Full wwPDB EM Validation Report ⓘ

Jun 20, 2024 – 03:29 AM JST

PDB ID	:	7WOO
EMDB ID	:	EMD-32653
Title	:	Cryo-EM structure of the inner ring protomer of the Saccharomyces cerevisiae nuclear pore complex
Authors	:	Li, Z.Q.; Chen, S.J.B.; Zhao, L.; Sui, S.F.
Deposited on	:	2022-01-22
Resolution	:	3.71 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

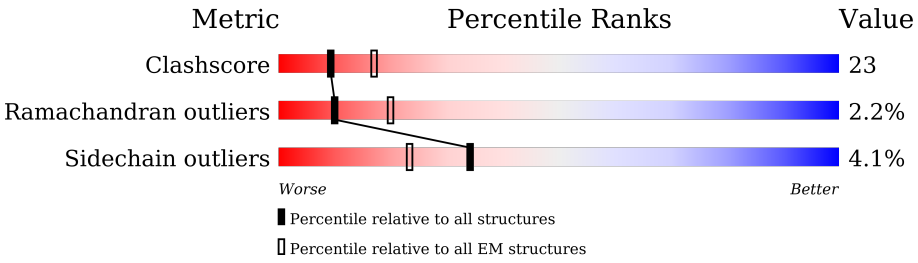
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance

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

The reported resolution of this entry is 3.71 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	839	83% 54% 31% • 13%
1	Z	839	53% 52% 30% 5% • 11%
2	C	1391	95% 88% 6% • 5%
3	D	1502	80% 67% 26% 7%
4	E	1655	14% 68% 25% • 6%
5	F	1683	33% 52% 36% 7% • •
6	G	472	24% 30% 12% • 58%
6	J	472	30% 17% 21% • 59%

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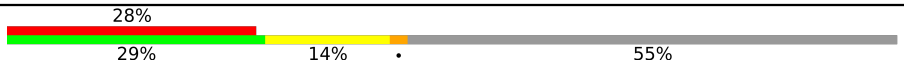
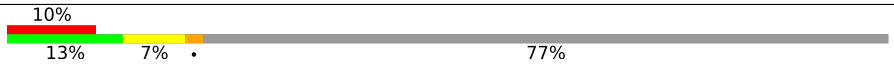
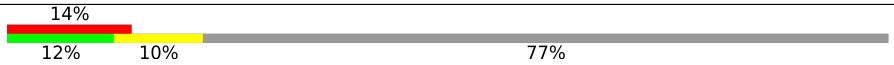
Mol	Chain	Length	Quality of chain
7	H	541	
7	K	541	
8	I	823	
8	L	823	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 66949 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 Nucleoporin NIC96.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	732	Total	C	N	O	S	0	0
			5723	3631	975	1101	16		
1	Z	746	Total	C	N	O	S	0	0
			5776	3660	981	1120	15		

- Molecule 2 is a protein called Nucleoporin NUP157.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1325	Total	C	N	O	S	0	0
			10452	6664	1736	2018	34		

- Molecule 3 is a protein called Nucleoporin NUP170.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1398	Total	C	N	O	S	0	0
			10976	7018	1811	2115	32		

- Molecule 4 is a protein called Nucleoporin NUP188.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	1552	Total	C	N	O	S	0	0
			12362	8017	1981	2337	27		

- Molecule 5 is a protein called Nucleoporin NUP192.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	1622	Total	C	N	O	S	0	0
			12232	7805	2031	2365	31		

- Molecule 6 is a protein called Nucleoporin NUP49/NSP49.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	200	Total	C	N	O	S	0	0
			1533	973	251	307	2		
6	J	195	Total	C	N	O	S	0	0
			1492	938	251	302	1		

- Molecule 7 is a protein called Nucleoporin NUP57.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	246	Total	C	N	O	S	0	0
			1811	1128	332	348	3		
7	K	254	Total	C	N	O	S	0	0
			1808	1126	334	345	3		

- Molecule 8 is a protein called Nucleoporin NSP1.

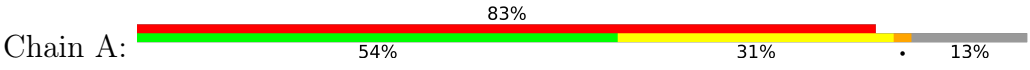
Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	187	Total	C	N	O	S	0	0
			1418	862	244	311	1		
8	L	187	Total	C	N	O	S	0	0
			1366	830	240	295	1		

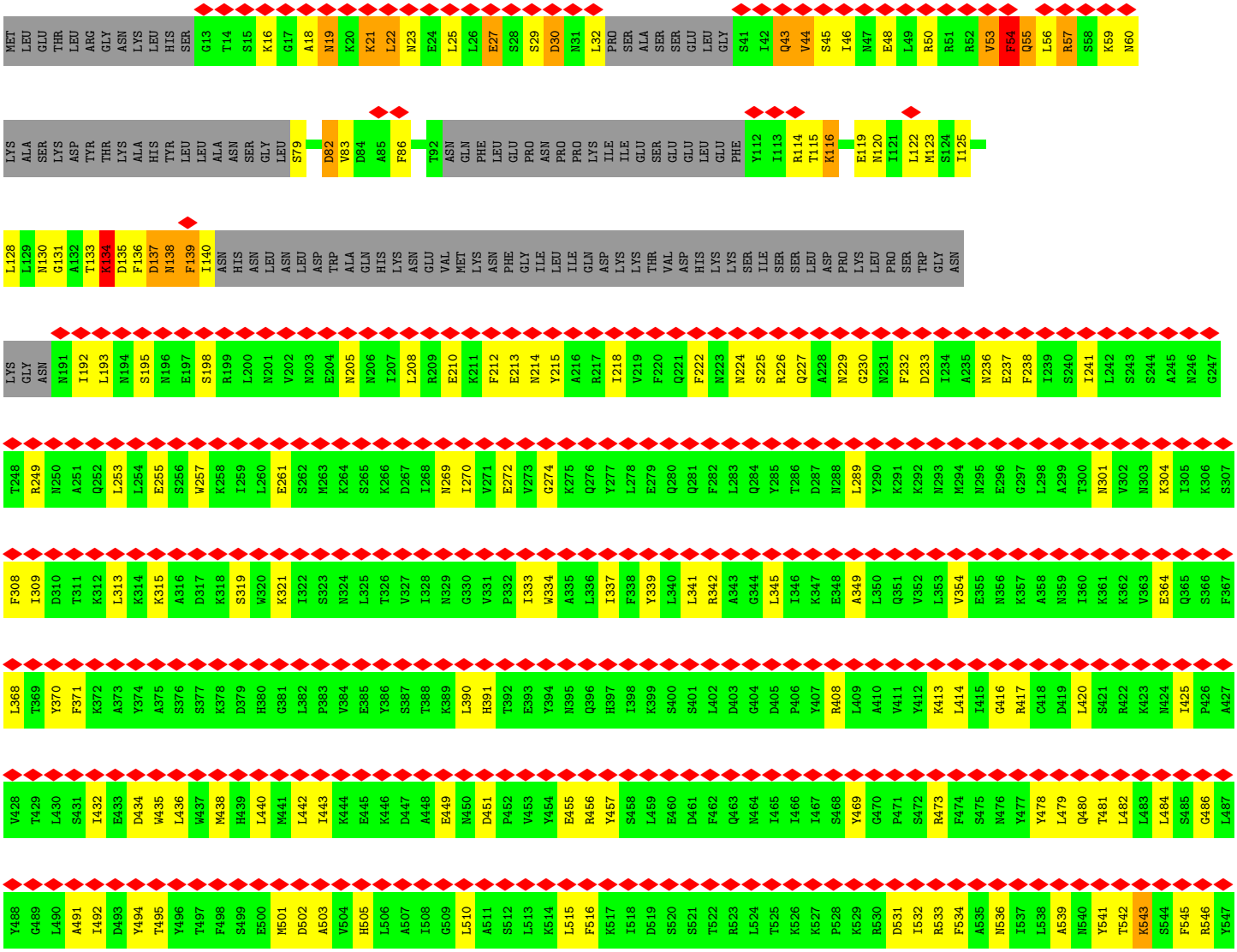
3 Residue-property plots (i)

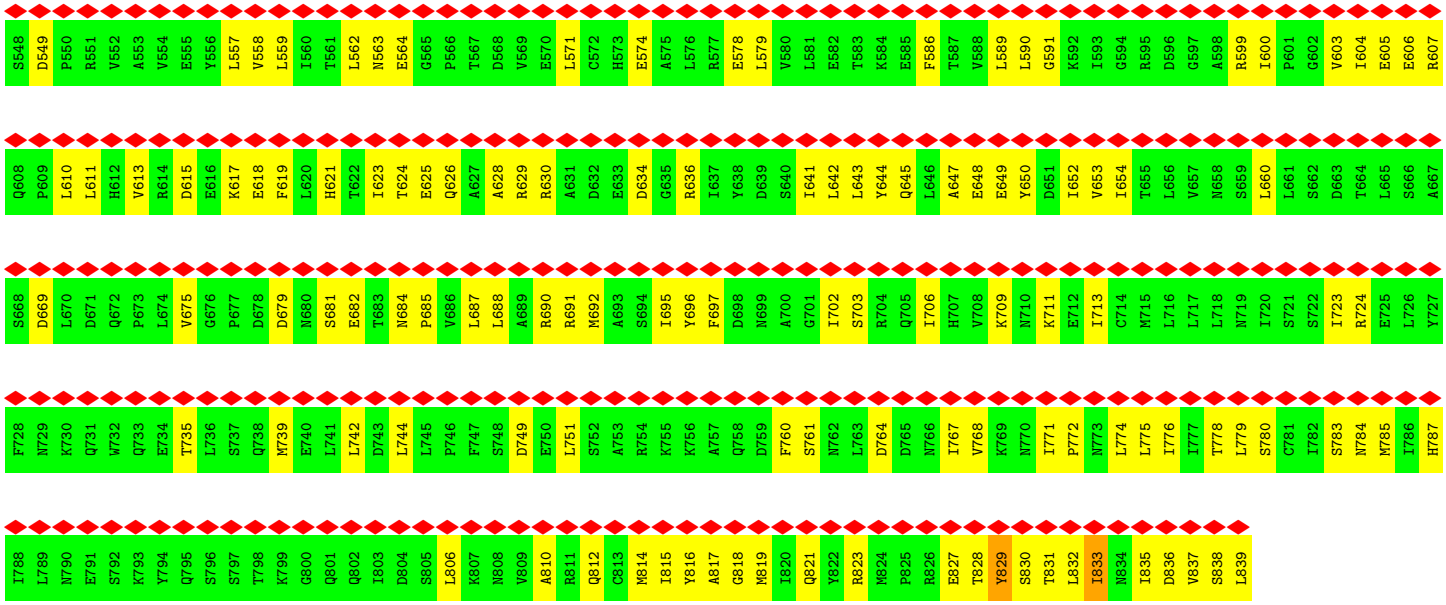
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Nucleoporin NIC96

Chain A:

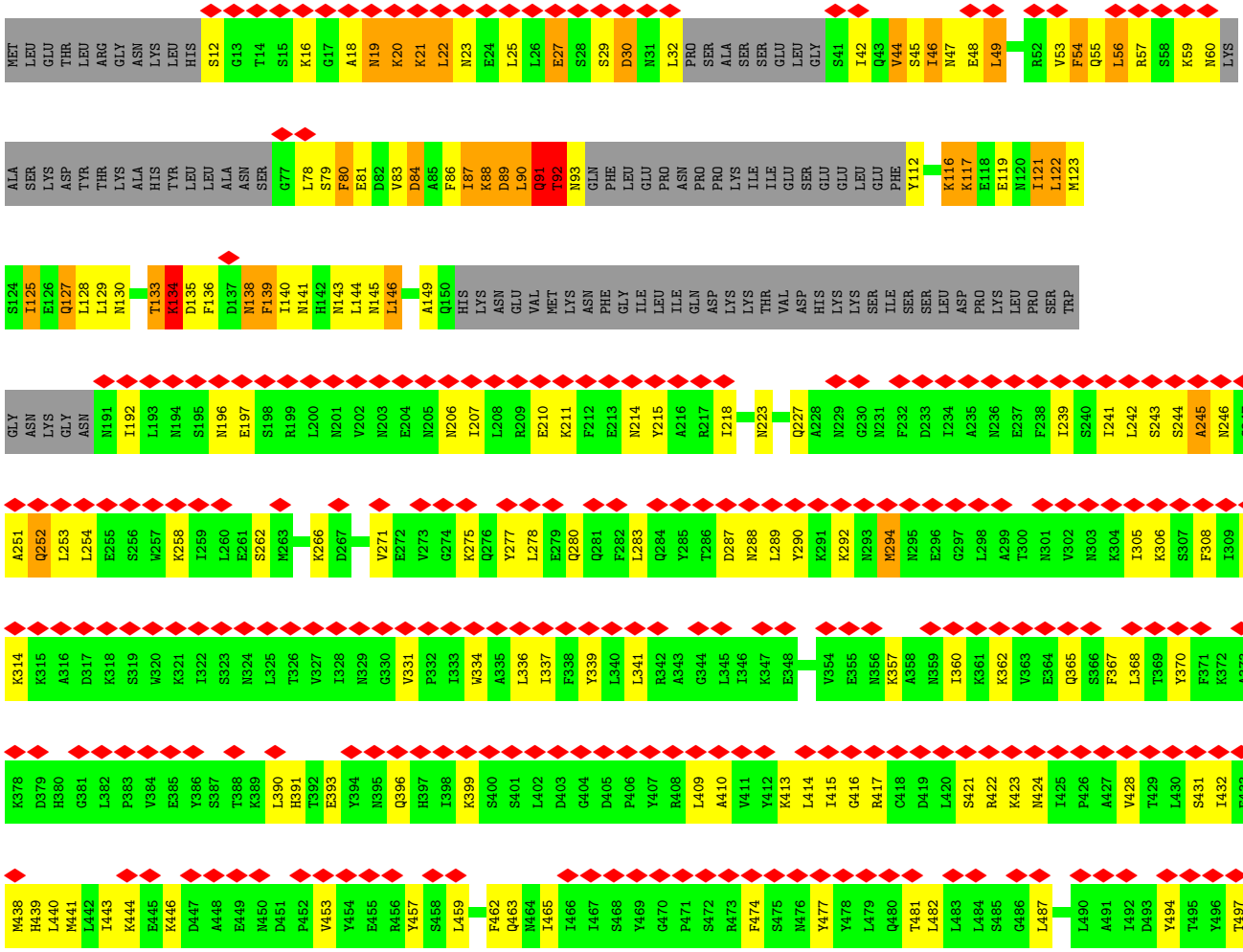


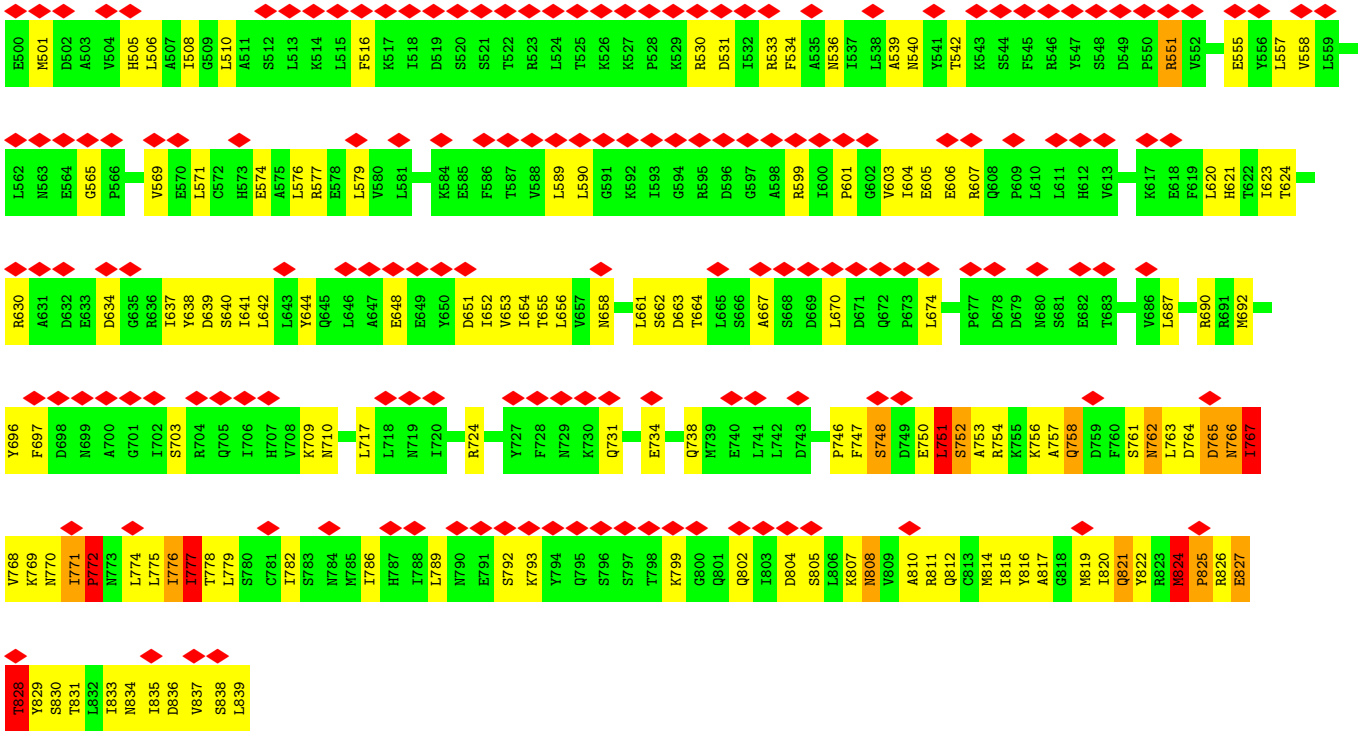




• Molecule 1: Nucleoporin NIC96

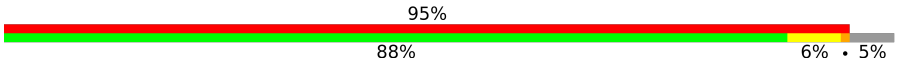
Chain Z:

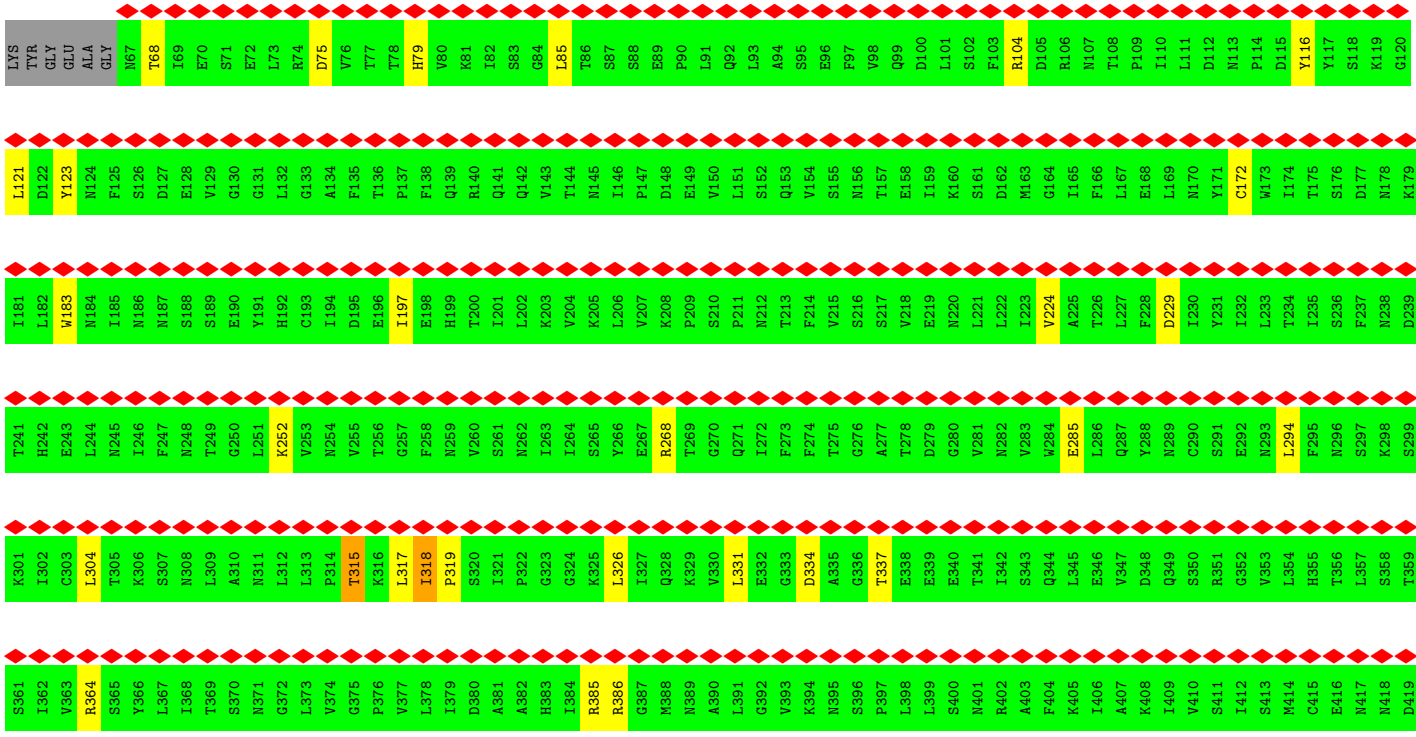


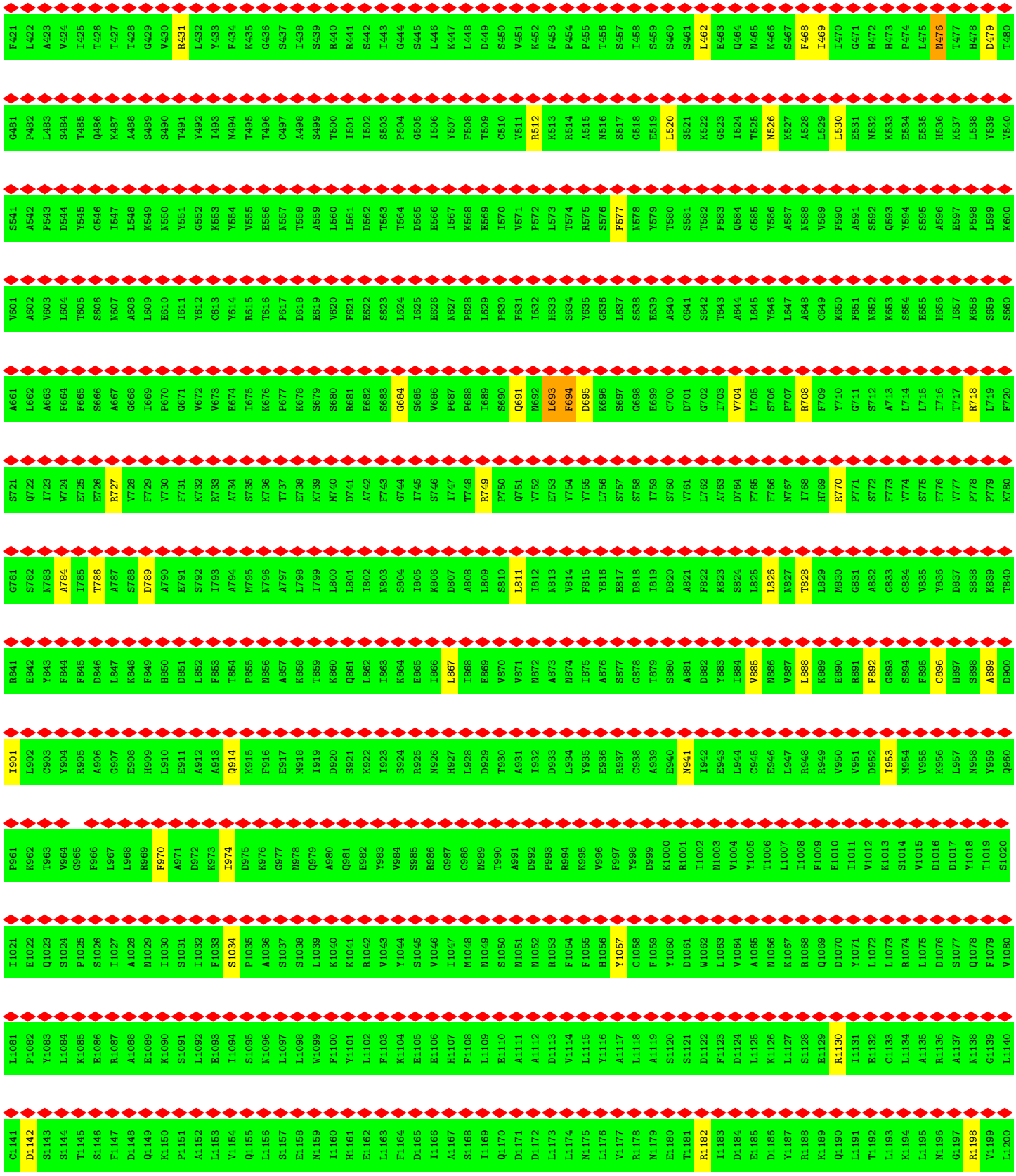


• Molecule 2: Nucleoporin NUP157

Chain C:



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G481 P482 L483 S484 T485 Q486 K487 A488 S489 S490 T491 Y492 I493 N494 T495 T496 C497 A498 S499 T500 I501 I502 S503 P504 G505 I506 Y507 F508 T509 C510 V511 R512 K513 R514 A515 N516 S517 G518 E519 L520 S521 K522 G523 I524 T525 N526 K527 A528 L529 L530 E531 N532 K533 E534 E535 H536 K537 L538 Y539 V540
S541 A542 P543 D544 Y545 G546 I547 L548 K549 N550 Y551 G552 K553 Y554 V555 E556 N557 T558 A559 L560 L561 D562 T563 T564 D565 E566 I567 K568 E569 I570 V571 P572 L573 T574 R575 S576 F577 N578 Y579 T580 S581 T582 P583 Q584 G585 Y586 A587 N588 V589 F590 A591 S592 Q593 Y594 S595 A596 E597 P598 L599 K600
V601 A602 V603 L604 T605 S606 N607 A608 L609 E610 I611 Y612 C613 Y614 R615 T616 P617 D618 E619 V620 F621 E622 S623 L624 I625 E626 N627 P628 L629 P630 F631 I632 H633 S634 Y635 G636 L637 S638 E639 A640 C641 S642 T643 A644 L645 Y646 L647 A648 C649 K650 F651 N652 K653 S654 E655 H656 I657 K658 S659 S660
A661 L662 A663 F664 F665 S666 A667 G668 I669 P670 G671 V672 V673 E674 I675 K676 P677 K678 S679 S680 R681 E682 S683 G684 S685 V686 P687 P688 I689 S690 Q691 N692 L693 F694 D695 K696 S697 G698 E699 C700 D701 G702 I703 V704 L705 S706 P707 R708 F709 Y710 G711 S712 A713 L714 L715 I716 T717 R718 L719 F720
S721 Q722 I723 W724 E725 E726 R727 V728 F729 V730 F731 K732 R733 A734 S735 K736 T737 E738 K739 M740 D741 A742 F743 G744 I745 S746 I747 T748 R749 P750 Q751 V752 E753 Y754 Y755 L756 S757 S758 I759 S760 V761 L762 A763 D764 F765 F766 N767 I768 H769 R770 P771 S772 F773 V774 S775 F776 V777 P778 P779 K780
G781 S782 N783 A784 I785 T786 A787 S788 D789 A790 E791 S792 I793 A794 M795 N796 A797 L798 I799 L800 L801 I802 N803 S804 I805 K806 D807 A808 L809 S810 L811 I812 N813 V814 F815 Y816 E817 D818 I819 D820 A821 F822 K823 S824 L825 L826 N827 T828 L829 M830 G831 A832 G833 G834 V835 Y836 D837 S838 K839 T840
R841 E842 Y843 F844 F845 D846 L847 K848 F849 H850 D851 L852 F853 T854 P855 N856 A857 K858 T859 K860 Q861 L862 I863 K864 E865 I866 L867 I868 E869 V870 V871 N872 A873 N874 I875 A876 S877 G878 T879 S880 A881 D882 Y883 I884 V885 N886 V887 L888 K889 E890 R891 F892 G893 S894 F895 C896 H897 S898 A899 D900
I901 L902 C903 Y904 R905 A906 G907 E908 H909 L910 E911 A912 A913 Q914 K915 F916 E917 M918 I919 D920 S921 K922 I923 S924 R925 N926 H927 L928 D929 T930 A931 I932 D933 L934 Y935 E936 R937 C938 A939 E940 N941 I942 E943 L944 C945 E946 L947 R948 R949 V950 V951 D952 I953 M954 V955 K956 L957 N958 Y959 Q960
P961 K962 T963 V964 G965 F966 L967 L968 R969 F970 A971 D972 K973 I974 D975 K976 G977 N978 Q979 A980 Q981 E982 Y983 V984 S985 R986 G987 C988 N989 T990 A991 D992 P993 R994 K995 V996 F997 Y998 D999 K1000 R1001 I1002 N1003 V1004 Y1005 T1006 L1007 I1008 F1009 E1010 I1011 V1012 K1013 S1014 V1015 D1016 D1017 Y1018 T1019 S1020
I1021 E1022 Q1023 S1024 P1025 S1026 I1027 A1028 N1029 I1030 S1031 I1032 F1033 S1034 P1035 A1036 S1037 S1038 L1039 K1040 K1041 R1042 V1043 Y1044 S1045 V1046 I1047 M1048 N1049 S1050 N1051 N1052 R1053 F1054 F1055 H1056 Y1057 C1058 F1059 Y1060 D1061 W1062 L1063 V1064 A1065 N1066 K1067 R1068 Q1069 D1070 Y1071 L1072 L1073 R1074 L1075 D1076 S1077 Q1078 F1079 V1080
L1081 P1082 Y1083 L1084 K1085 E1086 R1087 A1088 E1089 K1090 S1091 L1092 E1093 I1094 S1095 N1096 L1097 L1098 W1099 F1100 Y1101 L1102 F1103 K1104 E1105 E1106 H1107 F1108 L1109 E1110 A1111 A1112 D1113 V1114 L1115 Y1116 A1117 L1118 A1119 S1120 S1121 D1122 F1123 D1124 L1125 K1126 L1127 S1128 E1129 R1130 I1131 E1132 C1133 L1134 A1135 R1136 A1137 N1138 G1139 L1140
C1141 D1142 S1143 S1144 T1145 S1146 F1147 D1148 Q1149 K1150 P1151 A1152 L1153 V1154 Q1155 L1156 S1157 E1158 N1159 I1160 H1161 E1162 L1163 F1164 D1165 I1166 A1167 S1168 I1169 Q1170 D1171 D1172 L1173 L1174 N1175 L1176 V1177 R1178 N1179 E1180 T1181 R1182 I1183 D1184 E1185 D1186 Y1187 R1188 K1189 Q1190 L1191 T1192 L1193 K1194 L1195 N1196 G1197 R1198 V1199 L1200

P1201 L1202 S1203 D1204 L1205 F1206 N1207 D1208 C1209 A1210 D1211 P1212 L1213 D1214 Y1215 Y1216 E1217 I1218 K1219 L1220 R1221 I1222 F1223 K1224 V1225 S1226 Q1227 F1228 K1229 D1230 E1231 K1232 V1233 I1234 Q1235 G1236 E1237 W1238 M1239 R1240 L1241 L1242 D1243 S1244 M1245 K1246 N1247 A1248 P1249 S1250 P1251 D1252 V1253 G1254 S1255 V1256 G1257 Q1258 E1259 S1260

F1261 L1262 S1263 S1264 I1265 S1266 N1267 T1268 L1269 I1270 R1271 I1272 G1273 K1274 T1275 T1276 R1277 D1278 T1279 D1280 V1281 V1282 F1283 P1284 V1285 H1286 F1287 L1288 M1289 N1290 K1291 I1292 L1293 E1294 S1295 F1296 I1297 D1298 K1299 S1300 S1301 A1302 A1303 D1304 G1305 S1306 V1307 C1308 S1309 M1310 F1311 L1312 L1313 A1314 G1315 V1316 S1317 H1318 L1319 K1320

L1321 Y1322 Y1323 I1324 L1325 S1326 R1327 I1328 I1329 E1330 N1331 S1332 E1333 G1334 N1335 V1336 E1337 L1338 A1339 K1340 K1341 E1342 M1343 V1344 W1345 L1346 I1347 K1348 D1349 W1350 Y1351 Q1352 S1353 D1354 S1355 D1356 L1357 R1358 G1359 S1360 I1361 A1362 P1363 E1364 Q1365 I1366 K1367 K1368 P1369 D1373 P1374 N1375 T1376 D1377 P1378 V1379 Q1380

D1381 Y1382 V1383 K1384 D1385 R1386 H1387 H1388 G1389 L1390 K1391

- Molecule 3: Nucleoporin NUP170

Chain D:

MET PHE GLN SER PHE PHE HIS ASN ASN GLY PRO ALA ALA ALA GLY GLU THR PHE SER ASP SER ARG SER TYR PRO LEU THR ASN HIS GLN GLU VAL PRO ARG ASN GLY LEU ASN GLU LEU ALA SER SER ALA THR LYS ALA GLN GLN GLN PRO THR HIS ILE LEU ASN SER TYR PRO ILE

THR GLY SER ASN PRO LEU MET ARG ALA SER ALA MET GLY ALA THR SER GLY SER ILE ASN PRO ASN MET SER ASN MET ASN GLU HIS ILE ARG VAL SER GLY MET GLY THR S98 K99 P100 L101 D102 L103 A104 G105 K106 Y107 T108 D109 H110 L111 Q112 H113 K114 D115 S116 N117 T118 P119 V120

L121 D122 E123 R124 S125 Y126 Y127 N128 S129 G130 V131 D132 Y133 N134 F135 S136 R137 E138 K139 N140 G141 L142 G143 A144 F145 T146 P147 F148 E149 K150 Q151 D152 V153 F154 N155 I156 P157 D158 E159 I160 L161 H162 E163 F164 S165 T166 S167 Q168 T169 K170 T171 D172 M173 G174 I175 F176 P177 E178 L179 N180

R181 C182 W183 I184 T185 I186 D187 N188 K189 L190 I191 L192 W193 N194 I195 N196 N197 D198 N199 E200 Y201 Q202 V203 V204 D205 D206 M207 K208 H209 T210 I211 Q212 K213 V214 A215 L216 V217 R218 P219 K220 P221 N222 T223 F224 V225 P226 A227 V228 K229 H230 L231 L232 L233 I234 S235 T236 T237 M238 E239 L240

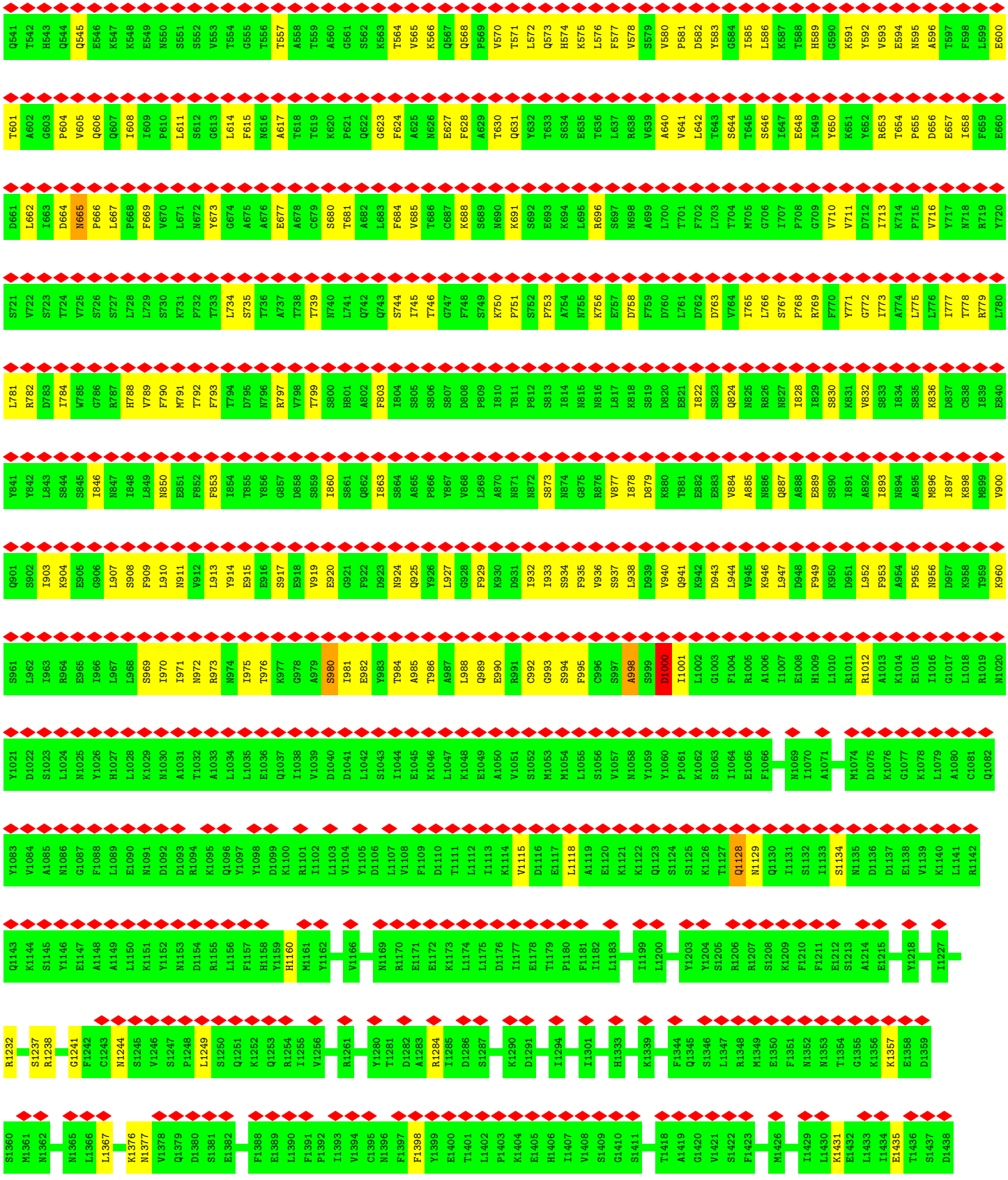
F241 M242 F243 A244 I245 S246 L247 D248 K249 A250 T251 N252 E253 L254 S255 V256 F257 N258 T259 H260 L261 S262 V263 P264 V265 Q266 G267 I268 D269 V270 I271 D272 I273 V274 S275 H276 E277 R278 S279 G280 R281 I282 F283 F284 A285 G286 Q287 A288 S289 G290 L291 N292 I293 W294 E295 L296 H297 Y298 S299 G300

S301 D302 D303 W304 F305 N306 S307 K308 C309 S310 K311 V312 C313 L314 T315 K316 S317 A318 L319 L320 S321 L322 L323 P324 T325 N326 M327 L328 S329 Q330 I331 P332 G333 V334 D335 F336 I337 Q338 A339 L340 F341 E342 D343 N344 S345 N346 G347 N348 G349 G350 F351 S352 Q353 E354 T355 I356 T357 Q358 L359 T360

I361 D362 Q363 Q364 R365 G366 I367 I368 Y369 S370 L371 S372 S373 K374 S375 T376 I377 R378 A379 Y380 V381 I382 T383 E384 K385 S386 L387 E388 G389 P390 M391 S392 I393 E394 P395 A396 Y397 I398 S399 R400 T401 I402 G403 T404 T405 T406 A407 R408 A409 A410 P411 I412 L413 G414 P415 K416 Y417 L418 K419 I420

V421 K422 I423 S424 S425 V426 A427 P428 E429 E430 N431 N432 N433 L434 F435 L436 V437 A438 L439 T440 V441 G442 G443 V444 R445 L446 Y447 F448 N449 G450 S451 M452 G453 R454 F455 N456 I457 E458 A459 L460 R461 L462 E463 S464 I465 K466 F467 P468 P469 S470 S471 V472 T473 P474 E475 V476 I477 Q478 Q479 E480

L481 L482 H483 Q484 Q485 Q486 E487 Q488 A489 K490 R491 S492 F493 P494 F495 F496 S497 N498 L499 M500 S501 S502 E503 P504 V505 L506 L507 K508 F509 Q510 K511 K512 S513 S514 V515 L516 L517 E518 T519 T520 K521 A522 S523 T524 I525 I526 S527 P528 G529 I530 F531 F532 S533 A534 V535 I536 K537 S538 S539 Q540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D661 L662 I663 D664 N665 P666 L667 P668 F669 V670 L671 N672 Y673 G674 A675 A676 E677 A678 C679 S680 T681 A682 L683 F684 V685 T686 C687 K688 S689 N690 K691 S692 E693 K694 L695 R696 S697 N698 A699 L700 T701 F702 L703 T704 M705 G706 I707 P708 G709 V710 V711 D712 I713 K714 P715 V716 Y717 N718 R719 Y720
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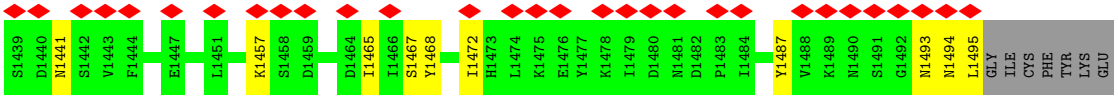
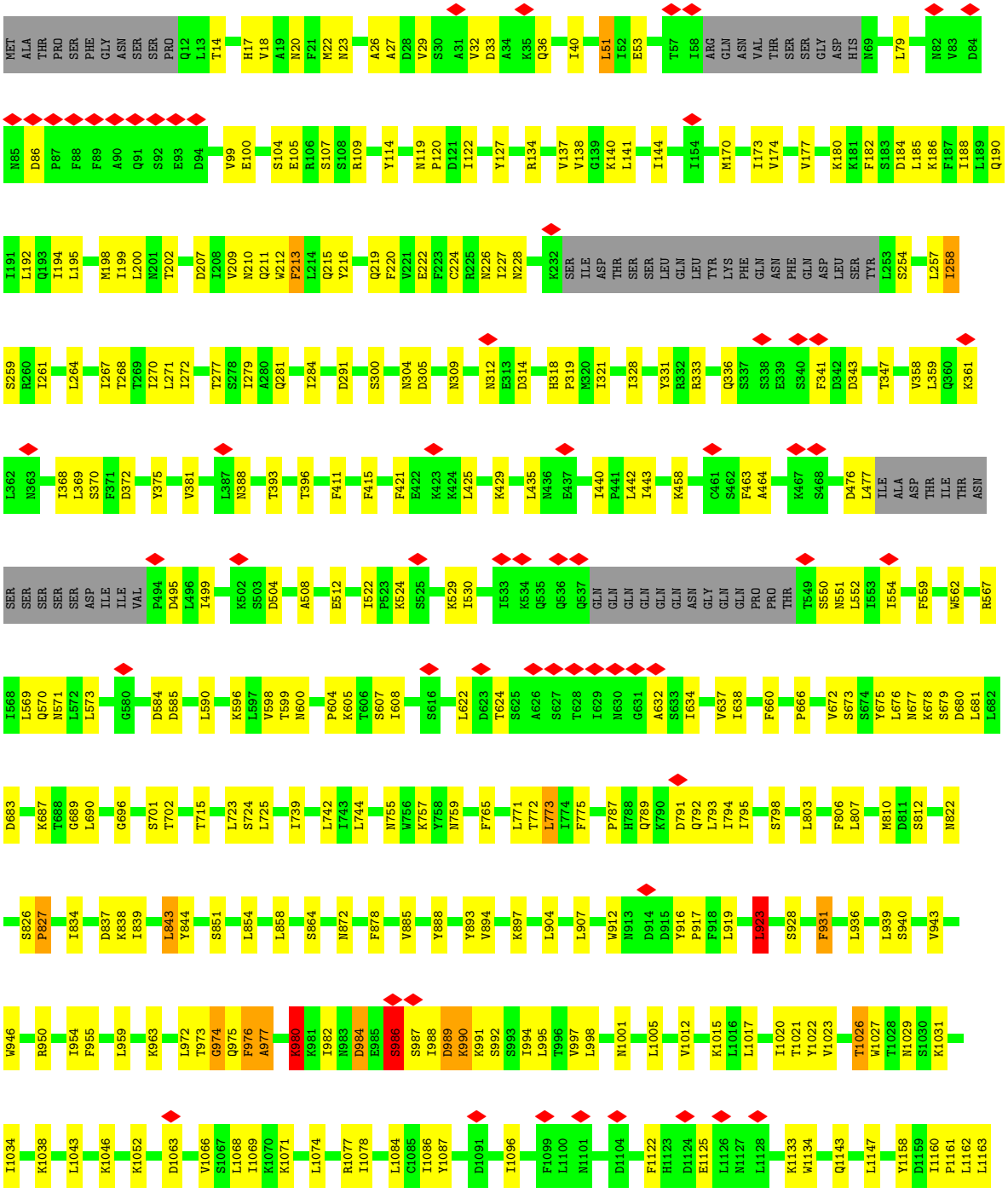
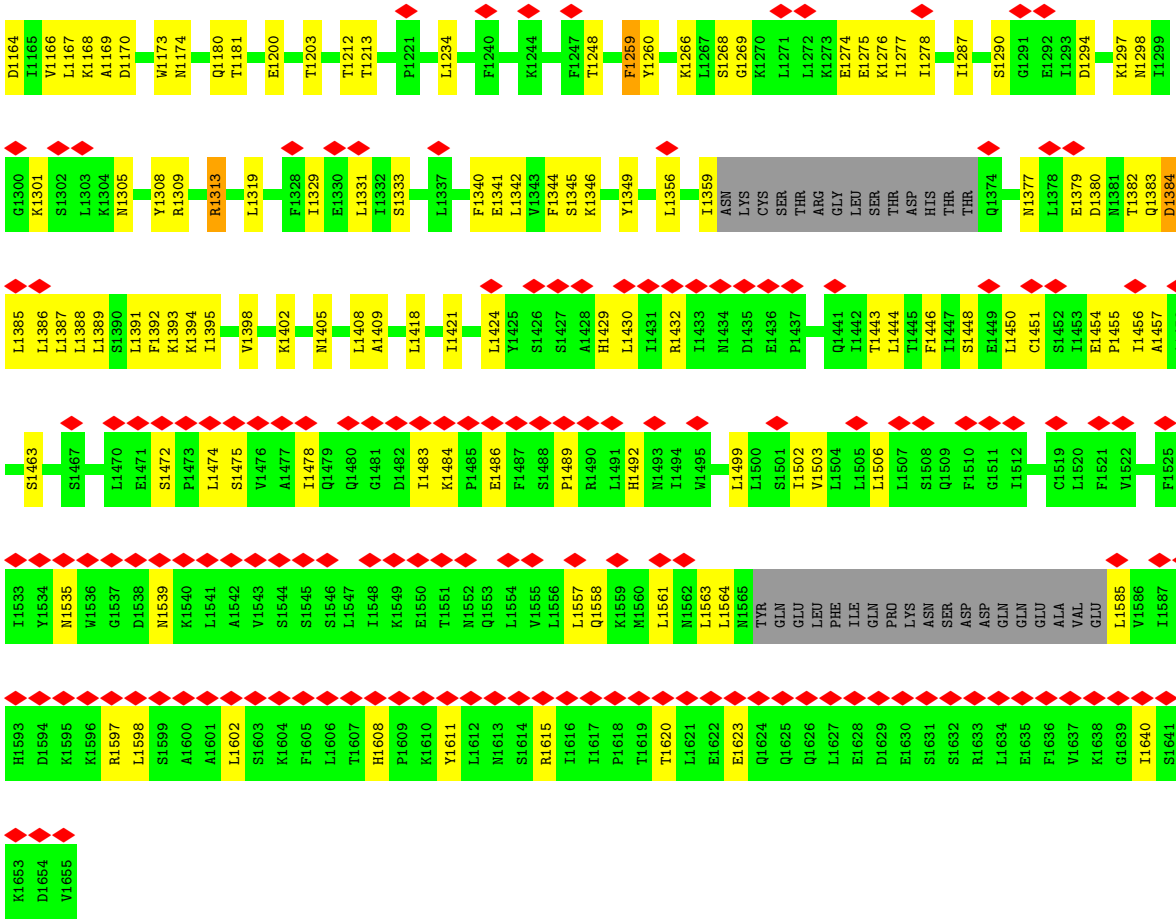
L781 R782 D783 I784 W785 G786 R787 H788 V789 F790 M791 T792 F793 T794 D795 N796 R797 V798 T799 S800 H801 A802 F803 I804 S805 S806 S807 D808 P809 I810 T811 P812 S813 I814 N815 N816 L817 K818 S819 D820 E821 I822 S823 Q824 N825 R826 N827 I828 I829 S830 K831 V832 S833 I834 S835 K836 D837 C838 I839 E840
Y841 Y842 L843 S844 S845 I846 N847 I848 L849 N850 E851 F852 F853 I854 T855 Y856 G857 D858 S859 I860 S861 Q862 I863 S864 A865 P866 Y867 V868 L869 A870 N871 N872 S873 N874 G875 R876 V877 I878 D879 K880 T881 E882 E883 V884 A885 N886 Q887 A888 E889 S890 I891 A892 I893 N894 A895 M896 I897 K898 M899 V900
Q901 S902 I903 K904 E905 G906 L907 S908 F909 L910 N911 V912 L913 Y914 E915 E916 S917 E918 V919 E920 G921 F922 D923 N924 Q925 Y926 L927 G928 F929 K930 D931 I932 I933 S934 F935 V936 S937 L938 D939 V940 Q941 K942 D943 L944 Y945 K946 L947 D948 F949 K950 D951 L952 F953 A954 P955 N956 D957 K958 T959 K960
S961 L962 I963 R964 E965 I966 L967 L968 S969 I970 I971 N972 R973 N974 I975 T976 K977 G978 A979 S980 I981 E982 Y983 T984 A985 T986 A987 L988 Q989 E990 R991 C992 G993 S994 F995 C996 S997 A998 S999 D1000 I1001 L1002 G1003 F1004 R1005 A1006 I1007 E1008 H1009 L1010 R1011 R1012 A1013 K1014 E1015 I1016 G1017 L1018 R1019 N1020
Y1021 D1022 S1023 L1024 N1025 Y1026 H1027 L1028 K1029 N1030 A1031 T1032 A1033 L1034 L1035 E1036 Q1037 I1038 V1039 D1040 D1041 L1042 S1043 I1044 E1045 K1046 L1047 K1048 E1049 A1050 V1051 S1052 M1053 M1054 L1055 S1056 V1057 N1058 Y1059 Y1060 P1061 K1062 S1063 I1064 E1065 F1066 N1069 I1070 A1071 M1074 D1075 K1076 G1077 K1078 L1079 A1080 C1081 Q1082
Y1083 V1084 A1085 N1086 G1087 F1088 L1089 E1090 N1091 D1092 D1093 R1094 K1095 Q1096 Y1097 Y1098 D1099 K1100 R1101 I1102 L1103 V1104 Y1105 D1106 L1107 V1108 F1109 D1110 T1111 L1112 I1113 K1114 V1115 D1116 E1117 L1118 A1119 E1120 K1121 K1122 Q1123 S1124 S1125 K1126 T1127 Q1128 N1129 Q1130 I1131 S1132 I1133 S1134 N1135 D1136 D1137 E1138 V1139 K1140 L1141 R1142
Q1143 K1144 S1145 Y1146 E1147 A1148 A1149 L1150 K1151 Y1152 N1153 D1154 R1155 L1156 F1157 H1158 Y1159 H1160 M1161 Y1162 V1166 N1169 R1170 E1171 E1172 K1173 L1174 L1175 D1176 I1177 E1178 T1179 P1180 F1181 I1182 L1183 I1199 L1200 Y1203 Y1204 S1205 R1206 R1207 S1208 K1209 F1210 F1211 E1212 S1213 A1214 E1215 Y1218 I1227
R1232 S1237 R1238 G1241 F1242 C1243 N1244 S1245 V1246 S1247 P1248 L1249 S1250 Q1251 K1252 Q1253 R1254 I1255 V1256 R1261 Y1280 T1281 D1282 A1283 R1284 I1285 D1286 S1287 K1290 D1291 I1294 I1301 H1333 K1339 F1344 Q1345 S1346 L1347 R1348 M1349 E1350 F1351 N1352 N1353 T1354 G1355 K1356 K1357 E1358 D1359
S1360 M1361 N1362 N1365 L1366 L1367 K1376 N1377 V1378 Q1379 D1380 S1381 E1382 F1388 E1389 L1390 F1391 P1392 I1393 V1394 C1395 N1396 F1397 F1398 Y1399 E1400 T1401 L1402 P1403 K1404 E1405 H1406 I1407 V1408 S1409 G1410 S1411 T1418 A1419 G1420 V1421 S1422 F1423 M1426 I1429 L1430 K1431 E1432 L1433 I1434 E1435 T1436 S1437 D1438



