Full wwPDB EM Validation Report ⓘ

Jun 3, 2025 – 12:42 PM EDT

PDB ID	:	9D9Z / pdb_00009d9z
EMDB ID	:	EMD-46686
Title	:	Structure of human UBR4-KCMF1-CaM E3 ligase complex (Silencing Factor of the Integrated stress response, SiFI)
Authors	:	Yang, Z.; Rape, M.
Deposited on	:	2024-08-21
Resolution	:	3.40 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:

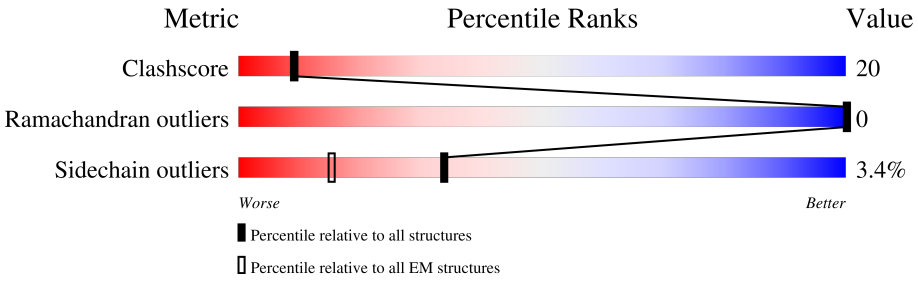
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.40 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	5205	50% 45% 29% · 25%
1	B	5205	50% 46% 28% · 24%
2	C	149	83% 51% 43% · ·
2	D	149	85% 47% 46% · ·
3	E	381	34% 30% 17% · 52%
3	F	381	35% 29% 18% · 52%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ZN	A	5202	-	-	X	-
4	ZN	B	5202	-	-	X	-
5	CA	D	202	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 66746 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 UBR4 (endogenously FLAG-tagged at the N-terminus),E3 ubiquitin-protein ligase UBR4,E3 ubiquitin-protein ligase UBR4,E3 ubiquitin-protein ligase UBR4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3917	Total	C	N	O	S	0	0
			30658	19475	5230	5749	204		
1	B	3946	Total	C	N	O	S	0	0
			30933	19647	5279	5802	205		

- Molecule 2 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	144	Total	C	N	O	S	0	0
			1134	696	182	247	9		
2	D	143	Total	C	N	O	S	0	0
			1127	692	181	245	9		

- Molecule 3 is a protein called E3 ubiquitin-protein ligase KCMF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	182	Total	C	N	O	S	0	0
			1435	881	250	288	16		
3	F	182	Total	C	N	O	S	0	0
			1435	881	250	288	16		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
4	A	6	Total	Zn	0
			6	6	
4	B	6	Total	Zn	0
			6	6	
4	E	4	Total	Zn	0
			4	4	

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Mol	Chain	Residues	Atoms	AltConf
4	F	4	Total Zn 4 4	0

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

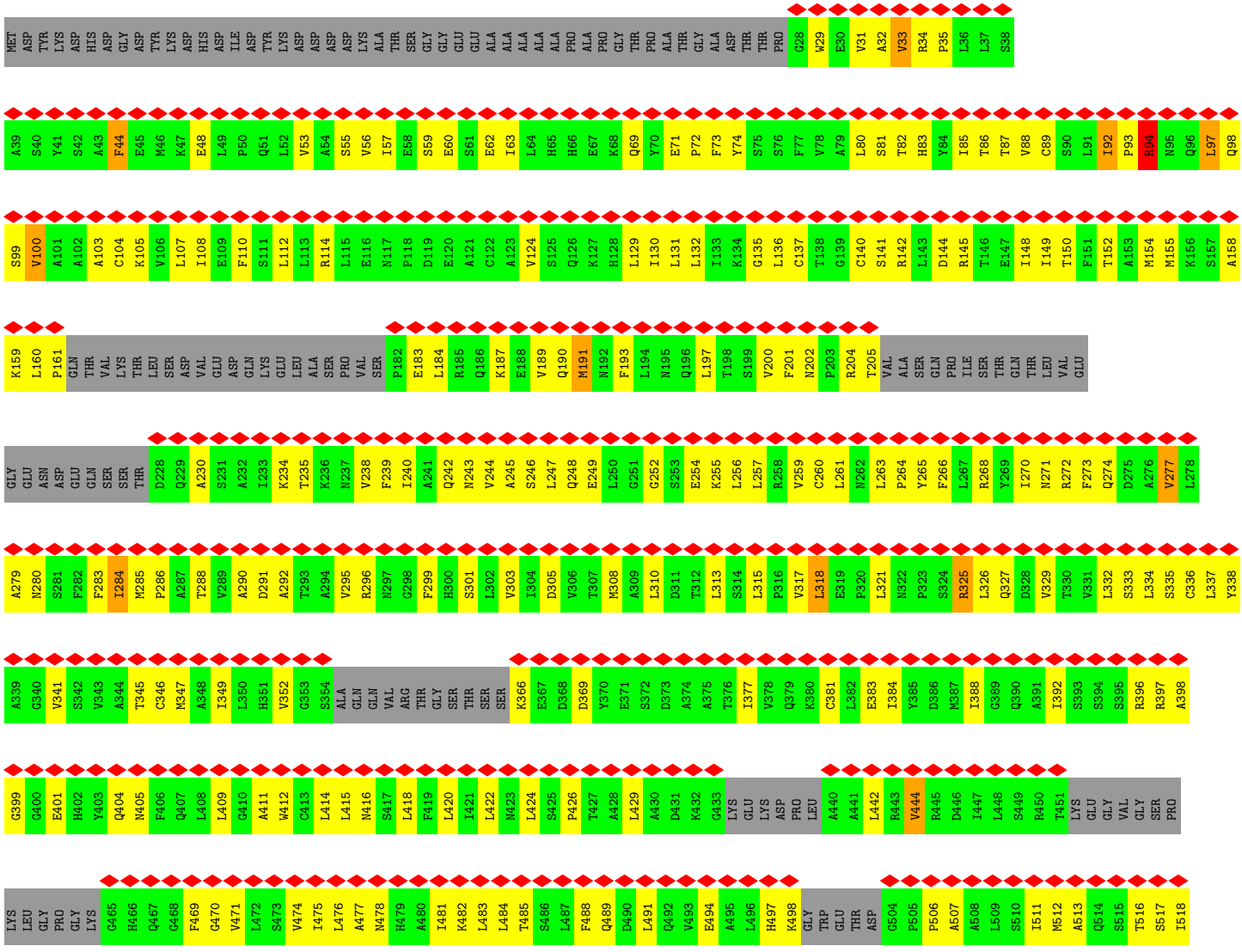
Mol	Chain	Residues	Atoms	AltConf
5	C	2	Total Ca 2 2	0
5	D	2	Total Ca 2 2	0

