



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:15 AM UTC

PDB ID : 8ZJ2 / pdb_00008zj2
EMDB ID : EMD-60136
Title : Cryo-EM structure of the RhoG/DOCK5/ELMO1/Rac1 complex
Authors : Kukimoto-Niino, M.; Katsura, K.; Ishizuka-Katsura, Y.; Mishima-Tsumagari, C.; Yonemochi, M.; Inoue, M.; Nakagawa, R.; Kaushik, R.; Zhang, K.Y.J.; Shirouzu, M.
Deposited on : 2024-05-14
Resolution : 4.66 Å (reported)
Based on initial models : 7Y4A, 6IE1, 7DPA

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

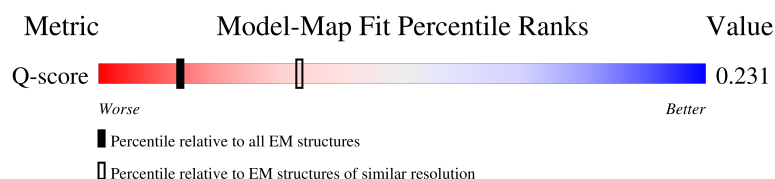
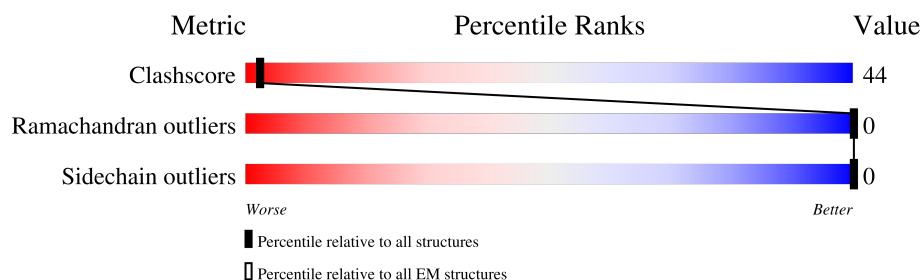
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.66 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2028 (4.16 - 5.16)

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

Mol	Chain	Length	Quality of chain
1	B	1648	 30% 69%
1	F	1648	 18% 37% 62%
2	C	184	 33% 64%

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Mol	Chain	Length	Quality of chain
2	G	184	32%64% .
3	A	733	48% 35%64% .
3	E	733	9%18% 73%
4	D	203	21% 33%56% 11%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 38587 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 Dedicator of cytokinesis protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	1642	Total	C	N	O	S	0	0
			13436	8618	2264	2484	70		
1	F	1642	Total	C	N	O	S	0	0
			13436	8618	2264	2484	70		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	GLY	-	expression tag	UNP Q9H7D0
B	-4	GLY	-	expression tag	UNP Q9H7D0
B	-3	SER	-	expression tag	UNP Q9H7D0
B	-2	GLY	-	expression tag	UNP Q9H7D0
B	-1	GLY	-	expression tag	UNP Q9H7D0
B	0	SER	-	expression tag	UNP Q9H7D0
B	1285	ARG	LYS	variant	UNP Q9H7D0
F	-5	GLY	-	expression tag	UNP Q9H7D0
F	-4	GLY	-	expression tag	UNP Q9H7D0
F	-3	SER	-	expression tag	UNP Q9H7D0
F	-2	GLY	-	expression tag	UNP Q9H7D0
F	-1	GLY	-	expression tag	UNP Q9H7D0
F	0	SER	-	expression tag	UNP Q9H7D0
F	1285	ARG	LYS	variant	UNP Q9H7D0

- Molecule 2 is a protein called Ras-related C3 botulinum toxin substrate 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	177	Total	C	N	O	S	0	0
			1385	890	228	259	8		
2	G	177	Total	C	N	O	S	0	0
			1385	890	228	259	8		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	GLY	-	expression tag	UNP P63000
C	-5	SER	-	expression tag	UNP P63000
C	-4	SER	-	expression tag	UNP P63000
C	-3	GLY	-	expression tag	UNP P63000
C	-2	SER	-	expression tag	UNP P63000
C	-1	SER	-	expression tag	UNP P63000
C	0	GLY	-	expression tag	UNP P63000
C	15	ALA	GLY	engineered mutation	UNP P63000
G	-6	GLY	-	expression tag	UNP P63000
G	-5	SER	-	expression tag	UNP P63000
G	-4	SER	-	expression tag	UNP P63000
G	-3	GLY	-	expression tag	UNP P63000
G	-2	SER	-	expression tag	UNP P63000
G	-1	SER	-	expression tag	UNP P63000
G	0	GLY	-	expression tag	UNP P63000
G	15	ALA	GLY	engineered mutation	UNP P63000

- Molecule 3 is a protein called Engulfment and cell motility protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	199	Total	C	N	O	S	0	0
			1617	1023	279	305	10		
3	A	727	Total	C	N	O	S	0	0
			5879	3721	1009	1108	41		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-5	GLY	-	expression tag	UNP Q92556
E	-4	GLY	-	expression tag	UNP Q92556
E	-3	SER	-	expression tag	UNP Q92556
E	-2	GLY	-	expression tag	UNP Q92556
E	-1	GLY	-	expression tag	UNP Q92556
E	0	SER	-	expression tag	UNP Q92556
A	-5	GLY	-	expression tag	UNP Q92556
A	-4	GLY	-	expression tag	UNP Q92556
A	-3	SER	-	expression tag	UNP Q92556
A	-2	GLY	-	expression tag	UNP Q92556
A	-1	GLY	-	expression tag	UNP Q92556
A	0	SER	-	expression tag	UNP Q92556

- Molecule 4 is a protein called Rho-related GTP-binding protein RhoG.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	181	Total	C	N	O	S	0	0
			1416	897	248	263	8		

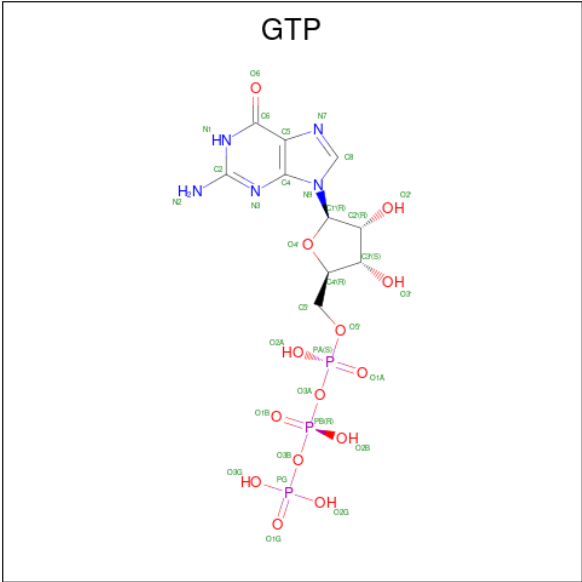
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-6	GLY	-	expression tag	UNP P84095
D	-5	SER	-	expression tag	UNP P84095
D	-4	SER	-	expression tag	UNP P84095
D	-3	GLY	-	expression tag	UNP P84095
D	-2	SER	-	expression tag	UNP P84095
D	-1	SER	-	expression tag	UNP P84095
D	0	GLY	-	expression tag	UNP P84095
D	61	LEU	GLN	engineered mutation	UNP P84095
D	185	SER	-	expression tag	UNP P84095
D	186	GLY	-	expression tag	UNP P84095
D	187	PRO	-	expression tag	UNP P84095
D	188	SER	-	expression tag	UNP P84095
D	189	SER	-	expression tag	UNP P84095
D	190	GLY	-	expression tag	UNP P84095
D	191	GLU	-	expression tag	UNP P84095
D	192	ASN	-	expression tag	UNP P84095
D	193	LEU	-	expression tag	UNP P84095
D	194	TYR	-	expression tag	UNP P84095
D	195	PHE	-	expression tag	UNP P84095
D	196	GLN	-	expression tag	UNP P84095

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	D	1	Total	Mg	0
			1	1	

- Molecule 6 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃) (labeled as "Ligand of Interest" by depositor).

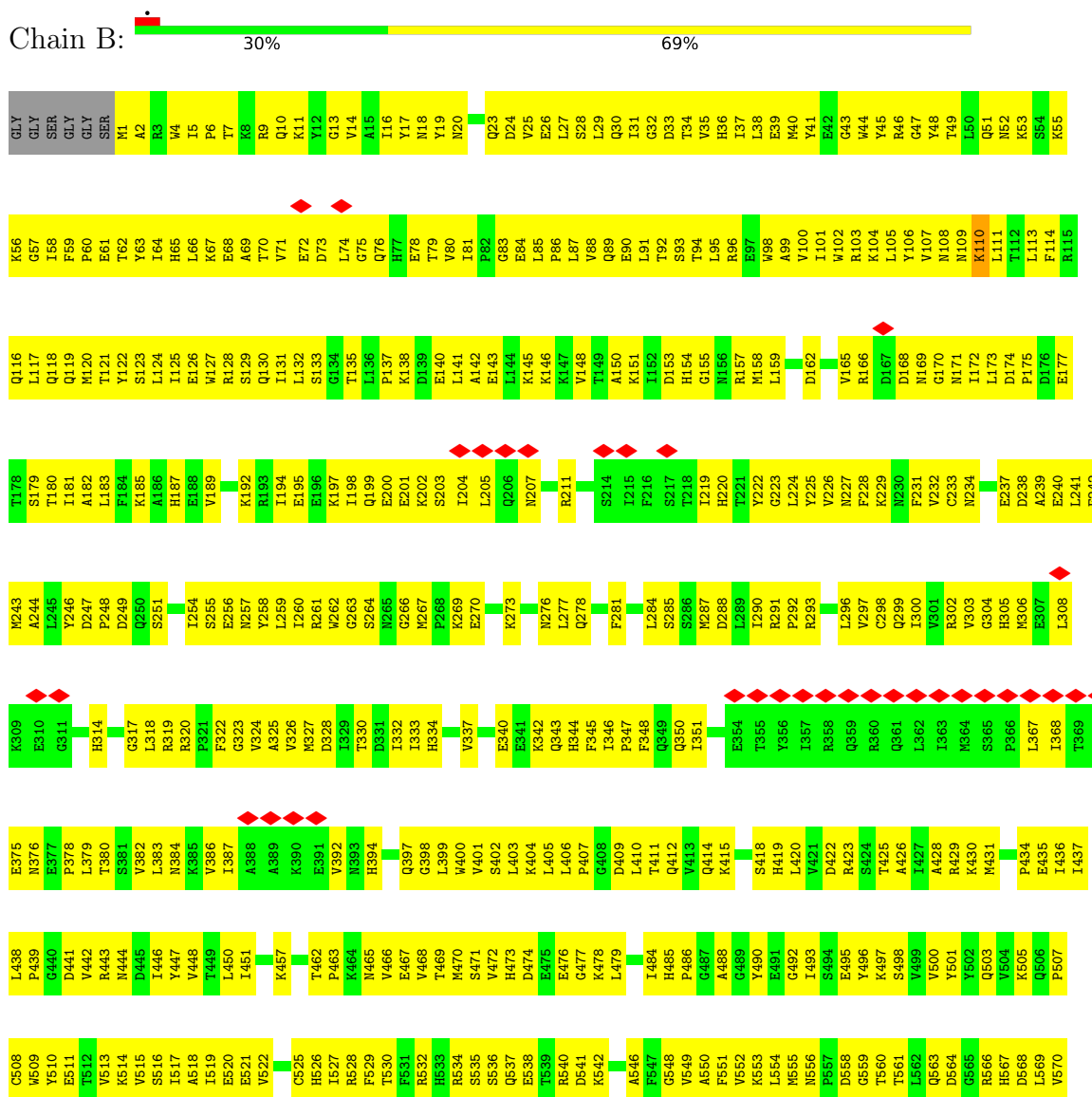


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
6	D	1	32	10	5	14	3	0

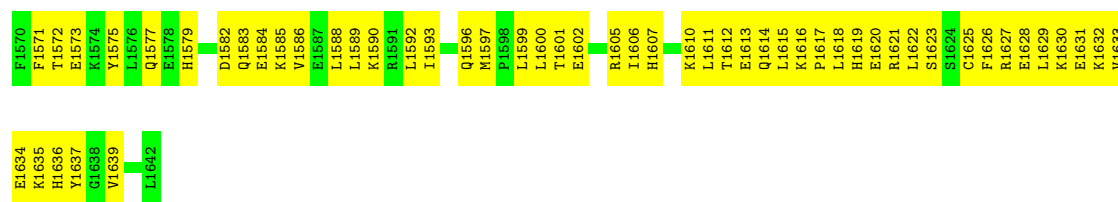
3 Residue-property plots

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

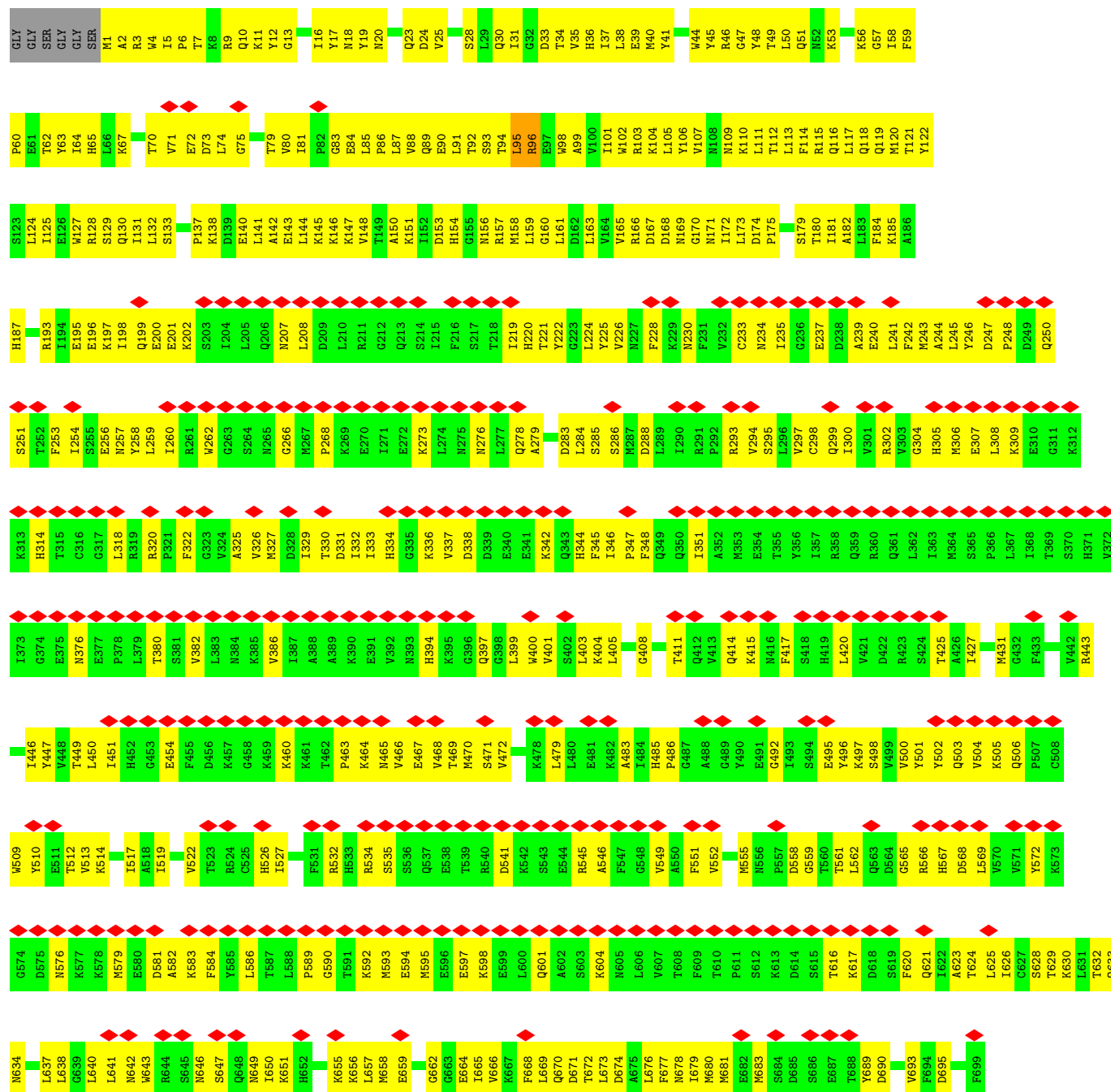
• Molecule 1: Dedicator of cytokinesis protein 5



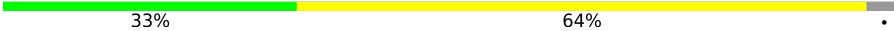
K1505	K1432	G1366	L1296	L1094	V1027	L961	S894	D832	I767	L703	L637	V671
Q1506	P1433	Y1367	K1299	H1097	L1028	Q962	N895	D833	I768	I704	L638	Y572
I1507	Y1364	Y1368	L1300	K1098	P1029	N963	K896	P833	G705	G705	G639	K573
T1508	M1435	Y1369	F1230	F1030	R1030	Q964	E900	V834	D706	D706	G638	K578
T1509	S1436	Q1370	Y1301	K1100	F1031	D965	A901	E835	S770	S770	L640	M579
E1511	E1510	Q1371	E1232	K1109	F1032	D966	S902	L836	R771	R772	L641	E580
P1514	P1438	G1372	E1233	F1101	M1033	S967	S903	V837	L773	F709	W642	D581
S1440	P1439	F1373	K1294	I1102	D1034	H968	S904	V838	Y774	Q710	W643	A582
Y1441	S1440	T1374	I1305	P1103	Q1035	Y969	Q904	L839	L775	H711	N646	F584
K1442	Y1441	E1375	L1172	S1104	S970	S970	L906	F840	R776	F712	N646	F584
D1443	D1443	E1376	E1173	M1105	A1037	H971	L906	C841	F777	N713	N646	F584
Q1449	Q1449	K1376	K1174	V1106	F1038	Y972	S907	F842	Y778	P714	N649	Y585
I1450	I1450	R1377	L1175	G1107	E1039	I973	N908	F843	Y779	V715	L650	L586
T1521	L1451	L1378	L1176	P1108	L1040	S974	I909	I844	Q780	L716	K651	T587
M1522	M1452	F1380	L1177	T1109	Q1041	F976	L910	Q845	S781	L718	H652	L588
E1523	Y1453	F1381	E1111	L1110	W1043	F976	L913	S846	K782	E717	H652	P589
L1524	Y1454	K1382	V1112	W1044	M1045	N982	R915	Q851	D783	Y719	L654	T591
T1525	R1455	L1383	T1115	Y1046	N1045	N983	K916	L852	D784	I720	L654	G590
N1526	N1456	G1384	P1116	F1047	Y1046	N983	K916	V853	D785	Y721	L657	K592
E1527	V1459	R1385	H1182	Y1046	Y1046	N983	K916	V853	E786	K722	L657	M593
R1528	Q1460	K1386	H1183	F1047	Y1046	N983	K916	V853	F787	H723	M658	E594
I1529	Q1461	E1387	E1117	H1048	N1048	N983	K916	V853	F788	F724	E659	E596
S1530	F1462	Y1388	Y1185	L1049	L1049	N983	K916	V853	N789	S725	V660	E596
N1531	R1463	E1389	L1186	A1050	Y1051	N983	K916	V853	A726	A726	D661	E597
C1532	Y1464	R1390	S1187	Y1051	Y1051	N983	K916	V853	T727	K598	G662	K598
E1533	Y1464	E1391	S1188	R1121	Y1051	N983	K916	V853	L728	E599	E599	E599
S1534	R1466	E1392	S1189	T1124	T1055	N983	K916	V853	A729	L600	V666	L600
Q1535	Y1467	E1393	H1190	F1125	H1056	N983	K916	V853	K667	Q801	Q801	Q801
H1536	F1468	S1395	E1191	F1125	Y1057	N983	K916	V853	F668	A802	F668	A802
D1539	R1470	L1398	Y1192	F1125	S1058	N983	K916	V853	L796	S803	L796	S803
S1540	K1471	L1399	F1193	F1125	L1059	N983	K916	V853	K732	K732	Q670	K604
L1542	Y1472	L1400	E1194	F1125	Q1060	N983	K916	V853	L733	L733	Q670	K604
S1543	N1477	E1401	L1195	F1125	Q1061	N983	K916	V853	N738	N738	T672	N605
V1544	E1478	F1402	L1196	D1130	E1062	N983	K916	V853	F739	F739	L673	L806
H1545	E1478	E1403	L1197	M1131	E1063	N983	K916	V853	N800	N800	L673	L806
P1546	T1481	M1404	L1198	Q1133	F1064	N983	K916	V853	F677	F677	E682	P811
L1547	M1482	E1406	L1200	Q1133	S1065	N983	K916	V853	N742	N742	E682	P811
S1548	W1483	E1407	L1201	F1136	K1068	N983	K916	V853	N743	N743	E682	P811
M1549	E1484	L1205	E1202	M1137	R1069	N983	K916	V853	A744	A744	E682	P811
E1485	E1485	D1206	E1203	M1137	R1069	N983	K916	V853	D745	D745	E682	P811
R1486	R1486	Y1207	L1204	M1143	I1072	N983	K916	V853	N802	N802	E682	P811
L1550	E1487	P1280	L1205	N1143	Y1073	N983	K916	V853	F677	F677	E682	P811
L1551	E1487	P1280	L1205	N1143	Y1073	N983	K916	V853	N742	N742	E682	P811
V1555	T1488	E1409	L1206	H1145	Y1076	N983	K916	V853	N742	N742	E682	P811
P1557	Y1489	P1413	L1207	H1145	Y1076	N983	K916	V853	N742	N742	E682	P811
M1560	T1490	E1416	L1211	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
G1561	T1491	E1416	L1212	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
G1562	T1494	E1416	L1213	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
F1563	F1495	E1416	L1214	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
S1564	P1496	E1416	L1215	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
N1565	L1499	E1416	L1216	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
Y1566	K1500	E1416	L1217	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
E1567	E1567	E1416	L1218	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
K1568	F1502	E1416	L1219	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
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		E1416	L1231	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1232	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1233	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
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		E1416	L1256	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1257	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1258	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1259	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1260	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1261	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1262	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1263	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1264	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1265	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1266	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1267	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1268	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1269	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1270	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1271	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1272	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1273	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1274	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1275	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1276	E1150	E1082	N983	K916	V853	N742	N742	E682	P811
		E1416	L1277	E1150	E1082	N983	K916	V853	N742	N74		

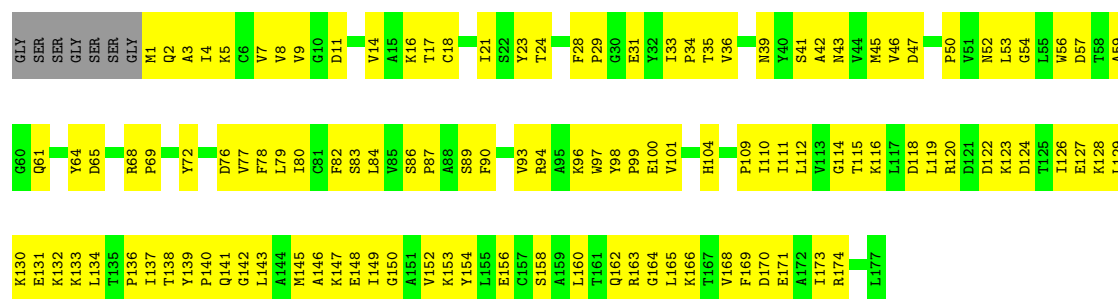


• Molecule 1: Dedicator of cytokinesis protein 5



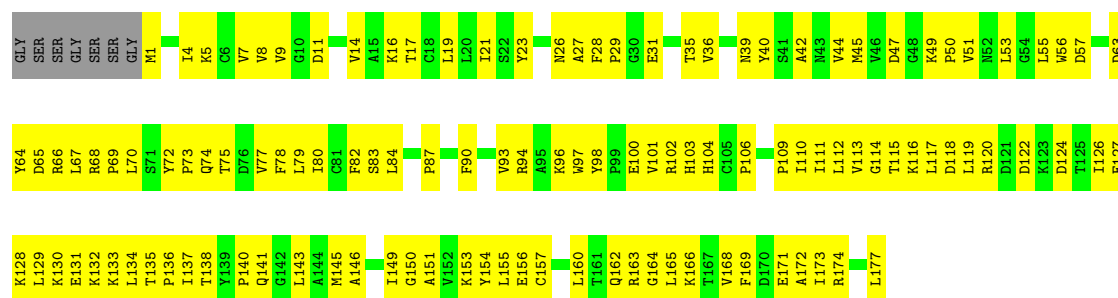
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I1529	Q1460	Y1388	K1319	I1239	K1174	I1109	A1036	Y969	Q904	L839	L775	Q705
S1530	Q1461	E1389	S1321	Y1240	L1176	E1110	S1037	S970	L905	F840	R776	Q710
M1531	F1462	E1390	S1321	I1241	L1177	E1111	F1038	S971	L906	C841	G779	N713
V1532	R1463	E1391	K1323	R1242	E1178	T1112	E1039	Y972	S907	K842	Y774	N713
Q1534	S1465	E1392	L1324	L1244	E1179	T1113	Q1041	Y973	N908	F843	P714	P714
Q1535	R1466	S1395	A1325	Y1245	R1181	T1114	L1042	Y974	I909	I844	V715	V715
L1536	P1467	E1396	E1326	R1248	H1182	T1115	W1043	Y975	L910	Q845	L716	L716
A1537	F1468	L1399	Y1328	D1249	H1183	P1116	E1117	F976	E911	S846	E717	E717
P1538	K1469	L1400	Y1328	R1250	H1184	V1118	N1044	Y977	D785	E786	T718	T718
D1539	K1470	Q1401	E1329	H1251	L1186	E1119	N1045	Y979	D914	F787	Y719	Y719
R1540	Q1471	Q1401	E1329	H1251	L1186	L1120	F1047	Y982	R915	N788	I720	I720
S1541	K1472	Q1401	E1329	H1251	L1186	R1121	H1048	Y982	K916	N789	Y721	Y721
L1542	K1473	Q1401	E1329	H1251	L1186	R1122	H1048	Y982	D917	S790	K722	K722
S1543	K1474	Q1401	E1329	H1251	L1186	R1123	L1054	Y985	S791	K854	H723	H723
V1544	K1475	Q1401	E1329	H1251	L1186	T1124	L1055	Y986	R792	K855	R792	R792
P1545	K1476	Q1401	E1329	H1251	L1186	T1125	H1056	Y987	Q793	K856	F724	F724
P1546	K1477	Q1401	E1329	H1251	L1186	P1126	E1057	Y988	L794	N858	S725	S725
L1547	K1478	Q1401	E1329	H1251	L1186	T1127	S1058	Y989	V923	C859	A726	A726
S1548	K1479	Q1401	E1329	H1251	L1186	F1128	L1059	Y990	H924	M860	Y730	Y730
M1549	K1480	Q1401	E1329	H1251	L1186	F1129	Q1060	Y991	I925	L796	V731	V731
L1550	K1481	Q1401	E1329	H1251	L1186	D1130	L1061	Y992	Q926	F797	L736	L736
P1551	K1482	Q1401	E1329	H1251	L1186	M1131	E1062	Y993	N927	N799	N737	N737
D1552	K1483	Q1401	E1329	H1251	L1186	M1132	T1063	Y994	I928	M800	N738	N738
P1553	K1484	Q1401	E1329	H1251	L1186	Q1133	F1064	Y995	M829	E865	F739	F739
P1554	K1485	Q1401	E1329	H1251	L1186	C1134	Q1065	Y996	E930	S866	Y740	Y740
P1555	K1486	Q1401	E1329	H1251	L1186	F1136	A1067	Y997	R931	T867	A742	A742
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P1557	K1488	Q1401	E1329	H1251	L1186	F1138	R1069	Y999	R804	P805	A744	A744
P1558	K1489	Q1401	E1329	H1251	L1186	S1139	I1072	Y999	L806	L806	D745	D745
P1559	K1490	Q1401	E1329	H1251	L1186	G1140	I1073	Y999	E807	E808	K748	K748
P1560	K1491	Q1401	E1329	H1251	L1186	M1141	V1073	Y999	V810	V810	T749	T749
P1561	K1492	Q1401	E1329	H1251	L1186	H1145	G1077	Y999	K811	K811	T750	T750
P1562	K1493	Q1401	E1329	H1251	L1186	H1146	D1078	Y999	L817	L817	E751	E751
P1563	K1494	Q1401	E1329	H1251	L1186	F1147	M1079	Y999	K818	K818	A755	A755
P1564	K1495	Q1401	E1329	H1251	L1186	E1148	K1080	Y999	Y819	Y819	A756	A756
P1565	K1496	Q1401	E1329	H1251	L1186	E1150	E1081	Y999	P821	P821	L757	L757
P1566	K1497	Q1401	E1329	H1251	L1186	L1151	I1083	Y999	S822	S822	K758	K758
P1567	K1498	Q1401	E1329	H1251	L1186	I1152	I1083	Y999	I824	I824	A759	A759
P1568	K1499	Q1401	E1329	H1251	L1186	D1156	R1086	Y999	D826	D826	L760	L760
P1569	K1500	Q1401	E1329	H1251	L1186	Q1157	I1087	Y999	K828	K828	K761	K761
P1570	K1501	Q1401	E1329	H1251	L1186	E1158	R1088	Y999	L829	L829	L762	L762
P1571	K1502	Q1401	E1329	H1251	L1186	V1159	M1090	Y999	V830	V830	F764	F764
P1572	K1503	Q1401	E1329	H1251	L1186	G1162	Y1092	Y999	N825	N825	R765	R765
P1573	K1504	Q1401	E1329	H1251	L1186	R1163	H1097	Y999	K896	K896	F766	F766
P1574	K1505	Q1401	E1329	H1251	L1186	D1165	K1098	Y999	P897	P897	I767	I767
P1575	K1506	Q1401	E1329	H1251	L1186	E1166	I1099	Y999	D832	D832	I768	I768
P1576	K1507	Q1401	E1329	H1251	L1186	Y1307	I1099	Y999	V833	V833	Q769	Q769
P1577	K1508	Q1401	E1329	H1251	L1186	Q1167	T1029	Y999	K896	K896	S770	S770
P1578	K1509	Q1401	E1329	H1251	L1186	E1168	F1101	Y999	D898	D898	L771	L771
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P1581	K1512	Q1401	E1329	H1251	L1186	L1171	L1172	Y999	M964	M964		
P1582	K1513	Q1401	E1329	H1251	L1186	L1172	L1173	Y999				
P1583	K1514	Q1401	E1329	H1251	L1186	L1173	L1174	Y999				
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P1585	K1516	Q1401	E1329	H1251	L1186	L1175	L1176	Y999				
P1586	K1517	Q1401	E1329	H1251	L1186	L1176	L1177	Y999				
P1587	K1518	Q1401	E1329	H1251	L1186	L1177	L1178	Y999				
P1588	K1519	Q1401	E1329	H1251	L1186	L1178	L1179	Y999				
P1589	K1520	Q1401	E1329	H1251	L1186	L1179	L1180	Y999				
P1590	K1521	Q1401	E1329	H1251	L1186	L1180	L1181	Y999				
P1591	K1522	Q1401	E1329	H1251	L1186	L1181	L1182	Y999				
P1592	K1523	Q1401	E1329	H1251	L1186	L1182	L1183	Y999				
P1593	K1524	Q1401	E1329	H1251	L1186	L1183	L1184	Y999				
P1594	K1525	Q1401	E1329	H1251	L1186	L1184	L1185	Y999				
P1595	K1526	Q1401	E1329	H1251	L1186	L1185	L1186	Y999				
P1596	K1527	Q1401	E1329	H1251	L1186	L1186	L1187	Y999				
P1597	K1528	Q1401	E1329	H1251	L1186	L1187	L1188	Y999				
P1598	K1529	Q1401	E1329	H1251	L1186	L1188	L1189	Y999				
P1599	K1530	Q1401	E1329	H1251	L1186	L1189	L1190	Y999				
P1600	K1531	Q1401	E1329	H1251	L1186	L1190	L1191	Y999				
P1601	K1532	Q1401	E1329	H1251	L1186	L1191	L1192	Y999				
P1602	K1533	Q1401	E1329	H1251	L1186	L1192	L1193	Y999				
P1603	K1534	Q1401	E1329	H1251	L1186	L1193	L1194	Y999				
P1604	K1535	Q1401	E1329	H1251	L1186	L1194	L1195	Y999				
P1605	K1536	Q1401	E1329	H1251	L1186	L1195	L1196	Y999				
P1606	K1537	Q1401	E1329	H1251	L1186	L1196	L1197	Y999				
P1607	K1538	Q1401	E1329	H1251	L1186	L1197	L1198	Y999				
P1608	K1539	Q1401	E1329	H1251	L1186	L1198	L1199	Y999				
P1609	K1540	Q1401	E1329	H1251	L1186	L1199	L1200	Y999				
P1610	K1541	Q1401	E1329	H1251	L1186	L1200	L1201	Y999				
P1611	K1542	Q1401	E1329	H1251	L1186	L1201	L1202	Y999				
P1612	K1543	Q1401	E1329	H1251	L1186	L1202	L1203	Y999				
P1613	K1544	Q1401	E1329	H1251	L1186	L1203	L1204	Y999				
P1614	K1545	Q1401	E1329	H1251	L1186	L1204	L1205	Y999				
P1615	K1546	Q1401	E1329	H1251	L1186	L1205	L1206	Y999				
P1616	K1547	Q1401	E1329	H1251	L1186	L1206	L1207	Y999				
P1617	K1548	Q1401	E1329	H1251	L1186	L1207	L1208	Y999				
P1618	K1549	Q1401	E1329	H1251	L1186	L1208	L1209	Y999				
P1619	K1550	Q1401	E1329	H1251	L1186	L1209	L1210	Y999				
P1620	K1551	Q1401	E1329	H1251	L1186	L1210	L1211	Y999				
P1621	K1552	Q1401	E1329	H1251	L1186	L1211	L1212	Y999				
P1622	K1553	Q1401	E1329	H1251	L1186	L1212	L1213	Y999				
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P1625	K1556	Q1401	E1329	H1251	L1186	L1215	L1216	Y999				
P1626	K1557	Q1401	E1329	H1251	L1186	L1216	L1217	Y999				
P1627	K1558	Q1401	E1329	H1251	L1186	L1217	L1218	Y999				
P1628	K1559	Q1401	E1329	H1251	L1186	L1218	L1219	Y999				
P1629	K1560	Q1401	E1329	H1251	L1186	L1219	L1220	Y999				
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P1631	K1562	Q1401	E1329	H1251	L1186	L1221	L1222	Y999				
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P1637	K1568	Q1401	E1329	H1251	L1186	L1227	L1228	Y999				
P1638	K1569	Q1401	E1329									

Chain C:  33% 64%



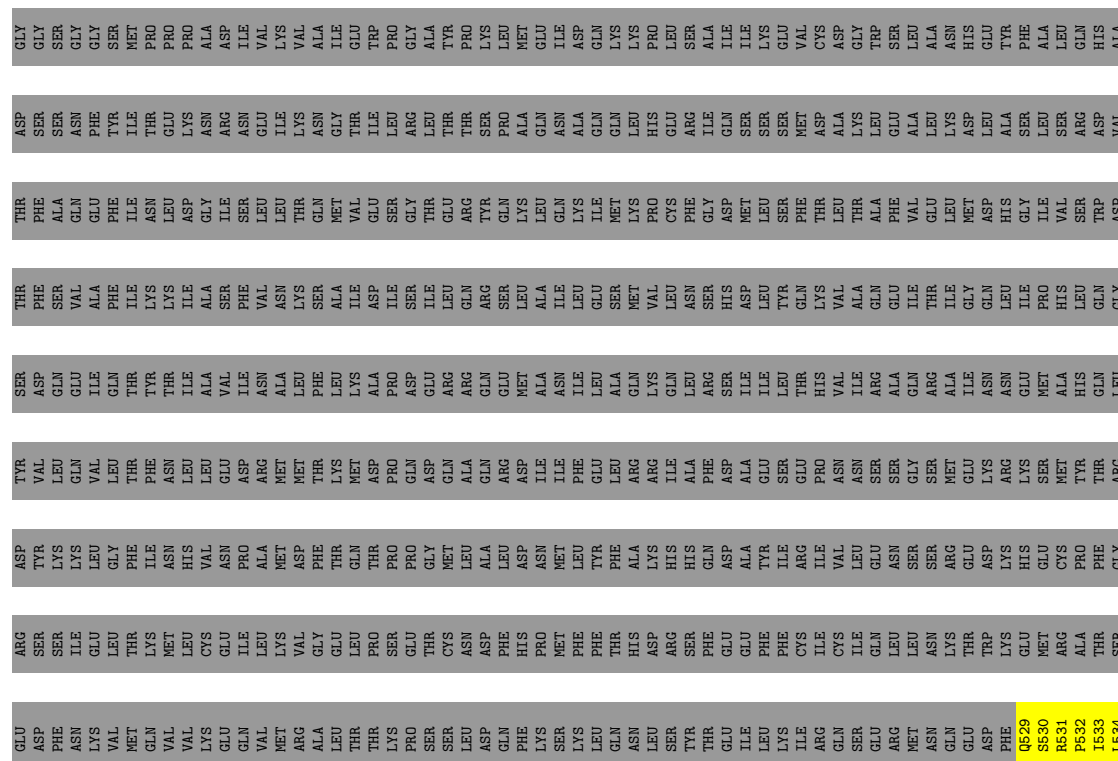
• Molecule 2: Ras-related C3 botulinum toxin substrate 1

Chain G:  32% 64%

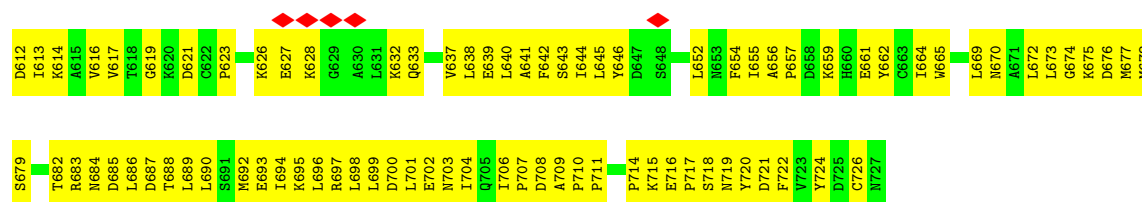


• Molecule 3: Engulfment and cell motility protein 1

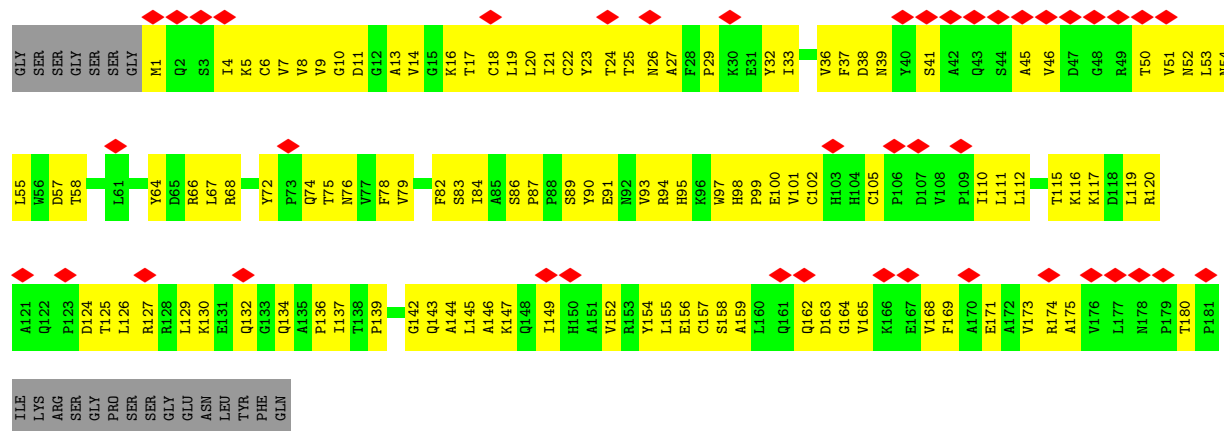
Chain E:  9% 18% 73%







• Molecule 4: Rho-related GTP-binding protein RhoG



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	169096	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.062	Depositor
Minimum map value	-0.021	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	452.2, 452.2, 452.2	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	Depositor

5 Model quality

5.1 Standard geometry

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

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	B	0.36	0/13722	0.61	1/18514 (0.0%)
1	F	0.29	0/13722	0.58	3/18514 (0.0%)
2	C	0.29	0/1415	0.53	0/1924
2	G	0.26	0/1415	0.54	0/1924
3	A	0.24	0/5992	0.57	1/8086 (0.0%)
3	E	0.24	0/1650	0.58	0/2230
4	D	0.22	0/1449	0.52	0/1977
All	All	0.30	0/39365	0.59	5/53169 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	96	ARG	CB-CG-CD	5.89	124.86	111.30
3	A	89	HIS	N-CA-CB	5.18	117.82	110.16
1	B	992	MET	CA-CB-CG	-5.05	104.00	114.10
1	F	95	LEU	CA-C-N	-5.05	112.29	120.72
1	F	95	LEU	C-N-CA	-5.05	112.29	120.72

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	110	LYS	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	13436	0	13516	1377	0
1	F	13436	0	13516	1102	0
2	C	1385	0	1407	120	0
2	G	1385	0	1407	147	0
3	A	5879	0	5902	508	0
3	E	1617	0	1625	160	0
4	D	1416	0	1413	123	0
5	D	1	0	0	0	0
6	D	32	0	12	3	0
All	All	38587	0	38798	3420	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 44.