• Molecule 4: Nucleoporin NUP188

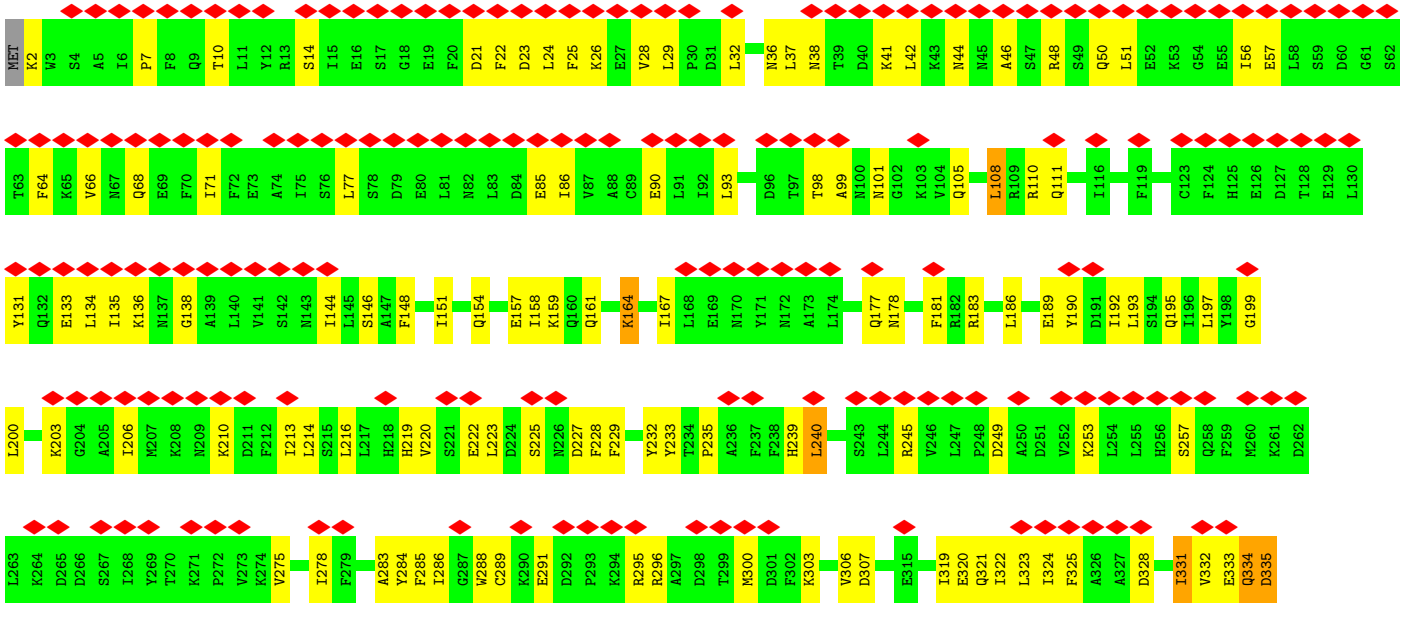
Chain E:

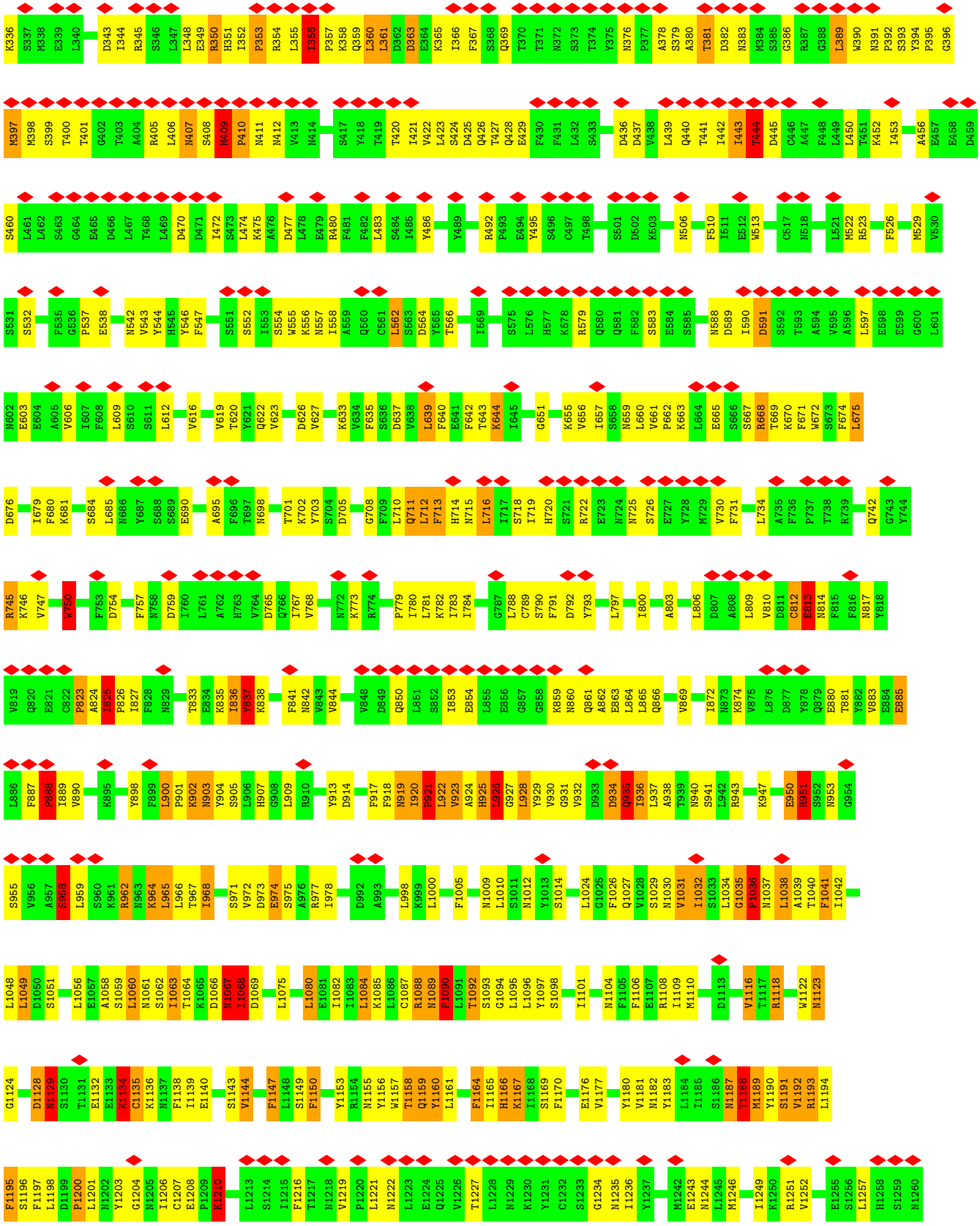




• Molecule 5: Nucleoporin NUP192

Chain F:

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M397 M398 S399 T400 T401 G402 T403 A404 R405 L406 N407 S408 N409 P410 N411 N412 V413 N414 S417 Y418 T419 T420 I421 V422 L423 S424 D425 Q426 T427 Q428 E429 F430 F431 L432 S433 D436 D437 V438 L439 Q440 T441 I442 I443 T444 D445 C446 A447 F448 L449 L450 T451 K452 I453 A456 E457 E458 D459
S460 L461 L462 S463 G464 E465 D466 L467 T468 L469 D470 D471 I472 S473 L474 K475 A476 D477 L478 E479 R480 F481 F482 L483 S484 I485 Y486 Y489 R492 P493 E494 Y495 S496 C497 T498 S501 D502 K503 N506 F510 I511 E512 W513 C517 N518 L521 M522 R523 F526 M529 V530
S531 S532 F535 G536 P537 E538 N542 V543 Y544 H545 Y546 F547 S551 S552 I553 S554 W555 K556 N557 I558 A559 Q560 C561 L562 S563 D564 Y565 T566 I569 S575 L576 H577 K578 R579 Q580 Q581 F582 S583 E584 S585 N588 D589 I590 D591 S592 T593 A594 V595 A596 L597 E598 E599 G600 L601
N602 E603 E604 A605 V606 I607 F608 L609 S610 S611 L612 V616 V619 T620 Y621 Q622 V623 D626 V627 K633 V634 F635 S636 D637 V638 L639 F640 E641 F642 T643 K644 I645 G651 K655 V656 I657 S658 N659 L660 V661 P662 K663 L664 E665 S666 S667 R668 T669 K670 F671 W672 S673 F674 L675
D676 I679 F680 K681 S684 L685 N686 Y687 S688 S689 E690 A695 F696 T697 N698 T701 K702 Y703 S704 D705 G708 F709 L710 Q711 L712 F713 H714 N715 L716 I717 S718 I719 H720 S721 R722 E723 N724 N725 S726 E727 Y728 M729 V730 F731 L734 A735 F736 P737 T738 R739 Q742 G743 Y744
R745 K746 V747 W750 F753 D754 F757 N758 D759 I760 L761 A762 H763 V764 D765 G766 I767 V768 N772 K773 R774 P779 I780 L781 K782 I783 I784 G787 L788 C789 S790 F791 D792 Y793 L797 I800 A803 L806 D807 A808 L809 V810 D811 C812 E813 N814 F815 F816 N817 Y818
V819 Q820 E821 C822 P823 A824 I825 P826 I827 F828 N829 T833 E834 K835 I836 Y837 K838 F841 N842 V843 V844 V848 D849 Q850 L851 S852 I853 E854 L855 E856 G857 G858 K859 N860 Q861 A862 E863 L864 L865 Q866 V869 I872 N873 K874 V875 L876 D877 Y878 Q879 E880 T881 Y882 V883 E884 E885
L886 F887 P888 I889 V890 K895 Y898 F899 L900 P901 K902 N903 Y904 S905 L906 H907 G908 L909 R910 Y913 D914 F917 F918 N919 I920 P921 L922 V923 A924 H925 L926 G927 L928 Y929 V930 G931 V932 D933 D934 Q935 I936 L937 A938 T939 N940 S941 L942 R943 K947 E950 R951 S952 N953 G954
S955 V956 A957 S958 L959 S960 K961 R962 N963 K964 L965 L966 T967 I968 S971 V972 D973 E974 S975 A976 R977 I978 D992 A993 L998 K999 L1000 F1005 N1009 L1010 S1011 N1012 Y1013 S1014 L1024 G1025 F1026 Q1027 V1028 S1029 N1030 V1031 I1032 S1033 L1034 G1035 P1036 N1037 L1038 A1039 T1040 F1041 I1042
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G1124 D1128 N1129 S1130 T1131 E1132 E1133 K1134 C1135 K1136 N1137 F1138 I1139 E1140 S1143 V1144 F1147 L1148 S1149 F1150 Y1153 R1154 N1155 Y1156 W1157 T1158 Q1159 Y1160 L1161 F1164 I1165 H1166 K1167 I1168 S1169 F1170 E1176 V1177 Y1180 V1181 N1182 Y1183 L1184 I1185 S1186 N1187 T1188 M1189 Y1190 S1191 V1192 R1193 L1194
F1195 S1196 F1197 L1198 D1199 P1200 L1201 N1202 Y1203 G1204 N1205 I1206 C1207 E1208 P1209 K1210 L1213 S1214 I1215 F1216 T1217 N1218 V1219 P1220 L1221 N1222 L1223 E1224 Q1225 V1226 T1227 L1228 N1229 K1230 Y1231 C1232 S1233 G1234 N1235 I1236 Y1237 M1242 E1243 N1244 L1245 M1246 I1249 K1250 R1251 V1252 E1255 S1256 L1257 H1258 S1259 N1260

S1261 F1262 S1263 L1264 T1265 V1266 S1267 K1268 E1269 Q1270 F1271 L1272 K1273 D1274 A1275 D1276 V1277 E1278 C1279 I1280 K1281 A1282 K1283 S1284 H1285 F1286 I1289 I1290 S1291 R1292 N1293 K1294 A1295 L1296 E1297 L1298 N1299 L1300 S1301 V1302 L1303 H1304 S1305 W1306 V1307 Q1308 L1309 V1314 T1315 D1316 G1317 LYS LEU GLU PRO SER THR ARG

SER ASN PHE ILE LEU GLU VAL PHE GLY THR ILE ILE PRO LYS ILE SER ASP TYR ILE GLU PHE N1346 F1349 L1353 L1356 A1357 V1358 F1359 L1360 F1361 D1362 I1363 Y1364 N1365 R1366 D1367 R1368 K1369 L1370 I1371 T1372 D1373 K1374 G1375 T1376 V1377 D1378 L1381 Y1382 Q1383 L1384 T1387 C1388 I1389 Q1390

G1391 I1392 N1393 S1394 P1395 L1396 V1399 A1400 L1401 R1402 S1403 D1404 F1405 Y1406 I1407 L1408 L1417 Q1420 V1421 G1422 S1423 E1424 K1425 V1426 L1427 Q1428 R1431 S1434 K1435 K1436 E1439 I1440 I1441 W1442 N1443 D1444 V1445 G1448 T1451 S1452 R1453 L1463 I1464 Q1465 L1466 A1467 N1468 R1469 S1470 K1471 E1472

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A1548 E1549 L1550 S1551 F1552 L1553 K1554 V1555 D1556 P1557 D1558 L1559 G1560 L1561 ASP LEU MET PHE ASP GLU VAL TYR VAL GLN ASN SER LYS PHE LEU LYS VAL ASN VAL THR LEU ASP ASN PRO LEU LEU VAL ASP LYS ASP A1592 N1593 G1594 V1595 S1596 L1597 F1598 E1599 L1600 I1601 I1604 F1605 Q1606 L1607 I1608

S1609 A1610 V1611 L1612 M1615 G1616 S1617 S1618 V1622 V1623 Q1624 T1625 V1626 K1627 G1628 L1629 L1630 N1631 T1632 Y1633 K1634 R1635 L1636 V1637 I1638 G1639 I1640 F1641 K1642 R1643 D1644 L1645 L1646 R1647 E1648 K1649 E1650 D1651 K1652 K1653 N1654 S1655 S1656 D1657 P1658 N1659 N1660 L1663 N1664 E1665 M1666 V1667 K1668 L1669 I1670 V1671 M1672

L1673 C1674 T1675 L1676 T1677 G1678 Y1679 Q1680 N1681 ASN ASP

- Molecule 6: Nucleoporin NUP49/NSP49

Chain G: 24% | 30% | 12% | • | 58%

MET PHE GLY LEU ASN LYS ALA SER SER THR PRO ALA GLY LEU PHE GLY GLN ALA SER GLY ALA SER THR GLY ASN ALA ASN THR GLY PHE SER PHE GLY THR GLN THR GLY GLN ASN THR GLY PRO SER THR GLY GLY LEU PHE GLY ALA LYS PRO ALA GLY SER THR GLY GLY

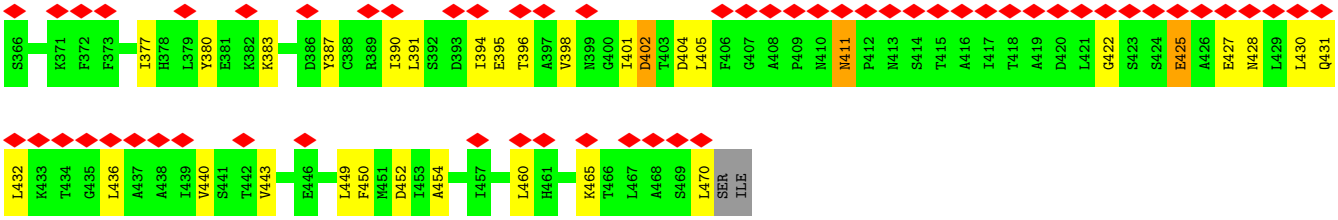
LEU GLY ALA SER PHE GLY GLN GLN GLN GLN GLN SER GLN THR ASN ALA PHE GLY GLY SER ALA THR THR GLY GLY GLY LEU PHE GLY ASN LYS PRO ASN ASN THR ALA ASN THR GLY GLY GLY LEU PHE GLY ALA ASN SER ASN SER ASN SER GLY SER LEU PHE GLY SER ASN ASN ALA

GLN THR SER ARG GLY LEU PHE GLY ASN ASN ASN THR ASN ILE ASN ASN SER SER SER GLY MET ASN ASN ALA SER ALA GLY LEU PHE GLY SER LYS PRO ALA GLY GLY THR SER LEU PHE GLY ASN THR SER THR THR SER SER ALA PRO ALA GLN ASN GLN GLY MET PHE GLY ALA LYS

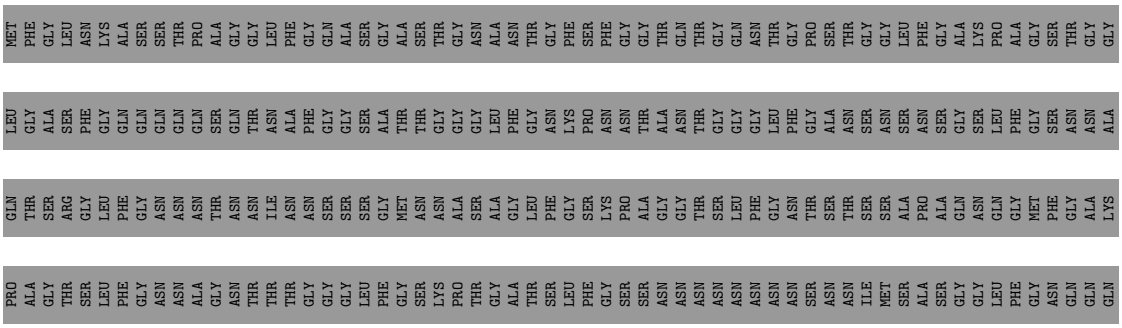
PRO ALA GLY THR SER LEU PHE GLY ASN ASN ALA GLY ASN THR THR THR GLY GLY GLY LEU PHE GLY SER LYS PRO THR GLY ALA THR SER LEU PHE GLY SER SER ASN ASN ASN ASN ASN ASN ASN ASN SER SER ASN ASN ILE MET SER ALA SER GLY GLY LEU PHE GLY ASN GLN GLN GLN

GLN LEU GLN GLN GLN PRO GLN MET GLN CYS ALA LEU GLN ASN LEU SER GLN LEU PRO ILE THR PRO MET THR ARG ILE SER GLU LEU PRO P271 Q272 I273 R274 Q275 E276 I277 E278 Q279 L280 D281 Q282 Y283 I284 Q285 V288 Q289 H292 K295 A296 D297 T298 I299 D300 H301 D302 E303

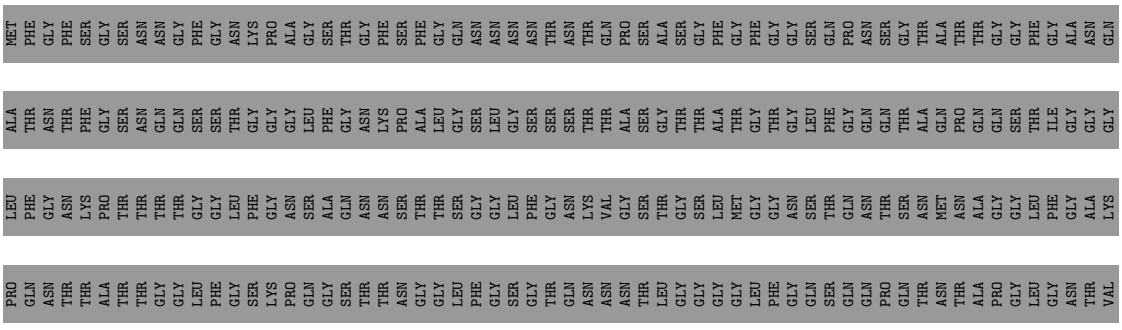
L304 I305 D306 S307 I308 P309 R310 Y314 L315 L316 K317 S318 E319 S320 A321 T322 S323 Q324 Y325 L326 K327 Q328 D329 L330 K331 K332 I333 S334 S335 F336 K337 S338 L339 I340 D341 E342 D343 L344 L345 D346 T347 Q348 T349 F350 S351 V352 L353 L354 Q355 Q356 L357 L358 T359 P360 G361 S362 K363 I364 S365

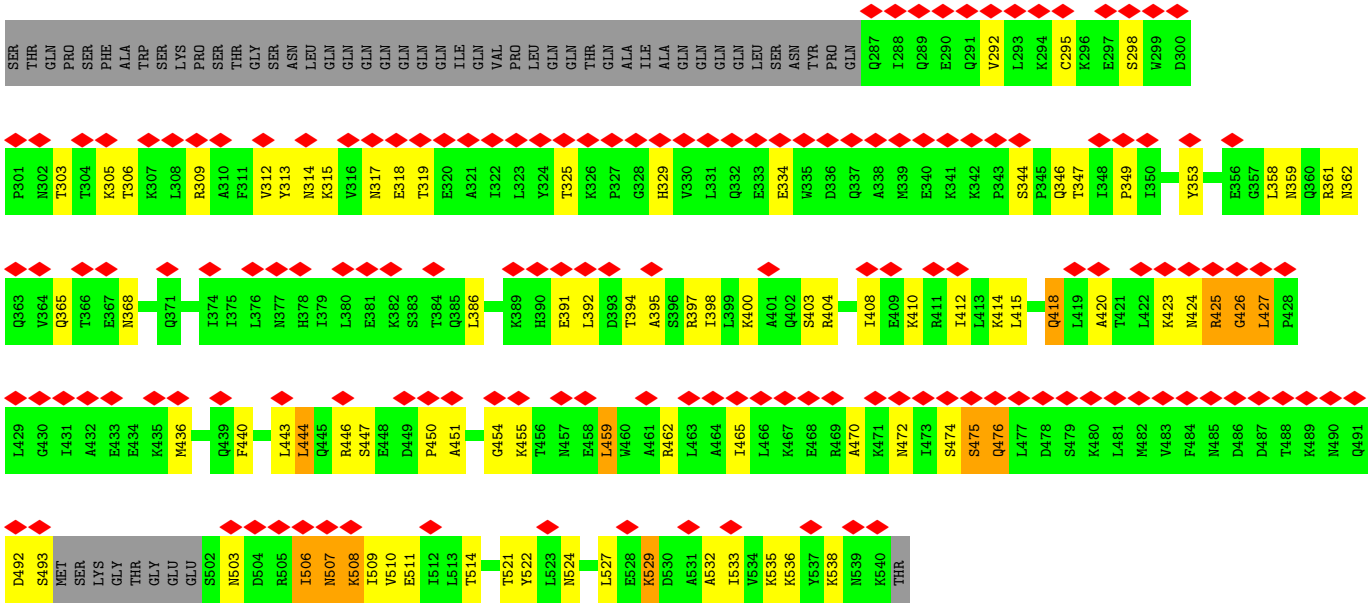


• Molecule 6: Nucleoporin NUP49/NSP49



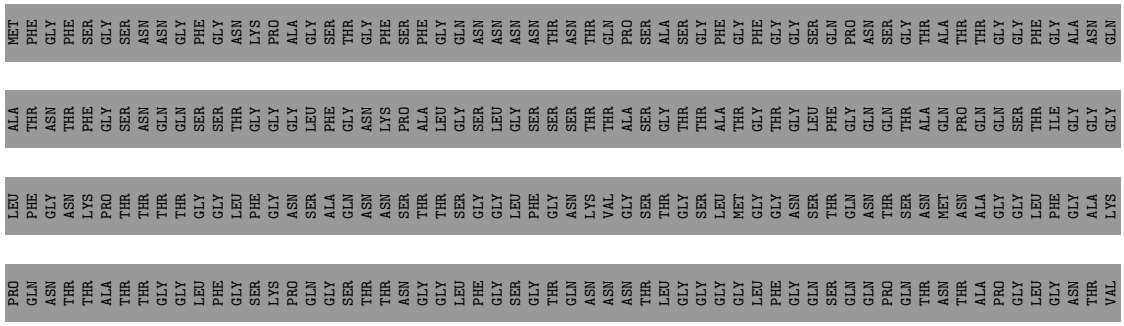
• Molecule 7: Nucleoporin NUP57

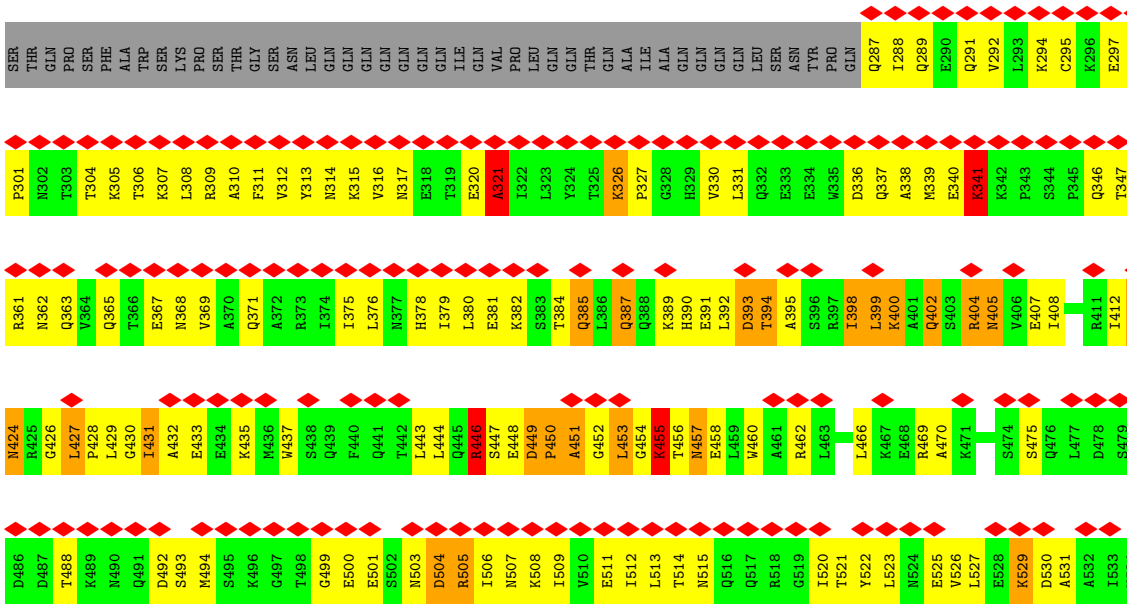




• Molecule 7: Nucleoporin NUP57

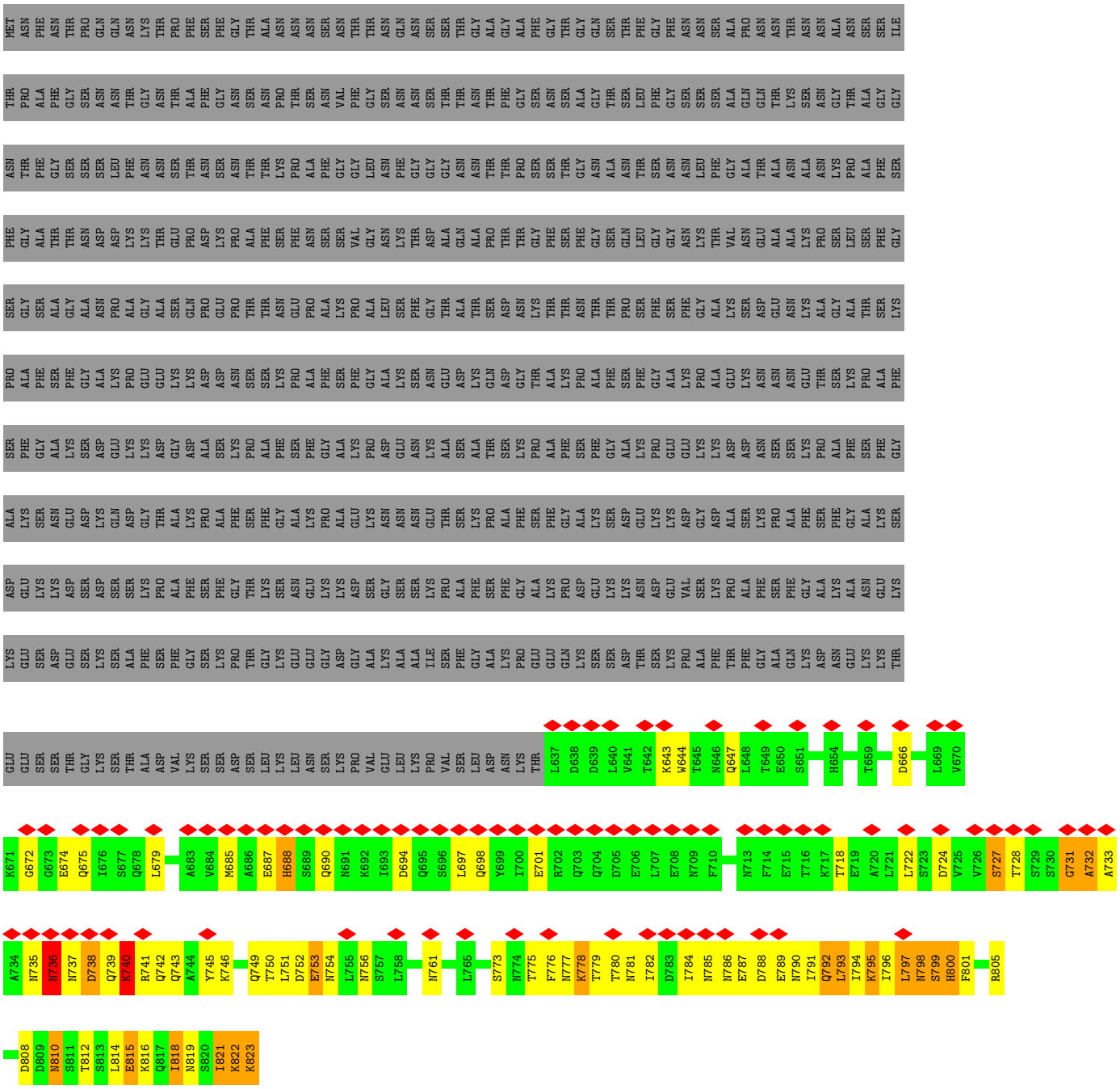
Chain K:





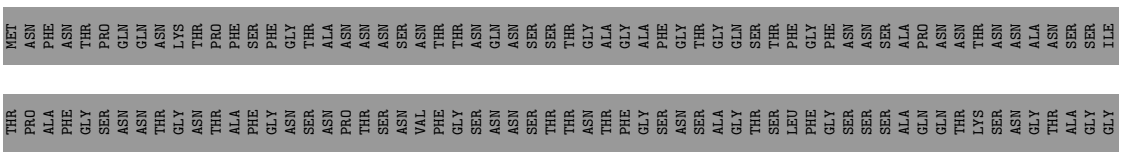
• Molecule 8: Nucleoporin NSP1

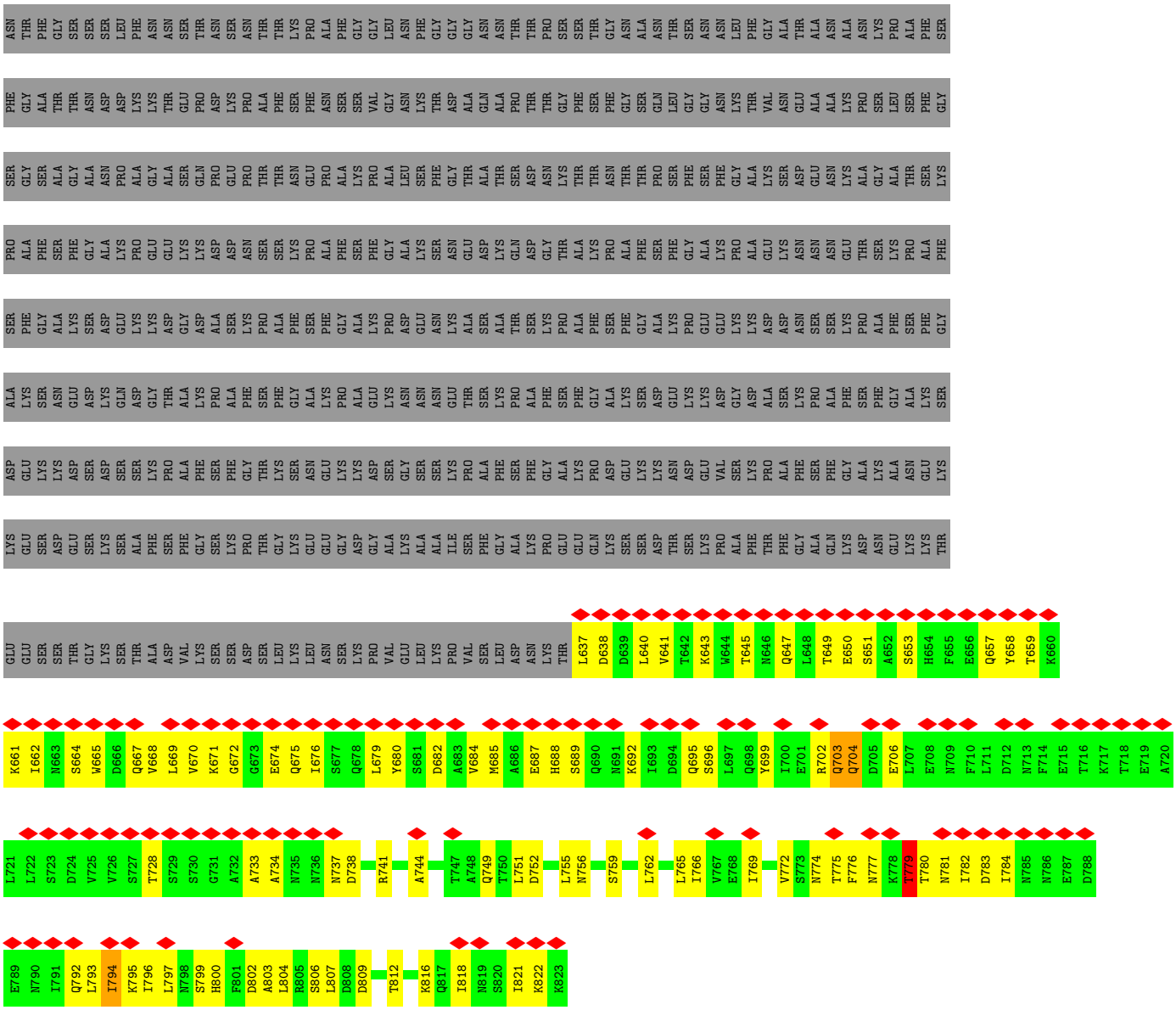
Chain I:



• Molecule 8: Nucleoporin NSP1

Chain L:




ASN THR PHE GLY SER SER SER LEU PHE ASN ASN SER THR ASN SER ASN THR THR LYS PRO ALA PHE GLY GLY LEU ASN PHE GLY GLY GLY ASN ASN THR THR PRO SER SER THR GLY ASN ALA ASN THR SER ASN ASN LEU LEU PHE GLY ALA THR ASN ALA ASN LYS PRO ALA PHE SER
PHE GLY ALA THR THR ASN ASP ASP LYS LYS THR GLU PRO ASP LYS PRO ALA PHE SER PHE ASN SER SER VAL GLY ASN LYS THR ASP GLY ALA GLN ALA PRO THR THR THR GLY PHE SER PHE GLY SER GLN LEU LEU GLY GLY ASN ASN LYS THR VAL ASN GLU ALA ALA LYS PRO SER LEU SER PHE GLY
SER GLY SER ALA GLY ALA ASN PRO ALA GLY ALA SER GLN PRO GLU PRO THR THR THR ASN SER PHE GLY THR ALA THR SER ASP ASN LYS THR THR THR PRO SER PHE SER PHE GLY GLY ALA LYS SER ASP GLU ASN LYS ALA GLY ALA THR SER LYS
PRO ALA PHE SER PHE GLY ALA LYS PRO GLU GLU LYS LYS ASP ASP ASN SER SER LYS PRO ALA PHE SER PHE GLY ALA LYS SER ASN GLU ASP LYS GLN ASP GLY THR ALA LYS PRO ALA PHE SER PHE GLY ALA LYS PRO GLU GLU LYS ASN ASN GLU THR SER LYS ALA PHE
SER PHE GLY ALA LYS SER ASP GLU LYS LYS ASP GLY ASP ALA SER LYS PRO ALA PHE SER PHE GLY ALA LYS PRO ASP GLU ASN ASN SER ALA THR SER LYS PRO ALA PHE SER PHE GLY ALA LYS PRO GLU GLU LYS LYS ASP ASP ASN SER SER LYS PRO ALA PHE SER PHE GLY
ALA LYS SER ASN GLU ASP GLY THR LYS SER PHE GLY ALA LYS PRO ALA PHE SER PHE GLY GLY ALA LYS SER ASP GLU LYS SER ASN ASN SER LYS PRO ALA PHE GLY GLY ALA LYS SER ASP GLU LYS LYS ASP GLY ASP ALA SER PHE GLY ALA LYS SER ASN ASN SER LYS PRO ALA PHE SER PHE GLY
ASP GLU LYS LYS ASP SER SER SER LYS PRO ALA PHE SER PHE GLY THR LYS SER ASN GLU LYS LYS SER GLY SER SER LYS PRO ALA PHE SER PHE GLY GLY ALA LYS PRO ASP GLU LYS LYS ASN ASP GLU VAL SER LYS PRO ALA PHE SER PHE GLY ALA LYS LYS ASN ASP GLU LYS LYS
LYS GLU SER ASP GLU SER LYS SER ALA PHE SER PHE GLY SER LYS PRO THR GLY LYS GLU GLU GLY ASP GLY ALA LYS ALA ILE SER PHE GLY ALA LYS PRO GLU GLU GLN LYS SER SER ASP THR SER LYS PRO ALA PHE THR PHE GLY ALA ALA GLN LYS ASP ASN GLU LYS LYS THR
GLU GLU SER SER THR GLY LYS SER THR ALA ASP VAL LYS SER ASP LEU LYS LEU ASN SER LYS PRO VAL GLU LEU LYS PRO VAL SER LEU ASP ASN LYS THR L637 D638 D639 L640 V641 T642 K643 W644 T645 N646 Q647 L648 T649 E650 S651 A652 S653 H654 F655 E656 Q657 Y658 T659 K660
K661 I662 N663 S664 W665 D666 Q667 V668 L669 V670 K671 G672 G673 E674 Q675 I676 S677 Q678 L679 Y680 S681 D682 A683 V684 M685 A686 E687 H688 S689 Q690 N691 K692 I693 D694 Q695 S696 L697 Q698 Y699 I700 E701 R702 Q703 Q704 D705 E706 L707 E708 N709 F710 L711 D712 N713 F714 E715 T716 K717 T718 E719 A720
L721 L722 S723 D724 V725 V726 S727 T728 S729 S730 G731 A732 A733 A734 N735 N736 N737 D738 R741 A744 T747 A748 Q749 T750 L751 D752 L755 N756 S759 L762 L765 I766 V767 E768 I769 V772 S773 N774 T775 F776 N777 K778 T779 T780 N781 I782 D783 I784 N785 N786 E787 D788
E789 N790 T791 Q792 L793 T794 K795 T796 L797 N798 S799 H800 F801 D802 A803 L804 R805 S806 L807 D808 D809 T812 K816 Q817 I818 N819 S820 I821 K822 K823

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1266268	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.677	Depositor
Minimum map value	-1.782	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.24	Depositor
Map size (Å)	467.59998, 467.59998, 467.59998	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.336, 1.336, 1.336	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.36	0/5813	0.58	5/7867 (0.1%)
1	Z	0.46	0/5862	0.82	9/7942 (0.1%)
2	C	0.66	0/10658	0.90	24/14443 (0.2%)
3	D	0.46	0/11192	0.63	5/15173 (0.0%)
4	E	0.43	0/12583	0.68	8/17054 (0.0%)
5	F	0.63	6/12435 (0.0%)	1.18	93/16887 (0.6%)
6	G	0.35	0/1553	0.62	1/2104 (0.0%)
6	J	0.49	0/1509	1.01	11/2042 (0.5%)
7	H	0.61	2/1832 (0.1%)	0.88	10/2482 (0.4%)
7	K	0.56	1/1829 (0.1%)	0.96	12/2485 (0.5%)
8	I	0.59	0/1431	0.93	4/1940 (0.2%)
8	L	0.40	0/1378	0.74	1/1873 (0.1%)
All	All	0.53	9/68075 (0.0%)	0.85	183/92292 (0.2%)

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	Z	0	1
5	F	0	3
6	G	0	1
7	H	0	1
7	K	0	2
All	All	0	8

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	750	TRP	C-N	10.13	1.53	1.34
7	H	427	LEU	C-N	9.99	1.53	1.34
7	H	425	ARG	C-N	8.96	1.49	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	K	326	LYS	C-N	8.60	1.50	1.34
5	F	1235	ASN	C-N	8.56	1.53	1.34
5	F	1394	SER	C-N	8.47	1.50	1.34
5	F	409	MET	C-N	8.27	1.50	1.34
5	F	356	ILE	C-N	7.34	1.48	1.34
5	F	1182	ASN	C-O	6.52	1.35	1.23

All (183) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	F	1090	PRO	CA-N-CD	-37.80	58.58	111.50
7	H	425	ARG	C-N-CA	-13.39	94.18	122.30
6	J	388	CYS	CB-CA-C	-12.59	85.22	110.40
5	F	1036	PRO	N-CA-CB	10.85	116.32	103.30
5	F	1089	ASN	C-N-CD	10.13	149.68	128.40
8	I	800	HIS	CB-CA-C	10.06	130.51	110.40
1	Z	772	PRO	CA-N-CD	-10.04	97.44	111.50
5	F	1067	ASN	CB-CA-C	-9.88	90.65	110.40
2	C	104	ARG	NE-CZ-NH1	9.61	125.11	120.30
5	F	837	TYR	CB-CA-C	9.41	129.22	110.40
5	F	1235	ASN	CA-C-N	9.20	137.45	117.20
5	F	823	PRO	N-CA-C	9.07	135.68	112.10
5	F	1089	ASN	CB-CA-C	8.77	127.94	110.40
5	F	711	GLN	CB-CA-C	8.75	127.89	110.40
1	Z	91	GLN	CB-CA-C	-8.72	92.97	110.40
5	F	1235	ASN	CA-C-O	-8.67	101.90	120.10
4	E	51	LEU	CA-CB-CG	8.39	134.60	115.30
7	K	450	PRO	N-CA-C	8.24	133.53	112.10
7	H	476	GLN	CB-CA-C	8.24	126.88	110.40
2	C	268	ARG	NE-CZ-NH1	8.22	124.41	120.30
5	F	1068	ILE	N-CA-C	-8.16	88.97	111.00
5	F	921	PRO	CA-N-CD	-8.12	100.14	111.50
5	F	1056	LEU	CA-CB-CG	8.11	133.94	115.30
5	F	1506	ILE	CG1-CB-CG2	-7.94	93.92	111.40
6	J	335	SER	O-C-N	7.83	135.23	122.70
2	C	512	ARG	NE-CZ-NH1	7.72	124.16	120.30
5	F	1090	PRO	N-CA-CB	7.70	112.54	103.30
5	F	750	TRP	CA-C-N	7.55	138.25	117.10
2	C	1221	ARG	NE-CZ-NH2	7.52	124.06	120.30
2	C	1130	ARG	NE-CZ-NH1	7.44	124.02	120.30
5	F	644	LYS	C-N-CA	7.36	140.09	121.70
5	F	668	ARG	NE-CZ-NH1	7.34	123.97	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	759	ASN	CB-CA-C	7.33	125.06	110.40
8	I	736	ASN	CB-CA-C	7.31	125.02	110.40
5	F	935	GLN	N-CA-CB	7.30	123.75	110.60
2	C	1277	ARG	NE-CZ-NH1	7.24	123.92	120.30
5	F	966	LEU	CA-CB-CG	7.18	131.82	115.30
5	F	1391	GLY	C-N-CA	7.17	139.62	121.70
5	F	1286	PHE	CB-CA-C	7.16	124.72	110.40
2	C	770	ARG	NE-CZ-NH1	7.15	123.88	120.30
5	F	1090	PRO	C-N-CA	-7.15	103.83	121.70
5	F	921	PRO	N-CA-CB	-7.09	94.79	103.30
5	F	1090	PRO	CA-CB-CG	-7.08	90.54	104.00
5	F	1164	PHE	CB-CA-C	-7.05	96.31	110.40
5	F	668	ARG	NE-CZ-NH2	-7.04	116.78	120.30
3	D	1232	ARG	NE-CZ-NH1	6.99	123.80	120.30
5	F	888	PRO	N-CA-C	6.87	129.96	112.10
5	F	797	LEU	CA-CB-CG	6.86	131.08	115.30
5	F	1234	GLY	O-C-N	6.83	133.63	122.70
1	Z	750	GLU	C-N-CA	6.77	138.62	121.70
5	F	716	LEU	CA-CB-CG	6.67	130.63	115.30
4	E	858	LEU	CA-CB-CG	-6.54	100.26	115.30
5	F	1378	ASP	CB-CA-C	6.53	123.46	110.40
2	C	364	ARG	NE-CZ-NH1	6.49	123.54	120.30
7	H	476	GLN	N-CA-CB	-6.48	98.94	110.60
2	C	693	LEU	C-N-CA	6.42	137.75	121.70
5	F	1049	LEU	CA-CB-CG	6.42	130.06	115.30
4	E	213	PHE	CB-CA-C	6.39	123.19	110.40
7	K	341	LYS	N-CA-C	-6.39	93.74	111.00
5	F	1182	ASN	CB-CA-C	-6.35	97.69	110.40
1	Z	506	LEU	CA-CB-CG	6.33	129.86	115.30
3	D	1012	ARG	NE-CZ-NH1	6.31	123.45	120.30
5	F	968	ILE	CG1-CB-CG2	-6.27	97.61	111.40
6	J	335	SER	CA-C-N	-6.27	103.41	117.20
5	F	1378	ASP	C-N-CA	6.26	135.45	122.30
5	F	1408	LEU	CB-CG-CD2	6.24	121.60	111.00
5	F	1061	ASN	CB-CA-C	6.21	122.82	110.40
7	K	423	LYS	C-N-CA	6.20	137.20	121.70
5	F	1222	ASN	C-N-CA	6.18	137.16	121.70
6	J	402	ASP	CB-CA-C	-6.18	98.04	110.40
5	F	1406	TYR	CA-CB-CG	6.17	125.13	113.40
2	C	1182	ARG	NE-CZ-NH1	6.15	123.38	120.30
5	F	1080	LEU	CA-CB-CG	6.15	129.45	115.30
6	J	335	SER	C-N-CA	6.15	137.07	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	F	935	GLN	CA-C-O	-6.14	107.20	120.10
4	E	435	LEU	CA-CB-CG	6.10	129.32	115.30
5	F	833	THR	CA-C-N	-6.09	103.79	117.20
8	I	731	GLY	C-N-CA	6.09	136.92	121.70
2	C	727	ARG	NE-CZ-NH2	-6.06	117.27	120.30
7	H	459	LEU	CA-CB-CG	6.05	129.21	115.30
5	F	344	ILE	C-N-CA	6.04	136.79	121.70
5	F	639	LEU	CB-CA-C	6.04	121.67	110.20
5	F	793	TYR	CA-CB-CG	6.01	124.83	113.40
5	F	925	HIS	C-N-CA	6.01	136.72	121.70
1	A	55	GLN	CB-CA-C	6.01	122.41	110.40
8	L	779	THR	C-N-CA	5.99	136.68	121.70
2	C	718	ARG	NE-CZ-NH1	5.99	123.29	120.30
5	F	1134	LYS	N-CA-CB	5.98	121.36	110.60
7	H	475	SER	O-C-N	5.96	132.24	122.70
7	K	424	ASN	CB-CA-C	5.96	122.31	110.40
5	F	1010	LEU	CB-CG-CD2	-5.93	100.92	111.00
2	C	431	ARG	NE-CZ-NH1	5.92	123.26	120.30
3	D	1128	GLN	N-CA-CB	5.91	121.23	110.60
7	K	446	ARG	CG-CD-NE	-5.90	99.40	111.80
7	K	450	PRO	CB-CA-C	-5.89	97.28	112.00
5	F	1234	GLY	CA-C-N	-5.88	104.27	117.20
5	F	644	LYS	O-C-N	5.87	132.09	122.70
5	F	750	TRP	O-C-N	-5.85	109.98	121.10
5	F	833	THR	O-C-N	5.84	132.05	122.70
2	C	385	ARG	NE-CZ-NH1	5.84	123.22	120.30
5	F	865	LEU	CB-CG-CD1	-5.83	101.09	111.00
7	H	426	GLY	O-C-N	5.82	132.02	122.70
5	F	1090	PRO	N-CD-CG	5.82	111.93	103.20
7	H	425	ARG	CA-C-O	-5.80	107.93	120.10
5	F	750	TRP	CA-CB-CG	5.76	124.65	113.70
5	F	186	LEU	CA-CB-CG	5.76	128.55	115.30
1	A	114	ARG	N-CA-CB	5.76	120.96	110.60
2	C	718	ARG	NE-CZ-NH2	-5.75	117.42	120.30
5	F	443	ILE	CG1-CB-CG2	-5.75	98.75	111.40
1	Z	54	PHE	CB-CA-C	-5.72	98.96	110.40
5	F	1158	THR	CB-CA-C	5.71	127.03	111.60
5	F	1088	ARG	O-C-N	5.71	131.83	122.70
1	Z	294	MET	CA-CB-CG	5.68	122.95	113.30
5	F	1075	LEU	CB-CG-CD1	-5.65	101.39	111.00
1	Z	283	LEU	CA-CB-CG	5.64	128.28	115.30
5	F	833	THR	C-N-CA	5.63	135.79	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	H	427	LEU	CA-C-N	5.63	132.87	117.10
5	F	366	ILE	C-N-CA	5.58	135.65	121.70
1	A	54	PHE	CB-CA-C	-5.58	99.25	110.40
5	F	77	LEU	CA-CB-CG	5.57	128.12	115.30
5	F	1401	LEU	CB-CG-CD2	5.56	120.45	111.00
7	K	320	GLU	C-N-CA	5.55	135.56	121.70
4	E	1384	ASP	CB-CA-C	5.53	121.45	110.40
5	F	1116	VAL	CG1-CB-CG2	-5.53	102.06	110.90
5	F	1188	THR	C-N-CA	5.51	135.49	121.70
5	F	889	ILE	CA-C-N	5.50	129.31	117.20
5	F	803	ALA	N-CA-CB	5.49	117.79	110.10
5	F	1314	VAL	N-CA-C	5.49	125.83	111.00
1	A	43	GLN	O-C-N	-5.48	113.93	122.70
5	F	193	LEU	CA-CB-CG	5.47	127.87	115.30
7	K	413	LEU	CA-CB-CG	5.45	127.83	115.30
5	F	803	ALA	C-N-CA	-5.45	108.08	121.70
5	F	356	ILE	C-N-CA	5.43	144.83	122.00
5	F	903	ASN	C-N-CA	5.41	135.22	121.70
6	J	380	TYR	CB-CA-C	5.39	121.19	110.40
2	C	1198	ARG	NE-CZ-NH1	5.38	122.99	120.30
7	K	452	GLY	C-N-CA	5.37	135.13	121.70
1	A	43	GLN	C-N-CA	-5.36	108.29	121.70
5	F	1075	LEU	CA-CB-CG	5.36	127.63	115.30
5	F	781	LEU	CA-CB-CG	5.34	127.59	115.30
6	J	406	PHE	C-N-CA	-5.34	111.09	122.30
5	F	1160	TYR	CB-CG-CD2	5.33	124.20	121.00
7	H	444	LEU	CA-CB-CG	5.33	127.55	115.30
5	F	827	ILE	C-N-CA	5.33	135.01	121.70
6	J	370	ASP	CA-CB-CG	5.31	125.08	113.40
5	F	1010	LEU	CA-CB-CG	5.30	127.50	115.30
7	K	451	ALA	N-CA-C	5.30	125.30	111.00
7	K	431	ILE	C-N-CA	-5.29	108.48	121.70
1	Z	642	LEU	CA-CB-CG	5.27	127.43	115.30
5	F	345	ARG	N-CA-CB	5.26	120.06	110.60
5	F	1382	TYR	CB-CG-CD1	5.25	124.15	121.00
8	I	753	GLU	CB-CA-C	-5.25	99.91	110.40
4	E	212	TRP	O-C-N	5.24	131.08	122.70
4	E	585	ASP	CB-CG-OD2	5.23	123.01	118.30
5	F	812	CYS	C-N-CA	5.23	134.77	121.70
2	C	1386	ARG	NE-CZ-NH1	5.21	122.91	120.30
3	D	1284	ARG	NE-CZ-NH1	5.21	122.91	120.30
5	F	1208	GLU	N-CA-C	-5.21	96.93	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	749	ARG	NE-CZ-NH1	5.18	122.89	120.30
2	C	1240	ARG	NE-CZ-NH1	5.18	122.89	120.30
2	C	104	ARG	NE-CZ-NH2	-5.17	117.71	120.30
7	K	321	ALA	N-CA-CB	5.17	117.34	110.10
5	F	597	LEU	CA-CB-CG	5.17	127.19	115.30
6	J	380	TYR	CB-CG-CD1	-5.16	117.90	121.00
5	F	108	LEU	CA-CB-CG	5.16	127.16	115.30
7	H	506	ILE	C-N-CA	5.16	134.60	121.70
5	F	1088	ARG	NE-CZ-NH1	-5.16	117.72	120.30
2	C	386	ARG	NE-CZ-NH1	5.14	122.87	120.30
5	F	675	LEU	CA-CB-CG	5.14	127.13	115.30
5	F	562	LEU	CA-CB-CG	5.09	127.01	115.30
1	Z	751	LEU	N-CA-CB	-5.08	100.24	110.40
5	F	1087	CYS	CA-CB-SG	5.07	123.13	114.00
3	D	528	PRO	CA-N-CD	-5.06	104.41	111.50
5	F	880	GLU	CB-CA-C	-5.06	100.28	110.40
6	J	373	PHE	N-CA-CB	5.06	119.70	110.60
6	J	370	ASP	CB-CA-C	5.05	120.50	110.40
2	C	1057	TYR	CB-CG-CD2	-5.05	117.97	121.00
2	C	116	TYR	CB-CG-CD2	-5.03	117.98	121.00
5	F	436	ASP	CB-CG-OD1	5.03	122.83	118.30
2	C	708	ARG	NE-CZ-NH1	5.03	122.81	120.30
5	F	240	LEU	CA-CB-CG	5.02	126.84	115.30
6	G	402	ASP	CB-CG-OD1	5.01	122.81	118.30
5	F	1405	PHE	C-N-CA	-5.01	109.18	121.70

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	F	1188	THR	Mainchain
5	F	360	LEU	Mainchain
5	F	813	GLU	Mainchain
6	G	422	GLY	Mainchain
7	H	509	ILE	Mainchain
7	K	380	LEU	Mainchain
7	K	488	THR	Mainchain
1	Z	748	SER	Mainchain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5723	0	5587	285	0
1	Z	5776	0	5607	420	0
2	C	10452	0	10392	49	0
3	D	10976	0	10827	406	0
4	E	12362	0	12566	349	0
5	F	12232	0	11559	829	0
6	G	1533	0	1515	118	0
6	J	1492	0	1465	274	0
7	H	1811	0	1697	146	0
7	K	1808	0	1614	305	0
8	I	1418	0	1293	170	0
8	L	1366	0	1211	166	0
All	All	66949	0	65333	3007	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 23.

