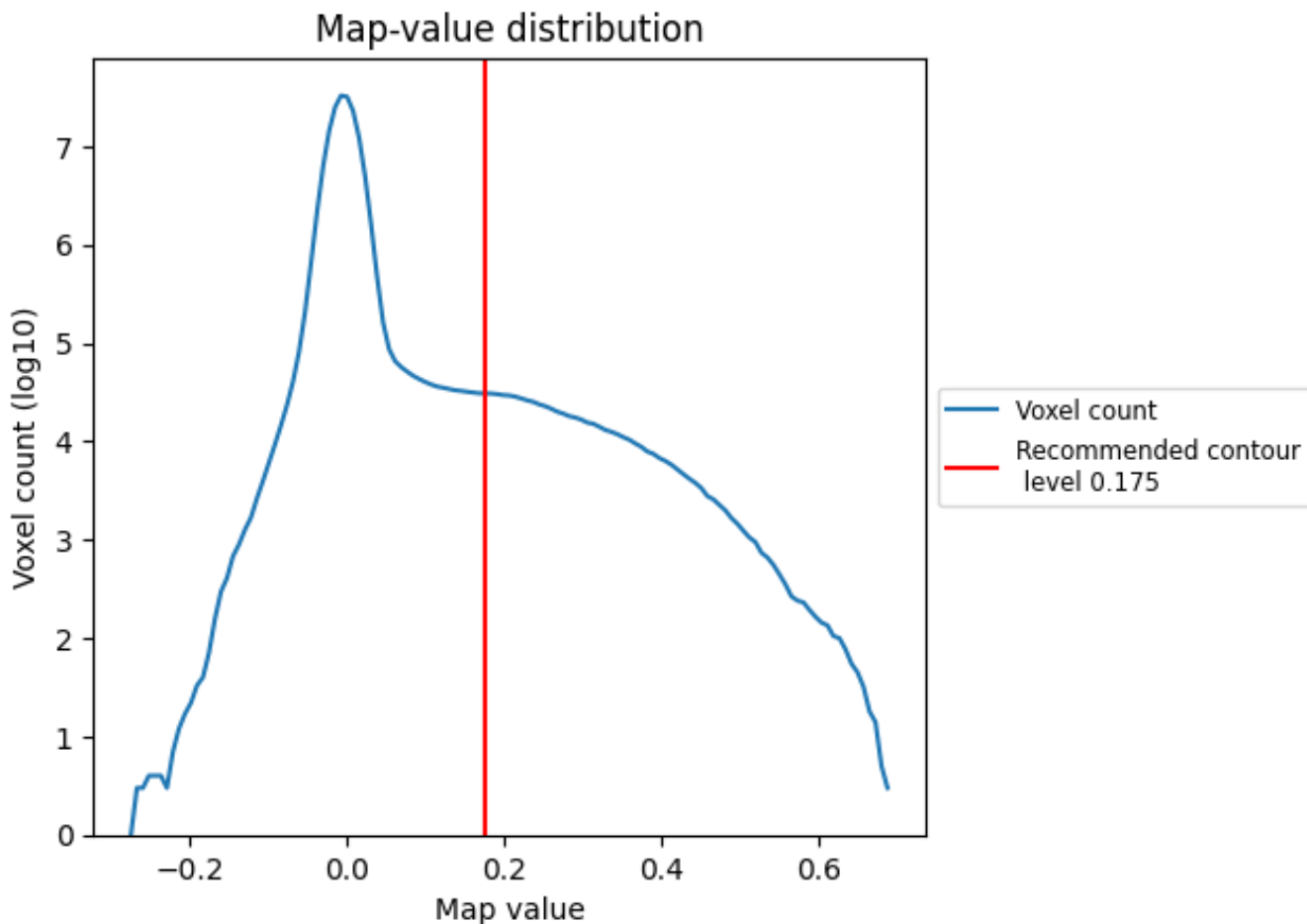
## 6.5 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