All (3420) 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:F:1028:LEU:O	1:F:1032:PHE:HB2	1.63	0.98
1:F:1217:LYS:HA	1:F:1220:ARG:HE	1.31	0.94
3:A:302:PHE:HB3	3:A:431:GLY:H	1.31	0.94
1:B:1462:PHE:HB2	1:B:1489:TYR:HB2	1.46	0.94
1:F:740:TYR:HA	1:F:749:LYS:HD3	1.47	0.94
1:B:19:TYR:HH	1:B:44:TRP:HH2	1.15	0.92
3:A:209:VAL:HG11	3:A:249:ALA:HB1	1.51	0.92
1:B:37:ILE:HA	1:B:47:GLY:HA3	1.53	0.90
1:B:1209:THR:O	1:B:1213:GLN:HB3	1.70	0.89
1:B:789:ASN:HB3	1:B:793:GLN:HE22	1.37	0.88
1:F:37:ILE:HA	1:F:47:GLY:HA3	1.55	0.88
1:F:153:ASP:OD1	1:F:197:LYS:NZ	2.07	0.88
3:A:306:GLU:HG3	3:A:310:MET:HE2	1.56	0.87
1:F:25:VAL:HG21	1:F:56:LYS:HG3	1.58	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1166:GLU:HA	1:B:1169:LYS:HE3	1.58	0.86
3:A:617:VAL:HB	3:A:621:ASP:HB3	1.57	0.86
1:F:1435:MET:HE3	1:F:1436:SER:H	1.40	0.86
1:B:1391:ARG:HD2	1:B:1429:PHE:HA	1.56	0.85
2:G:171:GLU:HA	2:G:174:ARG:HG2	1.58	0.85
1:B:655:LYS:HB2	1:B:656:LYS:HZ2	1.39	0.85
1:F:157:ARG:NH2	1:F:201:GLU:OE1	2.08	0.85
1:B:285:SER:H	1:B:288:ASP:HB2	1.42	0.84
1:F:35:VAL:HG12	1:F:49:THR:HG22	1.60	0.84
1:F:1284:GLN:HE21	1:F:1286:ASP:HB2	1.40	0.84
1:B:945:ARG:HH21	1:B:946:GLN:HG2	1.39	0.84
1:F:668:PHE:HB3	1:F:671:ASP:HB2	1.58	0.84
1:B:927:LEU:HB3	1:B:931:ARG:HH12	1.42	0.83
1:F:1057:GLU:HA	1:F:1061:LEU:HD13	1.60	0.83
1:F:806:LEU:HD12	1:F:813:LYS:HD3	1.60	0.83
1:F:1633:VAL:HA	1:F:1637:TYR:HB2	1.59	0.83
1:F:1291:TYR:HB3	1:F:1296:LEU:HD21	1.59	0.83
1:B:1353:ILE:O	1:B:1449:GLN:NE2	2.12	0.82
3:A:306:GLU:HA	3:A:309:MET:HG2	1.59	0.82
1:B:537:GLN:HB2	1:B:540:ARG:HB3	1.60	0.82
1:F:1221:MET:HE1	1:F:1250:LEU:HB3	1.61	0.82
1:F:1587:GLU:HA	1:F:1590:LYS:HD2	1.62	0.82
1:B:323:GLY:HA2	1:B:351:ILE:HG13	1.61	0.82
1:B:330:THR:HA	1:B:333:ILE:HG12	1.62	0.81
1:B:1184:LYS:HG3	1:B:1185:TYR:H	1.45	0.81
1:B:904:GLN:O	1:B:908:ASN:ND2	2.13	0.81
1:F:1233:GLU:O	1:F:1235:LYS:NZ	2.14	0.81
3:E:670:ASN:ND2	3:E:676:ASP:O	2.13	0.81
2:C:116:LYS:HB3	2:C:119:LEU:HB2	1.62	0.81
1:F:132:LEU:HD22	3:E:703:ASN:HB2	1.61	0.81
1:B:1284:GLN:HG2	1:B:1286:ASP:H	1.45	0.81
1:F:297:VAL:HG12	1:F:299:GLN:HE21	1.42	0.81
1:F:1245:TYR:HD2	1:F:1248:ARG:HH21	1.29	0.81
2:G:90:PHE:HE2	2:G:137:ILE:HB	1.46	0.80
1:B:1057:GLU:O	1:B:1080:ARG:NH1	2.14	0.80
1:B:1276:LYS:NZ	1:B:1277:PRO:O	2.14	0.80
1:B:666:VAL:HA	1:B:669:LEU:HD23	1.64	0.80
3:A:670:ASN:ND2	3:A:676:ASP:O	2.13	0.80
1:B:1028:LEU:O	1:B:1032:PHE:HB2	1.80	0.80
1:B:851:GLN:O	1:B:856:LYS:NZ	2.14	0.80
1:B:1315:GLU:OE2	1:B:1357:ARG:NH2	2.13	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:79:THR:HG21	3:A:87:GLN:HE22	1.47	0.80
1:B:769:GLN:OE1	1:B:776:ARG:NH2	2.15	0.80
1:F:879:LEU:HG	1:F:931:ARG:HH22	1.46	0.80
1:F:1301:TYR:HE2	1:F:1320:LEU:HD12	1.47	0.80
1:F:1056:HIS:ND1	1:F:1057:GLU:OE2	2.14	0.79
2:C:153:LYS:NZ	2:C:154:TYR:O	2.16	0.79
1:F:910:LEU:HA	1:F:913:LEU:HD12	1.63	0.79
2:G:45:MET:HB3	2:G:50:PRO:HA	1.64	0.79
1:F:45:TYR:HD2	1:F:64:ILE:HG13	1.48	0.79
3:E:537:LYS:HB2	3:E:694:ILE:HG21	1.65	0.79
3:A:241:THR:O	3:A:293:GLN:NE2	2.17	0.78
3:A:448:HIS:HB3	3:A:451:SER:HB3	1.65	0.78
1:B:19:TYR:H	1:B:28:SER:HA	1.47	0.78
1:B:954:VAL:HA	1:B:957:MET:HE3	1.64	0.78
1:B:1543:SER:OG	1:B:1545:HIS:ND1	2.17	0.78
2:C:39:ASN:H	2:C:57:ASP:HB3	1.47	0.78
1:B:95:LEU:HA	1:B:98:TRP:CD1	2.18	0.78
1:B:485:HIS:HA	1:B:492:GLY:HA2	1.66	0.78
1:B:560:THR:HG22	1:B:638:LEU:HG	1.66	0.78
1:B:1057:GLU:HA	1:B:1061:LEU:HD13	1.65	0.78
1:B:1245:TYR:HD2	1:B:1248:ARG:HH21	1.31	0.78
1:F:166:ARG:NH1	1:F:167:ASP:OD1	2.16	0.78
1:F:1217:LYS:HG2	1:F:1220:ARG:HH21	1.46	0.78
1:B:1360:PRO:HA	1:B:1387:GLU:HA	1.64	0.77
1:B:46:ARG:NH2	3:A:726:CYS:SG	2.57	0.77
1:B:940:VAL:HA	1:B:943:MET:HB3	1.65	0.77
1:F:1088:ARG:HG3	1:F:1127:ILE:HD11	1.64	0.77
1:B:476:GLU:HG3	1:B:583:LYS:HD2	1.67	0.77
1:B:1159:VAL:O	1:B:1208:ARG:NH1	2.18	0.77
1:B:1579:HIS:HB3	1:B:1582:ASP:HB2	1.66	0.77
1:F:986:LEU:HG	1:F:1028:LEU:HD21	1.67	0.77
1:F:1057:GLU:O	1:F:1080:ARG:NH1	2.17	0.77
1:F:1360:PRO:HA	1:F:1387:GLU:HA	1.64	0.77
1:F:904:GLN:OE1	1:F:908:ASN:ND2	2.17	0.77
3:A:126:ILE:HG21	3:A:166:MET:HE3	1.67	0.77
3:A:331:ALA:HB1	3:A:399:VAL:HG21	1.67	0.77
1:B:1612:THR:HG22	1:B:1615:LEU:HD13	1.66	0.77
1:B:741:VAL:HG23	1:B:801:LEU:HD11	1.66	0.77
1:B:566:ARG:HE	1:B:621:GLN:HG3	1.48	0.76
1:F:1368:TYR:HD1	1:F:1408:MET:HE1	1.50	0.76
4:D:93:VAL:HA	4:D:97:TRP:HB2	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:TYR:N	1:B:404:LYS:O	2.19	0.76
1:B:934:ARG:NH1	1:B:934:ARG:O	2.17	0.76
1:B:484:ILE:HG21	1:B:496:TYR:HB2	1.67	0.76
1:F:632:THR:HG23	1:F:664:GLU:HB3	1.67	0.76
1:F:883:THR:HG21	1:F:931:ARG:HG3	1.67	0.76
1:B:740:TYR:HA	1:B:749:LYS:HD3	1.67	0.76
1:B:1563:PHE:HA	1:B:1566:TYR:HD2	1.51	0.76
1:B:1167:GLN:OE1	1:B:1167:GLN:N	2.18	0.76
1:B:154:HIS:HB2	1:B:197:LYS:HZ2	1.51	0.76
1:B:1183:HIS:CE1	1:B:1186:LEU:HB3	2.21	0.76
1:B:1010:ASN:OD1	1:B:1013:GLN:NE2	2.18	0.75
1:B:37:ILE:HD13	1:B:45:TYR:HB3	1.67	0.75
1:B:1597:MET:HG3	1:B:1633:VAL:HG21	1.67	0.75
2:G:90:PHE:HB3	2:G:94:ARG:HH22	1.51	0.75
1:B:1408:MET:HB2	1:B:1427:GLN:HB3	1.67	0.75
2:G:98:TYR:HE1	2:G:149:ILE:HD13	1.51	0.75
1:B:1545:HIS:O	1:B:1548:SER:OG	2.03	0.75
3:A:677:MET:O	3:A:683:ARG:NH2	2.16	0.75
1:B:434:PRO:O	1:B:708:LYS:NZ	2.17	0.75
1:B:36:HIS:N	1:B:48:TYR:O	2.19	0.75
1:B:1010:ASN:O	1:B:1013:GLN:NE2	2.18	0.75
1:B:1620:GLU:OE2	1:B:1621:ARG:NH1	2.20	0.75
3:A:561:CYS:HB3	3:A:574:PHE:HB3	1.68	0.75
1:B:864:VAL:HG21	1:B:909:ILE:HG22	1.68	0.75
2:G:7:VAL:HA	2:G:56:TRP:HB2	1.69	0.74
1:F:165:VAL:HG23	1:F:175:PRO:HD3	1.68	0.74
1:B:1117:GLU:OE1	1:B:1119:GLU:N	2.20	0.74
1:F:1159:VAL:O	1:F:1208:ARG:NH1	2.20	0.74
1:F:1390:ARG:NH2	2:G:23:TYR:O	2.20	0.74
1:B:467:GLU:HB2	1:B:500:VAL:HG22	1.68	0.74
1:B:1561:GLY:O	1:B:1565:ASN:ND2	2.18	0.74
1:F:1219:ASN:OD1	1:F:1401:GLN:NE2	2.21	0.74
1:F:1248:ARG:NH1	1:F:1249:ASP:OD1	2.19	0.74
1:B:930:GLU:O	1:B:935:ARG:NH2	2.21	0.74
1:F:954:VAL:HA	1:F:957:MET:HE2	1.69	0.74
3:A:582:ASN:HB3	3:A:584:LYS:HG2	1.69	0.74
1:F:150:ALA:O	1:F:197:LYS:NZ	2.20	0.74
1:F:1525:THR:HA	1:F:1528:ARG:HH11	1.52	0.74
4:D:78:PHE:HE2	4:D:105:CYS:HB2	1.53	0.74
1:B:1315:GLU:OE1	1:B:1315:GLU:N	2.16	0.74
1:B:1463:ARG:HD3	1:B:1486:ARG:HD2	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:THR:HG22	1:B:85:LEU:HB2	1.69	0.74
1:F:145:LYS:HD2	1:F:169:ASN:H	1.53	0.74
3:E:530:SER:HB2	3:E:533:ILE:HD13	1.70	0.74
1:B:1111:GLU:O	1:B:1163:ARG:NH2	2.21	0.74
1:F:95:LEU:HD23	1:F:98:TRP:HD1	1.52	0.74
4:D:120:ARG:NH1	4:D:137:ILE:O	2.21	0.74
3:A:694:ILE:HA	3:A:697:ARG:HG2	1.69	0.73
1:B:875:ARG:NH1	1:B:920:ALA:O	2.20	0.73
3:A:97:MET:HE1	3:A:147:MET:HE1	1.69	0.73
1:B:199:GLN:HA	1:B:202:LYS:HZ3	1.53	0.73
4:D:51:VAL:HG11	4:D:173:VAL:HG11	1.70	0.73
1:B:1368:TYR:O	1:B:1425:TYR:N	2.17	0.73
1:F:5:ILE:H	1:F:40:MET:H	1.37	0.73
3:E:531:ARG:NH2	3:E:708:ASP:OD2	2.21	0.73
3:A:584:LYS:O	3:A:607:LYS:NZ	2.22	0.73
1:F:96:ARG:HH22	1:F:1067:ALA:HB2	1.54	0.73
1:F:1362:TYR:HE2	1:F:1459:VAL:HG21	1.53	0.73
1:B:95:LEU:HA	1:B:98:TRP:HD1	1.53	0.73
1:B:228:PHE:HE2	1:B:399:LEU:HB2	1.54	0.73
1:B:1275:ASP:O	1:B:1292:THR:OG1	2.07	0.73
1:F:705:GLY:O	1:F:710:GLN:NE2	2.19	0.73
1:F:961:LEU:HA	1:F:964:MET:HB3	1.69	0.73
1:B:79:THR:HG21	1:B:83:GLY:H	1.53	0.72
1:B:1063:THR:HA	1:B:1069:ARG:HH11	1.53	0.72
1:B:1633:VAL:HA	1:B:1637:TYR:HB2	1.70	0.72
1:F:33:ASP:HA	1:F:51:GLN:HE22	1.54	0.72
1:F:1156:ASP:OD2	1:F:1242:ARG:NH2	2.22	0.72
3:A:86:GLN:O	3:A:89:HIS:ND1	2.22	0.72
1:B:110:LYS:HZ2	1:B:113:LEU:HB2	1.55	0.72
1:F:102:TRP:HB2	1:F:114:PHE:HE1	1.53	0.72
1:F:1063:THR:HA	1:F:1069:ARG:HH11	1.54	0.72
1:F:72:GLU:HA	1:F:89:GLN:HE22	1.54	0.72
1:B:86:PRO:HA	1:B:89:GLN:HE21	1.53	0.72
1:B:140:GLU:N	1:B:140:GLU:OE1	2.21	0.72
1:B:474:ASP:O	1:B:526:HIS:ND1	2.23	0.72
1:B:498:SER:HB2	1:B:509:TRP:HE1	1.54	0.72
1:B:900:GLU:O	1:B:903:SER:OG	2.08	0.72
1:B:944:ASN:O	1:B:946:GLN:NE2	2.22	0.72
1:B:979:ARG:NH2	1:B:1031:PHE:O	2.23	0.72
1:B:1367:TYR:HH	1:B:1383:TYR:HH	1.36	0.72
1:F:60:PRO:HB3	3:E:714:PRO:HD2	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1248:ARG:HH11	1:F:1252:ARG:HH12	1.37	0.72
2:G:9:VAL:HG22	2:G:78:PHE:HZ	1.54	0.72
1:F:871:GLN:HB2	1:F:918:VAL:HG12	1.72	0.72
1:F:1359:GLN:NE2	1:F:1360:PRO:O	2.23	0.72
2:G:90:PHE:HB3	2:G:94:ARG:NH2	2.05	0.72
3:A:134:GLU:OE1	3:A:177:SER:OG	2.08	0.72
3:A:328:ARG:HE	3:A:329:ARG:HH21	1.37	0.72
1:F:59:PHE:HD2	1:F:64:ILE:HG12	1.54	0.72
1:B:154:HIS:HA	1:B:157:ARG:HE	1.55	0.72
1:B:446:ILE:HB	1:B:515:VAL:HB	1.71	0.72
1:B:1372:PHE:O	1:B:1377:ARG:NH2	2.23	0.72
1:F:1560:MET:HE1	2:G:36:VAL:HG12	1.72	0.72
3:A:619:GLY:HA3	3:A:638:LEU:HD12	1.71	0.72
2:G:100:GLU:O	2:G:104:HIS:ND1	2.23	0.71
1:B:890:LEU:HD22	1:B:935:ARG:HG3	1.72	0.71
2:C:130:LYS:HE3	2:C:136:PRO:HD3	1.72	0.71
1:F:242:PHE:HB3	1:F:257:ASN:HB3	1.72	0.71
1:B:150:ALA:O	1:B:197:LYS:NZ	2.24	0.71
1:F:761:LYS:HG3	1:F:765:ARG:HH21	1.55	0.71
1:F:1166:GLU:HA	1:F:1169:LYS:HE3	1.72	0.71
1:F:1277:PRO:HG3	1:F:1292:THR:HA	1.71	0.71
1:B:1200:LEU:HD23	1:B:1230:PHE:HE2	1.55	0.71
1:B:1439:PRO:HA	1:B:1442:LYS:HZ2	1.54	0.71
1:F:239:ALA:HB3	1:F:262:TRP:HB3	1.72	0.71
1:F:532:ARG:HA	1:F:546:ALA:HA	1.71	0.71
1:F:1545:HIS:HD2	2:G:5:LYS:HE3	1.54	0.71
1:B:1:MET:HE2	3:A:718:SER:HA	1.70	0.71
1:B:555:MET:HA	1:B:561:THR:HA	1.73	0.71
3:A:216:TYR:HE1	3:A:250:LEU:HA	1.54	0.71
3:A:235:SER:O	3:A:284:ARG:NH1	2.23	0.71
1:B:972:TYR:HA	1:B:975:THR:HB	1.70	0.71
1:B:122:TYR:CZ	3:A:692:MET:HE3	2.26	0.71
1:F:1623:SER:HB3	1:F:1627:ARG:HH22	1.55	0.71
4:D:19:LEU:HD21	4:D:168:VAL:HG11	1.72	0.71
3:A:509:LEU:HA	3:A:514:ILE:HD11	1.71	0.71
1:B:1155:LEU:HD21	1:B:1201:LEU:HD21	1.73	0.71
1:F:472:VAL:HB	1:F:483:ALA:HB1	1.72	0.71
1:F:1081:LYS:HD2	1:F:1120:LEU:HD23	1.71	0.71
2:G:7:VAL:HG23	2:G:75:THR:HG21	1.73	0.71
1:B:237:GLU:OE2	1:B:305:HIS:N	2.23	0.71
1:B:871:GLN:HG2	1:B:875:ARG:HD3	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:563:GLN:O	1:B:567:HIS:NE2	2.23	0.70
1:B:730:TYR:HB3	1:B:770:SER:HB3	1.71	0.70
1:F:495:GLU:O	1:F:497:LYS:NZ	2.23	0.70
1:B:843:PHE:O	1:B:846:SER:OG	2.09	0.70
1:B:1622:LEU:O	1:B:1626:PHE:HB2	1.91	0.70
2:C:9:VAL:HG22	2:C:78:PHE:HZ	1.53	0.70
3:A:564:LYS:HG3	3:A:575:TRP:NE1	2.06	0.70
1:B:638:LEU:HD13	1:B:641:LEU:HD12	1.72	0.70
1:B:1370:GLN:OE1	1:B:1377:ARG:NH1	2.25	0.70
1:F:237:GLU:OE2	1:F:305:HIS:N	2.24	0.70
3:A:529:GLN:HG3	3:A:534:LEU:HD11	1.74	0.70
1:B:2:ALA:H	3:A:717:PRO:HG2	1.55	0.70
1:B:138:LYS:HA	1:B:141:LEU:HD13	1.73	0.70
1:B:1525:THR:HA	1:B:1528:ARG:HH11	1.56	0.70
1:F:1185:TYR:O	1:F:1188:SER:OG	2.07	0.70
4:D:4:ILE:HD12	4:D:173:VAL:HG13	1.74	0.70
1:B:181:ILE:HG22	1:B:185:LYS:HZ1	1.57	0.70
1:F:904:GLN:O	1:F:908:ASN:ND2	2.25	0.70
1:F:1440:SER:H	1:F:1442:LYS:HZ2	1.38	0.70
3:E:561:CYS:HB3	3:E:574:PHE:HA	1.74	0.70
1:B:961:LEU:O	1:B:1019:ARG:NH1	2.25	0.70
1:B:1307:TYR:HD1	1:B:1310:LYS:HZ3	1.38	0.70
1:F:1:MET:HE1	1:F:23:GLN:HE21	1.55	0.70
1:F:1275:ASP:O	1:F:1292:THR:OG1	2.08	0.70
2:G:153:LYS:NZ	2:G:154:TYR:O	2.25	0.70
1:B:318:LEU:HD22	1:B:320:ARG:HH22	1.56	0.70
1:B:792:ARG:NE	1:B:835:GLU:OE1	2.19	0.70
1:B:871:GLN:HB2	1:B:918:VAL:HG12	1.74	0.70
1:F:745:ASP:HB3	1:F:804:ARG:HH22	1.56	0.70
2:G:14:VAL:HB	2:G:16:LYS:HZ3	1.55	0.70
1:B:680:MET:HE1	1:B:690:ASP:HA	1.74	0.70
1:F:870:ARG:NH1	1:F:872:SER:OG	2.24	0.70
1:B:1062:GLU:HB3	1:B:1069:ARG:HA	1.74	0.69
1:B:789:ASN:OD1	1:B:792:ARG:NH1	2.25	0.69
2:C:45:MET:HA	2:C:50:PRO:HA	1.74	0.69
1:F:1536:HIS:HA	1:F:1542:LEU:HD13	1.73	0.69
1:B:1152:ILE:HD12	1:B:1200:LEU:HD11	1.73	0.69
3:A:398:ILE:O	3:A:402:ASN:ND2	2.26	0.69
1:B:1356:MET:N	1:B:1356:MET:SD	2.65	0.69
1:F:1349:TYR:HA	1:F:1352:ILE:HD12	1.75	0.69
1:B:1007:MET:N	1:B:1007:MET:SD	2.61	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1486:ARG:NH2	1:B:1510:GLU:OE1	2.26	0.69
1:F:1114:LEU:HD22	1:F:1163:ARG:HB3	1.75	0.69
1:B:496:TYR:OH	1:B:511:GLU:OE2	2.10	0.69
1:B:1342:LEU:HD11	1:F:1346:ALA:HB2	1.75	0.69
1:B:327:MET:HE3	1:B:347:PRO:HD2	1.73	0.69
1:B:795:PHE:CE2	1:B:843:PHE:HB2	2.28	0.69
1:F:581:ASP:HB3	1:F:584:PHE:HB3	1.74	0.69
1:F:1335:TYR:HA	1:F:1338:LEU:HD23	1.73	0.69
1:B:1360:PRO:HG2	1:B:1362:TYR:HE1	1.58	0.69
1:F:70:THR:HG22	1:F:71:VAL:H	1.57	0.69
1:F:93:SER:O	1:F:96:ARG:HD3	1.92	0.69
1:F:852:LEU:HB2	1:F:856:LYS:HE2	1.75	0.69
1:F:1469:ARG:HA	1:F:1481:THR:HB	1.73	0.69
3:A:51:LEU:O	3:A:61:ILE:N	2.22	0.69
4:D:10:GLY:O	4:D:16:LYS:NZ	2.25	0.69
1:B:187:HIS:HD1	1:B:1006:TRP:HD1	1.38	0.69
1:B:646:ASN:OD1	1:B:649:ASN:ND2	2.26	0.69
1:B:802:MET:SD	1:B:846:SER:OG	2.50	0.69
1:F:35:VAL:HA	1:F:49:THR:HA	1.75	0.69
1:F:1532:CYS:O	1:F:1535:GLN:NE2	2.24	0.69
3:A:81:PRO:HB3	3:A:116:PHE:HA	1.75	0.69
3:A:309:MET:HE1	3:A:376:PRO:HB3	1.72	0.69
1:B:1056:HIS:ND1	1:B:1057:GLU:OE2	2.26	0.69
1:B:1231:TYR:HE2	1:B:1243:TYR:HE2	1.41	0.69
1:F:454:GLU:HA	1:F:506:GLN:HG2	1.74	0.69
1:F:1218:GLU:N	1:F:1218:GLU:OE1	2.25	0.69
1:B:913:LEU:HD23	1:B:925:ILE:HG22	1.73	0.68
1:F:110:LYS:HZ3	1:F:113:LEU:HB2	1.58	0.68
1:F:1121:ARG:HH11	1:F:1171:LEU:HD12	1.57	0.68
1:F:1438:PRO:HB2	1:F:1441:TYR:HB2	1.74	0.68
1:B:72:GLU:OE1	1:B:74:LEU:N	2.26	0.68
1:B:1522:MET:HE1	1:B:1593:ILE:HA	1.74	0.68
1:F:95:LEU:HA	1:F:98:TRP:CD1	2.29	0.68
3:A:138:GLU:OE2	3:A:139:ARG:NH1	2.26	0.68
4:D:32:TYR:HA	6:D:202:GTP:H5''	1.75	0.68
1:B:730:TYR:HB2	1:B:767:ILE:HG23	1.76	0.68
1:B:879:LEU:HB2	1:B:924:HIS:HE1	1.58	0.68
1:B:1584:GLU:HG3	1:B:1585:LYS:HD2	1.76	0.68
1:F:79:THR:HG22	1:F:85:LEU:HB2	1.75	0.68
1:F:376:ASN:ND2	1:F:502:TYR:O	2.24	0.68
1:F:678:ASN:HA	1:F:681:MET:HG2	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:789:ASN:OD1	1:F:792:ARG:NH1	2.26	0.68
1:F:824:ILE:HB	1:F:836:LEU:HD21	1.75	0.68
1:B:1238:ASP:HA	1:B:1241:ILE:HD12	1.75	0.68
3:A:315:PRO:O	3:A:320:GLN:NE2	2.25	0.68
4:D:11:ASP:OD1	4:D:97:TRP:NE1	2.17	0.68
1:F:1328:TYR:HA	1:F:1332:VAL:HG12	1.75	0.68
1:F:1365:VAL:O	1:F:1381:PHE:N	2.18	0.68
3:A:547:LEU:O	3:A:550:GLN:NE2	2.27	0.68
1:B:106:TYR:O	3:A:555:ARG:NH2	2.27	0.68
1:B:70:THR:HG22	1:B:71:VAL:H	1.59	0.68
1:F:565:GLY:N	1:F:624:THR:O	2.25	0.68
1:F:979:ARG:NH2	1:F:1031:PHE:O	2.27	0.68
3:A:58:ASN:OD1	3:A:76:ARG:NH2	2.27	0.68
1:B:344:HIS:N	1:B:401:VAL:O	2.27	0.68
1:B:669:LEU:O	1:B:672:THR:OG1	2.11	0.68
1:F:1097:HIS:HA	1:F:1100:LYS:HE2	1.75	0.68
2:G:4:ILE:H	2:G:53:LEU:HA	1.59	0.68
2:G:11:ASP:O	2:G:16:LYS:NZ	2.26	0.68
3:A:266:LEU:HA	3:A:271:LEU:HD13	1.76	0.68
1:B:876:GLU:N	1:B:876:GLU:OE1	2.27	0.68
3:E:608:LEU:HD11	3:E:613:ILE:HD11	1.76	0.68
3:A:526:GLU:O	3:A:530:SER:N	2.23	0.68
1:B:25:VAL:HG21	1:B:56:LYS:HG3	1.75	0.67
1:B:1111:GLU:N	1:B:1111:GLU:OE1	2.25	0.67
1:F:247:ASP:HB3	1:F:250:GLN:HB2	1.76	0.67
3:A:113:ASP:HB3	3:A:116:PHE:HB3	1.75	0.67
3:A:530:SER:HB2	3:A:533:ILE:HD13	1.76	0.67
1:B:719:TYR:CD1	1:B:723:HIS:HB2	2.30	0.67
1:F:241:LEU:HB2	1:F:260:ILE:HB	1.75	0.67
1:F:332:ILE:HD13	1:F:403:LEU:HD13	1.76	0.67
1:F:1062:GLU:HB3	1:F:1069:ARG:HA	1.76	0.67
1:B:34:THR:OG1	3:A:700:ASP:OD2	2.12	0.67
1:B:1218:GLU:OE1	1:B:1218:GLU:N	2.27	0.67
1:B:1390:ARG:NH2	2:C:23:TYR:O	2.28	0.67
1:F:1:MET:H3	3:E:717:PRO:HD2	1.58	0.67
1:F:4:TRP:O	3:E:724:TYR:N	2.28	0.67
3:E:557:VAL:O	3:E:578:ARG:NH1	2.28	0.67
3:A:87:GLN:O	3:A:91:ARG:HG2	1.94	0.67
1:B:85:LEU:HA	1:B:88:VAL:HG12	1.75	0.67
1:B:91:LEU:O	1:B:95:LEU:HG	1.94	0.67
1:B:129:SER:HA	1:B:132:LEU:HD12	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1065:SER:OG	1:B:1068:LYS:N	2.28	0.67
1:B:1374:SER:O	1:B:1379:LYS:NZ	2.27	0.67
3:A:108:ALA:O	3:A:112:ARG:NH1	2.27	0.67
1:B:73:ASP:HA	1:B:78:GLU:HB2	1.77	0.67
2:C:170:ASP:HB3	2:C:174:ARG:HH21	1.60	0.67
1:F:306:MET:H	1:F:314:HIS:HB3	1.59	0.67
1:F:519:ILE:HG21	1:F:630:LYS:HB3	1.77	0.67
3:E:551:GLN:HG2	3:E:552:ARG:HH21	1.60	0.67
3:E:692:MET:O	3:E:696:LEU:N	2.28	0.67
1:B:302:ARG:HG3	1:B:320:ARG:HB2	1.77	0.67
1:B:1180:CYS:O	1:B:1187:SER:OG	2.10	0.67
1:F:789:ASN:HA	1:F:792:ARG:HD2	1.75	0.67
1:F:1366:GLY:HA2	1:F:1380:ILE:HA	1.76	0.67
1:F:1631:GLU:OE1	1:F:1635:LYS:NZ	2.28	0.67
4:D:39:ASN:ND2	4:D:54:ASN:OD1	2.20	0.67
4:D:124:ASP:OD1	4:D:127:ARG:NH1	2.27	0.67
1:B:1532:CYS:O	1:B:1535:GLN:NE2	2.26	0.67
3:A:665:TRP:O	3:A:669:LEU:HG	1.94	0.67
1:B:965:ASP:OD1	1:B:966:ASP:N	2.28	0.67
1:B:1117:GLU:OE2	1:B:1121:ARG:N	2.25	0.67
1:F:1148:GLU:O	1:F:1152:ILE:HG12	1.94	0.67
1:B:31:ILE:HG21	3:A:698:LEU:HA	1.77	0.67
1:B:114:PHE:O	1:B:117:LEU:HB3	1.95	0.67
1:F:1490:THR:OG1	1:F:1506:GLN:HB3	1.95	0.67
3:A:83:GLN:OE1	3:A:86:GLN:NE2	2.28	0.67
1:B:590:GLY:N	1:B:594:GLU:OE2	2.28	0.66
1:B:1196:LEU:O	1:B:1199:SER:OG	2.13	0.66
1:F:1506:GLN:NE2	1:F:1508:SER:OG	2.22	0.66
3:A:13:GLU:O	3:A:77:LEU:N	2.27	0.66
1:B:844:ILE:HB	1:B:881:LEU:HD11	1.76	0.66
1:B:1259:GLU:OE1	1:B:1259:GLU:N	2.29	0.66
1:F:857:LEU:HA	1:F:860:MET:SD	2.35	0.66
1:F:930:GLU:O	1:F:935:ARG:NH2	2.28	0.66
3:A:352:TYR:O	3:A:356:TYR:HB2	1.95	0.66
1:B:1051:VAL:HG21	1:B:1108:PRO:HB3	1.77	0.66
1:F:102:TRP:HB2	1:F:114:PHE:CE1	2.31	0.66
1:F:943:MET:HE3	1:F:950:ILE:HG13	1.77	0.66
1:F:1362:TYR:HD2	1:F:1462:PHE:HE2	1.43	0.66
2:G:116:LYS:HB3	2:G:119:LEU:HB2	1.77	0.66
3:A:132:MET:HG3	3:A:133:VAL:HG13	1.76	0.66
3:A:579:LEU:HD11	3:A:583:HIS:HA	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:TRP:CD1	3:A:716:GLU:HG3	2.31	0.66
1:F:1451:LEU:HB3	1:F:1455:ARG:HH22	1.61	0.66
1:F:465:ASN:ND2	1:F:534:ARG:O	2.28	0.66
1:F:772:VAL:HA	1:F:775:LEU:HG	1.78	0.66
1:F:1418:ILE:HA	1:F:1421:SER:HB3	1.77	0.66
1:F:1484:ILE:HB	1:F:1512:ILE:HB	1.78	0.66
3:A:333:ASP:HA	3:A:336:SER:HB2	1.76	0.66
1:F:1167:GLN:OE1	1:F:1167:GLN:N	2.25	0.66
3:A:640:LEU:HB3	3:A:656:ALA:H	1.61	0.66
4:D:13:ALA:HA	6:D:202:GTP:H5'	1.76	0.66
1:B:860:MET:HA	1:B:863:ILE:HD13	1.78	0.66
2:C:11:ASP:OD1	2:C:16:LYS:NZ	2.29	0.66
3:A:308:ARG:NE	3:A:382:ASP:OD2	2.28	0.66
3:A:614:LYS:HB2	3:A:645:LEU:HB2	1.78	0.66
1:B:372:VAL:O	1:B:376:ASN:ND2	2.29	0.66
1:B:923:VAL:O	1:B:927:LEU:HG	1.96	0.66
1:B:1015:ARG:HA	1:B:1018:LEU:HD12	1.77	0.66
1:B:1120:LEU:O	1:B:1124:THR:OG1	2.09	0.66
1:F:1128:PHE:HA	1:F:1131:MET:SD	2.36	0.66
1:F:1549:MET:HE1	2:G:56:TRP:CE2	2.31	0.66
1:F:1590:LYS:HB3	1:F:1639:VAL:HG12	1.78	0.66
3:E:692:MET:HA	3:E:695:LYS:HE3	1.77	0.66
1:B:771:ARG:HH12	1:B:784:GLY:HA2	1.60	0.66
1:F:1607:HIS:NE2	1:F:1619:HIS:HB2	2.11	0.66
2:G:64:TYR:HB2	2:G:68:ARG:HH21	1.59	0.66
3:A:377:GLY:H	3:A:418:ILE:HD11	1.61	0.66
3:A:441:PHE:O	3:A:495:LYS:NZ	2.23	0.66
1:B:259:LEU:N	1:B:488:ALA:O	2.24	0.65
1:B:939:THR:O	1:B:943:MET:N	2.21	0.65
1:B:970:SER:O	1:B:974:SER:OG	2.14	0.65
1:B:1470:LYS:H	1:B:1481:THR:HB	1.60	0.65
1:F:1391:ARG:HH22	2:G:29:PRO:HD3	1.59	0.65
3:A:245:ALA:HB2	3:A:293:GLN:HE22	1.60	0.65
1:B:154:HIS:O	1:B:157:ARG:HG2	1.96	0.65
1:B:1231:TYR:O	1:B:1235:LYS:N	2.30	0.65
1:B:1469:ARG:HD2	1:B:1481:THR:OG1	1.95	0.65
1:F:115:ARG:O	1:F:119:GLN:NE2	2.29	0.65
1:F:1149:ASN:HA	1:F:1236:ARG:HH22	1.59	0.65
1:F:1307:TYR:O	1:F:1311:GLY:N	2.26	0.65
3:E:547:LEU:O	3:E:550:GLN:NE2	2.28	0.65
1:B:1169:LYS:HA	1:B:1172:LEU:HD12	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:485:HIS:HA	1:F:492:GLY:HA3	1.79	0.65
1:F:1568:LYS:O	1:F:1572:THR:OG1	2.13	0.65
3:A:141:GLN:HA	3:A:144:GLN:HG3	1.78	0.65
2:G:80:ILE:HD11	2:G:97:TRP:HB3	1.79	0.65
2:G:149:ILE:HG23	2:G:151:ALA:H	1.60	0.65
3:E:580:SER:O	3:E:583:HIS:ND1	2.30	0.65
4:D:11:ASP:O	4:D:16:LYS:NZ	2.28	0.65
1:B:330:THR:O	1:B:334:HIS:ND1	2.29	0.65
1:B:844:ILE:HG21	1:B:881:LEU:HD21	1.79	0.65
1:B:1024:PHE:HA	1:B:1027:VAL:HG12	1.78	0.65
1:F:297:VAL:HG13	1:F:326:VAL:HG22	1.79	0.65
2:G:7:VAL:HB	2:G:78:PHE:HD2	1.60	0.65
3:A:708:ASP:OD1	3:A:709:ALA:N	2.29	0.65
1:B:1416:GLU:HA	1:B:1419:LYS:HG2	1.77	0.65
1:F:463:PRO:HD2	1:F:503:GLN:HB3	1.79	0.65
1:B:517:ILE:HD12	1:B:522:VAL:HG23	1.77	0.65
3:E:603:SER:N	3:E:606:ASP:OD1	2.29	0.65
3:A:256:ASP:HA	3:A:259:ARG:HD3	1.79	0.65
3:A:358:LYS:HA	3:A:406:GLU:HA	1.78	0.65
1:B:446:ILE:HG12	1:B:626:ILE:HG23	1.78	0.65
1:B:789:ASN:HB3	1:B:793:GLN:NE2	2.10	0.65
1:F:555:MET:HA	1:F:561:THR:HA	1.79	0.65
1:F:1568:LYS:O	1:F:1574:LYS:NZ	2.30	0.65
3:E:588:TYR:N	3:E:603:SER:OG	2.29	0.65
3:E:591:LEU:HD21	3:E:604:LEU:H	1.62	0.65
1:B:44:TRP:CZ2	1:B:60:PRO:HG3	2.32	0.65
1:B:414:GLN:O	1:B:423:ARG:NH2	2.30	0.65
1:B:1525:THR:HA	1:B:1528:ARG:HD3	1.79	0.65
1:F:98:TRP:HA	1:F:101:ILE:HG22	1.78	0.65
1:F:99:ALA:HA	1:F:102:TRP:CD1	2.32	0.65
1:F:590:GLY:N	1:F:594:GLU:OE2	2.27	0.65
3:A:608:LEU:HD11	3:A:613:ILE:HD11	1.79	0.65
1:B:31:ILE:HG22	3:A:701:LEU:HD23	1.79	0.65
1:F:1534:GLN:HB3	1:F:1538:TRP:CH2	2.31	0.65
2:G:100:GLU:HB2	2:G:104:HIS:HE1	1.62	0.65
3:A:423:MET:HG2	3:A:481:MET:HE3	1.78	0.65
1:B:219:ILE:O	1:B:222:TYR:OH	2.15	0.64
1:B:1209:THR:O	1:B:1213:GLN:CB	2.44	0.64
1:B:1391:ARG:NH1	1:B:1428:CYS:O	2.30	0.64
1:F:166:ARG:HD3	1:F:173:LEU:HB2	1.79	0.64
2:G:49:LYS:NZ	2:G:50:PRO:O	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:LEU:HD22	1:B:83:GLY:HA2	1.79	0.64
2:C:5:LYS:HE2	2:C:56:TRP:HZ2	1.62	0.64
1:F:25:VAL:HG23	1:F:57:GLY:HA2	1.78	0.64
1:F:757:LEU:HA	1:F:760:LEU:HG	1.79	0.64
4:D:78:PHE:HB2	4:D:110:ILE:HG12	1.78	0.64
1:B:1275:ASP:OD2	1:B:1292:THR:OG1	2.15	0.64
1:B:1335:TYR:HA	1:B:1338:LEU:HD23	1.77	0.64
1:B:1549:MET:O	2:C:39:ASN:ND2	2.30	0.64
1:F:1225:VAL:HG21	1:F:1499:LEU:HD21	1.79	0.64
1:F:1452:ASN:OD1	1:F:1453:TYR:N	2.30	0.64
3:A:216:TYR:CE1	3:A:250:LEU:HA	2.32	0.64
3:A:566:ASN:OD1	3:A:633:GLN:NE2	2.31	0.64
3:A:616:VAL:HB	3:A:644:ILE:HG12	1.79	0.64
1:B:1183:HIS:HE1	1:B:1186:LEU:HB3	1.62	0.64
1:F:1536:HIS:CG	1:F:1542:LEU:HD22	2.32	0.64
3:E:564:LYS:HE3	3:E:590:ASP:HA	1.78	0.64
3:A:564:LYS:HB2	3:A:567:ALA:HB2	1.79	0.64
1:F:181:ILE:HA	1:F:184:PHE:HB3	1.80	0.64
1:F:1117:GLU:OE1	1:F:1119:GLU:N	2.30	0.64
3:E:719:ASN:ND2	3:E:721:ASP:OD2	2.31	0.64
1:B:789:ASN:HA	1:B:792:ARG:HD2	1.79	0.64
1:F:187:HIS:HD1	1:F:1006:TRP:HD1	1.46	0.64
1:F:551:PHE:HE1	1:F:579:MET:HE1	1.62	0.64
1:F:979:ARG:O	1:F:982:ILE:HG22	1.98	0.64
1:B:566:ARG:NH2	1:B:568:ASP:OD1	2.30	0.64
2:C:77:VAL:HG12	2:C:109:PRO:HG2	1.78	0.64
1:F:1029:THR:HB	1:F:1033:MET:HE3	1.79	0.64
1:F:1129:PHE:HZ	1:F:1183:HIS:HB3	1.63	0.64
1:F:1618:LEU:HD22	1:F:1621:ARG:HH21	1.62	0.64
2:G:5:LYS:NZ	2:G:73:PRO:O	2.30	0.64
2:G:23:TYR:HB2	2:G:165:LEU:HD21	1.80	0.64
3:A:486:GLU:O	3:A:490:ARG:HG2	1.98	0.64
1:B:1166:GLU:O	1:B:1169:LYS:HG2	1.97	0.64
2:C:98:TYR:HE1	2:C:149:ILE:HD13	1.61	0.64
2:C:116:LYS:HD3	2:C:119:LEU:HD12	1.80	0.64
1:F:1241:ILE:HA	1:F:1244:LEU:HD12	1.80	0.64
1:F:1370:GLN:OE1	1:F:1377:ARG:NH1	2.31	0.64
3:A:38:CYS:HB3	3:A:43:LEU:HB2	1.78	0.64
1:B:225:TYR:OH	1:B:227:ASN:ND2	2.27	0.64
1:B:811:LYS:HD2	1:B:812:ILE:HG13	1.80	0.64
2:C:52:ASN:OD1	2:C:53:LEU:N	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:266:LEU:HG	3:A:271:LEU:HB2	1.78	0.64
3:A:401:GLU:O	3:A:405:ARG:NE	2.30	0.64
3:A:685:ASP:OD1	3:A:686:LEU:N	2.31	0.64
1:B:1313:MET:HE1	1:B:1496:PRO:HG3	1.79	0.64
1:F:110:LYS:HD3	1:F:113:LEU:HD12	1.80	0.64
1:F:1438:PRO:HB3	1:F:1454:TYR:CE2	2.33	0.64
3:A:501:GLN:OE1	3:A:505:LYS:NZ	2.30	0.64
1:B:166:ARG:NH2	1:B:169:ASN:OD1	2.31	0.63
1:B:1555:VAL:HG21	1:B:1622:LEU:HD22	1.80	0.63
1:F:1211:ILE:HD13	1:F:1220:ARG:HG2	1.79	0.63
2:G:129:LEU:HB3	2:G:134:LEU:O	1.98	0.63
1:B:132:LEU:O	3:A:703:ASN:ND2	2.30	0.63
2:C:124:ASP:O	2:C:127:GLU:HG2	1.98	0.63
1:B:11:LYS:HB2	1:B:70:THR:HA	1.80	0.63
1:B:19:TYR:HB2	1:B:59:PHE:HE1	1.63	0.63
1:B:468:VAL:N	1:B:498:SER:OG	2.31	0.63
1:B:853:VAL:O	1:B:857:LEU:HG	1.99	0.63
1:B:940:VAL:HG13	1:B:992:MET:HE1	1.79	0.63
1:B:1627:ARG:HA	1:B:1630:LYS:HB2	1.80	0.63
1:F:187:HIS:ND1	1:F:1006:TRP:HD1	1.96	0.63
1:F:879:LEU:CG	1:F:931:ARG:HH22	2.11	0.63
1:F:1284:GLN:HG2	1:F:1286:ASP:H	1.63	0.63
3:A:26:GLN:OE1	3:A:66:ARG:NH1	2.30	0.63
1:F:102:TRP:HA	1:F:105:LEU:HG	1.81	0.63
3:A:21:LEU:HD13	4:D:37:PHE:CZ	2.33	0.63
1:B:1028:LEU:HD12	1:B:1043:TRP:CZ2	2.34	0.63
1:B:1165:ASP:O	1:B:1168:TYR:HB3	1.99	0.63
1:F:1506:GLN:NE2	1:F:1507:ILE:O	2.31	0.63
1:B:153:ASP:HB2	1:B:194:ILE:HD11	1.79	0.63
1:B:1274:SER:HB2	1:B:1293:GLN:HE21	1.64	0.63
1:F:93:SER:HB2	1:F:96:ARG:NH1	2.14	0.63
1:F:226:VAL:HB	1:F:279:ALA:HB3	1.80	0.63
1:F:1061:LEU:HA	1:F:1064:PHE:CZ	2.34	0.63
1:F:1301:TYR:CE2	1:F:1320:LEU:HD12	2.31	0.63
1:F:233:CYS:SG	1:F:234:ASN:N	2.71	0.63
2:G:174:ARG:HA	2:G:177:LEU:HB2	1.80	0.63
3:A:562:PHE:N	3:A:575:TRP:O	2.32	0.63
1:B:72:GLU:OE1	1:B:75:GLY:N	2.28	0.63
1:B:707:ILE:O	1:B:711:HIS:NE2	2.32	0.63
4:D:29:PRO:HB3	4:D:33:ILE:HD11	1.79	0.63
1:B:855:GLN:OE1	1:B:855:GLN:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1181:ARG:NH1	1:B:1191:GLU:OE2	2.32	0.63
1:B:1628:GLU:O	1:B:1632:LYS:HG2	1.98	0.63
1:F:761:LYS:HE3	1:F:765:ARG:NE	2.14	0.63
1:F:1002:TYR:HB3	1:F:1006:TRP:HE3	1.64	0.63
3:E:578:ARG:NH2	3:E:598:GLU:OE1	2.32	0.63
3:A:205:LEU:HB3	3:A:223:ILE:HD11	1.79	0.63
1:B:73:ASP:O	1:B:79:THR:N	2.32	0.62
1:B:945:ARG:HE	1:B:946:GLN:H	1.47	0.62
1:F:95:LEU:HA	1:F:98:TRP:HD1	1.63	0.62
1:F:761:LYS:HE3	1:F:765:ARG:HE	1.63	0.62
1:F:930:GLU:HG2	1:F:972:TYR:HB3	1.80	0.62
1:F:1478:GLU:HB2	1:F:1482:MET:HE3	1.81	0.62
3:E:529:GLN:HG3	3:E:534:LEU:HD11	1.80	0.62
3:A:13:GLU:N	3:A:75:LEU:O	2.25	0.62
3:A:268:GLN:HG3	3:A:269:LYS:HD2	1.80	0.62
1:B:1233:GLU:O	1:B:1235:LYS:NZ	2.31	0.62
1:B:1533:VAL:HG23	1:B:1606:ILE:HG13	1.81	0.62
2:C:65:ASP:HA	2:C:68:ARG:HE	1.63	0.62
1:F:460:LYS:HD2	1:F:464:LYS:HG2	1.82	0.62
1:B:11:LYS:HG3	1:B:70:THR:HG23	1.80	0.62
1:B:263:GLY:HA2	1:B:269:LYS:HG3	1.82	0.62
1:B:493:ILE:HD11	1:B:496:TYR:HD1	1.63	0.62
1:B:519:ILE:HG21	1:B:630:LYS:HB3	1.81	0.62
1:B:909:ILE:HG13	1:B:910:LEU:N	2.15	0.62
1:B:1060:GLN:OE1	1:B:1060:GLN:N	2.32	0.62
2:C:93:VAL:HA	2:C:97:TRP:HB2	1.81	0.62
3:A:409:HIS:HA	3:A:473:THR:HA	1.81	0.62
1:B:16:ILE:HG21	3:A:707:PRO:HG2	1.81	0.62
1:B:92:THR:HA	1:B:95:LEU:HD12	1.80	0.62
1:B:719:TYR:HD1	1:B:723:HIS:HB2	1.63	0.62
1:F:166:ARG:HH21	1:F:169:ASN:HD21	1.48	0.62
1:F:855:GLN:OE1	1:F:855:GLN:N	2.29	0.62
3:E:685:ASP:OD1	3:E:686:LEU:N	2.33	0.62
1:B:330:THR:HG22	1:B:334:HIS:CE1	2.35	0.62
1:B:579:MET:HA	1:B:585:TYR:HB3	1.81	0.62
2:C:59:ALA:O	2:C:68:ARG:NH2	2.32	0.62
1:F:1091:TRP:CZ2	1:F:1098:LYS:HG2	2.35	0.62
3:A:466:THR:O	3:A:470:MET:N	2.33	0.62
4:D:17:THR:HG21	4:D:33:ILE:HG21	1.80	0.62
1:F:5:ILE:HB	1:F:40:MET:HB3	1.82	0.62
1:F:306:MET:SD	1:F:320:ARG:NH2	2.73	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:929:MET:SD	1:F:968:HIS:HB3	2.40	0.62
1:F:1367:TYR:N	1:F:1379:LYS:O	2.33	0.62
1:B:651:LYS:HB3	1:B:689:TYR:CE1	2.34	0.62
2:C:14:VAL:HG13	2:C:116:LYS:NZ	2.15	0.62
2:C:111:ILE:HG12	2:C:153:LYS:HB3	1.82	0.62
1:F:1388:TYR:HB2	2:G:45:MET:HE3	1.81	0.62
3:A:211:ASN:HB2	3:A:215:LEU:HD12	1.82	0.62
3:A:548:ILE:O	3:A:552:ARG:HG2	2.00	0.62
1:B:463:PRO:HD2	1:B:503:GLN:HB3	1.82	0.62
1:B:1216:SER:OG	1:B:1401:GLN:NE2	2.33	0.62
1:F:1149:ASN:OD1	1:F:1236:ARG:NH2	2.33	0.62
1:F:1543:SER:OG	1:F:1545:HIS:ND1	2.25	0.62
1:B:759:ALA:O	1:B:763:LEU:HG	2.00	0.62
1:B:816:ALA:O	1:B:820:LEU:HG	2.00	0.62
1:B:1536:HIS:CD2	1:B:1542:LEU:HD13	2.34	0.62
1:F:876:GLU:OE1	1:F:876:GLU:N	2.30	0.62
1:F:913:LEU:HD22	1:F:925:ILE:HG22	1.80	0.62
1:F:972:TYR:HA	1:F:975:THR:HB	1.82	0.62
2:G:17:THR:O	2:G:21:ILE:HG22	2.00	0.62
3:A:524:ASN:OD1	3:A:525:GLN:NE2	2.32	0.62
1:B:1305:ILE:HD11	1:B:1320:LEU:HB2	1.82	0.61
1:F:964:MET:HE1	1:F:969:TYR:CD2	2.35	0.61
1:F:1196:LEU:O	1:F:1200:LEU:HG	2.00	0.61
3:A:225:ILE:HG21	3:A:265:ILE:HG21	1.80	0.61
3:A:320:GLN:HA	3:A:323:ILE:HG22	1.81	0.61
1:B:1146:MET:HA	1:B:1149:ASN:HD22	1.64	0.61
1:F:1032:PHE:HA	1:F:1036:ALA:HB3	1.81	0.61
1:F:1115:THR:O	1:F:1121:ARG:NH2	2.33	0.61
3:E:607:LYS:HG3	3:E:609:PRO:HD3	1.82	0.61
1:B:1133:GLN:OE1	1:B:1137:ASN:ND2	2.31	0.61
1:F:166:ARG:HB2	1:F:174:ASP:H	1.65	0.61
1:F:1381:PHE:HA	1:F:1503:GLU:HA	1.82	0.61
1:B:101:ILE:HG21	1:B:159:LEU:HD13	1.82	0.61
1:B:486:PRO:HA	1:B:513:VAL:HG12	1.81	0.61
1:B:527:ILE:N	1:B:552:VAL:O	2.30	0.61
1:B:1573:GLU:O	1:B:1577:GLN:NE2	2.33	0.61
1:B:1607:HIS:O	1:B:1611:LEU:N	2.33	0.61
2:G:69:PRO:HA	2:G:72:TYR:CD2	2.35	0.61
2:G:164:GLY:O	2:G:168:VAL:N	2.30	0.61
3:A:256:ASP:HA	3:A:259:ARG:HB2	1.82	0.61
3:A:564:LYS:HE3	3:A:590:ASP:HA	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:707:ILE:HA	1:B:710:GLN:CD	2.25	0.61
1:B:1467:PRO:HG3	2:C:33:ILE:HD13	1.83	0.61
1:B:1495:PHE:HE1	1:B:1502:PHE:HD2	1.47	0.61
1:F:773:LEU:HA	1:F:776:ARG:HG2	1.82	0.61
1:F:1487:THR:HA	1:F:1509:THR:HA	1.81	0.61
3:A:420:LEU:HD23	3:A:481:MET:HE1	1.83	0.61
1:B:1367:TYR:O	1:B:1378:ASN:N	2.31	0.61
2:C:129:LEU:HB3	2:C:134:LEU:O	2.00	0.61
1:F:30:GLN:HB2	3:E:697:ARG:HH21	1.65	0.61
1:F:643:TRP:HZ3	1:F:683:MET:HE1	1.65	0.61
3:A:270:GLN:HG2	3:A:273:SER:HB3	1.81	0.61
3:A:644:ILE:H	3:A:652:LEU:HB2	1.64	0.61
4:D:171:GLU:HA	4:D:174:ARG:HG2	1.82	0.61
1:B:98:TRP:O	1:B:101:ILE:HG22	1.99	0.61
1:F:1131:MET:O	1:F:1135:GLU:HG3	2.00	0.61
1:B:882:LEU:HA	1:B:885:GLN:HE21	1.65	0.61
1:B:1439:PRO:HA	1:B:1442:LYS:NZ	2.15	0.61
1:B:1590:LYS:HB3	1:B:1639:VAL:HG12	1.81	0.61
1:F:817:LEU:HD22	1:F:856:LYS:HD3	1.82	0.61
3:A:129:LEU:O	3:A:133:VAL:HG22	2.01	0.61
1:B:102:TRP:HA	1:B:105:LEU:HG	1.82	0.61
1:B:501:TYR:CG	1:B:507:PRO:HB3	2.35	0.61
1:B:1156:ASP:OD1	1:B:1243:TYR:OH	2.18	0.61
1:B:1277:PRO:HG3	1:B:1292:THR:HA	1.83	0.61
2:C:84:LEU:HD11	2:C:156:GLU:HG2	1.82	0.61
1:F:1390:ARG:HH11	2:G:44:VAL:HG21	1.66	0.61
1:F:1466:ARG:NH1	2:G:31:GLU:OE1	2.34	0.61
2:G:146:ALA:O	2:G:150:GLY:N	2.33	0.61
3:E:670:ASN:O	3:E:674:GLY:N	2.34	0.61
4:D:159:ALA:N	6:D:202:GTP:O6	2.34	0.61
1:F:1196:LEU:O	1:F:1199:SER:OG	2.15	0.61
3:A:719:ASN:ND2	3:A:721:ASP:OD2	2.34	0.61
1:B:241:LEU:HB2	1:B:260:ILE:HB	1.83	0.60
1:B:569:LEU:O	1:B:620:PHE:N	2.33	0.60
1:B:1195:LEU:O	1:B:1198:SER:OG	2.19	0.60
1:F:739:PHE:O	1:F:749:LYS:NZ	2.33	0.60
1:F:1626:PHE:HD2	1:F:1627:ARG:HD3	1.66	0.60
3:A:237:GLN:O	3:A:241:THR:HG23	2.01	0.60
1:F:147:LYS:O	1:F:151:LYS:HG2	2.02	0.60
1:F:330:THR:HA	1:F:333:ILE:HG12	1.81	0.60
1:F:638:LEU:O	1:F:642:ASN:ND2	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1536:HIS:O	1:F:1540:ARG:NH2	2.33	0.60
3:A:544:ILE:O	3:A:548:ILE:HG12	2.00	0.60
4:D:14:VAL:O	4:D:116:LYS:NZ	2.33	0.60
1:B:23:GLN:HG2	1:B:58:ILE:HB	1.83	0.60
1:B:246:TYR:CZ	1:B:383:LEU:HD21	2.35	0.60
1:B:247:ASP:HB2	1:B:254:ILE:HD11	1.82	0.60
1:B:536:SER:OG	1:B:537:GLN:OE1	2.16	0.60
1:B:1216:SER:OG	1:B:1219:ASN:OD1	2.18	0.60
1:B:1478:GLU:N	1:B:1478:GLU:OE2	2.32	0.60
1:B:1630:LYS:O	1:B:1634:GLU:HG2	2.01	0.60
1:F:44:TRP:CZ2	1:F:60:PRO:HG3	2.37	0.60
1:F:761:LYS:NZ	1:F:825:ASN:HD21	1.98	0.60
1:F:769:GLN:OE1	1:F:776:ARG:NH2	2.34	0.60
1:F:1164:GLY:HA3	1:F:1168:TYR:HD1	1.64	0.60
3:A:451:SER:HA	3:A:454:GLU:HG3	1.83	0.60
1:B:471:SER:HB2	1:B:479:LEU:HD13	1.83	0.60