All (3007) 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:Z:810:ALA:CB	1:Z:836:ASP:HA	1.26	1.59
3:D:955:PRO:CB	3:D:994:SER:CB	1.78	1.59
7:H:522:TYR:CB	1:Z:54:PHE:CB	1.82	1.56
5:F:841:PHE:CD2	5:F:918:PHE:HE1	1.21	1.55
5:F:1357:ALA:HB2	5:F:1381:LEU:CB	1.19	1.53
7:K:538:LYS:HA	8:L:822:LYS:CB	1.10	1.53
6:J:325:TYR:CE2	7:K:390:HIS:HA	1.44	1.52
5:F:376:ASN:CB	5:F:381:THR:CA	1.83	1.51
6:J:383:LYS:NZ	8:L:756:ASN:CA	1.73	1.50
7:H:420:ALA:HB1	8:I:745:TYR:CE1	1.49	1.46
1:A:772:PRO:CB	1:A:828:THR:HG21	1.47	1.44
7:H:418:GLN:NE2	8:I:718:THR:CG2	1.81	1.43
6:J:357:LEU:HB3	7:K:423:LYS:CE	1.46	1.43
7:K:483:VAL:O	7:K:492:ASP:CB	1.66	1.43
7:K:321:ALA:CA	7:K:348:ILE:HD11	1.50	1.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:753:ALA:HB1	1:Z:815:ILE:C	1.35	1.42
1:Z:757:ALA:CB	1:Z:819:MET:O	1.68	1.41
6:G:404:ASP:CB	6:G:425:GLU:CB	1.97	1.40
8:I:818:ILE:O	8:I:821:ILE:CG2	1.68	1.40
5:F:1353:LEU:CB	5:F:1384:LEU:CB	2.01	1.39
7:K:389:LYS:HA	7:K:393:ASP:CB	1.49	1.39
1:Z:746:PRO:CB	1:Z:753:ALA:HA	1.52	1.39
5:F:1116:VAL:HG11	5:F:1150:PHE:CE2	1.58	1.38
7:K:389:LYS:CA	7:K:393:ASP:HB3	1.49	1.38
5:F:841:PHE:CD2	5:F:918:PHE:CE1	2.11	1.38
7:K:483:VAL:CB	7:K:493:SER:O	1.72	1.37
5:F:334:GLN:NE2	5:F:859:LYS:NZ	1.73	1.36
7:K:538:LYS:CA	8:L:822:LYS:CB	2.01	1.36
4:E:1022:TYR:CE2	4:E:1026:THR:HG21	1.60	1.36
5:F:228:PHE:H	5:F:361:LEU:CB	1.37	1.36
5:F:334:GLN:HE21	5:F:859:LYS:NZ	1.24	1.35
5:F:1227:THR:CB	7:H:475:SER:OG	1.74	1.35
1:Z:810:ALA:CB	1:Z:836:ASP:CA	2.02	1.35
1:A:128:LEU:HD22	4:E:1260:TYR:CE2	1.61	1.35
6:J:383:LYS:NZ	8:L:756:ASN:HA	1.03	1.34
5:F:376:ASN:CB	5:F:381:THR:HA	0.88	1.34
5:F:1357:ALA:CB	5:F:1381:LEU:CB	2.05	1.34
5:F:902:LYS:HE2	7:H:414:LYS:CD	1.58	1.33
6:G:331:LYS:HE2	1:Z:49:LEU:CD1	1.56	1.33
5:F:1633:TYR:CE2	5:F:1635:ARG:HB2	1.63	1.33
1:Z:810:ALA:HB1	1:Z:836:ASP:CA	1.57	1.31
7:H:418:GLN:HE21	8:I:718:THR:CG2	1.38	1.30
8:L:775:THR:O	8:L:779:THR:CB	1.78	1.29
5:F:902:LYS:CE	7:H:414:LYS:HD2	1.62	1.29
5:F:1116:VAL:HG11	5:F:1150:PHE:CZ	1.68	1.29
5:F:1084:LEU:HA	5:F:1156:TYR:OH	1.29	1.28
1:A:140:ILE:CG2	4:E:1393:LYS:HD3	1.62	1.28
5:F:334:GLN:HG3	5:F:854:GLU:OE2	1.24	1.28
6:J:357:LEU:CB	7:K:423:LYS:HE3	1.60	1.28
1:A:128:LEU:HD13	4:E:1260:TYR:CZ	1.67	1.28
6:J:333:ILE:O	6:J:336:PHE:CB	1.82	1.27
1:A:43:GLN:O	1:A:44:VAL:CB	1.68	1.27
5:F:675:LEU:O	5:F:679:ILE:HG12	1.13	1.27
1:Z:753:ALA:CB	1:Z:815:ILE:C	2.02	1.27
7:K:321:ALA:N	7:K:348:ILE:HD11	1.47	1.27
3:D:242:MET:SD	3:D:298:TYR:CE2	2.28	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:LEU:HD22	4:E:1260:TYR:CD2	1.67	1.26
1:A:59:LYS:C	8:L:807:LEU:CB	2.03	1.26
7:K:321:ALA:HA	7:K:348:ILE:CG1	1.65	1.25
6:J:383:LYS:NZ	8:L:756:ASN:CG	1.89	1.25
6:J:405:LEU:O	6:J:409:PRO:CD	1.84	1.25
1:Z:810:ALA:HB3	1:Z:836:ASP:O	1.30	1.24
1:Z:251:ALA:O	1:Z:253:LEU:N	1.70	1.24
5:F:800:ILE:HG12	5:F:885:GLU:OE1	1.37	1.23
1:Z:746:PRO:CB	1:Z:816:TYR:CB	2.16	1.23
1:A:772:PRO:HB3	1:A:828:THR:CG2	1.68	1.22
6:G:431:GLN:HA	7:H:503:ASN:CB	1.67	1.22
1:Z:753:ALA:HB1	1:Z:816:TYR:N	1.54	1.22
6:G:327:LYS:NZ	1:Z:46:ILE:HB	1.54	1.21
7:H:418:GLN:NE2	8:I:718:THR:HG21	1.55	1.21
5:F:1129:ASN:ND2	5:F:1132:GLU:HB3	1.56	1.21
1:A:814:MET:HG3	1:A:833:ILE:CD1	1.71	1.19
5:F:800:ILE:CG1	5:F:885:GLU:OE1	1.90	1.19
6:J:383:LYS:HZ1	8:L:756:ASN:CA	1.39	1.19
1:Z:824:MET:HG2	1:Z:825:PRO:CD	1.70	1.19
3:D:1244:ASN:CB	1:Z:826:ARG:CB	2.21	1.19
6:J:364:ILE:HA	7:K:424:ASN:ND2	1.55	1.19
1:Z:241:ILE:HG22	1:Z:245:ALA:CB	1.72	1.19
1:Z:807:LYS:HA	1:Z:836:ASP:O	1.41	1.19
4:E:1022:TYR:CD2	4:E:1026:THR:HG21	1.76	1.19
4:E:1022:TYR:CE2	4:E:1026:THR:CG2	2.25	1.19
6:G:430:LEU:CB	8:I:780:THR:HA	1.74	1.17
8:I:773:SER:O	8:I:777:ASN:CB	1.90	1.17
1:Z:757:ALA:HB2	1:Z:819:MET:C	1.64	1.17
7:H:418:GLN:NE2	8:I:718:THR:HG23	1.42	1.16
6:J:383:LYS:NZ	8:L:756:ASN:CB	2.07	1.16
4:E:1309:ARG:O	4:E:1313:ARG:HG3	1.45	1.16
8:I:810:ASN:OD1	1:Z:59:LYS:CB	1.94	1.16
5:F:354:ARG:HB2	5:F:356:ILE:HG22	1.29	1.15
5:F:1529:ALA:HB2	5:F:1611:VAL:HG13	1.22	1.15
1:Z:814:MET:CB	1:Z:833:ILE:HD13	1.76	1.15
3:D:1238:ARG:HA	1:Z:830:SER:HB3	1.28	1.14
7:H:425:ARG:C	7:H:427:LEU:H	1.48	1.14
7:K:444:LEU:O	7:K:447:SER:CB	1.95	1.14
7:K:446:ARG:HH22	7:K:455:LYS:NZ	1.44	1.14
6:J:398:VAL:HG21	7:K:462:ARG:CA	1.78	1.14
1:A:775:LEU:HB3	1:A:832:LEU:CD1	1.79	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:753:ALA:CB	1:Z:816:TYR:N	2.11	1.12
7:K:321:ALA:CA	7:K:348:ILE:CD1	2.27	1.12
5:F:675:LEU:O	5:F:679:ILE:CG1	1.96	1.12
7:K:336:ASP:O	7:K:340:GLU:HB2	1.48	1.11
1:Z:810:ALA:CA	1:Z:836:ASP:HA	1.80	1.11
5:F:734:LEU:CD2	5:F:817:ASN:OD1	1.98	1.11
5:F:1203:TYR:CB	5:F:1299:ASN:HD21	1.63	1.11
1:Z:824:MET:CG	1:Z:825:PRO:HD3	1.80	1.11
5:F:922:LEU:HD23	7:H:400:LYS:CE	1.81	1.11
1:Z:810:ALA:HB3	1:Z:836:ASP:C	1.69	1.11
5:F:334:GLN:NE2	5:F:859:LYS:HZ2	1.30	1.11
1:Z:746:PRO:CB	1:Z:753:ALA:CA	2.29	1.11
5:F:841:PHE:HD2	5:F:918:PHE:CE1	1.55	1.10
3:D:1493:ASN:HA	5:F:1471:LYS:HD2	1.32	1.10
6:G:289:GLN:HE22	6:J:352:VAL:HG22	0.95	1.10
7:K:321:ALA:HA	7:K:348:ILE:CD1	1.80	1.10
5:F:800:ILE:CD1	5:F:885:GLU:OE1	1.98	1.10
5:F:1550:LEU:CD2	5:F:1552:PHE:CZ	2.34	1.10
6:G:289:GLN:NE2	6:J:352:VAL:HG22	1.67	1.10
6:J:380:TYR:HE2	8:L:751:LEU:HD21	1.09	1.10
5:F:334:GLN:CG	5:F:854:GLU:OE2	1.99	1.10
5:F:690:GLU:CD	8:I:722:LEU:HD21	1.69	1.10
1:Z:753:ALA:HB1	1:Z:815:ILE:O	1.52	1.10
1:A:783:SER:HA	1:A:839:LEU:HA	1.26	1.09
6:J:432:LEU:CB	8:L:782:ILE:O	2.00	1.09
6:J:431:GLN:HA	7:K:500:GLU:H	1.10	1.09
6:G:327:LYS:HZ3	1:Z:46:ILE:HB	0.96	1.09
6:J:432:LEU:CB	8:L:782:ILE:C	2.20	1.09
1:Z:757:ALA:HB1	1:Z:819:MET:O	1.40	1.08
6:J:405:LEU:O	6:J:409:PRO:HD3	0.93	1.08
1:Z:814:MET:CB	1:Z:833:ILE:CD1	2.32	1.08
5:F:922:LEU:HD23	7:H:400:LYS:NZ	1.68	1.08
5:F:1529:ALA:CB	5:F:1611:VAL:HG13	1.84	1.08
5:F:1550:LEU:CD1	5:F:1604:ILE:HD13	1.84	1.07
1:Z:824:MET:CB	1:Z:825:PRO:HD3	1.85	1.07
1:A:55:GLN:CB	7:K:521:THR:CB	2.32	1.07
6:G:331:LYS:HE2	1:Z:49:LEU:HD11	1.29	1.07
7:H:426:GLY:HA2	8:I:736:ASN:N	1.69	1.07
6:J:383:LYS:HZ2	8:L:756:ASN:CB	1.66	1.07
7:K:482:MET:CB	8:L:784:ILE:HA	1.83	1.07
7:K:317:ASN:CB	7:K:346:GLN:HB3	1.83	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:837:TYR:HB2	5:F:918:PHE:CE2	1.90	1.07
1:A:814:MET:HG3	1:A:833:ILE:HD11	1.07	1.06
3:D:242:MET:SD	3:D:298:TYR:CD2	2.48	1.06
5:F:228:PHE:N	5:F:361:LEU:CB	2.18	1.06
7:H:420:ALA:CB	8:I:745:TYR:CE1	2.36	1.06
6:G:430:LEU:CB	8:I:780:THR:HG22	1.83	1.06
7:H:412:ILE:HG23	7:H:415:LEU:HD22	1.38	1.06
7:H:532:ALA:HB2	8:I:818:ILE:HD12	1.34	1.06
4:E:227:ILE:HD11	4:E:258:ILE:HD13	1.37	1.06
7:K:513:LEU:HD21	8:L:800:HIS:CE1	1.90	1.06
5:F:1034:LEU:HD22	5:F:1092:THR:HB	1.37	1.06
7:K:535:LYS:HA	8:L:818:ILE:CB	1.86	1.06
7:H:535:LYS:CB	8:I:821:ILE:HD11	1.86	1.06
7:H:412:ILE:HG23	7:H:415:LEU:CD2	1.86	1.05
1:A:772:PRO:CA	1:A:828:THR:HG21	1.86	1.05
6:J:383:LYS:NZ	8:L:756:ASN:OD1	1.87	1.05
1:A:128:LEU:HD13	4:E:1260:TYR:OH	1.53	1.05
6:J:398:VAL:HG21	7:K:462:ARG:CB	1.86	1.05
1:A:814:MET:CG	1:A:833:ILE:HD11	1.86	1.05
5:F:928:LEU:H	5:F:928:LEU:HD12	1.15	1.05
5:F:841:PHE:CE2	5:F:918:PHE:CE1	2.44	1.05
1:Z:241:ILE:HG22	1:Z:245:ALA:HB1	1.33	1.05
4:E:977:ALA:O	7:K:460:TRP:CB	2.04	1.04
6:J:383:LYS:HZ2	8:L:756:ASN:CG	1.49	1.04
5:F:1203:TYR:CB	5:F:1299:ASN:ND2	2.20	1.04
2:C:1258:GLN:HG2	2:C:1299:LYS:CE	1.86	1.04
1:Z:751:LEU:O	1:Z:753:ALA:N	1.89	1.03
1:A:53:VAL:HG21	8:L:799:SER:OG	1.57	1.03
4:E:1022:TYR:CD2	4:E:1026:THR:CG2	2.40	1.03
6:J:325:TYR:CE2	7:K:390:HIS:CA	2.41	1.03
1:A:140:ILE:HG22	4:E:1393:LYS:NZ	1.73	1.03
2:C:318:ILE:H	2:C:318:ILE:HD12	1.17	1.03
5:F:350:ARG:O	5:F:393:SER:CB	2.06	1.03
4:E:1319:LEU:HD21	4:E:1398:VAL:CG2	1.88	1.02
5:F:159:LYS:HE3	5:F:363:ASP:HA	1.39	1.02
5:F:690:GLU:CD	8:I:722:LEU:CD2	2.28	1.02
4:E:1394:LYS:O	4:E:1398:VAL:HG23	1.58	1.02
1:Z:753:ALA:HB1	1:Z:816:TYR:CA	1.90	1.02
1:Z:810:ALA:HB3	1:Z:836:ASP:CA	1.86	1.02
5:F:1116:VAL:CG1	5:F:1150:PHE:CE2	2.42	1.02
8:I:739:GLN:O	8:I:741:ARG:N	1.91	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:GLU:OE2	1:A:30:ASP:HB3	1.58	1.02
1:Z:817:ALA:O	1:Z:821:GLN:N	1.91	1.02
1:A:59:LYS:CB	8:L:807:LEU:CB	2.38	1.01
1:A:814:MET:CG	1:A:833:ILE:CD1	2.37	1.01
5:F:920:ILE:HG21	5:F:924:ALA:O	1.59	1.01
6:G:331:LYS:CE	1:Z:49:LEU:HD11	1.91	1.01
1:Z:27:GLU:OE2	1:Z:30:ASP:HB3	1.58	1.01
1:Z:811:ARG:N	1:Z:836:ASP:CB	2.24	1.01
1:A:140:ILE:HG21	4:E:1393:LYS:HD3	1.05	1.01
7:K:482:MET:CB	8:L:784:ILE:CA	2.38	1.01
3:D:242:MET:SD	3:D:298:TYR:HE2	1.78	1.01
3:D:401:ILE:HG21	3:D:462:LEU:HB3	1.43	1.01
8:I:798:ASN:O	8:I:801:PHE:N	1.92	1.01
5:F:1129:ASN:HD21	5:F:1132:GLU:CB	1.73	1.00
5:F:1550:LEU:CD2	5:F:1552:PHE:CE2	2.44	1.00
4:E:210:ASN:HA	4:E:213:PHE:CB	1.90	1.00
5:F:228:PHE:CD1	5:F:360:LEU:O	2.15	1.00
5:F:909:LEU:CB	7:H:404:ARG:HA	1.91	1.00
7:K:321:ALA:HA	7:K:348:ILE:HG12	1.43	1.00
1:Z:824:MET:HG2	1:Z:825:PRO:HD2	1.36	1.00
4:E:1022:TYR:O	4:E:1026:THR:HG23	1.59	1.00
6:G:431:GLN:CA	7:H:503:ASN:CB	2.39	1.00
3:D:938:LEU:HB2	3:D:940:VAL:HG22	1.41	1.00
5:F:887:PHE:N	5:F:888:PRO:HD2	1.77	1.00
5:F:1167:LYS:HA	5:F:1167:LYS:HE3	1.44	0.99
1:A:140:ILE:HG21	4:E:1393:LYS:CD	1.91	0.99
1:Z:810:ALA:HB1	1:Z:836:ASP:HA	1.01	0.99
5:F:228:PHE:CE1	5:F:360:LEU:O	2.15	0.99
5:F:1529:ALA:HB2	5:F:1611:VAL:CG1	1.92	0.99
5:F:1550:LEU:HD22	5:F:1552:PHE:CE2	1.97	0.99
6:G:289:GLN:HE22	6:J:352:VAL:CG2	1.76	0.99
7:H:420:ALA:HB1	8:I:745:TYR:CZ	1.98	0.99
6:J:380:TYR:CE2	8:L:751:LEU:HD21	1.98	0.99
1:Z:757:ALA:HB2	1:Z:819:MET:O	1.46	0.99
6:G:331:LYS:CE	1:Z:49:LEU:CD1	2.41	0.98
5:F:1084:LEU:HA	5:F:1156:TYR:HH	1.16	0.98
6:J:365:SER:H	7:K:424:ASN:ND2	1.60	0.98
7:H:418:GLN:HE21	8:I:718:THR:HG23	0.86	0.98
1:Z:753:ALA:CA	1:Z:816:TYR:HA	1.92	0.98
5:F:1550:LEU:HD21	5:F:1552:PHE:CZ	1.98	0.98
7:K:446:ARG:HH22	7:K:455:LYS:CE	1.76	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:538:LYS:CB	8:L:818:ILE:O	2.13	0.97
3:D:1238:ARG:HA	1:Z:830:SER:CB	1.94	0.97
1:A:128:LEU:CD2	4:E:1260:TYR:CE2	2.47	0.97
1:Z:807:LYS:CA	1:Z:836:ASP:O	2.12	0.97
6:J:281:ASP:HA	6:J:284:ILE:HD12	1.46	0.97
1:Z:249:ARG:O	1:Z:251:ALA:N	1.98	0.97
1:Z:817:ALA:O	1:Z:821:GLN:CB	2.13	0.97
1:Z:824:MET:HG2	1:Z:825:PRO:HD3	1.43	0.97
1:A:775:LEU:HB3	1:A:832:LEU:HD11	1.44	0.97
5:F:951:ARG:HH21	5:F:953:ASN:H	1.08	0.97
6:G:331:LYS:HE2	1:Z:49:LEU:HD12	1.47	0.97
5:F:968:ILE:HG13	7:H:392:LEU:HD13	1.46	0.97
7:H:493:SER:O	8:I:784:ILE:O	1.83	0.97
5:F:1085:LYS:O	5:F:1089:ASN:CB	2.12	0.96
5:F:1550:LEU:HD22	5:F:1552:PHE:CZ	1.97	0.96
1:Z:133:THR:HG22	1:Z:134:LYS:N	1.77	0.96
7:H:426:GLY:CA	8:I:736:ASN:N	2.27	0.96
5:F:334:GLN:NE2	5:F:859:LYS:HZ3	1.56	0.96
5:F:1216:PHE:HE2	5:F:1282:ALA:CB	1.77	0.96
5:F:1034:LEU:CD2	5:F:1092:THR:HB	1.95	0.96
7:K:298:SER:HA	7:K:306:THR:HA	1.47	0.96
7:K:526:VAL:O	7:K:530:ASP:HB2	1.66	0.96
6:G:430:LEU:O	7:H:503:ASN:CB	2.13	0.95
6:J:380:TYR:HE2	8:L:751:LEU:CD2	1.79	0.95
6:J:325:TYR:HE2	7:K:390:HIS:HA	1.17	0.95
6:J:383:LYS:HZ2	8:L:756:ASN:CA	1.54	0.95
5:F:1129:ASN:HD21	5:F:1132:GLU:HB3	0.83	0.95
6:J:431:GLN:HA	7:K:500:GLU:N	1.81	0.95
1:Z:810:ALA:C	1:Z:836:ASP:CB	2.35	0.95
4:E:227:ILE:HD11	4:E:258:ILE:CD1	1.96	0.95
1:A:751:LEU:HD22	2:C:1313:LEU:HA	1.49	0.95
3:D:528:PRO:HG3	3:D:624:PHE:CE2	2.02	0.95
6:J:383:LYS:CD	8:L:756:ASN:OD1	2.13	0.95
1:Z:824:MET:CG	1:Z:825:PRO:CD	2.43	0.94
7:K:321:ALA:H	7:K:348:ILE:HD11	1.09	0.94
1:Z:824:MET:HB2	1:Z:825:PRO:HD3	1.47	0.94
5:F:920:ILE:CG2	5:F:924:ALA:O	2.15	0.94
6:J:398:VAL:HG21	7:K:462:ARG:HA	1.50	0.94
5:F:1550:LEU:HD11	5:F:1604:ILE:HD13	1.48	0.94
8:I:814:LEU:HD21	1:Z:59:LYS:CB	1.97	0.94
5:F:968:ILE:CG1	7:H:392:LEU:HD13	1.97	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:383:LYS:HD2	8:L:756:ASN:OD1	1.68	0.94
5:F:350:ARG:O	5:F:393:SER:HB3	1.68	0.94
6:J:383:LYS:CE	8:L:756:ASN:OD1	2.16	0.94
1:A:772:PRO:HB3	1:A:828:THR:HG21	0.95	0.93
8:I:818:ILE:O	8:I:821:ILE:HG22	0.76	0.93
5:F:1068:ILE:HD12	5:F:1150:PHE:CD2	2.04	0.93
6:J:383:LYS:HZ3	8:L:756:ASN:CG	1.65	0.93
1:Z:753:ALA:HA	1:Z:816:TYR:CB	1.98	0.93
6:G:465:LYS:HB2	1:Z:20:LYS:NZ	1.81	0.93
5:F:354:ARG:CB	5:F:356:ILE:HG22	1.98	0.93
6:J:433:LYS:N	7:K:499:GLY:HA3	1.84	0.93
5:F:1012:ASN:O	8:I:787:GLU:HG2	1.68	0.92
8:I:818:ILE:C	8:I:821:ILE:HG22	1.87	0.92
1:Z:241:ILE:CG2	1:Z:245:ALA:HB2	1.99	0.92
3:D:1467:SER:HB2	1:Z:621:HIS:NE2	1.84	0.92
6:G:327:LYS:NZ	1:Z:46:ILE:CB	2.31	0.92
3:D:515:VAL:HG12	3:D:644:SER:HB3	1.52	0.92
6:J:388:CYS:HB2	7:K:455:LYS:HD2	1.51	0.92
1:A:140:ILE:CG2	4:E:1393:LYS:CD	2.47	0.92
5:F:800:ILE:HD11	5:F:885:GLU:OE1	1.69	0.92
7:K:456:THR:O	7:K:458:GLU:N	2.03	0.92
3:D:483:HIS:HB2	3:D:486:GLN:HG2	1.52	0.91
4:E:1398:VAL:O	4:E:1398:VAL:HG12	1.69	0.91
4:E:687:LYS:CB	5:F:1391:GLY:HA3	2.00	0.91
1:Z:116:LYS:HB3	1:Z:116:LYS:HZ3	1.33	0.91
6:J:388:CYS:O	6:J:388:CYS:SG	2.28	0.91
4:E:989:ASP:O	4:E:991:LYS:N	2.03	0.91
7:K:525:GLU:O	7:K:529:LYS:HB3	1.70	0.91
5:F:334:GLN:HG2	5:F:860:ASN:ND2	1.85	0.91
5:F:837:TYR:HB2	5:F:918:PHE:HE2	1.30	0.91
7:H:425:ARG:C	7:H:427:LEU:N	2.21	0.91
7:K:321:ALA:H	7:K:348:ILE:CD1	1.83	0.91
3:D:118:THR:HB	3:D:623:GLY:HA2	1.50	0.91
3:D:971:ILE:HD11	3:D:984:THR:HB	1.52	0.91
5:F:711:GLN:OE1	5:F:779:PRO:HA	1.69	0.91
7:K:379:ILE:O	7:K:382:LYS:CB	2.19	0.91
1:Z:362:LYS:O	1:Z:365:GLN:HB2	1.71	0.91
1:A:59:LYS:CA	8:L:807:LEU:CB	2.48	0.90
4:E:1029:ASN:ND2	7:K:475:SER:CB	2.35	0.90
3:D:716:VAL:HG11	3:D:889:GLU:HB2	1.53	0.90
6:G:295:LYS:HG2	6:J:363:LYS:NZ	1.86	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:810:ALA:C	1:Z:836:ASP:HA	1.91	0.90
6:J:342:GLU:OE1	6:J:375:LYS:NZ	2.04	0.90
1:Z:810:ALA:HB3	1:Z:836:ASP:HA	1.46	0.90
2:C:1258:GLN:HG2	2:C:1299:LYS:NZ	1.87	0.90
7:K:484:PHE:O	7:K:492:ASP:CB	2.20	0.90
1:Z:810:ALA:CB	1:Z:836:ASP:O	2.20	0.90
6:J:364:ILE:CA	7:K:424:ASN:ND2	2.35	0.90
5:F:1038:LEU:C	5:F:1040:THR:H	1.74	0.89
7:K:326:LYS:CB	7:K:327:PRO:HD2	2.02	0.89
1:Z:817:ALA:O	1:Z:821:GLN:CA	2.20	0.89
5:F:887:PHE:H	5:F:888:PRO:HD2	1.37	0.89
5:F:1167:LYS:HA	5:F:1167:LYS:CE	1.99	0.89
7:K:446:ARG:NH1	7:K:446:ARG:O	2.06	0.89
5:F:750:TRP:HZ2	5:F:901:PRO:CB	1.86	0.89
5:F:967:THR:O	7:H:392:LEU:HD21	1.72	0.89
1:Z:753:ALA:CB	1:Z:816:TYR:CA	2.50	0.89
5:F:1672:MET:CB	1:Z:149:ALA:HB2	2.03	0.89
1:Z:127:GLN:HA	1:Z:127:GLN:HE21	1.38	0.89
3:D:499:LEU:HB2	3:D:502:SER:HB3	1.55	0.88
5:F:1116:VAL:HG11	5:F:1150:PHE:HE2	1.32	0.88
5:F:657:ILE:O	5:F:712:LEU:HD12	1.73	0.88
5:F:922:LEU:CD2	7:H:400:LYS:HE3	2.02	0.88
7:K:446:ARG:NH2	7:K:455:LYS:NZ	2.21	0.88
6:J:387:TYR:HA	8:L:762:LEU:HD22	1.55	0.88
5:F:1187:ASN:CB	5:F:1190:TYR:CB	2.52	0.88
1:A:27:GLU:OE2	1:A:30:ASP:CB	2.21	0.88
1:Z:27:GLU:OE2	1:Z:30:ASP:CB	2.21	0.88
6:G:292:HIS:ND1	6:J:352:VAL:HG11	1.87	0.88
7:H:535:LYS:CB	8:I:821:ILE:CD1	2.51	0.88
6:J:433:LYS:CB	7:K:499:GLY:HA2	2.03	0.88
5:F:968:ILE:HG13	7:H:392:LEU:CD1	2.03	0.88
1:Z:117:LYS:NZ	1:Z:117:LYS:HB3	1.87	0.88
6:J:459:VAL:O	6:J:463:LYS:HB2	1.73	0.88
5:F:1084:LEU:HA	5:F:1156:TYR:CZ	2.09	0.87
5:F:1294:LYS:O	5:F:1295:ALA:O	1.90	0.87
5:F:914:ASP:HA	5:F:917:PHE:CB	2.03	0.87
3:D:175:ILE:HD11	3:D:642:LEU:HB2	1.55	0.87
3:D:944:LEU:HD12	3:D:947:LEU:HD12	1.57	0.87
5:F:935:GLN:O	5:F:938:ALA:N	2.07	0.87
3:D:910:LEU:HD23	3:D:913:LEU:HD12	1.57	0.87
5:F:1251:ARG:HH22	5:F:1276:ASP:HB2	1.39	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:429:LEU:CB	6:J:434:THR:OG1	2.23	0.86
4:E:504:ASP:HA	4:E:522:ILE:O	1.73	0.86
3:D:830:SER:HB3	3:D:934:SER:HB3	1.58	0.86
7:H:426:GLY:HA2	8:I:736:ASN:H	1.38	0.86
5:F:734:LEU:HD21	5:F:817:ASN:OD1	1.74	0.86
1:Z:241:ILE:CG2	1:Z:245:ALA:CB	2.50	0.86
4:E:182:PHE:CE2	5:F:1189:MET:CB	2.59	0.86
7:K:455:LYS:HD3	7:K:455:LYS:N	1.91	0.86
1:Z:811:ARG:CA	1:Z:836:ASP:CB	2.53	0.86
5:F:354:ARG:HB2	5:F:356:ILE:CG2	2.04	0.86
1:Z:746:PRO:O	1:Z:812:GLN:O	1.93	0.86
5:F:389:LEU:H	5:F:389:LEU:HD12	1.41	0.86
5:F:968:ILE:HG23	7:H:392:LEU:HD11	1.56	0.86
7:K:315:LYS:HA	7:K:347:THR:HA	1.58	0.86
1:Z:807:LYS:CB	1:Z:837:VAL:O	2.24	0.85
1:A:751:LEU:CD2	2:C:1313:LEU:HD23	2.04	0.85
3:D:430:GLU:CD	3:D:528:PRO:HD3	1.95	0.85
5:F:1167:LYS:O	5:F:1167:LYS:HD3	1.76	0.85
1:A:57:ARG:HG2	1:A:57:ARG:HH11	1.38	0.85
3:D:768:PRO:HA	3:D:771:TYR:HB2	1.57	0.85
5:F:401:THR:CB	5:F:411:ASN:CB	2.53	0.85
7:K:321:ALA:HA	7:K:348:ILE:HD11	1.42	0.85
7:K:404:ARG:HA	7:K:404:ARG:NE	1.88	0.85
6:G:430:LEU:CB	8:I:780:THR:CA	2.53	0.85
1:A:783:SER:CA	1:A:839:LEU:HA	2.06	0.85
5:F:922:LEU:HD23	7:H:400:LYS:HE3	1.58	0.85
6:J:365:SER:N	7:K:424:ASN:ND2	2.25	0.85
5:F:1216:PHE:CE2	5:F:1282:ALA:CB	2.59	0.85
8:I:822:LYS:HZ1	8:I:822:LYS:HA	1.42	0.85
3:D:528:PRO:HG3	3:D:624:PHE:CD2	2.11	0.85
6:J:324:GLN:HA	6:J:327:LYS:HE2	1.56	0.85
6:J:405:LEU:CD2	7:K:469:ARG:HE	1.89	0.85
3:D:537:LYS:HE2	3:D:572:LEU:HD23	1.57	0.84
6:J:371:LYS:O	6:J:371:LYS:NZ	2.10	0.84
6:J:432:LEU:CB	8:L:782:ILE:CA	2.55	0.84
1:A:140:ILE:HG22	4:E:1393:LYS:HZ2	1.41	0.84
1:A:50:ARG:HA	1:A:53:VAL:HG12	1.58	0.84
5:F:1037:ASN:H	5:F:1040:THR:CB	1.91	0.84
1:Z:49:LEU:O	1:Z:49:LEU:HD22	1.76	0.84
1:Z:242:LEU:HA	1:Z:245:ALA:HB3	1.58	0.84
4:E:687:LYS:CB	5:F:1391:GLY:CA	2.56	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:772:PRO:CB	1:A:828:THR:CG2	2.39	0.84
6:G:295:LYS:CG	6:J:363:LYS:NZ	2.40	0.84
6:J:323:SER:HA	6:J:326:LEU:HD12	1.57	0.84
1:Z:811:ARG:HA	1:Z:836:ASP:CB	2.07	0.84
1:A:787:HIS:CE1	1:A:838:SER:O	2.31	0.83
5:F:1134:LYS:C	5:F:1136:LYS:H	1.81	0.83
6:G:465:LYS:HB2	1:Z:20:LYS:HZ3	1.42	0.83
4:E:1163:LEU:O	4:E:1167:LEU:HB2	1.78	0.83
5:F:1634:LYS:HD2	5:F:1635:ARG:HD3	1.58	0.83
1:Z:747:PHE:HA	1:Z:812:GLN:CB	2.09	0.83
1:Z:756:LYS:CB	1:Z:816:TYR:CB	2.57	0.83
5:F:929:TYR:O	5:F:932:VAL:HG13	1.79	0.83
1:Z:46:ILE:HD12	1:Z:46:ILE:O	1.78	0.83
1:Z:753:ALA:CB	1:Z:816:TYR:HA	2.09	0.82
1:Z:753:ALA:CA	1:Z:816:TYR:CA	2.57	0.82
5:F:690:GLU:CG	8:I:722:LEU:HD21	2.08	0.82
1:A:775:LEU:CB	1:A:832:LEU:CD1	2.57	0.82
6:J:390:ILE:HB	8:L:762:LEU:HD11	1.62	0.82
6:J:333:ILE:O	6:J:336:PHE:CA	2.28	0.82
5:F:1251:ARG:HH22	5:F:1276:ASP:CB	1.92	0.82
6:G:465:LYS:CB	1:Z:20:LYS:NZ	2.42	0.82
5:F:227:ASP:HA	5:F:379:SER:CB	2.10	0.82
5:F:1116:VAL:CG1	5:F:1150:PHE:HE2	1.87	0.82
3:D:1457:LYS:O	1:Z:651:ASP:CB	2.27	0.82
1:Z:782:ILE:CB	1:Z:839:LEU:C	2.48	0.81
1:A:46:ILE:HA	8:L:792:GLN:H	1.45	0.81
2:C:1258:GLN:HG2	2:C:1299:LYS:HZ1	1.42	0.81
4:E:923:LEU:HD11	4:E:931:PHE:HE2	1.44	0.81
5:F:914:ASP:HA	5:F:917:PHE:HB3	1.59	0.81
1:Z:753:ALA:HA	1:Z:816:TYR:CA	2.10	0.81
4:E:227:ILE:CD1	4:E:258:ILE:CD1	2.58	0.81
5:F:1109:ILE:HD11	5:F:1160:TYR:OH	1.80	0.81
3:D:1377:ASN:ND2	1:Z:758:GLN:HE21	1.76	0.81
1:A:772:PRO:HB3	1:A:828:THR:CB	2.09	0.81
3:D:734:LEU:HB3	3:D:739:THR:HG21	1.60	0.81
5:F:1357:ALA:HB2	5:F:1381:LEU:CA	2.10	0.81
6:G:430:LEU:CB	8:I:780:THR:CG2	2.58	0.81
1:Z:251:ALA:O	1:Z:252:GLN:C	2.19	0.81
4:E:258:ILE:CG2	4:E:261:ILE:HD11	2.10	0.81
6:J:369:LEU:HD13	7:K:419:LEU:HD22	1.62	0.80
1:Z:774:LEU:HA	1:Z:777:ILE:HG22	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:400:LYS:HD2	7:K:400:LYS:O	1.80	0.80
1:A:128:LEU:CD1	4:E:1260:TYR:CZ	2.60	0.80
5:F:1068:ILE:CD1	5:F:1150:PHE:CD2	2.63	0.80
8:I:814:LEU:CD2	1:Z:59:LYS:CB	2.59	0.80
6:J:386:ASP:HA	6:J:389:ARG:HB2	1.63	0.80
7:K:337:GLN:O	7:K:341:LYS:HE2	1.79	0.80
7:K:446:ARG:NH2	7:K:455:LYS:HZ1	1.79	0.80
8:I:805:ARG:CB	1:Z:88:LYS:NZ	2.45	0.80
1:Z:804:ASP:O	1:Z:808:ASN:HB3	1.81	0.80
5:F:1106:PHE:CD2	5:F:1164:PHE:CE2	2.69	0.80
3:D:160:ILE:HG23	3:D:191:ILE:HG21	1.64	0.80
7:H:412:ILE:CG2	7:H:415:LEU:HD23	2.11	0.80
5:F:1216:PHE:HE2	5:F:1282:ALA:HB2	1.47	0.80
3:D:368:ILE:HB	3:D:380:TYR:HB2	1.63	0.80
6:J:333:ILE:C	6:J:336:PHE:CB	2.50	0.80
8:L:643:LYS:HG3	8:L:647:GLN:HE22	1.47	0.80
1:Z:251:ALA:O	1:Z:254:LEU:N	2.15	0.80
1:Z:779:LEU:CB	1:Z:835:ILE:CB	2.60	0.80
5:F:1068:ILE:CD1	5:F:1150:PHE:HD2	1.95	0.79
7:K:385:GLN:HA	7:K:385:GLN:HE21	1.48	0.79
5:F:935:GLN:O	5:F:937:LEU:N	2.14	0.79
6:J:384:LEU:HD23	6:J:384:LEU:O	1.82	0.79
8:I:822:LYS:HA	8:I:822:LYS:CE	2.12	0.79
1:Z:810:ALA:CB	1:Z:836:ASP:C	2.37	0.79
2:C:1388:HIS:O	4:E:1331:LEU:CD1	2.31	0.79
4:E:988:ILE:O	4:E:990:LYS:N	2.16	0.79
6:J:353:LEU:HG	7:K:419:LEU:HD11	1.64	0.79
7:K:337:GLN:O	7:K:341:LYS:CE	2.30	0.79
6:J:305:ILE:HD11	8:L:668:VAL:HG12	1.61	0.79
1:Z:824:MET:CB	1:Z:825:PRO:CD	2.60	0.79
3:D:1376:LYS:CB	1:Z:762:ASN:CA	2.60	0.79
7:H:532:ALA:HB2	8:I:818:ILE:CD1	2.12	0.79
5:F:734:LEU:HD22	5:F:817:ASN:OD1	1.81	0.79
1:Z:753:ALA:HB1	1:Z:816:TYR:HA	1.61	0.79
5:F:928:LEU:H	5:F:928:LEU:CD1	1.92	0.79
6:J:325:TYR:CD2	7:K:390:HIS:HA	2.15	0.79
6:G:449:LEU:HD23	1:Z:84:ASP:CG	2.03	0.78
7:H:423:LYS:O	8:I:735:ASN:CB	2.31	0.78
1:Z:116:LYS:HB3	1:Z:116:LYS:NZ	1.95	0.78
7:K:314:ASN:HB2	7:K:361:ARG:HH12	1.46	0.78
3:D:515:VAL:HB	3:D:604:PRO:HG3	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1376:LYS:CB	1:Z:762:ASN:HA	2.13	0.78
5:F:1436:LYS:O	5:F:1440:ILE:HB	1.83	0.78
7:K:310:ALA:HB3	7:K:352:ILE:HB	1.64	0.78
5:F:922:LEU:CD2	7:H:400:LYS:CE	2.58	0.78
5:F:1134:LYS:O	5:F:1136:LYS:N	2.16	0.78
1:Z:133:THR:CG2	1:Z:134:LYS:N	2.46	0.78
6:G:295:LYS:HG2	6:J:363:LYS:HZ1	1.47	0.78
1:Z:663:ASP:O	1:Z:667:ALA:HB3	1.84	0.78
1:A:775:LEU:CB	1:A:832:LEU:HD11	2.13	0.78
5:F:1035:GLY:O	5:F:1042:ILE:CB	2.32	0.78
6:J:333:ILE:HA	6:J:336:PHE:CB	2.13	0.78
4:E:182:PHE:HE2	5:F:1189:MET:CB	1.96	0.78
5:F:1633:TYR:CZ	5:F:1635:ARG:HB2	2.19	0.78
7:K:358:LEU:HD22	8:L:662:ILE:HD13	1.64	0.78
1:A:82:ASP:OD1	1:A:82:ASP:N	2.14	0.77
3:D:445:ARG:HB2	3:D:466:LYS:HB2	1.67	0.77
1:A:53:VAL:CG2	8:L:799:SER:OG	2.31	0.77
1:A:253:LEU:HD22	1:A:502:ASP:HB3	1.67	0.77
5:F:1606:GLN:O	5:F:1610:ALA:HB2	1.83	0.77
6:J:319:GLU:HA	6:J:322:THR:HG22	1.66	0.77
3:D:263:VAL:HB	3:D:311:LYS:HE3	1.65	0.77
5:F:1139:ILE:HG12	5:F:1291:SER:OG	1.84	0.77
1:Z:91:GLN:O	1:Z:93:ASN:N	2.18	0.77
1:A:779:LEU:CB	1:A:835:ILE:CB	2.61	0.77
2:C:1258:GLN:CG	2:C:1299:LYS:CE	2.62	0.77
3:D:395:PRO:HB3	3:D:418:LEU:HD23	1.65	0.77
1:Z:768:VAL:HA	1:Z:771:ILE:HD12	1.66	0.77
3:D:1468:TYR:H	1:Z:621:HIS:CE1	2.02	0.77
5:F:968:ILE:HG23	7:H:392:LEU:CD1	2.14	0.77
5:F:1435:LYS:NZ	5:F:1484:ARG:NH2	2.32	0.77
6:G:465:LYS:CB	1:Z:20:LYS:HZ1	1.98	0.77
3:D:744:SER:HA	3:D:758:ASP:HB2	1.67	0.77
3:D:1238:ARG:HG2	1:Z:830:SER:HB2	1.66	0.77
8:I:737:ASN:OD1	8:I:738:ASP:OD1	2.01	0.77
4:E:973:THR:OG1	4:E:974:GLY:N	2.14	0.77
5:F:1038:LEU:O	5:F:1040:THR:N	2.18	0.77
4:E:1022:TYR:CE2	4:E:1026:THR:HG22	2.18	0.77
6:G:465:LYS:HE3	1:Z:20:LYS:HZ3	1.49	0.77
1:Z:810:ALA:HB2	1:Z:839:LEU:CA	2.15	0.77
1:Z:810:ALA:HB1	1:Z:835:ILE:O	1.84	0.76
4:E:1359:ILE:HG21	1:Z:453:VAL:HG11	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:327:LYS:HZ2	1:Z:46:ILE:HA	1.50	0.76
7:H:412:ILE:CG2	7:H:415:LEU:CD2	2.62	0.76
1:Z:810:ALA:C	1:Z:836:ASP:CA	2.54	0.76
8:I:822:LYS:HA	8:I:822:LYS:NZ	1.99	0.76
1:A:128:LEU:HD13	4:E:1260:TYR:CE2	2.20	0.76
4:E:1319:LEU:HD21	4:E:1398:VAL:HG23	1.67	0.76
5:F:1216:PHE:HE2	5:F:1282:ALA:HB1	1.48	0.76
7:K:483:VAL:CB	7:K:493:SER:C	2.53	0.76
5:F:1370:LEU:O	5:F:1371:ILE:HG12	1.86	0.76
5:F:1357:ALA:CA	5:F:1381:LEU:CB	2.63	0.76
6:J:387:TYR:CB	8:L:759:SER:OG	2.33	0.76
1:Z:146:LEU:O	1:Z:146:LEU:HD12	1.85	0.76
5:F:506:ASN:O	5:F:510:PHE:HB2	1.84	0.76
5:F:1606:GLN:HB3	1:Z:141:ASN:HD22	1.50	0.76
6:J:398:VAL:HB	7:K:462:ARG:O	1.85	0.76
7:K:321:ALA:C	7:K:348:ILE:HD11	2.06	0.76
3:D:509:PHE:HA	3:D:517:LEU:HG	1.68	0.76
1:Z:810:ALA:HB2	1:Z:839:LEU:HA	1.68	0.76
3:D:298:TYR:CE1	3:D:311:LYS:HE2	2.21	0.75
8:I:805:ARG:CB	1:Z:88:LYS:CE	2.64	0.75
7:K:359:ASN:HA	7:K:362:ASN:HD22	1.49	0.75
1:A:120:ASN:OD1	6:J:413:ASN:ND2	2.20	0.75
3:D:1249:LEU:CB	5:F:1502:THR:O	2.34	0.75
5:F:159:LYS:NZ	5:F:363:ASP:CB	2.49	0.75
7:K:313:TYR:HA	7:K:349:PRO:HB3	1.68	0.75
6:J:376:LYS:NZ	8:L:756:ASN:HD22	1.84	0.75
7:K:538:LYS:CB	8:L:821:ILE:CG2	2.64	0.75
5:F:1442:TRP:CE2	5:F:1484:ARG:HB3	2.21	0.75
7:K:446:ARG:HH22	7:K:455:LYS:HZ1	1.30	0.75
1:A:16:LYS:HE2	6:J:467:LEU:O	1.86	0.75
1:A:226:ARG:NH2	1:A:230:GLY:O	2.20	0.75
3:D:508:LYS:HG3	3:D:517:LEU:H	1.50	0.75
5:F:1034:LEU:O	5:F:1095:LEU:HD11	1.85	0.75
7:K:538:LYS:CB	8:L:821:ILE:HG23	2.16	0.75
4:E:923:LEU:HD11	4:E:931:PHE:CE2	2.21	0.75
1:Z:133:THR:HG22	1:Z:134:LYS:H	1.48	0.75
3:D:402:ILE:HG21	3:D:406:THR:H	1.51	0.75
3:D:576:LEU:HD22	3:D:601:THR:HB	1.69	0.75
5:F:227:ASP:CB	5:F:361:LEU:CB	2.65	0.75
5:F:922:LEU:HD23	7:H:400:LYS:HZ1	1.49	0.75
7:K:446:ARG:NH2	7:K:455:LYS:CE	2.50	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:LEU:CD2	4:E:1260:TYR:CD2	2.62	0.75
7:H:420:ALA:HB1	8:I:745:TYR:HE1	1.48	0.75
7:H:425:ARG:O	7:H:427:LEU:N	2.19	0.74
1:A:137:ASP:HB2	4:E:1386:LEU:HA	1.69	0.74
1:A:233:ASP:OD2	1:A:236:ASN:ND2	2.21	0.74
7:H:412:ILE:HA	7:H:415:LEU:HB2	1.67	0.74
6:J:365:SER:H	7:K:424:ASN:HD21	1.33	0.74
1:Z:116:LYS:HE2	1:Z:116:LYS:O	1.88	0.74
1:Z:44:VAL:CB	1:Z:47:ASN:ND2	2.50	0.74
1:A:192:ILE:HD12	1:A:571:LEU:HD11	1.68	0.74
5:F:1216:PHE:CZ	5:F:1282:ALA:HA	2.21	0.74
1:Z:753:ALA:HB2	1:Z:816:TYR:N	2.02	0.74
1:Z:810:ALA:HB1	1:Z:836:ASP:N	2.03	0.74
1:A:783:SER:HA	1:A:839:LEU:CA	2.12	0.74
3:D:490:LYS:HE2	3:D:533:SER:HB3	1.70	0.74
3:D:1241:GLY:HA2	1:Z:826:ARG:O	1.87	0.74
5:F:750:TRP:CZ2	5:F:901:PRO:CB	2.70	0.74
7:K:287:GLN:O	7:K:291:GLN:N	2.18	0.74
1:Z:117:LYS:HB3	1:Z:117:LYS:HZ1	1.52	0.74
5:F:1274:ASP:HA	5:F:1277:VAL:HB	1.68	0.74
5:F:1550:LEU:HD21	5:F:1552:PHE:CE2	2.19	0.74
6:G:431:GLN:CB	7:H:503:ASN:N	2.51	0.74
6:J:350:PHE:CD1	7:K:419:LEU:HD12	2.23	0.74
7:K:513:LEU:CD2	8:L:800:HIS:CE1	2.69	0.74
6:G:357:LEU:O	8:I:732:ALA:O	2.06	0.74
6:J:364:ILE:HA	7:K:424:ASN:HD22	1.52	0.73
7:K:379:ILE:O	7:K:382:LYS:N	2.20	0.73
7:K:387:GLN:HA	7:K:387:GLN:HE21	1.51	0.73
4:E:224:CYS:O	4:E:228:ASN:HB2	1.87	0.73
5:F:951:ARG:HH21	5:F:953:ASN:N	1.84	0.73
3:D:1238:ARG:CA	1:Z:830:SER:HB3	2.13	0.73
4:E:1359:ILE:CG2	1:Z:453:VAL:HG11	2.18	0.73
5:F:1635:ARG:O	5:F:1639:GLY:HA3	1.89	0.73
3:D:413:LEU:HD11	3:D:444:VAL:HG11	1.69	0.73
3:D:472:VAL:HG23	3:D:474:PRO:HD2	1.70	0.73
5:F:1216:PHE:CE2	5:F:1282:ALA:HB2	2.23	0.73
1:Z:365:GLN:O	1:Z:368:LEU:HB2	1.87	0.73
1:A:128:LEU:HB3	4:E:1260:TYR:HE2	1.54	0.73
2:C:1258:GLN:HG2	2:C:1299:LYS:HE2	1.69	0.73
4:E:182:PHE:CZ	5:F:1189:MET:CB	2.71	0.73
5:F:968:ILE:CG1	7:H:392:LEU:CD1	2.65	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1669:LEU:CB	1:Z:145:ASN:CB	2.67	0.73
1:Z:822:TYR:O	1:Z:828:THR:HG23	1.88	0.73
6:J:398:VAL:CG2	7:K:462:ARG:HA	2.19	0.73
1:Z:754:ARG:HA	1:Z:819:MET:CB	2.17	0.73
1:A:60:ASN:N	8:L:807:LEU:CB	2.52	0.73
3:D:155:ASN:HA	3:D:646:SER:HB3	1.71	0.73
5:F:951:ARG:NH2	5:F:953:ASN:H	1.84	0.73
7:K:312:VAL:HG23	7:K:352:ILE:HG13	1.71	0.73
5:F:424:SER:O	5:F:428:GLN:NE2	2.21	0.72
5:F:1283:LYS:HA	5:F:1283:LYS:CE	2.17	0.72
3:D:750:LYS:HB2	3:D:751:PRO:HD3	1.71	0.72
1:Z:771:ILE:HG22	1:Z:772:PRO:CD	2.19	0.72
5:F:159:LYS:HE3	5:F:363:ASP:CA	2.15	0.72
1:Z:822:TYR:O	1:Z:828:THR:CG2	2.37	0.72
6:J:432:LEU:CB	8:L:782:ILE:HA	2.19	0.72
6:J:433:LYS:H	7:K:499:GLY:HA3	1.52	0.72
7:K:404:ARG:HA	7:K:404:ARG:HE	1.55	0.72
7:K:520:ILE:HA	7:K:523:LEU:HB2	1.71	0.72
1:A:634:ASP:O	1:A:636:ARG:NH1	2.22	0.72
8:L:637:LEU:HD21	8:L:640:LEU:HD23	1.72	0.72
4:E:984:ASP:N	4:E:984:ASP:OD1	2.17	0.72
5:F:354:ARG:CZ	5:F:354:ARG:HB3	2.20	0.72
5:F:1363:ILE:HG22	1:Z:125:ILE:CD1	2.19	0.72
1:Z:127:GLN:HE21	1:Z:127:GLN:CA	2.01	0.72
4:E:258:ILE:HG23	4:E:261:ILE:HD11	1.70	0.72
1:A:315:LYS:HE3	1:A:321:LYS:HA	1.72	0.72
1:Z:753:ALA:C	1:Z:816:TYR:HA	2.09	0.72
3:D:915:GLU:OE1	3:D:980:SER:HB3	1.90	0.71
6:J:389:ARG:O	6:J:389:ARG:NH1	2.23	0.71
5:F:334:GLN:HE22	5:F:859:LYS:NZ	1.83	0.71
6:J:303:GLU:HG2	6:J:304:LEU:HD12	1.70	0.71
7:K:448:GLU:HA	7:K:448:GLU:OE2	1.89	0.71
5:F:1027:GLN:HG2	5:F:1036:PRO:HA	1.71	0.71
6:G:470:LEU:CB	7:H:538:LYS:NZ	2.50	0.71
1:A:775:LEU:HB3	1:A:832:LEU:HD12	1.72	0.71
3:D:268:ILE:HG21	3:D:284:PHE:HE2	1.54	0.71
5:F:837:TYR:CB	5:F:918:PHE:CE2	2.71	0.71
5:F:1435:LYS:CE	5:F:1484:ARG:NH2	2.53	0.71
6:J:376:LYS:O	6:J:376:LYS:HD2	1.89	0.71
7:K:378:HIS:O	7:K:381:GLU:CB	2.38	0.71
3:D:451:SER:H	3:D:458:GLU:HB3	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:724:ASP:O	8:I:727:SER:HB2	1.89	0.71
8:I:822:LYS:HA	8:I:822:LYS:HE3	1.70	0.71
6:G:470:LEU:HB2	7:H:538:LYS:NZ	2.05	0.71
1:Z:746:PRO:CB	1:Z:753:ALA:N	2.53	0.71
3:D:935:PHE:HD2	3:D:936:VAL:HG22	1.55	0.71
5:F:376:ASN:CB	5:F:382:ASP:H	2.04	0.71
5:F:1550:LEU:CD1	5:F:1604:ILE:CD1	2.68	0.71
4:E:227:ILE:CD1	4:E:258:ILE:HD13	2.17	0.71
5:F:1080:LEU:HG	5:F:1156:TYR:HD2	1.56	0.71
1:A:59:LYS:O	8:L:807:LEU:CB	2.39	0.70
3:D:528:PRO:CG	3:D:624:PHE:CE2	2.74	0.70
6:G:296:ALA:HB2	6:J:363:LYS:HD2	1.71	0.70
8:L:800:HIS:O	8:L:804:LEU:HB3	1.91	0.70
1:A:140:ILE:HG22	4:E:1393:LYS:HZ3	1.56	0.70
6:J:383:LYS:HE3	8:L:759:SER:HB2	1.73	0.70
1:Z:753:ALA:O	1:Z:816:TYR:HA	1.92	0.70
1:Z:601:PRO:HB3	1:Z:605:GLU:HB2	1.74	0.70
1:Z:746:PRO:CB	1:Z:752:SER:C	2.60	0.70
5:F:887:PHE:N	5:F:888:PRO:CD	2.54	0.70
7:K:317:ASN:CA	7:K:346:GLN:HB3	2.21	0.70
4:E:1309:ARG:O	4:E:1313:ARG:CG	2.35	0.70
6:G:295:LYS:CD	6:J:363:LYS:HZ3	2.05	0.70
1:Z:44:VAL:O	1:Z:47:ASN:HB2	1.91	0.70
5:F:1088:ARG:HH11	5:F:1088:ARG:HG3	1.56	0.70
6:J:429:LEU:HA	6:J:434:THR:H	1.57	0.70
1:A:16:LYS:HA	1:A:19:ASN:HD22	1.57	0.70
2:C:318:ILE:H	2:C:318:ILE:CD1	1.96	0.70
3:D:937:SER:HB3	3:D:941:GLN:HB2	1.73	0.70
5:F:841:PHE:CE2	5:F:918:PHE:CD1	2.79	0.70
5:F:900:LEU:C	5:F:900:LEU:HD12	2.12	0.70
5:F:1294:LYS:O	5:F:1295:ALA:C	2.28	0.70
6:J:376:LYS:HZ1	8:L:756:ASN:HD22	1.40	0.70
7:K:505:ARG:HA	7:K:508:LYS:HB3	1.73	0.70
5:F:1216:PHE:HZ	5:F:1282:ALA:HA	1.55	0.70
4:E:1029:ASN:HD21	7:K:475:SER:CB	2.04	0.70
7:H:412:ILE:O	7:H:415:LEU:HB3	1.92	0.70
3:D:475:GLU:O	3:D:486:GLN:NE2	2.24	0.69
5:F:328:ASP:HB3	5:F:331:ILE:HD11	1.74	0.69
5:F:1024:LEU:HA	5:F:1048:LEU:HB3	1.73	0.69
1:A:301:ASN:HB3	1:A:345:LEU:HD13	1.74	0.69
3:D:545:GLN:HG3	3:D:572:LEU:HD13	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:1356:LEU:HB2	1:Z:453:VAL:CG2	2.21	0.69
7:H:426:GLY:CA	8:I:736:ASN:H	1.98	0.69
7:H:508:LYS:HG3	7:H:510:VAL:HG13	1.74	0.69
1:Z:29:SER:HA	1:Z:32:LEU:HG	1.74	0.69
3:D:222:ASN:H	3:D:301:SER:HB2	1.57	0.69
3:D:763:ASP:HB3	3:D:765:ILE:HD11	1.74	0.69
5:F:333:GLU:O	5:F:335:ASP:N	2.23	0.69
5:F:914:ASP:OD1	5:F:917:PHE:HB2	1.91	0.69
6:J:383:LYS:HZ3	8:L:756:ASN:CB	1.94	0.69
1:Z:767:ILE:O	1:Z:771:ILE:N	2.20	0.69
3:D:617:ALA:HA	3:D:630:THR:HG21	1.73	0.69
7:K:310:ALA:O	7:K:352:ILE:N	2.25	0.69
7:K:426:GLY:HA2	8:L:738:ASP:HB3	1.72	0.69
1:A:29:SER:HA	1:A:32:LEU:HG	1.75	0.69
5:F:1157:TRP:CD1	5:F:1160:TYR:CE1	2.81	0.69
3:D:860:ILE:HG21	3:D:893:ILE:HG13	1.72	0.69
1:Z:16:LYS:HA	1:Z:19:ASN:HD22	1.57	0.69
1:Z:748:SER:OG	1:Z:752:SER:HB3	1.92	0.69
1:A:669:ASP:O	1:A:724:ARG:NH2	2.25	0.69
1:A:682:GLU:HG2	1:A:691:ARG:HH22	1.58	0.69
1:A:775:LEU:HD13	1:A:832:LEU:HD11	1.75	0.69
2:C:1388:HIS:O	4:E:1331:LEU:HD11	1.92	0.69
5:F:376:ASN:CB	5:F:382:ASP:N	2.55	0.69
6:G:327:LYS:NZ	1:Z:46:ILE:HA	2.08	0.69
1:Z:782:ILE:CB	1:Z:839:LEU:O	2.41	0.69
1:A:775:LEU:HD13	1:A:832:LEU:CD1	2.23	0.69
5:F:376:ASN:CB	5:F:381:THR:C	2.59	0.69
1:A:814:MET:HG2	1:A:833:ILE:HG12	1.75	0.69
5:F:376:ASN:CB	5:F:381:THR:N	2.55	0.69
8:I:821:ILE:HD13	8:I:821:ILE:C	2.13	0.69
1:Z:810:ALA:HB1	1:Z:835:ILE:C	2.12	0.69
5:F:1036:PRO:CB	5:F:1042:ILE:CB	2.70	0.68
1:A:133:THR:O	1:A:136:PHE:N	2.25	0.68
1:A:816:TYR:HA	1:A:819:MET:HG2	1.75	0.68
3:D:828:ILE:HD13	3:D:925:GLN:HA	1.73	0.68
5:F:968:ILE:HG12	7:H:392:LEU:HD13	1.74	0.68
5:F:1633:TYR:HE2	5:F:1635:ARG:HB2	1.47	0.68
5:F:926:LEU:HD12	5:F:926:LEU:O	1.93	0.68
5:F:967:THR:O	7:H:392:LEU:CD2	2.40	0.68
1:Z:753:ALA:HB2	1:Z:815:ILE:C	2.08	0.68
7:K:483:VAL:H	7:K:493:SER:C	1.96	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:242:LEU:CA	1:Z:245:ALA:HB3	2.18	0.68
5:F:1116:VAL:HG11	5:F:1150:PHE:HZ	1.51	0.68
8:I:738:ASP:HB2	8:I:740:LYS:HE2	1.74	0.68
3:D:421:VAL:HG21	3:D:490:LYS:HB3	1.74	0.68
6:G:465:LYS:HB2	1:Z:20:LYS:HZ1	1.57	0.68
6:G:430:LEU:C	7:H:503:ASN:CB	2.61	0.68
5:F:1303:LEU:O	5:F:1303:LEU:HD13	1.94	0.68
6:G:396:THR:CB	1:Z:89:ASP:OD2	2.41	0.68
5:F:320:GLU:OE1	5:F:351:HIS:CE1	2.47	0.68
8:L:728:THR:HB	8:L:734:ALA:HB2	1.76	0.68
1:A:364:GLU:OE1	1:A:408:ARG:NH1	2.26	0.68
5:F:661:VAL:HG11	5:F:712:LEU:CD1	2.23	0.68
6:G:470:LEU:HB2	7:H:538:LYS:HZ3	1.57	0.68
6:J:297:ASP:OD2	7:K:362:ASN:ND2	2.27	0.68
1:Z:774:LEU:HD23	1:Z:774:LEU:C	2.14	0.68
5:F:750:TRP:HE1	5:F:754:ASP:HB2	1.59	0.67
6:G:289:GLN:OE1	6:J:352:VAL:HA	1.94	0.67
5:F:249:ASP:OD2	5:F:295:ARG:NH1	2.27	0.67
5:F:334:GLN:HE21	5:F:859:LYS:HZ2	0.83	0.67
5:F:1359:PHE:CE1	5:F:1363:ILE:HG23	2.29	0.67
1:Z:133:THR:O	1:Z:136:PHE:N	2.25	0.67
1:A:57:ARG:HG2	1:A:57:ARG:NH1	2.01	0.67
1:A:249:ARG:NH1	1:A:494:TYR:OH	2.27	0.67
7:H:412:ILE:O	7:H:415:LEU:CB	2.42	0.67
7:K:451:ALA:HB3	7:K:453:LEU:HD12	1.76	0.67
7:K:513:LEU:CD2	8:L:800:HIS:HE1	2.07	0.67
1:Z:724:ARG:NH1	1:Z:724:ARG:O	2.27	0.67
6:G:327:LYS:NZ	1:Z:46:ILE:CA	2.57	0.67
1:Z:746:PRO:O	1:Z:812:GLN:C	2.33	0.67
6:J:365:SER:N	7:K:424:ASN:HD22	1.91	0.67
3:D:235:SER:HB2	3:D:240:LEU:HD13	1.77	0.67
3:D:261:LEU:HD13	3:D:311:LYS:HB2	1.75	0.67
5:F:667:SER:HA	5:F:670:LYS:HB3	1.77	0.67
6:J:405:LEU:HA	6:J:408:ALA:HB3	1.76	0.67
7:K:429:LEU:C	7:K:429:LEU:HD12	2.15	0.67
7:H:527:LEU:HD23	7:H:527:LEU:C	2.15	0.67
2:C:784:ALA:HB3	3:D:1357:LYS:H	1.59	0.67
5:F:860:ASN:HD22	5:F:861:GLN:HG3	1.60	0.67
5:F:1134:LYS:C	5:F:1136:LYS:N	2.45	0.67
7:H:532:ALA:CB	8:I:818:ILE:HD12	2.20	0.67
6:J:357:LEU:CB	7:K:423:LYS:CE	2.43	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:308:LEU:HD13	7:K:355:PHE:HE2	1.58	0.67
1:Z:810:ALA:HB2	1:Z:839:LEU:CB	2.24	0.67
1:A:218:ILE:HD11	1:A:241:ILE:HD12	1.77	0.66
6:G:295:LYS:C	6:J:363:LYS:NZ	2.48	0.66
7:K:326:LYS:CB	7:K:327:PRO:CD	2.72	0.66
7:K:538:LYS:C	8:L:822:LYS:CB	2.64	0.66
3:D:753:PRO:HD2	3:D:756:LYS:HD2	1.77	0.66
5:F:1642:LYS:HA	5:F:1645:LEU:HD23	1.77	0.66
6:J:380:TYR:CE2	8:L:751:LEU:CD2	2.68	0.66
4:E:440:ILE:HG12	4:E:590:LEU:HD13	1.77	0.66
5:F:159:LYS:HZ2	5:F:363:ASP:CB	2.07	0.66
7:K:513:LEU:HD21	8:L:800:HIS:HE1	1.53	0.66
5:F:690:GLU:OE1	8:I:722:LEU:HD23	1.95	0.66
5:F:926:LEU:HD12	5:F:926:LEU:C	2.15	0.66
1:Z:49:LEU:HD22	1:Z:49:LEU:C	2.15	0.66
5:F:883:VAL:O	8:I:761:ASN:ND2	2.28	0.66
6:G:331:LYS:HE2	1:Z:49:LEU:CG	2.25	0.66
3:D:292:ASN:ND2	3:D:380:TYR:OH	2.28	0.66
3:D:583:TYR:HE2	3:D:628:PHE:HB2	1.59	0.66
4:E:1398:VAL:O	4:E:1398:VAL:CG1	2.42	0.66
5:F:711:GLN:OE1	5:F:779:PRO:CA	2.44	0.66
5:F:1116:VAL:CG1	5:F:1150:PHE:CZ	2.64	0.66
6:G:295:LYS:CG	6:J:363:LYS:HZ3	2.07	0.66
6:J:404:ASP:O	6:J:408:ALA:N	2.29	0.66
6:J:405:LEU:CD2	7:K:469:ARG:NE	2.59	0.66
1:Z:746:PRO:CB	1:Z:752:SER:O	2.44	0.66
4:E:209:VAL:O	4:E:213:PHE:CB	2.44	0.66
1:Z:87:ILE:HD13	1:Z:87:ILE:N	2.10	0.66
5:F:1303:LEU:O	5:F:1303:LEU:HD22	1.96	0.66
3:D:260:HIS:CG	3:D:261:LEU:HA	2.31	0.65
7:K:399:LEU:HD12	7:K:399:LEU:O	1.96	0.65
5:F:809:LEU:HG	5:F:810:VAL:HG13	1.77	0.65
5:F:837:TYR:CB	5:F:918:PHE:HE2	2.04	0.65
3:D:863:ILE:HG21	3:D:887:GLN:HA	1.79	0.65
6:J:370:ASP:HA	6:J:373:PHE:HB2	1.78	0.65
7:K:352:ILE:HG21	7:K:358:LEU:HG	1.78	0.65
7:K:404:ARG:HG3	8:L:704:GLN:NE2	2.11	0.65
3:D:580:VAL:O	3:D:595:ASN:N	2.29	0.65
3:D:611:LEU:HD11	3:D:640:ALA:HB2	1.78	0.65
5:F:690:GLU:OE2	8:I:722:LEU:HD21	1.96	0.65
6:G:449:LEU:HD21	1:Z:84:ASP:O	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:387:GLN:HA	7:K:387:GLN:NE2	2.11	0.65
1:A:192:ILE:HA	1:A:195:SER:HB3	1.79	0.65
3:D:943:ASP:O	3:D:947:LEU:HG	1.96	0.65
5:F:1442:TRP:CD2	5:F:1484:ARG:HD2	2.31	0.65
6:J:339:LEU:CB	7:K:405:ASN:OD1	2.44	0.65
7:K:291:GLN:HA	7:K:294:LYS:HB2	1.79	0.65
1:Z:116:LYS:HE2	1:Z:116:LYS:C	2.17	0.65
1:Z:644:TYR:HB3	1:Z:653:VAL:HG22	1.77	0.65
3:D:362:ASP:HB2	3:D:369:TYR:HE2	1.61	0.65
5:F:1128:ASP:OD2	5:F:1206:ILE:HG23	1.96	0.65
5:F:1314:VAL:HG11	5:F:1373:ASP:HB3	1.78	0.65
7:H:404:ARG:O	7:H:408:ILE:HB	1.96	0.65
8:I:792:GLN:HB2	8:I:795:LYS:HG3	1.79	0.65
1:Z:827:GLU:HA	1:Z:827:GLU:OE2	1.97	0.65
3:D:449:ASN:HD22	3:D:463:GLU:HG2	1.61	0.65
3:D:971:ILE:HD11	3:D:984:THR:CB	2.26	0.65
4:E:1405:ASN:HB3	4:E:1455:PRO:HG2	1.78	0.65
5:F:900:LEU:HD12	5:F:900:LEU:O	1.97	0.65
5:F:1406:TYR:HH	5:F:1452:SER:HG	1.43	0.65
6:G:350:PHE:CE2	7:H:418:GLN:NE2	2.65	0.65
6:J:333:ILE:CA	6:J:336:PHE:CB	2.74	0.65
3:D:454:ARG:HB3	3:D:455:PHE:HD1	1.62	0.65
5:F:336:LYS:NZ	5:F:703:TYR:OH	2.29	0.65
5:F:382:ASP:HB3	5:F:386:GLY:H	1.62	0.65
5:F:355:LEU:N	5:F:355:LEU:HD12	2.11	0.65
5:F:844:VAL:HG22	5:F:862:ALA:HA	1.79	0.65
5:F:1633:TYR:CE2	5:F:1635:ARG:CB	2.59	0.65
7:K:527:LEU:O	7:K:531:ALA:CB	2.45	0.65
1:Z:804:ASP:O	1:Z:808:ASN:CB	2.45	0.65
3:D:915:GLU:OE1	3:D:980:SER:CB	2.44	0.65
4:E:1022:TYR:O	4:E:1026:THR:CG2	2.41	0.65
5:F:22:PHE:O	5:F:26:LYS:NZ	2.30	0.65
5:F:249:ASP:O	5:F:253:LYS:HB2	1.97	0.65
5:F:555:TRP:HB2	5:F:633:LYS:HD3	1.77	0.65
6:G:296:ALA:HA	6:J:363:LYS:HE3	1.79	0.65
6:G:327:LYS:HZ3	1:Z:46:ILE:CB	1.88	0.65
6:G:430:LEU:CB	8:I:780:THR:CB	2.75	0.65
8:I:643:LYS:HG3	8:I:647:GLN:HE22	1.62	0.65
1:Z:410:ALA:HB2	1:Z:428:VAL:HG11	1.79	0.65
1:A:449:GLU:O	1:A:456:ARG:NH2	2.31	0.64
5:F:914:ASP:CA	5:F:917:PHE:HB3	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:331:LYS:CE	1:Z:49:LEU:HD12	2.20	0.64
3:D:1376:LYS:CB	1:Z:762:ASN:N	2.60	0.64
4:E:1319:LEU:HD21	4:E:1398:VAL:HG22	1.79	0.64
5:F:1424:GLU:O	5:F:1428:GLN:HB2	1.97	0.64
8:I:786:ASN:O	8:I:786:ASN:ND2	2.29	0.64
5:F:690:GLU:OE1	8:I:722:LEU:CD2	2.44	0.64
3:D:919:VAL:HG21	3:D:927:LEU:H	1.62	0.64
4:E:687:LYS:CB	5:F:1391:GLY:HA2	2.27	0.64
5:F:1283:LYS:O	5:F:1284:SER:C	2.32	0.64
5:F:1084:LEU:CA	5:F:1156:TYR:OH	2.25	0.64
1:A:776:ILE:HG23	1:A:831:THR:HG22	1.79	0.64
3:D:260:HIS:CD2	3:D:261:LEU:HD23	2.33	0.64
5:F:718:SER:O	5:F:722:ARG:NH2	2.30	0.64
5:F:1129:ASN:CG	5:F:1132:GLU:HB3	2.17	0.64
8:I:731:GLY:C	8:I:733:ALA:H	2.01	0.64
1:Z:590:LEU:HD23	1:Z:604:ILE:HG21	1.79	0.64
1:A:772:PRO:CA	1:A:828:THR:CG2	2.72	0.64
5:F:1088:ARG:HG3	5:F:1088:ARG:NH1	2.12	0.64
5:F:1543:LEU:C	5:F:1543:LEU:HD12	2.18	0.64
1:Z:821:GLN:CB	1:Z:829:TYR:CB	2.76	0.64
3:D:529:GLY:O	3:D:581:PRO:HD3	1.98	0.64
1:Z:824:MET:SD	1:Z:824:MET:N	2.70	0.64
5:F:1435:LYS:HZ3	5:F:1484:ARG:NH2	1.94	0.64
6:J:377:ILE:HG22	6:J:378:HIS:HD2	1.62	0.64
5:F:177:GLN:NE2	5:F:178:ASN:OD1	2.31	0.64
5:F:350:ARG:O	5:F:393:SER:HB2	1.94	0.64
5:F:442:ILE:HG23	5:F:443:ILE:HG13	1.80	0.64
6:J:322:THR:O	6:J:326:LEU:HG	1.98	0.64
7:K:355:PHE:HD1	7:K:358:LEU:HD12	1.61	0.64
1:Z:45:SER:O	1:Z:48:GLU:N	2.31	0.64
1:A:210:GLU:O	1:A:213:GLU:N	2.31	0.63
2:C:885:VAL:HG13	2:C:901:ILE:HG23	1.79	0.63
5:F:1216:PHE:CE2	5:F:1282:ALA:HB1	2.29	0.63
3:D:581:PRO:HA	3:D:594:GLU:HA	1.79	0.63
3:D:1494:ASN:O	5:F:1471:LYS:HE2	1.98	0.63
4:E:1377:ASN:CB	4:E:1380:ASP:CB	2.76	0.63
5:F:389:LEU:HD12	5:F:389:LEU:N	2.11	0.63
5:F:1363:ILE:CG2	1:Z:125:ILE:HD12	2.28	0.63
6:J:334:SER:O	6:J:337:LYS:N	2.27	0.63
1:Z:577:ARG:HH21	1:Z:630:ARG:HE	1.46	0.63
5:F:1309:LEU:O	5:F:1309:LEU:HD22	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:439:HIS:HD1	1:Z:457:TYR:HH	1.47	0.63
4:E:258:ILE:HG22	4:E:261:ILE:CG1	2.28	0.63
5:F:321:GLN:HA	5:F:324:ILE:HG12	1.81	0.63
6:J:389:ARG:HG2	6:J:389:ARG:HH11	1.63	0.63
4:E:1418:LEU:HG	4:E:1421:ILE:HD12	1.81	0.63
5:F:36:ASN:HD22	5:F:110:ARG:HH11	1.46	0.63
5:F:101:ASN:OD1	5:F:105:GLN:NE2	2.31	0.63
5:F:841:PHE:HD2	5:F:918:PHE:HE1	0.69	0.63
8:L:703:GLN:HA	8:L:706:GLU:OE1	1.98	0.63
5:F:656:VAL:HG13	5:F:657:ILE:HG13	1.80	0.63
6:J:357:LEU:HB3	7:K:423:LYS:HE2	1.68	0.63
7:K:505:ARG:O	7:K:509:ILE:N	2.28	0.63
5:F:1297:GLU:OE1	5:F:1297:GLU:HA	1.96	0.63
1:Z:92:THR:O	1:Z:92:THR:OG1	2.15	0.63
3:D:412:ILE:HG13	3:D:413:LEU:HD12	1.79	0.63
5:F:334:GLN:CB	5:F:860:ASN:CG	2.59	0.63
7:H:511:GLU:CB	8:I:800:HIS:CE1	2.82	0.63
3:D:377:ILE:HD11	3:D:420:ILE:HD13	1.79	0.63
5:F:971:SER:HB3	7:H:392:LEU:HD21	1.80	0.63
5:F:1305:SER:C	5:F:1307:VAL:H	2.03	0.63
8:I:778:LYS:O	8:I:778:LYS:HD3	1.98	0.63
6:J:315:LEU:HD23	8:L:679:LEU:HG	1.81	0.63
8:L:640:LEU:HA	8:L:643:LYS:HB3	1.80	0.63
4:E:421:PHE:O	4:E:425:LEU:HB2	1.99	0.62
6:J:333:ILE:O	6:J:336:PHE:C	2.37	0.62
2:C:811:LEU:CD1	2:C:867:LEU:HD21	2.30	0.62
3:D:557:THR:HG21	3:D:571:THR:HG21	1.81	0.62
3:D:932:ILE:HG23	3:D:933:ILE:HG13	1.82	0.62
5:F:1363:ILE:C	5:F:1363:ILE:HD12	2.19	0.62
7:K:419:LEU:HD23	7:K:419:LEU:O	1.97	0.62
1:Z:422:ARG:HE	1:Z:424:ASN:H	1.48	0.62
5:F:657:ILE:HG23	5:F:660:LEU:HB3	1.80	0.62
5:F:1635:ARG:O	5:F:1639:GLY:CA	2.46	0.62
6:J:390:ILE:HG12	8:L:766:ILE:HD12	1.80	0.62
7:K:338:ALA:HA	7:K:341:LYS:HE2	1.80	0.62
1:Z:196:ASN:HD21	1:Z:530:ARG:HE	1.44	0.62
3:D:242:MET:SD	3:D:298:TYR:HD2	2.17	0.62
3:D:412:ILE:HB	3:D:476:VAL:HG21	1.82	0.62
4:E:1640:ILE:O	4:E:1644:ILE:HB	1.99	0.62
1:Z:44:VAL:O	1:Z:47:ASN:CB	2.46	0.62
7:H:521:THR:HA	7:H:524:ASN:HB2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L:643:LYS:O	8:L:647:GLN:NE2	2.33	0.62
8:L:685:MET:HA	8:L:688:HIS:ND1	2.14	0.62
1:A:123:MET:O	6:J:414:SER:HB2	2.00	0.62
1:A:654:ILE:HD11	1:A:696:TYR:HD2	1.63	0.62
4:E:1143:GLN:HA	4:E:1158:TYR:HA	1.81	0.62
5:F:603:GLU:HA	5:F:606:VAL:HG12	1.82	0.62
1:A:337:ILE:HG23	1:A:349:ALA:HB1	1.81	0.62
1:A:775:LEU:CB	1:A:832:LEU:HD12	2.27	0.62
4:E:258:ILE:HG22	4:E:261:ILE:HG13	1.81	0.62
5:F:1399:VAL:O	5:F:1399:VAL:HG12	2.00	0.62
7:H:426:GLY:HA2	8:I:736:ASN:CA	2.30	0.62
1:Z:814:MET:CB	1:Z:833:ILE:HD12	2.28	0.62
1:A:56:LEU:CB	8:L:804:LEU:HD13	2.30	0.62
1:A:60:ASN:CB	8:L:803:ALA:O	2.47	0.62
3:D:850:ASN:HD22	3:D:904:LYS:HD3	1.64	0.62
6:J:293:HIS:HB3	7:K:359:ASN:HD21	1.63	0.62
7:K:365:GLN:HB3	8:L:669:LEU:HD13	1.81	0.62
8:L:682:ASP:O	8:L:685:MET:HG2	2.00	0.62
1:Z:146:LEU:HD12	1:Z:146:LEU:C	2.17	0.62
1:A:313:LEU:HD11	1:A:339:TYR:HE2	1.64	0.62
4:E:980:LYS:O	4:E:980:LYS:HD2	2.00	0.62
5:F:1469:ARG:HH12	5:F:1530:GLU:HG2	1.65	0.62
7:K:295:CYS:O	7:K:299:TRP:HB2	2.00	0.62
1:A:742:LEU:HD13	1:A:744:LEU:HD12	1.82	0.62
5:F:38:ASN:HD22	5:F:41:LYS:HB2	1.63	0.62
5:F:334:GLN:HE22	5:F:859:LYS:CD	2.13	0.62
5:F:690:GLU:CD	8:I:722:LEU:HD23	2.19	0.62
5:F:1314:VAL:HG11	5:F:1373:ASP:CB	2.29	0.62
5:F:1314:VAL:HG23	5:F:1314:VAL:O	1.98	0.62
6:J:301:HIS:CE1	8:L:665:TRP:HB3	2.35	0.62
7:K:359:ASN:O	7:K:363:GLN:HG2	2.00	0.62
8:L:637:LEU:HD23	8:L:640:LEU:H	1.65	0.62
1:Z:753:ALA:HA	1:Z:816:TYR:HA	1.72	0.62
1:A:542:THR:HA	1:A:545:PHE:CE1	2.35	0.61
6:G:452:ASP:CB	1:Z:84:ASP:OD2	2.48	0.61
7:K:527:LEU:O	7:K:531:ALA:HB2	2.00	0.61
3:D:929:PHE:O	3:D:932:ILE:HG22	1.99	0.61
3:D:518:GLU:HA	3:D:536:ILE:HD12	1.82	0.61
3:D:971:ILE:CD1	3:D:984:THR:HB	2.29	0.61
4:E:567:ARG:O	4:E:571:ASN:ND2	2.33	0.61
5:F:1156:TYR:O	5:F:1159:GLN:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:317:ASN:HA	7:K:346:GLN:HB3	1.82	0.61
1:Z:310:ASP:HA	1:Z:314:LYS:HB3	1.80	0.61
3:D:483:HIS:HB2	3:D:486:GLN:CG	2.28	0.61
5:F:138:GLY:H	5:F:206:ILE:HD11	1.64	0.61
5:F:195:GLN:NE2	5:F:232:TYR:O	2.33	0.61
6:J:325:TYR:HE2	7:K:390:HIS:CA	1.96	0.61
1:A:137:ASP:CB	4:E:1386:LEU:HG	2.30	0.61
3:D:470:SER:HB3	3:D:475:GLU:HG2	1.82	0.61
6:G:427:GLU:CB	8:I:779:THR:HG21	2.31	0.61
1:Z:814:MET:HA	1:Z:817:ALA:HB3	1.82	0.61
1:A:557:LEU:HG	1:A:579:LEU:HD11	1.83	0.61
2:C:867:LEU:HD22	2:C:888:LEU:HD21	1.82	0.61
4:E:679:SER:OG	4:E:680:ASP:N	2.34	0.61
4:E:982:ILE:HG22	4:E:982:ILE:O	2.00	0.61
6:J:357:LEU:HB3	7:K:423:LYS:HE3	0.67	0.61
3:D:147:PRO:HB2	3:D:580:VAL:HG21	1.82	0.61
4:E:215:GLN:NE2	4:E:219:GLN:OE1	2.34	0.61
6:G:431:GLN:CB	7:H:503:ASN:CB	2.78	0.61
7:K:456:THR:C	7:K:458:GLU:H	2.03	0.61
3:D:421:VAL:HG22	3:D:491:ARG:HB3	1.82	0.61
5:F:303:LYS:O	5:F:307:ASP:HB2	2.00	0.61
3:D:927:LEU:HD13	3:D:973:ARG:HH22	1.66	0.61
5:F:690:GLU:HG3	8:I:722:LEU:HG	1.82	0.61
6:J:327:LYS:O	6:J:331:LYS:HG3	2.01	0.61
7:K:312:VAL:HG12	7:K:361:ARG:HH21	1.66	0.61
1:Z:459:LEU:O	1:Z:463:GLN:HB2	2.01	0.61
5:F:1435:LYS:HE2	5:F:1484:ARG:HH21	1.65	0.61
5:F:1653:LYS:HG2	5:F:1655:SER:H	1.66	0.61
7:H:386:LEU:O	8:I:690:GLN:NE2	2.33	0.61
8:I:739:GLN:C	8:I:741:ARG:H	1.97	0.61
4:E:673:SER:O	4:E:677:ASN:ND2	2.33	0.60
5:F:922:LEU:H	5:F:922:LEU:HD12	1.65	0.60
1:Z:46:ILE:HD12	1:Z:46:ILE:C	2.21	0.60
3:D:1241:GLY:CA	1:Z:826:ARG:O	2.48	0.60
5:F:398:MET:O	5:F:400:THR:HG23	2.01	0.60
7:K:308:LEU:HB3	7:K:355:PHE:CE2	2.36	0.60
3:D:454:ARG:HB3	3:D:455:PHE:CD1	2.37	0.60
6:J:308:ILE:HD11	7:K:369:VAL:HG13	1.83	0.60
1:Z:56:LEU:HD22	1:Z:60:ASN:HD21	1.65	0.60
1:Z:207:ILE:HB	1:Z:246:ASN:CB	2.31	0.60
3:D:237:THR:O	3:D:266:GLN:HA	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:987:SER:OG	4:E:987:SER:O	2.15	0.60
4:E:1620:THR:HB	4:E:1623:GLU:HB2	1.83	0.60
5:F:759:ASP:O	5:F:773:LYS:NZ	2.34	0.60
5:F:1118:ARG:HG2	5:F:1118:ARG:HH11	1.66	0.60
5:F:1157:TRP:CD1	5:F:1160:TYR:HE1	2.19	0.60
7:H:450:PRO:O	7:H:454:GLY:N	2.35	0.60
3:D:298:TYR:CD1	3:D:311:LYS:HE2	2.37	0.60