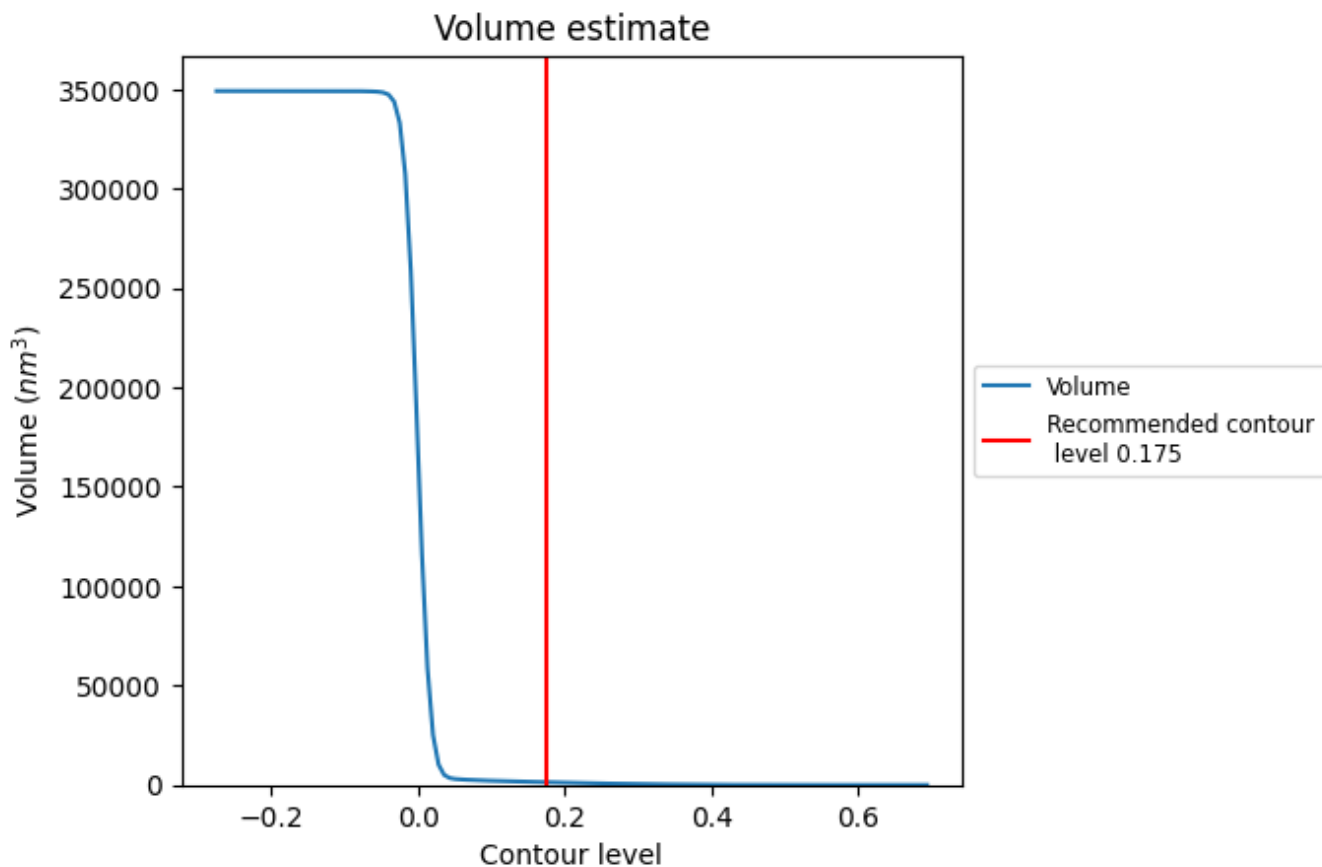
This section contains the results of statistical analysis of the map.