1:B:528:ARG:HA	1:B:551:PHE:HA	1.83	0.60
1:B:1391:ARG:NH2	2:C:28:PHE:HA	2.16	0.60
1:F:1111:GLU:O	1:F:1163:ARG:NH2	2.35	0.60
1:B:751:GLU:OE1	1:B:751:GLU:N	2.21	0.60
1:B:806:LEU:HD12	1:B:813:LYS:HD3	1.84	0.60
1:B:1557:PRO:HB2	1:B:1561:GLY:HA2	1.84	0.60
1:F:302:ARG:HG2	1:F:322:PHE:HB2	1.82	0.60
1:F:831:PHE:HE2	1:F:835:GLU:HB3	1.65	0.60
1:F:1512:ILE:HG23	1:F:1516:GLU:HB2	1.84	0.60
3:A:280:ILE:HG21	3:A:443:PRO:HB3	1.84	0.60
1:B:761:LYS:HG3	1:B:765:ARG:HE	1.65	0.60
1:B:1468:PHE:HB3	1:B:1483:TRP:O	2.02	0.60
1:F:662:GLY:HA2	1:F:665:ILE:HD12	1.83	0.60
1:F:938:ARG:HA	1:F:941:ILE:HD12	1.83	0.60
1:F:1436:SER:HB3	1:F:1454:TYR:HB3	1.82	0.60
2:G:87:PRO:HG2	2:G:135:THR:H	1.67	0.60
3:A:387:PHE:CE1	3:A:457:CYS:HB3	2.36	0.60
1:B:572:TYR:HB2	1:B:579:MET:HE1	1.83	0.60
1:B:1463:ARG:HA	1:B:1487:THR:O	2.02	0.60
1:F:95:LEU:HD23	1:F:98:TRP:CD1	2.34	0.60
1:F:140:GLU:OE1	1:F:140:GLU:N	2.35	0.60
1:F:166:ARG:HB3	1:F:171:ASN:HA	1.84	0.60
3:A:160:THR:HG22	3:A:200:ARG:HD2	1.84	0.60
3:A:692:MET:O	3:A:696:LEU:HG	2.00	0.60
1:B:498:SER:HB2	1:B:509:TRP:NE1	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:772:VAL:HA	1:B:775:LEU:HD12	1.83	0.60
1:B:1601:THR:HB	1:B:1605:ARG:HH21	1.66	0.60
2:C:69:PRO:HA	2:C:72:TYR:CG	2.37	0.60
1:F:127:TRP:HD1	1:F:130:GLN:NE2	1.99	0.60
1:F:449:THR:HB	1:F:623:ALA:HB3	1.81	0.60
1:F:594:GLU:HA	1:F:597:GLU:HG2	1.84	0.60
3:A:133:VAL:HB	3:A:155:LEU:HD13	1.84	0.60
3:A:327:LEU:HD21	3:A:385:LEU:HD23	1.84	0.60
3:A:587:HIS:ND1	3:A:606:ASP:OD1	2.34	0.60
1:B:591:THR:OG1	1:B:593:MET:SD	2.59	0.60
1:F:93:SER:HB2	1:F:96:ARG:HH11	1.66	0.60
1:F:1545:HIS:CD2	2:G:5:LYS:HE3	2.36	0.60
2:G:82:PHE:O	2:G:115:THR:OG1	2.14	0.60
3:E:692:MET:O	3:E:696:LEU:HG	2.00	0.60
3:A:288:ASN:HB2	3:A:439:ASN:HD21	1.66	0.60
3:A:309:MET:HB3	3:A:375:PRO:HB3	1.83	0.60
1:B:485:HIS:HB2	1:B:514:LYS:HB3	1.84	0.60
1:B:900:GLU:O	1:B:904:GLN:NE2	2.34	0.60
1:F:741:VAL:HA	1:F:753:LEU:HD11	1.83	0.60
1:B:256:GLU:HG3	1:B:488:ALA:HB2	1.84	0.59
1:B:757:LEU:HD12	1:B:816:ALA:HA	1.83	0.59
1:B:761:LYS:HD3	1:B:822:SER:HB2	1.84	0.59
1:B:993:PHE:O	1:B:997:ILE:HG12	2.01	0.59
1:F:764:PHE:CD1	1:F:826:ASP:HB2	2.36	0.59
1:F:1059:LEU:HD11	1:F:1117:GLU:HA	1.83	0.59
1:F:1164:GLY:HA3	1:F:1168:TYR:CD1	2.36	0.59
3:A:185:ALA:HA	3:A:188:VAL:HG12	1.84	0.59
3:A:555:ARG:O	3:A:559:GLY:N	2.32	0.59
1:B:5:ILE:H	1:B:40:MET:H	1.50	0.59
1:B:128:ARG:NH2	3:A:699:LEU:O	2.32	0.59
1:B:965:ASP:HB3	1:B:968:HIS:CD2	2.36	0.59
1:B:994:LYS:HB2	1:B:1049:LEU:HD21	1.84	0.59
1:F:44:TRP:CE3	1:F:58:ILE:HG22	2.37	0.59
1:F:1111:GLU:OE1	1:F:1111:GLU:N	2.28	0.59
2:G:93:VAL:HG13	2:G:94:ARG:HD3	1.84	0.59
1:B:422:ASP:OD1	1:B:425:THR:OG1	2.15	0.59
1:B:659:GLU:N	1:B:659:GLU:OE2	2.35	0.59
1:B:1470:LYS:N	1:B:1481:THR:HB	2.17	0.59
1:F:62:THR:HG21	3:E:712:PRO:HG2	1.85	0.59
1:F:226:VAL:N	1:F:279:ALA:O	2.34	0.59
1:F:380:THR:HG22	1:F:510:TYR:CZ	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1588:LEU:O	1:F:1592:LEU:HG	2.03	0.59
1:B:1611:LEU:HD12	1:B:1615:LEU:HB3	1.83	0.59
1:F:638:LEU:HD13	1:F:641:LEU:HD12	1.83	0.59
3:A:54:ALA:HB3	3:A:74:ILE:HB	1.85	0.59
4:D:45:ALA:HA	4:D:50:THR:HA	1.82	0.59
1:B:525:CYS:HB2	1:B:554:LEU:HD12	1.84	0.59
1:B:929:MET:HG3	1:B:933:LEU:HD11	1.84	0.59
1:F:37:ILE:HD13	1:F:45:TYR:HB3	1.83	0.59
1:F:106:TYR:O	3:E:555:ARG:NH2	2.35	0.59
1:F:486:PRO:HA	1:F:513:VAL:HG12	1.84	0.59
3:E:575:TRP:HZ3	3:E:588:TYR:HB2	1.65	0.59
1:B:832:ASP:OD2	1:B:835:GLU:N	2.34	0.59
1:B:1015:ARG:HD3	1:B:1076:TYR:HD1	1.68	0.59
1:F:1098:LYS:O	1:F:1102:ILE:N	2.33	0.59
1:F:1516:GLU:HA	1:F:1519:ILE:HD12	1.85	0.59
3:A:644:ILE:HB	3:A:652:LEU:HD12	1.85	0.59
1:B:187:HIS:ND1	1:B:1006:TRP:HD1	2.01	0.59
1:B:631:LEU:O	1:B:667:LYS:NZ	2.22	0.59
1:B:1264:LEU:HD21	1:B:1300:LEU:HD22	1.85	0.59
1:F:44:TRP:HZ2	3:E:713:ILE:HG23	1.68	0.59
3:A:408:LYS:HG3	3:A:474:SER:H	1.68	0.59
4:D:37:PHE:HA	4:D:57:ASP:O	2.03	0.59
1:B:237:GLU:HB2	1:B:308:LEU:HD21	1.85	0.59
1:B:706:ASP:HB3	1:B:709:PHE:HD2	1.67	0.59
1:B:941:ILE:O	1:B:944:ASN:HB2	2.03	0.59
1:B:972:TYR:C	1:B:975:THR:H	2.11	0.59
1:F:1197:VAL:O	1:F:1201:LEU:HG	2.03	0.59
3:A:591:LEU:HD21	3:A:604:LEU:H	1.67	0.59
1:B:73:ASP:HB2	1:B:86:PRO:HD3	1.85	0.59
1:B:450:LEU:HD23	1:B:622:ILE:HG12	1.84	0.59
1:B:1043:TRP:HA	1:B:1046:TYR:HB3	1.85	0.59
1:B:1470:LYS:HB3	1:B:1483:TRP:CD1	2.38	0.59
3:A:121:ILE:HG23	3:A:171:VAL:HB	1.85	0.59
3:A:419:GLU:HA	3:A:422:LYS:HG2	1.85	0.59
1:B:102:TRP:HB2	1:B:114:PHE:CE1	2.38	0.59
1:B:287:MET:HA	1:B:290:ILE:HG12	1.84	0.59
1:B:1284:GLN:HE22	1:B:1291:TYR:HE2	1.51	0.59
2:C:129:LEU:HA	2:C:132:LYS:HG2	1.85	0.59
1:F:826:ASP:HA	1:F:829:LEU:HD13	1.85	0.59
1:F:1344:LYS:O	1:F:1347:SER:OG	2.18	0.59
3:A:104:LEU:HD22	3:A:132:MET:HE1	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:66:ARG:NH1	4:D:67:LEU:HB2	2.18	0.59
4:D:117:LYS:HB3	4:D:156:GLU:HB3	1.85	0.59
1:B:119:GLN:HE21	1:B:122:TYR:HE2	1.50	0.58
1:B:569:LEU:HD12	1:B:620:PHE:HD2	1.68	0.58
1:B:934:ARG:NH1	1:B:938:ARG:HB2	2.18	0.58
1:F:1:MET:HG2	3:E:716:GLU:HB3	1.84	0.58
1:F:863:ILE:O	1:F:867:THR:OG1	2.20	0.58
1:B:7:THR:HG22	1:B:9:ARG:H	1.68	0.58
1:B:79:THR:HA	1:B:85:LEU:HD22	1.85	0.58
1:B:654:LEU:HA	1:B:657:LEU:HG	1.84	0.58
1:B:1357:ARG:HH21	1:B:1453:TYR:HB2	1.67	0.58
1:F:1043:TRP:NE1	1:F:1090:MET:HE2	2.18	0.58
1:F:1177:LEU:O	1:F:1181:ARG:HD3	2.03	0.58
2:G:102:ARG:HD3	2:G:149:ILE:HD11	1.85	0.58
1:B:65:HIS:ND1	1:B:65:HIS:O	2.37	0.58
1:B:926:GLN:O	1:B:930:GLU:HG3	2.04	0.58
1:B:966:ASP:HA	1:B:969:TYR:CD1	2.38	0.58
2:C:87:PRO:HA	2:C:90:PHE:CD2	2.38	0.58
1:F:127:TRP:O	1:F:131:ILE:HG12	2.04	0.58
1:F:138:LYS:HA	1:F:141:LEU:HD13	1.84	0.58
1:F:1289:TYR:HD2	1:F:1290:VAL:HG22	1.68	0.58
2:G:68:ARG:HG2	2:G:69:PRO:HD3	1.84	0.58
3:A:698:LEU:O	3:A:702:GLU:HG2	2.03	0.58
1:B:556:ASN:N	1:B:560:THR:O	2.35	0.58
1:B:713:ASN:HA	1:B:716:LEU:HD12	1.84	0.58
1:B:871:GLN:NE2	1:B:875:ARG:HH11	2.00	0.58
1:B:958:ILE:HG13	1:B:959:ALA:N	2.18	0.58
1:B:1094:LEU:HB3	1:B:1098:LYS:HE3	1.83	0.58
1:B:1467:PRO:HG2	2:C:31:GLU:O	2.03	0.58
1:F:86:PRO:HA	1:F:89:GLN:HE21	1.69	0.58
1:F:1102:ILE:HD11	1:F:1134:CYS:HB2	1.85	0.58
3:A:144:GLN:HA	3:A:147:MET:HB3	1.85	0.58
3:A:469:GLU:O	3:A:470:MET:HE2	2.04	0.58
1:B:654:LEU:HD13	1:B:692:LEU:HB2	1.84	0.58
1:B:772:VAL:HG23	1:B:776:ARG:HH22	1.67	0.58
1:B:1452:ASN:OD1	1:B:1453:TYR:N	2.35	0.58
1:F:1010:ASN:OD1	1:F:1013:GLN:NE2	2.36	0.58
1:B:10:GLN:NE2	1:B:38:LEU:O	2.33	0.58
1:B:553:LYS:HD2	1:B:586:LEU:HD22	1.86	0.58
1:B:652:HIS:O	1:B:656:LYS:HG2	2.03	0.58
1:B:1219:ASN:OD1	1:B:1401:GLN:NE2	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1407:LYS:HG3	1:B:1426:MET:SD	2.44	0.58
3:A:261:GLU:O	3:A:265:ILE:HG12	2.02	0.58
1:B:4:TRP:O	3:A:724:TYR:N	2.34	0.58
1:B:819:TYR:O	1:B:822:SER:OG	2.18	0.58
1:B:976:PHE:HB2	1:B:982:ILE:HD12	1.86	0.58
1:B:1344:LYS:O	1:B:1347:SER:OG	2.14	0.58
2:C:9:VAL:HG22	2:C:78:PHE:CZ	2.37	0.58
1:F:101:ILE:O	1:F:105:LEU:HG	2.03	0.58
1:F:1530:SER:O	1:F:1534:GLN:HG2	2.04	0.58
1:B:965:ASP:HA	1:B:1019:ARG:NH2	2.18	0.58
1:B:1207:TYR:O	1:B:1211:ILE:HG12	2.04	0.58
2:C:128:LYS:HA	2:C:131:GLU:HG2	1.85	0.58
2:C:138:THR:H	2:C:141:GLN:NE2	2.02	0.58
2:G:117:LEU:HD22	2:G:156:GLU:HG2	1.85	0.58
3:A:9:LYS:N	3:A:71:ASN:OD1	2.37	0.58
3:A:260:GLN:HG3	3:A:304:LEU:HD12	1.85	0.58
3:A:489:MET:HB3	3:A:490:ARG:HH21	1.68	0.58
3:A:588:TYR:N	3:A:603:SER:OG	2.36	0.58
1:B:62:THR:HG22	3:A:714:PRO:HD3	1.86	0.58
1:F:680:MET:HE1	1:F:690:ASP:HA	1.86	0.58
1:F:34:THR:HB	1:F:50:LEU:HB2	1.86	0.58
1:F:302:ARG:H	1:F:322:PHE:HB2	1.69	0.58
1:F:789:ASN:HB3	1:F:793:GLN:HE22	1.69	0.58
1:F:1565:ASN:O	1:F:1568:LYS:HG3	2.04	0.58
2:G:128:LYS:HA	2:G:131:GLU:HG2	1.85	0.58
1:B:18:ASN:HD21	3:A:536:LEU:HA	1.69	0.57
1:B:41:TYR:HD2	1:B:44:TRP:HB2	1.68	0.57
1:B:80:VAL:HG22	1:B:85:LEU:HD11	1.84	0.57
1:B:743:ASN:HB2	1:B:749:LYS:HD2	1.85	0.57
1:B:1217:LYS:HG3	1:B:1220:ARG:HH21	1.68	0.57
1:F:156:ASN:O	1:F:160:GLY:N	2.37	0.57
2:G:7:VAL:HG22	2:G:56:TRP:CG	2.39	0.57
3:A:445:PHE:HA	3:A:451:SER:OG	2.04	0.57
1:B:332:ILE:HG12	1:B:337:VAL:HB	1.86	0.57
1:B:1238:ASP:OD1	1:B:1239:ILE:N	2.37	0.57
2:C:146:ALA:O	2:C:150:GLY:N	2.37	0.57
1:F:376:ASN:HD22	1:F:504:VAL:HG22	1.69	0.57
1:F:845:GLN:HE22	1:F:881:LEU:HD12	1.68	0.57
1:F:914:ASP:HB2	1:F:963:GLN:CD	2.29	0.57
1:F:1372:PHE:HB2	1:F:1377:ARG:HA	1.86	0.57
1:F:1391:ARG:NH2	2:G:27:ALA:O	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1466:ARG:O	1:F:1484:ILE:HA	2.05	0.57
1:B:46:ARG:HA	1:B:57:GLY:O	2.05	0.57
1:B:224:LEU:HA	1:B:405:LEU:HA	1.86	0.57
1:B:257:ASN:O	1:B:488:ALA:N	2.35	0.57
1:B:538:GLU:OE1	1:B:542:LYS:NZ	2.33	0.57
1:B:1631:GLU:HA	1:B:1634:GLU:HG2	1.87	0.57
1:F:411:THR:O	1:F:415:LYS:HB2	2.05	0.57
1:F:1206:ASP:HA	1:F:1209:THR:HG22	1.85	0.57
3:A:9:LYS:HD3	4:D:38:ASP:OD1	2.05	0.57
3:A:302:PHE:CE1	3:A:430:VAL:HG22	2.39	0.57
3:A:474:SER:HA	3:A:477:PHE:HB2	1.85	0.57
1:B:228:PHE:CD1	1:B:277:LEU:HD13	2.39	0.57
1:B:320:ARG:CZ	1:B:500:VAL:HB	2.34	0.57
1:B:400:TRP:HZ2	4:D:127:ARG:HB2	1.68	0.57
1:B:744:ALA:HA	1:B:753:LEU:HD11	1.87	0.57
1:F:60:PRO:HG2	1:F:63:TYR:CD2	2.39	0.57
1:F:1461:GLN:OE1	1:F:1490:THR:HG22	2.04	0.57
3:A:379:LEU:O	3:A:383:ASN:ND2	2.37	0.57
3:A:485:LYS:HG2	3:A:489:MET:HE2	1.86	0.57
3:A:623:PRO:O	3:A:627:GLU:N	2.36	0.57
3:A:687:ASP:OD1	3:A:688:THR:N	2.37	0.57
1:B:19:TYR:OH	1:B:44:TRP:HH2	1.84	0.57
1:B:934:ARG:HH12	1:B:938:ARG:HB2	1.69	0.57
1:B:1568:LYS:O	1:B:1572:THR:OG1	2.21	0.57
1:F:1623:SER:HB3	1:F:1627:ARG:NH2	2.18	0.57
1:F:1628:GLU:O	1:F:1632:LYS:HG2	2.04	0.57
4:D:8:VAL:HG21	4:D:20:LEU:HD21	1.87	0.57
1:B:106:TYR:HE2	3:A:550:GLN:HE22	1.52	0.57
1:B:1040:LEU:HA	1:B:1043:TRP:CZ3	2.40	0.57
1:B:1217:LYS:H	1:B:1217:LYS:HD3	1.70	0.57
1:B:1582:ASP:HA	1:B:1584:GLU:HG2	1.87	0.57
2:C:41:SER:HA	2:C:54:GLY:HA2	1.86	0.57
1:F:417:PHE:HB3	1:F:420:LEU:HD12	1.85	0.57
1:F:859:CYS:O	1:F:863:ILE:HD12	2.05	0.57
1:B:879:LEU:HD21	1:B:931:ARG:HH22	1.69	0.57
1:B:1588:LEU:O	1:B:1592:LEU:HG	2.04	0.57
2:C:93:VAL:HG13	2:C:94:ARG:HD2	1.87	0.57
1:F:7:THR:HG22	1:F:9:ARG:H	1.70	0.57
1:F:1082:GLU:O	1:F:1086:ARG:HG2	2.04	0.57
1:B:181:ILE:HG22	1:B:185:LYS:NZ	2.19	0.57
1:B:701:ILE:HA	1:B:704:ILE:HD12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:994:LYS:N	1:B:1049:LEU:HD11	2.20	0.57
1:B:1079:MET:N	1:B:1079:MET:SD	2.78	0.57
1:B:1412:THR:HG21	1:B:1466:ARG:HD3	1.86	0.57
1:F:1362:TYR:CE1	1:F:1384:ARG:HG3	2.40	0.57
2:G:137:ILE:HG23	2:G:141:GLN:HE21	1.69	0.57
3:A:358:LYS:HG2	3:A:406:GLU:HG3	1.86	0.57
1:B:581:ASP:HB3	1:B:584:PHE:HB3	1.85	0.57
1:B:1062:GLU:O	1:B:1069:ARG:HD3	2.05	0.57
1:B:1102:ILE:O	1:B:1106:VAL:HG23	2.05	0.57
1:F:18:ASN:HD22	1:F:28:SER:HB3	1.70	0.57
1:F:806:LEU:HD22	1:F:851:GLN:HB3	1.86	0.57
3:E:578:ARG:HB3	3:E:587:HIS:HB2	1.87	0.57
4:D:154:TYR:OH	4:D:156:GLU:OE2	2.18	0.57
1:B:1328:TYR:HB3	1:B:1338:LEU:HD22	1.87	0.57
1:F:113:LEU:O	1:F:116:GLN:HG2	2.05	0.57
1:F:220:HIS:ND1	1:F:286:SER:HB3	2.20	0.57
1:F:1392:GLU:HA	1:F:1395:SER:HB3	1.86	0.57
4:D:6:CYS:HB3	4:D:55:LEU:HD23	1.87	0.57
1:B:203:SER:O	1:B:207:ASN:N	2.29	0.56
1:B:570:VAL:HG11	1:B:615:SER:OG	2.04	0.56
1:F:59:PHE:CD2	1:F:64:ILE:HG12	2.38	0.56
1:F:1174:LYS:O	1:F:1178:GLU:HG2	2.04	0.56
1:F:1563:PHE:O	1:F:1567:GLU:HG2	2.05	0.56
3:A:613:ILE:HD13	3:A:646:TYR:HB3	1.86	0.56
1:B:224:LEU:HD23	1:B:281:PHE:HD2	1.70	0.56
1:B:340:GLU:HG3	1:B:404:LYS:HE2	1.87	0.56
1:B:797:ALA:O	1:B:801:LEU:HG	2.06	0.56
1:F:62:THR:HG22	3:E:714:PRO:HD3	1.86	0.56
1:F:713:ASN:O	1:F:762:TYR:OH	2.22	0.56
1:F:1181:ARG:NH1	1:F:1191:GLU:OE2	2.38	0.56
1:F:1322:LYS:HA	1:F:1345:ARG:HH22	1.69	0.56
3:E:576:TYR:HB2	3:E:598:GLU:HG2	1.86	0.56
1:B:187:HIS:HB3	1:B:1006:TRP:CD1	2.40	0.56
1:B:457:LYS:HG2	1:B:463:PRO:HG3	1.87	0.56
1:B:795:PHE:HE2	1:B:843:PHE:HB2	1.68	0.56
1:B:859:CYS:O	1:B:863:ILE:HD12	2.04	0.56
1:B:883:THR:HG21	1:B:931:ARG:HE	1.70	0.56
1:B:969:TYR:O	1:B:974:SER:N	2.38	0.56
1:B:984:ASP:O	1:B:987:MET:HG3	2.05	0.56
1:B:1363:PHE:CE1	1:B:1391:ARG:HA	2.40	0.56
1:B:1506:GLN:NE2	1:B:1507:ILE:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1524:LEU:HA	1:B:1527:GLU:CD	2.29	0.56
1:B:1618:LEU:O	1:B:1622:LEU:HG	2.05	0.56
1:F:4:TRP:HD1	3:E:722:PHE:HA	1.70	0.56
1:F:1522:MET:O	1:F:1526:ASN:ND2	2.38	0.56
2:G:9:VAL:HG22	2:G:78:PHE:CZ	2.38	0.56
3:E:661:GLU:HA	3:E:664:ILE:HD12	1.87	0.56
3:A:295:TYR:OH	3:A:432:GLU:OE2	2.13	0.56
3:A:320:GLN:O	3:A:324:ILE:HG12	2.05	0.56
3:A:376:PRO:HG2	3:A:380:ALA:HB2	1.87	0.56
3:A:467:TRP:O	3:A:471:ARG:N	2.38	0.56
3:A:486:GLU:HA	3:A:489:MET:HE3	1.86	0.56
1:B:99:ALA:HB1	1:B:103:ARG:HH12	1.70	0.56
1:B:1007:MET:HA	1:B:1010:ASN:HB3	1.88	0.56
1:F:46:ARG:HA	1:F:57:GLY:O	2.05	0.56
1:F:247:ASP:HB2	1:F:254:ILE:HD11	1.87	0.56
1:F:1217:LYS:HG2	1:F:1220:ARG:NH2	2.19	0.56
1:F:1483:TRP:NE1	1:F:1514:PRO:HD3	2.20	0.56
3:E:532:PRO:HA	3:E:535:GLU:CD	2.31	0.56
3:A:126:ILE:HD13	3:A:171:VAL:HG11	1.86	0.56
3:A:642:PHE:HE2	3:A:652:LEU:HB3	1.69	0.56
3:A:642:PHE:CZ	3:A:654:PHE:HB2	2.40	0.56
1:B:64:ILE:HG22	1:B:66:LEU:N	2.21	0.56
1:B:255:SER:HA	1:B:430:LYS:HA	1.85	0.56
1:B:632:THR:HG21	1:B:637:LEU:HD23	1.86	0.56
1:B:854:ARG:NE	1:B:900:GLU:OE2	2.36	0.56
1:B:1174:LYS:O	1:B:1178:GLU:HG2	2.06	0.56
2:C:47:ASP:OD2	2:C:174:ARG:NH1	2.37	0.56
1:F:74:LEU:HD13	1:F:83:GLY:H	1.69	0.56
1:F:761:LYS:HZ3	1:F:825:ASN:HD21	1.52	0.56
1:F:1486:ARG:O	1:F:1510:GLU:N	2.39	0.56
4:D:94:ARG:HG2	4:D:145:LEU:HD13	1.88	0.56
1:F:887:SER:HA	1:F:890:LEU:HB2	1.88	0.56
1:F:1062:GLU:O	1:F:1069:ARG:HD3	2.05	0.56
1:F:1617:PRO:HG3	2:G:70:LEU:HD22	1.86	0.56
3:E:637:VAL:O	3:E:641:ALA:N	2.36	0.56
3:A:224:THR:H	3:A:227:GLN:HE21	1.54	0.56
3:A:637:VAL:HG12	3:A:640:LEU:HD12	1.87	0.56
4:D:19:LEU:HD12	4:D:165:VAL:HG13	1.88	0.56
1:B:73:ASP:O	1:B:79:THR:HG23	2.06	0.56
1:B:281:PHE:HA	1:B:428:ALA:O	2.05	0.56
1:B:578:LYS:HG2	1:B:584:PHE:HE2	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:16:ILE:HD13	3:E:711:PRO:HG2	1.87	0.56
1:F:99:ALA:HA	1:F:102:TRP:NE1	2.21	0.56
1:F:431:MET:HE2	1:F:512:THR:HG21	1.87	0.56
1:F:589:PRO:HG3	1:F:598:LYS:HD2	1.88	0.56
1:F:1391:ARG:HD2	1:F:1429:PHE:HA	1.87	0.56
1:F:1404:ASN:OD1	1:F:1424:GLN:HB2	2.06	0.56
1:F:1585:LYS:HA	1:F:1588:LEU:HD12	1.88	0.56
2:G:93:VAL:HA	2:G:97:TRP:CD1	2.40	0.56
3:E:541:GLN:HG3	3:E:545:LEU:HD23	1.87	0.56
1:B:166:ARG:HH22	1:B:168:ASP:HB2	1.71	0.56
1:B:243:MET:HB3	1:B:296:LEU:HD11	1.86	0.56
1:B:572:TYR:OH	1:B:595:MET:SD	2.54	0.56
2:C:83:SER:HA	2:C:115:THR:HB	1.86	0.56
1:F:1583:GLN:O	1:F:1586:VAL:HG12	2.06	0.56
2:G:93:VAL:HA	2:G:97:TRP:HD1	1.71	0.56
3:E:665:TRP:O	3:E:669:LEU:HG	2.05	0.56
3:A:532:PRO:HA	3:A:535:GLU:CD	2.31	0.56
1:B:59:PHE:CZ	1:B:63:TYR:HB3	2.40	0.56
1:B:472:VAL:HG13	1:B:527:ILE:HG13	1.86	0.56
1:B:1115:THR:O	1:B:1121:ARG:NH2	2.39	0.56
1:F:153:ASP:HA	1:F:156:ASN:ND2	2.20	0.56
1:F:166:ARG:HE	1:F:173:LEU:HD12	1.71	0.56
1:F:891:ASP:HB2	1:F:938:ARG:HH12	1.70	0.56
1:F:923:VAL:O	1:F:927:LEU:HG	2.06	0.56
1:F:964:MET:O	1:F:1019:ARG:NH1	2.39	0.56
1:F:1301:TYR:O	1:F:1305:ILE:HG12	2.05	0.56
1:F:1448:GLU:OE2	1:F:1448:GLU:N	2.29	0.56
3:E:708:ASP:OD1	3:E:709:ALA:N	2.38	0.56
1:B:1102:ILE:HG12	1:B:1131:MET:HB2	1.87	0.56
1:B:1316:LYS:HE3	1:B:1319:LYS:HD3	1.88	0.56
1:F:950:ILE:HA	1:F:953:PHE:HD1	1.71	0.56
1:F:970:SER:O	1:F:974:SER:OG	2.23	0.56
1:F:1275:ASP:OD2	1:F:1292:THR:OG1	2.24	0.56
3:E:620:LYS:HA	3:E:625:MET:HB3	1.88	0.56
3:A:52:GLN:HE21	3:A:76:ARG:HE	1.53	0.56
3:A:586:LEU:HB2	3:A:608:LEU:HB3	1.87	0.56
1:B:710:GLN:O	1:B:713:ASN:ND2	2.38	0.55
1:B:964:MET:O	1:B:1019:ARG:NH2	2.39	0.55
1:F:73:ASP:HB2	1:F:86:PRO:HD3	1.88	0.55
1:F:844:ILE:HG21	1:F:881:LEU:HD21	1.88	0.55
3:E:639:GLU:OE1	3:E:639:GLU:N	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:244:ILE:HA	3:A:247:ILE:HD12	1.88	0.55
3:A:309:MET:HE2	3:A:425:CYS:SG	2.46	0.55
3:A:309:MET:HE3	3:A:375:PRO:HB2	1.88	0.55
1:B:166:ARG:O	1:B:171:ASN:HA	2.06	0.55
1:B:651:LYS:HB3	1:B:689:TYR:HE1	1.70	0.55
1:B:1460:GLN:HB2	1:B:1494:THR:HG22	1.88	0.55
1:B:1607:HIS:NE2	1:B:1619:HIS:HB2	2.21	0.55
2:C:1:MET:HE3	2:C:2:GLN:H	1.71	0.55
1:F:105:LEU:HD13	1:F:110:LYS:NZ	2.21	0.55
1:F:714:PRO:O	1:F:718:THR:OG1	2.22	0.55
1:F:792:ARG:NE	1:F:835:GLU:OE1	2.36	0.55
1:F:879:LEU:HG	1:F:931:ARG:NH2	2.20	0.55
1:F:992:MET:O	1:F:996:LEU:HD23	2.06	0.55
2:G:169:PHE:HA	2:G:172:ALA:HB3	1.87	0.55
3:A:623:PRO:HA	3:A:626:LYS:HB2	1.89	0.55
1:B:11:LYS:HZ1	1:B:36:HIS:HB3	1.72	0.55
1:B:81:ILE:HD13	1:B:141:LEU:HD21	1.88	0.55
1:B:443:ARG:NH2	1:B:447:TYR:OH	2.39	0.55
1:B:569:LEU:HD11	1:B:622:ILE:HD12	1.87	0.55
1:B:1536:HIS:CE1	1:B:1610:LYS:HG2	2.42	0.55
1:F:1279:VAL:HG23	1:F:1282:LEU:HG	1.89	0.55
1:F:1378:ASN:ND2	1:F:1419:LYS:O	2.39	0.55
1:F:1612:THR:O	1:F:1616:LYS:N	2.39	0.55
3:A:26:GLN:HE22	3:A:69:ILE:HD12	1.71	0.55
1:F:875:ARG:HG2	1:F:924:HIS:CE1	2.41	0.55
1:F:958:ILE:HB	1:F:1016:VAL:HG21	1.89	0.55
1:F:1125:ILE:HD12	1:F:1172:LEU:HD23	1.88	0.55
1:F:1557:PRO:HB2	1:F:1560:MET:O	2.06	0.55
3:A:121:ILE:HD13	3:A:170:ILE:HB	1.89	0.55
3:A:533:ILE:HA	3:A:536:LEU:HD13	1.87	0.55
1:B:165:VAL:O	1:B:171:ASN:HA	2.06	0.55
1:B:247:ASP:O	1:B:251:SER:N	2.39	0.55
1:B:965:ASP:HB3	1:B:968:HIS:HD2	1.70	0.55
1:F:273:LYS:HA	1:F:276:ASN:HB3	1.89	0.55
1:F:1545:HIS:O	1:F:1548:SER:OG	2.21	0.55
2:G:96:LYS:HD2	2:G:100:GLU:HG2	1.88	0.55
4:D:116:LYS:N	4:D:157:CYS:O	2.38	0.55
1:B:37:ILE:HG23	1:B:46:ARG:C	2.31	0.55
1:B:1198:SER:O	1:B:1201:LEU:N	2.40	0.55
1:B:1514:PRO:HA	1:B:1517:ASN:HD22	1.71	0.55
1:F:120:MET:HA	1:F:120:MET:HE3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1469:ARG:NH1	1:F:1481:THR:OG1	2.40	0.55
3:E:565:LEU:HD21	3:E:653:ASN:HB3	1.87	0.55
3:A:361:PHE:HE1	3:A:415:ARG:HB2	1.72	0.55
4:D:22:CYS:O	4:D:162:GLN:NE2	2.40	0.55
1:B:122:TYR:HA	1:B:125:ILE:HG12	1.88	0.55
1:B:529:PHE:HB2	1:B:550:ALA:HB3	1.89	0.55
1:B:964:MET:SD	1:B:968:HIS:HB2	2.47	0.55
2:C:129:LEU:O	2:C:133:LYS:N	2.40	0.55
1:F:572:TYR:OH	1:F:589:PRO:O	2.21	0.55
1:F:634:ASN:OD1	1:F:637:LEU:N	2.28	0.55
1:F:1390:ARG:NH1	2:G:44:VAL:HG21	2.21	0.55
2:G:90:PHE:CE2	2:G:137:ILE:HB	2.36	0.55
3:A:88:LEU:HD13	3:A:107:LEU:HD13	1.89	0.55
3:A:334:ALA:HB3	3:A:400:LEU:HD11	1.88	0.55
4:D:9:VAL:N	4:D:79:VAL:O	2.39	0.55
1:B:60:PRO:HG2	1:B:63:TYR:CD2	2.42	0.55
2:C:61:GLN:HB3	2:C:64:TYR:HD1	1.71	0.55
2:C:96:LYS:C	2:C:99:PRO:HD2	2.32	0.55
1:F:6:PRO:HD3	3:E:724:TYR:HB2	1.89	0.55
1:F:241:LEU:HG	1:F:300:ILE:HG13	1.88	0.55
3:E:573:LYS:NZ	3:E:593:GLU:OE1	2.29	0.55
3:A:217:GLN:OE1	3:A:258:ARG:NH2	2.34	0.55
3:A:276:LEU:HD12	3:A:280:ILE:HB	1.88	0.55
1:B:224:LEU:HD12	1:B:404:LYS:O	2.06	0.55
1:B:232:VAL:N	1:B:398:GLY:O	2.32	0.55
1:B:1117:GLU:CD	1:B:1120:LEU:HG	2.32	0.55
1:B:1546:PRO:HA	1:B:1549:MET:HG2	1.87	0.55
1:F:1117:GLU:OE2	1:F:1120:LEU:N	2.40	0.55
1:F:1384:ARG:HD2	1:F:1495:PHE:HB3	1.89	0.55
1:B:526:HIS:CE1	1:B:585:TYR:HH	2.21	0.55
1:B:1065:SER:H	1:B:1068:LYS:HB3	1.72	0.55
1:F:569:LEU:HB2	1:F:620:PHE:HB3	1.88	0.55
1:F:1412:THR:HB	1:F:1413:PRO:HD3	1.89	0.55
1:F:1470:LYS:HD3	1:F:1483:TRP:CE2	2.42	0.55
2:G:94:ARG:HD2	2:G:145:MET:HG2	1.88	0.55
3:E:585:VAL:HG23	3:E:607:LYS:HA	1.88	0.55
3:E:586:LEU:HB2	3:E:608:LEU:HB3	1.87	0.55
1:B:133:SER:HB3	1:B:135:THR:HG23	1.88	0.54
1:B:229:LYS:HE3	1:B:343:GLN:HG2	1.88	0.54
1:B:319:ARG:NH1	1:B:497:LYS:O	2.41	0.54
1:B:646:ASN:ND2	1:B:653:ASN:HD21	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1353:ILE:HG21	1:F:1335:TYR:HB2	1.89	0.54
1:F:932:LEU:N	1:F:935:ARG:HH21	2.05	0.54
1:F:1158:GLU:OE1	1:F:1158:GLU:N	2.40	0.54
1:F:1630:LYS:O	1:F:1634:GLU:HG2	2.07	0.54
3:A:405:ARG:HB2	3:A:407:ASP:OD1	2.07	0.54
3:A:692:MET:O	3:A:696:LEU:N	2.38	0.54
1:B:231:PHE:CE2	1:B:233:CYS:HB3	2.42	0.54
1:B:840:PHE:O	1:B:844:ILE:HG12	2.06	0.54
1:B:936:ILE:O	1:B:940:VAL:HG12	2.07	0.54
1:F:720:ILE:HG12	1:F:766:PHE:CE1	2.42	0.54
1:F:1384:ARG:NH2	1:F:1457:ASN:OD1	2.39	0.54
3:E:687:ASP:OD1	3:E:688:THR:N	2.40	0.54
3:A:564:LYS:HA	3:A:654:PHE:HD1	1.73	0.54
1:B:688:THR:O	1:B:692:LEU:HG	2.06	0.54
1:B:1465:SER:HA	1:B:1486:ARG:HG2	1.89	0.54
1:B:1482:MET:HA	1:B:1482:MET:HE3	1.88	0.54
1:F:1162:GLY:HA2	1:F:1208:ARG:CZ	2.38	0.54
2:G:39:ASN:H	2:G:57:ASP:HB3	1.72	0.54
3:E:640:LEU:O	3:E:656:ALA:N	2.36	0.54
4:D:98:HIS:CE1	4:D:149:ILE:HB	2.43	0.54
1:B:18:ASN:ND2	1:B:28:SER:HB3	2.22	0.54
1:B:342:LYS:O	1:B:402:SER:HA	2.07	0.54
1:B:859:CYS:HA	1:B:862:LYS:HE2	1.90	0.54
1:B:972:TYR:O	1:B:975:THR:N	2.40	0.54
1:B:1148:GLU:O	1:B:1152:ILE:HG12	2.07	0.54
1:B:1280:PRO:HA	1:B:1283:LEU:HD23	1.89	0.54
1:B:1611:LEU:HD11	1:B:1616:LYS:HA	1.88	0.54
2:C:69:PRO:HA	2:C:72:TYR:CD2	2.42	0.54
2:C:139:TYR:HD1	2:C:156:GLU:OE1	1.89	0.54
1:F:926:GLN:HE21	1:F:930:GLU:CD	2.14	0.54
1:F:1117:GLU:OE2	1:F:1120:LEU:HG	2.08	0.54
1:F:1483:TRP:CE2	1:F:1514:PRO:HD3	2.42	0.54
1:F:1609:GLU:HB2	1:F:1610:LYS:HZ2	1.73	0.54
1:B:669:LEU:HD12	1:B:670:GLN:N	2.23	0.54
2:C:98:TYR:CE1	2:C:149:ILE:HD13	2.41	0.54
1:F:19:TYR:CG	1:F:20:ASN:N	2.76	0.54
1:F:80:VAL:HG22	1:F:85:LEU:HD21	1.88	0.54
1:F:85:LEU:O	1:F:88:VAL:HG12	2.08	0.54
1:F:738:ASN:HA	1:F:741:VAL:HG12	1.89	0.54
1:F:1485:GLU:HG3	1:F:1511:GLU:OE1	2.08	0.54
2:G:96:LYS:O	2:G:100:GLU:HG3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:164:GLY:O	2:G:168:VAL:HG23	2.08	0.54
3:E:578:ARG:HG2	3:E:587:HIS:HD2	1.72	0.54
3:A:669:LEU:HA	3:A:672:LEU:HD12	1.89	0.54
3:A:715:LYS:NZ	3:A:716:GLU:O	2.37	0.54
1:B:6:PRO:HG3	3:A:724:TYR:CD1	2.42	0.54
1:B:979:ARG:O	1:B:982:ILE:HG22	2.07	0.54
1:B:1088:ARG:HG2	1:B:1092:TYR:CE2	2.43	0.54
1:F:4:TRP:CZ3	1:F:46:ARG:HG2	2.43	0.54
1:F:181:ILE:O	1:F:185:LYS:NZ	2.41	0.54
1:F:1339:GLY:O	1:F:1343:LYS:HG3	2.08	0.54
3:A:272:ARG:NH1	3:A:273:SER:HB2	2.23	0.54
1:B:4:TRP:CE3	1:B:46:ARG:HG2	2.43	0.54
1:B:882:LEU:HA	1:B:885:GLN:NE2	2.22	0.54
1:B:1008:VAL:O	1:B:1012:THR:HG23	2.08	0.54
1:B:1602:GLU:HA	1:B:1605:ARG:NE	2.23	0.54
1:F:318:LEU:HD22	1:F:320:ARG:HH22	1.72	0.54
1:F:1184:LYS:H	1:F:1184:LYS:HD2	1.73	0.54
3:E:544:ILE:HG21	3:E:690:LEU:HD22	1.89	0.54
3:A:380:ALA:O	3:A:384:MET:HG2	2.07	0.54
3:A:511:TYR:HE1	3:A:518:ARG:HH21	1.55	0.54
3:A:678:MET:N	3:A:678:MET:SD	2.81	0.54
1:B:89:GLN:O	1:B:92:THR:OG1	2.22	0.54
1:B:561:THR:HG21	1:B:631:LEU:HD22	1.90	0.54
2:C:21:ILE:HD11	2:C:35:THR:HG23	1.89	0.54
1:F:41:TYR:CZ	3:E:717:PRO:HD3	2.41	0.54
1:F:1478:GLU:O	1:F:1482:MET:HG2	2.08	0.54
2:G:82:PHE:HD1	2:G:112:LEU:HD11	1.73	0.54
3:E:579:LEU:HD13	3:E:586:LEU:HD22	1.90	0.54
3:A:619:GLY:N	3:A:641:ALA:O	2.39	0.54
4:D:21:ILE:O	4:D:26:ASN:N	2.41	0.54
1:B:1086:ARG:O	1:B:1090:MET:HG2	2.08	0.54
1:B:1485:GLU:OE1	1:B:1485:GLU:N	2.40	0.54
1:F:128:ARG:NH1	1:F:128:ARG:O	2.34	0.54
1:F:843:PHE:O	1:F:846:SER:OG	2.17	0.54
1:F:857:LEU:HB3	1:F:905:LEU:HD21	1.90	0.54
1:F:1028:LEU:O	1:F:1032:PHE:CB	2.48	0.54
1:F:1178:GLU:O	1:F:1182:LYS:HD2	2.08	0.54
1:F:1391:ARG:NE	2:G:26:ASN:O	2.39	0.54
3:A:133:VAL:HG21	3:A:158:THR:HG21	1.90	0.54
1:B:746:ASP:CG	1:B:748:SER:HG	2.15	0.54
1:B:1036:ALA:C	1:B:1038:PHE:H	2.16	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1069:ARG:O	1:B:1073:VAL:HG23	2.07	0.54
1:B:1633:VAL:HG12	1:B:1637:TYR:HD2	1.71	0.54
2:C:123:LYS:HA	2:C:126:ILE:HG12	1.88	0.54
2:C:163:ARG:C	2:C:165:LEU:H	2.15	0.54
1:F:167:ASP:OD1	1:F:168:ASP:N	2.36	0.54
1:F:198:ILE:O	1:F:201:GLU:HG2	2.07	0.54
1:F:719:TYR:HD1	1:F:723:HIS:HB2	1.72	0.54
1:F:896:LYS:HG2	1:F:897:PRO:HD3	1.90	0.54
3:A:251:PHE:HB3	3:A:300:LEU:HD22	1.89	0.54
3:A:552:ARG:HD3	3:A:664:ILE:HG23	1.90	0.54
1:B:154:HIS:O	1:B:158:MET:HG2	2.08	0.53
1:B:962:GLN:O	1:B:1019:ARG:NH1	2.40	0.53
1:B:1363:PHE:HE1	1:B:1391:ARG:HA	1.73	0.53
1:F:198:ILE:HG13	1:F:202:LYS:NZ	2.23	0.53
1:F:1043:TRP:HA	1:F:1046:TYR:HB3	1.90	0.53
3:A:331:ALA:HB2	3:A:395:TYR:CE2	2.44	0.53
4:D:79:VAL:HG22	4:D:111:LEU:HD23	1.90	0.53
1:B:630:LYS:HG3	1:B:668:PHE:HZ	1.73	0.53
1:B:800:MET:HE1	1:B:804:ARG:HE	1.72	0.53
1:F:141:LEU:O	1:F:145:LYS:HG3	2.07	0.53
3:A:294:LEU:HA	3:A:297:LEU:HD12	1.89	0.53
4:D:5:LYS:HG2	4:D:75:THR:HA	1.91	0.53
4:D:46:VAL:HG11	4:D:174:ARG:HB3	1.90	0.53
1:B:228:PHE:CE2	1:B:399:LEU:HB2	2.40	0.53
1:B:1125:ILE:HD13	1:B:1175:LEU:HB2	1.88	0.53
1:F:31:ILE:HB	3:E:697:ARG:HB3	1.91	0.53
1:F:450:LEU:HB3	1:F:509:TRP:CE3	2.42	0.53
1:F:1109:ILE:O	1:F:1112:VAL:HG22	2.08	0.53
3:A:424:LEU:O	3:A:428:LEU:HB2	2.08	0.53
4:D:82:PHE:CE1	4:D:90:TYR:HD2	2.26	0.53
4:D:152:VAL:HG21	4:D:175:ALA:HB2	1.90	0.53
1:B:821:PRO:O	1:B:824:ILE:HG12	2.08	0.53
1:B:1221:MET:HG3	1:B:1250:LEU:HD13	1.90	0.53
2:C:90:PHE:HE2	2:C:137:ILE:HB	1.73	0.53
1:F:219:ILE:HD12	1:F:408:GLY:HA2	1.90	0.53
1:F:245:LEU:O	1:F:254:ILE:N	2.33	0.53
1:F:666:VAL:HA	1:F:669:LEU:HB3	1.91	0.53
1:F:785:ASP:OD1	1:F:786:GLU:N	2.41	0.53
2:G:98:TYR:CE1	2:G:149:ILE:HD13	2.39	0.53
3:E:616:VAL:HA	3:E:644:ILE:HA	1.91	0.53
3:E:670:ASN:HA	3:E:673:LEU:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:51:LEU:HA	3:A:77:LEU:HA	1.89	0.53
3:A:408:LYS:HG2	3:A:475:GLU:OE1	2.09	0.53
1:B:942:GLY:C	1:B:944:ASN:H	2.14	0.53
1:B:1082:GLU:OE1	1:B:1082:GLU:N	2.27	0.53
1:F:643:TRP:HZ2	1:F:678:ASN:HB3	1.73	0.53
1:F:819:TYR:O	1:F:822:SER:OG	2.25	0.53
1:F:1240:TYR:O	1:F:1244:LEU:HG	2.09	0.53
3:A:52:GLN:HG2	3:A:76:ARG:O	2.09	0.53
3:A:323:ILE:O	3:A:326:GLU:HG3	2.08	0.53
1:B:182:ALA:HA	1:B:185:LYS:HZ3	1.73	0.53
1:B:1328:TYR:HA	1:B:1332:VAL:HG22	1.91	0.53
2:C:162:GLN:HA	2:C:165:LEU:HD13	1.89	0.53
1:F:4:TRP:CE3	1:F:46:ARG:HG2	2.43	0.53
1:F:1601:THR:O	1:F:1605:ARG:HG2	2.08	0.53
2:G:83:SER:HA	2:G:115:THR:HB	1.90	0.53
3:A:181:ILE:HD11	3:A:219:VAL:HA	1.90	0.53
1:B:118:GLN:HB3	1:B:122:TYR:CZ	2.44	0.53
1:B:486:PRO:HD3	1:B:492:GLY:HA2	1.91	0.53
1:B:727:THR:O	1:B:774:TYR:HB2	2.08	0.53
1:F:300:ILE:O	1:F:322:PHE:HB3	2.08	0.53
1:F:467:GLU:OE1	1:F:534:ARG:HD3	2.08	0.53
1:F:921:THR:OG1	1:F:924:HIS:HB3	2.09	0.53
1:F:1024:PHE:HA	1:F:1027:VAL:HG12	1.90	0.53
1:F:1063:THR:HA	1:F:1069:ARG:CD	2.39	0.53
1:F:1066:GLN:HA	1:F:1069:ARG:NH2	2.23	0.53
1:F:1089:ASP:HA	1:F:1092:TYR:CD2	2.43	0.53
3:A:129:LEU:HA	3:A:132:MET:HG2	1.90	0.53
3:A:457:CYS:O	3:A:460:ILE:HG22	2.08	0.53
3:A:563:ARG:HG2	3:A:573:LYS:O	2.08	0.53
1:B:46:ARG:HB3	1:B:58:ILE:HG12	1.90	0.53
1:B:154:HIS:HA	1:B:157:ARG:NE	2.21	0.53
1:B:979:ARG:O	1:B:983:ILE:HG13	2.09	0.53
1:B:1143:ASN:HB2	1:B:1145:HIS:CD2	2.43	0.53
1:B:1443:ASP:OD1	1:B:1443:ASP:N	2.40	0.53
1:F:730:TYR:CZ	1:F:731:VAL:HG23	2.44	0.53
1:F:936:ILE:HD12	1:F:939:THR:HB	1.91	0.53
1:F:1618:LEU:HD22	1:F:1621:ARG:NH2	2.23	0.53
2:G:93:VAL:HG23	2:G:97:TRP:HB2	1.89	0.53
1:B:470:MET:SD	1:B:496:TYR:HB3	2.49	0.53
1:B:529:PHE:N	1:B:550:ALA:O	2.24	0.53
1:B:725:SER:HA	1:B:773:LEU:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:852:LEU:HB3	1:B:855:GLN:HB2	1.90	0.53
1:B:1386:LYS:HB3	1:B:1389:GLU:HB2	1.90	0.53
1:F:154:HIS:O	1:F:158:MET:HG2	2.08	0.53
1:F:221:THR:O	1:F:408:GLY:N	2.42	0.53
1:F:828:LYS:NZ	1:F:867:THR:HA	2.24	0.53
1:F:1440:SER:H	1:F:1442:LYS:NZ	2.06	0.53
1:F:1529:ILE:HD13	1:F:1550:LEU:HD23	1.91	0.53
2:G:11:ASP:OD1	2:G:11:ASP:N	2.41	0.53
3:A:45:ASN:HB3	3:A:48:TYR:CD2	2.44	0.53
3:A:202:LEU:HD23	3:A:205:LEU:HD12	1.91	0.53
1:B:142:ALA:HA	1:B:145:LYS:HE2	1.91	0.53
1:B:306:MET:HB2	1:B:314:HIS:CE1	2.43	0.53
1:B:589:PRO:HG3	1:B:598:LYS:HD2	1.90	0.53
1:B:593:MET:HA	1:B:596:GLU:CD	2.34	0.53
1:B:1056:HIS:HD1	1:B:1057:GLU:CD	2.16	0.53
1:B:1231:TYR:HE2	1:B:1243:TYR:CE2	2.23	0.53
1:B:1599:LEU:HA	1:B:1602:GLU:OE1	2.09	0.53
2:C:82:PHE:HD1	2:C:112:LEU:HD11	1.73	0.53
1:F:166:ARG:O	1:F:171:ASN:HA	2.09	0.53
1:F:674:ASP:O	1:F:678:ASN:ND2	2.43	0.53
3:E:548:ILE:O	3:E:552:ARG:HG2	2.09	0.53
3:A:111:SER:O	3:A:168:HIS:NE2	2.41	0.53
3:A:178:VAL:O	3:A:182:LYS:HG2	2.09	0.53
3:A:224:THR:HB	3:A:227:GLN:HG2	1.91	0.53
3:A:276:LEU:HA	3:A:280:ILE:HD12	1.91	0.53
3:A:309:MET:SD	3:A:379:LEU:HD13	2.48	0.53
3:A:646:TYR:CE1	3:A:652:LEU:HG	2.44	0.53
1:B:204:ILE:HA	1:B:207:ASN:O	2.09	0.52
1:B:936:ILE:HD12	1:B:939:THR:HB	1.91	0.52
1:B:1307:TYR:O	1:B:1311:GLY:N	2.42	0.52
1:F:297:VAL:O	1:F:299:GLN:NE2	2.42	0.52
1:F:414:GLN:NE2	1:F:427:ILE:HD11	2.24	0.52
1:F:1362:TYR:OH	1:F:1384:ARG:NE	2.36	0.52
3:A:457:CYS:SG	3:A:458:ILE:N	2.82	0.52
3:A:590:ASP:O	3:A:604:LEU:HD22	2.09	0.52
4:D:145:LEU:O	4:D:149:ILE:HG12	2.09	0.52
1:B:2:ALA:N	3:A:717:PRO:HG2	2.23	0.52
1:B:43:GLY:O	1:B:61:GLU:N	2.37	0.52
1:B:1516:GLU:O	1:B:1519:ILE:N	2.41	0.52
1:F:18:ASN:HD21	3:E:536:LEU:HA	1.73	0.52
1:F:19:TYR:CG	1:F:59:PHE:HE1	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:72:GLU:HA	1:F:89:GLN:NE2	2.21	0.52
1:F:187:HIS:HD1	1:F:1006:TRP:CD1	2.25	0.52
1:F:1245:TYR:HD2	1:F:1248:ARG:NH2	2.02	0.52
2:G:28:PHE:HB3	2:G:31:GLU:HG3	1.92	0.52
2:G:84:LEU:HD13	2:G:120:ARG:HH11	1.74	0.52
3:A:423:MET:SD	3:A:424:LEU:N	2.82	0.52
3:A:588:TYR:O	3:A:603:SER:OG	2.23	0.52
1:B:19:TYR:CG	1:B:20:ASN:N	2.76	0.52
1:B:697:LEU:HA	1:B:700:ILE:HD12	1.90	0.52
1:F:72:GLU:CD	1:F:75:GLY:H	2.17	0.52
1:F:73:ASP:O	1:F:79:THR:N	2.39	0.52
1:F:225:TYR:HE1	1:F:278:GLN:HB3	1.73	0.52
1:F:1306:SER:O	1:F:1310:LYS:HG2	2.09	0.52
3:A:541:GLN:HG3	3:A:545:LEU:HD23	1.91	0.52
4:D:86:SER:O	4:D:89:SER:OG	2.13	0.52
1:B:246:TYR:OH	1:B:383:LEU:HD21	2.09	0.52
1:B:566:ARG:HA	1:B:623:ALA:HA	1.90	0.52
1:B:704:ILE:HG21	1:B:716:LEU:HD11	1.92	0.52
1:B:1086:ARG:NH2	1:B:1089:ASP:OD2	2.35	0.52
2:C:82:PHE:CZ	2:C:114:GLY:HA2	2.45	0.52
1:F:172:ILE:C	1:F:175:PRO:HD2	2.34	0.52
1:F:871:GLN:HG2	1:F:875:ARG:HB2	1.90	0.52
1:F:1220:ARG:O	1:F:1224:THR:HG22	2.08	0.52
2:G:87:PRO:HA	2:G:90:PHE:CD2	2.44	0.52
3:E:537:LYS:HE3	3:E:690:LEU:HD23	1.92	0.52
3:A:241:THR:HG22	3:A:290:MET:HE2	1.91	0.52
3:A:408:LYS:O	3:A:474:SER:N	2.43	0.52
1:B:261:ARG:HB2	1:B:270:GLU:HG3	1.91	0.52
1:B:380:THR:HG22	1:B:510:TYR:CZ	2.44	0.52
1:B:468:VAL:HG12	1:B:470:MET:HE3	1.91	0.52
1:B:570:VAL:HB	1:B:572:TYR:CE2	2.44	0.52
1:B:958:ILE:HG13	1:B:959:ALA:H	1.72	0.52
1:B:1518:ALA:HB1	1:B:1566:TYR:HE1	1.73	0.52
1:B:1535:GLN:OE1	1:B:1542:LEU:HD11	2.09	0.52
2:C:5:LYS:N	2:C:76:ASP:OD2	2.42	0.52
2:C:23:TYR:HB2	2:C:165:LEU:HD21	1.90	0.52
1:F:957:MET:HA	1:F:960:LEU:HD12	1.91	0.52
1:F:1469:ARG:HD2	1:F:1481:THR:HB	1.90	0.52
1:F:1470:LYS:HB3	1:F:1483:TRP:CD1	2.45	0.52
2:G:163:ARG:C	2:G:165:LEU:H	2.17	0.52
3:A:464:ASN:O	3:A:468:LYS:HG2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:511:TYR:HE1	3:A:518:ARG:NH2	2.07	0.52
1:B:249:ASP:OD2	1:B:293:ARG:N	2.43	0.52
1:B:330:THR:HG23	1:B:333:ILE:HD11	1.91	0.52
1:B:457:LYS:HA	1:B:463:PRO:HA	1.90	0.52
1:B:643:TRP:HA	1:B:646:ASN:HB3	1.90	0.52
1:B:925:ILE:HA	1:B:928:ILE:HD12	1.91	0.52
1:B:1514:PRO:HA	1:B:1517:ASN:HB2	1.90	0.52
1:F:1032:PHE:HB3	1:F:1043:TRP:HH2	1.75	0.52
1:F:1208:ARG:HB3	1:F:1212:MET:HE1	1.92	0.52
1:F:1483:TRP:HE3	1:F:1511:GLU:HG3	1.74	0.52