5:F:389:LEU:C	5:F:389:LEU:HD13	2.22	0.60
5:F:920:ILE:HB	5:F:924:ALA:C	2.21	0.60
7:H:436:MET:O	7:H:440:PHE:HB3	2.02	0.60
6:J:432:LEU:CA	8:L:782:ILE:O	2.50	0.60
6:J:433:LYS:N	7:K:499:GLY:CA	2.63	0.60
7:K:385:GLN:HE21	7:K:385:GLN:CA	2.12	0.60
1:Z:218:ILE:HD11	1:Z:241:ILE:HD12	1.84	0.60
1:A:57:ARG:HH11	1:A:57:ARG:CG	2.08	0.60
1:A:590:LEU:HD23	1:A:604:ILE:HG21	1.84	0.60
7:K:523:LEU:O	7:K:527:LEU:CB	2.49	0.60
1:Z:777:ILE:HG23	1:Z:777:ILE:O	2.00	0.60
1:A:208:LEU:O	1:A:212:PHE:HB2	2.02	0.60
5:F:29:LEU:HD13	5:F:134:LEU:HG	1.84	0.60
6:J:371:LYS:O	6:J:371:LYS:HD2	2.01	0.60
1:A:510:LEU:HD22	1:A:515:LEU:HD22	1.82	0.60
3:D:789:VAL:HG11	3:D:952:LEU:HD11	1.84	0.60
3:D:1467:SER:HA	1:Z:621:HIS:HE1	1.67	0.60
3:D:1493:ASN:OD1	5:F:1471:LYS:HG2	2.02	0.60
5:F:668:ARG:HH22	5:F:719:ILE:HA	1.66	0.60
5:F:1349:PHE:N	5:F:1349:PHE:CD1	2.70	0.60
6:J:364:ILE:CA	7:K:424:ASN:HD22	2.07	0.60
5:F:332:VAL:HG13	5:F:335:ASP:HA	1.84	0.60
7:H:361:ARG:NH2	8:I:666:ASP:OD2	2.35	0.60
8:L:776:PHE:HA	8:L:779:THR:CB	2.32	0.60
1:Z:751:LEU:C	1:Z:753:ALA:H	2.03	0.60
1:Z:753:ALA:CB	1:Z:815:ILE:O	2.29	0.60
1:A:613:VAL:HG11	1:A:619:PHE:HB2	1.84	0.60
3:D:449:ASN:HD21	3:D:461:ARG:HB2	1.65	0.60
3:D:989:GLN:HA	3:D:998:ALA:HA	1.82	0.60
7:K:444:LEU:HA	7:K:447:SER:CB	2.32	0.60
1:Z:287:ASP:HA	1:Z:290:TYR:HB3	1.83	0.60
1:A:193:LEU:HA	1:A:539:ALA:HB1	1.84	0.59
3:D:863:ILE:CG2	3:D:887:GLN:HA	2.32	0.59
5:F:1084:LEU:CA	5:F:1156:TYR:CZ	2.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:334:GLN:NE2	5:F:859:LYS:CD	2.65	0.59
5:F:661:VAL:O	5:F:667:SER:OG	2.21	0.59
5:F:1032:ILE:HG22	5:F:1032:ILE:O	2.01	0.59
8:L:702:ARG:O	8:L:706:GLU:OE1	2.20	0.59
5:F:633:LYS:HZ2	5:F:635:PHE:HB2	1.67	0.59
5:F:1139:ILE:CG1	5:F:1291:SER:OG	2.49	0.59
7:K:298:SER:CA	7:K:306:THR:HA	2.27	0.59
1:Z:393:GLU:HA	1:Z:396:GLN:HG2	1.84	0.59
1:Z:766:ASN:O	1:Z:769:LYS:CB	2.50	0.59
1:A:128:LEU:CG	4:E:1260:TYR:CE2	2.86	0.59
2:C:318:ILE:HD12	2:C:318:ILE:N	2.01	0.59
2:C:811:LEU:HD11	2:C:867:LEU:HD21	1.83	0.59
3:D:268:ILE:HG21	3:D:284:PHE:CE2	2.36	0.59
5:F:405:ARG:NH1	5:F:407:ASN:HB3	2.17	0.59
6:J:324:GLN:OE1	6:J:328:GLN:NE2	2.35	0.59
6:J:351:SER:O	6:J:355:GLN:NE2	2.36	0.59
1:Z:531:ASP:OD2	1:Z:540:ASN:ND2	2.36	0.59
1:A:814:MET:CG	1:A:833:ILE:CG1	2.81	0.59
1:A:814:MET:HG2	1:A:833:ILE:CD1	2.28	0.59
3:D:641:VAL:HB	3:D:648:GLU:HG2	1.83	0.59
5:F:725:ASN:ND2	5:F:789:CYS:SG	2.76	0.59
1:Z:501:MET:O	1:Z:505:HIS:ND1	2.34	0.59
1:Z:771:ILE:HB	1:Z:772:PRO:HD2	1.83	0.59
1:A:16:LYS:HD3	6:J:468:ALA:HA	1.84	0.59
1:A:775:LEU:CG	1:A:832:LEU:HD11	2.33	0.59
3:D:713:ILE:HD12	3:D:769:ARG:HD3	1.83	0.59
3:D:744:SER:HA	3:D:758:ASP:CB	2.33	0.59
4:E:757:LYS:HG3	5:F:1195:PHE:HB2	1.85	0.59
5:F:235:PRO:O	5:F:239:HIS:ND1	2.35	0.59
2:C:786:THR:CB	2:C:789:ASP:OD2	2.50	0.59
4:E:258:ILE:HG22	4:E:261:ILE:HD11	1.84	0.59
5:F:323:LEU:HD11	5:F:483:LEU:HD23	1.84	0.59
5:F:353:PRO:HA	5:F:393:SER:HA	1.85	0.59
5:F:837:TYR:CG	5:F:918:PHE:CE2	2.90	0.59
5:F:935:GLN:CB	5:F:998:LEU:HD23	2.33	0.59
7:K:379:ILE:HG21	8:L:680:TYR:CE1	2.38	0.59
1:Z:227:GLN:NE2	1:Z:606:GLU:O	2.30	0.59
1:A:123:MET:CB	6:J:413:ASN:HB3	2.32	0.59
4:E:1031:LYS:NZ	4:E:1084:LEU:O	2.36	0.59
5:F:510:PHE:HA	5:F:513:TRP:HB3	1.85	0.59
5:F:51:LEU:HD23	5:F:71:ILE:HG13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:292:HIS:ND1	6:J:352:VAL:CG1	2.63	0.59
6:G:295:LYS:CB	6:J:363:LYS:NZ	2.65	0.59
7:H:412:ILE:HG23	7:H:415:LEU:HD23	1.67	0.59
4:E:793:LEU:HD11	4:E:1162:LEU:HD21	1.83	0.58
6:G:401:ILE:O	6:G:405:LEU:HB2	2.03	0.58
1:A:589:LEU:HA	1:A:603:VAL:HG22	1.84	0.58
3:D:353:GLN:HB3	3:D:372:SER:HB2	1.84	0.58
5:F:1434:SER:OG	5:F:1435:LYS:N	2.36	0.58
7:K:312:VAL:CG2	7:K:352:ILE:HG13	2.33	0.58
1:Z:531:ASP:OD1	1:Z:531:ASP:N	2.36	0.58
1:Z:767:ILE:O	1:Z:770:ASN:N	2.36	0.58
1:A:440:LEU:HA	1:A:443:ILE:HD12	1.85	0.58
5:F:1093:SER:O	5:F:1096:LEU:CB	2.51	0.58
5:F:1110:MET:HE3	5:F:1157:TRP:HZ2	1.68	0.58
5:F:1116:VAL:HG21	5:F:1150:PHE:HZ	1.67	0.58
5:F:1246:MET:CB	5:F:1279:CYS:CB	2.81	0.58
5:F:1303:LEU:HD22	5:F:1303:LEU:C	2.23	0.58
5:F:1468:ASN:ND2	5:F:1530:GLU:OE1	2.36	0.58
7:K:321:ALA:C	7:K:348:ILE:CD1	2.69	0.58
4:E:267:ILE:HA	4:E:270:ILE:HD12	1.85	0.58
5:F:679:ILE:O	5:F:679:ILE:HG22	2.03	0.58
5:F:746:LYS:HD2	5:F:898:TYR:H	1.68	0.58
5:F:883:VAL:O	8:I:761:ASN:CG	2.41	0.58
5:F:1031:VAL:CB	6:G:314:TYR:HB3	2.34	0.58
5:F:1538:LEU:HD11	5:F:1543:LEU:HD23	1.84	0.58
1:A:22:LEU:O	1:A:25:LEU:HB3	2.04	0.58
3:D:491:ARG:HG3	3:D:521:LYS:HB2	1.86	0.58
5:F:2:LYS:HG2	5:F:7:PRO:HG2	1.84	0.58
5:F:1084:LEU:CA	5:F:1156:TYR:HH	2.05	0.58
1:Z:22:LEU:O	1:Z:25:LEU:HB3	2.04	0.58
1:Z:751:LEU:C	1:Z:753:ALA:N	2.57	0.58
1:A:46:ILE:HA	8:L:792:GLN:N	2.16	0.58
5:F:492:ARG:HH12	5:F:495:TYR:H	1.51	0.58
8:L:774:ASN:HD22	8:L:777:ASN:HD22	1.51	0.58
8:L:793:LEU:O	8:L:796:ILE:N	2.36	0.58
3:D:860:ILE:CG2	3:D:893:ILE:HG13	2.33	0.58
3:D:1467:SER:HA	1:Z:621:HIS:CE1	2.38	0.58
4:E:1022:TYR:CZ	4:E:1026:THR:HG22	2.37	0.58
5:F:199:GLY:O	5:F:203:LYS:NZ	2.37	0.58
5:F:227:ASP:CA	5:F:379:SER:CB	2.79	0.58
5:F:1473:ASN:HB2	5:F:1475:ILE:H	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1508:ILE:HA	5:F:1511:LEU:HB3	1.85	0.58
1:Z:133:THR:O	1:Z:135:ASP:N	2.37	0.58
1:A:236:ASN:ND2	1:A:261:GLU:OE1	2.35	0.58
3:D:119:PRO:HB3	3:D:739:THR:HG22	1.84	0.58
3:D:298:TYR:HE1	3:D:311:LYS:CE	2.17	0.58
3:D:507:LEU:HG	3:D:512:LYS:HB3	1.85	0.58
8:I:795:LYS:HZ2	8:I:795:LYS:C	2.04	0.58
6:J:332:LYS:HE3	7:K:402:GLN:HG3	1.86	0.58
7:K:429:LEU:HD12	7:K:429:LEU:O	2.03	0.58
2:C:121:LEU:HD23	2:C:123:TYR:CZ	2.38	0.58
5:F:334:GLN:CG	5:F:854:GLU:CD	2.72	0.58
5:F:1005:PHE:O	5:F:1009:ASN:HB2	2.03	0.58
5:F:1129:ASN:OD1	5:F:1132:GLU:N	2.36	0.58
5:F:1492:LEU:O	5:F:1495:THR:OG1	2.22	0.58
6:G:449:LEU:HA	1:Z:84:ASP:OD2	2.03	0.58
7:H:426:GLY:HA3	8:I:736:ASN:N	2.18	0.58
1:Z:421:SER:O	1:Z:423:LYS:NZ	2.37	0.58
1:A:133:THR:O	1:A:135:ASP:N	2.37	0.58
5:F:914:ASP:CB	5:F:917:PHE:HB3	2.34	0.58
6:G:295:LYS:HB3	6:J:363:LYS:HZ2	1.68	0.58
3:D:799:THR:HA	3:D:803:PHE:HB2	1.85	0.57
1:Z:44:VAL:O	1:Z:47:ASN:N	2.37	0.57
3:D:853:PHE:CE2	3:D:900:VAL:HG21	2.39	0.57
7:H:397:ARG:NH2	8:I:698:GLN:OE1	2.37	0.57
8:I:785:ASN:CB	1:Z:112:TYR:HA	2.34	0.57
8:I:823:LYS:HD2	8:I:823:LYS:O	2.04	0.57
7:K:313:TYR:HD1	7:K:349:PRO:HB3	1.68	0.57
5:F:1014:SER:H	8:I:788:ASP:H	1.49	0.57
5:F:1435:LYS:NZ	5:F:1484:ARG:HH22	2.00	0.57
8:I:737:ASN:OD1	8:I:738:ASP:CG	2.41	0.57
7:K:444:LEU:O	7:K:447:SER:N	2.38	0.57
7:K:513:LEU:HD11	8:L:800:HIS:ND1	2.20	0.57
8:L:765:LEU:O	8:L:769:ILE:HB	2.03	0.57
1:A:706:ILE:HB	1:A:711:LYS:HE2	1.86	0.57
3:D:298:TYR:CE1	3:D:311:LYS:CE	2.87	0.57
5:F:579:ARG:HH11	5:F:698:ASN:HB3	1.69	0.57
5:F:841:PHE:CD2	5:F:918:PHE:CD1	2.89	0.57
6:J:308:ILE:HB	6:J:309:PRO:HD3	1.86	0.57
1:Z:810:ALA:CB	1:Z:835:ILE:O	2.51	0.57
3:D:328:LEU:HD11	3:D:334:VAL:HG22	1.86	0.57
3:D:515:VAL:HB	3:D:604:PRO:CG	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:753:PRO:HG2	3:D:756:LYS:HE3	1.87	0.57
5:F:712:LEU:HG	5:F:716:LEU:HD23	1.86	0.57
5:F:1063:ILE:HG22	5:F:1063:ILE:O	2.05	0.57
5:F:1467:ALA:HB1	5:F:1473:ASN:HB3	1.84	0.57
4:E:888:TYR:O	4:E:897:LYS:NZ	2.37	0.57
5:F:354:ARG:HB3	5:F:354:ARG:NH1	2.20	0.57
5:F:1118:ARG:HG2	5:F:1118:ARG:NH1	2.19	0.57
5:F:1650:GLU:OE1	5:F:1659:ASN:ND2	2.37	0.57
1:A:23:ASN:C	1:A:25:LEU:H	2.08	0.57
1:A:417:ARG:NH2	1:A:442:LEU:O	2.38	0.57
1:A:559:LEU:HA	1:A:562:LEU:HD13	1.86	0.57
3:D:853:PHE:HE2	3:D:900:VAL:HG21	1.70	0.57
5:F:702:LYS:HA	5:F:767:ILE:HD11	1.87	0.57
7:H:397:ARG:HB2	8:I:697:LEU:HD21	1.86	0.57
1:A:751:LEU:HD22	2:C:1313:LEU:HD23	1.86	0.57
5:F:397:MET:N	5:F:397:MET:SD	2.77	0.57
5:F:590:ILE:HG13	5:F:591:ASP:H	1.69	0.57
5:F:712:LEU:HG	5:F:716:LEU:CD2	2.35	0.57
8:L:799:SER:O	8:L:803:ALA:HB3	2.05	0.57
1:A:435:TRP:HA	1:A:438:MET:SD	2.44	0.57
1:A:775:LEU:HB3	1:A:832:LEU:CG	2.34	0.57
4:E:812:SER:O	4:E:872:ASN:ND2	2.38	0.57
4:E:837:ASP:HB3	4:E:839:ILE:H	1.69	0.57
6:J:398:VAL:CB	7:K:462:ARG:O	2.53	0.57
1:Z:23:ASN:C	1:Z:25:LEU:H	2.08	0.57
1:Z:824:MET:HB2	1:Z:825:PRO:CD	2.30	0.57
3:D:832:VAL:H	3:D:929:PHE:HE2	1.52	0.56
4:E:216:TYR:HD1	4:E:220:PHE:HB2	1.70	0.56
4:E:997:VAL:O	4:E:1001:ASN:ND2	2.38	0.56
5:F:28:VAL:O	5:F:32:LEU:N	2.30	0.56
5:F:353:PRO:O	5:F:356:ILE:CG2	2.53	0.56
5:F:620:THR:HG23	5:F:627:VAL:HG21	1.87	0.56
5:F:750:TRP:NE1	5:F:754:ASP:HB2	2.20	0.56
8:I:818:ILE:HD13	8:I:818:ILE:N	2.20	0.56
7:K:321:ALA:N	7:K:348:ILE:CD1	2.39	0.56
7:K:427:LEU:N	7:K:428:PRO:HD3	2.20	0.56
3:D:186:ILE:HG22	3:D:189:LYS:HB2	1.87	0.56
3:D:481:LEU:HD23	3:D:488:GLN:HB3	1.86	0.56
3:D:485:GLN:HA	3:D:577:PHE:CZ	2.40	0.56
3:D:527:SER:HB3	3:D:528:PRO:HD2	1.87	0.56
3:D:970:ILE:HG23	3:D:975:ILE:HD12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:358:VAL:HG13	4:E:359:LEU:HG	1.87	0.56
5:F:562:LEU:O	5:F:566:THR:OG1	2.23	0.56
5:F:1123:ASN:HB3	5:F:1143:SER:OG	2.05	0.56
6:G:465:LYS:HE3	1:Z:20:LYS:NZ	2.18	0.56
7:H:358:LEU:O	7:H:362:ASN:ND2	2.38	0.56
8:I:778:LYS:HZ2	8:I:778:LYS:HA	1.70	0.56
6:J:398:VAL:HG23	7:K:466:LEU:HD11	1.87	0.56
3:D:242:MET:CE	3:D:298:TYR:CD2	2.88	0.56
3:D:535:VAL:HB	3:D:575:LYS:HB2	1.87	0.56
3:D:773:ILE:O	3:D:777:ILE:HG12	2.04	0.56
4:E:986:SER:O	4:E:986:SER:OG	2.22	0.56
4:E:1319:LEU:CD2	4:E:1398:VAL:CG2	2.76	0.56
4:E:1443:THR:O	4:E:1446:PHE:HB2	2.06	0.56
4:E:1611:TYR:O	4:E:1615:ARG:HB2	2.04	0.56
5:F:909:LEU:O	7:H:403:SER:HB2	2.05	0.56
5:F:1110:MET:HE1	5:F:1161:LEU:HD11	1.87	0.56
5:F:1118:ARG:HH11	5:F:1118:ARG:CG	2.18	0.56
5:F:1270:GLN:O	5:F:1274:ASP:HB2	2.06	0.56
5:F:1435:LYS:O	5:F:1439:GLU:N	2.28	0.56
5:F:1666:MET:O	5:F:1670:ILE:HB	2.05	0.56
6:G:295:LYS:CB	6:J:363:LYS:HZ2	2.19	0.56
1:Z:277:TYR:O	1:Z:280:GLN:NE2	2.37	0.56
1:Z:638:TYR:HA	1:Z:641:ILE:HG22	1.88	0.56
5:F:668:ARG:HD2	5:F:716:LEU:HD13	1.88	0.56
5:F:1431:ARG:HD2	5:F:1474:PHE:H	1.70	0.56
6:G:402:ASP:OD2	7:H:462:ARG:NH1	2.38	0.56
6:J:309:PRO:HA	6:J:312:VAL:CG2	2.35	0.56
6:J:391:LEU:HD13	7:K:455:LYS:HA	1.86	0.56
6:J:405:LEU:HD22	7:K:469:ARG:HE	1.67	0.56
6:J:405:LEU:HD23	7:K:469:ARG:HE	1.66	0.56
1:Z:241:ILE:CG2	1:Z:245:ALA:HB1	2.22	0.56
3:D:611:LEU:CD1	3:D:640:ALA:HB2	2.35	0.56
4:E:1644:ILE:HD13	4:E:1647:LEU:HD21	1.86	0.56
5:F:661:VAL:HG11	5:F:712:LEU:HD12	1.87	0.56
5:F:825:ILE:HG22	5:F:890:VAL:HG13	1.87	0.56
5:F:1501:SER:OG	5:F:1502:THR:N	2.38	0.56
6:J:296:ALA:O	6:J:299:ILE:HG12	2.06	0.56
1:Z:80:PHE:CD1	1:Z:80:PHE:N	2.73	0.56
3:D:398:ILE:O	3:D:402:ILE:HG12	2.06	0.56
3:D:985:ALA:O	3:D:988:LEU:CB	2.54	0.56
4:E:972:LEU:HD23	4:E:995:LEU:HD11	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:537:PRO:HA	5:F:622:GLN:HB3	1.86	0.56
5:F:1550:LEU:HD13	5:F:1552:PHE:CE1	2.40	0.56
8:I:822:LYS:HZ1	8:I:822:LYS:CA	2.18	0.56
7:K:389:LYS:CB	7:K:393:ASP:HB3	2.32	0.56
1:Z:409:LEU:O	1:Z:413:LYS:HB2	2.04	0.56
1:A:16:LYS:HG2	6:J:468:ALA:HA	1.87	0.56
4:E:765:PHE:HB3	4:E:843:LEU:HD22	1.88	0.56
7:H:418:GLN:HE22	8:I:718:THR:CG2	2.03	0.56
1:Z:334:TRP:HA	1:Z:337:ILE:HD12	1.87	0.56
1:Z:692:MET:O	1:Z:696:TYR:HB2	2.06	0.56
2:C:1388:HIS:C	4:E:1331:LEU:HD11	2.26	0.56
3:D:449:ASN:HB3	3:D:463:GLU:HG2	1.86	0.56
4:E:928:SER:HA	4:E:931:PHE:HB2	1.88	0.56
5:F:552:SER:O	5:F:557:ASN:ND2	2.37	0.56
5:F:690:GLU:CG	8:I:722:LEU:CD2	2.80	0.56
6:J:319:GLU:HA	6:J:322:THR:CG2	2.36	0.56
7:K:404:ARG:O	7:K:407:GLU:N	2.37	0.56
7:K:446:ARG:HH22	7:K:455:LYS:HZ3	1.48	0.56
1:Z:251:ALA:C	1:Z:253:LEU:N	2.51	0.56
5:F:1251:ARG:NH2	5:F:1276:ASP:CB	2.66	0.56
5:F:1595:VAL:O	5:F:1599:GLU:HB2	2.06	0.56
6:G:351:SER:O	6:G:355:GLN:NE2	2.39	0.56
7:K:297:GLU:HB3	7:K:304:THR:OG1	2.04	0.56
7:K:538:LYS:O	8:L:822:LYS:CB	2.54	0.56
8:L:658:TYR:O	8:L:662:ILE:HG22	2.06	0.56
3:D:545:GLN:HG3	3:D:572:LEU:CD1	2.36	0.56
3:D:710:VAL:HG22	3:D:711:VAL:H	1.71	0.56
5:F:333:GLU:HA	5:F:420:THR:CB	2.36	0.56
5:F:679:ILE:O	5:F:745:ARG:NH1	2.39	0.56
5:F:869:VAL:HA	5:F:872:ILE:HD12	1.86	0.56
5:F:1403:SER:OG	5:F:1451:THR:O	2.22	0.56
5:F:1598:PHE:HA	5:F:1601:ILE:HB	1.86	0.56
8:I:778:LYS:HD3	8:I:778:LYS:C	2.26	0.56
6:J:388:CYS:HA	6:J:391:LEU:HB2	1.89	0.56
1:Z:289:LEU:HD21	1:Z:312:LYS:HG2	1.88	0.56
1:Z:652:ILE:HA	1:Z:655:THR:HG22	1.87	0.56
1:A:46:ILE:HA	8:L:792:GLN:CB	2.36	0.55
1:A:779:LEU:C	1:A:835:ILE:CB	2.74	0.55
5:F:637:ASP:HA	5:F:640:PHE:HD2	1.71	0.55
5:F:1176:GLU:OE1	5:F:1176:GLU:N	2.39	0.55
3:D:441:VAL:HA	3:D:490:LYS:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:134:ARG:NH2	4:E:198:MET:O	2.39	0.55
5:F:885:GLU:HG3	5:F:885:GLU:O	2.07	0.55
6:G:391:LEU:O	6:G:395:GLU:HB2	2.06	0.55
1:A:776:ILE:HD11	1:A:828:THR:HA	1.88	0.55
3:D:222:ASN:O	3:D:301:SER:N	2.40	0.55
4:E:277:THR:HG22	4:E:381:VAL:HG21	1.88	0.55
4:E:331:TYR:OH	4:E:388:ASN:ND2	2.40	0.55
4:E:1450:LEU:HD22	4:E:1456:ILE:HG21	1.88	0.55
6:G:449:LEU:HA	1:Z:84:ASP:CG	2.26	0.55
7:H:533:ILE:HA	7:H:536:LYS:HB2	1.87	0.55
6:J:384:LEU:HD23	6:J:384:LEU:C	2.26	0.55
1:Z:249:ARG:C	1:Z:251:ALA:H	2.02	0.55
1:A:607:ARG:HD2	1:A:610:LEU:HD12	1.87	0.55
3:D:654:THR:HB	3:D:655:PRO:HD2	1.87	0.55
3:D:1237:SER:CB	1:Z:829:TYR:CB	2.84	0.55
4:E:312:ASN:ND2	4:E:314:ASP:O	2.39	0.55
5:F:657:ILE:HG12	5:F:660:LEU:HD13	1.87	0.55
5:F:902:LYS:HD3	5:F:903:ASN:H	1.71	0.55
5:F:1063:ILE:HB	5:F:1066:ASP:HB3	1.87	0.55
3:D:508:LYS:HB3	3:D:516:LEU:HA	1.87	0.55
4:E:264:LEU:O	4:E:268:THR:OG1	2.23	0.55
5:F:1243:GLU:HB3	5:F:1283:LYS:HD2	1.89	0.55
5:F:1435:LYS:CE	5:F:1484:ARG:HH21	2.18	0.55
6:G:411:ASN:OD1	6:G:411:ASN:N	2.37	0.55
6:J:309:PRO:HA	6:J:312:VAL:HB	1.88	0.55
1:Z:589:LEU:HA	1:Z:603:VAL:HG22	1.88	0.55
1:A:814:MET:CG	1:A:833:ILE:HG12	2.35	0.55
3:D:139:LYS:HE3	3:D:600:GLU:HB2	1.88	0.55
3:D:484:GLN:HG2	3:D:568:GLN:OE1	2.07	0.55
3:D:911:ASN:HA	3:D:914:TYR:CD2	2.42	0.55
4:E:318:HIS:H	4:E:321:ILE:HD11	1.71	0.55
4:E:1309:ARG:HH21	4:E:1313:ARG:HH12	1.55	0.55
4:E:1585:LEU:N	4:E:1590:ASP:OD2	2.40	0.55
5:F:1606:GLN:HB3	1:Z:141:ASN:ND2	2.19	0.55
5:F:1674:CYS:HA	5:F:1677:THR:OG1	2.07	0.55
6:G:357:LEU:O	8:I:732:ALA:C	2.44	0.55
6:J:405:LEU:HD11	7:K:470:ALA:HA	1.87	0.55
8:L:640:LEU:HD13	8:L:643:LYS:HG2	1.88	0.55
8:L:672:GLY:HA2	8:L:675:GLN:HG2	1.87	0.55
1:Z:766:ASN:C	1:Z:770:ASN:HD22	2.09	0.55
1:A:309:ILE:HG23	1:A:313:LEU:HD12	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:492:ILE:HD11	1:A:510:LEU:HD12	1.89	0.55
1:A:642:LEU:HA	1:A:645:GLN:NE2	2.22	0.55
3:D:175:ILE:HG12	3:D:182:CYS:SG	2.47	0.55
3:D:903:ILE:HG23	3:D:953:PHE:CE1	2.42	0.55
3:D:956:ASN:O	3:D:960:LYS:N	2.37	0.55
5:F:355:LEU:H	5:F:355:LEU:CD1	2.20	0.55
5:F:554:SER:OG	5:F:555:TRP:N	2.39	0.55
5:F:1068:ILE:HG22	5:F:1068:ILE:O	2.05	0.55
5:F:1376:THR:O	5:F:1376:THR:OG1	2.24	0.55
6:J:324:GLN:OE1	6:J:327:LYS:HE3	2.06	0.55
1:Z:25:LEU:O	1:Z:25:LEU:HD23	2.07	0.55
3:D:155:ASN:HA	3:D:646:SER:CB	2.36	0.55
3:D:475:GLU:OE2	3:D:487:GLU:N	2.40	0.55
3:D:507:LEU:HG	3:D:512:LYS:CB	2.37	0.55
4:E:258:ILE:HG22	4:E:261:ILE:CD1	2.37	0.55
4:E:1356:LEU:HB2	1:Z:453:VAL:HG21	1.88	0.55
5:F:227:ASP:CB	5:F:379:SER:CB	2.84	0.55
5:F:788:LEU:HD12	5:F:874:LYS:HE2	1.88	0.55
5:F:928:LEU:HD12	5:F:928:LEU:N	2.01	0.55
5:F:1040:THR:O	5:F:1042:ILE:N	2.40	0.55
5:F:1356:LEU:HG	5:F:1356:LEU:O	2.03	0.55
7:K:400:LYS:HD2	7:K:400:LYS:C	2.20	0.55
7:K:431:ILE:O	7:K:435:LYS:CB	2.55	0.55
8:L:682:ASP:HA	8:L:685:MET:CE	2.37	0.55
8:L:792:GLN:HA	8:L:796:ILE:HB	1.88	0.55
1:Z:288:ASN:O	1:Z:292:LYS:HB2	2.06	0.55
5:F:334:GLN:NE2	5:F:859:LYS:CE	2.68	0.55
5:F:1067:ASN:HD22	5:F:1069:ASP:HB2	1.71	0.55
6:G:295:LYS:C	6:J:363:LYS:HZ2	2.11	0.55
8:I:674:GLU:OE1	8:I:675:GLN:NE2	2.40	0.55
6:J:398:VAL:HG21	7:K:462:ARG:C	2.28	0.55
3:D:467:PHE:CG	3:D:473:THR:HG23	2.42	0.55
4:E:20:ASN:ND2	4:E:894:VAL:O	2.40	0.55
4:E:137:VAL:HA	4:E:140:LYS:HG2	1.88	0.55
5:F:1088:ARG:HH12	8:I:785:ASN:HA	1.72	0.55
5:F:1309:LEU:HD22	5:F:1309:LEU:C	2.27	0.55
5:F:1362:ASP:CB	1:Z:125:ILE:HG21	2.37	0.55
7:H:529:LYS:HB2	8:I:814:LEU:HD11	1.88	0.55
1:A:128:LEU:CD1	4:E:1260:TYR:CE2	2.88	0.54
1:A:660:LEU:HG	1:A:685:PRO:HB3	1.88	0.54
3:D:187:ASP:O	3:D:210:THR:HA	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1286:PHE:O	5:F:1286:PHE:HD1	1.89	0.54
6:G:281:ASP:HA	6:G:284:ILE:HD12	1.89	0.54
8:I:751:LEU:HA	8:I:754:ASN:HD22	1.72	0.54
6:J:334:SER:C	6:J:337:LYS:H	2.09	0.54
1:A:25:LEU:HD23	1:A:25:LEU:O	2.07	0.54
1:A:215:TYR:HB3	1:A:505:HIS:NE2	2.23	0.54
3:D:1238:ARG:HA	1:Z:830:SER:HB2	1.87	0.54
4:E:14:THR:HB	4:E:17:HIS:HB2	1.88	0.54
5:F:10:THR:O	5:F:14:SER:HB3	2.06	0.54
5:F:837:TYR:CG	5:F:918:PHE:HE2	2.25	0.54
5:F:1038:LEU:C	5:F:1040:THR:N	2.45	0.54
5:F:1200:PRO:O	5:F:1299:ASN:OD1	2.26	0.54
5:F:1445:VAL:HG12	5:F:1453:ARG:HG3	1.89	0.54
5:F:1473:ASN:OD1	5:F:1476:LEU:N	2.34	0.54
8:I:752:ASP:OD1	8:I:756:ASN:ND2	2.40	0.54
8:I:795:LYS:C	8:I:795:LYS:HD3	2.28	0.54
1:Z:197:GLU:O	1:Z:530:ARG:NH2	2.40	0.54
1:A:501:MET:HA	1:A:541:TYR:CE1	2.41	0.54
1:A:814:MET:CG	1:A:833:ILE:HD13	2.35	0.54
3:D:164:PHE:HA	3:D:186:ILE:HD12	1.88	0.54
3:D:528:PRO:HG3	3:D:624:PHE:HE2	1.67	0.54
3:D:691:LYS:O	3:D:696:ARG:NH2	2.41	0.54
4:E:723:LEU:HD23	4:E:794:ILE:HD12	1.88	0.54
5:F:788:LEU:HA	5:F:791:PHE:HB3	1.88	0.54
5:F:837:TYR:CD2	5:F:918:PHE:HE2	2.26	0.54
6:G:465:LYS:HE3	1:Z:20:LYS:CE	2.37	0.54
7:K:352:ILE:HG21	7:K:358:LEU:CG	2.38	0.54
1:Z:661:LEU:HB2	1:Z:717:LEU:HD13	1.89	0.54
3:D:402:ILE:HG13	3:D:406:THR:HB	1.88	0.54
3:D:1377:ASN:CG	1:Z:758:GLN:HE21	2.11	0.54
5:F:225:SER:HA	5:F:383:ASN:HD21	1.73	0.54
5:F:579:ARG:HH22	5:F:701:THR:HG21	1.71	0.54
5:F:1364:TYR:HD1	5:F:1364:TYR:O	1.90	0.54
6:J:305:ILE:HD11	8:L:668:VAL:CG1	2.35	0.54
6:J:398:VAL:CG2	7:K:462:ARG:CB	2.76	0.54
7:K:379:ILE:O	7:K:382:LYS:CA	2.55	0.54
1:A:775:LEU:CD1	1:A:832:LEU:HD11	2.37	0.54
3:D:605:VAL:HG13	3:D:641:VAL:HG13	1.88	0.54
4:E:227:ILE:CD1	4:E:258:ILE:HD11	2.36	0.54
4:E:1022:TYR:CZ	4:E:1026:THR:CG2	2.89	0.54
5:F:46:ALA:O	5:F:50:GLN:HB3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:133:GLU:HA	5:F:136:LYS:HD3	1.88	0.54
5:F:349:GLU:O	5:F:480:ARG:NH2	2.40	0.54
1:Z:262:SER:O	1:Z:266:LYS:NZ	2.41	0.54
1:Z:462:PHE:HA	1:Z:465:ILE:HD12	1.89	0.54
1:Z:463:GLN:HE21	1:Z:487:LEU:HD11	1.72	0.54
1:A:116:LYS:O	1:A:116:LYS:HD3	2.08	0.54
1:A:814:MET:HG2	1:A:833:ILE:CG1	2.37	0.54
3:D:103:LEU:HG	3:D:107:TYR:CE2	2.41	0.54
3:D:443:GLY:HA2	3:D:490:LYS:HG3	1.90	0.54
4:E:210:ASN:CA	4:E:213:PHE:CB	2.76	0.54
4:E:333:ARG:NH1	4:E:341:PHE:O	2.40	0.54
5:F:389:LEU:H	5:F:389:LEU:CD1	2.16	0.54
8:L:645:THR:O	8:L:649:THR:HG23	2.08	0.54
2:C:786:THR:H	2:C:789:ASP:HB2	1.72	0.54
2:C:1258:GLN:CG	2:C:1299:LYS:HE3	2.36	0.54
3:D:784:ILE:O	3:D:949:PHE:HB2	2.08	0.54
5:F:354:ARG:CB	5:F:354:ARG:CZ	2.86	0.54
6:J:405:LEU:CD1	7:K:470:ALA:HA	2.38	0.54
1:Z:779:LEU:CB	1:Z:835:ILE:HA	2.37	0.54
1:A:391:HIS:NE2	1:A:416:GLY:O	2.33	0.54
3:D:403:GLY:O	3:D:408:ARG:NE	2.37	0.54
4:E:180:LYS:NZ	4:E:184:ASP:OD1	2.40	0.54
5:F:1498:LEU:HG	5:F:1514:GLU:HB3	1.88	0.54
1:Z:789:LEU:HB3	1:Z:799:LYS:HD2	1.90	0.54
1:A:691:ARG:O	1:A:695:ILE:HG12	2.07	0.54
3:D:222:ASN:HB3	3:D:301:SER:HA	1.90	0.54
3:D:662:LEU:HB3	3:D:667:LEU:HD13	1.90	0.54
4:E:885:VAL:HG21	4:E:923:LEU:HD21	1.90	0.54
5:F:1550:LEU:CD1	5:F:1604:ILE:HG21	2.38	0.54
5:F:1635:ARG:O	5:F:1639:GLY:N	2.40	0.54
7:H:298:SER:HA	7:H:306:THR:HA	1.90	0.54
7:H:426:GLY:HA3	8:I:735:ASN:C	2.27	0.54
6:J:382:LYS:HE2	6:J:382:LYS:N	2.22	0.54
7:K:433:GLU:HB2	8:L:741:ARG:HH11	1.73	0.54
3:D:284:PHE:CE1	3:D:296:LEU:HG	2.42	0.54
1:A:545:PHE:HD2	1:A:549:ASP:HB2	1.74	0.53
4:E:463:PHE:O	4:E:554:ILE:HA	2.07	0.53
5:F:1363:ILE:HG23	1:Z:125:ILE:HD12	1.89	0.53
5:F:1363:ILE:CG2	1:Z:125:ILE:CD1	2.85	0.53
6:G:295:LYS:HD3	6:J:363:LYS:HZ3	1.72	0.53
8:I:814:LEU:HD21	1:Z:59:LYS:CA	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:814:MET:HG3	1:A:833:ILE:HD13	1.79	0.53
4:E:757:LYS:HA	5:F:1195:PHE:CD2	2.43	0.53
4:E:1290:SER:OG	4:E:1297:LYS:NZ	2.40	0.53
4:E:1319:LEU:HD22	4:E:1394:LYS:HB3	1.90	0.53
5:F:334:GLN:HG3	5:F:854:GLU:CD	2.18	0.53
5:F:1283:LYS:CE	5:F:1283:LYS:CA	2.84	0.53
8:I:785:ASN:CB	1:Z:112:TYR:CB	2.85	0.53
1:Z:674:LEU:HD21	1:Z:724:ARG:HG3	1.90	0.53
2:C:197:ILE:HD13	2:C:224:VAL:HG11	1.91	0.53
3:D:440:THR:OG1	3:D:444:VAL:HG12	2.07	0.53
5:F:44:ASN:OD1	5:F:44:ASN:N	2.40	0.53
5:F:333:GLU:C	5:F:335:ASP:N	2.61	0.53
1:A:255:GLU:OE2	1:A:480:GLN:NE2	2.40	0.53
2:C:172:CYS:HB2	2:C:183:TRP:CE2	2.44	0.53
2:C:786:THR:N	2:C:789:ASP:HB2	2.24	0.53
4:E:29:VAL:HG12	4:E:32:VAL:HG11	1.91	0.53
4:E:170:MET:HA	4:E:173:ILE:HG22	1.89	0.53
5:F:1014:SER:N	8:I:788:ASP:O	2.41	0.53
7:K:321:ALA:HA	7:K:348:ILE:HG13	1.76	0.53
7:K:337:GLN:O	7:K:341:LYS:CD	2.56	0.53
4:E:826:SER:OG	4:E:844:TYR:OH	2.26	0.53
4:E:1531:SER:O	4:E:1535:ASN:ND2	2.42	0.53
5:F:286:ILE:HA	5:F:289:CYS:HB2	1.91	0.53
5:F:824:ALA:O	5:F:826:PRO:N	2.41	0.53
5:F:1024:LEU:HD22	5:F:1049:LEU:HD23	1.90	0.53
6:G:296:ALA:HA	6:J:363:LYS:CE	2.39	0.53
1:Z:127:GLN:HA	1:Z:127:GLN:NE2	2.16	0.53
3:D:585:ILE:HG21	3:D:593:VAL:HB	1.90	0.53
4:E:1341:GLU:OE1	4:E:1346:LYS:NZ	2.42	0.53
5:F:427:THR:OG1	5:F:428:GLN:NE2	2.41	0.53
5:F:835:LYS:O	5:F:838:LYS:N	2.42	0.53
5:F:909:LEU:O	7:H:403:SER:C	2.47	0.53
5:F:917:PHE:CE2	5:F:922:LEU:HD21	2.43	0.53
7:K:367:GLU:O	7:K:371:GLN:HG3	2.09	0.53
8:L:751:LEU:HA	8:L:755:LEU:HD13	1.90	0.53
1:A:625:GLU:OE1	1:A:629:ARG:NH2	2.33	0.53
3:D:606:GLN:N	3:D:642:LEU:O	2.36	0.53
4:E:607:SER:OG	4:E:608:ILE:N	2.40	0.53
4:E:715:THR:HB	4:E:742:LEU:HD22	1.90	0.53
4:E:1234:LEU:HD12	4:E:1287:ILE:HG13	1.90	0.53
4:E:1259:PHE:CD1	4:E:1259:PHE:C	2.82	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:1382:THR:OG1	4:E:1383:GLN:NE2	2.41	0.53
5:F:159:LYS:CE	5:F:363:ASP:HA	2.26	0.53
5:F:333:GLU:C	5:F:335:ASP:H	2.11	0.53
5:F:936:ILE:O	5:F:940:ASN:ND2	2.42	0.53
5:F:1634:LYS:O	5:F:1638:ILE:N	2.34	0.53
6:G:327:LYS:HZ2	1:Z:46:ILE:CA	2.18	0.53
7:K:394:THR:HB	7:K:398:ILE:HG13	1.90	0.53
7:K:427:LEU:N	7:K:428:PRO:CD	2.72	0.53
1:A:767:ILE:O	1:A:771:ILE:HG12	2.08	0.53
3:D:515:VAL:CG1	3:D:644:SER:HB3	2.32	0.53
3:D:576:LEU:HD13	3:D:601:THR:O	2.08	0.53
5:F:320:GLU:OE1	5:F:351:HIS:HE1	1.92	0.53
6:G:465:LYS:HB3	1:Z:20:LYS:NZ	2.20	0.53
6:J:389:ARG:CB	6:J:389:ARG:CZ	2.84	0.53
6:J:429:LEU:HA	6:J:434:THR:N	2.24	0.53
6:J:433:LYS:CB	7:K:499:GLY:CA	2.81	0.53
7:K:311:PHE:CD2	7:K:341:LYS:NZ	2.58	0.53
3:D:150:LYS:HD3	3:D:153:VAL:CG2	2.39	0.53
4:E:258:ILE:O	4:E:261:ILE:N	2.41	0.53
5:F:1370:LEU:O	5:F:1371:ILE:CG1	2.56	0.53
8:I:752:ASP:O	8:I:756:ASN:ND2	2.42	0.53
7:K:483:VAL:H	7:K:494:MET:N	2.07	0.53
1:Z:87:ILE:N	1:Z:87:ILE:CD1	2.72	0.53
1:Z:623:ILE:HG23	1:Z:624:THR:HG23	1.91	0.53
1:A:289:LEU:HD22	1:A:308:PHE:HA	1.91	0.53
1:A:451:ASP:O	1:A:456:ARG:NE	2.38	0.53
1:A:681:SER:HB2	1:A:691:ARG:HD3	1.91	0.53
4:E:107:SER:HB2	4:E:190:GLN:HE22	1.74	0.53
5:F:902:LYS:CE	7:H:414:LYS:CD	2.46	0.53
6:J:310:ARG:HG2	6:J:314:TYR:CZ	2.44	0.53
6:J:390:ILE:N	6:J:390:ILE:CD1	2.72	0.53
7:K:511:GLU:O	7:K:515:ASN:ND2	2.42	0.53
1:Z:127:GLN:CA	1:Z:127:GLN:NE2	2.72	0.53
1:Z:799:LYS:HA	1:Z:802:GLN:HE21	1.73	0.53
1:A:83:VAL:HA	1:A:86:PHE:CD2	2.43	0.52
1:A:812:GLN:HA	1:A:815:ILE:HD12	1.91	0.52
3:D:470:SER:HB3	3:D:475:GLU:CG	2.39	0.52
3:D:775:LEU:O	3:D:779:ARG:HG3	2.08	0.52
4:E:864:SER:OG	4:E:1147:LEU:O	2.24	0.52
5:F:1037:ASN:N	5:F:1040:THR:CB	2.69	0.52
5:F:1098:SER:O	5:F:1101:ILE:HB	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1672:MET:CB	1:Z:149:ALA:CB	2.84	0.52
6:G:427:GLU:HG2	8:I:779:THR:HG21	1.90	0.52
7:K:385:GLN:CA	7:K:385:GLN:NE2	2.72	0.52
1:Z:289:LEU:HD23	1:Z:308:PHE:HA	1.91	0.52
1:Z:807:LYS:O	1:Z:836:ASP:O	2.27	0.52
1:A:48:GLU:O	7:K:514:THR:HG23	2.09	0.52
1:A:590:LEU:HD13	1:A:624:THR:HG23	1.92	0.52
1:A:772:PRO:HA	1:A:828:THR:HG21	1.87	0.52
2:C:693:LEU:HB3	2:C:694:PHE:HD1	1.74	0.52
4:E:368:ILE:HG22	4:E:369:LEU:HD12	1.92	0.52
4:E:1170:ASP:O	4:E:1174:ASN:ND2	2.42	0.52
5:F:812:CYS:SG	5:F:813:GLU:N	2.83	0.52
5:F:1360:LEU:CD1	5:F:1360:LEU:N	2.73	0.52
7:H:303:THR:OG1	7:H:329:HIS:O	2.22	0.52
6:J:384:LEU:HD21	7:K:455:LYS:HG2	1.91	0.52
6:J:388:CYS:CB	7:K:455:LYS:HD2	2.32	0.52
1:A:643:LEU:O	1:A:647:ALA:N	2.38	0.52
2:C:1261:PHE:CZ	2:C:1265:ILE:HD11	2.43	0.52
4:E:584:ASP:N	4:E:584:ASP:OD1	2.38	0.52
4:E:739:ILE:HG21	4:E:795:ILE:HG22	1.92	0.52
4:E:789:GLN:OE1	4:E:792:GLN:NE2	2.40	0.52
4:E:954:ILE:HG12	4:E:1015:LYS:HG2	1.92	0.52
4:E:1563:LEU:HD12	4:E:1564:LEU:HG	1.92	0.52
5:F:920:ILE:HG13	5:F:924:ALA:HA	1.89	0.52
5:F:1522:VAL:HA	5:F:1525:LEU:HD12	1.91	0.52
8:I:778:LYS:HG2	8:I:794:ILE:CB	2.39	0.52
6:J:311:ASP:HA	6:J:314:TYR:CD2	2.43	0.52
6:J:324:GLN:O	6:J:328:GLN:HG2	2.09	0.52
1:Z:536:ASN:O	1:Z:540:ASN:ND2	2.42	0.52
3:D:421:VAL:HG13	3:D:491:ARG:CB	2.40	0.52
3:D:664:ASP:O	3:D:667:LEU:N	2.42	0.52
4:E:989:ASP:O	4:E:992:SER:N	2.36	0.52
4:E:1409:ALA:HB1	4:E:1459:LYS:HG3	1.90	0.52
5:F:210:LYS:HG2	5:F:214:LEU:HD13	1.92	0.52
5:F:922:LEU:N	5:F:922:LEU:CD1	2.72	0.52
5:F:1392:ILE:CB	5:F:1405:PHE:CE2	2.93	0.52
5:F:1634:LYS:HD3	5:F:1638:ILE:HD12	1.91	0.52
8:I:805:ARG:CB	1:Z:88:LYS:HZ1	2.22	0.52
1:A:274:GLY:HA2	1:A:484:LEU:HD22	1.91	0.52
3:D:1467:SER:HB2	1:Z:621:HIS:CE1	2.45	0.52
4:E:724:SER:HA	4:E:1166:VAL:HA	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1094:GLY:O	5:F:1098:SER:N	2.42	0.52
5:F:1529:ALA:HB1	5:F:1611:VAL:HG13	1.83	0.52
6:J:406:PHE:O	6:J:409:PRO:HD2	2.09	0.52
3:D:186:ILE:CG2	3:D:189:LYS:HB2	2.40	0.52
3:D:662:LEU:HB3	3:D:667:LEU:CD1	2.40	0.52
4:E:33:ASP:OD1	4:E:33:ASP:N	2.42	0.52
5:F:154:GLN:HA	5:F:157:GLU:HG3	1.92	0.52
5:F:757:PHE:HD1	5:F:780:ILE:HD11	1.74	0.52
5:F:1027:GLN:CG	5:F:1036:PRO:HA	2.37	0.52
5:F:1251:ARG:NH2	5:F:1276:ASP:HB3	2.25	0.52
8:I:781:ASN:HD22	8:I:781:ASN:N	2.08	0.52
8:I:814:LEU:HD23	1:Z:59:LYS:CB	2.39	0.52
6:J:364:ILE:HG22	6:J:367:ASN:HD21	1.75	0.52
6:J:432:LEU:HA	8:L:782:ILE:O	2.10	0.52
7:K:352:ILE:HG21	7:K:358:LEU:CD2	2.40	0.52
8:L:692:LYS:HD2	8:L:695:GLN:HE21	1.75	0.52
1:A:140:ILE:CG2	4:E:1393:LYS:NZ	2.61	0.52
3:D:944:LEU:O	3:D:947:LEU:HB2	2.10	0.52
5:F:389:LEU:N	5:F:389:LEU:CD1	2.72	0.52
5:F:1360:LEU:C	5:F:1362:ASP:H	2.13	0.52
5:F:1605:PHE:HA	5:F:1608:ILE:HG12	1.91	0.52
7:H:522:TYR:CB	1:Z:54:PHE:C	2.77	0.52
6:J:332:LYS:HG2	7:K:398:ILE:HG21	1.91	0.52
7:K:309:ARG:HG3	7:K:353:TYR:CZ	2.44	0.52
4:E:141:LEU:HA	4:E:144:ILE:HD12	1.92	0.52
4:E:827:PRO:HB3	4:E:893:TYR:CZ	2.44	0.52
4:E:1005:LEU:HD13	4:E:1046:LYS:HZ1	1.75	0.52
5:F:690:GLU:HG2	8:I:722:LEU:HD21	1.92	0.52
5:F:711:GLN:HG2	5:F:779:PRO:HB3	1.92	0.52
5:F:1664:ASN:HA	5:F:1667:VAL:HG12	1.92	0.52
8:I:795:LYS:CA	8:I:795:LYS:NZ	2.73	0.52
8:L:692:LYS:HD2	8:L:695:GLN:NE2	2.25	0.52
1:Z:414:LEU:HD11	1:Z:438:MET:HB2	1.92	0.52
1:A:687:LEU:HD23	1:A:690:ARG:HH11	1.74	0.52
3:D:233:LEU:HD11	3:D:282:ILE:HD13	1.92	0.52
3:D:969:SER:O	3:D:972:ASN:HB2	2.10	0.52
4:E:976:PHE:CZ	7:K:457:ASN:HB3	2.44	0.52
5:F:837:TYR:CD2	5:F:918:PHE:CE2	2.97	0.52
5:F:1227:THR:HA	7:H:472:ASN:HB3	1.92	0.52
7:H:314:ASN:HB2	7:H:361:ARG:HH12	1.75	0.52
7:K:387:GLN:NE2	7:K:387:GLN:CA	2.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:444:LEU:C	7:K:447:SER:CB	2.75	0.52
3:D:792:THR:HA	3:D:830:SER:HB2	1.92	0.52
4:E:1268:SER:OG	4:E:1269:GLY:N	2.42	0.52
5:F:639:LEU:HA	5:F:642:PHE:HB3	1.91	0.52
5:F:836:ILE:N	5:F:836:ILE:CD1	2.72	0.52
5:F:958:SER:HB3	5:F:962:ARG:HA	1.91	0.52
6:G:295:LYS:C	6:J:363:LYS:HZ1	2.12	0.52
7:H:391:GLU:O	7:H:395:ALA:HB3	2.10	0.52
6:J:442:THR:CB	7:K:509:ILE:CD1	2.88	0.52
1:Z:215:TYR:HA	1:Z:218:ILE:HD12	1.92	0.52
3:D:160:ILE:CG2	3:D:191:ILE:HG21	2.37	0.51
4:E:681:LEU:HA	4:E:690:LEU:CB	2.40	0.51
5:F:177:GLN:O	5:F:181:PHE:HB2	2.10	0.51
5:F:328:ASP:O	5:F:331:ILE:HD11	2.09	0.51
5:F:543:VAL:HA	5:F:546:TYR:HB2	1.91	0.51
5:F:690:GLU:HG3	8:I:722:LEU:CG	2.40	0.51
5:F:1067:ASN:N	5:F:1067:ASN:OD1	2.42	0.51
6:G:387:TYR:HA	6:G:390:ILE:HB	1.92	0.51
8:I:818:ILE:CD1	8:I:818:ILE:N	2.72	0.51
1:Z:482:LEU:O	1:Z:487:LEU:N	2.43	0.51
1:Z:767:ILE:HD12	1:Z:768:VAL:H	1.74	0.51
1:A:641:ILE:HG23	1:A:653:VAL:HG13	1.91	0.51
3:D:263:VAL:HB	3:D:311:LYS:CE	2.37	0.51
3:D:501:SER:O	3:D:508:LYS:NZ	2.41	0.51
4:E:207:ASP:OD1	4:E:207:ASP:N	2.40	0.51
5:F:1150:PHE:CD1	5:F:1150:PHE:C	2.83	0.51
7:H:309:ARG:NE	7:H:353:TYR:OH	2.37	0.51
6:J:433:LYS:CA	7:K:499:GLY:CA	2.88	0.51
7:K:337:GLN:O	7:K:341:LYS:HD3	2.10	0.51
8:L:675:GLN:O	8:L:679:LEU:HD13	2.10	0.51
1:Z:391:HIS:NE2	1:Z:417:ARG:O	2.42	0.51
1:Z:431:SER:OG	1:Z:432:ILE:N	2.42	0.51
1:A:128:LEU:HB3	4:E:1260:TYR:CE2	2.40	0.51
3:D:915:GLU:OE2	3:D:980:SER:OG	2.23	0.51
5:F:157:GLU:OE1	5:F:183:ARG:NH1	2.42	0.51
5:F:355:LEU:N	5:F:355:LEU:CD1	2.72	0.51
5:F:809:LEU:HD13	5:F:1252:VAL:HG23	1.93	0.51
5:F:1427:LEU:HD22	5:F:1466:LEU:HG	1.91	0.51
5:F:1496:ASP:HA	5:F:1499:LEU:HG	1.93	0.51
5:F:1550:LEU:HD12	5:F:1604:ILE:HD13	1.87	0.51
6:J:383:LYS:CE	8:L:756:ASN:HA	2.23	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:390:ILE:CG1	8:L:766:ILE:HD12	2.40	0.51
1:Z:670:LEU:HD13	1:Z:724:ARG:HD3	1.92	0.51
2:C:885:VAL:CG1	2:C:901:ILE:HG23	2.39	0.51
3:D:240:LEU:HB3	3:D:263:VAL:CG1	2.40	0.51
3:D:484:GLN:HG3	3:D:564:THR:O	2.10	0.51
3:D:484:GLN:NE2	3:D:565:VAL:HA	2.24	0.51
5:F:343:ASP:OD2	5:F:702:LYS:NZ	2.38	0.51
5:F:1177:VAL:HA	5:F:1180:TYR:CB	2.41	0.51
5:F:1363:ILE:HD12	5:F:1364:TYR:N	2.25	0.51
7:H:397:ARG:NH1	8:I:701:GLU:OE1	2.43	0.51
1:Z:139:PHE:CD1	1:Z:139:PHE:C	2.84	0.51
1:A:817:ALA:HB2	1:A:832:LEU:HD13	1.92	0.51
3:D:863:ILE:HD12	3:D:887:GLN:HG3	1.92	0.51
4:E:86:ASP:OD1	4:E:86:ASP:N	2.44	0.51
4:E:508:ALA:HB1	4:E:512:GLU:HG2	1.93	0.51
5:F:929:TYR:O	5:F:931:GLY:N	2.43	0.51
5:F:1132:GLU:HG3	5:F:1135:CYS:HB2	1.93	0.51
5:F:1439:GLU:HA	5:F:1442:TRP:HB3	1.93	0.51
6:J:382:LYS:N	6:J:382:LYS:CE	2.73	0.51
7:K:321:ALA:HB2	7:K:346:GLN:HA	1.92	0.51
1:Z:734:GLU:OE2	1:Z:738:GLN:NE2	2.43	0.51
1:A:48:GLU:HA	7:K:514:THR:HG21	1.93	0.51
1:A:139:PHE:CD1	1:A:139:PHE:C	2.84	0.51
3:D:377:ILE:HB	3:D:393:ILE:HB	1.93	0.51
4:E:1340:PHE:O	4:E:1344:PHE:HB2	2.11	0.51
4:E:1342:LEU:HA	4:E:1346:LYS:HD3	1.92	0.51
5:F:544:TYR:HA	5:F:547:PHE:HD2	1.76	0.51
5:F:920:ILE:HB	5:F:924:ALA:CA	2.41	0.51
5:F:950:GLU:N	5:F:950:GLU:OE2	2.43	0.51
1:A:760:PHE:CZ	1:A:768:VAL:HG13	2.45	0.51
3:D:832:VAL:HG23	3:D:929:PHE:CE2	2.46	0.51
4:E:550:SER:OG	4:E:551:ASN:N	2.44	0.51
5:F:378:ALA:O	5:F:383:ASN:HA	2.11	0.51
7:K:308:LEU:HB3	7:K:355:PHE:CZ	2.46	0.51
1:Z:23:ASN:C	1:Z:25:LEU:N	2.64	0.51
1:A:621:HIS:ND1	1:A:625:GLU:OE2	2.32	0.51
3:D:170:LYS:NZ	3:D:212:GLN:O	2.37	0.51
3:D:242:MET:O	3:D:259:THR:OG1	2.21	0.51
3:D:568:GLN:HE21	3:D:573:GLN:HG2	1.76	0.51
3:D:790:PHE:HB3	3:D:933:ILE:HG21	1.92	0.51
3:D:887:GLN:OE1	3:D:887:GLN:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:332:VAL:CG1	5:F:335:ASP:HA	2.40	0.51
5:F:838:LYS:HA	5:F:841:PHE:HB2	1.92	0.51
5:F:1012:ASN:O	8:I:787:GLU:CG	2.52	0.51
6:J:437:ALA:O	6:J:439:ILE:N	2.44	0.51
8:L:643:LYS:HG3	8:L:647:GLN:NE2	2.22	0.51
2:C:1258:GLN:CD	2:C:1299:LYS:HE3	2.31	0.51
3:D:421:VAL:HG13	3:D:491:ARG:HB3	1.92	0.51
5:F:841:PHE:HZ	5:F:922:LEU:HD22	1.75	0.51
5:F:914:ASP:HA	5:F:917:PHE:H	1.76	0.51
5:F:1300:LEU:HD23	5:F:1300:LEU:C	2.31	0.51
7:K:389:LYS:CB	7:K:393:ASP:CB	2.88	0.51
1:A:123:MET:O	6:J:414:SER:CB	2.59	0.51
3:D:528:PRO:CG	3:D:624:PHE:HE2	2.21	0.51
4:E:182:PHE:HZ	5:F:1189:MET:CB	2.23	0.51
5:F:334:GLN:NE2	5:F:859:LYS:HD2	2.26	0.51
5:F:452:LYS:HE3	5:F:456:ALA:HB2	1.92	0.51
5:F:1510:ASP:N	5:F:1510:ASP:OD1	2.42	0.51
5:F:1532:ARG:NH1	5:F:1615:MET:SD	2.84	0.51
8:I:794:ILE:HA	8:I:797:LEU:HD13	1.93	0.51
7:K:365:GLN:HA	7:K:368:ASN:HD22	1.76	0.51
1:A:193:LEU:HB3	1:A:546:ARG:HH12	1.76	0.50
1:A:837:VAL:HG11	2:C:1142:ASP:HB2	1.93	0.50
4:E:757:LYS:HA	5:F:1195:PHE:HD2	1.76	0.50
4:E:810:MET:SD	4:E:810:MET:N	2.84	0.50
4:E:1402:LYS:NZ	4:E:1454:GLU:OE1	2.43	0.50
5:F:726:SER:O	5:F:726:SER:OG	2.27	0.50
5:F:836:ILE:N	5:F:836:ILE:HD12	2.26	0.50
6:G:350:PHE:CZ	7:H:418:GLN:NE2	2.79	0.50
8:I:643:LYS:O	8:I:647:GLN:NE2	2.44	0.50
1:Z:278:LEU:HD22	1:Z:437:TRP:HB2	1.92	0.50
1:A:787:HIS:HE1	1:A:838:SER:O	1.90	0.50
2:C:970:PHE:CE2	2:C:974:ILE:HD11	2.46	0.50
3:D:353:GLN:OE1	3:D:374:LYS:HB2	2.11	0.50
3:D:970:ILE:HG23	3:D:975:ILE:CD1	2.40	0.50
5:F:713:PHE:HA	5:F:716:LEU:HB2	1.93	0.50
5:F:1370:LEU:O	5:F:1371:ILE:CB	2.59	0.50
5:F:1618:SER:HB2	1:Z:634:ASP:O	2.10	0.50
5:F:1674:CYS:C	5:F:1676:LEU:H	2.13	0.50
6:J:310:ARG:NE	6:J:314:TYR:OH	2.44	0.50
6:J:404:ASP:O	6:J:408:ALA:HB2	2.11	0.50
6:J:462:GLN:HE22	8:L:812:THR:HG23	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:535:LYS:CA	8:L:818:ILE:CB	2.75	0.50
1:A:224:ASN:OD1	1:A:607:ARG:NH2	2.41	0.50
1:A:414:LEU:HD21	1:A:438:MET:HB2	1.94	0.50
2:C:317:LEU:HB2	2:C:318:ILE:HD12	1.92	0.50
3:D:507:LEU:HA	3:D:512:LYS:O	2.12	0.50
5:F:355:LEU:HD12	5:F:355:LEU:H	1.74	0.50
5:F:681:LYS:HE3	5:F:685:LEU:HA	1.93	0.50
5:F:968:ILE:CG2	7:H:392:LEU:HD11	2.36	0.50
7:K:355:PHE:CD1	7:K:358:LEU:HD12	2.45	0.50
8:L:647:GLN:HA	8:L:650:GLU:HG2	1.93	0.50
8:L:671:LYS:O	8:L:675:GLN:HG2	2.10	0.50
1:Z:251:ALA:O	1:Z:253:LEU:CA	2.54	0.50
1:Z:639:ASP:OD1	1:Z:639:ASP:N	2.43	0.50
1:A:626:GLN:O	1:A:630:ARG:HG2	2.11	0.50
3:D:586:LEU:HD21	3:D:592:TYR:HD1	1.76	0.50
3:D:828:ILE:CD1	3:D:925:GLN:HA	2.41	0.50
3:D:873:SER:CB	3:D:877:VAL:HB	2.42	0.50
4:E:1259:PHE:O	4:E:1259:PHE:HD1	1.94	0.50
4:E:1294:ASP:O	4:E:1298:ASN:N	2.42	0.50
5:F:1088:ARG:NH1	5:F:1088:ARG:CG	2.73	0.50
5:F:1373:ASP:O	5:F:1376:THR:N	2.28	0.50
8:I:742:GLN:HB3	8:I:746:LYS:HZ2	1.76	0.50
8:L:637:LEU:HD22	8:L:640:LEU:HB2	1.92	0.50
1:A:27:GLU:OE2	1:A:30:ASP:HB2	2.11	0.50
1:A:684:ASN:HB3	1:A:687:LEU:HB2	1.93	0.50
3:D:518:GLU:HA	3:D:536:ILE:CD1	2.41	0.50
5:F:665:GLU:HB2	5:F:720:HIS:NE2	2.25	0.50
5:F:1167:LYS:HD3	5:F:1167:LYS:C	2.30	0.50
5:F:1472:GLU:OE1	5:F:1531:THR:OG1	2.25	0.50
5:F:1502:THR:H	5:F:1510:ASP:HB2	1.77	0.50
6:G:465:LYS:HB3	1:Z:20:LYS:CE	2.42	0.50
6:G:470:LEU:CB	7:H:538:LYS:HZ1	1.94	0.50
6:J:389:ARG:NH1	6:J:389:ARG:CG	2.72	0.50
6:J:390:ILE:N	6:J:390:ILE:HD12	2.26	0.50
7:K:313:TYR:CD1	7:K:349:PRO:HB3	2.45	0.50
7:K:336:ASP:HB3	7:K:340:GLU:OE1	2.11	0.50
7:K:375:ILE:O	7:K:379:ILE:HG22	2.11	0.50
7:K:456:THR:C	7:K:458:GLU:N	2.64	0.50
1:A:599:ARG:NH1	1:A:605:GLU:OE2	2.44	0.50
3:D:358:GLN:OE1	3:D:422:LYS:HG3	2.11	0.50
4:E:1275:GLU:HA	4:E:1278:ILE:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:359:ASN:HA	7:H:362:ASN:HD22	1.75	0.50
7:H:412:ILE:HG22	7:H:415:LEU:HD23	1.94	0.50
6:J:281:ASP:O	6:J:284:ILE:HB	2.11	0.50
7:K:536:LYS:HA	7:K:539:ASN:HB2	1.94	0.50
5:F:838:LYS:O	5:F:842:ASN:HB2	2.12	0.50
5:F:1674:CYS:C	5:F:1676:LEU:N	2.65	0.50
1:A:137:ASP:OD2	4:E:1385:LEU:HD12	2.11	0.50
4:E:200:LEU:HD13	4:E:271:LEU:HD22	1.94	0.50
7:H:317:ASN:HA	7:H:346:GLN:HB3	1.94	0.50
7:K:402:GLN:HE21	7:K:402:GLN:C	2.14	0.50
8:L:650:GLU:HG3	8:L:651:SER:N	2.27	0.50
1:Z:440:LEU:HA	1:Z:443:ILE:HG12	1.94	0.50
1:Z:771:ILE:CB	1:Z:772:PRO:HD2	2.42	0.50
1:A:516:PHE:HZ	1:A:532:ILE:HG22	1.76	0.50
1:A:814:MET:HB2	1:A:836:ASP:OD2	2.11	0.50
4:E:185:LEU:HD23	4:E:188:ILE:HD11	1.94	0.50
5:F:900:LEU:HD22	5:F:904:TYR:CZ	2.47	0.50
8:I:750:THR:O	8:I:753:GLU:HB3	2.11	0.50
6:J:277:ILE:CD1	6:J:280:LEU:HD23	2.42	0.50
7:K:289:GLN:O	7:K:292:VAL:HB	2.11	0.50
8:L:667:GLN:NE2	8:L:668:VAL:HG23	2.26	0.50
1:Z:533:ARG:HH21	1:Z:534:PHE:HB3	1.76	0.50
1:Z:771:ILE:HG22	1:Z:772:PRO:HD3	1.94	0.50
4:E:411:PHE:O	4:E:415:PHE:HB3	2.11	0.49
4:E:1429:HIS:HD2	4:E:1474:LEU:HD22	1.77	0.49
5:F:669:THR:HA	5:F:672:TRP:HB2	1.94	0.49
5:F:1370:LEU:O	5:F:1371:ILE:HB	2.12	0.49
7:H:443:LEU:HA	7:H:446:ARG:HB2	1.94	0.49
8:I:739:GLN:C	8:I:741:ARG:N	2.61	0.49
8:I:822:LYS:CE	8:I:822:LYS:CA	2.84	0.49
6:J:370:ASP:HA	6:J:373:PHE:CB	2.40	0.49
7:K:429:LEU:HB2	8:L:741:ARG:CZ	2.42	0.49
8:L:637:LEU:CD2	8:L:640:LEU:H	2.24	0.49
8:L:692:LYS:O	8:L:695:GLN:HG3	2.11	0.49
1:Z:136:PHE:C	1:Z:136:PHE:CD1	2.85	0.49
1:Z:576:LEU:HA	1:Z:579:LEU:HB2	1.94	0.49
3:D:449:ASN:HB3	3:D:463:GLU:CG	2.41	0.49
3:D:932:ILE:CG2	3:D:933:ILE:HG13	2.41	0.49
4:E:477:LEU:HA	4:E:499:ILE:HA	1.94	0.49
4:E:725:LEU:HD23	4:E:1167:LEU:HA	1.93	0.49
5:F:50:GLN:NE2	5:F:57:GLU:OE2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:616:VAL:HG12	5:F:656:VAL:HG21	1.92	0.49
5:F:684:SER:HB3	5:F:695:ALA:HB2	1.94	0.49
5:F:1529:ALA:HB2	5:F:1611:VAL:CG2	2.42	0.49
8:I:740:LYS:O	8:I:743:GLN:NE2	2.45	0.49
6:J:309:PRO:O	6:J:312:VAL:HB	2.12	0.49
6:J:364:ILE:C	7:K:424:ASN:HD22	2.15	0.49
3:D:412:ILE:HG22	3:D:476:VAL:HB	1.93	0.49
5:F:555:TRP:HA	5:F:558:ILE:HG12	1.94	0.49
5:F:668:ARG:O	5:F:672:TRP:HB2	2.12	0.49
5:F:1543:LEU:O	5:F:1547:ILE:HG22	2.12	0.49
6:G:427:GLU:CG	8:I:779:THR:HG21	2.41	0.49
6:G:431:GLN:CB	7:H:503:ASN:H	2.22	0.49
8:I:795:LYS:HE3	8:I:799:SER:HB3	1.94	0.49
8:L:696:SER:O	8:L:699:TYR:HB2	2.11	0.49
1:Z:25:LEU:HD23	1:Z:25:LEU:C	2.33	0.49
1:A:764:ASP:O	1:A:768:VAL:HG23	2.12	0.49
1:A:818:GLY:O	1:A:821:GLN:NE2	2.40	0.49
3:D:119:PRO:HB3	3:D:739:THR:CG2	2.42	0.49
3:D:442:GLY:HA2	3:D:488:GLN:HG2	1.94	0.49
4:E:114:TYR:HB2	4:E:194:ILE:HD11	1.93	0.49
4:E:476:ASP:OD1	4:E:476:ASP:N	2.45	0.49
5:F:806:LEU:O	5:F:814:ASN:CB	2.60	0.49
5:F:1357:ALA:HA	5:F:1381:LEU:CB	2.42	0.49
5:F:1469:ARG:HH22	5:F:1530:GLU:HB3	1.76	0.49
5:F:1667:VAL:HA	5:F:1670:ILE:HG22	1.95	0.49
8:I:822:LYS:NZ	8:I:822:LYS:CA	2.73	0.49
6:J:433:LYS:CA	7:K:499:GLY:HA3	2.42	0.49
7:K:315:LYS:HA	7:K:347:THR:CA	2.38	0.49
1:A:23:ASN:C	1:A:25:LEU:N	2.64	0.49
1:A:205:ASN:OD1	1:A:208:LEU:HB2	2.12	0.49
1:A:505:HIS:HE1	1:A:541:TYR:OH	1.96	0.49
1:A:558:VAL:HG22	1:A:611:LEU:HD21	1.93	0.49
3:D:375:SER:HB3	3:D:420:ILE:HG13	1.94	0.49
4:E:1017:LEU:O	4:E:1021:THR:OG1	2.26	0.49
5:F:900:LEU:HD13	5:F:904:TYR:CE1	2.47	0.49
5:F:913:TYR:O	5:F:917:PHE:N	2.46	0.49
5:F:1092:THR:O	5:F:1092:THR:OG1	2.23	0.49
5:F:1139:ILE:HG12	5:F:1291:SER:CB	2.42	0.49
5:F:1628:GLY:O	5:F:1632:THR:HB	2.13	0.49
8:I:816:LYS:HE2	8:I:816:LYS:N	2.28	0.49
1:Z:116:LYS:HZ3	1:Z:116:LYS:CB	2.17	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:820:ILE:O	1:Z:821:GLN:C	2.49	0.49
3:D:491:ARG:CB	3:D:520:THR:HB	2.42	0.49
3:D:631:GLN:NE2	3:D:656:ASP:OD2	2.44	0.49
3:D:653:ARG:HG3	3:D:657:GLU:HB2	1.93	0.49
4:E:27:ALA:O	4:E:119:ASN:ND2	2.45	0.49
4:E:186:LYS:HE2	4:E:834:ILE:HG23	1.95	0.49
4:E:822:ASN:O	4:E:826:SER:HB3	2.13	0.49
4:E:995:LEU:HA	4:E:998:LEU:HB2	1.95	0.49
5:F:973:ASP:O	5:F:975:SER:N	2.44	0.49
5:F:1477:ASP:O	5:F:1481:LYS:N	2.45	0.49
5:F:1550:LEU:HD21	5:F:1552:PHE:HZ	1.66	0.49
5:F:1641:PHE:HA	5:F:1644:ASP:HB2	1.95	0.49
7:H:309:ARG:NH2	7:H:334:GLU:OE2	2.45	0.49
7:H:418:GLN:CD	8:I:718:THR:HG21	2.26	0.49
7:H:511:GLU:CB	8:I:800:HIS:HE1	2.24	0.49
7:H:522:TYR:CB	1:Z:55:GLN:N	2.75	0.49
6:J:398:VAL:CG2	7:K:462:ARG:CA	2.69	0.49
7:K:310:ALA:CB	7:K:352:ILE:HB	2.38	0.49
7:K:504:ASP:O	7:K:507:ASN:N	2.44	0.49
1:Z:771:ILE:CG2	1:Z:772:PRO:HD2	2.42	0.49
1:A:54:PHE:HA	1:A:57:ARG:HD3	1.94	0.49
5:F:334:GLN:HG2	5:F:860:ASN:HD21	1.73	0.49
5:F:472:ILE:HG23	5:F:474:LEU:H	1.76	0.49
5:F:665:GLU:HA	5:F:668:ARG:HG2	1.94	0.49
5:F:959:LEU:CB	6:G:325:TYR:HB2	2.43	0.49
7:H:344:SER:O	7:H:347:THR:OG1	2.31	0.49
3:D:175:ILE:CD1	3:D:642:LEU:HB2	2.36	0.49
3:D:499:LEU:CB	3:D:502:SER:HB3	2.35	0.49
3:D:586:LEU:HD11	3:D:592:TYR:HA	1.94	0.49
3:D:753:PRO:HD2	3:D:756:LYS:CD	2.40	0.49
3:D:896:MET:O	3:D:900:VAL:HG23	2.13	0.49
3:D:971:ILE:HD11	3:D:984:THR:CG2	2.43	0.49
3:D:1494:ASN:O	5:F:1471:LYS:CE	2.59	0.49
5:F:288:TRP:O	5:F:295:ARG:NH2	2.45	0.49
5:F:334:GLN:HE22	5:F:859:LYS:HZ3	1.46	0.49
5:F:1269:GLU:O	5:F:1273:LYS:HB3	2.13	0.49
6:G:449:LEU:HD23	1:Z:84:ASP:OD1	2.12	0.49
6:J:350:PHE:HD1	7:K:419:LEU:HD12	1.73	0.49
8:L:774:ASN:HA	8:L:777:ASN:HB2	1.95	0.49
4:E:1460:LEU:O	4:E:1463:SER:OG	2.31	0.49
5:F:159:LYS:CE	5:F:363:ASP:CA	2.88	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:914:ASP:HA	5:F:917:PHE:HB2	1.93	0.49
7:H:315:LYS:HA	7:H:347:THR:HA	1.95	0.49
6:J:376:LYS:NZ	8:L:756:ASN:ND2	2.57	0.49
7:K:430:GLY:C	7:K:432:ALA:N	2.65	0.49
1:Z:140:ILE:HA	1:Z:143:ASN:HB3	1.93	0.49
1:A:270:ILE:HD13	1:A:486:GLY:HA3	1.95	0.49
3:D:1468:TYR:N	1:Z:621:HIS:CE1	2.77	0.49
4:E:795:ILE:O	4:E:798:SER:OG	2.29	0.49
4:E:994:ILE:HG13	4:E:995:LEU:HD12	1.95	0.49
5:F:161:GLN:HA	5:F:164:LYS:HG3	1.94	0.49
5:F:914:ASP:CA	5:F:917:PHE:CB	2.85	0.49
5:F:1373:ASP:O	5:F:1375:GLY:N	2.45	0.49
5:F:1671:VAL:HG13	1:Z:149:ALA:HB1	1.94	0.49
6:G:395:GLU:HA	6:G:398:VAL:HB	1.95	0.49
6:G:436:LEU:HD13	7:H:503:ASN:CB	2.43	0.49
1:Z:211:LYS:CB	1:Z:246:ASN:O	2.60	0.49
3:D:449:ASN:ND2	3:D:461:ARG:HB2	2.27	0.48
3:D:578:VAL:O	3:D:596:ALA:HA	2.12	0.48
3:D:745:ILE:HG13	3:D:746:THR:H	1.77	0.48
3:D:836:LYS:HB2	3:D:914:TYR:CD1	2.47	0.48
5:F:835:LYS:HD3	5:F:835:LYS:N	2.28	0.48
5:F:1465:GLN:HG3	5:F:1527:ARG:NH2	2.28	0.48
6:J:364:ILE:C	7:K:424:ASN:ND2	2.65	0.48
6:J:380:TYR:O	6:J:380:TYR:CD1	2.66	0.48
7:K:538:LYS:CB	8:L:821:ILE:HG22	2.42	0.48
1:Z:223:ASN:ND2	1:Z:555:GLU:OE2	2.35	0.48
1:Z:275:LYS:NZ	1:Z:441:MET:SD	2.81	0.48
1:A:341:LEU:HD21	1:A:371:PHE:HZ	1.78	0.48
1:A:642:LEU:HA	1:A:645:GLN:CD	2.33	0.48
3:D:421:VAL:HG21	3:D:490:LYS:CB	2.41	0.48
3:D:453:GLY:O	3:D:456:ASN:N	2.45	0.48
3:D:539:SER:HA	3:D:545:GLN:NE2	2.29	0.48
4:E:1598:LEU:O	4:E:1602:LEU:HB2	2.13	0.48
5:F:866:GLN:HA	5:F:869:VAL:HG12	1.95	0.48
5:F:923:VAL:HG23	5:F:925:HIS:H	1.77	0.48
6:G:428:ASN:HD21	6:G:432:LEU:HD23	1.78	0.48
8:L:638:ASP:HA	8:L:641:VAL:CG2	2.42	0.48
2:C:914:GLN:HE21	2:C:953:ILE:HG23	1.78	0.48
3:D:503:GLU:OE1	3:D:508:LYS:HD3	2.14	0.48
3:D:919:VAL:CG2	3:D:927:LEU:H	2.26	0.48
4:E:570:GLN:HE21	4:E:622:LEU:HB3	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1304:HIS:CG	5:F:1304:HIS:O	2.66	0.48
6:G:449:LEU:HD23	1:Z:84:ASP:CB	2.42	0.48
8:I:795:LYS:CE	8:I:799:SER:HB3	2.43	0.48
6:J:370:ASP:HA	6:J:373:PHE:CG	2.48	0.48
1:Z:305:ILE:HG21	1:Z:336:LEU:HA	1.94	0.48
1:A:315:LYS:HD2	1:A:319:SER:OG	2.13	0.48
1:A:571:LEU:O	1:A:574:GLU:HG3	2.13	0.48
3:D:539:SER:HA	3:D:545:GLN:HE22	1.78	0.48
4:E:573:LEU:HD22	4:E:637:VAL:HG13	1.96	0.48
4:E:1063:ASP:N	4:E:1063:ASP:OD1	2.44	0.48
5:F:922:LEU:HD12	5:F:922:LEU:N	2.23	0.48
5:F:951:ARG:NE	5:F:951:ARG:CA	2.76	0.48
1:Z:761:SER:C	1:Z:763:LEU:H	2.15	0.48
1:A:140:ILE:HG22	4:E:1393:LYS:CE	2.43	0.48
1:A:413:LYS:HD2	1:A:425:ILE:HD11	1.94	0.48
3:D:927:LEU:HD13	3:D:973:ARG:NH2	2.29	0.48
4:E:134:ARG:NH1	4:E:198:MET:SD	2.87	0.48
4:E:1259:PHE:C	4:E:1259:PHE:HD1	2.16	0.48
4:E:1384:ASP:HA	4:E:1388:LEU:HB2	1.96	0.48
5:F:291:GLU:HG3	5:F:295:ARG:HG2	1.95	0.48
5:F:1463:LEU:HD12	5:F:1463:LEU:HA	1.73	0.48
6:J:324:GLN:HA	6:J:327:LYS:CE	2.35	0.48
6:J:389:ARG:CZ	6:J:389:ARG:HB3	2.44	0.48
1:Z:494:TYR:O	1:Z:497:THR:OG1	2.27	0.48
1:A:25:LEU:HD23	1:A:25:LEU:C	2.33	0.48
3:D:481:LEU:CD2	3:D:488:GLN:HB3	2.43	0.48
4:E:936:LEU:O	4:E:940:SER:OG	2.26	0.48
5:F:971:SER:OG	5:F:972:VAL:N	2.46	0.48
7:H:292:VAL:HG22	8:I:644:TRP:HZ3	1.79	0.48
8:I:795:LYS:HZ3	8:I:795:LYS:HA	1.78	0.48
7:K:535:LYS:O	7:K:539:ASN:N	2.43	0.48
3:D:491:ARG:HA	3:D:520:THR:HB	1.96	0.48
3:D:976:THR:CB	3:D:981:ILE:CB	2.91	0.48
5:F:927:GLY:HA3	5:F:978:ILE:HD11	1.95	0.48
5:F:1058:ALA:C	5:F:1060:LEU:H	2.16	0.48
6:J:283:TYR:O	6:J:286:LYS:HG2	2.14	0.48
6:J:445:GLU:O	6:J:449:LEU:HB2	2.13	0.48
1:A:829:TYR:CD1	1:A:829:TYR:C	2.85	0.48
3:D:503:GLU:HB2	3:D:507:LEU:N	2.29	0.48
4:E:675:TYR:HA	4:E:678:LYS:HG2	1.96	0.48
5:F:837:TYR:CG	5:F:918:PHE:CZ	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1529:ALA:HB2	5:F:1611:VAL:HG22	1.95	0.48
6:G:465:LYS:HE3	1:Z:20:LYS:HE2	1.94	0.48
8:I:750:THR:O	8:I:754:ASN:ND2	2.46	0.48
8:I:814:LEU:HD21	1:Z:59:LYS:HA	1.96	0.48
6:J:390:ILE:HG23	6:J:394:ILE:HG23	1.94	0.48
7:K:433:GLU:HB3	7:K:437:TRP:CZ3	2.49	0.48
1:Z:341:LEU:HD22	1:Z:415:ILE:HD11	1.96	0.48
1:Z:753:ALA:HB2	1:Z:815:ILE:CB	2.43	0.48
1:Z:767:ILE:HD12	1:Z:768:VAL:HG23	1.95	0.48
1:A:18:ALA:HA	1:A:21:LYS:HB2	1.96	0.48
1:A:128:LEU:CD1	4:E:1260:TYR:OH	2.44	0.48
1:A:342:ARG:NE	1:A:434:ASP:OD1	2.41	0.48
1:A:723:ILE:HG23	1:A:735:THR:HG23	1.96	0.48
2:C:1216:TYR:HB2	2:C:1241:LEU:HD13	1.95	0.48
3:D:585:ILE:HG12	3:D:591:LYS:HB2	1.94	0.48
3:D:628:PHE:O	3:D:779:ARG:HD2	2.14	0.48
4:E:878:PHE:HZ	4:E:917:PRO:HB3	1.77	0.48
5:F:275:VAL:HA	5:F:278:ILE:HB	1.96	0.48
5:F:320:GLU:CD	5:F:351:HIS:CE1	2.87	0.48
5:F:965:LEU:O	5:F:965:LEU:HG	2.13	0.48
5:F:1031:VAL:CB	6:G:314:TYR:O	2.61	0.48
5:F:1300:LEU:HD23	5:F:1301:SER:HA	1.96	0.48
6:J:384:LEU:CD2	7:K:455:LYS:HG2	2.43	0.48
6:J:398:VAL:CG2	7:K:462:ARG:O	2.62	0.48
7:K:314:ASN:H	7:K:349:PRO:HA	1.79	0.48
8:L:774:ASN:HB3	8:L:795:LYS:HE2	1.96	0.48
8:L:777:ASN:HD22	8:L:795:LYS:HA	1.79	0.48
3:D:538:SER:OG	3:D:545:GLN:HB2	2.14	0.48
3:D:910:LEU:HA	3:D:913:LEU:HD12	1.96	0.48
3:D:1238:ARG:CG	1:Z:830:SER:HB2	2.40	0.48
4:E:1022:TYR:CD2	4:E:1026:THR:HG22	2.38	0.48
4:E:1499:LEU:HA	4:E:1502:ILE:HG12	1.95	0.48
5:F:925:HIS:HA	5:F:928:LEU:CD1	2.44	0.48