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



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

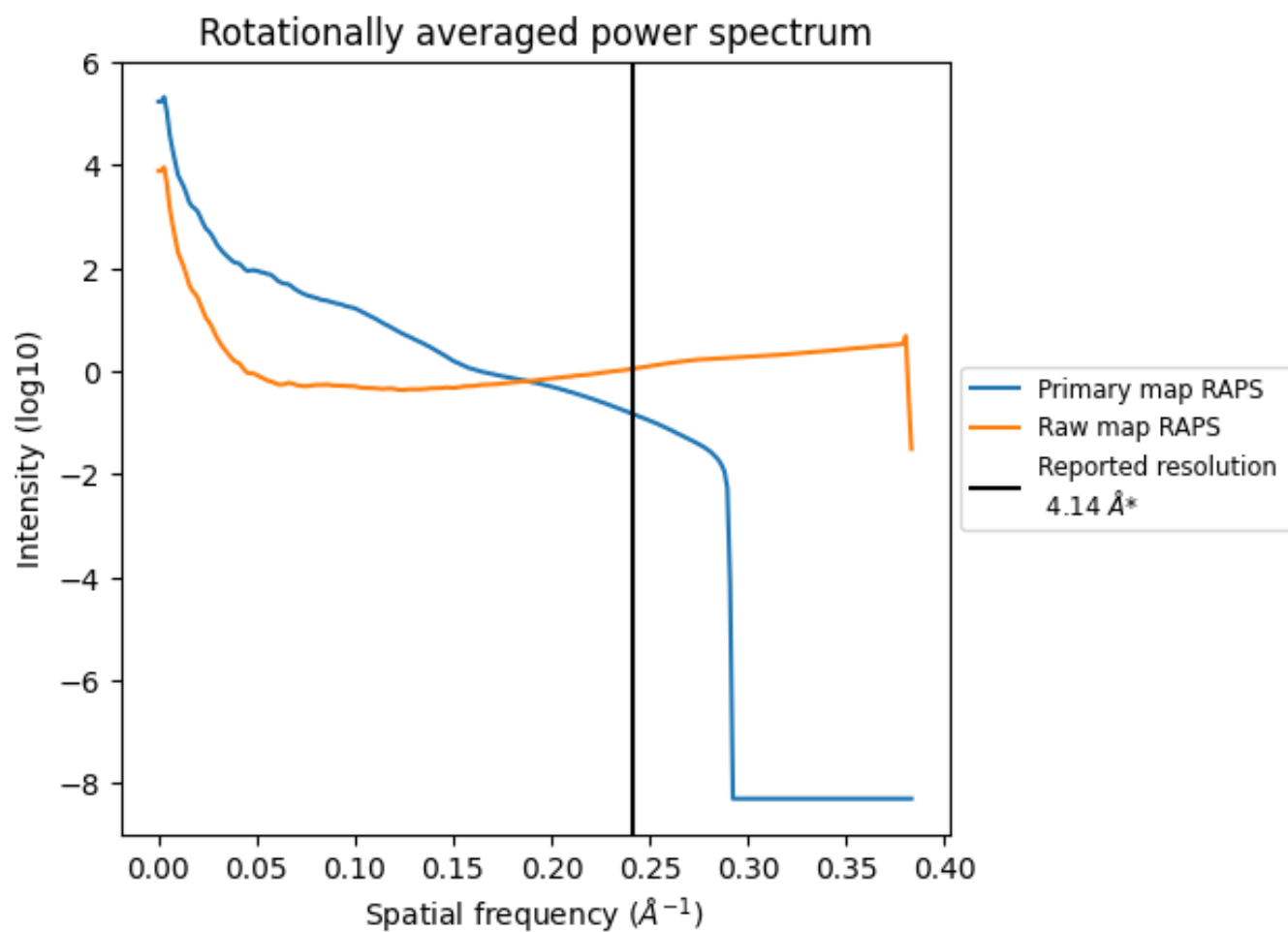
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is  $1371 \text{ nm}^3$ ; this corresponds to an approximate mass of 1239 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 i