2:G:45:MET:HE2	2:G:50:PRO:HB3	1.91	0.52
2:G:129:LEU:O	2:G:134:LEU:N	2.37	0.52
3:A:259:ARG:HB3	3:A:304:LEU:HD11	1.91	0.52
3:A:609:PRO:HD2	3:A:612:ASP:OD1	2.09	0.52
1:B:273:LYS:O	1:B:277:LEU:HG	2.09	0.52
1:B:1178:GLU:O	1:B:1182:LYS:HD2	2.10	0.52
1:B:1368:TYR:O	1:B:1372:PHE:HE2	1.93	0.52
1:F:79:THR:HA	1:F:85:LEU:HD22	1.91	0.52
1:F:81:ILE:HG21	1:F:141:LEU:HD21	1.91	0.52
3:E:556:LEU:HD21	3:E:665:TRP:CD1	2.45	0.52
3:A:612:ASP:HB2	3:A:646:TYR:HB2	1.90	0.52
1:B:106:TYR:HA	1:B:111:LEU:HD11	1.91	0.52
1:B:306:MET:HG2	1:B:320:ARG:HH21	1.75	0.52
1:B:772:VAL:HG23	1:B:776:ARG:NH2	2.25	0.52
1:B:909:ILE:HG13	1:B:910:LEU:H	1.73	0.52
1:F:714:PRO:HA	1:F:717:GLU:HG2	1.92	0.52
1:F:1054:LEU:HB2	1:F:1083:ILE:HG21	1.92	0.52
1:F:1229:ASN:HA	1:F:1232:LYS:HE2	1.91	0.52
1:F:1248:ARG:NH1	1:F:1252:ARG:HH12	2.06	0.52
1:F:1549:MET:HE1	2:G:56:TRP:CD2	2.44	0.52
3:E:698:LEU:O	3:E:702:GLU:HG2	2.10	0.52
1:B:41:TYR:CE1	3:A:717:PRO:HD3	2.45	0.52
1:B:437:ILE:HG13	1:B:708:LYS:HE3	1.92	0.52
1:B:706:ASP:OD1	1:B:708:LYS:N	2.31	0.52
1:B:1089:ASP:HA	1:B:1092:TYR:CD2	2.45	0.52
1:B:1154:LYS:HA	1:B:1157:GLN:OE1	2.10	0.52
1:B:1391:ARG:HH11	1:B:1429:PHE:HA	1.75	0.52
1:F:187:HIS:HB3	1:F:1006:TRP:CD1	2.44	0.52
1:F:1065:SER:OG	1:F:1068:LYS:N	2.43	0.52
3:E:678:MET:HA	3:E:683:ARG:HH12	1.75	0.52
3:A:425:CYS:HA	3:A:430:VAL:HB	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:670:ASN:HA	3:A:673:LEU:HB2	1.91	0.52
1:B:60:PRO:HB3	3:A:714:PRO:HD2	1.92	0.52
1:B:1136:PHE:HZ	1:B:1185:TYR:CE2	2.28	0.52
1:B:1274:SER:HB2	1:B:1293:GLN:NE2	2.25	0.52
1:B:1623:SER:HB3	1:B:1627:ARG:NH2	2.25	0.52
1:F:48:TYR:HB3	1:F:53:LYS:HA	1.92	0.52
1:F:59:PHE:CZ	1:F:63:TYR:HB3	2.45	0.52
1:F:221:THR:HG23	1:F:283:ASP:HA	1.92	0.52
1:F:583:LYS:HG3	1:F:586:LEU:HD12	1.90	0.52
1:F:724:PHE:CZ	1:F:726:ALA:HB3	2.44	0.52
1:F:945:ARG:NH1	1:F:946:GLN:HB2	2.24	0.52
1:F:1573:GLU:O	1:F:1577:GLN:NE2	2.43	0.52
1:F:1607:HIS:NE2	1:F:1615:LEU:HB3	2.24	0.52
2:G:5:LYS:HG2	2:G:56:TRP:HE1	1.75	0.52
3:A:198:LEU:HD11	3:A:231:HIS:CD2	2.44	0.52
3:A:387:PHE:O	3:A:392:GLN:N	2.43	0.52
1:B:110:LYS:HD3	1:B:113:LEU:HD12	1.91	0.51
1:B:297:VAL:HG22	1:B:326:VAL:HG22	1.91	0.51
1:B:411:THR:O	1:B:415:LYS:HD3	2.11	0.51
1:B:469:THR:HB	1:B:530:THR:OG1	2.10	0.51
1:B:970:SER:HA	1:B:974:SER:HB3	1.93	0.51
1:B:1165:ASP:HB2	1:B:1168:TYR:HB2	1.92	0.51
1:F:677:PHE:HE2	1:F:766:PHE:CE1	2.28	0.51
1:F:879:LEU:HD13	1:F:924:HIS:CE1	2.45	0.51
1:F:1026:GLU:O	1:F:1029:THR:OG1	2.22	0.51
1:F:1291:TYR:HB3	1:F:1296:LEU:CD2	2.35	0.51
1:F:1405:ALA:H	3:E:584:LYS:HZ1	1.55	0.51
3:E:578:ARG:O	3:E:587:HIS:N	2.23	0.51
3:E:588:TYR:OH	3:E:607:LYS:O	2.20	0.51
3:A:299:VAL:O	3:A:303:ASN:ND2	2.43	0.51
4:D:158:SER:HB3	4:D:163:ASP:HB3	1.92	0.51
1:B:520:GLU:OE1	1:B:520:GLU:N	2.32	0.51
1:B:716:LEU:O	1:B:720:ILE:HG13	2.10	0.51
1:B:1370:GLN:O	1:B:1377:ARG:NH2	2.43	0.51
2:C:90:PHE:O	2:C:94:ARG:HD3	2.11	0.51
1:F:17:TYR:CZ	3:E:710:PRO:HB3	2.45	0.51
2:G:124:ASP:O	2:G:127:GLU:HG2	2.09	0.51
2:G:137:ILE:HG23	2:G:141:GLN:NE2	2.24	0.51
3:A:491:ALA:O	3:A:496:PRO:HD3	2.09	0.51
1:B:4:TRP:CZ3	1:B:46:ARG:HG2	2.44	0.51
1:B:166:ARG:HE	1:B:173:LEU:HD12	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:232:VAL:O	1:B:397:GLN:HA	2.09	0.51
1:B:241:LEU:HB3	1:B:243:MET:HE1	1.92	0.51
1:B:383:LEU:HD22	1:B:510:TYR:CE2	2.46	0.51
1:B:556:ASN:ND2	1:B:560:THR:OG1	2.25	0.51
1:B:1372:PHE:CZ	1:B:1424:GLN:HB3	2.45	0.51
1:F:34:THR:O	1:F:50:LEU:N	2.31	0.51
1:F:764:PHE:CD1	1:F:823:ILE:HB	2.44	0.51
1:F:1360:PRO:HG2	1:F:1362:TYR:CE1	2.45	0.51
3:A:52:GLN:HA	3:A:61:ILE:HG12	1.91	0.51
1:B:1:MET:N	3:A:716:GLU:HB3	2.25	0.51
1:B:4:TRP:CD1	3:A:722:PHE:HD1	2.29	0.51
1:B:1586:VAL:HA	1:B:1589:LEU:HD12	1.91	0.51
1:F:866:SER:C	1:F:868:LEU:H	2.19	0.51
1:F:1090:MET:O	1:F:1090:MET:HE3	2.10	0.51
3:A:51:LEU:HD22	3:A:75:LEU:HB3	1.91	0.51
3:A:224:THR:HG22	3:A:226:GLY:H	1.75	0.51
3:A:386:TYR:CD1	3:A:453:GLU:HB3	2.45	0.51
4:D:1:MET:HG3	4:D:52:ASN:HB2	1.91	0.51
1:B:694:PHE:O	1:B:697:LEU:HG	2.11	0.51
1:B:720:ILE:HG12	1:B:766:PHE:CE1	2.46	0.51
1:B:1539:ASP:OD1	1:B:1542:LEU:HB2	2.11	0.51
1:B:1557:PRO:HB2	1:B:1562:GLY:H	1.75	0.51
1:F:36:HIS:N	1:F:48:TYR:O	2.41	0.51
1:F:193:ARG:HA	1:F:196:GLU:CD	2.36	0.51
3:A:237:GLN:HG3	3:A:290:MET:HE3	1.93	0.51
3:A:348:ARG:NH1	3:A:352:TYR:OH	2.44	0.51
3:A:491:ALA:O	3:A:494:THR:OG1	2.24	0.51
3:A:496:PRO:HG2	3:A:502:PHE:HD1	1.76	0.51
3:A:644:ILE:HD11	3:A:669:LEU:HD13	1.92	0.51
3:A:670:ASN:O	3:A:674:GLY:N	2.43	0.51
1:B:105:LEU:HD13	1:B:110:LYS:NZ	2.24	0.51
1:B:127:TRP:O	1:B:131:ILE:HG12	2.09	0.51
1:B:438:LEU:N	1:B:441:ASP:OD2	2.44	0.51
1:B:794:LEU:HG	1:B:798:PHE:CZ	2.45	0.51
1:B:1002:TYR:CZ	1:B:1009:MET:HE1	2.45	0.51
1:B:1220:ARG:O	1:B:1224:THR:HG22	2.11	0.51
2:C:8:VAL:HG22	2:C:79:LEU:HB2	1.93	0.51
2:C:65:ASP:HA	2:C:68:ARG:NE	2.26	0.51
1:F:817:LEU:HD11	1:F:855:GLN:HB3	1.93	0.51
1:F:1062:GLU:O	1:F:1069:ARG:N	2.44	0.51
1:F:1336:GLU:O	1:F:1340:ASN:ND2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1361:GLU:OE2	1:F:1388:TYR:HA	2.11	0.51
1:F:1593:ILE:O	1:F:1596:GLN:HB3	2.11	0.51
3:A:582:ASN:HB2	3:A:585:VAL:HG12	1.91	0.51
1:B:87:LEU:O	1:B:90:GLU:HG3	2.11	0.51
1:B:744:ALA:HB3	1:B:804:ARG:NH1	2.25	0.51
1:B:1398:LEU:HD23	1:B:1426:MET:HE3	1.93	0.51
1:B:1478:GLU:HG3	2:C:34:PRO:HB2	1.93	0.51
1:F:333:ILE:O	1:F:405:LEU:HD22	2.11	0.51
1:F:337:VAL:HG11	1:F:344:HIS:CE1	2.46	0.51
1:F:864:VAL:HG11	1:F:909:ILE:HG22	1.93	0.51
1:F:889:GLN:OE1	1:F:895:ASN:HB3	2.11	0.51
1:F:1110:LEU:O	1:F:1114:LEU:N	2.43	0.51
1:F:1340:ASN:HA	1:F:1343:LYS:HE2	1.92	0.51
1:F:1567:GLU:HA	1:F:1571:PHE:CD1	2.45	0.51
1:F:1613:GLU:OE2	1:F:1614:GLN:NE2	2.43	0.51
4:D:90:TYR:CE1	4:D:94:ARG:HD2	2.46	0.51
1:B:972:TYR:CE2	1:B:976:PHE:HA	2.45	0.51
1:B:1200:LEU:HD23	1:B:1230:PHE:CE2	2.42	0.51
1:B:1495:PHE:CE1	1:B:1502:PHE:HD2	2.28	0.51
1:F:914:ASP:OD1	1:F:916:LYS:NZ	2.38	0.51
1:F:1372:PHE:O	1:F:1377:ARG:NH2	2.44	0.51
3:E:543:GLU:O	3:E:546:GLU:HG2	2.11	0.51
3:E:680:ASP:OD1	3:E:681:LEU:HD12	2.11	0.51
3:A:72:GLY:HA3	4:D:64:TYR:HE2	1.76	0.51
3:A:546:GLU:HA	3:A:549:LYS:HE3	1.93	0.51
1:B:69:ALA:HB2	1:B:76:GLN:HB2	1.93	0.51
1:B:299:GLN:HG3	1:B:324:VAL:HG22	1.92	0.51
1:B:927:LEU:CB	1:B:931:ARG:HH12	2.17	0.51
1:B:1148:GLU:HA	1:B:1151:LEU:HB3	1.93	0.51
1:B:1306:SER:O	1:B:1310:LYS:HG2	2.11	0.51
1:B:1474:ASP:OD2	1:B:1477:ASN:ND2	2.37	0.51
1:F:44:TRP:HE3	1:F:58:ILE:HG22	1.76	0.51
1:F:98:TRP:HZ3	1:F:159:LEU:HD13	1.75	0.51
1:F:129:SER:O	1:F:132:LEU:HB2	2.11	0.51
1:F:1489:TYR:HE1	1:F:1507:ILE:HG13	1.74	0.51
3:A:8:VAL:HG22	3:A:10:VAL:HG13	1.93	0.51
3:A:198:LEU:HD21	3:A:231:HIS:HD2	1.75	0.51
1:B:45:TYR:CE2	1:B:66:LEU:HD12	2.46	0.51
1:B:111:LEU:O	1:B:114:PHE:HB3	2.11	0.51
1:B:127:TRP:O	1:B:130:GLN:HG2	2.11	0.51
1:B:240:GLU:O	1:B:300:ILE:HA	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:409:ASP:CG	1:B:411:THR:HG1	2.18	0.51
1:B:985:PHE:O	1:B:989:THR:HG23	2.11	0.51
1:B:1322:LYS:HD3	1:B:1345:ARG:NH1	2.26	0.51
2:C:7:VAL:HG22	2:C:56:TRP:CD1	2.46	0.51
2:C:29:PRO:HG3	2:C:162:GLN:CD	2.35	0.51
1:F:195:GLU:O	1:F:199:GLN:HG2	2.11	0.51
1:F:616:THR:OG1	1:F:617:LYS:N	2.44	0.51
1:F:787:PHE:O	1:F:791:ILE:HG12	2.11	0.51
1:F:872:SER:HA	1:F:875:ARG:HH12	1.76	0.51
1:F:1306:SER:HB3	1:F:1310:LYS:NZ	2.25	0.51
1:F:1579:HIS:HB3	1:F:1582:ASP:HB2	1.93	0.51
3:E:563:ARG:HG3	3:E:657:PRO:HG3	1.92	0.51
3:A:462:LEU:HD22	3:A:506:LEU:HB3	1.93	0.51
3:A:533:ILE:HD11	3:A:706:ILE:HD13	1.93	0.51
1:B:729:ALA:O	1:B:733:LEU:HG	2.11	0.50
1:B:1546:PRO:O	1:B:1549:MET:HB2	2.11	0.50
2:C:130:LYS:HE2	2:C:130:LYS:HA	1.93	0.50
1:F:101:ILE:HD12	1:F:104:LYS:HG3	1.93	0.50
1:F:569:LEU:HD12	1:F:620:PHE:CD2	2.47	0.50
1:F:809:ALA:O	1:F:813:LYS:HG3	2.11	0.50
1:F:941:ILE:O	1:F:944:ASN:HB2	2.10	0.50
3:E:613:ILE:HD12	3:E:644:ILE:HG22	1.93	0.50
3:E:637:VAL:HA	3:E:640:LEU:HD12	1.92	0.50
3:A:548:ILE:O	3:A:551:GLN:HB3	2.11	0.50
1:B:166:ARG:HG2	1:B:173:LEU:HB2	1.92	0.50
1:B:628:SER:OG	1:B:629:THR:N	2.43	0.50
1:B:652:HIS:HA	1:B:655:LYS:HD2	1.92	0.50
1:B:761:LYS:HG3	1:B:765:ARG:NE	2.26	0.50
1:B:1167:GLN:O	1:B:1171:LEU:HG	2.11	0.50
1:B:1366:GLY:HA3	1:B:1380:ILE:HD13	1.94	0.50
1:B:1522:MET:HE1	1:B:1593:ILE:CA	2.41	0.50
1:F:89:GLN:O	1:F:92:THR:OG1	2.27	0.50
1:F:878:LEU:O	1:F:882:LEU:HG	2.10	0.50
1:F:950:ILE:HA	1:F:953:PHE:CD1	2.46	0.50
1:F:1008:VAL:O	1:F:1012:THR:HG23	2.10	0.50
1:F:1216:SER:OG	1:F:1401:GLN:NE2	2.31	0.50
1:F:1605:ARG:O	1:F:1609:GLU:HG3	2.11	0.50
2:G:87:PRO:HD2	2:G:134:LEU:HD22	1.92	0.50
2:G:116:LYS:O	2:G:120:ARG:N	2.45	0.50
3:A:200:ARG:NH2	3:A:242:TYR:OH	2.44	0.50
3:A:271:LEU:HA	3:A:274:ILE:HG22	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:90:TYR:O	4:D:94:ARG:HG3	2.11	0.50
4:D:91:GLU:O	4:D:95:HIS:ND1	2.44	0.50
1:B:256:GLU:HA	1:B:431:MET:HE2	1.93	0.50
1:B:879:LEU:HD13	1:B:924:HIS:CE1	2.47	0.50
1:B:1593:ILE:O	1:B:1596:GLN:HB3	2.12	0.50
1:F:31:ILE:HG23	3:E:701:LEU:HD23	1.94	0.50
3:A:309:MET:CE	3:A:376:PRO:HB3	2.39	0.50
1:B:88:VAL:O	1:B:92:THR:HG23	2.11	0.50
1:B:122:TYR:O	1:B:126:GLU:HG3	2.12	0.50
1:B:304:GLY:CA	1:B:317:GLY:H	2.25	0.50
1:B:346:ILE:N	1:B:399:LEU:O	2.42	0.50
1:B:877:VAL:O	1:B:880:PRO:HD2	2.11	0.50
1:B:914:ASP:HB2	1:B:963:GLN:CD	2.37	0.50
1:B:1079:MET:HA	1:B:1082:GLU:OE2	2.11	0.50
1:B:1165:ASP:HB3	1:B:1167:GLN:CD	2.36	0.50
1:B:1336:GLU:OE2	1:B:1340:ASN:ND2	2.34	0.50
2:C:96:LYS:HD2	2:C:100:GLU:HG2	1.93	0.50
2:C:114:GLY:HA3	2:C:156:GLU:HG3	1.94	0.50
1:F:329:ILE:HB	1:F:332:ILE:HB	1.93	0.50
1:F:847:ILE:HD13	1:F:856:LYS:HD2	1.94	0.50
1:F:1183:HIS:CG	1:F:1184:LYS:H	2.28	0.50
3:E:645:LEU:HA	3:E:651:GLN:HG3	1.93	0.50
3:A:386:TYR:O	3:A:390:HIS:N	2.40	0.50
3:A:537:LYS:HB2	3:A:694:ILE:HG21	1.93	0.50
3:A:561:CYS:HB3	3:A:574:PHE:CB	2.37	0.50
3:A:564:LYS:CE	3:A:590:ASP:HA	2.41	0.50
3:A:642:PHE:CE2	3:A:652:LEU:HB3	2.46	0.50
1:B:239:ALA:HB3	1:B:262:TRP:CD1	2.47	0.50
1:B:288:ASP:HA	1:B:291:ARG:HD2	1.92	0.50
1:B:477:GLY:H	1:B:526:HIS:HE1	1.59	0.50
1:B:786:GLU:HA	1:B:789:ASN:ND2	2.27	0.50
1:B:1019:ARG:O	1:B:1023:GLN:NE2	2.41	0.50
1:B:1449:GLN:HA	1:B:1452:ASN:ND2	2.27	0.50
1:B:1545:HIS:HD2	2:C:5:LYS:HE3	1.76	0.50
1:B:1567:GLU:HA	1:B:1571:PHE:HB2	1.94	0.50
2:C:139:TYR:O	2:C:142:GLY:N	2.45	0.50
1:F:127:TRP:CH2	1:F:151:LYS:HE3	2.47	0.50
1:F:853:VAL:O	1:F:857:LEU:HG	2.10	0.50
1:F:1468:PHE:CE2	1:F:1470:LYS:HB2	2.46	0.50
2:G:39:ASN:HA	2:G:57:ASP:H	1.77	0.50
2:G:40:TYR:C	2:G:55:LEU:HB2	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:78:PHE:CE1	2:G:101:VAL:HG11	2.46	0.50
3:E:541:GLN:N	3:E:542:PRO:HD3	2.26	0.50
3:A:38:CYS:O	3:A:43:LEU:N	2.31	0.50
3:A:274:ILE:HA	3:A:277:THR:HG22	1.93	0.50
3:A:276:LEU:HB2	3:A:446:PHE:HB3	1.92	0.50
3:A:551:GLN:O	3:A:555:ARG:HD3	2.11	0.50
3:A:562:PHE:HB3	3:A:575:TRP:CZ2	2.47	0.50
4:D:72:TYR:HE2	4:D:100:GLU:HG2	1.75	0.50
1:B:102:TRP:HA	1:B:105:LEU:CG	2.42	0.50
1:B:204:ILE:HG12	1:B:211:ARG:HD3	1.92	0.50
2:C:158:SER:O	2:C:162:GLN:N	2.43	0.50
1:F:84:GLU:OE1	1:F:141:LEU:HD23	2.11	0.50
1:F:717:GLU:HA	1:F:720:ILE:HD12	1.93	0.50
1:F:1063:THR:HA	1:F:1069:ARG:HD3	1.93	0.50
1:F:1365:VAL:N	1:F:1381:PHE:O	2.34	0.50
1:F:1545:HIS:CD2	2:G:5:LYS:HG3	2.47	0.50
2:G:65:ASP:HA	2:G:68:ARG:HG2	1.92	0.50
2:G:129:LEU:HA	2:G:132:LYS:HG2	1.94	0.50
3:E:609:PRO:O	3:E:613:ILE:HG12	2.11	0.50
3:A:230:PRO:O	3:A:234:GLY:N	2.42	0.50
1:B:568:ASP:OD2	1:B:569:LEU:N	2.43	0.50
1:B:568:ASP:HB3	1:B:592:LYS:HG3	1.94	0.50
1:B:892:ASP:H	1:B:895:ASN:CG	2.19	0.50
1:B:1125:ILE:HD12	1:B:1172:LEU:HA	1.94	0.50
1:F:1532:CYS:SG	1:F:1533:VAL:N	2.85	0.50
1:F:1593:ILE:O	1:F:1597:MET:HG2	2.12	0.50
3:A:120:PHE:CZ	3:A:125:GLY:HA3	2.47	0.50
3:A:147:MET:HE3	3:A:151:PHE:HB2	1.94	0.50
1:B:740:TYR:C	1:B:753:LEU:HD21	2.37	0.50
1:B:923:VAL:O	1:B:926:GLN:HB3	2.12	0.50
1:B:1549:MET:HE1	2:C:56:TRP:CE2	2.47	0.50
1:F:973:ILE:HA	1:F:976:PHE:CE1	2.46	0.50
1:F:1632:LYS:HD3	1:F:1636:HIS:CD2	2.47	0.50
1:F:1633:VAL:O	1:F:1639:VAL:N	2.39	0.50
2:G:69:PRO:O	2:G:73:PRO:HD3	2.12	0.50
3:E:586:LEU:HD23	3:E:608:LEU:HB3	1.94	0.50
3:E:685:ASP:HA	3:E:688:THR:HG22	1.94	0.50
3:A:564:LYS:HZ3	3:A:575:TRP:CD1	2.30	0.50
4:D:36:VAL:O	4:D:37:PHE:HB3	2.11	0.50
1:B:16:ILE:HG23	3:A:706:ILE:HG13	1.93	0.50
1:B:41:TYR:CZ	3:A:717:PRO:HD3	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:GLN:HA	1:B:122:TYR:CD2	2.47	0.50
1:B:143:GLU:HA	1:B:146:LYS:HZ3	1.77	0.50
1:B:596:GLU:O	1:B:600:LEU:HG	2.12	0.50
1:B:720:ILE:HA	1:B:724:PHE:HB2	1.94	0.50
1:B:1094:LEU:HD22	1:B:1098:LYS:HG3	1.94	0.50
2:C:110:ILE:O	2:C:152:VAL:HG12	2.12	0.50
1:F:13:GLY:HA3	1:F:35:VAL:HG23	1.93	0.50
1:F:446:ILE:HG23	1:F:626:ILE:HG12	1.94	0.50
1:F:794:LEU:HG	1:F:798:PHE:CZ	2.47	0.50
1:F:1328:TYR:HB3	1:F:1338:LEU:CD2	2.42	0.50
3:A:51:LEU:HD13	3:A:75:LEU:HD13	1.92	0.50
3:A:89:HIS:HB3	3:A:123:LEU:HD21	1.94	0.50
3:A:321:ARG:HH12	3:A:366:ASN:ND2	2.10	0.50
3:A:560:THR:O	3:A:576:TYR:HA	2.12	0.50
3:A:619:GLY:HA2	3:A:641:ALA:HB3	1.92	0.50
1:B:306:MET:HA	1:B:320:ARG:HG3	1.94	0.49
1:B:713:ASN:O	1:B:717:GLU:HG2	2.12	0.49
1:B:789:ASN:O	1:B:792:ARG:N	2.45	0.49
1:B:883:THR:HG21	1:B:931:ARG:NE	2.26	0.49
1:F:30:GLN:OE1	3:E:697:ARG:NH2	2.45	0.49
1:F:45:TYR:CD2	1:F:64:ILE:HG13	2.38	0.49
1:F:809:ALA:HB1	1:F:812:ILE:HB	1.94	0.49
1:F:1392:GLU:HB2	2:G:166:LYS:HE2	1.94	0.49
1:F:1441:TYR:HE2	1:F:1450:ILE:HG21	1.75	0.49
1:B:677:PHE:HB3	1:B:681:MET:HE1	1.94	0.49
1:B:1258:THR:HG21	1:B:1496:PRO:HB2	1.94	0.49
1:B:1329:GLU:HB3	1:B:1338:LEU:HD11	1.93	0.49
2:C:14:VAL:HG21	2:C:83:SER:HB2	1.94	0.49
2:C:171:GLU:HA	2:C:174:ARG:HG2	1.94	0.49
1:F:908:ASN:O	1:F:911:GLU:HG3	2.12	0.49
1:F:928:ILE:HG23	1:F:932:LEU:HD12	1.94	0.49
1:F:1489:TYR:CE1	1:F:1507:ILE:HG13	2.47	0.49
1:F:1599:LEU:HA	1:F:1602:GLU:OE1	2.12	0.49
3:A:515:LEU:HD12	3:A:516:LYS:N	2.27	0.49
3:A:720:TYR:HB3	3:A:722:PHE:CZ	2.48	0.49
1:B:997:ILE:HG13	1:B:998:GLY:H	1.76	0.49
1:B:1436:SER:OG	1:B:1437:LEU:N	2.44	0.49
1:B:1466:ARG:H	1:B:1484:ILE:HG23	1.77	0.49
1:B:1470:LYS:HD3	1:B:1483:TRP:CD2	2.47	0.49
1:F:562:LEU:HD11	1:F:567:HIS:CG	2.47	0.49
3:E:580:SER:HB2	3:E:587:HIS:NE2	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:166:ARG:HH12	1:B:168:ASP:HB2	1.77	0.49
1:B:534:ARG:NH2	1:B:541:ASP:OD2	2.46	0.49
1:B:879:LEU:HD22	1:B:924:HIS:CE1	2.47	0.49
1:B:1151:LEU:O	1:B:1155:LEU:HB2	2.13	0.49
1:F:94:THR:HG22	1:F:98:TRP:CE2	2.47	0.49
1:F:943:MET:HE1	1:F:953:PHE:CG	2.46	0.49
1:F:1184:LYS:HD2	1:F:1184:LYS:N	2.27	0.49
1:F:1236:ARG:HG3	1:F:1239:ILE:HG12	1.94	0.49
1:F:1368:TYR:HA	1:F:1378:ASN:HA	1.94	0.49
1:F:1416:GLU:HA	1:F:1419:LYS:HG2	1.93	0.49
1:F:1438:PRO:HB3	1:F:1454:TYR:CD2	2.46	0.49
1:F:1611:LEU:HD21	1:F:1616:LYS:HE2	1.94	0.49
3:A:222:GLU:O	3:A:227:GLN:NE2	2.45	0.49
3:A:541:GLN:N	3:A:542:PRO:HD3	2.26	0.49
1:B:44:TRP:HE3	1:B:58:ILE:HG22	1.77	0.49
1:B:197:LYS:O	1:B:200:GLU:HG2	2.12	0.49
1:B:273:LYS:O	1:B:276:ASN:N	2.45	0.49
1:B:436:ILE:HG23	1:B:711:HIS:NE2	2.28	0.49
1:B:551:PHE:CZ	1:B:585:TYR:HB2	2.47	0.49
1:B:817:LEU:HD11	1:B:855:GLN:HB3	1.94	0.49
1:B:1015:ARG:HD3	1:B:1076:TYR:CD1	2.45	0.49
1:B:1153:THR:O	1:B:1156:ASP:HB3	2.12	0.49
1:F:103:ARG:HA	1:F:106:TYR:HE1	1.77	0.49
1:F:110:LYS:O	1:F:112:THR:N	2.45	0.49
1:F:242:PHE:CD2	1:F:259:LEU:HD13	2.48	0.49
1:F:297:VAL:HG22	1:F:326:VAL:HG13	1.94	0.49
1:F:470:MET:HB2	1:F:527:ILE:CG2	2.42	0.49
1:F:993:PHE:O	1:F:997:ILE:HG12	2.12	0.49
1:F:1176:LEU:HD12	1:F:1177:LEU:N	2.27	0.49
1:F:1387:GLU:HG2	1:F:1388:TYR:CD2	2.47	0.49
3:E:550:GLN:HA	3:E:553:LEU:HD12	1.94	0.49
3:A:607:LYS:HG3	3:A:609:PRO:HD3	1.95	0.49
1:B:44:TRP:NE1	3:A:714:PRO:O	2.44	0.49
1:B:166:ARG:HB3	1:B:171:ASN:C	2.38	0.49
1:B:237:GLU:C	1:B:264:SER:HA	2.37	0.49
1:B:517:ILE:HB	1:B:522:VAL:HB	1.93	0.49
1:B:1193:PHE:O	1:B:1196:LEU:HB2	2.12	0.49
1:B:1206:ASP:O	1:B:1209:THR:HG22	2.11	0.49
1:B:1584:GLU:O	1:B:1588:LEU:HG	2.13	0.49
1:B:1630:LYS:O	1:B:1633:VAL:HG22	2.12	0.49
1:F:471:SER:HB2	1:F:479:LEU:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:721:TYR:HB2	1:F:722:LYS:NZ	2.27	0.49
1:F:854:ARG:H	1:F:854:ARG:HD2	1.76	0.49
1:F:1361:GLU:C	1:F:1362:TYR:HD1	2.20	0.49
3:A:384:MET:SD	3:A:395:TYR:HE1	2.36	0.49
4:D:11:ASP:CG	4:D:97:TRP:HE1	2.15	0.49
1:B:249:ASP:OD2	1:B:292:PRO:HB2	2.13	0.49
1:B:776:ARG:HG3	1:B:777:PHE:HD2	1.78	0.49
1:B:840:PHE:O	1:B:843:PHE:HB3	2.13	0.49
1:B:1125:ILE:N	1:B:1126:PRO:HD2	2.28	0.49
2:C:96:LYS:O	2:C:100:GLU:HG3	2.13	0.49
1:F:256:GLU:HB3	1:F:447:TYR:CE1	2.48	0.49
1:F:632:THR:HG21	1:F:637:LEU:HD23	1.95	0.49
1:F:1221:MET:HE2	1:F:1250:LEU:HD13	1.95	0.49
2:G:39:ASN:OD1	2:G:56:TRP:HA	2.13	0.49
3:E:591:LEU:HD21	3:E:603:SER:HB2	1.94	0.49
3:A:244:ILE:HG21	3:A:293:GLN:HB3	1.95	0.49
3:A:387:PHE:HA	3:A:391:HIS:H	1.77	0.49
4:D:142:GLY:HA3	4:D:154:TYR:CE2	2.48	0.49
1:B:228:PHE:HB2	1:B:401:VAL:HG12	1.95	0.49
1:B:319:ARG:HD2	1:B:497:LYS:HB2	1.95	0.49
1:B:439:PRO:HG3	1:B:712:PHE:CD2	2.47	0.49
1:B:864:VAL:HG23	1:B:868:LEU:HD22	1.94	0.49
1:B:1035:GLN:HG2	1:B:1036:ALA:N	2.27	0.49
1:B:1136:PHE:CG	1:B:1186:LEU:HD22	2.48	0.49
1:B:1435:MET:HE3	1:B:1436:SER:HB3	1.95	0.49
1:B:1483:TRP:CE3	1:B:1511:GLU:HG3	2.48	0.49
1:B:1488:THR:N	1:B:1508:SER:O	2.32	0.49
1:F:4:TRP:HB3	1:F:39:GLU:HB3	1.95	0.49
1:F:81:ILE:HD13	1:F:141:LEU:HD21	1.95	0.49
1:F:1044:ASN:O	1:F:1048:HIS:ND1	2.45	0.49
1:F:1098:LYS:O	1:F:1102:ILE:HG13	2.12	0.49
2:G:102:ARG:NH1	2:G:106:PRO:O	2.42	0.49
3:A:11:ALA:HB3	3:A:74:ILE:HG12	1.94	0.49
3:A:361:PHE:CE1	3:A:415:ARG:HB2	2.47	0.49
3:A:500:ASP:OD2	3:A:501:GLN:N	2.46	0.49
4:D:19:LEU:HG	4:D:169:PHE:CE2	2.48	0.49
4:D:46:VAL:CG1	4:D:174:ARG:HB3	2.42	0.49
1:B:246:TYR:CE2	1:B:387:ILE:HD11	2.48	0.49
1:B:347:PRO:HB2	1:B:392:VAL:HB	1.94	0.49
1:B:444:ASN:HA	1:B:628:SER:HA	1.94	0.49
1:B:518:ALA:HB3	1:B:521:GLU:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1013:GLN:HA	1:B:1016:VAL:HG22	1.94	0.49
1:B:1300:LEU:O	1:B:1304:ILE:HG13	2.12	0.49
1:F:124:LEU:HD21	1:F:151:LYS:HB2	1.93	0.49
1:F:320:ARG:CZ	1:F:500:VAL:HB	2.43	0.49
1:F:1412:THR:OG1	1:F:1466:ARG:NE	2.46	0.49
1:F:1462:PHE:HB2	1:F:1489:TYR:HB2	1.94	0.49
1:F:1466:ARG:HG2	1:F:1485:GLU:HB2	1.95	0.49
1:F:1586:VAL:HA	1:F:1589:LEU:HD12	1.95	0.49
1:F:1617:PRO:HB2	1:F:1621:ARG:HH22	1.78	0.49
3:E:620:LYS:HD3	3:E:625:MET:HB3	1.93	0.49
3:A:470:MET:C	3:A:471:ARG:HD3	2.38	0.49
1:B:9:ARG:HH21	1:B:69:ALA:C	2.21	0.49
1:B:564:ASP:CG	1:B:633:GLN:HE22	2.21	0.49
1:B:584:PHE:O	1:B:587:THR:OG1	2.21	0.49
1:B:745:ASP:OD1	1:B:804:ARG:NH1	2.45	0.49
1:B:1183:HIS:CG	1:B:1184:LYS:N	2.81	0.49
1:F:44:TRP:CH2	1:F:60:PRO:HG3	2.48	0.49
1:F:94:THR:HG22	1:F:98:TRP:NE1	2.28	0.49
1:F:1017:PHE:O	1:F:1021:ILE:HG12	2.13	0.49
1:F:1193:PHE:O	1:F:1197:VAL:HG23	2.13	0.49
1:F:1232:LYS:HB2	1:F:1240:TYR:CE2	2.48	0.49
1:F:1464:TYR:O	1:F:1486:ARG:HA	2.11	0.49
3:A:188:VAL:HG23	3:A:231:HIS:CE1	2.47	0.49
3:A:532:PRO:HG2	3:A:708:ASP:HB2	1.94	0.49
4:D:90:TYR:HE2	4:D:142:GLY:HA2	1.77	0.49
1:B:121:THR:HA	1:B:124:LEU:HD12	1.94	0.48
1:B:166:ARG:HD3	1:B:174:ASP:OD1	2.13	0.48
1:B:700:ILE:O	1:B:703:LEU:HB3	2.13	0.48
1:B:1381:PHE:HD2	1:B:1501:TRP:HD1	1.61	0.48
1:B:1563:PHE:O	1:B:1567:GLU:HG2	2.12	0.48
1:F:72:GLU:OE1	1:F:74:LEU:N	2.46	0.48
1:F:526:HIS:HB2	1:F:552:VAL:O	2.13	0.48
1:F:1019:ARG:O	1:F:1023:GLN:NE2	2.33	0.48
2:G:5:LYS:HE2	2:G:56:TRP:HZ2	1.78	0.48
3:E:614:LYS:HB2	3:E:645:LEU:HB2	1.95	0.48
3:A:204:ILE:HG22	3:A:208:MET:HE3	1.93	0.48
3:A:509:LEU:HD23	3:A:514:ILE:HD11	1.94	0.48
4:D:126:LEU:O	4:D:130:LYS:HG2	2.13	0.48
1:B:228:PHE:O	1:B:277:LEU:HB2	2.13	0.48
1:B:909:ILE:O	1:B:913:LEU:HD13	2.14	0.48
1:B:1206:ASP:HA	1:B:1209:THR:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:39:ASN:HA	2:C:57:ASP:H	1.78	0.48
1:F:505:LYS:HD2	1:F:506:GLN:HG3	1.95	0.48
1:F:743:ASN:HB3	1:F:749:LYS:HD2	1.95	0.48
1:F:1043:TRP:HE1	1:F:1090:MET:HE2	1.77	0.48
3:A:397:ARG:HH22	3:A:461:GLN:CD	2.21	0.48
4:D:87:PRO:HD2	4:D:129:LEU:HD21	1.95	0.48
1:B:227:ASN:HB3	1:B:402:SER:OG	2.14	0.48
1:B:239:ALA:HB3	1:B:262:TRP:HB3	1.94	0.48
1:B:304:GLY:HA2	1:B:317:GLY:H	1.77	0.48
1:B:637:LEU:O	1:B:641:LEU:HG	2.13	0.48
1:B:1125:ILE:HD12	1:B:1172:LEU:HD23	1.94	0.48
1:B:1602:GLU:O	1:B:1606:ILE:HG12	2.14	0.48
1:F:224:LEU:HD23	1:F:245:LEU:HD21	1.95	0.48
1:F:1019:ARG:O	1:F:1023:GLN:HG2	2.13	0.48
1:F:1192:VAL:O	1:F:1196:LEU:HG	2.14	0.48
1:F:1206:ASP:O	1:F:1210:ILE:HG12	2.13	0.48
1:F:1488:THR:OG1	1:F:1508:SER:HB2	2.13	0.48
3:E:576:TYR:HB2	3:E:598:GLU:HA	1.96	0.48
3:E:660:HIS:CG	3:E:661:GLU:N	2.81	0.48
3:A:155:LEU:O	3:A:159:LEU:HG	2.14	0.48
3:A:303:ASN:HA	3:A:431:GLY:HA2	1.95	0.48
4:D:38:ASP:HB2	4:D:57:ASP:HB3	1.95	0.48
1:B:187:HIS:HD1	1:B:1006:TRP:CD1	2.26	0.48
1:B:233:CYS:SG	1:B:234:ASN:N	2.86	0.48
1:B:910:LEU:HA	1:B:913:LEU:HD22	1.94	0.48
1:B:1362:TYR:HD2	1:B:1462:PHE:CE2	2.31	0.48
2:C:89:SER:O	2:C:93:VAL:HG12	2.13	0.48
1:F:240:GLU:OE1	1:F:259:LEU:HD11	2.13	0.48
1:F:741:VAL:HG11	1:F:794:LEU:HD12	1.96	0.48
1:F:1395:SER:O	1:F:1399:LEU:HG	2.11	0.48
1:F:1435:MET:SD	1:F:1455:ARG:NE	2.87	0.48
3:A:202:LEU:HA	3:A:205:LEU:HD12	1.94	0.48
3:A:307:ASP:OD1	3:A:308:ARG:N	2.47	0.48
3:A:514:ILE:HG22	3:A:517:ILE:HD12	1.94	0.48
4:D:66:ARG:HH11	4:D:67:LEU:HB2	1.77	0.48
1:B:35:VAL:HA	1:B:49:THR:HA	1.96	0.48
1:B:239:ALA:HB3	1:B:262:TRP:HD1	1.77	0.48
1:B:570:VAL:HB	1:B:572:TYR:CZ	2.48	0.48
1:B:654:LEU:HD23	1:B:657:LEU:HD12	1.94	0.48
1:F:45:TYR:O	1:F:59:PHE:N	2.41	0.48
1:F:256:GLU:HB3	1:F:447:TYR:HE1	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1183:HIS:CG	1:F:1184:LYS:N	2.81	0.48
1:F:1519:ILE:O	1:F:1523:GLU:HG3	2.13	0.48
2:G:111:ILE:HG23	2:G:153:LYS:O	2.13	0.48
3:A:33:ILE:O	3:A:36:GLU:HG3	2.12	0.48
3:A:191:SER:OG	3:A:192:ALA:N	2.46	0.48
3:A:194:ASP:OD1	3:A:195:ILE:N	2.46	0.48
3:A:356:TYR:CE2	3:A:367:PRO:HB3	2.49	0.48
1:B:29:LEU:HD12	1:B:59:PHE:CE1	2.49	0.48
1:B:450:LEU:O	1:B:510:TYR:N	2.46	0.48
1:B:815:ALA:O	1:B:819:TYR:HD2	1.97	0.48
1:B:1284:GLN:NE2	1:B:1291:TYR:HE2	2.10	0.48
1:B:1399:LEU:HD11	1:B:1407:LYS:HD2	1.96	0.48
1:F:771:ARG:NH2	1:F:784:GLY:HA2	2.28	0.48
1:F:987:MET:HE2	1:F:1042:LEU:HD13	1.95	0.48
1:F:1055:THR:O	1:F:1055:THR:HG22	2.14	0.48
2:G:78:PHE:CD1	2:G:101:VAL:HG11	2.48	0.48
3:A:415:ARG:O	3:A:418:ILE:HG22	2.12	0.48
4:D:11:ASP:HB2	4:D:14:VAL:HG11	1.95	0.48
1:B:122:TYR:CE1	3:A:692:MET:HE3	2.48	0.48
1:B:157:ARG:HB3	1:B:194:ILE:HD12	1.96	0.48
1:B:241:LEU:HD13	1:B:262:TRP:HB2	1.96	0.48
1:B:1013:GLN:O	1:B:1017:PHE:HD2	1.97	0.48
1:B:1117:GLU:OE2	1:B:1120:LEU:HG	2.13	0.48
1:B:1176:LEU:HD12	1:B:1177:LEU:N	2.29	0.48
1:F:24:ASP:N	1:F:24:ASP:OD1	2.46	0.48
1:F:31:ILE:HB	3:E:697:ARG:CB	2.44	0.48
1:F:235:ILE:HD12	1:F:262:TRP:CD1	2.48	0.48
1:F:1089:ASP:HA	1:F:1092:TYR:HD2	1.79	0.48
1:F:1390:ARG:HD3	2:G:44:VAL:HG11	1.96	0.48
1:F:1607:HIS:CD2	1:F:1619:HIS:HB2	2.48	0.48
2:G:29:PRO:HB3	2:G:160:LEU:O	2.13	0.48
3:A:97:MET:CE	3:A:147:MET:HE1	2.42	0.48
3:A:150:CYS:O	3:A:154:MET:HG3	2.14	0.48
1:B:243:MET:HB2	1:B:258:TYR:HB3	1.95	0.48
1:B:555:MET:SD	1:B:559:GLY:HA2	2.54	0.48
1:B:556:ASN:HB2	1:B:558:ASP:OD1	2.14	0.48
1:B:931:ARG:HG3	1:B:932:LEU:HD12	1.94	0.48
1:B:1091:TRP:CD1	1:B:1127:ILE:HD12	2.49	0.48
1:B:1238:ASP:HB3	1:B:1281:HIS:HB3	1.95	0.48
2:C:118:ASP:OD1	2:C:119:LEU:N	2.47	0.48
1:F:582:ALA:C	1:F:583:LYS:HD3	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1371:GLY:C	1:F:1424:GLN:HE21	2.21	0.48
1:F:1576:LEU:HD22	1:F:1583:GLN:HB2	1.95	0.48
1:F:1632:LYS:HA	1:F:1636:HIS:CD2	2.48	0.48
2:G:100:GLU:HB2	2:G:104:HIS:CE1	2.46	0.48
3:A:60:TYR:CE1	3:A:110:LEU:HD11	2.49	0.48
1:B:29:LEU:HD22	1:B:33:ASP:HB3	1.95	0.48
1:B:96:ARG:NH1	3:A:696:LEU:O	2.40	0.48
1:B:224:LEU:HD23	1:B:281:PHE:CD2	2.49	0.48
1:B:285:SER:HB2	1:B:435:GLU:CD	2.39	0.48
1:B:593:MET:HA	1:B:596:GLU:OE2	2.14	0.48
1:B:827:VAL:HG11	1:B:836:LEU:HD13	1.96	0.48
1:F:468:VAL:O	1:F:498:SER:HB3	2.14	0.48
1:F:1177:LEU:HD22	1:F:1181:ARG:HH22	1.79	0.48
1:F:1290:VAL:HG23	1:F:1291:TYR:H	1.78	0.48
2:G:64:TYR:HB2	2:G:68:ARG:NH2	2.27	0.48
3:A:204:ILE:HG22	3:A:208:MET:CE	2.43	0.48
3:A:215:LEU:HA	3:A:218:LYS:HG3	1.96	0.48
3:A:526:GLU:HB2	3:A:531:ARG:H	1.78	0.48
3:A:575:TRP:HB3	3:A:591:LEU:O	2.14	0.48
1:B:10:GLN:OE1	1:B:10:GLN:N	2.47	0.48
1:B:414:GLN:O	1:B:418:SER:HB3	2.14	0.48
1:B:463:PRO:O	1:B:503:GLN:HA	2.14	0.48
1:B:601:GLN:HA	1:B:604:LYS:HG2	1.96	0.48
1:B:871:GLN:HB2	1:B:918:VAL:CG1	2.42	0.48
1:B:1055:THR:HG22	1:B:1055:THR:O	2.12	0.48
1:B:1211:ILE:O	1:B:1212:MET:HE2	2.14	0.48
2:C:153:LYS:HG2	2:C:171:GLU:HG2	1.95	0.48
1:F:979:ARG:HD3	1:F:1039:GLU:OE2	2.14	0.48
1:F:1231:TYR:O	1:F:1235:LYS:N	2.46	0.48
1:F:1328:TYR:HB3	1:F:1338:LEU:HD21	1.95	0.48
1:F:1370:GLN:OE1	1:F:1377:ARG:HD3	2.14	0.48
1:F:1627:ARG:HA	1:F:1630:LYS:HB2	1.94	0.48
1:F:1632:LYS:O	1:F:1637:TYR:N	2.37	0.48
2:G:7:VAL:O	2:G:79:LEU:N	2.41	0.48
3:E:580:SER:OG	3:E:582:ASN:OD1	2.25	0.48
3:A:21:LEU:O	3:A:22:MET:HE2	2.13	0.48
3:A:477:PHE:O	3:A:481:MET:HB2	2.14	0.48
4:D:78:PHE:CD2	4:D:101:VAL:HB	2.49	0.48
1:B:239:ALA:HB1	1:B:300:ILE:HG23	1.96	0.47
1:B:248:PRO:C	1:B:251:SER:H	2.22	0.47
1:B:342:LYS:HG2	1:B:344:HIS:NE2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:345:PHE:HB2	1:B:400:TRP:CZ3	2.48	0.47
1:B:934:ARG:HH12	1:B:938:ARG:N	2.12	0.47
1:B:1224:THR:O	1:B:1227:VAL:HG12	2.14	0.47
2:C:1:MET:HE3	2:C:2:GLN:N	2.29	0.47
2:C:164:GLY:O	2:C:168:VAL:N	2.29	0.47
1:F:1248:ARG:HH11	1:F:1252:ARG:NH1	2.08	0.47
1:F:1262:TYR:HB3	1:F:1498:ILE:HG22	1.96	0.47
3:E:646:TYR:C	3:E:648:SER:H	2.21	0.47
3:A:216:TYR:OH	3:A:250:LEU:O	2.27	0.47
3:A:306:GLU:HA	3:A:309:MET:CG	2.37	0.47
3:A:467:TRP:CG	3:A:472:ALA:HB3	2.49	0.47
3:A:509:LEU:HD23	3:A:514:ILE:CD1	2.44	0.47
4:D:111:LEU:HD13	4:D:171:GLU:OE1	2.14	0.47
1:B:1:MET:HB3	3:A:720:TYR:CD1	2.49	0.47
1:B:293:ARG:HG2	1:B:328:ASP:CG	2.39	0.47
1:B:1042:LEU:O	1:B:1045:ASN:HB3	2.12	0.47
1:B:1132:MET:HE1	1:B:1144:PHE:CD2	2.48	0.47
1:B:1545:HIS:HD2	2:C:5:LYS:NZ	2.11	0.47
1:B:1625:CYS:HA	1:B:1628:GLU:HB3	1.96	0.47
1:B:1632:LYS:HD3	1:B:1636:HIS:ND1	2.29	0.47
1:F:241:LEU:HD13	1:F:262:TRP:HB2	1.96	0.47
1:F:673:LEU:HD11	1:F:716:LEU:HD22	1.96	0.47
1:F:680:MET:HE3	1:F:693:VAL:HG21	1.95	0.47
1:F:858:ASN:O	1:F:861:THR:HB	2.14	0.47
1:F:879:LEU:HD11	1:F:928:ILE:HG12	1.96	0.47
2:G:138:THR:H	2:G:141:GLN:NE2	2.11	0.47
2:G:141:GLN:N	2:G:141:GLN:OE1	2.44	0.47
3:A:325:PHE:O	3:A:328:ARG:HG2	2.14	0.47
4:D:23:TYR:HB2	4:D:165:VAL:HG12	1.95	0.47
1:B:5:ILE:H	1:B:40:MET:N	2.12	0.47
1:B:113:LEU:O	1:B:116:GLN:HG2	2.15	0.47
1:B:223:GLY:HA2	1:B:281:PHE:O	2.14	0.47
1:B:305:HIS:HB3	1:B:314:HIS:HB2	1.95	0.47
1:B:400:TRP:HH2	4:D:127:ARG:HD2	1.78	0.47
1:B:471:SER:N	1:B:528:ARG:O	2.42	0.47
1:B:721:TYR:C	1:B:722:LYS:HD2	2.39	0.47
1:B:1128:PHE:HA	1:B:1131:MET:SD	2.53	0.47
1:B:1154:LYS:O	1:B:1157:GLN:N	2.47	0.47
1:B:1484:ILE:HG22	1:B:1486:ARG:HG3	1.96	0.47
1:B:1617:PRO:O	1:B:1620:GLU:HG3	2.13	0.47
1:F:248:PRO:HG2	1:F:293:ARG:NE	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:555:MET:HE2	1:F:559:GLY:O	2.13	0.47
1:F:852:LEU:O	1:F:856:LYS:HG2	2.15	0.47
1:F:1626:PHE:O	1:F:1629:LEU:HG	2.14	0.47
3:A:52:GLN:NE2	3:A:76:ARG:HH21	2.12	0.47
3:A:356:TYR:CD1	3:A:359:LEU:HD12	2.49	0.47
3:A:505:LYS:O	3:A:509:LEU:HG	2.14	0.47
4:D:142:GLY:HA3	4:D:154:TYR:CZ	2.50	0.47
1:B:11:LYS:NZ	1:B:36:HIS:HB3	2.28	0.47
1:B:120:MET:O	1:B:123:SER:OG	2.29	0.47
1:B:300:ILE:O	1:B:322:PHE:HB3	2.14	0.47
1:B:330:THR:HG22	1:B:334:HIS:HE1	1.78	0.47
1:B:926:GLN:O	1:B:929:MET:HB3	2.14	0.47
1:B:1231:TYR:CE2	1:B:1243:TYR:HE2	2.26	0.47
1:F:643:TRP:CZ3	1:F:683:MET:HE1	2.46	0.47
1:F:749:LYS:HG3	1:F:752:LEU:HB2	1.95	0.47
1:F:796:LEU:HA	1:F:799:ASN:HD22	1.80	0.47
1:F:814:GLY:O	1:F:817:LEU:HG	2.14	0.47
1:F:887:SER:O	1:F:890:LEU:HB3	2.15	0.47
1:F:1117:GLU:CD	1:F:1120:LEU:HG	2.39	0.47
1:F:1273:TRP:CD2	1:F:1297:LYS:HD3	2.50	0.47
1:F:1407:LYS:HG3	1:F:1426:MET:SD	2.55	0.47
1:F:1438:PRO:HB2	1:F:1441:TYR:CB	2.44	0.47
3:A:11:ALA:HA	3:A:21:LEU:HD11	1.95	0.47
3:A:167:ASP:OD1	3:A:168:HIS:N	2.48	0.47
3:A:412:PRO:HB2	3:A:415:ARG:HB3	1.96	0.47
1:B:5:ILE:HB	1:B:40:MET:HB3	1.96	0.47
1:B:13:GLY:O	1:B:35:VAL:N	2.35	0.47
1:B:137:PRO:HB2	1:B:140:GLU:OE1	2.14	0.47
1:B:263:GLY:N	1:B:267:MET:O	2.30	0.47
1:B:467:GLU:OE1	1:B:534:ARG:NH1	2.48	0.47
1:B:591:THR:O	1:B:595:MET:HG3	2.14	0.47
1:B:669:LEU:O	1:B:673:LEU:HG	2.14	0.47
1:B:954:VAL:O	1:B:958:ILE:HG12	2.14	0.47
1:B:1327:THR:HA	1:B:1331:LYS:NZ	2.30	0.47
1:B:1372:PHE:HB3	1:B:1376:LEU:HB2	1.95	0.47
1:B:1617:PRO:HA	1:B:1620:GLU:HG3	1.95	0.47
1:F:875:ARG:HG2	1:F:924:HIS:NE2	2.29	0.47
1:F:1145:HIS:O	1:F:1148:GLU:HG3	2.15	0.47
1:F:1380:ILE:HB	1:F:1504:VAL:HG12	1.96	0.47
2:G:118:ASP:OD1	2:G:118:ASP:N	2.48	0.47
3:E:576:TYR:CB	3:E:598:GLU:HA	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:113:ASP:OD1	3:A:115:THR:OG1	2.32	0.47
3:A:265:ILE:HA	3:A:268:GLN:HG2	1.96	0.47
3:A:529:GLN:CG	3:A:534:LEU:HD11	2.43	0.47
4:D:78:PHE:CE2	4:D:105:CYS:HB2	2.41	0.47
1:B:225:TYR:OH	1:B:278:GLN:NE2	2.41	0.47
1:B:226:VAL:O	1:B:278:GLN:HG2	2.14	0.47
1:B:800:MET:O	1:B:804:ARG:HG3	2.14	0.47
1:B:1033:MET:H	1:B:1035:GLN:NE2	2.12	0.47
1:B:1198:SER:O	1:B:1199:SER:C	2.58	0.47
1:B:1410:SER:O	1:B:1413:PRO:HD2	2.15	0.47
2:C:17:THR:OG1	2:C:18:CYS:N	2.46	0.47
1:F:170:GLY:C	1:F:172:ILE:H	2.21	0.47
1:F:549:VAL:N	1:F:572:TYR:O	2.44	0.47
1:F:1028:LEU:HD12	1:F:1043:TRP:CH2	2.49	0.47
1:F:1303:GLU:O	1:F:1306:SER:HB2	2.15	0.47
1:F:1360:PRO:HG2	1:F:1362:TYR:HE1	1.80	0.47
3:E:531:ARG:HD3	3:E:532:PRO:HD3	1.95	0.47
3:E:587:HIS:HD1	3:E:606:ASP:CG	2.22	0.47
3:E:690:LEU:O	3:E:694:ILE:HG12	2.15	0.47
3:A:26:GLN:NE2	3:A:66:ARG:O	2.48	0.47
3:A:127:SER:O	3:A:130:THR:HB	2.13	0.47
3:A:588:TYR:HE1	3:A:608:LEU:HB2	1.79	0.47
3:A:599:VAL:HG23	3:A:601:HIS:HD2	1.78	0.47
3:A:617:VAL:HG23	3:A:643:SER:HB2	1.96	0.47
3:A:673:LEU:HB3	3:A:675:LYS:NZ	2.30	0.47
1:B:48:TYR:HA	1:B:55:LYS:O	2.15	0.47
1:B:51:GLN:H	1:B:51:GLN:CD	2.21	0.47
1:B:179:SER:OG	1:B:182:ALA:HB3	2.14	0.47
1:B:258:TYR:HA	1:B:488:ALA:HB3	1.97	0.47
1:B:394:HIS:HD1	1:B:394:HIS:H	1.61	0.47
1:B:442:VAL:HA	1:B:629:THR:OG1	2.14	0.47
1:B:568:ASP:CG	1:B:592:LYS:HG3	2.39	0.47
1:B:595:MET:HE1	1:B:615:SER:OG	2.15	0.47
1:B:806:LEU:HG	1:B:810:VAL:HB	1.96	0.47
1:B:866:SER:C	1:B:868:LEU:H	2.22	0.47
1:B:932:LEU:N	1:B:935:ARG:HH21	2.12	0.47
1:B:1009:MET:O	1:B:1012:THR:OG1	2.25	0.47
1:B:1117:GLU:OE2	1:B:1120:LEU:N	2.48	0.47
1:B:1144:PHE:O	1:B:1147:PHE:HB3	2.14	0.47
1:B:1156:ASP:OD2	1:B:1242:ARG:NH2	2.39	0.47
1:F:220:HIS:CE1	1:F:286:SER:HB3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:228:PHE:HE2	1:F:399:LEU:HB2	1.79	0.47
1:F:293:ARG:HH21	1:F:295:SER:HB3	1.80	0.47
1:F:351:ILE:HG12	1:F:382:VAL:HG11	1.95	0.47