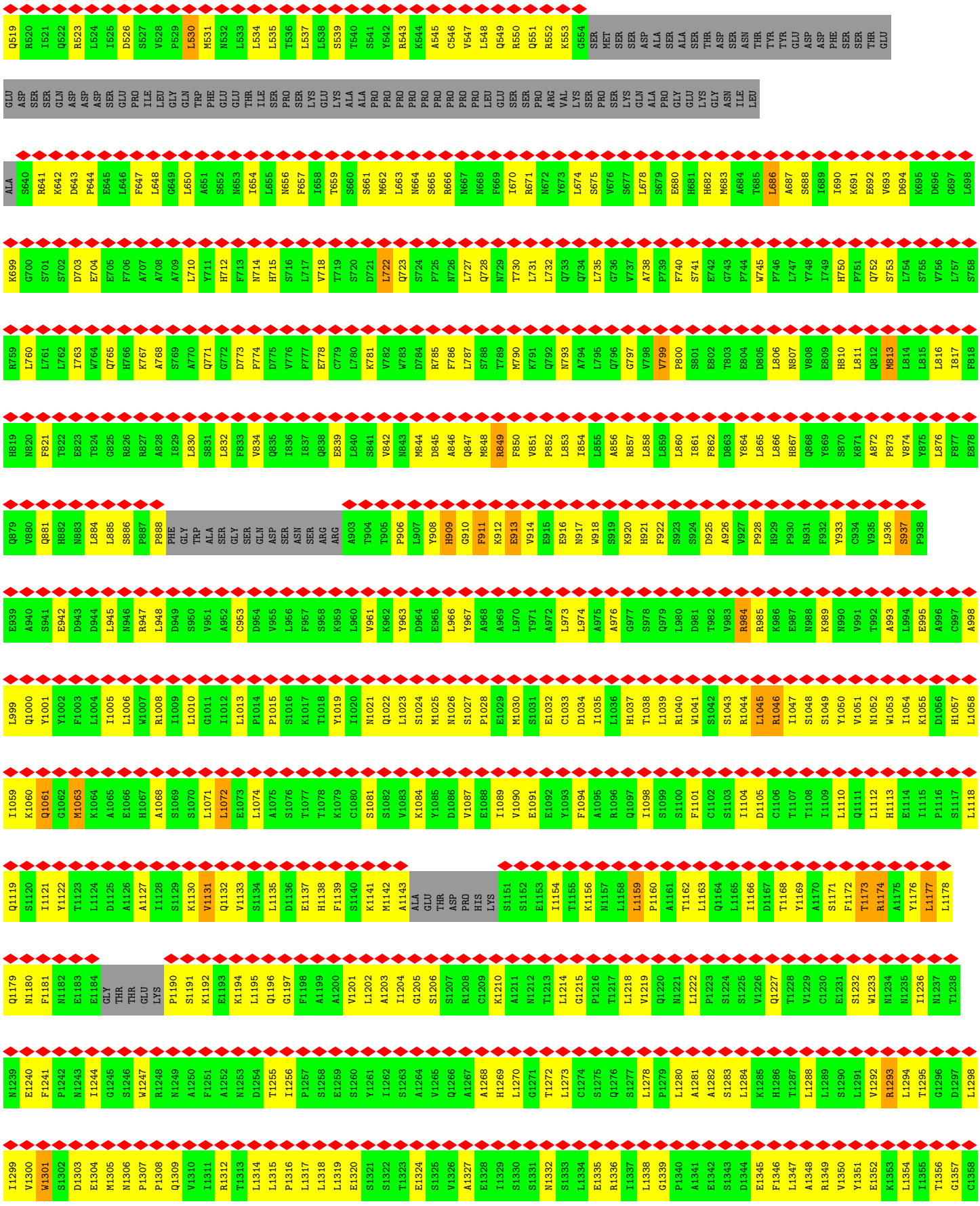
3 Residue-property plots (i)