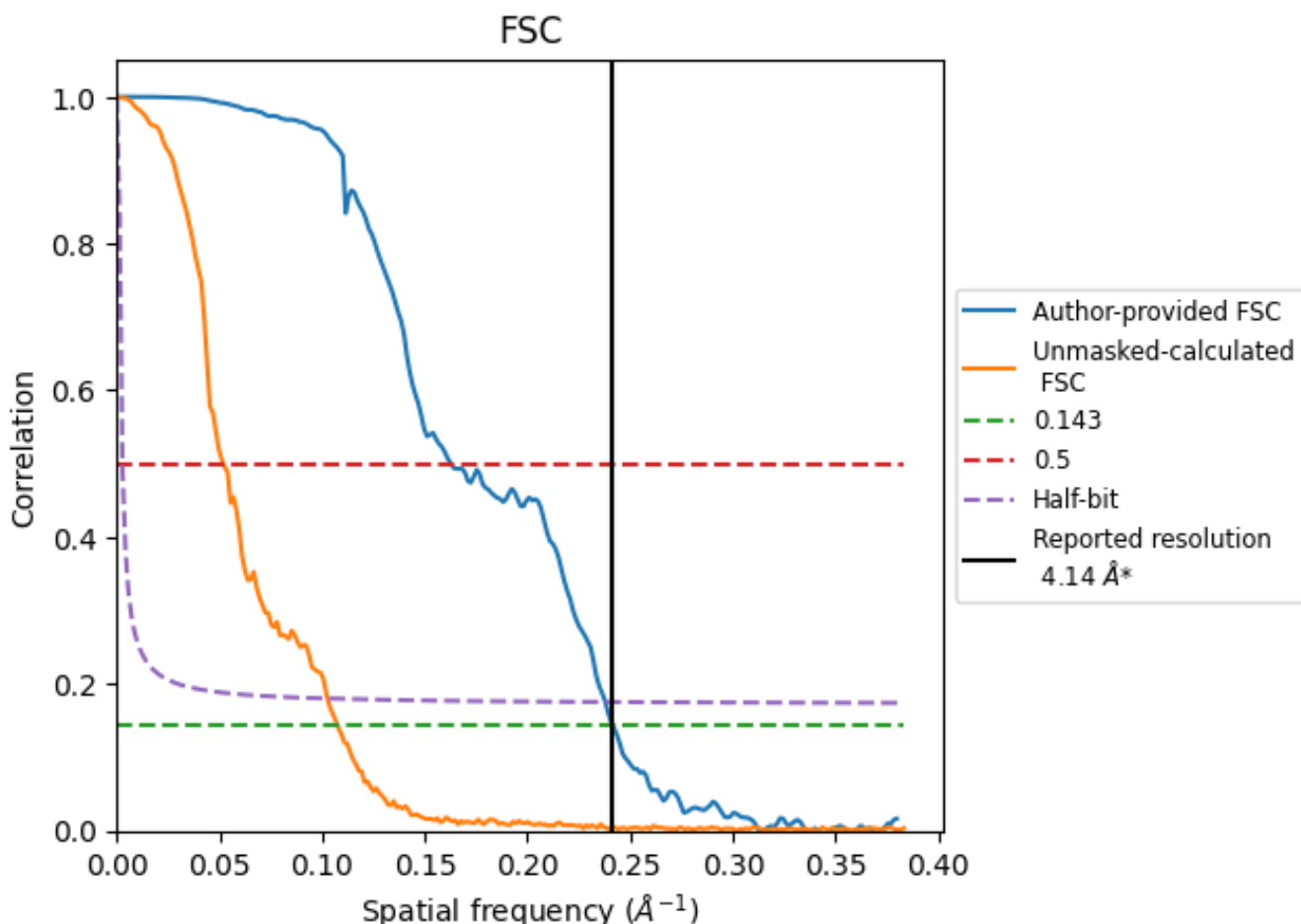


\*Reported resolution corresponds to spatial frequency of  $0.242 \text{ \AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.242 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.14	-	-
Author-provided FSC curve	4.14	6.14	4.20
Unmasked-calculated*	9.30	19.27	9.74

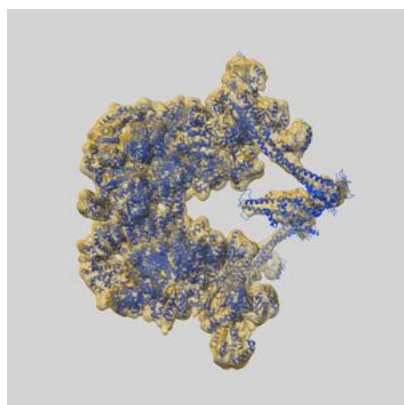
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.30 differs from the reported value 4.14 by more than 10 %



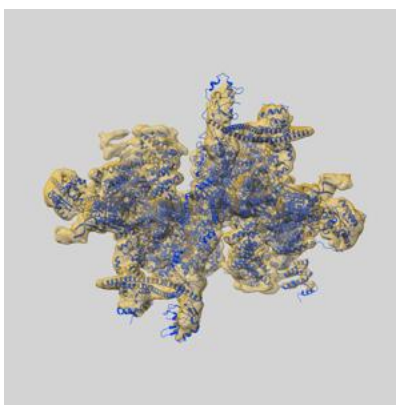
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12299 and PDB model 7NFC. Per-residue inclusion information can be found in section 3 on page 6.