1:F:810:VAL:HG23	1:F:852:LEU:HD11	1.96	0.47
1:F:882:LEU:HA	1:F:885:GLN:NE2	2.30	0.47
1:F:1174:LYS:HE2	1:F:1174:LYS:HB3	1.62	0.47
1:F:1529:ILE:O	1:F:1533:VAL:HG23	2.15	0.47
1:F:1536:HIS:CD2	1:F:1542:LEU:HB3	2.50	0.47
3:A:104:LEU:HD21	3:A:158:THR:N	2.30	0.47
3:A:189:ASN:HA	3:A:227:GLN:OE1	2.14	0.47
3:A:588:TYR:CE1	3:A:608:LEU:HB2	2.50	0.47
4:D:18:CYS:HA	4:D:29:PRO:HG2	1.97	0.47
4:D:120:ARG:HH12	4:D:156:GLU:CD	2.23	0.47
1:B:32:GLY:HA2	3:A:700:ASP:HB2	1.96	0.47
1:B:44:TRP:CE3	1:B:58:ILE:HG22	2.50	0.47
1:B:696:ALA:O	1:B:700:ILE:HG13	2.15	0.47
1:B:783:ASP:O	1:B:786:GLU:HG3	2.13	0.47
1:B:1470:LYS:HD3	1:B:1483:TRP:CG	2.50	0.47
1:F:30:GLN:HB3	3:E:697:ARG:HE	1.80	0.47
1:F:890:LEU:HD11	1:F:935:ARG:C	2.40	0.47
1:F:915:ARG:HE	1:F:916:LYS:H	1.63	0.47
1:F:943:MET:HG3	1:F:950:ILE:HD12	1.96	0.47
1:F:1279:VAL:HB	1:F:1281:HIS:ND1	2.30	0.47
1:F:1506:GLN:HE22	1:F:1508:SER:HG	1.54	0.47
2:G:63:ASP:OD1	2:G:63:ASP:N	2.47	0.47
2:G:113:VAL:HA	2:G:155:LEU:O	2.15	0.47
2:G:157:CYS:HB2	2:G:163:ARG:O	2.15	0.47
3:A:334:ALA:HB3	3:A:400:LEU:HD21	1.96	0.47
3:A:428:LEU:HD21	3:A:455:PHE:CZ	2.50	0.47
3:A:537:LYS:HB2	3:A:694:ILE:HD13	1.95	0.47
1:B:94:THR:HG22	1:B:98:TRP:CE2	2.50	0.47
1:B:717:GLU:O	1:B:721:TYR:HD2	1.97	0.47
1:B:1027:VAL:HG13	1:B:1028:LEU:HD22	1.96	0.47
1:B:1038:PHE:C	1:B:1039:GLU:HG2	2.40	0.47
1:B:1186:LEU:HD12	1:B:1189:SER:HB2	1.96	0.47
1:B:1483:TRP:NE1	1:B:1514:PRO:HD3	2.29	0.47
1:B:1623:SER:HB3	1:B:1627:ARG:NH1	2.30	0.47
1:F:220:HIS:HD1	1:F:286:SER:HB3	1.79	0.47
1:F:754:PHE:CD1	1:F:811:LYS:HD3	2.50	0.47
1:F:969:TYR:CG	1:F:1023:GLN:HG3	2.50	0.47
1:F:1166:GLU:HA	1:F:1169:LYS:CE	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1209:THR:O	1:F:1213:GLN:HB3	2.14	0.47
1:F:1230:PHE:O	1:F:1234:LYS:HG2	2.15	0.47
1:F:1248:ARG:NH1	1:F:1252:ARG:HH22	2.13	0.47
1:F:1276:LYS:HD2	1:F:1277:PRO:HD2	1.97	0.47
2:G:151:ALA:O	2:G:153:LYS:N	2.48	0.47
3:A:202:LEU:HB3	3:A:242:TYR:HB3	1.97	0.47
3:A:576:TYR:HB2	3:A:598:GLU:CG	2.44	0.47
3:A:695:LYS:O	3:A:698:LEU:HG	2.14	0.47
1:B:226:VAL:HG22	1:B:403:LEU:HD22	1.97	0.47
1:B:406:LEU:HD11	1:B:420:LEU:HD12	1.97	0.47
1:B:741:VAL:HG21	1:B:798:PHE:CD1	2.49	0.47
1:B:1232:LYS:HB2	1:B:1240:TYR:CE2	2.49	0.47
2:C:43:ASN:HA	2:C:52:ASN:HA	1.96	0.47
1:F:329:ILE:O	1:F:333:ILE:N	2.39	0.47
1:F:658:MET:N	1:F:658:MET:SD	2.88	0.47
1:F:883:THR:OG1	1:F:931:ARG:NH2	2.48	0.47
1:F:1033:MET:HB2	1:F:1035:GLN:HG3	1.97	0.47
2:G:42:ALA:O	2:G:53:LEU:HG	2.15	0.47
3:E:642:PHE:CZ	3:E:654:PHE:HB2	2.50	0.47
3:E:695:LYS:HG2	3:E:698:LEU:HD21	1.96	0.47
3:A:448:HIS:HB2	3:A:499:LEU:HD21	1.96	0.47
4:D:126:LEU:HD23	4:D:136:PRO:HG2	1.96	0.47
1:B:4:TRP:CE2	1:B:46:ARG:HD3	2.50	0.46
1:B:10:GLN:NE2	1:B:40:MET:HB2	2.30	0.46
1:B:141:LEU:O	1:B:145:LYS:HG3	2.15	0.46
1:B:222:TYR:HB2	1:B:284:LEU:HB2	1.97	0.46
1:B:306:MET:HG3	1:B:318:LEU:HD13	1.97	0.46
1:B:318:LEU:HB3	1:B:320:ARG:NH1	2.30	0.46
1:B:806:LEU:HD22	1:B:851:GLN:CD	2.40	0.46
1:B:860:MET:HG3	1:B:905:LEU:HD11	1.97	0.46
1:B:1117:GLU:OE1	1:B:1118:VAL:N	2.48	0.46
1:B:1367:TYR:HB2	1:B:1376:LEU:O	2.15	0.46
1:B:1391:ARG:NH2	2:C:29:PRO:HD3	2.29	0.46
1:B:1408:MET:N	1:B:1426:MET:O	2.37	0.46
2:C:137:ILE:HG23	2:C:141:GLN:CG	2.45	0.46
1:F:945:ARG:HH11	1:F:946:GLN:H	1.63	0.46
1:F:1114:LEU:HD23	1:F:1168:TYR:CE1	2.50	0.46
1:F:1329:GLU:HB3	1:F:1338:LEU:HD11	1.97	0.46
1:F:1451:LEU:HB3	1:F:1455:ARG:NH2	2.27	0.46
3:E:670:ASN:HB2	3:E:678:MET:HE1	1.96	0.46
3:A:157:PHE:O	3:A:160:THR:OG1	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:295:TYR:CZ	3:A:438:CYS:HB2	2.49	0.46
3:A:692:MET:O	3:A:695:LYS:HB3	2.15	0.46
1:B:457:LYS:HD3	1:B:505:LYS:HD2	1.98	0.46
1:B:466:VAL:O	1:B:500:VAL:HA	2.14	0.46
1:B:1404:ASN:HB2	1:B:1406:GLU:OE2	2.14	0.46
1:F:106:TYR:HA	1:F:111:LEU:HD11	1.96	0.46
1:F:163:LEU:HD13	1:F:1005:ASP:O	2.14	0.46
1:F:332:ILE:CG2	1:F:403:LEU:HB3	2.45	0.46
1:F:842:LYS:O	1:F:846:SER:N	2.46	0.46
1:F:866:SER:OG	1:F:867:THR:HG23	2.15	0.46
1:F:915:ARG:HE	1:F:916:LYS:N	2.13	0.46
1:F:1206:ASP:O	1:F:1209:THR:HG22	2.15	0.46
3:E:562:PHE:HB2	3:E:575:TRP:CZ2	2.49	0.46
3:E:613:ILE:HA	3:E:645:LEU:O	2.15	0.46
3:A:555:ARG:HA	3:A:558:GLU:HG3	1.97	0.46
4:D:14:VAL:HA	4:D:83:SER:HB2	1.97	0.46
1:B:101:ILE:O	1:B:105:LEU:HG	2.15	0.46
1:B:109:ASN:HA	1:B:111:LEU:HG	1.97	0.46
1:B:143:GLU:HA	1:B:146:LYS:HE2	1.98	0.46
1:B:246:TYR:HE2	1:B:387:ILE:HD11	1.81	0.46
1:B:410:LEU:O	1:B:414:GLN:HB2	2.16	0.46
1:B:478:LYS:HB3	1:B:478:LYS:HE3	1.77	0.46
1:B:1371:GLY:C	1:B:1424:GLN:HE21	2.24	0.46
1:F:228:PHE:HA	1:F:401:VAL:HG12	1.97	0.46
1:F:716:LEU:O	1:F:720:ILE:HG13	2.16	0.46
1:F:821:PRO:O	1:F:824:ILE:HG12	2.16	0.46
1:F:857:LEU:O	1:F:861:THR:OG1	2.26	0.46
1:F:1362:TYR:HD2	1:F:1462:PHE:CE2	2.29	0.46
1:F:1575:TYR:O	1:F:1579:HIS:N	2.32	0.46
2:G:8:VAL:HA	2:G:79:LEU:O	2.16	0.46
2:G:114:GLY:N	2:G:155:LEU:O	2.37	0.46
3:E:695:LYS:O	3:E:698:LEU:HG	2.16	0.46
3:A:639:GLU:CD	3:A:639:GLU:H	2.21	0.46
4:D:129:LEU:HD12	4:D:136:PRO:HG3	1.96	0.46
1:B:634:ASN:O	1:B:638:LEU:HD23	2.15	0.46
1:B:795:PHE:CZ	1:B:843:PHE:HB2	2.50	0.46
1:B:853:VAL:HA	1:B:856:LYS:HG2	1.97	0.46
1:B:940:VAL:HG11	1:B:957:MET:HE1	1.97	0.46
1:B:1256:ASN:OD1	1:B:1500:LYS:HE2	2.15	0.46
1:B:1318:ILE:O	1:B:1322:LYS:HG2	2.15	0.46
1:B:1433:PRO:HA	1:B:1462:PHE:CD2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:197:LYS:HA	1:F:200:GLU:CD	2.40	0.46
1:F:320:ARG:NH1	1:F:500:VAL:HB	2.31	0.46
1:F:485:HIS:O	1:F:514:LYS:N	2.47	0.46
1:F:713:ASN:HA	1:F:716:LEU:HD12	1.97	0.46
1:F:940:VAL:HA	1:F:943:MET:HE2	1.98	0.46
1:F:1114:LEU:HA	1:F:1168:TYR:CZ	2.51	0.46
1:F:1519:ILE:HG13	1:F:1589:LEU:HD21	1.97	0.46
1:F:1545:HIS:N	1:F:1546:PRO:HD2	2.31	0.46
3:E:693:GLU:OE2	3:E:697:ARG:HD3	2.14	0.46
3:A:225:ILE:HG21	3:A:265:ILE:CG2	2.46	0.46
3:A:479:LYS:O	3:A:483:VAL:HG23	2.16	0.46
3:A:613:ILE:HA	3:A:645:LEU:O	2.16	0.46
3:A:702:GLU:C	3:A:704:ILE:H	2.22	0.46
4:D:119:LEU:HB3	4:D:125:THR:OG1	2.16	0.46
1:B:182:ALA:HA	1:B:185:LYS:HG2	1.97	0.46
1:B:256:GLU:OE1	1:B:429:ARG:N	2.30	0.46
1:B:469:THR:HG23	1:B:497:LYS:HD3	1.97	0.46
1:B:823:ILE:O	1:B:827:VAL:HG23	2.16	0.46
1:B:933:LEU:HD21	1:B:960:LEU:HD22	1.98	0.46
1:B:1299:LYS:HA	1:B:1302:GLN:OE1	2.16	0.46
1:B:1466:ARG:O	1:B:1484:ILE:HA	2.16	0.46
1:B:1632:LYS:O	1:B:1637:TYR:N	2.28	0.46
1:F:87:LEU:O	1:F:90:GLU:HG3	2.16	0.46
1:F:88:VAL:CG2	1:F:128:ARG:HG2	2.46	0.46
1:F:230:ASN:ND2	1:F:268:PRO:HD3	2.31	0.46
1:F:601:GLN:HA	1:F:604:LYS:HG2	1.97	0.46
1:F:833:PRO:HD2	1:F:873:GLU:OE2	2.15	0.46
1:F:1495:PHE:HZ	1:F:1502:PHE:HB2	1.81	0.46
3:A:79:THR:OG1	3:A:84:ASN:OD1	2.33	0.46
3:A:679:SER:O	3:A:682:THR:HB	2.16	0.46
4:D:84:ILE:HG12	4:D:137:ILE:HB	1.98	0.46
1:B:1189:SER:O	1:B:1192:VAL:HG22	2.15	0.46
1:B:1268:ALA:HA	1:B:1271:LEU:HD13	1.98	0.46
2:C:129:LEU:O	2:C:134:LEU:N	2.48	0.46
1:F:5:ILE:H	1:F:40:MET:N	2.06	0.46
1:F:11:LYS:HZ1	1:F:36:HIS:C	2.23	0.46
1:F:181:ILE:HD11	1:F:955:ALA:O	2.16	0.46
1:F:306:MET:H	1:F:314:HIS:CB	2.27	0.46
1:F:669:LEU:HD12	1:F:670:GLN:N	2.30	0.46
1:F:1132:MET:O	1:F:1135:GLU:HB2	2.16	0.46
1:F:1602:GLU:HA	1:F:1605:ARG:HG2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:115:THR:HG22	4:D:157:CYS:SG	2.56	0.46
1:B:448:VAL:HB	1:B:513:VAL:HG23	1.97	0.46
1:B:1003:ALA:H	1:B:1006:TRP:HZ3	1.58	0.46
1:B:1034:ASP:HA	1:B:1037:SER:HA	1.96	0.46
1:B:1175:LEU:HB3	1:B:1179:HIS:CE1	2.51	0.46
1:B:1256:ASN:O	1:B:1259:GLU:N	2.48	0.46
1:B:1363:PHE:O	1:B:1382:ILE:HD12	2.15	0.46
1:B:1451:LEU:HG	1:B:1455:ARG:HH12	1.81	0.46
1:B:1491:THR:HA	1:B:1505:LYS:H	1.80	0.46
1:B:1516:GLU:O	1:B:1517:ASN:C	2.58	0.46
1:F:113:LEU:HA	1:F:116:GLN:CD	2.40	0.46
1:F:329:ILE:HA	1:F:332:ILE:HD12	1.98	0.46
1:F:646:ASN:ND2	1:F:649:ASN:HB2	2.31	0.46
1:F:668:PHE:O	1:F:672:THR:N	2.38	0.46
1:F:800:MET:O	1:F:804:ARG:N	2.47	0.46
1:F:1135:GLU:O	1:F:1139:SER:OG	2.25	0.46
2:G:68:ARG:NH1	2:G:96:LYS:HZ1	2.14	0.46
3:E:694:ILE:HA	3:E:697:ARG:HG2	1.97	0.46
1:B:65:HIS:HE1	1:B:67:LYS:HD2	1.81	0.46
1:B:113:LEU:HA	1:B:116:GLN:CD	2.41	0.46
1:B:306:MET:O	1:B:320:ARG:HG3	2.15	0.46
1:B:378:PRO:HB3	1:B:508:CYS:SG	2.55	0.46
1:B:527:ILE:HB	1:B:552:VAL:HG12	1.96	0.46
1:B:534:ARG:HH21	1:B:541:ASP:CG	2.24	0.46
1:B:928:ILE:O	1:B:932:LEU:HB2	2.15	0.46
1:F:197:LYS:HA	1:F:200:GLU:HG2	1.96	0.46
1:F:651:LYS:HD2	1:F:655:LYS:HE3	1.96	0.46
1:F:956:CYS:O	1:F:960:LEU:HG	2.14	0.46
1:F:1201:LEU:O	1:F:1205:LEU:HD23	2.16	0.46
2:G:35:THR:OG1	2:G:40:TYR:OH	2.34	0.46
3:E:551:GLN:O	3:E:555:ARG:HD3	2.16	0.46
3:E:720:TYR:HB3	3:E:722:PHE:CE1	2.50	0.46
3:A:359:LEU:O	3:A:412:PRO:HB3	2.16	0.46
3:A:458:ILE:HD11	3:A:503:LYS:HA	1.98	0.46
1:B:19:TYR:HB3	1:B:27:LEU:O	2.15	0.46
1:B:107:VAL:HA	3:A:555:ARG:HH12	1.81	0.46
1:B:222:TYR:HD1	1:B:407:PRO:HA	1.80	0.46
1:B:1035:GLN:HG2	1:B:1036:ALA:H	1.81	0.46
1:B:1394:PHE:HD2	1:B:1428:CYS:HG	1.64	0.46
1:B:1623:SER:HB3	1:B:1627:ARG:CZ	2.46	0.46
2:C:86:SER:O	2:C:89:SER:OG	2.25	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:96:ARG:O	1:F:99:ALA:HB3	2.16	0.46
1:F:246:TYR:HB3	1:F:297:VAL:HG21	1.98	0.46
1:F:1068:LYS:O	1:F:1072:ILE:HG12	2.15	0.46
1:F:1557:PRO:HG2	1:F:1561:GLY:HA2	1.97	0.46
2:G:47:ASP:O	2:G:49:LYS:N	2.43	0.46
3:A:37:VAL:HG12	3:A:77:LEU:HD22	1.97	0.46
1:B:13:GLY:O	1:B:34:THR:HA	2.16	0.46
1:B:242:PHE:O	1:B:298:CYS:HA	2.15	0.46
1:B:325:ALA:HB2	1:B:348:PHE:HD1	1.80	0.46
1:B:640:LEU:HD11	1:B:657:LEU:HD21	1.98	0.46
1:B:1156:ASP:O	1:B:1160:GLU:HG3	2.16	0.46
1:B:1358:PRO:HB2	1:B:1387:GLU:HB2	1.98	0.46
1:B:1545:HIS:HD2	2:C:5:LYS:CE	2.27	0.46
1:B:1613:GLU:CD	1:B:1614:GLN:HG3	2.40	0.46
1:F:860:MET:O	1:F:864:VAL:HG12	2.16	0.46
1:F:1617:PRO:O	1:F:1620:GLU:HG3	2.16	0.46
3:E:634:ASN:O	3:E:637:VAL:HG22	2.16	0.46
3:A:545:LEU:HD12	3:A:546:GLU:N	2.31	0.46
3:A:576:TYR:HB2	3:A:598:GLU:HG2	1.97	0.46
4:D:78:PHE:CE2	4:D:101:VAL:HB	2.51	0.46
1:B:128:ARG:NH1	1:B:132:LEU:HD21	2.31	0.45
1:B:651:LYS:HB2	1:B:655:LYS:HE3	1.97	0.45
1:B:757:LEU:HD13	1:B:760:LEU:HD11	1.98	0.45
1:B:1105:MET:O	1:B:1108:PRO:HD2	2.15	0.45
1:B:1193:PHE:HA	1:B:1196:LEU:HD12	1.97	0.45
1:B:1386:LYS:HD3	1:B:1386:LYS:HA	1.79	0.45
1:B:1575:TYR:O	1:B:1579:HIS:N	2.27	0.45
1:F:31:ILE:HG21	3:E:698:LEU:HA	1.97	0.45
1:F:721:TYR:C	1:F:722:LYS:HD3	2.41	0.45
1:F:764:PHE:CE1	1:F:826:ASP:HB2	2.51	0.45
1:F:879:LEU:HD21	1:F:931:ARG:HH12	1.82	0.45
1:F:948:PRO:C	1:F:950:ILE:H	2.24	0.45
1:F:1283:LEU:HB3	1:F:1288:TYR:CD1	2.51	0.45
1:F:1535:GLN:OE1	1:F:1542:LEU:HD11	2.16	0.45
3:E:625:MET:HE1	3:E:633:GLN:O	2.16	0.45
3:A:240:GLN:HA	3:A:243:THR:HG22	1.97	0.45
3:A:328:ARG:NE	3:A:329:ARG:HH21	2.11	0.45
3:A:526:GLU:CB	3:A:531:ARG:H	2.29	0.45
4:D:98:HIS:HA	4:D:101:VAL:HG22	1.99	0.45
1:B:25:VAL:HG23	1:B:57:GLY:HA2	1.97	0.45
1:B:901:ALA:HA	1:B:904:GLN:NE2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:914:ASP:HB2	1:B:963:GLN:NE2	2.31	0.45
1:B:1068:LYS:O	1:B:1072:ILE:HG12	2.15	0.45
1:B:1610:LYS:HD2	1:B:1610:LYS:N	2.31	0.45
2:C:80:ILE:HD11	2:C:97:TRP:HB3	1.97	0.45
2:C:87:PRO:O	2:C:90:PHE:HB2	2.16	0.45
1:F:1218:GLU:O	1:F:1221:MET:HB2	2.16	0.45
1:F:1478:GLU:OE2	1:F:1478:GLU:N	2.41	0.45
1:F:1504:VAL:HG22	1:F:1506:GLN:H	1.81	0.45
3:A:82:ALA:HB2	3:A:119:GLU:HG2	1.98	0.45
3:A:223:ILE:HD13	3:A:246:VAL:CG1	2.46	0.45
3:A:523:MET:O	3:A:526:GLU:HG2	2.16	0.45
3:A:591:LEU:HD21	3:A:603:SER:HB2	1.97	0.45
3:A:613:ILE:HD12	3:A:644:ILE:HG22	1.97	0.45
1:B:382:VAL:O	1:B:386:VAL:HG23	2.17	0.45
1:B:532:ARG:NH1	1:B:541:ASP:O	2.46	0.45
1:B:809:ALA:O	1:B:810:VAL:C	2.59	0.45
1:B:934:ARG:HH12	1:B:938:ARG:H	1.64	0.45
1:B:934:ARG:HB3	1:B:935:ARG:NH1	2.31	0.45
1:B:1292:THR:O	1:B:1295:GLU:N	2.48	0.45
1:B:1390:ARG:HB2	2:C:166:LYS:NZ	2.31	0.45
1:B:1518:ALA:HB1	1:B:1566:TYR:CE1	2.50	0.45
2:C:97:TRP:O	2:C:101:VAL:HG22	2.16	0.45
1:F:3:ARG:HA	3:E:723:VAL:HG23	1.98	0.45
1:F:207:ASN:C	1:F:208:LEU:HD12	2.42	0.45
1:F:258:TYR:CE2	1:F:279:ALA:HB2	2.52	0.45
1:F:717:GLU:O	1:F:721:TYR:HD2	1.99	0.45
1:F:932:LEU:O	1:F:936:ILE:HG22	2.17	0.45
1:F:1220:ARG:HA	1:F:1223:CYS:SG	2.56	0.45
1:F:1238:ASP:HA	1:F:1241:ILE:HD12	1.98	0.45
1:F:1277:PRO:HA	1:F:1293:GLN:HG3	1.98	0.45
1:F:1444:LYS:O	1:F:1446:VAL:N	2.44	0.45
3:A:11:ALA:HB3	3:A:74:ILE:HA	1.97	0.45
3:A:72:GLY:HA2	4:D:36:VAL:HG11	1.98	0.45
3:A:96:SER:OG	3:A:99:ALA:HB3	2.16	0.45
3:A:104:LEU:HD11	3:A:158:THR:HA	1.97	0.45
3:A:140:TYR:HD1	3:A:144:GLN:HB3	1.81	0.45
3:A:272:ARG:HH21	3:A:449:ASP:CG	2.25	0.45
3:A:299:VAL:HA	3:A:302:PHE:HB2	1.98	0.45
3:A:328:ARG:CZ	3:A:351:MET:HE1	2.46	0.45
3:A:420:LEU:HD22	3:A:459:CYS:SG	2.57	0.45
3:A:425:CYS:HG	3:A:452:PHE:HE1	1.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:685:ASP:O	3:A:689:LEU:HG	2.15	0.45
4:D:72:TYR:CZ	4:D:101:VAL:HG12	2.50	0.45
1:B:127:TRP:CE3	1:B:148:VAL:HG12	2.52	0.45
1:B:883:THR:HA	1:B:886:LEU:HG	1.97	0.45
1:B:891:ASP:OD1	1:B:938:ARG:NH2	2.46	0.45
1:B:1262:TYR:HE2	1:B:1496:PRO:O	1.98	0.45
1:B:1324:LEU:HB3	1:B:1341:LEU:HD21	1.99	0.45
1:F:11:LYS:NZ	1:F:38:LEU:HD22	2.32	0.45
1:F:757:LEU:HD12	1:F:819:TYR:HB2	1.98	0.45
1:F:795:PHE:HA	1:F:798:PHE:CD2	2.52	0.45
1:F:969:TYR:CD1	1:F:1023:GLN:HG3	2.51	0.45
1:F:1013:GLN:HA	1:F:1016:VAL:HG22	1.97	0.45
1:F:1628:GLU:O	1:F:1631:GLU:HG3	2.17	0.45
3:E:561:CYS:SG	3:E:597:GLY:HA2	2.56	0.45
3:A:166:MET:HB3	3:A:173:TRP:CZ3	2.50	0.45
3:A:180:PHE:HE1	3:A:204:ILE:HD13	1.82	0.45
3:A:472:ALA:HB1	3:A:480:VAL:HG11	1.98	0.45
3:A:580:SER:HB3	3:A:585:VAL:HG13	1.99	0.45
4:D:4:ILE:HG23	4:D:76:ASN:HB2	1.98	0.45
1:B:35:VAL:O	1:B:37:ILE:HG13	2.16	0.45
1:B:285:SER:H	1:B:288:ASP:CB	2.23	0.45
1:B:384:ASN:HA	1:B:387:ILE:HD12	1.98	0.45
1:B:871:GLN:CG	1:B:875:ARG:HD3	2.43	0.45
1:B:1115:THR:HA	1:B:1163:ARG:HH21	1.81	0.45
1:B:1516:GLU:HA	1:B:1519:ILE:HD12	1.98	0.45
1:B:1557:PRO:HB2	1:B:1560:MET:O	2.17	0.45
1:B:1557:PRO:HD3	1:B:1563:PHE:HE2	1.82	0.45
2:C:82:PHE:CD1	2:C:112:LEU:HD11	2.51	0.45
1:F:166:ARG:HH21	1:F:169:ASN:ND2	2.11	0.45
1:F:179:SER:OG	1:F:182:ALA:HB3	2.17	0.45
1:F:338:ASP:OD1	1:F:338:ASP:N	2.45	0.45
1:F:451:ILE:HD12	1:F:621:GLN:HG2	1.99	0.45
1:F:501:TYR:CE2	1:F:509:TRP:HD1	2.34	0.45
1:F:1145:HIS:HA	1:F:1148:GLU:HG3	1.98	0.45
1:F:1596:GLN:O	1:F:1600:LEU:HG	2.17	0.45
1:B:263:GLY:HA3	1:B:267:MET:SD	2.56	0.45
1:B:649:ASN:O	1:B:653:ASN:N	2.28	0.45
1:B:1519:ILE:HG23	1:B:1592:LEU:HD11	1.99	0.45
1:F:91:LEU:O	1:F:95:LEU:HG	2.16	0.45
1:F:285:SER:N	1:F:288:ASP:OD2	2.30	0.45
1:F:331:ASP:HB2	1:F:336:LYS:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:345:PHE:HZ	1:F:394:HIS:CD2	2.35	0.45
1:F:718:THR:O	1:F:722:LYS:HB2	2.17	0.45
1:F:743:ASN:O	1:F:749:LYS:HD2	2.16	0.45
1:F:871:GLN:NE2	1:F:875:ARG:HD3	2.31	0.45
1:F:1237:GLU:O	1:F:1240:TYR:HB3	2.17	0.45
1:F:1249:ASP:HA	1:F:1252:ARG:NH2	2.32	0.45
1:F:1292:THR:HG23	1:F:1295:GLU:H	1.82	0.45
2:G:5:LYS:HD2	2:G:74:GLN:O	2.15	0.45
3:E:531:ARG:O	3:E:535:GLU:HG3	2.17	0.45
3:E:581:PRO:HA	3:E:583:HIS:CE1	2.52	0.45
3:E:688:THR:O	3:E:691:SER:OG	2.27	0.45
3:A:86:GLN:HA	3:A:89:HIS:ND1	2.32	0.45
3:A:141:GLN:HA	3:A:144:GLN:CG	2.46	0.45
3:A:238:GLU:O	3:A:241:THR:OG1	2.24	0.45
3:A:419:GLU:OE1	3:A:481:MET:HG2	2.16	0.45
1:B:1082:GLU:O	1:B:1086:ARG:HG2	2.16	0.45
1:B:1190:GLY:HA2	1:B:1193:PHE:CD2	2.51	0.45
2:C:3:ALA:HA	2:C:52:ASN:O	2.17	0.45
2:C:61:GLN:HB3	2:C:64:TYR:CD1	2.51	0.45
1:F:333:ILE:HG13	1:F:334:HIS:N	2.32	0.45
1:F:797:ALA:O	1:F:801:LEU:HG	2.17	0.45
3:E:564:LYS:HG3	3:E:575:TRP:CE2	2.51	0.45
3:E:702:GLU:C	3:E:704:ILE:H	2.23	0.45
3:A:41:TRP:HD1	3:A:43:LEU:HD21	1.82	0.45
3:A:328:ARG:O	3:A:332:PHE:HB2	2.17	0.45
3:A:514:ILE:HA	3:A:517:ILE:HD12	1.99	0.45
3:A:659:LYS:O	3:A:662:TYR:HB3	2.17	0.45
4:D:18:CYS:HA	4:D:29:PRO:HD2	1.98	0.45
4:D:27:ALA:O	4:D:29:PRO:HD3	2.17	0.45
4:D:37:PHE:HB2	4:D:58:THR:HA	1.97	0.45
1:B:99:ALA:HA	1:B:102:TRP:NE1	2.32	0.45
1:B:662:GLY:HA2	1:B:703:LEU:HD21	1.99	0.45
1:B:666:VAL:HB	1:B:712:PHE:CE2	2.52	0.45
1:B:700:ILE:O	1:B:704:ILE:HG13	2.17	0.45
1:B:730:TYR:CD1	1:B:771:ARG:HB2	2.52	0.45
1:B:893:ASN:O	1:B:896:LYS:NZ	2.50	0.45
1:B:901:ALA:HA	1:B:904:GLN:HE21	1.82	0.45
1:B:1033:MET:HB2	1:B:1035:GLN:OE1	2.17	0.45
1:B:1080:ARG:HA	1:B:1083:ILE:HD12	1.99	0.45
1:B:1354:LYS:HD2	1:B:1355:ALA:N	2.32	0.45
1:B:1462:PHE:O	1:B:1489:TYR:N	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1628:GLU:O	1:B:1631:GLU:HG3	2.17	0.45
1:F:247:ASP:O	1:F:251:SER:N	2.49	0.45
1:F:344:HIS:CG	1:F:403:LEU:HD12	2.52	0.45
1:F:710:GLN:HA	1:F:713:ASN:HD22	1.82	0.45
1:F:1119:GLU:O	1:F:1122:LYS:N	2.50	0.45
2:G:45:MET:HA	2:G:51:VAL:HG22	1.98	0.45
3:A:94:SER:O	3:A:100:LYS:HD2	2.16	0.45
3:A:259:ARG:HB3	3:A:304:LEU:HD21	1.98	0.45
3:A:530:SER:O	3:A:534:LEU:N	2.49	0.45
3:A:612:ASP:O	3:A:646:TYR:HA	2.16	0.45
1:B:529:PHE:O	1:B:549:VAL:HG13	2.17	0.45
1:B:534:ARG:NE	1:B:541:ASP:OD1	2.40	0.45
1:B:1036:ALA:O	1:B:1038:PHE:N	2.49	0.45
1:B:1091:TRP:CD1	1:B:1127:ILE:HG23	2.52	0.45
1:B:1280:PRO:HB3	1:B:1288:TYR:OH	2.17	0.45
1:B:1391:ARG:HB3	1:B:1392:GLU:OE1	2.17	0.45
1:B:1404:ASN:OD1	1:B:1424:GLN:HB2	2.16	0.45
1:B:1597:MET:O	1:B:1601:THR:OG1	2.19	0.45
2:C:46:VAL:HG13	2:C:47:ASP:N	2.32	0.45
1:F:6:PRO:HG3	3:E:724:TYR:CD1	2.52	0.45
1:F:1183:HIS:HB3	1:F:1187:SER:OG	2.17	0.45
1:F:1485:GLU:N	1:F:1485:GLU:OE1	2.50	0.45
3:E:579:LEU:HD11	3:E:583:HIS:HA	1.99	0.45
3:E:639:GLU:H	3:E:639:GLU:CD	2.22	0.45
3:A:166:MET:SD	3:A:173:TRP:HA	2.57	0.45
3:A:307:ASP:HA	3:A:310:MET:HE3	1.99	0.45
1:B:1:MET:H1	3:A:716:GLU:HB3	1.82	0.45
1:B:287:MET:HE3	1:B:435:GLU:OE2	2.17	0.45
1:B:932:LEU:HA	1:B:935:ARG:HE	1.81	0.45
1:B:1127:ILE:HG22	1:B:1131:MET:HE1	1.98	0.45
1:B:1146:MET:HG2	1:B:1147:PHE:N	2.31	0.45
1:B:1231:TYR:CE2	1:B:1239:ILE:HD12	2.52	0.45
2:C:7:VAL:HB	2:C:78:PHE:CD2	2.52	0.45
2:C:93:VAL:HG13	2:C:94:ARG:N	2.32	0.45
1:F:262:TRP:HE1	1:F:266:GLY:HA2	1.82	0.45
1:F:325:ALA:HB2	1:F:348:PHE:HD1	1.82	0.45
1:F:566:ARG:HE	1:F:621:GLN:HE21	1.63	0.45
1:F:593:MET:HG3	1:F:594:GLU:N	2.32	0.45
1:F:656:LYS:HD2	1:F:659:GLU:HG3	1.99	0.45
1:F:668:PHE:O	1:F:672:THR:HG23	2.17	0.45
1:F:879:LEU:HD22	1:F:924:HIS:NE2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1483:TRP:CE3	1:F:1511:GLU:HG3	2.52	0.45
1:F:1604:ILE:CD1	1:F:1622:LEU:HB3	2.47	0.45
2:G:69:PRO:HB3	2:G:104:HIS:CD2	2.52	0.45
3:E:602:ASP:N	3:E:602:ASP:OD1	2.49	0.45
3:A:216:TYR:OH	3:A:254:ALA:HB2	2.17	0.45
3:A:476:ASP:O	3:A:480:VAL:HG12	2.17	0.45
3:A:608:LEU:HD12	3:A:608:LEU:HA	1.71	0.45
3:A:657:PRO:HB2	3:A:661:GLU:OE2	2.17	0.45
1:B:39:GLU:OE1	1:B:46:ARG:NE	2.50	0.44
1:B:231:PHE:CZ	1:B:233:CYS:HB3	2.52	0.44
1:B:501:TYR:OH	1:B:508:CYS:O	2.18	0.44
1:B:795:PHE:HZ	1:B:840:PHE:HA	1.82	0.44
1:B:921:THR:OG1	1:B:924:HIS:HB3	2.17	0.44
1:B:1300:LEU:HA	1:B:1303:GLU:OE1	2.16	0.44
1:F:80:VAL:HG11	1:F:133:SER:HA	1.98	0.44
1:F:105:LEU:HD13	1:F:110:LYS:HZ1	1.83	0.44
1:F:634:ASN:O	1:F:638:LEU:HD23	2.17	0.44
1:F:745:ASP:N	1:F:745:ASP:OD1	2.50	0.44
1:F:882:LEU:O	1:F:885:GLN:HG2	2.18	0.44
1:F:906:LEU:HG	1:F:910:LEU:HD23	1.99	0.44
1:F:1125:ILE:N	1:F:1126:PRO:HD2	2.32	0.44
1:F:1195:LEU:O	1:F:1198:SER:OG	2.33	0.44
2:G:42:ALA:HB3	2:G:53:LEU:HD11	1.97	0.44
3:A:89:HIS:HB3	3:A:123:LEU:HD11	2.00	0.44
3:A:180:PHE:O	3:A:184:ILE:HG12	2.16	0.44
1:B:31:ILE:HD12	3:A:697:ARG:HB2	1.99	0.44
1:B:44:TRP:CH2	1:B:60:PRO:HG3	2.53	0.44
1:B:227:ASN:ND2	1:B:278:GLN:HE21	2.15	0.44
1:B:322:PHE:O	1:B:350:GLN:HA	2.18	0.44
1:B:563:GLN:OE1	1:B:633:GLN:HB3	2.18	0.44
1:B:630:LYS:HG3	1:B:668:PHE:CZ	2.51	0.44
1:B:738:ASN:HA	1:B:741:VAL:HG12	1.98	0.44
1:B:932:LEU:CA	1:B:935:ARG:HE	2.30	0.44
1:B:1217:LYS:HD3	1:B:1217:LYS:N	2.32	0.44
1:B:1545:HIS:CD2	2:C:5:LYS:HE3	2.52	0.44
1:F:118:GLN:HB3	1:F:122:TYR:CZ	2.51	0.44
1:F:628:SER:OG	1:F:629:THR:N	2.49	0.44
1:F:843:PHE:O	1:F:847:ILE:HG13	2.17	0.44
1:F:1015:ARG:N	1:F:1079:MET:HE1	2.32	0.44
1:F:1177:LEU:HD22	1:F:1181:ARG:NH2	2.31	0.44
1:F:1284:GLN:OE1	1:F:1284:GLN:N	2.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:77:VAL:HG12	2:G:109:PRO:HG2	1.98	0.44
3:E:678:MET:N	3:E:678:MET:SD	2.90	0.44
3:A:419:GLU:OE1	3:A:481:MET:HE2	2.17	0.44
3:A:613:ILE:HD12	3:A:644:ILE:CG2	2.46	0.44
1:B:19:TYR:CB	1:B:59:PHE:HE1	2.29	0.44
1:B:29:LEU:HD12	1:B:59:PHE:CZ	2.53	0.44
1:B:59:PHE:HD2	1:B:64:ILE:HD13	1.82	0.44
1:B:95:LEU:HD23	1:B:98:TRP:CD1	2.52	0.44
1:B:706:ASP:OD1	1:B:707:ILE:N	2.51	0.44
1:B:771:ARG:HH22	1:B:784:GLY:CA	2.29	0.44
1:B:982:ILE:O	1:B:986:LEU:HD23	2.17	0.44
1:B:1015:ARG:O	1:B:1018:LEU:HB2	2.18	0.44
1:B:1125:ILE:HG21	1:B:1175:LEU:HG	1.99	0.44
1:B:1197:VAL:O	1:B:1200:LEU:HB2	2.16	0.44
1:B:1392:GLU:HA	1:B:1395:SER:HB3	1.99	0.44
1:B:1601:THR:CB	1:B:1605:ARG:HH21	2.28	0.44
2:C:83:SER:HB3	2:C:86:SER:HB3	2.00	0.44
2:C:100:GLU:O	2:C:104:HIS:ND1	2.40	0.44
1:F:31:ILE:HG13	3:E:536:LEU:HD22	1.99	0.44
1:F:109:ASN:OD1	3:E:555:ARG:NE	2.51	0.44
1:F:985:PHE:CD2	1:F:986:LEU:HD22	2.53	0.44
1:F:1435:MET:HE3	1:F:1436:SER:N	2.21	0.44
3:A:80:SER:O	3:A:84:ASN:ND2	2.50	0.44
4:D:7:VAL:H	4:D:75:THR:HG23	1.81	0.44
4:D:41:SER:HA	4:D:53:LEU:O	2.17	0.44
4:D:83:SER:HB3	4:D:86:SER:HB3	1.99	0.44
4:D:139:PRO:O	4:D:143:GLN:HB2	2.17	0.44
1:B:24:ASP:OD1	1:B:24:ASP:N	2.49	0.44
1:B:45:TYR:CD2	1:B:64:ILE:HG13	2.52	0.44
1:B:52:ASN:HB3	1:B:55:LYS:HE2	1.98	0.44
1:B:300:ILE:HB	1:B:322:PHE:HD2	1.82	0.44
1:B:470:MET:HA	1:B:529:PHE:HA	1.98	0.44
1:B:651:LYS:O	1:B:655:LYS:HG3	2.17	0.44
1:B:1129:PHE:CD1	1:B:1179:HIS:HB2	2.52	0.44
1:B:1560:MET:O	1:B:1560:MET:HG3	2.17	0.44
1:F:106:TYR:HB2	3:E:551:GLN:NE2	2.32	0.44
1:F:304:GLY:O	1:F:318:LEU:HB2	2.18	0.44
1:F:647:SER:HA	1:F:650:ILE:HD12	1.98	0.44
1:F:753:LEU:HD23	1:F:753:LEU:HA	1.74	0.44
1:F:835:GLU:HA	1:F:838:VAL:HG22	1.99	0.44
1:F:937:ASN:ND2	1:F:989:THR:HG22	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1166:GLU:O	1:F:1169:LYS:HG2	2.18	0.44
3:E:663:CYS:HB3	3:E:679:SER:OG	2.16	0.44
3:A:33:ILE:HG13	3:A:66:ARG:HH12	1.82	0.44
1:B:247:ASP:OD1	1:B:249:ASP:HB2	2.16	0.44
1:B:754:PHE:HB2	1:B:812:ILE:HG12	1.98	0.44
1:B:893:ASN:N	1:B:895:ASN:OD1	2.47	0.44
1:B:1440:SER:H	1:B:1442:LYS:HZ2	1.66	0.44
2:C:14:VAL:HG13	2:C:116:LYS:HZ3	1.82	0.44
1:F:242:PHE:CE2	1:F:259:LEU:HD13	2.52	0.44
1:F:470:MET:HB2	1:F:527:ILE:HG21	2.00	0.44
1:F:527:ILE:HB	1:F:552:VAL:HG12	2.00	0.44
1:F:910:LEU:O	1:F:913:LEU:HB2	2.18	0.44
1:F:985:PHE:O	1:F:989:THR:HG23	2.18	0.44
1:F:1322:LYS:HG2	1:F:1345:ARG:HH12	1.81	0.44
2:G:117:LEU:HD13	2:G:156:GLU:HG3	1.98	0.44
3:E:563:ARG:O	3:E:655:ILE:N	2.47	0.44
3:E:652:LEU:HD23	3:E:652:LEU:HA	1.78	0.44
3:E:679:SER:HB2	3:E:682:THR:OG1	2.18	0.44
3:A:485:LYS:O	3:A:489:MET:HG3	2.17	0.44
1:B:114:PHE:O	1:B:118:GLN:OE1	2.34	0.44
1:B:775:LEU:CD2	1:B:781:SER:HB2	2.48	0.44
1:B:800:MET:O	1:B:804:ARG:N	2.48	0.44
1:B:1384:ARG:HB2	1:B:1495:PHE:CD2	2.53	0.44
2:C:145:MET:O	2:C:148:GLU:HB3	2.18	0.44
1:F:327:MET:CE	1:F:347:PRO:HD2	2.47	0.44
1:F:821:PRO:HG3	1:F:863:ILE:HD11	1.99	0.44
1:F:900:GLU:O	1:F:903:SER:OG	2.29	0.44
2:G:110:ILE:HG23	2:G:151:ALA:HA	1.98	0.44
3:E:657:PRO:HD2	3:E:665:TRP:HH2	1.82	0.44
3:A:107:LEU:HD11	3:A:165:LEU:HD11	1.98	0.44
4:D:14:VAL:HB	4:D:83:SER:N	2.33	0.44
1:B:220:HIS:HA	1:B:222:TYR:CZ	2.53	0.44
1:B:450:LEU:HB2	1:B:511:GLU:HB2	1.99	0.44
1:B:1136:PHE:CD1	1:B:1186:LEU:HD22	2.53	0.44
1:B:1232:LYS:HB2	1:B:1232:LYS:HE3	1.89	0.44
1:B:1387:GLU:HG2	1:B:1388:TYR:N	2.33	0.44
1:B:1435:MET:SD	1:B:1455:ARG:HA	2.58	0.44
1:B:1568:LYS:HD2	1:B:1569:ALA:N	2.33	0.44
1:F:795:PHE:CZ	1:F:843:PHE:HB2	2.53	0.44
1:F:891:ASP:HB2	1:F:938:ARG:NH1	2.31	0.44
1:F:903:SER:HB3	1:F:953:PHE:CE2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1283:LEU:HB3	1:F:1288:TYR:HD1	1.83	0.44
1:F:1359:GLN:HG2	1:F:1456:ALA:HB2	2.00	0.44
1:F:1368:TYR:HD2	1:F:1419:LYS:HE3	1.83	0.44
3:A:156:SER:O	3:A:160:THR:HG23	2.18	0.44
3:A:178:VAL:O	3:A:181:ILE:HG22	2.18	0.44
3:A:295:TYR:HB2	3:A:440:ASP:O	2.18	0.44
3:A:359:LEU:HD22	3:A:412:PRO:HA	2.00	0.44
3:A:408:LYS:HE3	3:A:474:SER:C	2.42	0.44
4:D:37:PHE:CB	4:D:58:THR:HA	2.48	0.44
1:B:37:ILE:HD13	1:B:45:TYR:CB	2.44	0.44
1:B:98:TRP:CZ3	1:B:159:LEU:HD12	2.53	0.44
1:B:180:THR:O	1:B:183:LEU:HB2	2.18	0.44
1:B:450:LEU:N	1:B:511:GLU:O	2.47	0.44
1:B:714:PRO:O	1:B:718:THR:OG1	2.27	0.44
1:B:787:PHE:O	1:B:791:ILE:HG12	2.17	0.44
1:B:869:PHE:HA	1:B:918:VAL:HG13	2.00	0.44
1:B:887:SER:O	1:B:890:LEU:HB3	2.18	0.44
1:B:940:VAL:HG13	1:B:992:MET:SD	2.57	0.44
1:B:950:ILE:O	1:B:954:VAL:HG23	2.18	0.44
1:B:1296:LEU:HD12	1:B:1296:LEU:HA	1.65	0.44
2:C:169:PHE:O	2:C:173:ILE:HG22	2.17	0.44
1:F:114:PHE:O	1:F:117:LEU:HB3	2.18	0.44
1:F:329:ILE:HG22	1:F:332:ILE:HD12	2.00	0.44
1:F:1405:ALA:H	3:E:584:LYS:NZ	2.14	0.44
1:F:1436:SER:OG	1:F:1437:LEU:N	2.49	0.44
1:F:1455:ARG:CZ	1:F:1455:ARG:HB2	2.47	0.44
1:F:1606:ILE:HG23	1:F:1610:LYS:NZ	2.33	0.44
3:E:535:GLU:O	3:E:539:LYS:HB2	2.18	0.44
3:A:356:TYR:C	3:A:359:LEU:H	2.26	0.44
3:A:386:TYR:HE1	3:A:391:HIS:HD2	1.64	0.44
3:A:542:PRO:HA	3:A:545:LEU:HG	1.99	0.44
1:B:30:GLN:H	1:B:33:ASP:CG	2.21	0.44
1:B:526:HIS:HA	1:B:553:LYS:HA	1.99	0.44
1:B:985:PHE:CD2	1:B:986:LEU:HD22	2.53	0.44
1:B:1145:HIS:O	1:B:1149:ASN:ND2	2.51	0.44
1:B:1198:SER:OG	1:B:1199:SER:N	2.51	0.44
1:B:1361:GLU:C	1:B:1362:TYR:HD1	2.26	0.44
1:F:2:ALA:HB3	3:E:717:PRO:HB2	2.00	0.44
1:F:558:ASP:OD1	1:F:559:GLY:N	2.51	0.44
1:F:642:ASN:OD1	1:F:646:ASN:HB2	2.17	0.44
1:F:730:TYR:HB2	1:F:767:ILE:HG23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1028:LEU:HD11	1:F:1042:LEU:HD23	2.00	0.44
1:F:1102:ILE:O	1:F:1105:MET:HG3	2.18	0.44
1:F:1321:SER:OG	1:F:1341:LEU:HD11	2.17	0.44
1:F:1328:TYR:CD2	1:F:1338:LEU:HD22	2.52	0.44
1:F:1578:GLU:HG3	1:F:1579:HIS:ND1	2.33	0.44
2:G:68:ARG:HH11	2:G:96:LYS:HZ1	1.65	0.44
3:A:100:LYS:HE2	3:A:132:MET:HE3	2.00	0.44
3:A:212:SER:HB2	3:A:215:LEU:HG	2.00	0.44
4:D:110:ILE:O	4:D:152:VAL:HG22	2.17	0.44
1:B:18:ASN:HD22	1:B:28:SER:HB3	1.82	0.43
1:B:98:TRP:CH2	1:B:155:GLY:HA3	2.53	0.43
1:B:166:ARG:HA	1:B:166:ARG:HD2	1.89	0.43
1:B:232:VAL:HG21	1:B:400:TRP:HE1	1.83	0.43
1:B:679:ILE:O	1:B:683:MET:N	2.44	0.43
1:B:1063:THR:CA	1:B:1069:ARG:HH11	2.27	0.43
1:B:1097:HIS:HA	1:B:1100:LYS:NZ	2.33	0.43
1:B:1154:LYS:O	1:B:1155:LEU:C	2.61	0.43
1:F:65:HIS:ND1	1:F:65:HIS:O	2.51	0.43
1:F:1207:TYR:CD2	1:F:1208:ARG:HG3	2.53	0.43
1:F:1323:GLU:O	1:F:1327:THR:HG23	2.18	0.43
1:F:1386:LYS:HG3	1:F:1387:GLU:OE1	2.18	0.43
1:F:1419:LYS:HD2	1:F:1419:LYS:HA	1.74	0.43
3:A:12:ILE:HA	3:A:75:LEU:HB2	1.99	0.43
3:A:130:THR:HG23	3:A:134:GLU:OE2	2.18	0.43
1:B:110:LYS:CD	1:B:113:LEU:HB2	2.48	0.43
1:B:238:ASP:O	1:B:303:VAL:N	2.51	0.43
1:B:966:ASP:HA	1:B:969:TYR:HD1	1.79	0.43
1:B:1183:HIS:ND1	1:B:1184:LYS:O	2.52	0.43
1:B:1546:PRO:HA	1:B:1549:MET:CG	2.48	0.43
1:F:107:VAL:C	3:E:555:ARG:HH22	2.26	0.43
1:F:517:ILE:HB	1:F:522:VAL:HB	2.01	0.43
1:F:741:VAL:HG21	1:F:798:PHE:CD1	2.53	0.43
1:F:1207:TYR:CZ	1:F:1211:ILE:HG13	2.54	0.43
3:E:578:ARG:HG2	3:E:587:HIS:CD2	2.53	0.43
1:B:109:ASN:OD1	3:A:555:ARG:NH2	2.42	0.43
1:B:306:MET:H	1:B:314:HIS:CG	2.36	0.43
1:B:400:TRP:CZ2	4:D:127:ARG:HB2	2.50	0.43
1:B:473:HIS:HB3	1:B:478:LYS:N	2.33	0.43
1:B:1102:ILE:HG23	1:B:1131:MET:HG3	2.01	0.43
1:B:1185:TYR:CD1	1:B:1185:TYR:N	2.86	0.43
1:B:1557:PRO:HG3	1:B:1563:PHE:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:243:MET:O	1:F:258:TYR:N	2.38	0.43
1:F:795:PHE:CD2	1:F:839:LEU:HD22	2.53	0.43
1:F:975:THR:HG22	1:F:975:THR:O	2.18	0.43
1:F:1038:PHE:O	1:F:1039:GLU:HG2	2.18	0.43
3:A:586:LEU:HD23	3:A:608:LEU:O	2.18	0.43
4:D:10:GLY:N	4:D:16:LYS:HD3	2.34	0.43
1:B:101:ILE:HD12	1:B:104:LYS:HE3	2.00	0.43
1:B:166:ARG:O	1:B:166:ARG:HG3	2.18	0.43
1:B:248:PRO:HB3	1:B:387:ILE:HD13	2.00	0.43
1:B:472:VAL:HA	1:B:527:ILE:HA	2.01	0.43
1:B:566:ARG:HE	1:B:621:GLN:CG	2.26	0.43
1:B:570:VAL:HG11	1:B:615:SER:HG	1.81	0.43
1:B:1115:THR:C	1:B:1121:ARG:HH21	2.27	0.43
1:B:1264:LEU:HD22	1:B:1304:ILE:CG1	2.48	0.43
1:B:1328:TYR:HB3	1:B:1338:LEU:CD2	2.48	0.43
1:B:1382:ILE:HD12	1:B:1382:ILE:HA	1.85	0.43
1:B:1432:LYS:HB2	1:B:1463:ARG:HG2	2.00	0.43
1:B:1632:LYS:HA	1:B:1636:HIS:HB2	2.00	0.43
2:C:160:LEU:HD12	2:C:160:LEU:HA	1.78	0.43
1:F:876:GLU:O	1:F:880:PRO:HD3	2.17	0.43
1:F:1159:VAL:HB	1:F:1204:LEU:HD22	2.00	0.43
1:F:1173:GLU:O	1:F:1176:LEU:HG	2.18	0.43
1:F:1230:PHE:O	1:F:1233:GLU:HB3	2.18	0.43
1:F:1326:GLU:HA	1:F:1329:GLU:HG2	2.01	0.43
1:F:1556:ASP:O	1:F:1558:ALA:N	2.51	0.43
3:A:300:LEU:HA	3:A:303:ASN:ND2	2.32	0.43
3:A:502:PHE:CZ	3:A:506:LEU:HD11	2.54	0.43
3:A:578:ARG:NH2	3:A:598:GLU:OE1	2.52	0.43
1:B:101:ILE:O	1:B:104:LYS:HG2	2.19	0.43
1:B:598:LYS:HA	1:B:601:GLN:HG3	2.01	0.43
1:B:904:GLN:O	1:B:907:SER:OG	2.33	0.43
1:B:932:LEU:O	1:B:935:ARG:HB2	2.18	0.43
1:B:1086:ARG:HG2	1:B:1086:ARG:HH11	1.82	0.43
1:B:1237:GLU:O	1:B:1240:TYR:HB3	2.19	0.43
1:B:1395:SER:O	1:B:1399:LEU:HG	2.19	0.43
1:B:1466:ARG:N	1:B:1484:ILE:HG23	2.33	0.43
1:F:142:ALA:O	1:F:146:LYS:HG3	2.19	0.43
1:F:154:HIS:O	1:F:157:ARG:HG2	2.18	0.43
1:F:783:ASP:O	1:F:786:GLU:HG3	2.19	0.43
1:F:926:GLN:O	1:F:929:MET:HG2	2.19	0.43
1:F:1325:ALA:O	1:F:1328:TYR:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:394:ALA:HA	3:A:397:ARG:NE	2.34	0.43
3:A:531:ARG:HD2	3:A:534:LEU:HD12	2.00	0.43
4:D:146:ALA:HB2	4:D:154:TYR:HB2	2.01	0.43
1:B:195:GLU:HA	1:B:198:ILE:HG22	2.01	0.43
1:B:927:LEU:HB3	1:B:931:ARG:NH1	2.21	0.43
1:B:1291:TYR:O	1:B:1292:THR:C	2.60	0.43
1:B:1516:GLU:O	1:B:1519:ILE:HB	2.17	0.43
1:B:1602:GLU:HA	1:B:1605:ARG:HG2	2.00	0.43
1:B:1634:GLU:C	1:B:1635:LYS:HD2	2.43	0.43
1:F:242:PHE:HB2	1:F:299:GLN:OE1	2.18	0.43
1:F:725:SER:HA	1:F:773:LEU:HD11	2.00	0.43
1:F:990:PHE:HD2	1:F:1042:LEU:HD11	1.84	0.43
1:F:1031:PHE:C	1:F:1035:GLN:HE22	2.27	0.43
1:F:1054:LEU:HD22	1:F:1083:ILE:HG22	1.99	0.43
1:F:1396:LEU:O	1:F:1399:LEU:N	2.52	0.43
1:F:1469:ARG:HD2	1:F:1481:THR:CB	2.48	0.43
1:F:1609:GLU:HB2	1:F:1610:LYS:NZ	2.33	0.43
3:E:677:MET:O	3:E:683:ARG:NH1	2.52	0.43
4:D:5:LYS:HB3	4:D:74:GLN:O	2.19	0.43
1:B:48:TYR:HB3	1:B:53:LYS:HD2	2.00	0.43
1:B:305:HIS:HB3	1:B:314:HIS:ND1	2.34	0.43
1:B:468:VAL:HG21	1:B:620:PHE:CE1	2.54	0.43
1:B:552:VAL:HG23	1:B:591:THR:HG21	2.01	0.43
1:B:740:TYR:HB3	1:B:753:LEU:CD2	2.49	0.43
1:B:801:LEU:O	1:B:804:ARG:HB2	2.18	0.43
1:B:1121:ARG:O	1:B:1125:ILE:HG22	2.18	0.43
1:B:1236:ARG:HD3	1:B:1236:ARG:HA	1.90	0.43
1:B:1488:THR:OG1	1:B:1508:SER:N	2.52	0.43
1:F:226:VAL:HG22	1:F:403:LEU:HD23	2.00	0.43
1:F:589:PRO:HB2	1:F:595:MET:HG2	2.01	0.43
1:F:680:MET:HE3	1:F:693:VAL:HG11	1.99	0.43
1:F:908:ASN:O	1:F:912:VAL:HG22	2.18	0.43
1:F:1010:ASN:O	1:F:1013:GLN:NE2	2.52	0.43
1:F:1135:GLU:OE2	1:F:1147:PHE:CG	2.72	0.43
1:F:1354:LYS:HE2	1:F:1354:LYS:HB2	1.84	0.43
1:F:1391:ARG:NH2	2:G:162:GLN:OE1	2.52	0.43
2:G:45:MET:CB	2:G:50:PRO:HA	2.42	0.43
2:G:49:LYS:HZ3	2:G:51:VAL:HG12	1.84	0.43