5:F:929:TYR:C	5:F:931:GLY:H	2.17	0.48
5:F:1027:GLN:HG3	5:F:1027:GLN:O	2.13	0.48
5:F:1147:PHE:C	5:F:1147:PHE:CD1	2.85	0.48
5:F:1493:LYS:HD2	5:F:1493:LYS:HA	1.66	0.48
6:G:380:TYR:HA	6:G:383:LYS:HE3	1.95	0.48
7:H:426:GLY:CA	8:I:735:ASN:C	2.83	0.48
8:I:778:LYS:HA	8:I:778:LYS:NZ	2.29	0.48
8:I:805:ARG:CB	1:Z:88:LYS:HZ3	2.24	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:18:ALA:HA	1:Z:21:LYS:HB2	1.95	0.48
1:Z:641:ILE:HD13	1:Z:656:LEU:HD12	1.96	0.48
1:Z:771:ILE:HG22	1:Z:772:PRO:HD2	1.94	0.48
1:A:255:GLU:HB3	1:A:480:GLN:HE21	1.79	0.47
3:D:315:THR:HG22	3:D:317:SER:H	1.79	0.47
3:D:426:VAL:CG2	3:D:437:VAL:HG23	2.44	0.47
4:E:18:VAL:HA	4:E:40:ILE:HD11	1.96	0.47
4:E:1345:SER:O	4:E:1349:TYR:HB2	2.14	0.47
5:F:1289:ILE:HD12	5:F:1289:ILE:HA	1.64	0.47
7:K:313:TYR:HA	7:K:349:PRO:CB	2.40	0.47
1:A:301:ASN:HA	1:A:304:LYS:HE3	1.96	0.47
3:D:442:GLY:O	3:D:468:PRO:HG3	2.15	0.47
4:E:1163:LEU:HB3	4:E:1173:TRP:HH2	1.78	0.47
5:F:1439:GLU:O	5:F:1443:ASN:N	2.34	0.47
5:F:1550:LEU:CD1	5:F:1552:PHE:CZ	2.97	0.47
6:G:315:LEU:HD23	8:I:679:LEU:HD23	1.95	0.47
8:L:769:ILE:HA	8:L:772:VAL:HG12	1.95	0.47
1:Z:116:LYS:HE2	1:Z:116:LYS:CA	2.44	0.47
1:Z:123:MET:SD	1:Z:123:MET:C	2.93	0.47
1:Z:271:VAL:HG22	1:Z:459:LEU:HD22	1.96	0.47
1:Z:786:ILE:CD1	1:Z:838:SER:HA	2.44	0.47
3:D:517:LEU:HB2	3:D:540:GLN:OE1	2.14	0.47
3:D:789:VAL:HG11	3:D:952:LEU:CD1	2.44	0.47
3:D:917:SER:OG	3:D:975:ILE:HA	2.15	0.47
4:E:1260:TYR:O	4:E:1260:TYR:CD1	2.67	0.47
5:F:951:ARG:NE	5:F:951:ARG:HA	2.29	0.47
5:F:1370:LEU:C	5:F:1371:ILE:HG12	2.33	0.47
6:J:300:ASP:HA	6:J:303:GLU:OE1	2.14	0.47
7:K:427:LEU:H	7:K:428:PRO:HD3	1.79	0.47
7:K:538:LYS:CB	8:L:822:LYS:CB	2.85	0.47
1:Z:810:ALA:O	1:Z:836:ASP:CB	2.62	0.47
3:D:445:ARG:HH11	3:D:466:LYS:HB3	1.79	0.47
4:E:105:GLU:O	4:E:109:ARG:N	2.47	0.47
4:E:725:LEU:HG	4:E:1169:ALA:HB3	1.97	0.47
4:E:954:ILE:HD11	4:E:1015:LYS:HE3	1.97	0.47
4:E:1031:LYS:HB2	4:E:1034:ILE:HG12	1.96	0.47
5:F:161:GLN:HB2	5:F:183:ARG:HH12	1.79	0.47
5:F:609:LEU:HA	5:F:612:LEU:HB2	1.96	0.47
6:J:326:LEU:HD22	8:L:689:SER:OG	2.14	0.47
2:C:888:LEU:HA	2:C:892:PHE:CD2	2.49	0.47
3:D:182:CYS:SG	3:D:195:ILE:HD11	2.55	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:893:ILE:O	3:D:897:ILE:HG13	2.15	0.47
5:F:710:LEU:HA	5:F:713:PHE:HB3	1.96	0.47
5:F:900:LEU:HD22	5:F:904:TYR:CE2	2.49	0.47
5:F:1486:LEU:HA	5:F:1489:ILE:HB	1.96	0.47
6:G:353:LEU:HD11	6:G:365:SER:HB2	1.97	0.47
7:H:492:ASP:O	7:H:493:SER:CB	2.62	0.47
6:J:311:ASP:HA	6:J:314:TYR:CG	2.48	0.47
8:L:818:ILE:HA	8:L:821:ILE:HG22	1.97	0.47
1:Z:710:ASN:OD1	1:Z:710:ASN:N	2.48	0.47
1:A:687:LEU:HA	1:A:690:ARG:HG2	1.96	0.47
3:D:1376:LYS:CB	1:Z:762:ASN:CB	2.93	0.47
4:E:803:LEU:HG	4:E:807:LEU:HD12	1.96	0.47
4:E:1200:GLU:HA	4:E:1203:THR:HG22	1.97	0.47
5:F:110:ARG:NH2	5:F:190:TYR:OH	2.47	0.47
5:F:1392:ILE:CB	5:F:1405:PHE:HE2	2.28	0.47
8:I:738:ASP:O	8:I:740:LYS:HG3	2.14	0.47
7:K:446:ARG:C	7:K:446:ARG:HD3	2.34	0.47
1:A:133:THR:O	1:A:134:LYS:C	2.52	0.47
2:C:285:GLU:HB2	2:C:304:LEU:HD11	1.96	0.47
3:D:412:ILE:HG13	3:D:413:LEU:CD1	2.43	0.47
3:D:568:GLN:NE2	3:D:573:GLN:HG2	2.30	0.47
3:D:911:ASN:HA	3:D:914:TYR:CE2	2.49	0.47
4:E:51:LEU:HA	4:E:109:ARG:HD3	1.97	0.47
4:E:141:LEU:HD11	4:E:195:LEU:HD13	1.97	0.47
4:E:604:PRO:HG3	4:E:666:PRO:HG2	1.95	0.47
4:E:1166:VAL:HG23	4:E:1167:LEU:HD23	1.96	0.47
4:E:1608:HIS:HB3	4:E:1611:TYR:HB3	1.97	0.47
5:F:46:ALA:O	5:F:50:GLN:CB	2.62	0.47
5:F:219:HIS:NE2	5:F:222:GLU:OE2	2.48	0.47
5:F:665:GLU:HG2	5:F:668:ARG:HG3	1.97	0.47
5:F:850:GLN:HA	5:F:853:ILE:HD12	1.97	0.47
5:F:907:HIS:CB	7:H:410:LYS:HD3	2.44	0.47
5:F:938:ALA:O	5:F:941:SER:OG	2.22	0.47
5:F:1058:ALA:C	5:F:1060:LEU:N	2.67	0.47
5:F:1506:ILE:HG22	5:F:1507:ASN:H	1.79	0.47
6:G:404:ASP:CB	6:G:425:GLU:O	2.63	0.47
7:H:472:ASN:O	7:H:476:GLN:CB	2.63	0.47
8:I:792:GLN:O	8:I:794:ILE:N	2.46	0.47
8:I:795:LYS:CA	8:I:795:LYS:HZ3	2.28	0.47
6:J:277:ILE:HD12	6:J:280:LEU:HD23	1.97	0.47
6:J:376:LYS:HD2	6:J:376:LYS:C	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:389:ARG:HH11	6:J:389:ARG:CG	2.23	0.47
8:L:661:LYS:HE2	8:L:665:TRP:CH2	2.50	0.47
1:Z:133:THR:O	1:Z:134:LYS:C	2.52	0.47
1:Z:539:ALA:HA	1:Z:542:THR:HG22	1.97	0.47
1:Z:551:ARG:HH12	1:Z:607:ARG:HH12	1.63	0.47
1:Z:807:LYS:CB	1:Z:836:ASP:O	2.63	0.47
1:A:193:LEU:HB3	1:A:546:ARG:NH1	2.30	0.47
1:A:615:ASP:HB2	1:A:618:GLU:HG3	1.97	0.47
1:A:688:LEU:O	1:A:692:MET:HG2	2.14	0.47
3:D:447:TYR:O	3:D:462:LEU:HD12	2.15	0.47
3:D:1465:ILE:HG23	3:D:1487:TYR:CZ	2.49	0.47
5:F:21:ASP:HB2	5:F:24:LEU:HB2	1.97	0.47
5:F:711:GLN:NE2	5:F:714:HIS:HB2	2.29	0.47
5:F:1423:SER:HA	5:F:1426:VAL:HG12	1.97	0.47
6:G:295:LYS:NZ	6:J:363:LYS:HZ3	2.12	0.47
7:K:358:LEU:O	7:K:362:ASN:ND2	2.48	0.47
8:L:643:LYS:CG	8:L:647:GLN:HE22	2.23	0.47
2:C:1389:GLY:HA2	4:E:1331:LEU:CD1	2.45	0.47
3:D:149:GLU:OE2	3:D:653:ARG:NH1	2.37	0.47
3:D:903:ILE:HG12	3:D:953:PHE:CG	2.50	0.47
4:E:33:ASP:OD2	4:E:946:TRP:NE1	2.40	0.47
4:E:1380:ASP:C	4:E:1382:THR:N	2.68	0.47
5:F:623:VAL:HG11	5:F:626:ASP:HB2	1.97	0.47
5:F:1622:VAL:HA	5:F:1625:THR:HG22	1.97	0.47
8:I:694:ASP:OD2	8:I:698:GLN:NE2	2.37	0.47
7:K:312:VAL:CG1	7:K:361:ARG:HH21	2.27	0.47
1:Z:574:GLU:HA	1:Z:577:ARG:HB2	1.96	0.47
1:A:16:LYS:CD	6:J:468:ALA:HA	2.45	0.47
1:A:817:ALA:CB	1:A:832:LEU:HD13	2.45	0.47
3:D:830:SER:CB	3:D:934:SER:HB3	2.38	0.47
5:F:655:LYS:HG3	5:F:708:GLY:HA2	1.95	0.47
5:F:1210:LYS:HB2	5:F:1289:ILE:HD11	1.96	0.47
5:F:1249:ILE:HA	5:F:1252:VAL:HG12	1.95	0.47
6:J:383:LYS:HZ1	8:L:756:ASN:HA	0.47	0.47
1:Z:138:ASN:C	1:Z:138:ASN:HD22	2.19	0.47
4:E:1052:LYS:HZ2	4:E:1068:LEU:HD23	1.79	0.46
4:E:1484:LYS:HZ2	4:E:1486:GLU:HB2	1.80	0.46
4:E:1558:GLN:NE2	4:E:1590:ASP:OD1	2.48	0.46
5:F:228:PHE:CE2	5:F:359:GLN:HA	2.50	0.46
5:F:657:ILE:O	5:F:712:LEU:CD1	2.56	0.46
5:F:1104:ASN:O	5:F:1108:ARG:NH1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1281:LYS:HD2	5:F:1281:LYS:HA	1.54	0.46
5:F:1635:ARG:HA	5:F:1635:ARG:HD2	1.55	0.46
6:J:432:LEU:CA	8:L:782:ILE:HA	2.45	0.46
7:K:402:GLN:CA	7:K:402:GLN:NE2	2.76	0.46
7:K:413:LEU:HG	8:L:749:GLN:HE21	1.80	0.46
3:D:260:HIS:NE2	3:D:261:LEU:HD23	2.30	0.46
3:D:361:ILE:HD12	3:D:368:ILE:HG12	1.97	0.46
3:D:611:LEU:CG	3:D:640:ALA:HB2	2.45	0.46
3:D:797:ARG:NH2	3:D:799:THR:OG1	2.49	0.46
5:F:10:THR:O	5:F:14:SER:CB	2.63	0.46
5:F:975:SER:HA	5:F:978:ILE:HG22	1.97	0.46
5:F:1014:SER:N	8:I:788:ASP:H	2.12	0.46
5:F:1167:LYS:HE3	5:F:1167:LYS:CA	2.27	0.46
5:F:1283:LYS:NZ	5:F:1286:PHE:HB3	2.30	0.46
7:H:312:VAL:HG12	7:H:361:ARG:HH21	1.80	0.46
8:I:788:ASP:N	8:I:788:ASP:OD1	2.49	0.46
6:J:293:HIS:CB	7:K:359:ASN:HD21	2.27	0.46
6:J:433:LYS:CA	7:K:499:GLY:HA2	2.44	0.46
7:K:310:ALA:HB3	7:K:352:ILE:CB	2.40	0.46
8:L:664:SER:HA	8:L:667:GLN:HE21	1.80	0.46
1:A:269:ASN:HB3	1:A:272:GLU:HB2	1.96	0.46
1:A:420:LEU:HD13	1:A:457:TYR:HB2	1.97	0.46
3:D:125:SER:OG	3:D:734:LEU:HD13	2.15	0.46
4:E:207:ASP:O	4:E:211:GLN:HB2	2.15	0.46
4:E:284:ILE:HD11	4:E:328:ILE:HD12	1.96	0.46
4:E:1160:ILE:HG13	4:E:1161:PRO:HD3	1.98	0.46
5:F:425:ASP:OD1	5:F:425:ASP:N	2.48	0.46
5:F:538:GLU:O	5:F:542:ASN:ND2	2.49	0.46
5:F:902:LYS:HE2	7:H:414:LYS:HD2	0.67	0.46
8:I:821:ILE:HD13	8:I:821:ILE:O	2.16	0.46
1:Z:192:ILE:HG22	1:Z:539:ALA:HB3	1.97	0.46
1:Z:210:GLU:O	1:Z:214:ASN:ND2	2.49	0.46
1:Z:306:LYS:HE2	1:Z:331:VAL:HG22	1.97	0.46
1:A:810:ALA:HB1	1:A:836:ASP:OD1	2.15	0.46
3:D:495:PHE:O	3:D:499:LEU:HG	2.16	0.46
4:E:458:LYS:HG3	4:E:562:TRP:HE1	1.81	0.46
4:E:1503:VAL:HA	4:E:1506:LEU:HG	1.96	0.46
5:F:322:ILE:HA	5:F:325:PHE:HB3	1.97	0.46
5:F:750:TRP:CG	5:F:750:TRP:O	2.68	0.46
5:F:1364:TYR:O	5:F:1364:TYR:CD1	2.68	0.46
6:G:310:ARG:NE	6:G:314:TYR:OH	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:281:ASP:HA	6:J:284:ILE:CD1	2.31	0.46
6:J:371:LYS:C	6:J:371:LYS:CE	2.84	0.46
6:J:434:THR:OG1	6:J:435:GLY:N	2.47	0.46
3:D:430:GLU:HA	3:D:624:PHE:CD2	2.50	0.46
3:D:608:ILE:CD1	3:D:641:VAL:HG22	2.46	0.46
3:D:713:ILE:HD12	3:D:769:ARG:CG	2.46	0.46
4:E:596:LYS:O	4:E:600:ASN:ND2	2.49	0.46
5:F:154:GLN:HG3	5:F:190:TYR:HE2	1.81	0.46
5:F:320:GLU:CD	5:F:351:HIS:HD1	2.19	0.46
5:F:439:LEU:HA	5:F:442:ILE:HG22	1.97	0.46
5:F:1406:TYR:OH	5:F:1452:SER:O	2.33	0.46
8:I:822:LYS:HG3	8:I:822:LYS:O	2.15	0.46
6:J:353:LEU:HD12	7:K:423:LYS:HG2	1.98	0.46
7:K:301:PRO:HB3	7:K:353:TYR:O	2.16	0.46
7:K:379:ILE:C	7:K:382:LYS:H	2.19	0.46
7:K:447:SER:CB	8:L:751:LEU:CD1	2.94	0.46
1:Z:697:PHE:HA	1:Z:703:SER:HB3	1.96	0.46
1:Z:807:LYS:CB	1:Z:837:VAL:C	2.84	0.46
2:C:229:ASP:CG	2:C:252:LYS:HE2	2.36	0.46
3:D:234:ILE:HD12	3:D:243:PHE:CE2	2.51	0.46
3:D:430:GLU:OE2	3:D:528:PRO:HA	2.16	0.46
4:E:1029:ASN:HD22	7:K:475:SER:CB	2.26	0.46
4:E:1086:ILE:HD11	4:E:1096:ILE:HB	1.97	0.46
5:F:319:ILE:HD11	5:F:477:ASP:HB2	1.97	0.46
5:F:526:PHE:HA	5:F:529:MET:HB3	1.97	0.46
5:F:1110:MET:CE	5:F:1157:TRP:CZ2	2.99	0.46
7:K:399:LEU:HD12	7:K:399:LEU:C	2.35	0.46
1:Z:768:VAL:HA	1:Z:771:ILE:CD1	2.41	0.46
1:A:563:ASN:O	1:A:564:GLU:HG3	2.15	0.46
3:D:503:GLU:OE1	3:D:503:GLU:N	2.45	0.46
3:D:519:THR:HG21	3:D:605:VAL:N	2.31	0.46
3:D:863:ILE:CD1	3:D:887:GLN:HG3	2.46	0.46
4:E:100:GLU:O	4:E:104:SER:OG	2.26	0.46
5:F:303:LYS:HA	5:F:306:VAL:HG22	1.96	0.46
5:F:334:GLN:HE21	5:F:859:LYS:HZ3	1.26	0.46
5:F:750:TRP:O	5:F:750:TRP:CD1	2.69	0.46
5:F:1136:LYS:CB	5:F:1207:CYS:HA	2.45	0.46
7:H:386:LEU:HG	8:I:690:GLN:HE21	1.81	0.46
6:J:371:LYS:C	6:J:371:LYS:HZ2	2.09	0.46
6:J:431:GLN:C	7:K:499:GLY:H	2.19	0.46
1:Z:820:ILE:O	1:Z:822:TYR:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:PHE:HZ	1:A:505:HIS:CD2	2.34	0.46
3:D:462:LEU:HD21	3:D:465:ILE:CG2	2.46	0.46
4:E:559:PHE:HZ	4:E:567:ARG:HH22	1.64	0.46
4:E:851:SER:O	4:E:851:SER:OG	2.33	0.46
5:F:671:PHE:HA	5:F:674:PHE:HB2	1.96	0.46
5:F:1067:ASN:ND2	5:F:1069:ASP:HB2	2.31	0.46
5:F:1139:ILE:HD12	5:F:1139:ILE:H	1.80	0.46
6:J:357:LEU:CD2	7:K:423:LYS:HE3	2.45	0.46
7:K:314:ASN:O	7:K:348:ILE:N	2.48	0.46
1:A:761:SER:CB	2:C:1355:SER:OG	2.64	0.46
3:D:515:VAL:HA	3:D:644:SER:HB3	1.97	0.46
4:E:1134:TRP:NE1	4:E:1170:ASP:OD2	2.40	0.46
5:F:98:THR:HG22	5:F:99:ALA:H	1.81	0.46
5:F:917:PHE:CD1	5:F:917:PHE:O	2.69	0.46
5:F:1363:ILE:C	5:F:1363:ILE:CD1	2.85	0.46
5:F:1480:MET:HG2	5:F:1537:ALA:HB1	1.98	0.46
7:K:483:VAL:O	7:K:493:SER:N	2.48	0.46
1:Z:86:PHE:N	1:Z:86:PHE:CD1	2.79	0.46
1:Z:555:GLU:HA	1:Z:607:ARG:HH21	1.81	0.46
3:D:1000:ASP:N	3:D:1000:ASP:OD1	2.49	0.46
4:E:393:THR:H	4:E:396:THR:HG22	1.80	0.46
5:F:564:ASP:N	5:F:564:ASP:OD1	2.49	0.46
8:I:778:LYS:HB2	8:I:794:ILE:CB	2.46	0.46
7:K:288:ILE:O	7:K:292:VAL:HG23	2.16	0.46
7:K:426:GLY:CA	8:L:738:ASP:HB3	2.45	0.46
7:K:429:LEU:HB2	8:L:741:ARG:NH2	2.31	0.46
1:Z:390:LEU:HD21	1:Z:416:GLY:HA2	1.96	0.46
1:A:140:ILE:CG2	4:E:1393:LYS:CE	2.94	0.45
1:A:210:GLU:OE2	1:A:214:ASN:ND2	2.49	0.45
1:A:469:TYR:HB3	1:A:473:ARG:HB2	1.97	0.45
2:C:914:GLN:HE21	2:C:953:ILE:CG2	2.29	0.45
3:D:665:ASN:CG	3:D:666:PRO:HD3	2.36	0.45
3:D:1494:ASN:O	5:F:1471:LYS:NZ	2.49	0.45
4:E:1038:LYS:HD2	4:E:1038:LYS:HA	1.78	0.45
5:F:159:LYS:CE	5:F:363:ASP:CB	2.93	0.45
5:F:1080:LEU:HG	5:F:1156:TYR:CD2	2.45	0.45
5:F:1608:ILE:HA	5:F:1612:LEU:HD13	1.98	0.45
7:H:318:GLU:CB	7:H:346:GLN:HA	2.46	0.45
6:J:405:LEU:HD22	7:K:469:ARG:NE	2.26	0.45
7:K:444:LEU:O	7:K:447:SER:CA	2.61	0.45
7:K:522:TYR:HA	7:K:525:GLU:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:774:LEU:HD23	1:Z:774:LEU:O	2.14	0.45
1:A:354:VAL:HA	1:A:368:LEU:HD11	1.98	0.45
3:D:111:LEU:HD22	3:D:775:LEU:HD21	1.97	0.45
4:E:23:ASN:HD22	4:E:838:LYS:HD2	1.81	0.45
5:F:56:ILE:HD13	5:F:86:ILE:HD13	1.97	0.45
5:F:1034:LEU:HD22	5:F:1092:THR:CB	2.28	0.45
5:F:1036:PRO:CB	5:F:1042:ILE:H	2.30	0.45
5:F:1110:MET:HE3	5:F:1157:TRP:CZ2	2.48	0.45
5:F:1285:HIS:ND1	5:F:1285:HIS:C	2.70	0.45
7:H:314:ASN:HB2	7:H:361:ARG:HH22	1.82	0.45
7:H:412:ILE:CA	7:H:415:LEU:HB2	2.42	0.45
8:I:793:LEU:HA	8:I:796:ILE:HG13	1.97	0.45
8:I:795:LYS:HZ3	8:I:795:LYS:CB	2.29	0.45
6:J:275:GLN:NE2	6:J:278:GLU:OE1	2.49	0.45
7:K:315:LYS:CG	7:K:347:THR:HG22	2.46	0.45
8:L:684:VAL:HA	8:L:687:GLU:OE1	2.16	0.45
1:A:545:PHE:CD2	1:A:549:ASP:HB2	2.50	0.45
1:A:739:MET:O	1:A:742:LEU:HB2	2.16	0.45
1:A:749:ASP:HB2	2:C:1274:LYS:HZ3	1.81	0.45
3:D:789:VAL:HG21	3:D:952:LEU:CD1	2.47	0.45
4:E:279:ILE:HG23	4:E:281:GLN:HG2	1.97	0.45
4:E:624:THR:HG23	4:E:632:ALA:HB2	1.97	0.45
5:F:444:THR:HB	5:F:445:ASP:H	1.53	0.45
5:F:672:TRP:CD1	5:F:675:LEU:HD22	2.51	0.45
5:F:1090:PRO:HD3	5:F:1093:SER:OG	2.16	0.45
1:Z:88:LYS:O	1:Z:92:THR:HG23	2.15	0.45
1:A:138:ASN:HD22	1:A:138:ASN:C	2.19	0.45
1:A:679:ASP:HB3	1:A:684:ASN:HB2	1.99	0.45
2:C:229:ASP:CG	2:C:252:LYS:CE	2.85	0.45
4:E:174:VAL:HA	4:E:177:VAL:HG12	1.97	0.45
6:J:380:TYR:CD1	6:J:383:LYS:HD3	2.51	0.45
7:K:315:LYS:HB2	8:L:670:VAL:HB	1.99	0.45
7:K:404:ARG:CG	8:L:704:GLN:NE2	2.80	0.45
1:Z:555:GLU:OE1	1:Z:607:ARG:NH2	2.49	0.45
1:A:195:SER:OG	1:A:536:ASN:OD1	2.34	0.45
3:D:641:VAL:HB	3:D:648:GLU:CG	2.45	0.45
4:E:982:ILE:HD12	4:E:982:ILE:N	2.31	0.45
5:F:690:GLU:CG	8:I:722:LEU:CG	2.95	0.45
5:F:1048:LEU:O	5:F:1051:SER:OG	2.26	0.45
5:F:1157:TRP:O	5:F:1158:THR:C	2.55	0.45
5:F:1617:SER:O	5:F:1617:SER:OG	2.28	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:289:GLN:OE1	6:J:352:VAL:HG13	2.16	0.45
7:H:295:CYS:HA	7:H:298:SER:HB2	1.99	0.45
8:I:778:LYS:CG	8:I:794:ILE:CB	2.94	0.45
8:I:794:ILE:HA	8:I:797:LEU:CD1	2.46	0.45
7:K:466:LEU:O	7:K:470:ALA:N	2.40	0.45
1:Z:831:THR:HA	1:Z:834:ASN:HB2	1.98	0.45
1:A:48:GLU:CA	7:K:514:THR:HG21	2.47	0.45
1:A:630:ARG:O	1:A:634:ASP:N	2.41	0.45
1:A:654:ILE:HG13	1:A:706:ILE:HG21	1.98	0.45
3:D:100:PRO:HG2	3:D:898:LYS:NZ	2.32	0.45
3:D:393:ILE:HD11	3:D:460:LEU:HB2	1.98	0.45
4:E:504:ASP:OD1	4:E:524:LYS:NZ	2.49	0.45
4:E:696:GLY:HA2	5:F:1383:GLN:CB	2.47	0.45
4:E:772:THR:HA	4:E:775:PHE:HB2	1.99	0.45
4:E:1472:SER:HB2	4:E:1475:SER:H	1.81	0.45
5:F:1680:GLN:OE1	5:F:1680:GLN:HA	2.12	0.45
8:I:685:MET:O	8:I:688:HIS:ND1	2.44	0.45
7:K:316:VAL:H	7:K:347:THR:HA	1.81	0.45
7:K:466:LEU:O	7:K:469:ARG:N	2.49	0.45
1:Z:239:ILE:HD12	1:Z:258:LYS:HD3	1.99	0.45
1:A:128:LEU:CB	4:E:1260:TYR:HE2	2.26	0.45
3:D:434:LEU:HD22	3:D:447:TYR:HB3	1.99	0.45
3:D:437:VAL:HA	3:D:446:LEU:O	2.16	0.45
3:D:476:VAL:HG13	3:D:488:GLN:HG3	1.99	0.45
3:D:763:ASP:O	3:D:765:ILE:HG12	2.17	0.45
3:D:789:VAL:HA	3:D:949:PHE:CE1	2.51	0.45
3:D:873:SER:OG	3:D:877:VAL:HB	2.17	0.45
4:E:912:TRP:CD1	4:E:917:PRO:HD3	2.52	0.45
4:E:1356:LEU:CB	1:Z:453:VAL:CG2	2.94	0.45
5:F:859:LYS:HD2	5:F:860:ASN:H	1.81	0.45
5:F:920:ILE:HB	5:F:924:ALA:HA	1.97	0.45
5:F:1138:PHE:C	5:F:1140:GLU:H	2.20	0.45
5:F:1219:VAL:O	5:F:1221:LEU:N	2.44	0.45
7:H:298:SER:OG	7:H:305:LYS:O	2.25	0.45
7:H:470:ALA:O	7:H:474:SER:HB2	2.17	0.45
7:H:508:LYS:HD2	7:H:508:LYS:HA	1.43	0.45
6:J:384:LEU:C	6:J:384:LEU:CD2	2.85	0.45
1:Z:658:ASN:O	1:Z:662:SER:HB2	2.17	0.45
1:Z:767:ILE:H	1:Z:767:ILE:HG13	1.47	0.45
1:Z:771:ILE:CG2	1:Z:772:PRO:CD	2.93	0.45
4:E:53:GLU:HB2	4:E:140:LYS:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:359:GLN:CB	5:F:421:ILE:HA	2.47	0.45
5:F:588:ASN:HB3	5:F:768:VAL:HG12	1.98	0.45
5:F:792:ASP:OD2	5:F:1244:ASN:ND2	2.43	0.45
5:F:900:LEU:C	5:F:900:LEU:CD1	2.82	0.45
5:F:1166:HIS:ND1	5:F:1166:HIS:C	2.70	0.45
6:J:284:ILE:O	6:J:288:VAL:HG23	2.17	0.45
1:Z:599:ARG:NE	1:Z:605:GLU:OE1	2.39	0.45
3:D:654:THR:O	3:D:658:ILE:HG13	2.16	0.45
4:E:1180:GLN:NE2	4:E:1181:THR:O	2.40	0.45
5:F:1472:GLU:OE2	5:F:1473:ASN:ND2	2.50	0.45
5:F:1638:ILE:HA	5:F:1641:PHE:CD2	2.52	0.45
6:J:389:ARG:NH1	6:J:389:ARG:CA	2.79	0.45
6:J:389:ARG:CZ	6:J:389:ARG:C	2.85	0.45
7:K:389:LYS:CA	7:K:393:ASP:CB	2.39	0.45
8:L:802:ASP:O	8:L:806:SER:CB	2.65	0.45
1:Z:542:THR:HG21	1:Z:557:LEU:HD21	1.99	0.45
1:A:775:LEU:HD22	1:A:832:LEU:HD11	1.99	0.45
3:D:615:PHE:CE2	3:D:627:GLU:HG2	2.52	0.45
5:F:320:GLU:OE2	5:F:351:HIS:ND1	2.50	0.45
7:H:527:LEU:C	7:H:527:LEU:CD2	2.85	0.45
6:J:404:ASP:O	6:J:408:ALA:CB	2.65	0.45
7:K:395:ALA:O	7:K:399:LEU:HB3	2.17	0.45
1:Z:239:ILE:O	1:Z:243:SER:OG	2.30	0.45
1:A:137:ASP:HB2	4:E:1386:LEU:HG	1.98	0.44
3:D:234:ILE:O	3:D:240:LEU:HD12	2.16	0.44
4:E:755:ASN:CB	5:F:1376:THR:OG1	2.64	0.44
4:E:955:PHE:O	4:E:959:LEU:HB2	2.17	0.44
4:E:963:LYS:HB2	4:E:963:LYS:HE3	1.84	0.44
4:E:1395:ILE:HD12	4:E:1398:VAL:HB	2.00	0.44
4:E:1421:ILE:HA	4:E:1424:LEU:HD23	1.99	0.44
5:F:23:ASP:OD1	5:F:23:ASP:N	2.47	0.44
5:F:943:ARG:HB3	5:F:947:LYS:NZ	2.32	0.44
5:F:1495:THR:HA	5:F:1498:LEU:HB2	1.97	0.44
6:G:427:GLU:HB3	8:I:779:THR:HG21	1.99	0.44
7:H:451:ALA:O	7:H:455:LYS:N	2.45	0.44
8:I:795:LYS:HZ3	8:I:795:LYS:HB2	1.82	0.44
6:J:286:LYS:O	6:J:290:ILE:HG12	2.18	0.44
6:J:372:PHE:O	6:J:372:PHE:CD1	2.69	0.44
7:K:389:LYS:HA	7:K:393:ASP:HB3	0.61	0.44
1:Z:27:GLU:OE2	1:Z:30:ASP:HB2	2.11	0.44
1:Z:54:PHE:HA	1:Z:57:ARG:CZ	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:661:LEU:HA	1:Z:664:THR:HG22	1.99	0.44
1:A:54:PHE:HA	1:A:57:ARG:CD	2.47	0.44
1:A:123:MET:CB	6:J:413:ASN:CB	2.95	0.44
1:A:125:ILE:CB	4:E:1212:THR:OG1	2.65	0.44
1:A:128:LEU:CB	4:E:1260:TYR:CE2	3.00	0.44
1:A:212:PHE:CE2	1:A:541:TYR:CZ	3.05	0.44
1:A:675:VAL:HA	1:A:684:ASN:HD21	1.81	0.44
3:D:123:GLU:HG2	3:D:124:ARG:H	1.82	0.44
3:D:910:LEU:HD23	3:D:913:LEU:CD1	2.38	0.44
3:D:937:SER:HB3	3:D:941:GLN:CB	2.43	0.44
4:E:495:ASP:HB2	4:E:529:LYS:HG3	1.99	0.44
6:G:289:GLN:CD	6:J:352:VAL:HG22	2.32	0.44
6:J:364:ILE:HG23	7:K:424:ASN:HB3	1.99	0.44
1:Z:12:SER:O	1:Z:12:SER:OG	2.31	0.44
1:A:739:MET:SD	1:A:778:THR:OG1	2.63	0.44
3:D:399:SER:O	3:D:407:ALA:HB2	2.17	0.44
3:D:445:ARG:O	3:D:465:ILE:HA	2.18	0.44
3:D:527:SER:HB2	3:D:614:LEU:HD22	1.99	0.44
4:E:1071:LYS:HD3	4:E:1071:LYS:HA	1.82	0.44
5:F:159:LYS:HE3	5:F:363:ASP:CB	2.45	0.44
5:F:253:LYS:NZ	5:F:257:SER:OG	2.44	0.44
5:F:378:ALA:O	5:F:383:ASN:OD1	2.35	0.44
5:F:1118:ARG:NH1	5:F:1118:ARG:CG	2.80	0.44
5:F:1285:HIS:O	5:F:1285:HIS:CG	2.70	0.44
6:J:389:ARG:NH1	6:J:389:ARG:C	2.71	0.44
8:L:638:ASP:HA	8:L:641:VAL:HG23	1.99	0.44
1:Z:766:ASN:O	1:Z:769:LYS:N	2.50	0.44
1:Z:792:SER:OG	1:Z:799:LYS:NZ	2.43	0.44
1:A:16:LYS:CG	6:J:468:ALA:HA	2.47	0.44
1:A:333:ILE:HG13	1:A:334:TRP:N	2.33	0.44
1:A:644:TYR:O	1:A:648:GLU:N	2.51	0.44
3:D:716:VAL:HB	3:D:885:ALA:HB1	1.99	0.44
3:D:878:ILE:HG22	3:D:879:ASP:H	1.83	0.44
3:D:908:SER:O	3:D:911:ASN:HB3	2.17	0.44
4:E:300:SER:O	4:E:304:ASN:HB2	2.16	0.44
4:E:1020:ILE:HA	4:E:1023:VAL:HG12	1.98	0.44
5:F:48:ARG:NH1	5:F:85:GLU:OE2	2.48	0.44
5:F:210:LYS:HE2	5:F:210:LYS:HB3	1.78	0.44
5:F:389:LEU:C	5:F:389:LEU:CD1	2.86	0.44
5:F:841:PHE:HE2	5:F:918:PHE:CE1	2.22	0.44
5:F:1084:LEU:CB	5:F:1156:TYR:CE1	3.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1359:PHE:O	5:F:1359:PHE:CG	2.69	0.44
7:H:313:TYR:HD1	7:H:349:PRO:HB3	1.82	0.44
7:H:455:LYS:O	7:H:459:LEU:HB2	2.17	0.44
6:J:300:ASP:O	6:J:304:LEU:HD13	2.17	0.44
6:J:372:PHE:CD2	6:J:372:PHE:C	2.89	0.44
1:A:589:LEU:O	1:A:604:ILE:HG22	2.17	0.44
4:E:442:LEU:HD23	4:E:442:LEU:HA	1.86	0.44
5:F:148:PHE:HA	5:F:151:ILE:HG12	1.99	0.44
5:F:365:LYS:HA	5:F:369:GLN:CB	2.47	0.44
5:F:663:LYS:HA	5:F:720:HIS:CE1	2.53	0.44
5:F:905:SER:CB	8:I:753:GLU:HB2	2.48	0.44
5:F:1026:PHE:HD2	5:F:1034:LEU:HD11	1.83	0.44
5:F:1026:PHE:HE1	5:F:1049:LEU:HD11	1.83	0.44
5:F:1084:LEU:CB	5:F:1156:TYR:CZ	3.00	0.44
5:F:1606:GLN:O	5:F:1610:ALA:CB	2.60	0.44
7:K:430:GLY:C	7:K:432:ALA:H	2.20	0.44
1:Z:357:LYS:HA	1:Z:360:ILE:HB	2.00	0.44
1:Z:807:LYS:C	1:Z:836:ASP:O	2.56	0.44
3:D:617:ALA:HB1	3:D:782:ARG:HH22	1.82	0.44
4:E:1122:PHE:HA	4:E:1125:GLU:HG2	1.99	0.44
4:E:1379:GLU:OE1	4:E:1383:GLN:NE2	2.50	0.44
5:F:56:ILE:HG13	5:F:66:VAL:HG21	2.00	0.44
5:F:351:HIS:O	5:F:351:HIS:CG	2.70	0.44
5:F:881:THR:HA	5:F:885:GLU:HB3	2.00	0.44
5:F:1068:ILE:CD1	5:F:1150:PHE:CE2	3.00	0.44
5:F:1191:SER:HB3	5:F:1192:VAL:H	1.51	0.44
5:F:1286:PHE:O	5:F:1286:PHE:CD1	2.70	0.44
1:Z:822:TYR:HB3	1:Z:824:MET:CE	2.48	0.44
1:A:193:LEU:CD1	1:A:578:GLU:HG3	2.48	0.44
1:A:628:ALA:HB1	1:A:644:TYR:CE2	2.53	0.44
3:D:331:ILE:O	3:D:334:VAL:HG23	2.18	0.44
3:D:445:ARG:NH1	3:D:466:LYS:HB3	2.32	0.44
3:D:735:SER:O	3:D:739:THR:OG1	2.32	0.44
4:E:22:MET:HA	4:E:26:ALA:HB3	1.99	0.44
4:E:119:ASN:N	4:E:119:ASN:OD1	2.50	0.44
4:E:1087:TYR:HB2	4:E:1213:THR:HG21	2.00	0.44
4:E:1359:ILE:HD12	4:E:1430:LEU:HD23	2.00	0.44
5:F:148:PHE:HE2	5:F:216:LEU:HD11	1.83	0.44
5:F:616:VAL:O	5:F:620:THR:OG1	2.24	0.44
5:F:1543:LEU:HD12	5:F:1543:LEU:O	2.18	0.44
5:F:1623:VAL:HA	5:F:1626:VAL:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:778:LYS:C	8:I:778:LYS:CD	2.85	0.44
7:K:315:LYS:CD	7:K:347:THR:HG22	2.48	0.44
7:K:413:LEU:HD21	8:L:749:GLN:HB3	2.00	0.44
3:D:353:GLN:HG2	3:D:374:LYS:H	1.82	0.44
3:D:929:PHE:HA	3:D:932:ILE:HG22	1.99	0.44
3:D:1494:ASN:N	5:F:1471:LYS:HE2	2.32	0.44
4:E:773:LEU:O	4:E:773:LEU:HD22	2.18	0.44
4:E:1305:ASN:OD1	4:E:1305:ASN:N	2.51	0.44
4:E:1475:SER:HA	4:E:1478:ILE:HD12	2.00	0.44
5:F:452:LYS:HA	5:F:452:LYS:HD2	1.70	0.44
5:F:1490:ARG:HE	5:F:1493:LYS:HB3	1.83	0.44
6:J:377:ILE:HG22	6:J:378:HIS:CD2	2.47	0.44
6:J:389:ARG:HH22	6:J:393:ASP:HB2	1.82	0.44
7:K:444:LEU:CA	7:K:447:SER:CB	2.95	0.44
8:L:637:LEU:O	8:L:641:VAL:HG23	2.18	0.44
1:Z:757:ALA:HA	1:Z:820:ILE:CB	2.47	0.44
1:A:137:ASP:OD2	4:E:1386:LEU:HG	2.16	0.44
1:A:341:LEU:HD21	1:A:371:PHE:CZ	2.53	0.44
5:F:659:ASN:N	5:F:659:ASN:OD1	2.51	0.44
5:F:1363:ILE:HG22	1:Z:125:ILE:HD11	1.97	0.44
6:J:277:ILE:HG12	8:L:641:VAL:HG22	1.99	0.44
6:J:391:LEU:CD1	7:K:455:LYS:HA	2.48	0.44
1:Z:391:HIS:HE2	1:Z:417:ARG:HB3	1.82	0.44
1:A:222:PHE:HD1	1:A:232:PHE:HB3	1.83	0.43
1:A:253:LEU:HG	1:A:257:TRP:CD1	2.53	0.43
1:A:760:PHE:HD2	1:A:823:ARG:HH11	1.66	0.43
3:D:713:ILE:CD1	3:D:769:ARG:HD3	2.48	0.43
3:D:936:VAL:O	3:D:936:VAL:HG12	2.18	0.43
4:E:773:LEU:HD23	4:E:773:LEU:HA	1.50	0.43
4:E:806:PHE:HE2	4:E:854:LEU:HD21	1.82	0.43
4:E:1430:LEU:O	4:E:1432:ARG:NH1	2.51	0.43
5:F:662:PRO:HA	5:F:668:ARG:HE	1.83	0.43
5:F:672:TRP:CE2	5:F:716:LEU:HD12	2.53	0.43
5:F:935:GLN:C	5:F:937:LEU:N	2.71	0.43
5:F:1227:THR:HA	7:H:472:ASN:CB	2.47	0.43
6:G:436:LEU:CD1	7:H:503:ASN:CB	2.96	0.43
7:H:394:THR:HA	8:I:697:LEU:HD22	2.00	0.43
7:H:511:GLU:HA	7:H:514:THR:CB	2.48	0.43
7:K:385:GLN:HA	7:K:385:GLN:NE2	2.23	0.43
8:L:682:ASP:HA	8:L:685:MET:HE2	2.00	0.43
1:Z:196:ASN:HD21	1:Z:530:ARG:NE	2.13	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:585:ILE:O	3:D:589:HIS:HB2	2.17	0.43
5:F:1349:PHE:N	5:F:1349:PHE:HD1	2.15	0.43
1:Z:436:LEU:HD21	1:Z:481:THR:HG23	2.00	0.43
1:Z:767:ILE:CD1	1:Z:768:VAL:HG23	2.49	0.43
3:D:568:GLN:NE2	3:D:570:VAL:O	2.52	0.43
3:D:608:ILE:CD1	3:D:641:VAL:HG13	2.48	0.43
3:D:781:LEU:HD11	3:D:903:ILE:HG21	2.00	0.43
3:D:799:THR:HG23	3:D:803:PHE:O	2.18	0.43
4:E:216:TYR:CD1	4:E:220:PHE:HB2	2.51	0.43
5:F:547:PHE:HE2	5:F:619:VAL:HG11	1.82	0.43
5:F:726:SER:HA	5:F:730:VAL:HG22	2.01	0.43
5:F:742:GLN:HG3	5:F:747:VAL:HA	2.01	0.43
5:F:920:ILE:CG2	5:F:926:LEU:HG	2.48	0.43
8:I:795:LYS:C	8:I:795:LYS:CD	2.85	0.43
6:J:372:PHE:O	6:J:372:PHE:CG	2.70	0.43
6:J:406:PHE:O	6:J:406:PHE:CD1	2.70	0.43
1:Z:56:LEU:HD22	1:Z:60:ASN:ND2	2.32	0.43
1:A:227:GLN:NE2	1:A:606:GLU:O	2.50	0.43
1:A:619:PHE:O	1:A:623:ILE:HG22	2.18	0.43
1:A:703:SER:OG	1:A:711:LYS:NZ	2.39	0.43
1:A:771:ILE:HD13	1:A:774:LEU:HD12	2.00	0.43
2:C:79:HIS:CE1	2:C:704:VAL:HG11	2.54	0.43
3:D:235:SER:CB	3:D:240:LEU:HD13	2.45	0.43
3:D:909:PHE:O	3:D:913:LEU:HG	2.18	0.43
3:D:1377:ASN:HD21	1:Z:758:GLN:HE21	1.59	0.43
4:E:36:GLN:HE22	4:E:943:VAL:HA	1.83	0.43
4:E:919:LEU:HA	4:E:919:LEU:HD12	1.86	0.43
4:E:1408:LEU:HD21	4:E:1456:ILE:HD11	2.00	0.43
5:F:583:SER:O	5:F:583:SER:OG	2.28	0.43
5:F:1000:LEU:HD13	5:F:1000:LEU:HA	1.82	0.43
5:F:1257:LEU:HD23	5:F:1257:LEU:HA	1.84	0.43
5:F:1519:LYS:HA	5:F:1522:VAL:HG12	2.00	0.43
6:G:350:PHE:HE2	7:H:418:GLN:HE22	1.63	0.43
7:H:303:THR:HG23	7:H:353:TYR:CZ	2.53	0.43
6:J:383:LYS:CD	8:L:756:ASN:CG	2.85	0.43
8:L:664:SER:O	8:L:668:VAL:HG23	2.18	0.43
1:A:198:SER:HB3	1:A:543:LYS:HE2	2.01	0.43
1:A:591:GLY:HA3	1:A:600:ILE:O	2.18	0.43
1:A:735:THR:O	1:A:739:MET:HG2	2.18	0.43
3:D:394:GLU:O	3:D:398:ILE:HG13	2.17	0.43
3:D:1467:SER:CA	1:Z:621:HIS:CE1	3.02	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:598:VAL:HG11	4:E:638:ILE:HD11	2.00	0.43
4:E:950:ARG:HG3	4:E:1012:VAL:HA	2.01	0.43
4:E:1444:LEU:O	4:E:1448:SER:N	2.49	0.43
5:F:213:ILE:HB	5:F:240:LEU:HD13	2.00	0.43
5:F:421:ILE:C	5:F:423:LEU:N	2.72	0.43
5:F:1110:MET:CE	5:F:1157:TRP:HZ2	2.29	0.43
5:F:1305:SER:C	5:F:1307:VAL:N	2.69	0.43
6:G:297:ASP:HA	6:G:300:ASP:HB2	1.99	0.43
7:H:386:LEU:HD21	8:I:687:GLU:HA	2.00	0.43
7:H:412:ILE:O	7:H:415:LEU:HB2	2.17	0.43
8:I:798:ASN:O	8:I:801:PHE:CB	2.66	0.43
8:L:667:GLN:O	8:L:670:VAL:HG22	2.18	0.43
1:Z:505:HIS:HA	1:Z:508:ILE:HD12	2.00	0.43
3:D:118:THR:HB	3:D:623:GLY:CA	2.35	0.43
3:D:491:ARG:HB2	3:D:521:LYS:H	1.84	0.43
3:D:508:LYS:CG	3:D:516:LEU:HA	2.49	0.43
3:D:986:THR:C	3:D:988:LEU:H	2.20	0.43
4:E:530:ILE:HA	4:E:552:LEU:O	2.19	0.43
4:E:1274:GLU:HA	4:E:1277:ILE:HD12	1.99	0.43
5:F:227:ASP:CA	5:F:361:LEU:CB	2.97	0.43
5:F:320:GLU:CD	5:F:351:HIS:ND1	2.72	0.43
5:F:676:ASP:HA	5:F:679:ILE:HB	1.99	0.43
5:F:905:SER:CB	8:I:749:GLN:O	2.66	0.43
5:F:1283:LYS:HA	5:F:1283:LYS:NZ	2.33	0.43
6:G:452:ASP:CB	1:Z:84:ASP:CG	2.87	0.43
7:K:395:ALA:O	7:K:399:LEU:HD23	2.19	0.43
8:L:695:GLN:NE2	8:L:696:SER:OG	2.51	0.43
8:L:809:ASP:HA	8:L:812:THR:HB	2.00	0.43
1:Z:786:ILE:HD11	1:Z:838:SER:HA	2.01	0.43
1:A:649:GLU:OE1	1:A:652:ILE:HD12	2.19	0.43
3:D:214:VAL:HA	3:D:233:LEU:O	2.18	0.43
3:D:451:SER:HB2	3:D:458:GLU:HB2	2.01	0.43
3:D:509:PHE:CD1	3:D:515:VAL:HG23	2.54	0.43
4:E:291:ASP:OD1	4:E:291:ASP:N	2.52	0.43
5:F:783:ILE:HG13	5:F:784:ILE:H	1.83	0.43
5:F:1088:ARG:HH11	5:F:1088:ARG:CG	2.23	0.43
5:F:1489:ILE:HA	5:F:1492:LEU:HD12	2.01	0.43
8:I:731:GLY:C	8:I:733:ALA:N	2.71	0.43
8:I:795:LYS:C	8:I:795:LYS:NZ	2.72	0.43
6:J:379:LEU:HG	6:J:379:LEU:O	2.19	0.43
6:J:406:PHE:CD1	6:J:406:PHE:C	2.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:454:GLY:C	7:K:456:THR:H	2.22	0.43
8:L:637:LEU:CD2	8:L:640:LEU:HB2	2.48	0.43
1:Z:444:LYS:HA	1:Z:444:LYS:HD3	1.89	0.43
1:A:131:GLY:HA2	1:A:134:LYS:HD3	2.01	0.43
1:A:436:LEU:HD21	1:A:481:THR:HG23	2.00	0.43
3:D:484:GLN:NE2	3:D:566:LYS:H	2.16	0.43
3:D:713:ILE:HD12	3:D:769:ARG:CD	2.48	0.43
4:E:40:ILE:HD12	4:E:40:ILE:HA	1.90	0.43
4:E:605:LYS:O	4:E:605:LYS:NZ	2.37	0.43
4:E:787:PRO:HG2	4:E:1143:GLN:HE21	1.84	0.43
5:F:131:TYR:O	5:F:135:ILE:HG12	2.19	0.43
5:F:334:GLN:HB3	5:F:860:ASN:CG	2.37	0.43
5:F:900:LEU:HD13	5:F:904:TYR:CD1	2.53	0.43
5:F:1618:SER:CB	1:Z:634:ASP:O	2.67	0.43
8:I:805:ARG:CB	1:Z:88:LYS:HE2	2.47	0.43
6:J:305:ILE:HG21	8:L:665:TRP:NE1	2.34	0.43
6:J:435:GLY:O	6:J:440:VAL:CB	2.67	0.43
8:L:682:ASP:OD1	8:L:685:MET:HE3	2.19	0.43
1:Z:78:LEU:HB3	1:Z:83:VAL:CG2	2.48	0.43
1:A:138:ASN:C	1:A:138:ASN:ND2	2.72	0.43
1:A:531:ASP:OD2	1:A:536:ASN:ND2	2.41	0.43
3:D:447:TYR:O	3:D:463:GLU:N	2.52	0.43
4:E:185:LEU:HD23	4:E:185:LEU:HA	1.89	0.43
4:E:305:ASP:O	4:E:309:ASN:CB	2.67	0.43
4:E:1387:LEU:O	4:E:1391:LEU:N	2.51	0.43
4:E:1561:LEU:HD13	4:E:1585:LEU:HD11	2.01	0.43
5:F:135:ILE:HG23	5:F:206:ILE:HA	2.01	0.43
5:F:229:PHE:O	5:F:233:TYR:N	2.52	0.43
5:F:522:MET:SD	5:F:523:ARG:N	2.92	0.43
5:F:680:PHE:HA	5:F:745:ARG:HH12	1.83	0.43
5:F:909:LEU:O	7:H:403:SER:CB	2.66	0.43
5:F:1362:ASP:CB	1:Z:125:ILE:CG2	2.97	0.43
5:F:1550:LEU:HD11	5:F:1604:ILE:HG21	2.00	0.43
8:I:792:GLN:HG2	1:Z:42:ILE:HD12	1.49	0.43
8:I:821:ILE:CD1	8:I:821:ILE:C	2.85	0.43
6:J:365:SER:N	7:K:424:ASN:HD21	2.04	0.43
1:Z:138:ASN:C	1:Z:138:ASN:ND2	2.72	0.43
1:Z:474:PHE:HB3	1:Z:477:TYR:HB3	2.00	0.43
1:Z:637:ILE:O	1:Z:640:SER:OG	2.28	0.43
3:D:401:ILE:CG2	3:D:462:LEU:HB3	2.30	0.43
3:D:491:ARG:HG3	3:D:521:LYS:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:582:ASP:O	3:D:585:ILE:HG22	2.19	0.43
3:D:766:LEU:HD22	3:D:889:GLU:HA	2.01	0.43
5:F:300:MET:HG3	5:F:303:LYS:HE2	2.00	0.43
5:F:841:PHE:CZ	5:F:922:LEU:HB2	2.54	0.43
5:F:925:HIS:HA	5:F:928:LEU:HD11	2.00	0.43
5:F:1545:ARG:HA	5:F:1548:ALA:HB3	2.01	0.43
6:J:311:ASP:CG	7:K:376:LEU:HD21	2.39	0.43
6:J:334:SER:HA	6:J:337:LYS:HB2	2.01	0.43
6:J:431:GLN:O	8:L:782:ILE:HA	2.19	0.43
7:K:437:TRP:HB3	8:L:744:ALA:HB3	2.00	0.43
8:L:664:SER:O	8:L:667:GLN:HG3	2.19	0.43
1:Z:136:PHE:CD1	1:Z:136:PHE:O	2.71	0.43
1:Z:709:LYS:NZ	1:Z:764:ASP:HB3	2.34	0.43
1:A:681:SER:HA	1:A:687:LEU:HB3	2.01	0.42
3:D:793:PHE:CZ	3:D:934:SER:HB2	2.54	0.42
4:E:370:SER:O	4:E:372:ASP:N	2.48	0.42
4:E:916:TYR:CZ	4:E:963:LYS:HB2	2.54	0.42
4:E:1276:LYS:HA	4:E:1276:LYS:HD2	1.71	0.42
5:F:606:VAL:HA	5:F:609:LEU:HG	2.01	0.42
5:F:731:PHE:CD2	5:F:790:SER:HA	2.54	0.42
6:G:296:ALA:CB	6:J:363:LYS:HD2	2.45	0.42
6:G:449:LEU:HA	1:Z:84:ASP:OD1	2.19	0.42
8:L:733:ALA:HA	8:L:737:ASN:HD21	1.84	0.42
1:Z:510:LEU:HB3	1:Z:516:PHE:HB2	2.00	0.42
1:A:225:SER:O	1:A:229:ASN:N	2.51	0.42
3:D:822:ILE:HG22	3:D:824:GLN:H	1.84	0.42
3:D:884:VAL:HB	3:D:887:GLN:OE1	2.19	0.42
5:F:200:LEU:HA	5:F:200:LEU:HD13	1.79	0.42
5:F:825:ILE:O	5:F:825:ILE:HG23	2.19	0.42
5:F:935:GLN:CB	5:F:998:LEU:CD2	2.97	0.42
6:J:371:LYS:C	6:J:371:LYS:CD	2.88	0.42
7:K:311:PHE:HD1	7:K:351:GLN:HG3	1.85	0.42
7:K:321:ALA:O	7:K:339:MET:HE3	2.19	0.42
7:K:402:GLN:C	7:K:402:GLN:NE2	2.72	0.42
1:A:681:SER:OG	1:A:691:ARG:NH1	2.52	0.42
1:A:709:LYS:O	1:A:713:ILE:HG12	2.18	0.42
3:D:375:SER:O	3:D:420:ILE:HD12	2.18	0.42
3:D:648:GLU:HG3	3:D:650:TYR:HE1	1.83	0.42
3:D:988:LEU:HA	3:D:992:CYS:CB	2.49	0.42
4:E:982:ILE:HD12	4:E:982:ILE:H	1.85	0.42
4:E:1356:LEU:CB	1:Z:453:VAL:HG21	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:158:ILE:HA	5:F:183:ARG:CZ	2.49	0.42
5:F:437:ASP:HA	5:F:440:GLN:HG3	2.01	0.42
6:G:440:VAL:HA	6:G:443:VAL:HB	2.01	0.42
7:H:420:ALA:CB	8:I:745:TYR:CD1	2.96	0.42
7:H:444:LEU:HA	7:H:447:SER:HB3	2.02	0.42
7:H:532:ALA:HA	8:I:821:ILE:HG13	2.01	0.42
7:K:525:GLU:O	7:K:529:LYS:CB	2.56	0.42
8:L:640:LEU:CD1	8:L:643:LYS:HG2	2.49	0.42
1:Z:551:ARG:NH2	1:Z:606:GLU:OE2	2.46	0.42
1:Z:687:LEU:HD23	1:Z:690:ARG:HD2	2.01	0.42
3:D:168:GLN:N	3:D:187:ASP:OD2	2.38	0.42
3:D:381:VAL:O	3:D:385:LYS:HA	2.19	0.42
3:D:491:ARG:HB2	3:D:520:THR:HB	2.01	0.42
3:D:605:VAL:HG11	3:D:608:ILE:HD11	2.01	0.42
3:D:611:LEU:HG	3:D:640:ALA:HB2	2.01	0.42
3:D:1367:LEU:HD23	3:D:1398:PHE:CE1	2.54	0.42
4:E:319:PRO:HG2	4:E:361:LYS:HD3	2.00	0.42
5:F:390:TRP:CB	5:F:393:SER:HB3	2.50	0.42
5:F:426:GLN:HA	5:F:429:GLU:HG3	2.00	0.42
5:F:1508:ILE:HG22	5:F:1511:LEU:HD23	2.02	0.42
7:H:415:LEU:HD12	7:H:415:LEU:HA	1.79	0.42
8:I:815:GLU:HB3	8:I:816:LYS:HE3	2.02	0.42
6:J:283:TYR:CD2	6:J:286:LYS:HE2	2.55	0.42
6:J:311:ASP:OD2	7:K:376:LEU:HD11	2.20	0.42
1:Z:117:LYS:HB3	1:Z:117:LYS:HZ2	1.79	0.42
1:Z:432:ILE:HD12	1:Z:432:ILE:HA	1.90	0.42
1:Z:779:LEU:CB	1:Z:835:ILE:CA	2.97	0.42
1:A:140:ILE:HG23	4:E:1393:LYS:HD3	1.84	0.42
1:A:532:ILE:HG22	1:A:532:ILE:O	2.19	0.42
2:C:888:LEU:HA	2:C:892:PHE:HD2	1.85	0.42
3:D:467:PHE:CD1	3:D:473:THR:HG23	2.54	0.42
3:D:919:VAL:HG12	3:D:920:GLU:N	2.34	0.42
3:D:1241:GLY:O	1:Z:826:ARG:CB	2.67	0.42
4:E:343:ASP:O	4:E:347:THR:OG1	2.36	0.42
4:E:976:PHE:HZ	7:K:457:ASN:HB3	1.83	0.42
5:F:917:PHE:O	5:F:919:ASN:N	2.52	0.42
6:G:343:ASP:O	6:G:347:THR:OG1	2.30	0.42
6:J:298:THR:HA	8:L:658:TYR:CE1	2.54	0.42
7:K:365:GLN:O	7:K:369:VAL:HG23	2.20	0.42
1:A:370:TYR:CD2	1:A:390:LEU:HD13	2.54	0.42
1:A:516:PHE:CE2	1:A:534:PHE:HB2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:295:GLU:CD	3:D:316:LYS:HE3	2.40	0.42
3:D:367:ILE:HA	3:D:380:TYR:O	2.20	0.42
3:D:667:LEU:HD12	3:D:669:PHE:HB2	2.00	0.42
3:D:684:PHE:O	3:D:688:LYS:HB2	2.19	0.42
4:E:569:LEU:HD22	4:E:634:ILE:HD11	2.01	0.42
4:E:683:ASP:OD1	4:E:689:GLY:N	2.36	0.42
5:F:1090:PRO:CD	5:F:1093:SER:HB3	2.50	0.42
5:F:1545:ARG:HA	5:F:1545:ARG:HD2	1.91	0.42
6:G:465:LYS:CE	1:Z:20:LYS:HE2	2.49	0.42
7:H:365:GLN:HA	7:H:368:ASN:HD22	1.84	0.42
7:K:358:LEU:HD22	8:L:662:ILE:CD1	2.41	0.42
1:Z:116:LYS:C	1:Z:116:LYS:CE	2.85	0.42
1:Z:122:LEU:HD23	1:Z:122:LEU:HA	1.73	0.42
1:Z:254:LEU:HG	1:Z:258:LYS:HE2	2.02	0.42
1:Z:599:ARG:HH22	1:Z:620:LEU:HD21	1.84	0.42
1:A:679:ASP:OD2	1:A:684:ASN:ND2	2.50	0.42
1:A:776:ILE:CD1	1:A:828:THR:HG23	2.49	0.42
2:C:899:ALA:HB3	2:C:941:ASN:HD22	1.83	0.42
3:D:514:SER:O	3:D:515:VAL:HG13	2.20	0.42
3:D:681:THR:O	3:D:685:VAL:HG23	2.20	0.42
4:E:443:ILE:HD12	4:E:590:LEU:HD11	2.01	0.42
4:E:599:THR:HG23	4:E:660:PHE:HA	2.02	0.42
4:E:1539:ASN:ND2	4:E:1611:TYR:OH	2.48	0.42
7:K:483:VAL:CB	7:K:494:MET:HA	2.49	0.42
7:K:483:VAL:N	7:K:493:SER:C	2.70	0.42
1:Z:239:ILE:HG23	1:Z:258:LYS:HZ2	1.84	0.42
1:A:478:TYR:O	1:A:482:LEU:HG	2.20	0.42
4:E:36:GLN:NE2	4:E:36:GLN:O	2.53	0.42
4:E:120:PRO:HB3	4:E:127:TYR:CG	2.54	0.42
4:E:421:PHE:O	4:E:425:LEU:CB	2.68	0.42
5:F:296:ARG:H	5:F:296:ARG:HG3	1.71	0.42
5:F:1293:ASN:ND2	5:F:1293:ASN:C	2.73	0.42
5:F:1305:SER:O	5:F:1307:VAL:N	2.49	0.42
6:G:295:LYS:HB3	6:J:363:LYS:NZ	2.33	0.42
6:G:377:ILE:HD12	6:G:377:ILE:HA	1.96	0.42
7:H:462:ARG:HA	7:H:465:ILE:HB	2.02	0.42
7:K:455:LYS:HD3	7:K:455:LYS:H	1.75	0.42
8:L:671:LYS:O	8:L:675:GLN:NE2	2.47	0.42
1:Z:654:ILE:HG22	1:Z:710:ASN:HB2	2.01	0.42
1:A:137:ASP:HB2	4:E:1386:LEU:CA	2.43	0.42
1:A:215:TYR:CD2	1:A:238:PHE:HE1	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:381:VAL:HB	3:D:457:ILE:CG2	2.50	0.42
4:E:222:GLU:O	4:E:226:ASN:HB2	2.20	0.42
4:E:1043:LEU:HB3	4:E:1078:ILE:HD11	2.00	0.42
5:F:864:LEU:HD12	5:F:864:LEU:HA	1.81	0.42
5:F:929:TYR:C	5:F:931:GLY:N	2.73	0.42
5:F:1144:VAL:HG11	5:F:1291:SER:OG	2.20	0.42
5:F:1550:LEU:HD12	5:F:1604:ILE:HG21	2.01	0.42
5:F:1634:LYS:HA	5:F:1637:VAL:HG22	2.00	0.42
8:I:672:GLY:HA2	8:I:675:GLN:HG2	2.00	0.42
8:I:822:LYS:NZ	8:I:822:LYS:CB	2.82	0.42
6:J:371:LYS:O	6:J:371:LYS:CD	2.68	0.42
7:K:462:ARG:O	7:K:466:LEU:HD12	2.20	0.42
8:L:749:GLN:NE2	8:L:752:ASP:OD2	2.51	0.42
1:Z:121:ILE:HD12	1:Z:121:ILE:HA	1.64	0.42
1:Z:367:PHE:O	1:Z:370:TYR:HB2	2.20	0.42
1:A:775:LEU:CD1	1:A:832:LEU:CD1	2.95	0.42
2:C:1388:HIS:O	4:E:1331:LEU:HD13	2.19	0.42
3:D:292:ASN:OD1	3:D:293:ILE:N	2.53	0.42
3:D:680:SER:OG	3:D:772:GLY:HA2	2.20	0.42
3:D:873:SER:HB3	3:D:877:VAL:HB	2.01	0.42
3:D:976:THR:CB	3:D:981:ILE:CA	2.97	0.42
3:D:988:LEU:CB	3:D:1001:ILE:CB	2.98	0.42
4:E:429:LYS:HA	4:E:429:LYS:HD2	1.80	0.42
4:E:672:VAL:HG12	4:E:676:LEU:HD12	2.02	0.42
5:F:968:ILE:HA	7:H:392:LEU:HD11	2.02	0.42
5:F:1177:VAL:C	5:F:1180:TYR:CB	2.88	0.42
6:J:304:LEU:O	6:J:308:ILE:HG12	2.19	0.42
6:J:334:SER:C	6:J:336:PHE:H	2.15	0.42
7:K:352:ILE:HG21	7:K:358:LEU:HD21	2.01	0.42
8:L:794:ILE:HA	8:L:797:LEU:HB3	2.02	0.42
1:Z:776:ILE:C	1:Z:778:THR:H	2.23	0.42
1:A:785:MET:SD	1:A:806:LEU:HD11	2.60	0.41
2:C:693:LEU:HB3	2:C:694:PHE:CD1	2.54	0.41
3:D:131:VAL:HG21	3:D:467:PHE:H	1.84	0.41
3:D:508:LYS:HE3	3:D:518:GLU:HG2	2.01	0.41
3:D:662:LEU:HD23	3:D:662:LEU:HA	1.88	0.41
4:E:199:ILE:O	4:E:202:THR:OG1	2.38	0.41
4:E:1266:LYS:HD3	4:E:1266:LYS:HA	1.74	0.41
5:F:285:PHE:O	5:F:289:CYS:N	2.49	0.41
5:F:640:PHE:O	5:F:643:THR:C	2.58	0.41
5:F:917:PHE:HZ	7:H:400:LYS:HZ2	1.66	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1196:SER:HB2	5:F:1198:LEU:H	1.84	0.41
5:F:1198:LEU:HD22	5:F:1201:LEU:HD13	2.02	0.41
6:G:398:VAL:HA	6:G:401:ILE:HG12	2.01	0.41
6:J:290:ILE:HD12	7:K:356:GLU:OE2	2.20	0.41
1:Z:641:ILE:HD12	1:Z:641:ILE:HA	1.88	0.41
1:A:432:ILE:HD12	1:A:435:TRP:HB3	2.02	0.41
3:D:135:PHE:CZ	3:D:485:GLN:HB2	2.55	0.41
4:E:989:ASP:C	4:E:991:LYS:N	2.72	0.41
5:F:672:TRP:O	5:F:675:LEU:HB3	2.19	0.41
5:F:1068:ILE:HD12	5:F:1150:PHE:HD2	1.52	0.41
8:L:659:THR:HA	8:L:662:ILE:HG22	2.02	0.41
2:C:1389:GLY:HA2	4:E:1331:LEU:HD11	2.02	0.41
3:D:402:ILE:CG2	3:D:406:THR:H	2.29	0.41
3:D:846:ILE:HG13	3:D:907:LEU:CD1	2.51	0.41
4:E:1483:ILE:HG21	4:E:1492:HIS:CE1	2.56	0.41
5:F:765:ASP:OD1	5:F:765:ASP:N	2.51	0.41
5:F:1251:ARG:HH22	5:F:1276:ASP:HB3	1.73	0.41
6:J:327:LYS:HG3	6:J:328:GLN:NE2	2.34	0.41
6:J:381:GLU:HA	6:J:381:GLU:OE2	2.19	0.41
6:J:389:ARG:NH1	6:J:389:ARG:HA	2.35	0.41
7:K:311:PHE:CD1	7:K:351:GLN:HG3	2.55	0.41
7:K:352:ILE:CG2	7:K:358:LEU:HG	2.47	0.41
7:K:503:ASN:HB2	7:K:506:ILE:CD1	2.50	0.41
1:Z:436:LEU:HA	1:Z:439:HIS:HB2	2.02	0.41
1:Z:807:LYS:CB	1:Z:837:VAL:HA	2.50	0.41
1:A:682:GLU:HG2	1:A:691:ARG:NH2	2.30	0.41
1:A:780:SER:O	1:A:784:ASN:ND2	2.53	0.41
3:D:178:GLU:HB3	3:D:230:HIS:NE2	2.35	0.41
4:E:268:THR:O	4:E:272:ILE:HG13	2.21	0.41
4:E:464:ALA:HB1	4:E:552:LEU:HD21	2.01	0.41
4:E:923:LEU:C	4:E:923:LEU:CD2	2.87	0.41
5:F:42:LEU:HD12	5:F:42:LEU:HA	1.95	0.41
5:F:189:GLU:HA	5:F:192:ILE:HG12	2.02	0.41
5:F:321:GLN:O	5:F:325:PHE:CB	2.68	0.41
5:F:470:ASP:N	5:F:470:ASP:OD1	2.53	0.41
5:F:589:ASP:OD1	5:F:589:ASP:N	2.52	0.41
5:F:866:GLN:OE1	5:F:940:ASN:HB2	2.20	0.41
5:F:1027:GLN:CG	5:F:1027:GLN:O	2.69	0.41
6:J:411:ASN:OD1	6:J:411:ASN:N	2.41	0.41
7:K:454:GLY:O	7:K:456:THR:N	2.52	0.41
1:Z:558:VAL:HG21	1:Z:607:ARG:HE	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:182:CYS:HB2	3:D:193:TRP:CE2	2.56	0.41
4:E:1066:VAL:HA	4:E:1069:ILE:HD12	2.02	0.41
4:E:1389:LEU:HA	4:E:1392:PHE:HD2	1.85	0.41
5:F:348:LEU:HD22	5:F:483:LEU:HD22	2.03	0.41
5:F:386:GLY:HA3	5:F:392:PRO:O	2.20	0.41
5:F:885:GLU:O	5:F:885:GLU:CG	2.68	0.41
8:I:816:LYS:N	8:I:816:LYS:CE	2.83	0.41
6:J:306:ASP:O	6:J:309:PRO:HD2	2.20	0.41
6:J:371:LYS:NZ	6:J:371:LYS:C	2.70	0.41
1:Z:90:LEU:HD23	1:Z:90:LEU:HA	1.69	0.41
3:D:903:ILE:HG12	3:D:953:PHE:CD1	2.56	0.41
5:F:159:LYS:HA	5:F:159:LYS:HD3	1.82	0.41
5:F:164:LYS:HA	5:F:167:ILE:HG12	2.02	0.41
5:F:220:VAL:HA	5:F:223:LEU:HG	2.01	0.41
5:F:450:LEU:HA	5:F:453:ILE:HG12	2.02	0.41
5:F:719:ILE:HG12	5:F:731:PHE:CD2	2.56	0.41
5:F:1158:THR:HG22	5:F:1197:PHE:CD2	2.55	0.41
5:F:1193:ARG:HA	5:F:1193:ARG:HD3	1.85	0.41
5:F:1282:ALA:O	5:F:1286:PHE:N	2.47	0.41
7:H:313:TYR:O	7:H:361:ARG:NH2	2.53	0.41
8:L:676:ILE:HD13	8:L:679:LEU:HD22	2.01	0.41
1:Z:49:LEU:C	1:Z:49:LEU:HD13	2.40	0.41
3:D:274:VAL:HG23	3:D:283:PHE:HB2	2.02	0.41
4:E:192:LEU:HD23	4:E:195:LEU:HD23	2.01	0.41
4:E:369:LEU:HD23	4:E:375:TYR:CD2	2.56	0.41
5:F:108:LEU:O	5:F:111:GLN:HB3	2.20	0.41
5:F:633:LYS:NZ	5:F:635:PHE:HB2	2.35	0.41
7:K:305:LYS:O	7:K:307:LYS:HE2	2.20	0.41
1:Z:822:TYR:HB3	1:Z:824:MET:SD	2.60	0.41
1:A:650:TYR:CG	1:A:702:ILE:HG23	2.55	0.41
3:D:135:PHE:HD1	3:D:596:ALA:HB3	1.86	0.41
3:D:421:VAL:HG22	3:D:491:ARG:N	2.35	0.41
3:D:617:ALA:HA	3:D:630:THR:CG2	2.47	0.41
3:D:788:HIS:ND1	3:D:946:LYS:HA	2.35	0.41
4:E:331:TYR:HD1	4:E:331:TYR:HA	1.72	0.41
4:E:1133:LYS:HD2	4:E:1133:LYS:HA	1.90	0.41
5:F:245:ARG:NH2	5:F:284:TYR:O	2.45	0.41
5:F:321:GLN:O	5:F:325:PHE:HB3	2.21	0.41
8:I:694:ASP:O	8:I:698:GLN:NE2	2.54	0.41
8:I:822:LYS:HE3	8:I:822:LYS:CA	2.44	0.41
6:J:389:ARG:O	6:J:389:ARG:CZ	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:315:LYS:HG3	7:K:347:THR:HG22	2.02	0.41
7:K:506:ILE:HG13	7:K:507:ASN:H	1.85	0.41
1:Z:206:ASN:OD1	1:Z:206:ASN:N	2.53	0.41
1:A:232:PHE:CZ	1:A:237:GLU:HG3	2.56	0.41
1:A:479:LEU:HD12	1:A:491:ALA:HB1	2.02	0.41
3:D:585:ILE:HG23	3:D:586:LEU:HD12	2.03	0.41
3:D:791:MET:O	3:D:830:SER:OG	2.27	0.41
4:E:22:MET:HE1	4:E:122:ILE:HG21	2.03	0.41
4:E:744:LEU:HD12	4:E:744:LEU:HA	1.90	0.41
5:F:26:LYS:HZ3	5:F:26:LYS:HG2	1.72	0.41
5:F:37:LEU:HD22	5:F:146:SER:HB2	2.02	0.41
5:F:68:GLN:HA	5:F:71:ILE:HD13	2.03	0.41
5:F:144:ILE:HD13	5:F:197:LEU:HD23	2.01	0.41
5:F:633:LYS:HA	5:F:633:LYS:HD2	1.82	0.41
5:F:835:LYS:HD2	5:F:835:LYS:HA	1.75	0.41
5:F:920:ILE:CB	5:F:924:ALA:O	2.69	0.41
5:F:1550:LEU:HD23	5:F:1550:LEU:HA	1.88	0.41
7:H:394:THR:O	7:H:398:ILE:HB	2.21	0.41
8:I:795:LYS:NZ	8:I:799:SER:HB3	2.35	0.41
6:J:371:LYS:O	6:J:371:LYS:CE	2.68	0.41
7:K:509:ILE:HA	7:K:512:ILE:HB	2.01	0.41
1:Z:249:ARG:C	1:Z:251:ALA:N	2.65	0.41
1:Z:571:LEU:HA	1:Z:574:GLU:HG3	2.03	0.41
1:A:776:ILE:HD11	1:A:828:THR:HG23	2.03	0.41
3:D:716:VAL:HG13	3:D:767:SER:HB3	2.02	0.41
3:D:778:THR:O	3:D:782:ARG:HB2	2.20	0.41
4:E:904:LEU:HD23	4:E:907:LEU:HD23	2.02	0.41
4:E:1529:ILE:HG21	4:E:1589:LEU:HD21	2.03	0.41
5:F:25:PHE:HB3	5:F:26:LYS:NZ	2.36	0.41
5:F:486:TYR:HD1	5:F:532:SER:HB3	1.86	0.41
5:F:1097:TYR:OH	5:F:1164:PHE:CD1	2.49	0.41
5:F:1300:LEU:HD23	5:F:1301:SER:N	2.36	0.41
6:J:381:GLU:OE2	6:J:381:GLU:CA	2.69	0.41
6:J:420:ASP:HB2	6:J:436:LEU:HD22	2.04	0.41
7:K:330:VAL:C	7:K:331:LEU:HD12	2.41	0.41
7:K:433:GLU:HB2	8:L:741:ARG:HE	1.85	0.41
7:K:503:ASN:HB2	7:K:506:ILE:HD13	2.03	0.41
1:A:451:ASP:OD1	1:A:455:GLU:HB2	2.22	0.40
1:A:533:ARG:HE	1:A:534:PHE:N	2.19	0.40
1:A:586:PHE:CD2	1:A:642:LEU:HD11	2.56	0.40
1:A:603:VAL:O	1:A:606:GLU:HG2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:212:GLN:N	3:D:235:SER:O	2.47	0.40
3:D:328:LEU:CD1	3:D:334:VAL:HG22	2.50	0.40
3:D:1431:LYS:HE2	3:D:1435:GLU:OE1	2.20	0.40
4:E:923:LEU:CD1	4:E:931:PHE:HE2	2.26	0.40
4:E:1319:LEU:CD2	4:E:1398:VAL:HG22	2.46	0.40
5:F:90:GLU:HA	5:F:93:LEU:HB2	2.03	0.40
5:F:460:SER:HB2	5:F:475:LYS:HB3	2.02	0.40
5:F:863:GLU:HA	5:F:866:GLN:HE21	1.87	0.40
5:F:964:LYS:CG	5:F:964:LYS:O	2.69	0.40
5:F:971:SER:HB3	7:H:392:LEU:CD2	2.50	0.40
5:F:1082:ILE:HA	5:F:1082:ILE:HD13	1.87	0.40
5:F:1626:VAL:HA	5:F:1629:LEU:HB3	2.03	0.40
8:I:815:GLU:HB3	8:I:816:LYS:CE	2.51	0.40
8:I:818:ILE:HD12	8:I:818:ILE:HA	1.80	0.40
6:J:356:GLN:HB3	7:K:423:LYS:NZ	2.36	0.40
6:J:402:ASP:HB2	7:K:466:LEU:CD2	2.51	0.40
7:K:446:ARG:O	7:K:446:ARG:CD	2.69	0.40
8:L:653:SER:O	8:L:657:GLN:HG2	2.21	0.40
8:L:679:LEU:O	8:L:682:ASP:HB2	2.20	0.40
8:L:800:HIS:O	8:L:804:LEU:CB	2.65	0.40
3:D:371:LEU:HD21	3:D:420:ILE:HG22	2.04	0.40
3:D:586:LEU:HD11	3:D:593:VAL:H	1.86	0.40
3:D:673:TYR:O	3:D:677:GLU:HB2	2.22	0.40
4:E:79:LEU:HD11	4:E:99:VAL:HG22	2.04	0.40
4:E:1305:ASN:HA	4:E:1308:TYR:CZ	2.56	0.40
4:E:1329:ILE:O	4:E:1333:SER:HB3	2.21	0.40
5:F:651:GLY:HA3	5:F:705:ASP:HA	2.03	0.40
5:F:662:PRO:HG3	5:F:715:ASN:ND2	2.36	0.40
5:F:914:ASP:CG	5:F:917:PHE:CB	2.89	0.40
5:F:974:GLU:OE1	5:F:977:ARG:NH2	2.51	0.40
5:F:1431:ARG:HD2	5:F:1474:PHE:N	2.36	0.40
8:I:795:LYS:NZ	8:I:795:LYS:CB	2.84	0.40
7:K:315:LYS:HD2	7:K:347:THR:HG22	2.03	0.40
7:K:408:ILE:O	7:K:412:ILE:HG13	2.22	0.40
7:K:529:LYS:HB3	7:K:529:LYS:HE3	1.98	0.40
7:K:538:LYS:CB	8:L:818:ILE:CA	2.98	0.40
8:L:703:GLN:OE1	8:L:704:GLN:N	2.54	0.40
1:Z:757:ALA:CB	1:Z:819:MET:C	2.39	0.40
1:A:697:PHE:CD1	1:A:697:PHE:N	2.88	0.40
3:D:422:LYS:HE2	3:D:524:THR:OG1	2.21	0.40
3:D:574:HIS:HD1	3:D:576:LEU:HD12	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:924:ASN:O	3:D:925:GLN:HB2	2.21	0.40
4:E:1046:LYS:HZ3	4:E:1074:LEU:HD11	1.86	0.40
4:E:1168:LYS:O	4:E:1174:ASN:ND2	2.45	0.40
4:E:1380:ASP:C	4:E:1382:THR:H	2.24	0.40
5:F:245:ARG:HH22	5:F:288:TRP:N	2.18	0.40
5:F:409:MET:CB	5:F:410:PRO:HD2	2.51	0.40
5:F:661:VAL:CG1	5:F:712:LEU:HD12	2.50	0.40
5:F:1080:LEU:O	5:F:1156:TYR:CE2	2.74	0.40
6:G:319:GLU:HA	6:G:322:THR:HG22	2.03	0.40
6:J:309:PRO:HA	6:J:312:VAL:CB	2.50	0.40
6:J:357:LEU:HD22	7:K:423:LYS:HE3	2.03	0.40
1:A:687:LEU:O	1:A:691:ARG:HG3	2.22	0.40
1:A:696:TYR:CD1	1:A:702:ILE:HG21	2.57	0.40
3:D:157:PRO:HD2	3:D:160:ILE:HD12	2.03	0.40
4:E:939:LEU:HB3	4:E:997:VAL:HG11	2.04	0.40
4:E:1451:CYS:HA	4:E:1457:ALA:HB2	2.04	0.40
5:F:283:ALA:HA	5:F:441:THR:HG21	2.04	0.40
5:F:1157:TRP:CD1	5:F:1161:LEU:HD13	2.56	0.40
5:F:1360:LEU:N	5:F:1360:LEU:HD12	2.37	0.40
5:F:1364:TYR:HB2	5:F:1374:LYS:CB	2.51	0.40
5:F:1442:TRP:NE1	5:F:1484:ARG:HB3	2.36	0.40
5:F:1660:ASN:O	5:F:1664:ASN:ND2	2.54	0.40
6:G:275:GLN:NE2	6:G:278:GLU:OE1	2.40	0.40
6:G:450:PHE:O	6:G:454:ALA:HB2	2.21	0.40
8:I:775:THR:OG1	8:I:776:PHE:N	2.55	0.40
8:I:778:LYS:HZ2	8:I:778:LYS:CA	2.34	0.40
7:K:339:MET:HG3	7:K:339:MET:O	2.22	0.40
8:L:658:TYR:HE1	8:L:665:TRP:HZ3	1.70	0.40
8:L:674:GLU:OE1	8:L:675:GLN:NE2	2.55	0.40
8:L:816:LYS:HD2	8:L:816:LYS:HA	1.83	0.40
1:A:495:THR:HG22	1:A:503:ALA:HB2	2.03	0.40
3:D:484:GLN:HE22	3:D:566:LYS:H	1.70	0.40
3:D:491:ARG:CA	3:D:520:THR:HB	2.51	0.40
5:F:918:PHE:HA	5:F:922:LEU:HD11	2.04	0.40
6:G:305:ILE:HD12	6:G:305:ILE:HA	1.91	0.40
6:G:391:LEU:HA	6:G:394:ILE:HG12	2.03	0.40
7:K:427:LEU:N	7:K:427:LEU:HD22	2.36	0.40
7:K:429:LEU:C	7:K:429:LEU:CD1	2.85	0.40
1:Z:305:ILE:HD12	1:Z:339:TYR:HB3	2.02	0.40
1:Z:565:GLY:O	1:Z:569:VAL:N	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	A	722/839 (86%)	700 (97%)	20 (3%)	2 (0%)	41 74
1	Z	736/839 (88%)	675 (92%)	39 (5%)	22 (3%)	4 32
2	C	1323/1391 (95%)	1269 (96%)	41 (3%)	13 (1%)	15 51
3	D	1396/1502 (93%)	1275 (91%)	113 (8%)	8 (1%)	25 61
4	E	1538/1655 (93%)	1376 (90%)	149 (10%)	13 (1%)	19 56
5	F	1616/1683 (96%)	1203 (74%)	317 (20%)	96 (6%)	1 19
6	G	198/472 (42%)	188 (95%)	9 (4%)	1 (0%)	29 65
6	J	191/472 (40%)	175 (92%)	13 (7%)	3 (2%)	9 43
7	H	242/541 (45%)	202 (84%)	36 (15%)	4 (2%)	9 42
7	K	252/541 (47%)	209 (83%)	32 (13%)	11 (4%)	2 24
8	I	185/823 (22%)	158 (85%)	16 (9%)	11 (6%)	1 19
8	L	185/823 (22%)	164 (89%)	15 (8%)	6 (3%)	4 31
All	All	8584/11581 (74%)	7594 (88%)	800 (9%)	190 (2%)	10 38