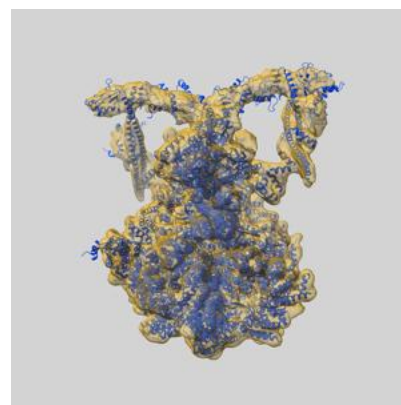
### 9.1 Map-model overlay [i](#)



X



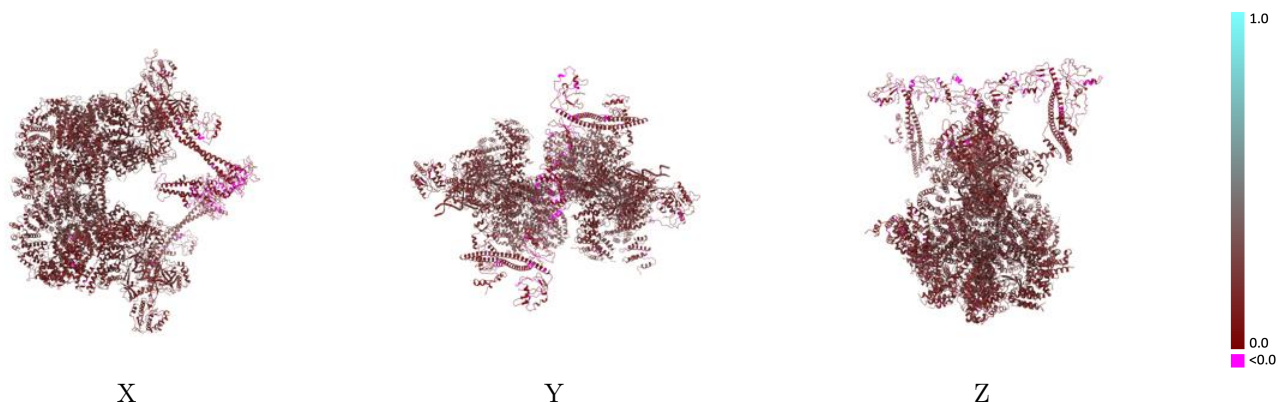
Y



Z

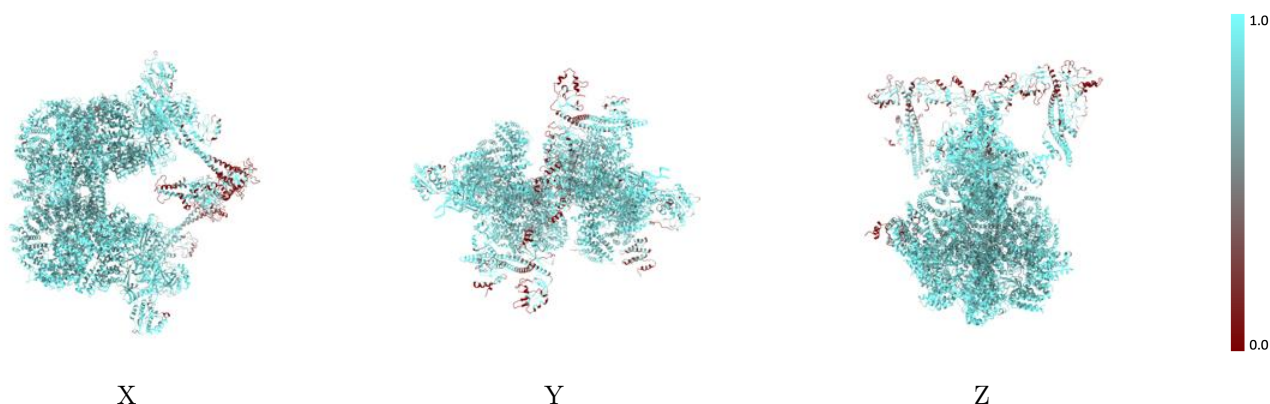
The images above show the 3D surface view of the map at the recommended contour level 0.175 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