3:E:681:LEU:HA	3:E:684:ASN:OD1	2.19	0.43
3:A:126:ILE:HG23	3:A:129:LEU:HD12	2.01	0.43
3:A:304:LEU:HD13	3:A:304:LEU:HA	1.89	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:563:ARG:C	3:A:575:TRP:HE1	2.25	0.43
4:D:21:ILE:HG23	4:D:25:THR:OG1	2.18	0.43
1:B:19:TYR:N	1:B:28:SER:HA	2.24	0.43
1:B:60:PRO:O	1:B:64:ILE:HG12	2.19	0.43
1:B:84:GLU:O	1:B:87:LEU:HB3	2.18	0.43
1:B:170:GLY:C	1:B:172:ILE:H	2.27	0.43
1:B:719:TYR:O	1:B:724:PHE:N	2.48	0.43
1:B:783:ASP:HB2	1:B:786:GLU:HG3	2.01	0.43
1:B:992:MET:O	1:B:996:LEU:HD23	2.19	0.43
1:B:1166:GLU:O	1:B:1170:VAL:HG23	2.18	0.43
1:B:1179:HIS:HA	1:B:1182:LYS:HD3	2.00	0.43
1:B:1211:ILE:HG22	1:B:1212:MET:HE3	2.01	0.43
1:B:1295:GLU:OE2	1:B:1299:LYS:HD3	2.19	0.43
1:F:1:MET:HB2	3:E:717:PRO:O	2.19	0.43
1:F:297:VAL:HG22	1:F:326:VAL:HG22	2.01	0.43
1:F:679:ILE:HG23	1:F:683:MET:SD	2.59	0.43
1:F:683:MET:HG3	1:F:689:TYR:CD2	2.54	0.43
1:F:871:GLN:HB2	1:F:918:VAL:CG1	2.47	0.43
1:F:1124:THR:O	1:F:1127:ILE:HB	2.18	0.43
1:F:1276:LYS:O	1:F:1278:CYS:N	2.52	0.43
1:F:1495:PHE:HA	1:F:1496:PRO:C	2.44	0.43
3:A:50:ALA:HB3	3:A:80:SER:HA	2.01	0.43
3:A:232:LEU:HA	3:A:240:GLN:HG2	1.99	0.43
3:A:272:ARG:HG2	3:A:446:PHE:CD1	2.54	0.43
3:A:297:LEU:HB2	3:A:446:PHE:HZ	1.82	0.43
3:A:420:LEU:CD2	3:A:481:MET:HE1	2.48	0.43
4:D:11:ASP:O	4:D:14:VAL:HG22	2.18	0.43
4:D:139:PRO:HA	4:D:154:TYR:HE2	1.84	0.43
1:B:306:MET:HG2	1:B:320:ARG:NH2	2.33	0.43
1:B:419:HIS:CD2	1:B:420:LEU:HG	2.54	0.43
1:B:450:LEU:HD12	1:B:511:GLU:HB2	1.99	0.43
1:B:485:HIS:CE1	1:B:516:SER:HB2	2.53	0.43
1:B:537:GLN:O	1:B:541:ASP:N	2.47	0.43
1:B:730:TYR:HA	1:B:733:LEU:HD12	2.00	0.43
1:B:841:CYS:HA	1:B:881:LEU:CD1	2.49	0.43
1:B:1521:THR:O	1:B:1524:LEU:HG	2.19	0.43
1:F:44:TRP:CD1	3:E:716:GLU:HG3	2.53	0.43
1:F:342:LYS:HG2	1:F:344:HIS:CE1	2.53	0.43
1:F:351:ILE:H	1:F:351:ILE:HG13	1.63	0.43
1:F:472:VAL:HG11	1:F:517:ILE:HD11	2.01	0.43
1:F:472:VAL:HG22	1:F:527:ILE:HG13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1618:LEU:O	1:F:1622:LEU:HG	2.19	0.43
3:E:533:ILE:HD12	3:E:533:ILE:H	1.84	0.43
4:D:95:HIS:O	4:D:99:PRO:HG2	2.19	0.43
1:B:10:GLN:HG3	1:B:37:ILE:HG22	1.99	0.43
1:B:100:VAL:HA	1:B:103:ARG:HB2	2.01	0.43
1:B:192:LYS:HE2	1:B:192:LYS:HA	2.01	0.43
1:B:240:GLU:OE1	1:B:261:ARG:HD2	2.19	0.43
1:B:834:VAL:HG22	1:B:873:GLU:O	2.17	0.43
1:B:1175:LEU:HB3	1:B:1179:HIS:HE1	1.84	0.43
1:B:1191:GLU:O	1:B:1195:LEU:HG	2.19	0.43
1:B:1269:GLU:OE1	1:B:1270:LEU:HD22	2.18	0.43
1:B:1315:GLU:HG2	1:B:1453:TYR:CE2	2.53	0.43
1:B:1517:ASN:O	1:B:1521:THR:HG23	2.19	0.43
1:F:1:MET:C	1:F:4:TRP:HE1	2.27	0.43
1:F:156:ASN:HB3	1:F:161:LEU:HB2	2.01	0.43
1:F:382:VAL:O	1:F:386:VAL:HG23	2.19	0.43
1:F:1014:ASN:O	1:F:1018:LEU:HG	2.19	0.43
1:F:1026:GLU:O	1:F:1030:ARG:HG2	2.18	0.43
1:F:1039:GLU:O	1:F:1040:LEU:HD23	2.19	0.43
1:F:1185:TYR:CG	1:F:1186:LEU:N	2.86	0.43
1:F:1217:LYS:O	1:F:1220:ARG:HB2	2.18	0.43
1:F:1221:MET:CE	1:F:1250:LEU:HD13	2.48	0.43
1:F:1444:LYS:N	1:F:1444:LYS:HD2	2.34	0.43
1:F:1470:LYS:HD3	1:F:1483:TRP:CD2	2.54	0.43
1:F:1617:PRO:HB2	1:F:1621:ARG:NH2	2.34	0.43
3:E:565:LEU:HD23	3:E:565:LEU:HA	1.77	0.43
3:E:613:ILE:HD13	3:E:646:TYR:HB3	2.00	0.43
3:A:2:PRO:HA	3:A:3:PRO:HD3	1.88	0.43
3:A:279:VAL:HG11	3:A:290:MET:SD	2.58	0.43
3:A:693:GLU:OE2	3:A:697:ARG:HD3	2.19	0.43
1:B:17:TYR:CE1	3:A:711:PRO:HD2	2.54	0.42
1:B:70:THR:HG22	1:B:71:VAL:N	2.30	0.42
1:B:73:ASP:O	1:B:78:GLU:N	2.52	0.42
1:B:86:PRO:HA	1:B:89:GLN:HG2	2.00	0.42
1:B:108:ASN:HD21	1:B:110:LYS:HG2	1.84	0.42
1:B:114:PHE:CZ	1:B:118:GLN:NE2	2.87	0.42
1:B:129:SER:O	1:B:132:LEU:HB2	2.19	0.42
1:B:379:LEU:HD23	1:B:379:LEU:HA	1.92	0.42
1:B:814:GLY:O	1:B:817:LEU:HG	2.19	0.42
1:B:905:LEU:O	1:B:906:LEU:C	2.62	0.42
1:B:905:LEU:O	1:B:909:ILE:HG12	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1029:THR:HA	1:B:1033:MET:SD	2.59	0.42
1:B:1086:ARG:NE	1:B:1086:ARG:HA	2.34	0.42
1:B:1156:ASP:O	1:B:1157:GLN:C	2.61	0.42
1:B:1205:LEU:HD13	1:B:1205:LEU:HA	1.91	0.42
1:B:1532:CYS:SG	1:B:1550:LEU:HD12	2.59	0.42
1:B:1593:ILE:O	1:B:1597:MET:HG2	2.19	0.42
2:C:24:THR:HG22	2:C:42:ALA:HB2	2.01	0.42
1:F:132:LEU:HD21	3:E:702:GLU:HB3	2.01	0.42
1:F:241:LEU:O	1:F:260:ILE:N	2.50	0.42
1:F:327:MET:HE3	1:F:346:ILE:HD13	2.01	0.42
1:F:431:MET:HB3	1:F:625:LEU:HD23	2.00	0.42
1:F:446:ILE:HG12	1:F:626:ILE:HG12	2.00	0.42
1:F:775:LEU:O	1:F:779:GLY:N	2.52	0.42
1:F:840:PHE:HA	1:F:843:PHE:HB3	2.00	0.42
1:F:1114:LEU:HD23	1:F:1168:TYR:HE1	1.83	0.42
1:F:1469:ARG:NH1	1:F:1473:LYS:HG3	2.34	0.42
2:G:64:TYR:HA	2:G:66:ARG:NH1	2.34	0.42
2:G:82:PHE:CE1	2:G:154:TYR:HE1	2.37	0.42
3:A:317:ASP:HB3	3:A:320:GLN:HG3	2.00	0.42
4:D:129:LEU:HB3	4:D:134:GLN:O	2.19	0.42
1:B:24:ASP:OD1	1:B:25:VAL:HG22	2.20	0.42
1:B:85:LEU:O	1:B:89:GLN:HG2	2.19	0.42
1:B:293:ARG:HA	1:B:330:THR:OG1	2.19	0.42
1:B:612:SER:OG	1:B:614:ASP:OD1	2.32	0.42
1:B:933:LEU:HD21	1:B:960:LEU:CD2	2.49	0.42
1:B:940:VAL:HG21	1:B:957:MET:HE1	2.01	0.42
1:B:987:MET:O	1:B:991:ILE:HG23	2.20	0.42
1:B:1011:MET:O	1:B:1014:ASN:HB2	2.19	0.42
1:B:1193:PHE:N	1:B:1193:PHE:CD1	2.85	0.42
1:B:1196:LEU:O	1:B:1200:LEU:HG	2.18	0.42
1:B:1231:TYR:CE2	1:B:1243:TYR:CE2	3.04	0.42
1:B:1599:LEU:HA	1:B:1599:LEU:HD12	1.91	0.42
1:B:1607:HIS:C	1:B:1607:HIS:CD2	2.98	0.42
2:C:138:THR:OG1	2:C:140:PRO:HD2	2.19	0.42
1:F:41:TYR:HD2	1:F:44:TRP:HB2	1.84	0.42
1:F:934:ARG:NH1	1:F:934:ARG:O	2.52	0.42
1:F:1015:ARG:HG3	1:F:1079:MET:HE2	2.02	0.42
1:F:1133:GLN:O	1:F:1136:PHE:HB3	2.19	0.42
1:F:1375:PHE:O	1:F:1379:LYS:HG3	2.19	0.42
1:F:1540:ARG:HA	1:F:1540:ARG:CZ	2.49	0.42
1:F:1540:ARG:O	1:F:1542:LEU:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:169:PHE:O	2:G:173:ILE:HG12	2.19	0.42
3:E:575:TRP:HB2	3:E:591:LEU:HB2	2.01	0.42
3:A:69:ILE:HG12	3:A:75:LEU:HD21	2.02	0.42
3:A:129:LEU:O	3:A:132:MET:HG2	2.20	0.42
3:A:260:GLN:NE2	3:A:307:ASP:OD2	2.52	0.42
3:A:522:ARG:HG3	3:A:531:ARG:NH1	2.34	0.42
3:A:609:PRO:HB2	3:A:611:ALA:H	1.83	0.42
3:A:646:TYR:HE1	3:A:652:LEU:HG	1.82	0.42
4:D:152:VAL:HB	4:D:180:THR:HG21	2.02	0.42
1:B:44:TRP:C	1:B:45:TYR:HD1	2.26	0.42
1:B:228:PHE:CE2	1:B:399:LEU:HD12	2.54	0.42
1:B:351:ILE:HD12	1:B:375:GLU:OE1	2.19	0.42
1:B:890:LEU:CD2	1:B:935:ARG:HG3	2.46	0.42
1:B:1022:ASN:O	1:B:1025:ALA:N	2.53	0.42
1:B:1024:PHE:O	1:B:1028:LEU:HD23	2.18	0.42
1:B:1328:TYR:HA	1:B:1332:VAL:CG2	2.50	0.42
1:F:12:TYR:HB2	1:F:67:LYS:HB2	2.01	0.42
1:F:137:PRO:HB2	1:F:140:GLU:OE1	2.20	0.42
1:F:598:LYS:HA	1:F:601:GLN:HG3	2.01	0.42
1:F:874:CYS:HA	1:F:877:VAL:HG12	2.00	0.42
1:F:1298:GLU:HG2	1:F:1302:GLN:OE1	2.19	0.42
1:F:1440:SER:C	1:F:1441:TYR:HD1	2.26	0.42
2:G:119:LEU:HA	2:G:122:ASP:HB2	2.00	0.42
3:A:88:LEU:O	3:A:92:ILE:HB	2.20	0.42
3:A:208:MET:SD	3:A:218:LYS:NZ	2.85	0.42
3:A:246:VAL:O	3:A:250:LEU:HG	2.19	0.42
3:A:526:GLU:C	3:A:529:GLN:H	2.27	0.42
3:A:552:ARG:HB3	3:A:664:ILE:HG23	2.01	0.42
1:B:88:VAL:O	1:B:91:LEU:HB3	2.20	0.42
1:B:128:ARG:O	1:B:132:LEU:HG	2.19	0.42
1:B:330:THR:CA	1:B:333:ILE:HG12	2.42	0.42
1:B:367:LEU:O	1:B:368:ILE:HG13	2.19	0.42
1:B:462:THR:HB	1:B:503:GLN:HG2	2.01	0.42
1:B:614:ASP:OD1	1:B:615:SER:N	2.53	0.42
1:B:768:ILE:O	1:B:772:VAL:HG22	2.20	0.42
1:B:809:ALA:O	1:B:813:LYS:HG3	2.20	0.42
1:B:910:LEU:HA	1:B:913:LEU:HB2	2.00	0.42
1:B:1279:VAL:HB	1:B:1281:HIS:ND1	2.34	0.42
1:B:1279:VAL:HA	1:B:1280:PRO:HD3	1.89	0.42
1:B:1372:PHE:CE2	1:B:1424:GLN:HB3	2.55	0.42
1:B:1452:ASN:OD1	1:B:1452:ASN:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1466:ARG:HB2	1:B:1485:GLU:H	1.84	0.42
1:F:318:LEU:HD22	1:F:320:ARG:NH2	2.34	0.42
1:F:710:GLN:HA	1:F:713:ASN:ND2	2.35	0.42
1:F:879:LEU:HD22	1:F:924:HIS:CE1	2.54	0.42
1:F:1013:GLN:O	1:F:1016:VAL:HG22	2.19	0.42
1:F:1073:VAL:O	1:F:1077:GLY:N	2.48	0.42
3:E:643:SER:OG	3:E:653:ASN:HA	2.20	0.42
4:D:19:LEU:HD13	4:D:157:CYS:SG	2.59	0.42
1:B:380:THR:HA	1:B:510:TYR:CE2	2.54	0.42
1:B:532:ARG:HA	1:B:546:ALA:HA	2.00	0.42
1:B:585:TYR:HA	1:B:588:LEU:HB2	2.00	0.42
1:B:694:PHE:O	1:B:698:VAL:HG23	2.20	0.42
1:B:818:LYS:HA	1:B:862:LYS:HE3	2.02	0.42
1:B:1169:LYS:HZ2	1:B:1202:GLU:HA	1.83	0.42
1:B:1279:VAL:HB	1:B:1281:HIS:HD1	1.85	0.42
1:B:1289:TYR:CE2	1:B:1291:TYR:CE1	3.07	0.42
1:B:1467:PRO:HG3	2:C:33:ILE:CD1	2.48	0.42
1:B:1499:LEU:HD23	1:B:1499:LEU:HA	1.80	0.42
1:B:1514:PRO:CA	1:B:1517:ASN:HD22	2.31	0.42
1:B:1529:ILE:O	1:B:1533:VAL:HG12	2.19	0.42
1:B:1583:GLN:HA	1:B:1586:VAL:HG12	2.01	0.42
1:F:105:LEU:HD22	1:F:110:LYS:CE	2.49	0.42
1:F:809:ALA:O	1:F:812:ILE:N	2.52	0.42
1:F:880:PRO:HA	1:F:931:ARG:HH21	1.85	0.42
1:F:910:LEU:C	1:F:963:GLN:HE22	2.24	0.42
1:F:1473:LYS:HD3	1:F:1481:THR:HG21	2.02	0.42
1:F:1514:PRO:O	1:F:1517:ASN:HB3	2.19	0.42
1:B:1:MET:C	1:B:4:TRP:HE1	2.28	0.42
1:B:323:GLY:HA3	1:B:350:GLN:HA	2.00	0.42
1:B:411:THR:OG1	1:B:412:GLN:N	2.52	0.42
1:B:527:ILE:HD13	1:B:552:VAL:HG13	2.02	0.42
1:B:566:ARG:NE	1:B:621:GLN:HG3	2.27	0.42
1:B:569:LEU:HB2	1:B:620:PHE:HB3	2.02	0.42
1:B:743:ASN:HB2	1:B:749:LYS:CD	2.50	0.42
1:B:1044:ASN:O	1:B:1048:HIS:ND1	2.53	0.42
1:B:1132:MET:HE1	1:B:1144:PHE:CE2	2.55	0.42
1:B:1211:ILE:HG22	1:B:1212:MET:CE	2.50	0.42
1:B:1216:SER:O	1:B:1220:ARG:HG3	2.19	0.42
1:B:1256:ASN:O	1:B:1257:TYR:C	2.63	0.42
2:C:80:ILE:O	2:C:112:LEU:HD12	2.19	0.42
1:F:676:LEU:HG	1:F:693:VAL:HG13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:678:ASN:HA	1:F:681:MET:CG	2.47	0.42
1:F:1066:GLN:HA	1:F:1069:ARG:HH22	1.84	0.42
1:F:1148:GLU:HA	1:F:1151:LEU:HB3	2.01	0.42
1:F:1362:TYR:N	1:F:1362:TYR:CD1	2.87	0.42
3:A:52:GLN:O	3:A:76:ARG:N	2.37	0.42
3:A:317:ASP:O	3:A:321:ARG:HB2	2.19	0.42
3:A:356:TYR:CE1	3:A:359:LEU:HD12	2.54	0.42
3:A:526:GLU:O	3:A:529:GLN:N	2.49	0.42
3:A:547:LEU:CA	3:A:550:GLN:HE21	2.33	0.42
4:D:9:VAL:HB	4:D:97:TRP:CZ3	2.54	0.42
4:D:22:CYS:HB3	4:D:162:GLN:NE2	2.35	0.42
1:B:104:LYS:O	1:B:107:VAL:HG22	2.20	0.42
1:B:162:ASP:HB2	1:B:1007:MET:SD	2.59	0.42
1:B:626:ILE:HD12	1:B:633:GLN:NE2	2.35	0.42
1:B:771:ARG:O	1:B:775:LEU:HG	2.20	0.42
1:B:784:GLY:O	1:B:787:PHE:HB3	2.20	0.42
1:B:809:ALA:O	1:B:812:ILE:N	2.53	0.42
1:B:1059:LEU:HD23	1:B:1080:ARG:HH22	1.84	0.42
1:B:1169:LYS:HE2	1:B:1169:LYS:HB3	1.83	0.42
2:C:46:VAL:HG13	2:C:47:ASP:H	1.84	0.42
2:C:116:LYS:O	2:C:120:ARG:N	2.44	0.42
2:C:122:ASP:O	2:C:126:ILE:HG23	2.20	0.42
1:F:934:ARG:HB3	1:F:935:ARG:NH1	2.34	0.42
1:F:953:PHE:O	1:F:956:CYS:HB2	2.20	0.42
1:F:1114:LEU:HB3	1:F:1163:ARG:HG2	2.02	0.42
1:F:1297:LYS:HG2	1:F:1301:TYR:HE1	1.83	0.42
1:F:1386:LYS:HD3	1:F:1386:LYS:HA	1.75	0.42
3:A:670:ASN:HA	3:A:673:LEU:HD12	2.01	0.42
4:D:20:LEU:O	4:D:24:THR:N	2.45	0.42
4:D:143:GLN:OE1	4:D:154:TYR:HB3	2.20	0.42
1:B:473:HIS:HA	1:B:478:LYS:O	2.19	0.42
1:B:883:THR:HG21	1:B:931:ARG:CD	2.50	0.42
1:B:1033:MET:O	1:B:1036:ALA:N	2.53	0.42
1:B:1335:TYR:O	1:B:1338:LEU:HB2	2.20	0.42
1:B:1585:LYS:HA	1:B:1588:LEU:HD12	2.00	0.42
1:F:31:ILE:CG2	3:E:701:LEU:HD23	2.48	0.42
1:F:244:ALA:HB2	1:F:257:ASN:HA	2.02	0.42
1:F:332:ILE:HG23	1:F:403:LEU:HB3	2.00	0.42
1:F:945:ARG:HH12	1:F:946:GLN:HB2	1.84	0.42
1:F:1372:PHE:N	1:F:1424:GLN:HG2	2.35	0.42
2:G:27:ALA:O	2:G:162:GLN:NE2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:292:HIS:ND1	3:A:436:GLU:HG3	2.35	0.42
3:A:394:ALA:O	3:A:398:ILE:HG12	2.19	0.42
1:B:55:LYS:HG2	1:B:56:LYS:N	2.35	0.42
1:B:102:TRP:HB2	1:B:114:PHE:HE1	1.82	0.42
1:B:291:ARG:HA	1:B:292:PRO:HD3	1.91	0.42
1:B:473:HIS:O	1:B:525:CYS:HB3	2.20	0.42
1:B:566:ARG:NH2	1:B:621:GLN:HE21	2.18	0.42
1:B:787:PHE:O	1:B:790:SER:HB3	2.20	0.42
1:B:789:ASN:O	1:B:790:SER:C	2.63	0.42
1:B:820:LEU:O	1:B:823:ILE:HG12	2.20	0.42
1:B:824:ILE:O	1:B:828:LYS:HG2	2.20	0.42
1:B:940:VAL:HG13	1:B:992:MET:CE	2.46	0.42
1:B:1036:ALA:C	1:B:1038:PHE:N	2.78	0.42
2:C:114:GLY:HA3	2:C:156:GLU:CG	2.50	0.42
1:F:127:TRP:HA	1:F:130:GLN:HG2	2.02	0.42
1:F:465:ASN:CB	1:F:534:ARG:H	2.32	0.42
1:F:651:LYS:HE2	1:F:689:TYR:CE1	2.54	0.42
1:F:862:LYS:O	1:F:865:GLU:HB3	2.19	0.42
1:F:1060:GLN:HA	1:F:1063:THR:OG1	2.19	0.42
1:F:1217:LYS:CG	1:F:1220:ARG:HH21	2.26	0.42
1:F:1316:LYS:HE3	1:F:1319:LYS:HD3	2.02	0.42
1:F:1560:MET:SD	1:F:1565:ASN:ND2	2.93	0.42
2:G:80:ILE:HG23	2:G:112:LEU:HA	2.01	0.42
2:G:122:ASP:O	2:G:126:ILE:HG23	2.19	0.42
3:A:393:ASP:OD1	3:A:393:ASP:N	2.52	0.42
3:A:531:ARG:HA	3:A:534:LEU:HD12	2.01	0.42
3:A:552:ARG:HH21	3:A:555:ARG:NE	2.18	0.42
3:A:644:ILE:HD12	3:A:652:LEU:HD12	2.01	0.42
1:B:99:ALA:HB1	1:B:103:ARG:NH1	2.33	0.42
1:B:237:GLU:HG2	1:B:303:VAL:O	2.20	0.42
1:B:474:ASP:O	1:B:526:HIS:CE1	2.73	0.42
1:B:1094:LEU:HD23	1:B:1094:LEU:O	2.20	0.42
1:B:1217:LYS:HE2	1:B:1217:LYS:HB2	1.87	0.42
1:F:105:LEU:HD22	1:F:110:LYS:HE2	2.00	0.42
1:F:121:THR:HA	1:F:124:LEU:HD12	2.01	0.42
1:F:197:LYS:HG2	1:F:200:GLU:OE2	2.20	0.42
1:F:683:MET:HG2	1:F:683:MET:O	2.20	0.42
1:F:1120:LEU:O	1:F:1124:THR:OG1	2.35	0.42
1:F:1199:SER:HA	1:F:1202:GLU:CD	2.44	0.42
1:F:1525:THR:HA	1:F:1528:ARG:NH1	2.27	0.42
2:G:68:ARG:NH1	2:G:97:TRP:HZ3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:544:ILE:HA	3:E:547:LEU:HG	2.02	0.42
3:E:579:LEU:HD12	3:E:585:VAL:O	2.20	0.42
3:A:302:PHE:HB3	3:A:431:GLY:N	2.15	0.42
3:A:303:ASN:HA	3:A:306:GLU:HB2	2.01	0.42
3:A:673:LEU:HB3	3:A:675:LYS:HE2	2.01	0.42
4:D:98:HIS:CE1	4:D:102:CYS:SG	3.13	0.42
1:B:59:PHE:HD2	1:B:64:ILE:CD1	2.33	0.41
1:B:175:PRO:C	1:B:177:GLU:H	2.28	0.41
1:B:262:TRP:HE1	1:B:266:GLY:HA2	1.85	0.41
1:B:469:THR:HA	1:B:496:TYR:O	2.19	0.41
1:B:535:SER:OG	1:B:536:SER:N	2.53	0.41
1:B:571:VAL:H	1:B:619:SER:HA	1.84	0.41
1:B:817:LEU:HD12	1:B:818:LYS:N	2.35	0.41
1:B:868:LEU:HD12	1:B:868:LEU:HA	1.89	0.41
1:B:1109:ILE:HA	1:B:1112:VAL:HG12	2.02	0.41
1:B:1124:THR:C	1:B:1126:PRO:HD2	2.45	0.41
1:B:1125:ILE:HG23	1:B:1126:PRO:HD3	2.02	0.41
1:B:1284:GLN:OE1	1:B:1284:GLN:N	2.43	0.41
1:B:1524:LEU:HA	1:B:1527:GLU:OE2	2.19	0.41
1:F:23:GLN:HG2	1:F:58:ILE:HB	2.01	0.41
1:F:105:LEU:HB3	1:F:110:LYS:HE3	2.02	0.41
1:F:224:LEU:HD12	1:F:404:LYS:O	2.20	0.41
1:F:469:THR:HA	1:F:496:TYR:O	2.20	0.41
1:F:736:VAL:HA	1:F:739:PHE:HB3	2.01	0.41
1:F:749:LYS:HA	1:F:752:LEU:HB2	2.02	0.41
1:F:853:VAL:HA	1:F:856:LYS:HG2	2.02	0.41
1:F:900:GLU:C	1:F:903:SER:HG	2.25	0.41
1:F:1134:CYS:HA	1:F:1137:ASN:OD1	2.20	0.41
1:F:1136:PHE:CD1	1:F:1186:LEU:HD22	2.55	0.41
1:F:1491:THR:HA	1:F:1505:LYS:H	1.84	0.41
2:G:113:VAL:HG12	2:G:155:LEU:HB2	2.01	0.41
2:G:129:LEU:O	2:G:133:LYS:N	2.53	0.41
3:E:560:THR:HG21	3:E:661:GLU:OE1	2.20	0.41
3:E:620:LYS:HA	3:E:620:LYS:HD3	1.82	0.41
4:D:58:THR:HB	4:D:68:ARG:HG3	2.02	0.41
4:D:97:TRP:O	4:D:101:VAL:HG13	2.20	0.41
4:D:98:HIS:CD2	4:D:149:ILE:HB	2.54	0.41
1:B:262:TRP:C	1:B:269:LYS:HB2	2.45	0.41
1:B:278:GLN:O	1:B:426:ALA:HB3	2.20	0.41
1:B:718:THR:O	1:B:722:LYS:HB2	2.18	0.41
1:B:924:HIS:CD2	1:B:928:ILE:HD11	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:929:MET:SD	1:B:968:HIS:HB3	2.60	0.41
1:B:1060:GLN:O	1:B:1063:THR:HB	2.20	0.41
1:B:1086:ARG:O	1:B:1089:ASP:OD1	2.37	0.41
1:B:1125:ILE:CD1	1:B:1172:LEU:HA	2.50	0.41
1:B:1344:LYS:HA	1:B:1344:LYS:HD2	1.79	0.41
1:B:1452:ASN:O	1:B:1455:ARG:HB3	2.20	0.41
1:B:1536:HIS:HD2	1:B:1539:ASP:O	2.03	0.41
1:B:1562:GLY:HA3	2:C:36:VAL:HB	2.02	0.41
1:B:1600:LEU:CB	1:B:1626:PHE:HE1	2.34	0.41
1:F:4:TRP:CZ3	1:F:41:TYR:HB3	2.54	0.41
1:F:470:MET:O	1:F:495:GLU:HG3	2.20	0.41
1:F:720:ILE:HG12	1:F:766:PHE:CZ	2.55	0.41
2:G:171:GLU:HG3	2:G:174:ARG:HD2	2.03	0.41
3:E:531:ARG:HG2	3:E:532:PRO:HD3	2.02	0.41
3:A:408:LYS:C	3:A:410:GLU:H	2.27	0.41
3:A:564:LYS:HZ1	3:A:590:ASP:HA	1.85	0.41
4:D:68:ARG:HG2	4:D:72:TYR:CE1	2.56	0.41
1:B:125:ILE:HG13	1:B:126:GLU:N	2.34	0.41
1:B:159:LEU:HD23	1:B:159:LEU:HA	1.79	0.41
1:B:297:VAL:HG12	1:B:299:GLN:NE2	2.34	0.41
1:B:473:HIS:HB2	1:B:526:HIS:CE1	2.55	0.41
1:B:724:PHE:CD2	1:B:769:GLN:HG3	2.55	0.41
1:B:838:VAL:HA	1:B:841:CYS:SG	2.60	0.41
1:B:866:SER:O	1:B:867:THR:OG1	2.34	0.41
1:B:1143:ASN:OD1	1:B:1145:HIS:N	2.54	0.41
1:B:1362:TYR:CD2	1:B:1462:PHE:CE2	3.07	0.41
1:B:1462:PHE:HB2	1:B:1489:TYR:CB	2.34	0.41
1:F:875:ARG:HE	1:F:924:HIS:CD2	2.38	0.41
1:F:1032:PHE:CB	1:F:1043:TRP:HH2	2.33	0.41
1:F:1033:MET:H	1:F:1035:GLN:HE21	1.68	0.41
1:F:1105:MET:O	1:F:1108:PRO:HD2	2.20	0.41
1:F:1318:ILE:HG12	1:F:1345:ARG:HG3	2.02	0.41
1:F:1322:LYS:HG2	1:F:1345:ARG:NH1	2.35	0.41
3:A:591:LEU:HD13	3:A:591:LEU:HA	1.81	0.41
4:D:164:GLY:O	4:D:168:VAL:HG23	2.20	0.41
1:B:10:GLN:HG2	1:B:37:ILE:O	2.20	0.41
1:B:45:TYR:OH	1:B:61:GLU:HG3	2.20	0.41
1:B:192:LYS:HE2	1:B:195:GLU:OE1	2.21	0.41
1:B:451:ILE:HB	1:B:621:GLN:OE1	2.20	0.41
1:B:465:ASN:OD1	1:B:503:GLN:N	2.53	0.41
1:B:741:VAL:HG21	1:B:798:PHE:HD1	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:879:LEU:HB3	1:B:880:PRO:HD3	2.03	0.41
1:B:1010:ASN:C	1:B:1013:GLN:HE21	2.24	0.41
1:B:1038:PHE:O	1:B:1039:GLU:HG2	2.20	0.41
1:B:1401:GLN:HB3	1:B:1402:PHE:HD2	1.86	0.41
1:B:1633:VAL:O	1:B:1639:VAL:HG22	2.20	0.41
1:F:4:TRP:HZ3	1:F:45:TYR:HA	1.86	0.41
1:F:896:LYS:CG	1:F:897:PRO:HD3	2.48	0.41
1:F:929:MET:HE3	1:F:933:LEU:HD11	2.01	0.41
1:F:937:ASN:O	1:F:940:VAL:HG12	2.20	0.41
1:F:1012:THR:HG22	1:F:1015:ARG:HH21	1.85	0.41
1:F:1272:GLN:OE1	1:F:1272:GLN:N	2.53	0.41
1:F:1602:GLU:HA	1:F:1605:ARG:CG	2.50	0.41
2:G:90:PHE:CD2	2:G:137:ILE:HD12	2.55	0.41
2:G:135:THR:O	2:G:137:ILE:N	2.52	0.41
3:A:236:ASP:HA	3:A:284:ARG:HH12	1.85	0.41
1:B:14:VAL:HG13	3:A:700:ASP:OD2	2.20	0.41
1:B:79:THR:HB	1:B:81:ILE:O	2.20	0.41
1:B:322:PHE:O	1:B:322:PHE:CG	2.73	0.41
1:B:900:GLU:CD	1:B:901:ALA:N	2.78	0.41
1:B:933:LEU:HD23	1:B:933:LEU:HA	1.84	0.41
1:B:1206:ASP:O	1:B:1210:ILE:HG12	2.20	0.41
1:B:1607:HIS:HE2	1:B:1619:HIS:HB2	1.86	0.41
1:F:248:PRO:HD2	1:F:294:VAL:HA	2.00	0.41
1:F:466:VAL:O	1:F:500:VAL:HA	2.21	0.41
1:F:505:LYS:HE3	1:F:505:LYS:HB3	1.89	0.41
1:F:866:SER:O	1:F:867:THR:OG1	2.38	0.41
1:F:1111:GLU:HA	1:F:1114:LEU:HD12	2.02	0.41
1:F:1297:LYS:HG2	1:F:1301:TYR:CE1	2.55	0.41
2:G:130:LYS:HE2	2:G:130:LYS:HA	2.01	0.41
2:G:130:LYS:HE3	2:G:136:PRO:HD3	2.03	0.41
3:E:616:VAL:HB	3:E:644:ILE:HG12	2.02	0.41
3:E:660:HIS:O	3:E:664:ILE:HG13	2.20	0.41
3:A:128:LEU:HA	3:A:131:GLN:OE1	2.21	0.41
3:A:305:LEU:HB3	3:A:379:LEU:HD11	2.03	0.41
3:A:307:ASP:OD1	3:A:308:ARG:HG3	2.21	0.41
3:A:572:ASP:HA	3:A:593:GLU:OE2	2.21	0.41
3:A:581:PRO:HA	3:A:583:HIS:CE1	2.55	0.41
4:D:16:LYS:HE3	4:D:58:THR:O	2.20	0.41
4:D:23:TYR:OH	4:D:53:LEU:HD12	2.20	0.41
1:B:548:GLY:HA2	1:B:573:LYS:HG2	2.01	0.41
1:B:594:GLU:HA	1:B:597:GLU:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:652:HIS:O	1:B:656:LYS:NZ	2.53	0.41
1:B:914:ASP:O	1:B:916:LYS:HD2	2.21	0.41
1:B:1540:ARG:O	1:B:1542:LEU:N	2.53	0.41
1:B:1561:GLY:C	1:B:1565:ASN:HD22	2.21	0.41
1:B:1629:LEU:HA	1:B:1632:LYS:CG	2.51	0.41
2:C:78:PHE:HB3	2:C:110:ILE:HD13	2.03	0.41
1:F:102:TRP:HA	1:F:105:LEU:CG	2.49	0.41
1:F:246:TYR:HB3	1:F:297:VAL:CG2	2.50	0.41
1:F:1127:ILE:HG22	1:F:1131:MET:CE	2.51	0.41
1:F:1150:GLU:H	1:F:1150:GLU:CD	2.29	0.41
2:G:100:GLU:HA	2:G:103:HIS:ND1	2.35	0.41
3:E:545:LEU:HD12	3:E:546:GLU:N	2.35	0.41
3:A:38:CYS:HB3	3:A:43:LEU:O	2.20	0.41
3:A:543:GLU:CD	3:A:544:ILE:N	2.79	0.41
3:A:652:LEU:HD23	3:A:652:LEU:HA	1.79	0.41
4:D:22:CYS:SG	4:D:159:ALA:HB1	2.61	0.41
4:D:87:PRO:O	4:D:90:TYR:HB3	2.21	0.41
1:B:85:LEU:CA	1:B:88:VAL:HG12	2.47	0.41
1:B:165:VAL:CG2	1:B:175:PRO:HD3	2.50	0.41
1:B:243:MET:N	1:B:243:MET:SD	2.94	0.41
1:B:729:ALA:O	1:B:732:LYS:N	2.53	0.41
1:B:775:LEU:O	1:B:779:GLY:N	2.54	0.41
1:B:957:MET:O	1:B:960:LEU:HB3	2.21	0.41
1:B:1483:TRP:CZ3	1:B:1511:GLU:HG3	2.56	0.41
1:F:79:THR:HB	1:F:81:ILE:O	2.20	0.41
1:F:220:HIS:O	1:F:285:SER:HA	2.21	0.41
1:F:1579:HIS:CD2	1:F:1582:ASP:HB2	2.55	0.41
3:A:26:GLN:HE22	3:A:66:ARG:HB2	1.86	0.41
3:A:300:LEU:HA	3:A:303:ASN:HD21	1.85	0.41
3:A:483:VAL:HG13	3:A:511:TYR:OH	2.21	0.41
3:A:641:ALA:O	3:A:662:TYR:OH	2.23	0.41
4:D:124:ASP:HA	4:D:127:ARG:HE	1.86	0.41
1:B:25:VAL:CG2	1:B:57:GLY:HA2	2.51	0.41
1:B:90:GLU:O	1:B:93:SER:OG	2.33	0.41
1:B:150:ALA:HA	1:B:153:ASP:OD2	2.20	0.41
1:B:240:GLU:HB3	1:B:242:PHE:CE1	2.55	0.41
1:B:578:LYS:HA	1:B:584:PHE:CE2	2.55	0.41
1:B:670:GLN:OE1	1:B:719:TYR:HB2	2.20	0.41
1:B:1154:LYS:O	1:B:1158:GLU:OE1	2.39	0.41
1:B:1300:LEU:HA	1:B:1300:LEU:HD23	1.78	0.41
1:B:1392:GLU:OE1	1:B:1392:GLU:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:122:TYR:HA	1:F:125:ILE:HG12	2.02	0.41
1:F:222:TYR:HB2	1:F:284:LEU:HB2	2.02	0.41
1:F:308:LEU:HD23	1:F:308:LEU:HA	1.88	0.41
1:F:545:ARG:NH1	1:F:576:ASN:OD1	2.54	0.41
1:F:695:ASP:OD1	1:F:752:LEU:HD22	2.21	0.41
1:F:824:ILE:O	1:F:827:VAL:HB	2.21	0.41
1:F:914:ASP:O	1:F:916:LYS:HD3	2.20	0.41
1:F:964:MET:HE1	1:F:969:TYR:CG	2.55	0.41
1:F:982:ILE:O	1:F:986:LEU:HD23	2.20	0.41
1:F:1060:GLN:OE1	1:F:1060:GLN:N	2.44	0.41
1:F:1444:LYS:HA	1:F:1445:PRO:HD3	1.96	0.41
1:F:1451:LEU:HA	1:F:1451:LEU:HD13	1.81	0.41
2:G:1:MET:HE2	2:G:1:MET:HB3	1.99	0.41
2:G:162:GLN:HA	2:G:165:LEU:HD13	2.02	0.41
3:E:644:ILE:HB	3:E:652:LEU:HB2	2.02	0.41
3:A:301:THR:O	3:A:305:LEU:HG	2.21	0.41
3:A:396:ILE:O	3:A:400:LEU:HD23	2.20	0.41
1:B:17:TYR:CZ	3:A:710:PRO:HA	2.56	0.41
1:B:41:TYR:CD2	1:B:44:TRP:HB2	2.52	0.41
1:B:110:LYS:HD2	1:B:110:LYS:C	2.46	0.41
1:B:151:LYS:HA	1:B:151:LYS:HD3	1.87	0.41
1:B:306:MET:HE1	1:B:534:ARG:O	2.21	0.41
1:B:423:ARG:HA	1:B:423:ARG:HD3	1.97	0.41
1:B:446:ILE:HG23	1:B:626:ILE:HG12	2.03	0.41
1:B:469:THR:HG22	1:B:495:GLU:CD	2.45	0.41
1:B:474:ASP:CG	1:B:478:LYS:HB3	2.46	0.41
1:B:772:VAL:O	1:B:776:ARG:HG2	2.21	0.41
1:B:883:THR:CB	1:B:931:ARG:HE	2.34	0.41
1:B:886:LEU:O	1:B:889:GLN:HB3	2.20	0.41
1:B:940:VAL:C	1:B:992:MET:HE1	2.45	0.41
1:B:941:ILE:HG12	1:B:992:MET:HE3	2.02	0.41
1:B:965:ASP:H	1:B:968:HIS:CD2	2.39	0.41
1:B:1170:VAL:O	1:B:1174:LYS:HG3	2.21	0.41
1:B:1218:GLU:N	1:B:1218:GLU:CD	2.78	0.41
1:B:1330:SER:C	1:B:1331:LYS:HD3	2.45	0.41
1:B:1362:TYR:HE2	1:B:1459:VAL:HG21	1.85	0.41
1:B:1377:ARG:O	1:B:1379:LYS:NZ	2.44	0.41
1:B:1551:LEU:HD23	1:B:1551:LEU:HA	1.91	0.41
2:C:93:VAL:HG13	2:C:94:ARG:H	1.86	0.41
1:F:1:MET:HB3	3:E:720:TYR:CE1	2.56	0.41
1:F:246:TYR:HA	1:F:253:PHE:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:278:GLN:HB2	1:F:425:THR:HG23	2.03	0.41
1:F:568:ASP:HB3	1:F:592:LYS:HB2	2.02	0.41
1:F:743:ASN:C	1:F:743:ASN:HD22	2.28	0.41
1:F:824:ILE:HG13	1:F:867:THR:HG21	2.02	0.41
1:F:1038:PHE:HB2	1:F:1039:GLU:OE1	2.20	0.41
1:F:1417:ASP:N	1:F:1417:ASP:OD1	2.53	0.41
1:F:1581:GLU:HG2	1:F:1582:ASP:OD1	2.21	0.41
1:F:1598:PRO:O	1:F:1602:GLU:OE1	2.39	0.41
2:G:66:ARG:HG2	2:G:67:LEU:HD23	2.02	0.41
2:G:78:PHE:O	2:G:110:ILE:HD12	2.21	0.41
2:G:82:PHE:HE1	2:G:154:TYR:HE1	1.69	0.41
3:E:643:SER:HA	3:E:652:LEU:O	2.20	0.41
3:A:91:ARG:HG3	3:A:103:ALA:HB1	2.03	0.41
3:A:276:LEU:HD22	3:A:446:PHE:O	2.21	0.41
3:A:422:LYS:HB2	3:A:422:LYS:HE3	1.82	0.41
3:A:463:LEU:HG	3:A:484:VAL:HG21	2.03	0.41
3:A:617:VAL:O	3:A:643:SER:N	2.54	0.41
4:D:21:ILE:HG22	4:D:27:ALA:O	2.20	0.41
4:D:111:LEU:HD12	4:D:112:LEU:N	2.35	0.41
1:B:85:LEU:O	1:B:88:VAL:HG12	2.21	0.41
1:B:172:ILE:HA	1:B:175:PRO:CG	2.51	0.41
1:B:225:TYR:CZ	1:B:420:LEU:HD22	2.56	0.41
1:B:785:ASP:OD1	1:B:785:ASP:N	2.53	0.41
1:B:795:PHE:O	1:B:798:PHE:HB2	2.21	0.41
1:B:1059:LEU:HG	1:B:1116:PRO:HB2	2.02	0.41
1:B:1582:ASP:HB3	1:B:1585:LYS:HD3	2.03	0.41
1:B:1596:GLN:HG2	1:B:1600:LEU:HG	2.03	0.41
1:F:19:TYR:N	1:F:28:SER:HA	2.36	0.41
1:F:51:GLN:H	1:F:51:GLN:CD	2.29	0.41
1:F:113:LEU:HA	1:F:116:GLN:OE1	2.21	0.41
1:F:144:LEU:O	1:F:148:VAL:HG22	2.21	0.41
1:F:246:TYR:HB2	1:F:253:PHE:CD1	2.56	0.41
1:F:300:ILE:HG22	1:F:322:PHE:HD2	1.86	0.41
1:F:307:GLU:C	1:F:309:LYS:H	2.29	0.41
1:F:345:PHE:CD2	1:F:347:PRO:HD3	2.56	0.41
1:F:443:ARG:O	1:F:629:THR:OG1	2.31	0.41
1:F:792:ARG:HE	1:F:835:GLU:CD	2.29	0.41
1:F:1138:PHE:O	1:F:1141:ASN:N	2.44	0.41
1:F:1146:MET:HA	1:F:1149:ASN:HD22	1.86	0.41
1:F:1251:HIS:CD2	1:F:1259:GLU:HB3	2.56	0.41
1:F:1273:TRP:CE3	1:F:1297:LYS:HD3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:616:VAL:HA	3:A:644:ILE:HA	2.03	0.41
1:B:110:LYS:HD3	1:B:113:LEU:HB2	2.02	0.40
1:B:865:GLU:CD	1:B:866:SER:HB3	2.46	0.40
1:B:949:HIS:HD1	1:B:949:HIS:H	1.69	0.40
1:B:1563:PHE:HA	1:B:1566:TYR:CD2	2.42	0.40
2:C:8:VAL:HG22	2:C:79:LEU:HD12	2.04	0.40
2:C:139:TYR:OH	2:C:143:LEU:HD12	2.21	0.40
1:F:10:GLN:OE1	1:F:10:GLN:N	2.54	0.40
1:F:743:ASN:O	1:F:743:ASN:ND2	2.54	0.40
1:F:828:LYS:HZ3	1:F:867:THR:HA	1.86	0.40
1:F:1032:PHE:HE2	1:F:1039:GLU:HG3	1.86	0.40
1:F:1250:LEU:HA	1:F:1250:LEU:HD23	1.79	0.40
3:E:695:LYS:HE3	3:E:695:LYS:HB3	1.92	0.40
3:A:11:ALA:HA	3:A:21:LEU:CD1	2.51	0.40
3:A:159:LEU:HD22	3:A:204:ILE:HD12	2.03	0.40
3:A:328:ARG:NE	3:A:351:MET:HE1	2.37	0.40
3:A:526:GLU:C	3:A:530:SER:H	2.20	0.40
3:A:543:GLU:O	3:A:546:GLU:HG2	2.21	0.40
3:A:547:LEU:HA	3:A:550:GLN:HG3	2.04	0.40
1:B:185:LYS:O	1:B:189:VAL:HG23	2.20	0.40
1:B:201:GLU:O	1:B:205:LEU:HB2	2.21	0.40
1:B:657:LEU:HA	1:B:660:VAL:HG23	2.04	0.40
1:B:910:LEU:O	1:B:913:LEU:HB2	2.21	0.40
1:B:1064:PHE:HD1	1:B:1068:LYS:HZ2	1.70	0.40
1:B:1101:PHE:O	1:B:1104:SER:OG	2.36	0.40
1:B:1204:LEU:O	1:B:1207:TYR:HB3	2.21	0.40
1:B:1316:LYS:CE	1:B:1319:LYS:HD3	2.50	0.40
2:C:7:VAL:HB	2:C:78:PHE:HD2	1.85	0.40
2:C:65:ASP:O	2:C:69:PRO:HD3	2.21	0.40
1:F:81:ILE:HG21	1:F:141:LEU:CD2	2.51	0.40
1:F:535:SER:HB3	1:F:541:ASP:HA	2.03	0.40
1:F:642:ASN:O	1:F:646:ASN:N	2.54	0.40
1:F:817:LEU:HD13	1:F:855:GLN:O	2.21	0.40
1:F:839:LEU:HA	1:F:842:LYS:HE2	2.03	0.40
1:F:959:ALA:O	1:F:963:GLN:HG3	2.21	0.40
1:F:1066:GLN:HA	1:F:1069:ARG:CZ	2.51	0.40
1:F:1127:ILE:HG22	1:F:1131:MET:HE3	2.02	0.40
1:F:1176:LEU:HD13	1:F:1194:ALA:HB1	2.03	0.40
1:F:1231:TYR:CE2	1:F:1239:ILE:HD12	2.55	0.40
1:F:1344:LYS:HD2	1:F:1344:LYS:HA	1.75	0.40
2:G:140:PRO:O	2:G:143:LEU:HB3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:184:ILE:HA	3:A:187:PHE:CD2	2.56	0.40
3:A:628:LYS:HA	3:A:632:LYS:HD3	2.04	0.40
3:A:684:ASN:HA	3:A:687:ASP:OD2	2.21	0.40
4:D:144:ALA:O	4:D:147:LYS:HG3	2.21	0.40
1:B:26:GLU:OE2	1:B:59:PHE:HB2	2.20	0.40
1:B:342:LYS:HG2	1:B:344:HIS:CE1	2.57	0.40
1:B:786:GLU:O	1:B:789:ASN:HB2	2.21	0.40
1:B:800:MET:CE	1:B:804:ARG:HE	2.33	0.40
1:B:1116:PRO:HA	1:B:1121:ARG:NH2	2.36	0.40
1:B:1197:VAL:O	1:B:1201:LEU:HG	2.21	0.40
1:B:1279:VAL:HB	1:B:1281:HIS:CE1	2.56	0.40
1:B:1485:GLU:N	1:B:1485:GLU:CD	2.80	0.40
1:B:1516:GLU:HG3	1:B:1520:GLU:OE1	2.21	0.40
1:B:1524:LEU:HD12	1:B:1525:THR:N	2.36	0.40
1:B:1531:ASN:O	1:B:1535:GLN:HG3	2.22	0.40
1:B:1557:PRO:CB	1:B:1562:GLY:H	2.33	0.40
2:C:147:LYS:C	2:C:150:GLY:H	2.29	0.40
1:F:298:CYS:N	1:F:325:ALA:O	2.53	0.40
1:F:626:ILE:HD12	1:F:633:GLN:NE2	2.36	0.40
1:F:640:LEU:HD11	1:F:657:LEU:HD21	2.03	0.40
1:F:759:ALA:O	1:F:763:LEU:HG	2.20	0.40
1:F:854:ARG:HG3	1:F:898:ASP:OD1	2.20	0.40
1:F:929:MET:CE	1:F:964:MET:HE2	2.52	0.40
1:F:943:MET:O	1:F:950:ILE:HD12	2.22	0.40
1:F:1458:GLU:N	1:F:1458:GLU:OE2	2.54	0.40
1:F:1495:PHE:N	1:F:1495:PHE:CD1	2.89	0.40
2:G:163:ARG:C	2:G:165:LEU:N	2.80	0.40
3:E:535:GLU:HB3	3:E:539:LYS:NZ	2.36	0.40
3:A:228:LEU:HD23	3:A:247:ILE:HG13	2.04	0.40
3:A:397:ARG:HH12	3:A:461:GLN:HG3	1.86	0.40
3:A:405:ARG:NH1	3:A:468:LYS:HZ3	2.20	0.40
4:D:124:ASP:HA	4:D:127:ARG:NE	2.35	0.40
4:D:129:LEU:HA	4:D:132:GLN:HE21	1.86	0.40
1:B:9:ARG:NE	1:B:68:GLU:O	2.52	0.40
1:B:400:TRP:CH2	4:D:127:ARG:HD2	2.57	0.40
1:B:474:ASP:HA	1:B:525:CYS:SG	2.61	0.40
1:B:616:THR:OG1	1:B:617:LYS:N	2.49	0.40
1:B:828:LYS:HA	1:B:828:LYS:HD2	1.97	0.40
1:B:861:THR:HA	1:B:864:VAL:HG12	2.04	0.40
1:B:933:LEU:O	1:B:934:ARG:C	2.64	0.40
1:B:1342:LEU:CD1	1:F:1346:ALA:HB2	2.49	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1406:GLU:HG3	1:B:1425:TYR:CE1	2.56	0.40
1:B:1564:SER:HA	1:B:1567:GLU:HG2	2.03	0.40
1:B:1611:LEU:HD12	1:B:1615:LEU:CB	2.50	0.40
2:C:2:GLN:HE22	2:C:4:ILE:HG12	1.87	0.40
2:C:114:GLY:O	2:C:115:THR:OG1	2.29	0.40
2:C:124:ASP:O	2:C:128:LYS:HD3	2.21	0.40
1:F:10:GLN:HG2	1:F:37:ILE:HB	2.03	0.40
1:F:41:TYR:HD2	1:F:44:TRP:N	2.20	0.40
1:F:180:THR:HG22	1:F:181:ILE:HD13	2.02	0.40
1:F:228:PHE:CD2	1:F:399:LEU:HD12	2.56	0.40
1:F:568:ASP:OD2	1:F:569:LEU:N	2.53	0.40
1:F:1424:GLN:H	1:F:1424:GLN:HG3	1.70	0.40
1:F:1436:SER:HB2	1:F:1454:TYR:O	2.21	0.40
1:F:1468:PHE:O	1:F:1469:ARG:HD3	2.22	0.40
2:G:78:PHE:C	2:G:79:LEU:HD22	2.45	0.40
2:G:94:ARG:HA	2:G:98:TYR:HB3	2.03	0.40
2:G:174:ARG:C	2:G:177:LEU:H	2.29	0.40
3:A:286:ILE:HG21	3:A:441:PHE:CE2	2.56	0.40
3:A:299:VAL:HA	3:A:302:PHE:HD2	1.87	0.40
3:A:302:PHE:CG	3:A:430:VAL:HA	2.56	0.40
3:A:690:LEU:HA	3:A:690:LEU:HD12	1.78	0.40
1:B:18:ASN:OD1	3:A:536:LEU:HD12	2.21	0.40
1:B:244:ALA:HB2	1:B:257:ASN:HA	2.04	0.40
1:B:259:LEU:HD23	1:B:490:TYR:HB3	2.04	0.40
1:B:683:MET:HE3	1:B:686:SER:N	2.35	0.40
1:B:841:CYS:O	1:B:844:ILE:N	2.55	0.40
1:B:1177:LEU:HD22	1:B:1181:ARG:HH12	1.87	0.40
1:B:1490:THR:OG1	1:B:1506:GLN:HB3	2.22	0.40
1:B:1516:GLU:O	1:B:1520:GLU:OE1	2.39	0.40
1:B:1562:GLY:O	1:B:1565:ASN:HB2	2.22	0.40
1:F:143:GLU:O	1:F:147:LYS:HD3	2.21	0.40
1:F:195:GLU:HA	1:F:198:ILE:HG22	2.03	0.40
1:F:233:CYS:HB2	1:F:397:GLN:HA	2.04	0.40
1:F:345:PHE:HD1	1:F:400:TRP:CE2	2.40	0.40
1:F:637:LEU:O	1:F:641:LEU:HG	2.22	0.40
1:F:753:LEU:O	1:F:757:LEU:HD23	2.22	0.40
1:F:771:ARG:O	1:F:774:TYR:HB3	2.21	0.40
1:F:1125:ILE:CD1	1:F:1172:LEU:HA	2.51	0.40
1:F:1200:LEU:HD23	1:F:1230:PHE:HE2	1.86	0.40
1:F:1372:PHE:CZ	1:F:1424:GLN:HB3	2.56	0.40
2:G:16:LYS:O	2:G:19:LEU:HB3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:560:THR:HG22	3:E:562:PHE:HE1	1.86	0.40
3:A:637:VAL:HB	3:A:655:ILE:HD12	2.03	0.40
4:D:155:LEU:CD1	4:D:168:VAL:HA	2.51	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	B	1640/1648 (100%)	1416 (86%)	224 (14%)	0	100	100
1	F	1640/1648 (100%)	1466 (89%)	174 (11%)	0	100	100
2	C	175/184 (95%)	156 (89%)	19 (11%)	0	100	100
2	G	175/184 (95%)	157 (90%)	18 (10%)	0	100	100
3	A	725/733 (99%)	657 (91%)	68 (9%)	0	100	100
3	E	197/733 (27%)	162 (82%)	35 (18%)	0	100	100
4	D	179/203 (88%)	161 (90%)	18 (10%)	0	100	100
All	All	4731/5333 (89%)	4175 (88%)	556 (12%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	1495/1497 (100%)	1495 (100%)	0	100	100
1	F	1495/1497 (100%)	1495 (100%)	0	100	100
2	C	153/157 (98%)	153 (100%)	0	100	100
2	G	153/157 (98%)	153 (100%)	0	100	100
3	A	662/664 (100%)	662 (100%)	0	100	100
3	E	184/664 (28%)	184 (100%)	0	100	100
4	D	157/174 (90%)	157 (100%)	0	100	100
All	All	4299/4810 (89%)	4299 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (89) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	30	GLN
1	B	36	HIS
1	B	89	GLN
1	B	171	ASN
1	B	230	ASN
1	B	250	GLN
1	B	265	ASN
1	B	278	GLN
1	B	419	HIS
1	B	452	HIS
1	B	621	GLN
1	B	652	HIS
1	B	653	ASN
1	B	871	GLN
1	B	885	GLN
1	B	904	GLN
1	B	924	HIS
1	B	946	GLN
1	B	968	HIS
1	B	1000	ASN
1	B	1010	ASN
1	B	1013	GLN
1	B	1149	ASN
1	B	1179	HIS
1	B	1203	ASN
1	B	1293	GLN