All (190) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	VAL
2	C	319	PRO
2	C	468	PHE
2	C	476	ASN
2	C	694	PHE
2	C	1255	SER
3	D	528	PRO
3	D	665	ASN
3	D	1000	ASP
3	D	1128	GLN
3	D	1134	SER
4	E	923	LEU

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Mol	Chain	Res	Type
4	E	986	SER
4	E	989	ASP
4	E	990	LYS
5	F	353	PRO
5	F	357	PRO
5	F	380	ALA
5	F	391	ASN
5	F	394	TYR
5	F	395	PRO
5	F	410	PRO
5	F	823	PRO
5	F	825	ILE
5	F	885	GLU
5	F	888	PRO
5	F	919	ASN
5	F	921	PRO
5	F	934	ASP
5	F	935	GLN
5	F	1031	VAL
5	F	1036	PRO
5	F	1090	PRO
5	F	1183	TYR
5	F	1187	ASN
5	F	1188	THR
5	F	1195	PHE
5	F	1295	ALA
5	F	1314	VAL
5	F	1371	ILE
5	F	1381	LEU
5	F	1387	THR
5	F	1392	ILE
5	F	1395	PRO
5	F	1680	GLN
6	G	425	GLU
7	H	506	ILE
7	H	507	ASN
8	I	732	ALA
8	I	740	LYS
8	I	793	LEU
8	I	799	SER
6	J	338	SER
6	J	339	LEU