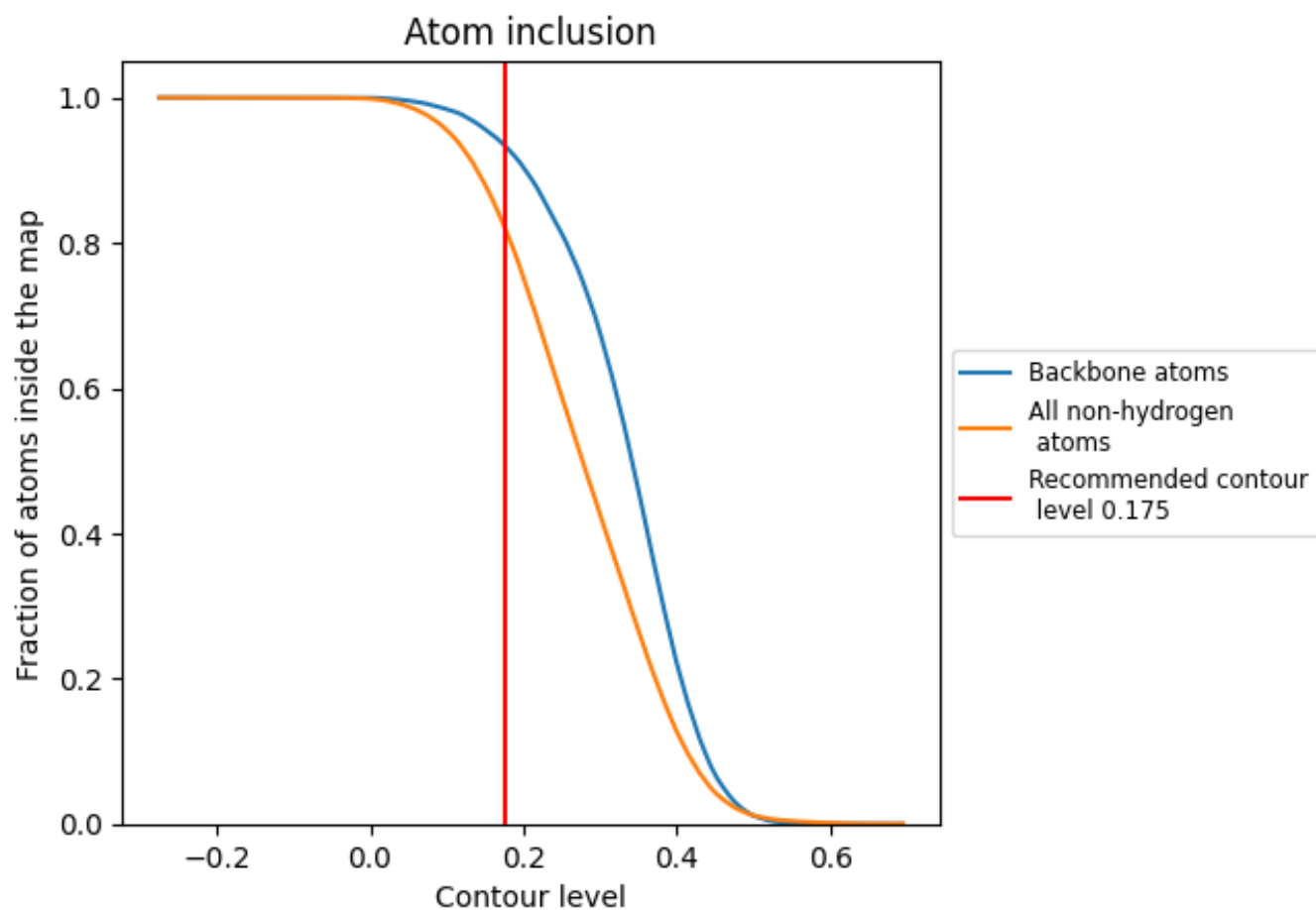
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.175).







































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 82% 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 (0.175) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8224	 0.2000
A	 0.8612	 0.2150
B	 0.8785	 0.2140
C	 0.8575	 0.2000
D	 0.9191	 0.2360
E	 0.9288	 0.2190
F	 0.8628	 0.2170
G	 0.8787	 0.2170
H	 0.7593	 0.1840
I	 0.9288	 0.2420
J	 0.9318	 0.2470
K	 0.6287	 0.1220
L	 0.5850	 0.1210
M	 0.7294	 0.1570
N	 0.5899	 0.1080
O	 0.5000	 0.1150
P	 0.8410	 0.1680
Q	 0.5409	 0.1000
R	 0.5341	 0.0830