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Mol	Chain	Res	Type
1	B	1517	ASN
1	B	1536	HIS
2	C	39	ASN
1	F	51	GLN
1	F	89	GLN
1	F	119	GLN
1	F	154	HIS
1	F	199	GLN
1	F	227	ASN
1	F	230	ASN
1	F	257	ASN
1	F	278	GLN
1	F	299	GLN
1	F	305	HIS
1	F	334	HIS
1	F	376	ASN
1	F	414	GLN
1	F	537	GLN
1	F	556	ASN
1	F	567	HIS
1	F	633	GLN
1	F	646	ASN
1	F	649	ASN
1	F	670	GLN
1	F	713	ASN
1	F	723	HIS
1	F	743	ASN
1	F	793	GLN
1	F	799	ASN
1	F	825	ASN
1	F	889	GLN
1	F	937	ASN
1	F	946	GLN
1	F	1013	GLN
1	F	1022	ASN
1	F	1035	GLN
1	F	1526	ASN
1	F	1614	GLN
3	E	551	GLN
3	E	605	GLN
3	E	633	GLN
3	A	52	GLN

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Mol	Chain	Res	Type
3	A	86	GLN
3	A	87	GLN
3	A	231	HIS
3	A	248	ASN
3	A	287	ASN
3	A	288	ASN
3	A	293	GLN
3	A	340	ASN
3	A	383	ASN
3	A	391	HIS
3	A	402	ASN
3	A	439	ASN
3	A	464	ASN
3	A	550	GLN
3	A	583	HIS
3	A	633	GLN
3	A	703	ASN
4	D	76	ASN
4	D	98	HIS
4	D	140	GLN
4	D	178	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	GTP	D	202	5	33,34,34	0.94	1 (3%)	50,54,54	1.56	9 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GTP	D	202	5	-	2/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	202	GTP	C2-N3	2.15	1.38	1.33