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Mol	Chain	Res	Type
6	J	438	ALA
7	K	321	ALA
7	K	449	ASP
7	K	450	PRO
7	K	457	ASN
8	L	780	THR
8	L	781	ASN
1	Z	44	VAL
1	Z	92	THR
1	Z	248	THR
1	Z	249	ARG
1	Z	250	ASN
1	Z	252	GLN
1	Z	751	LEU
1	Z	752	SER
1	Z	765	ASP
1	Z	767	ILE
1	Z	824	MET
2	C	526	ASN
4	E	259	SER
4	E	701	SER
4	E	1248	THR
5	F	361	LEU
5	F	396	GLY
5	F	412	ASN
5	F	922	LEU
5	F	926	LEU
5	F	936	ILE
5	F	958	SER
5	F	964	LYS
5	F	974	GLU
5	F	1039	ALA
5	F	1041	PHE
5	F	1059	SER
5	F	1062	SER
5	F	1124	GLY
5	F	1134	LYS
5	F	1135	CYS
5	F	1189	MET
5	F	1204	GLY
5	F	1210	LYS
5	F	1374	LYS

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Mol	Chain	Res	Type
5	F	1389	ILE
5	F	1421	VAL
7	H	319	THR
7	H	424	ASN
8	I	728	THR
7	K	405	ASN
7	K	501	GLU
7	K	504	ASP
7	K	505	ARG
8	L	779	THR
1	Z	245	ALA
1	Z	821	GLN
1	A	134	LYS
2	C	75	ASP
2	C	334	ASP
2	C	479	ASP
4	E	980	LYS
5	F	335	ASP
5	F	350	ARG
5	F	358	LYS
5	F	367	PHE
5	F	381	THR
5	F	406	LEU
5	F	591	ASP
5	F	902	LYS
5	F	1030	ASN
5	F	1035	GLY
5	F	1038	LEU
5	F	1064	THR
5	F	1084	LEU
5	F	1123	ASN
5	F	1193	ARG
5	F	1200	PRO
5	F	1269	GLU
5	F	1370	LEU
5	F	1396	LEU
5	F	1675	THR
8	I	738	ASP
8	I	789	GLU
8	I	790	ASN
7	K	392	LEU
8	L	783	ASP