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	202	GTP	C5-C4-N3	-5.03	120.39	128.39
6	D	202	GTP	C2-N3-C4	4.50	120.05	112.30
6	D	202	GTP	N9-C4-N3	3.19	132.34	125.95
6	D	202	GTP	C2-N1-C6	-2.93	119.80	125.11
6	D	202	GTP	C5-C6-N1	2.50	119.61	113.25
6	D	202	GTP	O6-C6-C5	-2.46	120.03	126.53
6	D	202	GTP	N9-C8-N7	-2.46	108.84	113.40
6	D	202	GTP	C8-N7-C5	2.37	108.48	104.26
6	D	202	GTP	C3'-C2'-C1'	2.09	105.42	101.46

There are no chirality outliers.

All (2) torsion outliers are listed below:

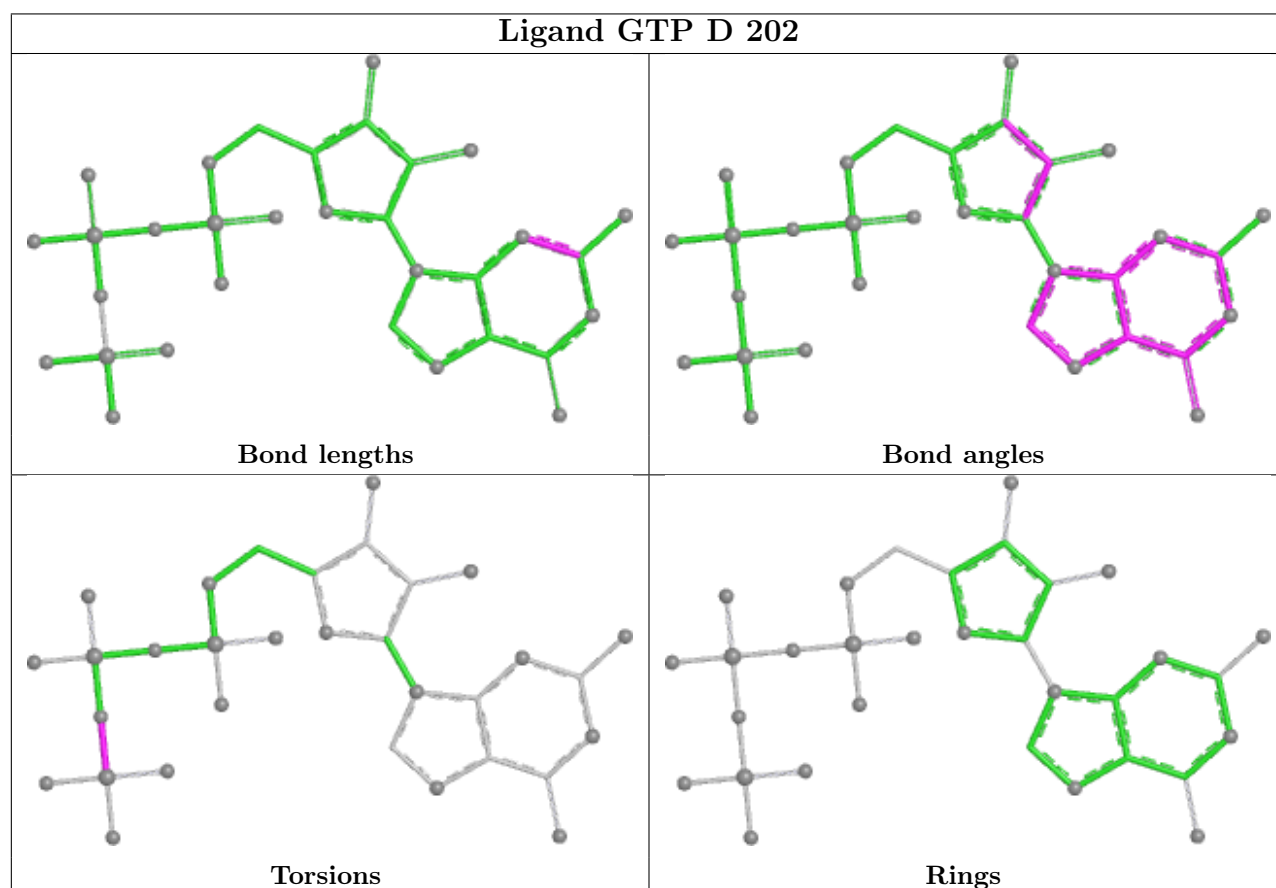
Mol	Chain	Res	Type	Atoms
6	D	202	GTP	PB-O3B-PG-O3G
6	D	202	GTP	PB-O3B-PG-O1G

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	202	GTP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

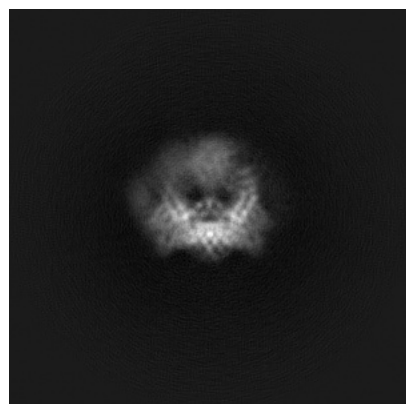
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60136. These allow visual inspection of the internal detail of the map and identification of artifacts.

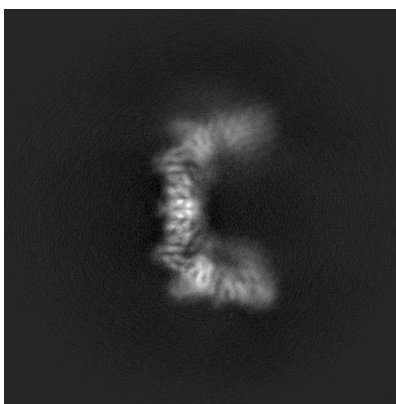
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

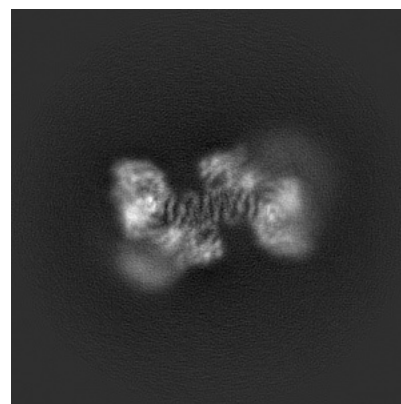
6.1.1 Primary map



X

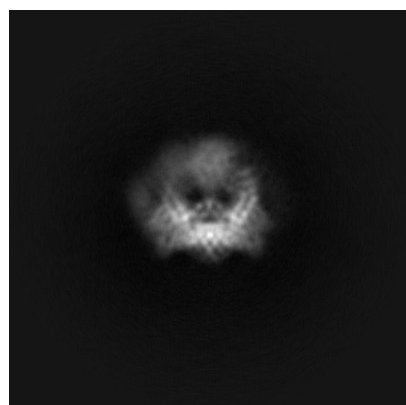


Y

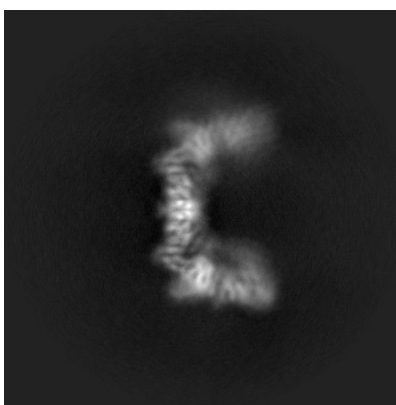


Z

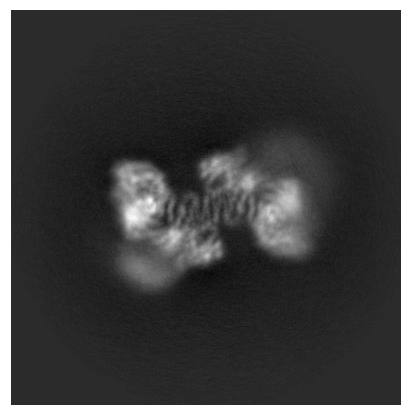
6.1.2 Raw map



X



Y

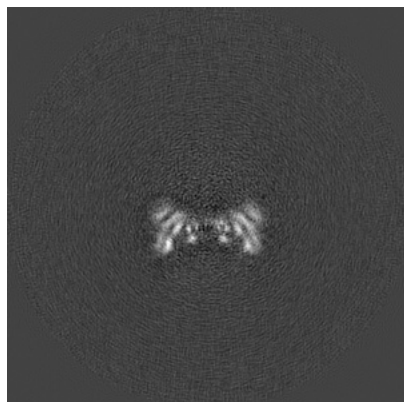


Z

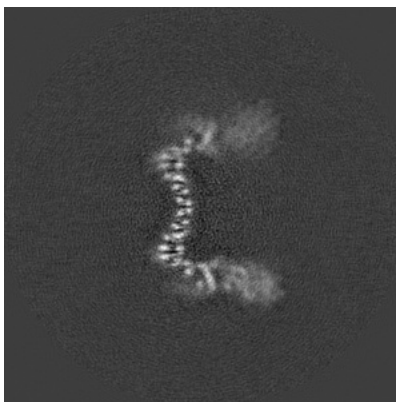
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

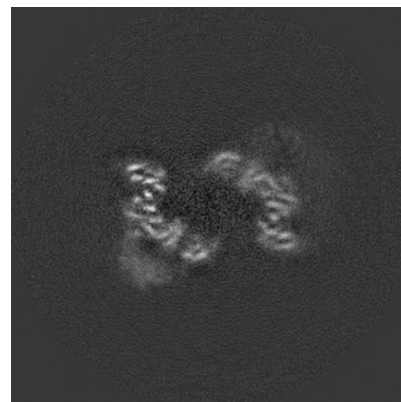
6.2.1 Primary map



X Index: 170

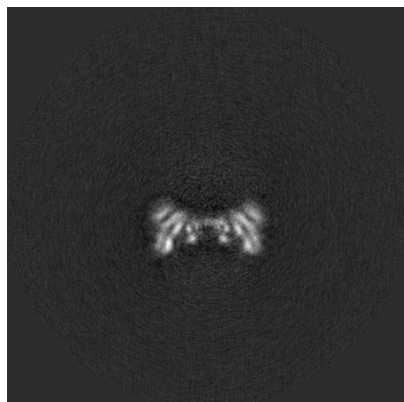


Y Index: 170

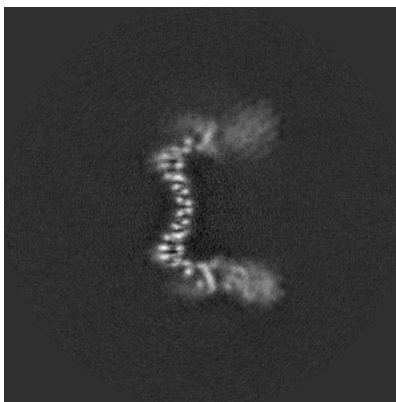


Z Index: 170

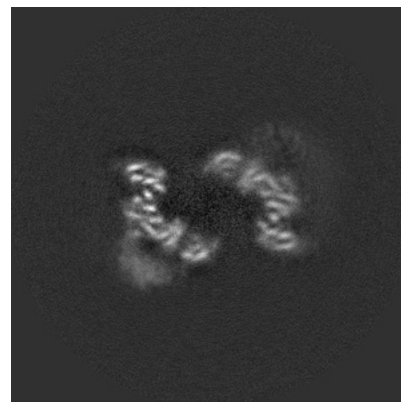
6.2.2 Raw map



X Index: 170



Y Index: 170

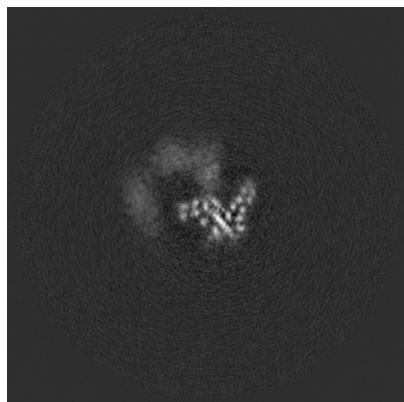


Z Index: 170

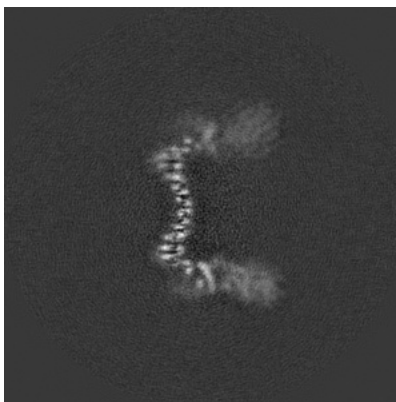
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

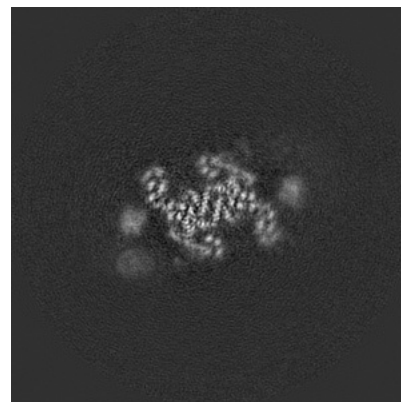
6.3.1 Primary map



X Index: 118

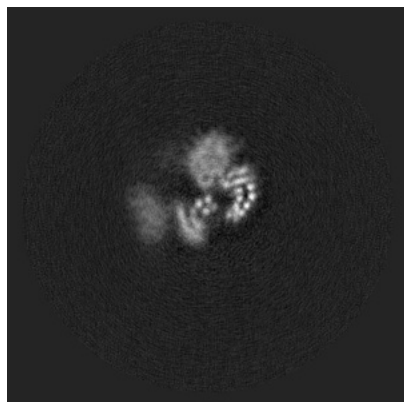


Y Index: 169

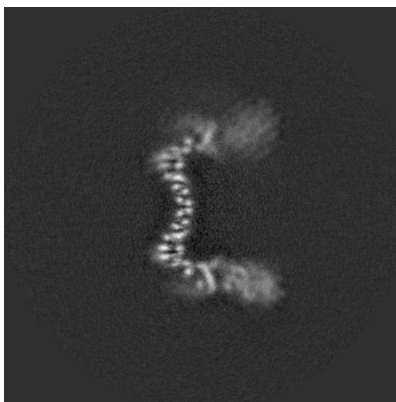


Z Index: 149

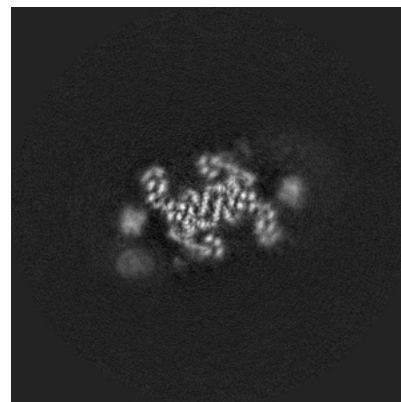
6.3.2 Raw map



X Index: 104



Y Index: 170

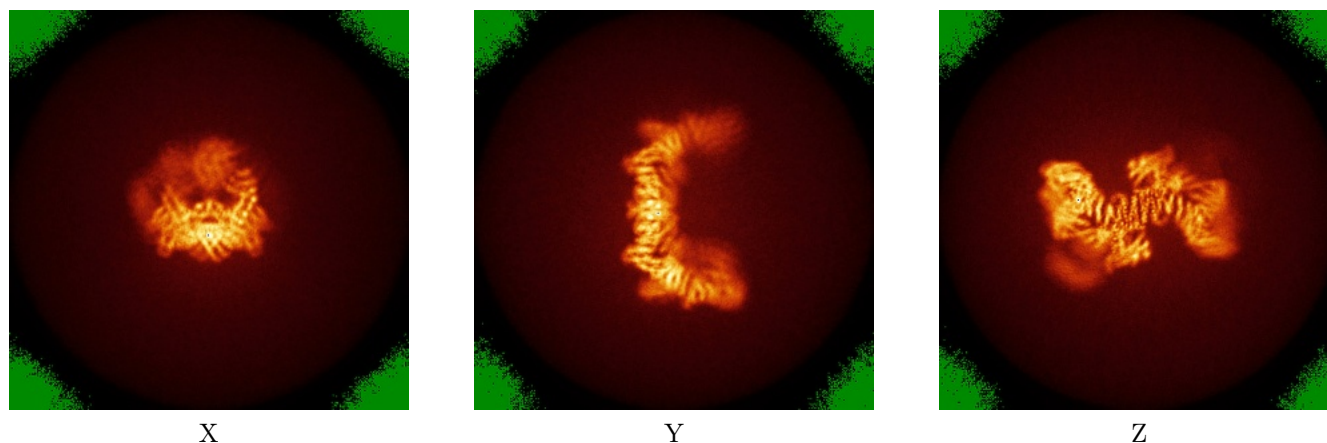


Z Index: 149

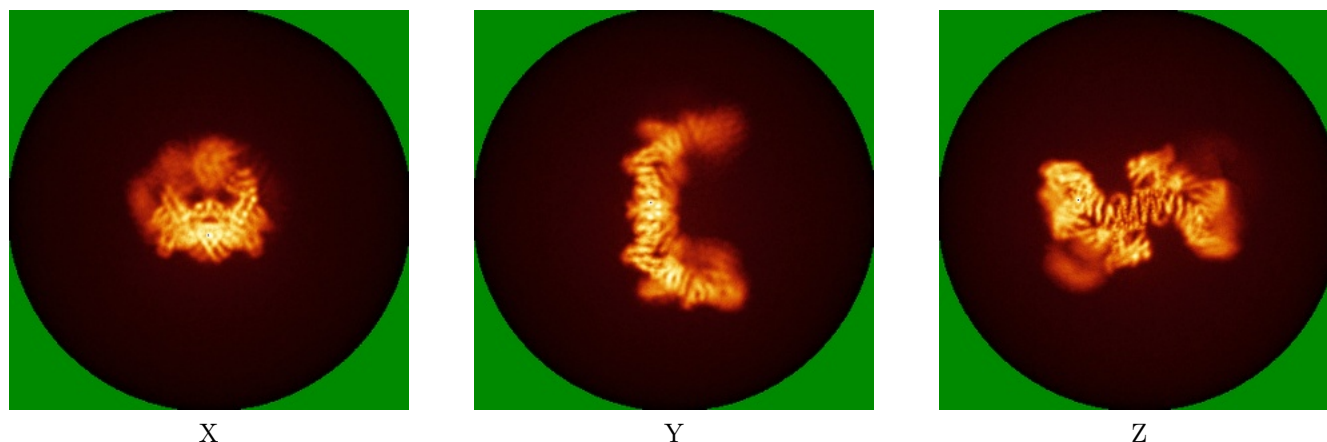
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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

6.5 Orthogonal surface views [i](#)

This section was not generated.

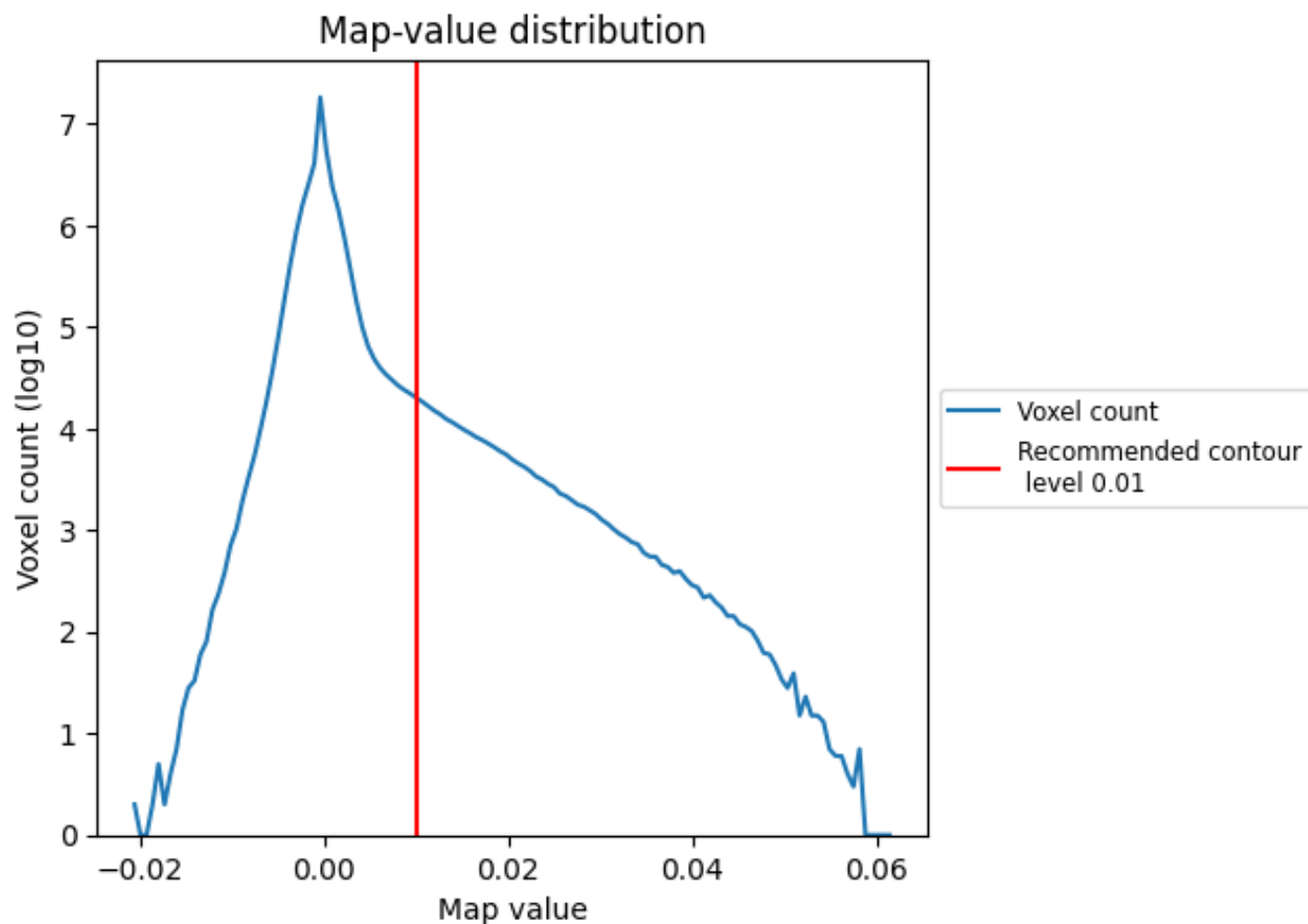
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

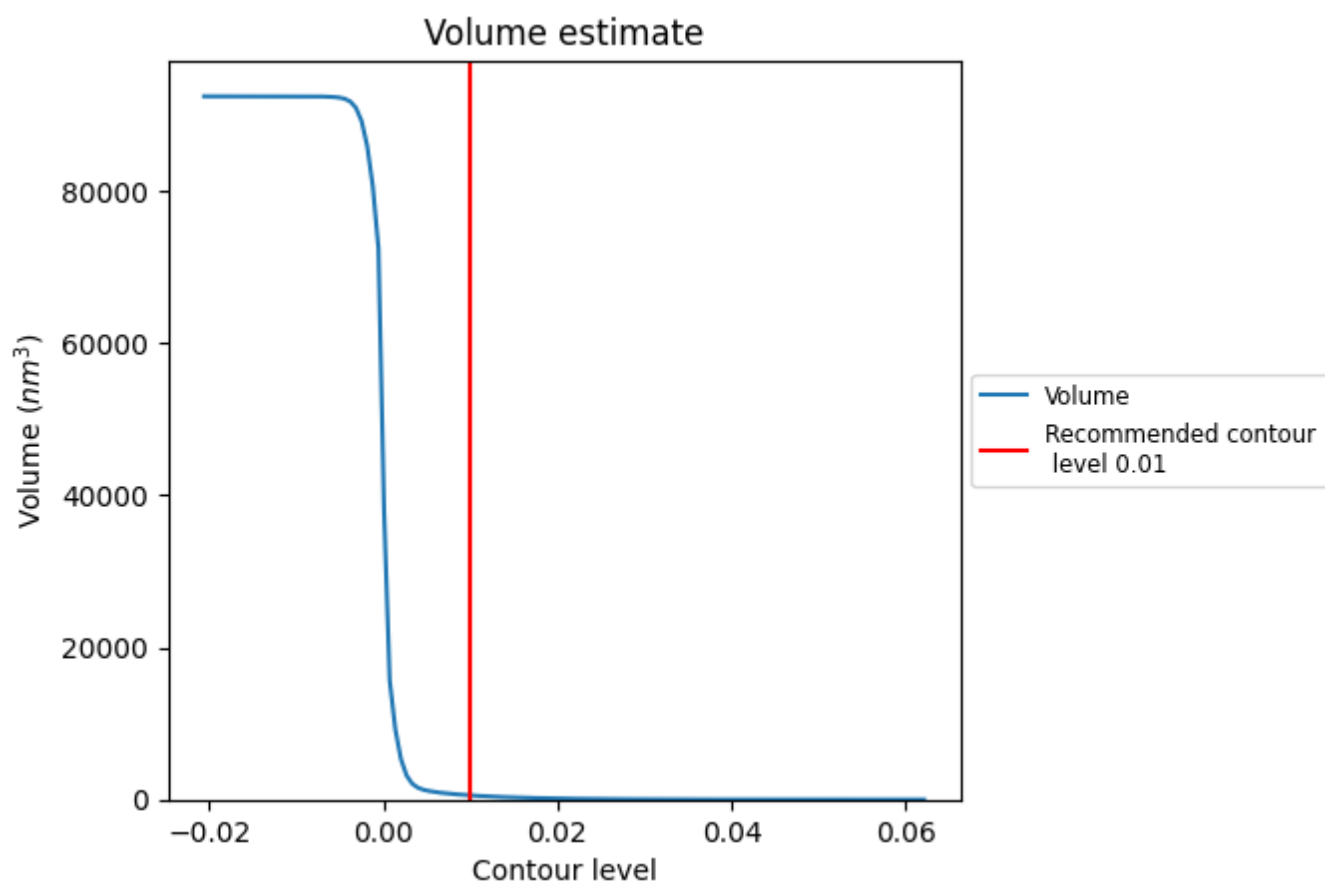
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

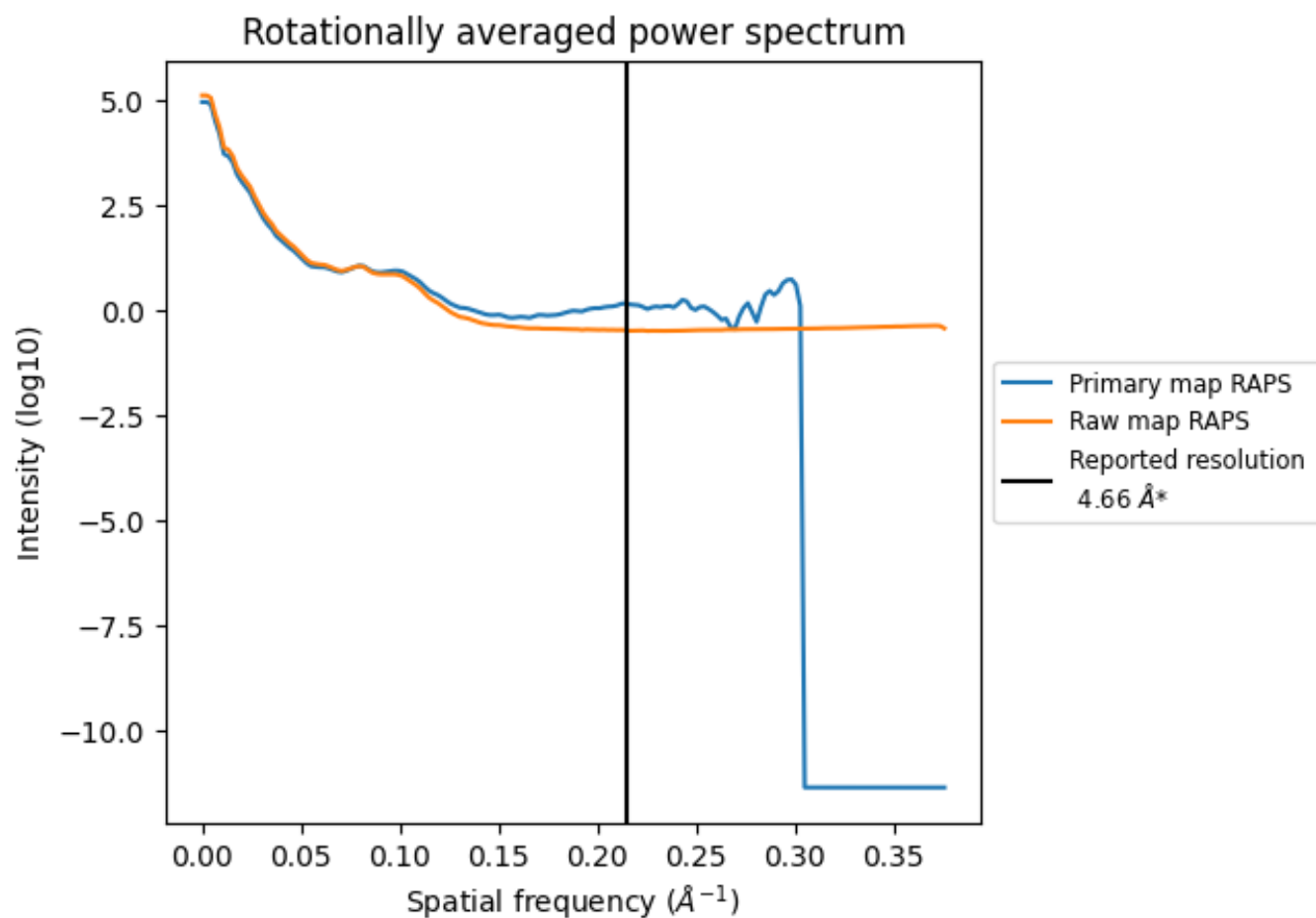
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 551 nm^3 ; this corresponds to an approximate mass of 498 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

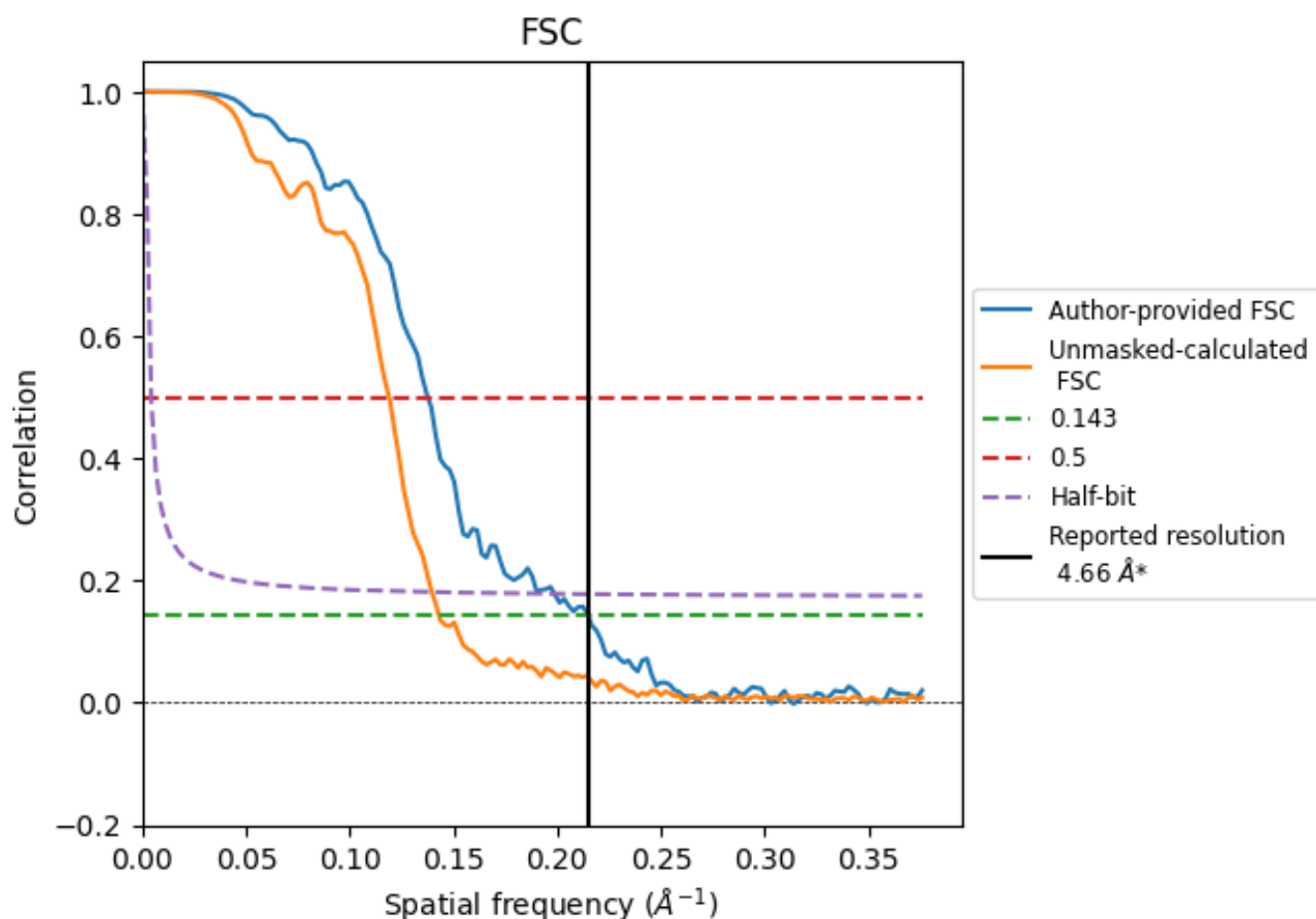


*Reported resolution corresponds to spatial frequency of 0.215 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.215 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

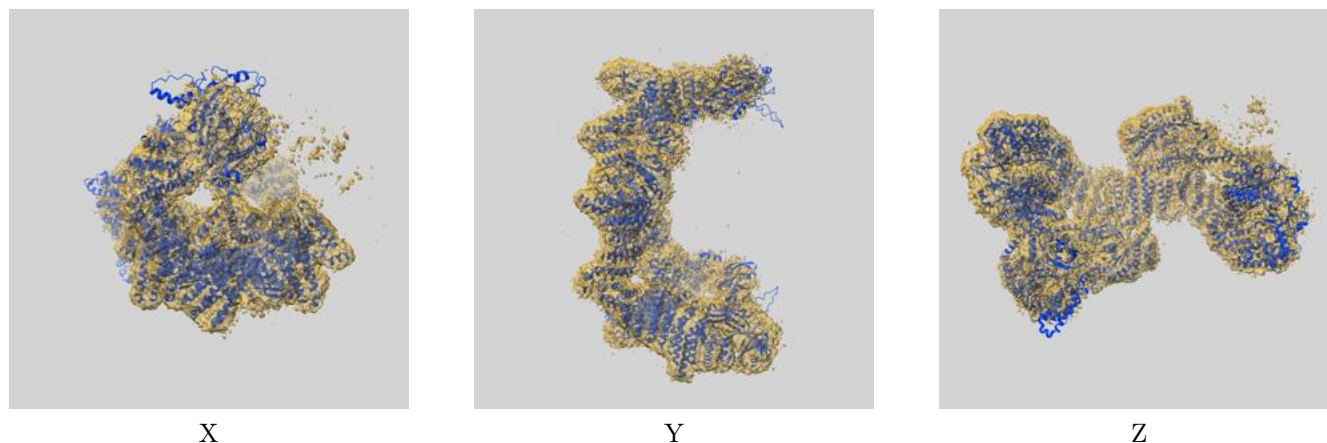
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.66	-	-
Author-provided FSC curve	4.65	7.27	5.03
Unmasked-calculated*	6.99	8.40	7.16

*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 6.99 differs from the reported value 4.66 by more than 10 %

9 Map-model fit [i](#)

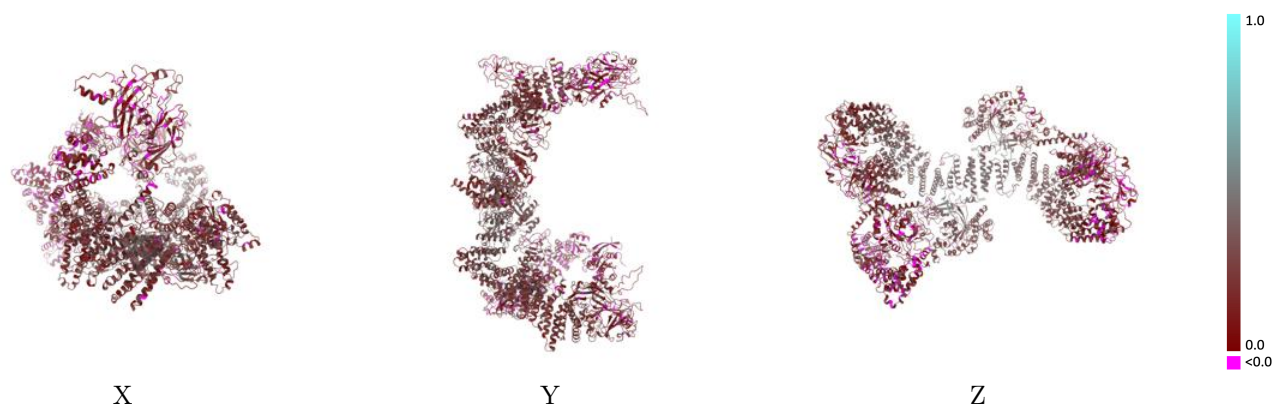
This section contains information regarding the fit between EMDB map EMD-60136 and PDB model 8ZJ2. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



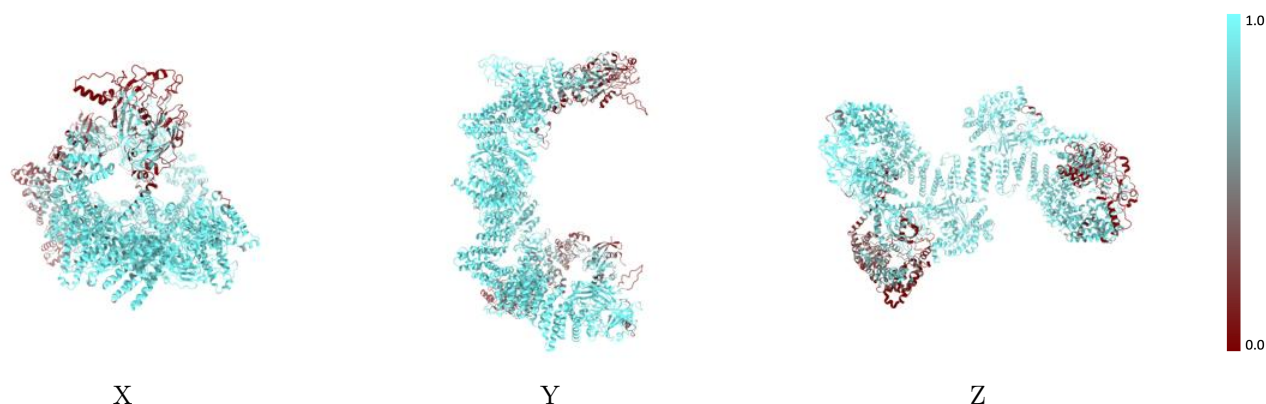
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



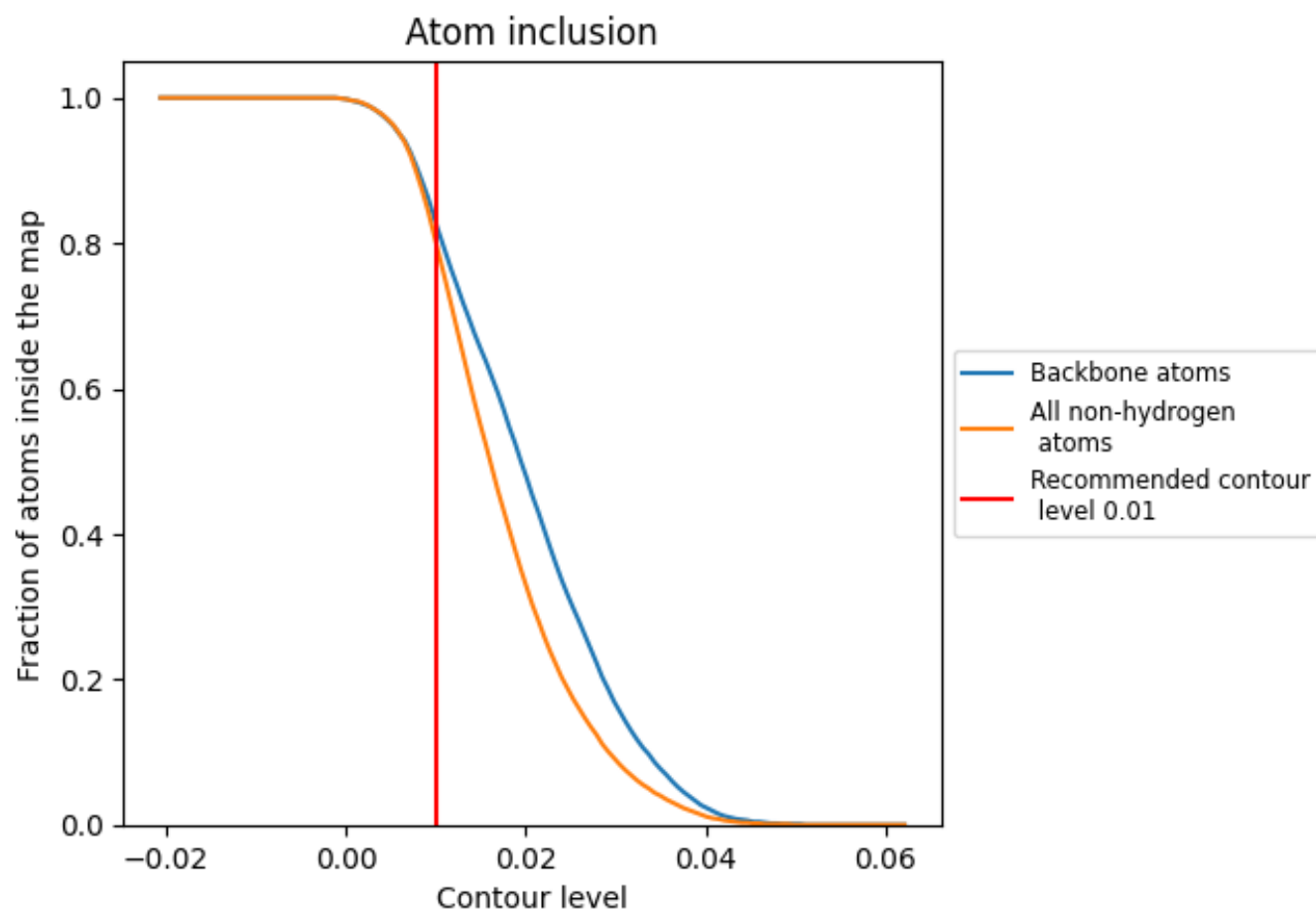
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 80% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8010	0.2310
A	0.4950	0.1540
B	0.9400	0.2700
C	0.9660	0.3030
D	0.6550	0.1510
E	0.8810	0.2070
F	0.7700	0.2260
G	0.9550	0.2650

1.0

0.0

<0.0