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Mol	Chain	Res	Type
1	Z	134	LYS
1	Z	825	PRO
2	C	315	THR
2	C	1252	ASP
3	D	1441	ASN
5	F	363	ASP
5	F	444	THR
5	F	930	VAL
5	F	951	ARG
5	F	1067	ASN
5	F	1129	ASN
5	F	1236	ILE
5	F	1361	PHE
5	F	1372	THR
5	F	1676	LEU
7	K	455	LYS
1	Z	91	GLN
1	Z	648	GLU
1	Z	762	ASN
1	Z	771	ILE
1	Z	777	ILE
3	D	998	ALA
4	E	702	THR
4	E	977	ALA
4	E	1027	TRP
5	F	1122	TRP
5	F	1194	LEU
5	F	1420	GLN
1	Z	244	SER
1	Z	828	THR
5	F	352	ILE
5	F	713	PHE
5	F	923	VAL
5	F	1296	LEU
5	F	1307	VAL
5	F	1365	ASN
5	F	1390	GLN
8	I	798	ASN
8	L	704	GLN
2	C	684	GLY
4	E	1489	PRO
8	L	794	ILE

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Mol	Chain	Res	Type
8	I	782	ILE
7	K	427	LEU
3	D	993	GLY
4	E	974	GLY
5	F	1032	ILE
5	F	1063	ILE
5	F	422	VAL
5	F	1266	VAL
8	I	791	ILE
2	C	469	ILE

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	609/762 (80%)	583 (96%)	26 (4%)	29 58
1	Z	611/762 (80%)	556 (91%)	55 (9%)	9 37
2	C	1177/1250 (94%)	1152 (98%)	25 (2%)	53 74
3	D	1215/1353 (90%)	1202 (99%)	13 (1%)	73 85
4	E	1421/1557 (91%)	1396 (98%)	25 (2%)	59 77
5	F	1260/1538 (82%)	1164 (92%)	96 (8%)	13 43
6	G	167/377 (44%)	165 (99%)	2 (1%)	71 84
6	J	162/377 (43%)	147 (91%)	15 (9%)	9 35
7	H	171/439 (39%)	166 (97%)	5 (3%)	42 66
7	K	153/439 (35%)	134 (88%)	19 (12%)	4 24
8	I	152/674 (23%)	135 (89%)	17 (11%)	6 28
8	L	138/674 (20%)	137 (99%)	1 (1%)	84 91
All	All	7236/10202 (71%)	6937 (96%)	299 (4%)	34 59

All (299) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	21	LYS
1	A	22	LEU
1	A	27	GLU
1	A	30	ASP
1	A	45	SER
1	A	53	VAL
1	A	54	PHE
1	A	57	ARG
1	A	79	SER
1	A	82	ASP
1	A	115	THR
1	A	116	LYS
1	A	119	GLU
1	A	122	LEU
1	A	130	ASN
1	A	134	LYS
1	A	137	ASP
1	A	138	ASN
1	A	139	PHE
1	A	543	LYS
1	A	617	LYS
1	A	827	GLU
1	A	829	TYR
1	A	830	SER
1	A	833	ILE
2	C	68	THR
2	C	85	LEU
2	C	294	LEU
2	C	315	THR
2	C	318	ILE
2	C	326	LEU
2	C	331	LEU
2	C	337	THR
2	C	462	LEU
2	C	476	ASN
2	C	520	LEU
2	C	530	LEU
2	C	577	PHE
2	C	691	GLN
2	C	695	ASP
2	C	826	LEU
2	C	828	THR

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Mol	Chain	Res	Type
2	C	896	CYS
2	C	1034	SER
2	C	1252	ASP
2	C	1253	VAL
2	C	1262	LEU
2	C	1299	LYS
2	C	1301	SER
2	C	1387	HIS
3	D	445	ARG
3	D	528	PRO
3	D	980	SER
3	D	982	GLU
3	D	990	GLU
3	D	995	PHE
3	D	1000	ASP
3	D	1115	VAL
3	D	1118	LEU
3	D	1129	ASN
3	D	1160	HIS
3	D	1472	ILE
3	D	1495	LEU
4	E	138	VAL
4	E	254	SER
4	E	257	LEU
4	E	258	ILE
4	E	336	GLN
4	E	771	LEU
4	E	773	LEU
4	E	791	ASP
4	E	827	PRO
4	E	843	LEU
4	E	923	LEU
4	E	931	PHE
4	E	975	GLN
4	E	976	PHE
4	E	980	LYS
4	E	984	ASP
4	E	986	SER
4	E	1026	THR
4	E	1077	ARG
4	E	1164	ASP
4	E	1259	PHE

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Mol	Chain	Res	Type
4	E	1301	LYS
4	E	1313	ARG
4	E	1557	LEU
4	E	1597	ARG
5	F	64	PHE
5	F	164	LYS
5	F	331	ILE
5	F	334	GLN
5	F	356	ILE
5	F	389	LEU
5	F	397	MET
5	F	399	SER
5	F	407	ASN
5	F	408	SER
5	F	409	MET
5	F	444	THR
5	F	556	LYS
5	F	644	LYS
5	F	712	LEU
5	F	745	ARG
5	F	750	TRP
5	F	782	LYS
5	F	813	GLU
5	F	825	ILE
5	F	836	ILE
5	F	837	TYR
5	F	888	PRO
5	F	900	LEU
5	F	920	ILE
5	F	921	PRO
5	F	926	LEU
5	F	928	LEU
5	F	934	ASP
5	F	950	GLU
5	F	951	ARG
5	F	955	SER
5	F	958	SER
5	F	962	ARG
5	F	965	LEU
5	F	1029	SER
5	F	1041	PHE
5	F	1060	LEU

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Mol	Chain	Res	Type
5	F	1068	ILE
5	F	1090	PRO
5	F	1092	THR
5	F	1118	ARG
5	F	1128	ASP
5	F	1129	ASN
5	F	1144	VAL
5	F	1147	PHE
5	F	1149	SER
5	F	1150	PHE
5	F	1153	TYR
5	F	1155	ASN
5	F	1159	GLN
5	F	1165	ILE
5	F	1166	HIS
5	F	1167	LYS
5	F	1169	SER
5	F	1170	PHE
5	F	1181	VAL
5	F	1191	SER
5	F	1192	VAL
5	F	1210	LYS
5	F	1273	LYS
5	F	1276	ASP
5	F	1277	VAL
5	F	1278	GLU
5	F	1280	ILE
5	F	1281	LYS
5	F	1283	LYS
5	F	1285	HIS
5	F	1286	PHE
5	F	1289	ILE
5	F	1291	SER
5	F	1293	ASN
5	F	1296	LEU
5	F	1297	GLU
5	F	1300	LEU
5	F	1301	SER
5	F	1302	VAL
5	F	1303	LEU
5	F	1309	LEU
5	F	1314	VAL

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Mol	Chain	Res	Type
5	F	1315	THR
5	F	1349	PHE
5	F	1356	LEU
5	F	1361	PHE
5	F	1364	TYR
5	F	1365	ASN
5	F	1372	THR
5	F	1373	ASP
5	F	1382	TYR
5	F	1387	THR
5	F	1417	LEU
5	F	1484	ARG
5	F	1550	LEU
5	F	1634	LYS
5	F	1635	ARG
5	F	1680	GLN
6	G	411	ASN
6	G	460	LEU
7	H	325	THR
7	H	418	GLN
7	H	507	ASN
7	H	508	LYS
7	H	529	LYS
8	I	688	HIS
8	I	727	SER
8	I	736	ASN
8	I	740	LYS
8	I	778	LYS
8	I	792	GLN
8	I	795	LYS
8	I	797	LEU
8	I	808	ASP
8	I	810	ASN
8	I	812	THR
8	I	815	GLU
8	I	818	ILE
8	I	819	ASN
8	I	821	ILE
8	I	822	LYS
8	I	823	LYS
6	J	357	LEU
6	J	368	ASP

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Mol	Chain	Res	Type
6	J	370	ASP
6	J	371	LYS
6	J	372	PHE
6	J	375	LYS
6	J	376	LYS
6	J	385	GLU
6	J	389	ARG
6	J	391	LEU
6	J	395	GLU
6	J	399	ASN
6	J	401	ILE
6	J	411	ASN
6	J	430	LEU
7	K	341	LYS
7	K	384	THR
7	K	385	GLN
7	K	387	GLN
7	K	391	GLU
7	K	393	ASP
7	K	394	THR
7	K	398	ILE
7	K	399	LEU
7	K	400	LYS
7	K	402	GLN
7	K	404	ARG
7	K	423	LYS
7	K	443	LEU
7	K	446	ARG
7	K	449	ASP
7	K	453	LEU
7	K	455	LYS
7	K	529	LYS
8	L	703	GLN
1	Z	19	ASN
1	Z	20	LYS
1	Z	21	LYS
1	Z	22	LEU
1	Z	27	GLU
1	Z	30	ASP
1	Z	46	ILE
1	Z	49	LEU
1	Z	53	VAL

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Mol	Chain	Res	Type
1	Z	56	LEU
1	Z	79	SER
1	Z	80	PHE
1	Z	81	GLU
1	Z	84	ASP
1	Z	87	ILE
1	Z	88	LYS
1	Z	89	ASP
1	Z	90	LEU
1	Z	92	THR
1	Z	116	LYS
1	Z	117	LYS
1	Z	119	GLU
1	Z	121	ILE
1	Z	122	LEU
1	Z	125	ILE
1	Z	127	GLN
1	Z	128	LEU
1	Z	129	LEU
1	Z	130	ASN
1	Z	133	THR
1	Z	134	LYS
1	Z	138	ASN
1	Z	139	PHE
1	Z	144	LEU
1	Z	146	LEU
1	Z	248	THR
1	Z	294	MET
1	Z	399	LYS
1	Z	446	LYS
1	Z	551	ARG
1	Z	731	GLN
1	Z	758	GLN
1	Z	765	ASP
1	Z	766	ASN
1	Z	767	ILE
1	Z	772	PRO
1	Z	775	LEU
1	Z	776	ILE
1	Z	777	ILE
1	Z	793	LYS
1	Z	805	SER

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Mol	Chain	Res	Type
1	Z	808	ASN
1	Z	824	MET
1	Z	827	GLU
1	Z	828	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (115) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	130	ASN
1	A	138	ASN
1	A	540	ASN
1	A	733	GLN
1	A	787	HIS
2	C	199	HIS
2	C	691	GLN
2	C	827	ASN
2	C	914	GLN
2	C	941	ASN
2	C	1387	HIS
3	D	449	ASN
3	D	484	GLN
3	D	850	ASN
3	D	1086	ASN
3	D	1129	ASN
4	E	36	GLN
4	E	190	GLN
4	E	210	ASN
4	E	299	ASN
4	E	388	ASN
4	E	571	ASN
4	E	600	ASN
4	E	636	GLN
4	E	677	ASN
4	E	759	ASN
4	E	763	GLN
4	E	770	HIS
4	E	822	ASN
4	E	1001	ASN
4	E	1029	ASN
4	E	1383	GLN
4	E	1429	HIS

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Mol	Chain	Res	Type
4	E	1493	ASN
4	E	1535	ASN
4	E	1539	ASN
4	E	1558	GLN
5	F	38	ASN
5	F	163	ASN
5	F	177	GLN
5	F	195	GLN
5	F	258	GLN
5	F	334	GLN
5	F	428	GLN
5	F	539	ASN
5	F	542	ASN
5	F	714	HIS
5	F	725	ASN
5	F	1293	ASN
5	F	1299	ASN
5	F	1365	ASN
5	F	1541	ASN
6	G	328	GLN
6	G	355	GLN
6	G	428	ASN
7	H	362	ASN
7	H	365	GLN
7	H	368	ASN
7	H	377	ASN
7	H	524	ASN
8	I	647	GLN
8	I	654	HIS
8	I	690	GLN
8	I	695	GLN
8	I	743	GLN
8	I	754	ASN
8	I	781	ASN
8	I	786	ASN
8	I	800	HIS
8	I	819	ASN
6	J	324	GLN
6	J	328	GLN
6	J	355	GLN
6	J	367	ASN
6	J	374	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	J	378	HIS
6	J	399	ASN
7	K	359	ASN
7	K	362	ASN
7	K	365	GLN
7	K	368	ASN
7	K	377	ASN
7	K	385	GLN
7	K	387	GLN
7	K	402	GLN
7	K	424	ASN
7	K	515	ASN
7	K	539	ASN
8	L	647	GLN
8	L	654	HIS
8	L	695	GLN
8	L	704	GLN
8	L	749	GLN
8	L	754	ASN
8	L	774	ASN
8	L	800	HIS
1	Z	19	ASN
1	Z	60	ASN
1	Z	127	GLN
1	Z	130	ASN
1	Z	138	ASN
1	Z	141	ASN
1	Z	196	ASN
1	Z	214	ASN
1	Z	396	GLN
1	Z	463	GLN
1	Z	464	ASN
1	Z	621	HIS
1	Z	658	ASN
1	Z	738	GLN
1	Z	758	GLN
1	Z	770	ASN
1	Z	802	GLN
1	Z	834	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

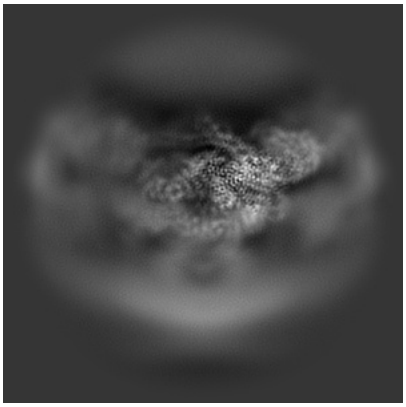
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-32653. These allow visual inspection of the internal detail of the map and identification of artifacts.

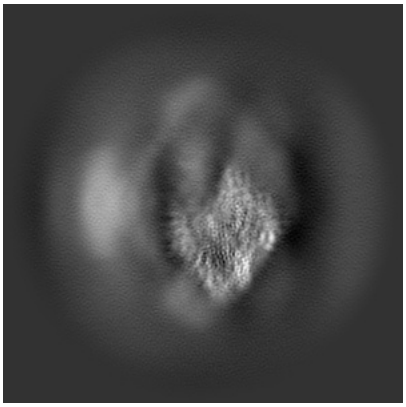
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

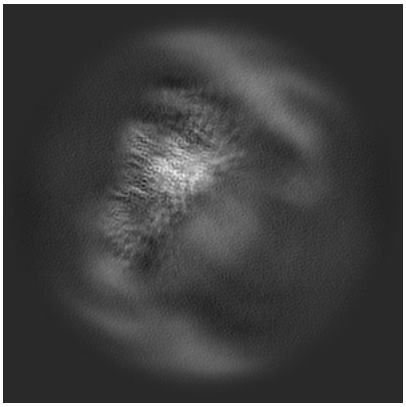
6.1.1 Primary map



X



Y

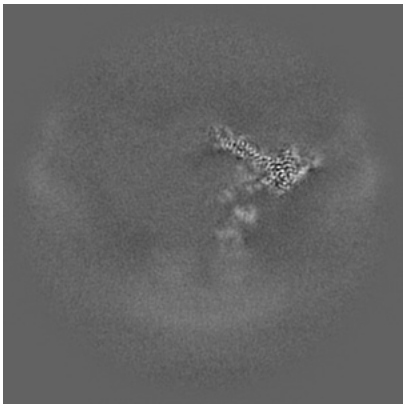


Z

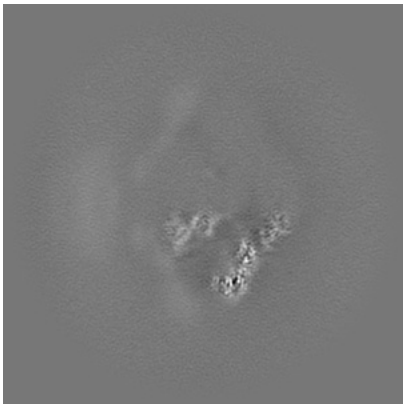
The images above show the map projected in three orthogonal directions.

6.2 Central slices

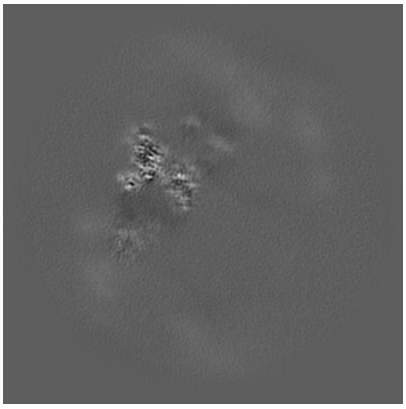
6.2.1 Primary map



X Index: 175



Y Index: 175

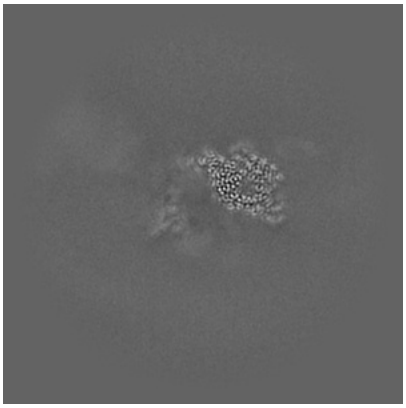


Z Index: 175

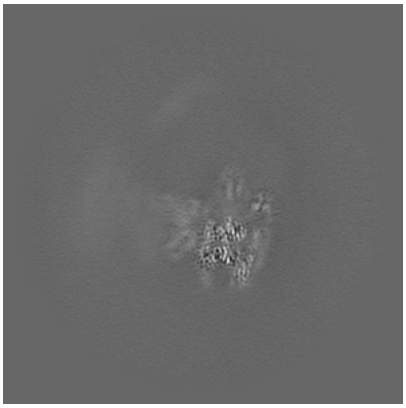
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

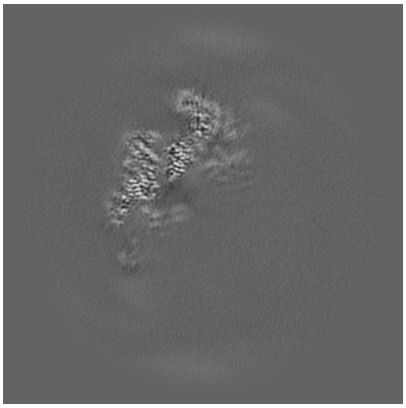
6.3.1 Primary map



X Index: 124



Y Index: 203

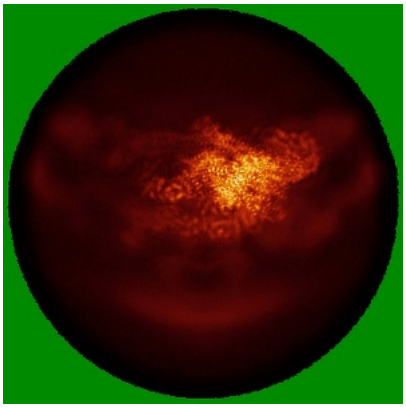


Z Index: 204

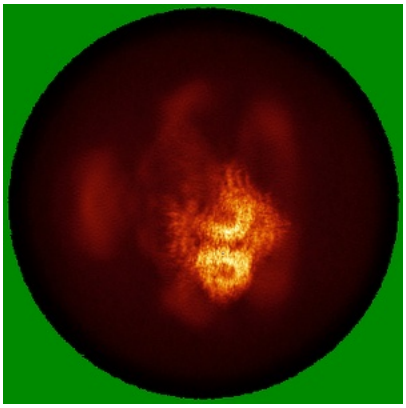
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

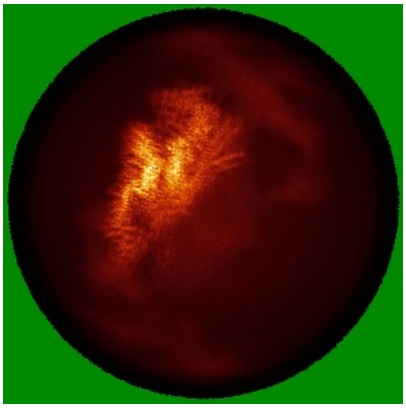
6.4.1 Primary map



X



Y

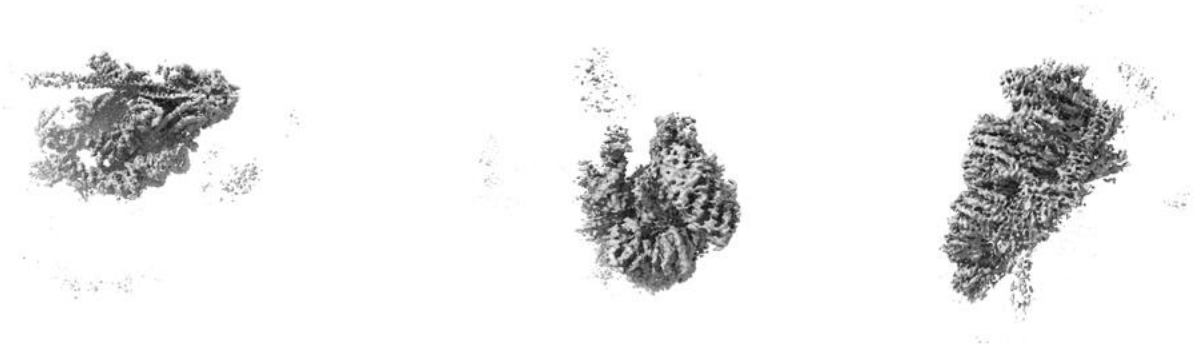


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.24. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

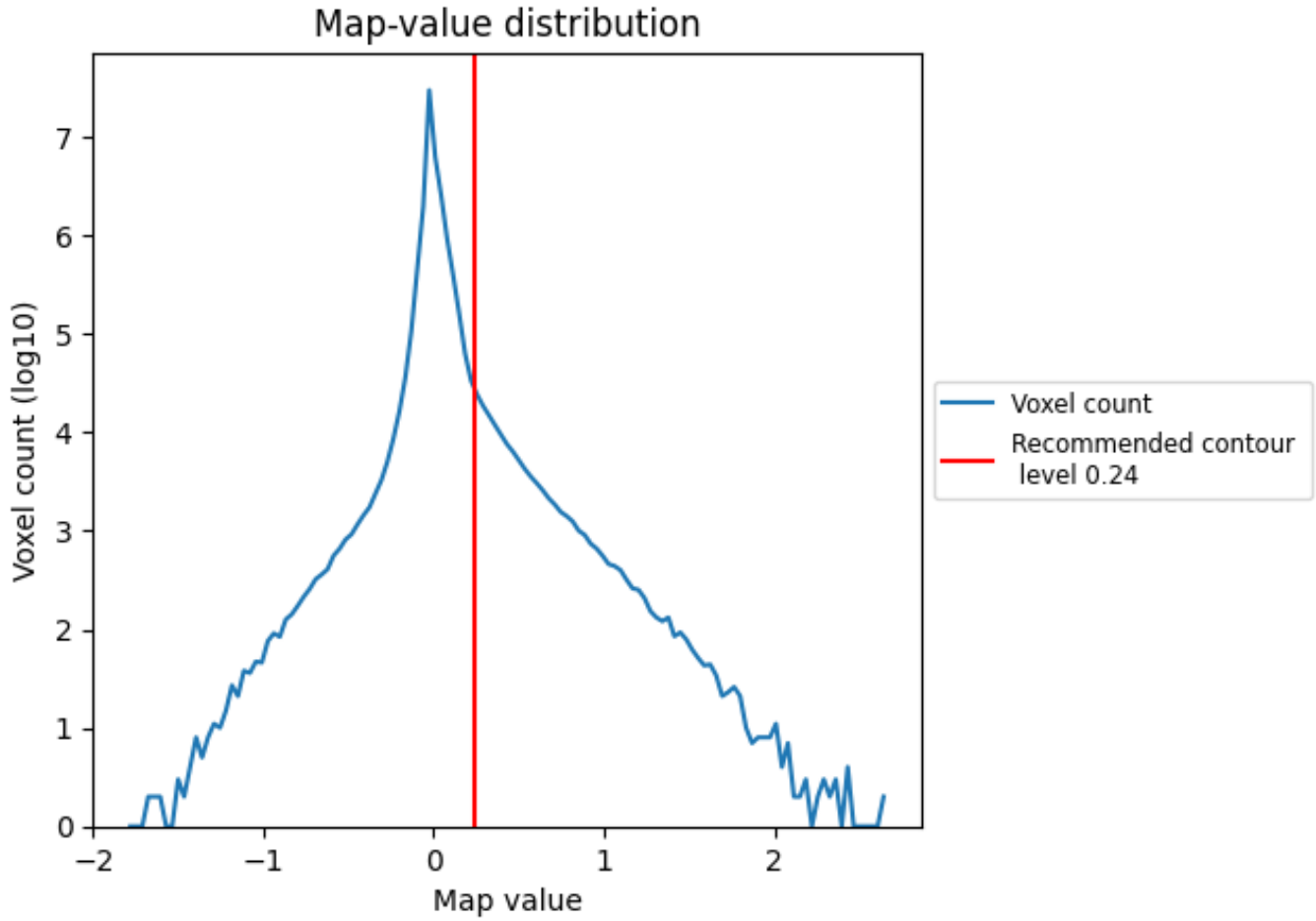
6.6 Mask visualisation (i)

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

7 Map analysis

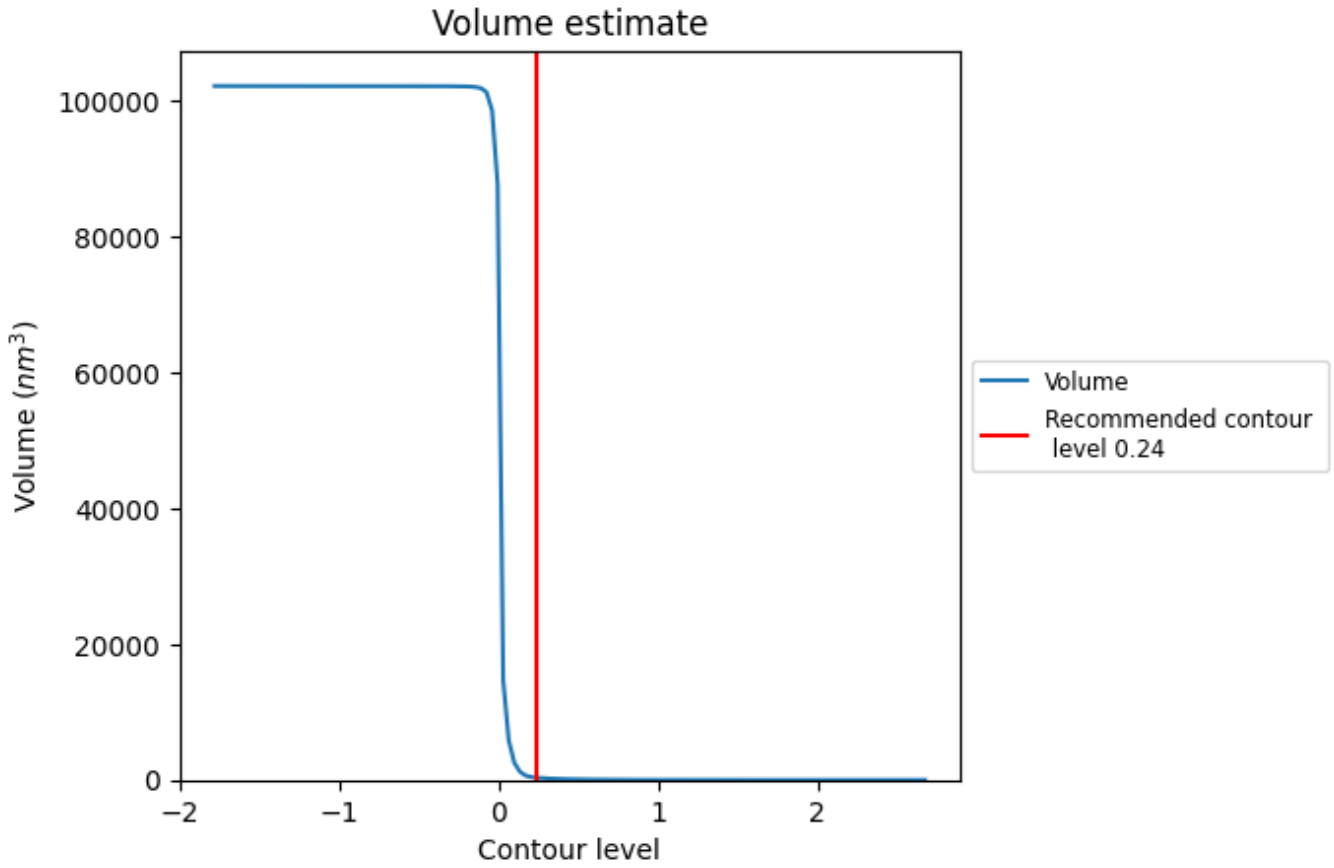
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

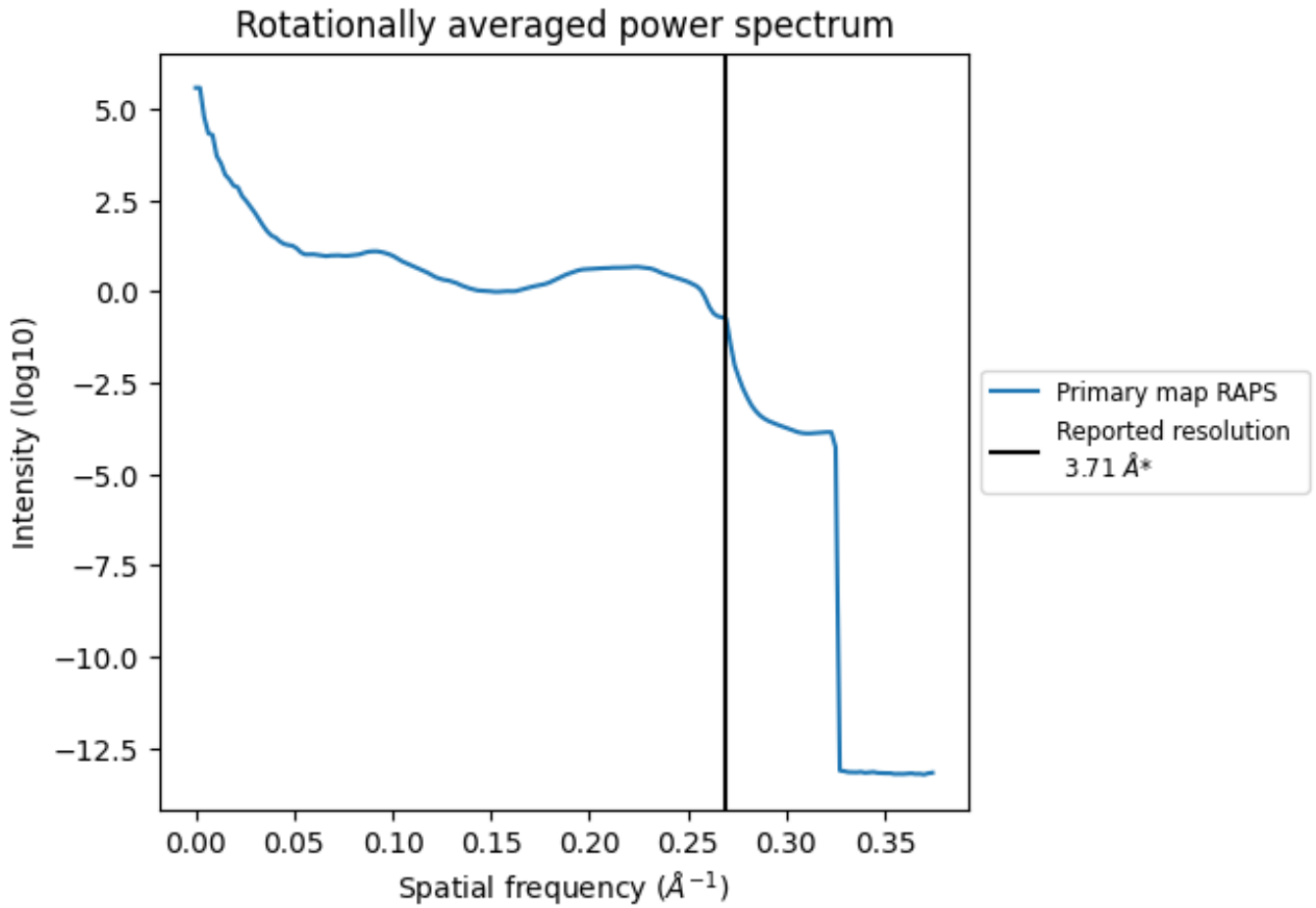
7.2 Volume estimate



The volume at the recommended contour level is 332 nm^3; this corresponds to an approximate mass of 300 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.270 $Å^{-1}$

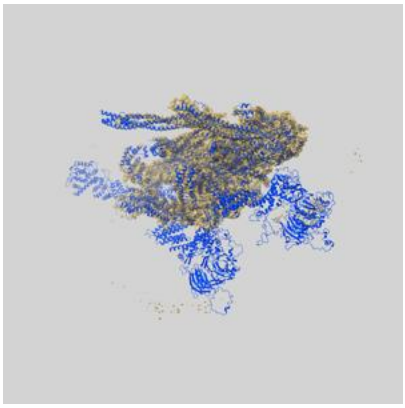
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

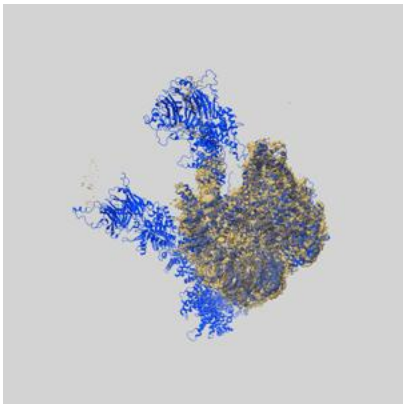
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-32653 and PDB model 7WOO. Per-residue inclusion information can be found in section 3 on page 6.

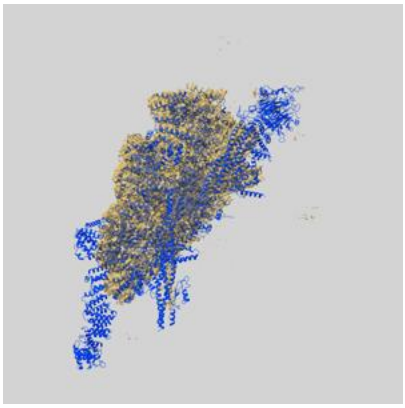
9.1 Map-model overlay



X



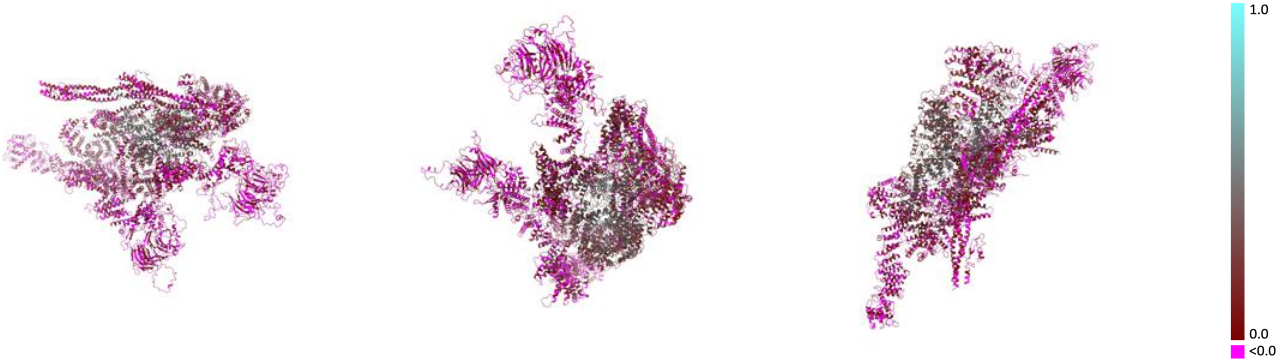
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.24 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.

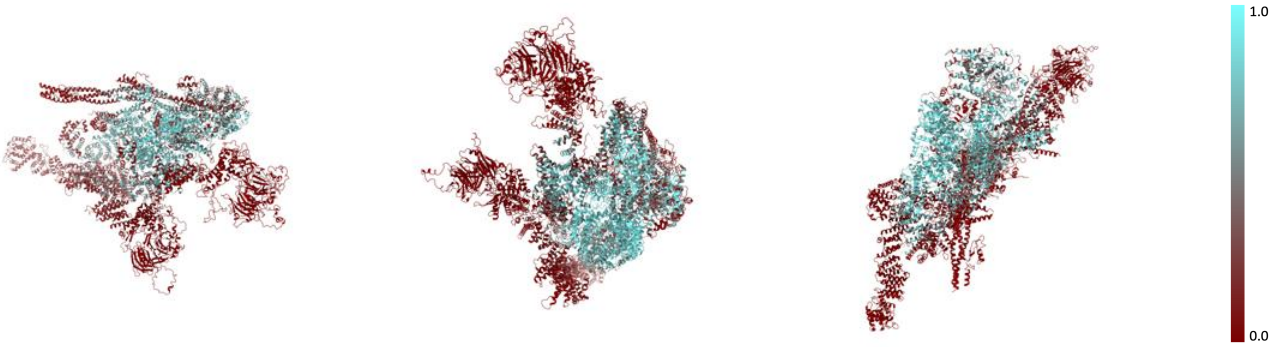
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

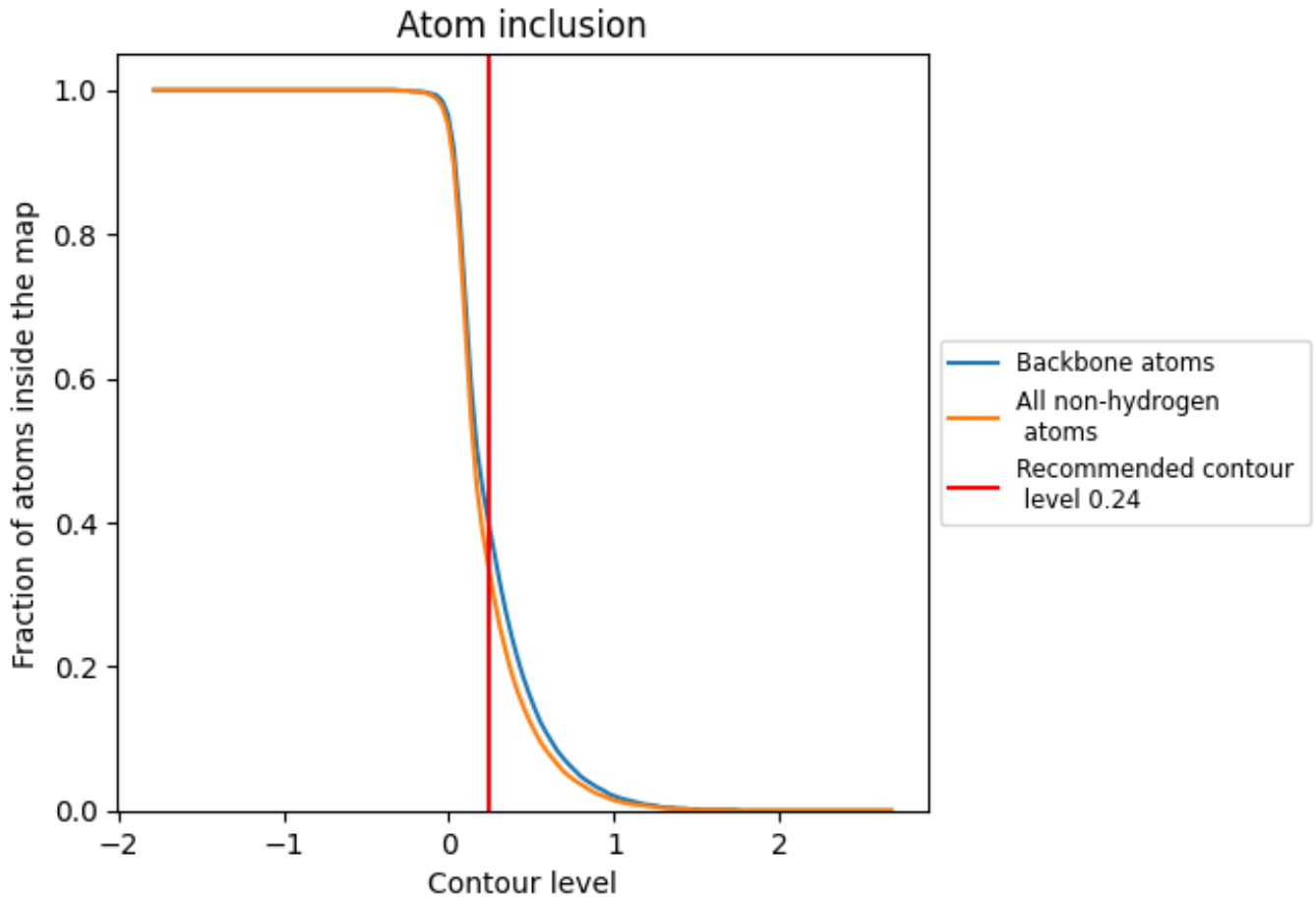
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.24).

9.4 Atom inclusion (i)



At the recommended contour level, 40% of all backbone atoms, 34% 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 (0.24) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3370	0.1340
A	0.0350	0.0150
C	0.0010	0.0220
D	0.1240	0.0320
E	0.7100	0.3120
F	0.5690	0.2180
G	0.3910	0.0730
H	0.3420	0.0980
I	0.4900	0.1220
J	0.2860	0.1480
K	0.2420	0.1210
L	0.3040	0.0820
Z	0.3470	0.1290