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: UBR4 (endogenously FLAG-tagged at the N-terminus),E3 ubiquitin-protein ligase UBR4,E3 ubiquitin-protein ligase UBR4,E3 ubiquitin-protein ligase UBR4

Chain A:

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SER MET SER SER ASP ALA SER ALA SER THR ASP SER ASN THR TYR TYR GLU ASP ASP PHE SER SER THR GLU
GLU ASP SER SER GLN ASP ASP ASP SER GLU PRO ILE LEU GLY GLN TRP PHE GLU GLU THR ILE SER PRO SER LYS GLU LYS ALA ALA PRO PRO PRO PRO PRO PRO PRO PRO PRO LEU GLU SER SER PRO ARG VAL LYS SER PRO SER LYS SER GLN LYS ALA ALA PRO GLY GLU LYS GLY ASN ILE LEU
ALA S640 R641 K642 D643 P644 E645 L646 F647 L648 G649 L650 A651 S652 N653 I654 L655 N656 F657 I658 T659 S660 S661 M662 L663 N664 S665 R666 N667 N668 F669 I670 R671 N672 Y673 L674 S675 V676 S677 L678 S679 E680 H681 H682 M683 A684 T685 L686 A687 S688 I689 I690 K691 E692 V693 D694 K695 D696 G697 L698
K699 G700 S701 S702 D703 E704 E705 F706 A707 A708 A709 L710 Y711 H712 F713 N714 H715 S716 L717 V718 T719 S720 D721 L722 Q723 S724 P725 N726 L727 Q728 N729 T730 L731 L732 Q733 Q734 L735 G736 V737 A738 P739 F740 S741 E742 G743 P744 W745 P746 L747 Y748 I749 H750 P751 Q752 S753 L754 S755 V756 L757 S758
R759 L760 L761 L762 I763 W764 Q765 H766 K767 A768 S769 A770 Q771 G772 D773 P774 D775 V776 P777 E778 C779 L780 K781 V782 W783 D784 R785 F786 L787 S788 T789 M790 K791 Q792 N793 A794 L795 Q796 G797 V798 V799 P800 S801 E802 T803 E804 D805 L806 N807 V808 E809 H810 L811 Q812 M813 L814 L815 L816 I817 F818
H819 N820 F821 T822 E823 T824 G825 R826 R827 A828 I829 L830 S831 L832 F833 V834 Q835 I836 I837 Q838 E839 L840 S841 V842 N843 M844 D845 A846 Q847 M848 R849 F850 V851 P852 L853 I854 L855 A856 R857 L858 L859 L860 I861 F862 D863 Y864 L865 L866 H867 Q868 Y869 S870 K871 A872 P873 V874 Y875 L876 F877 E878
Q879 V880 Q881 H882 N883 L884 L885 S886 P887 P888 PHE GLY TRP ALA SER GLY SER GLN ASP SER ASN SER ARG ARG A903 T904 T905 P906 L907 Y908 H909 G910 F911 K912 E913 V914 E915 E916 N917 W918 S919 K920 H921 F922 S923 S924 D925 A926 V927 P928 H929 P930 R931 F932 Y933 C934 V935 L936 S937 P938
E939 A940 S941 E942 D943 D944 L945 N946 R947 L948 D949 S950 V951 A952 C953 D954 V955 L956 F957 S958 K959 L960 V961 K962 Y963 D964 E965 L966 Y967 A968 A969 L970 T971 A972 L973 L974 A975 A976 G977 S978 Q979 L980 D981 T982 V983 R984 R985 K986 E987 N988 K989 N990 V991 T992 A993 L994 E995 A996 C997 A998
L999 Q1000 Y1001 Y1002 F1003 L1004 I1005 L1006 W1007 R1008 I1009 L1010 G1011 I1012 L1013 P1014 P1015 S1016 K1017 T1018 Y1019 I1020 N1021 Q1022 L1023 S1024 M1025 N1026 S1027 P1028 E1029 M1030 S1031 E1032 C1033 D1034 I1035 L1036 H1037 T1038 L1039 R1040 W1041 S1042 S1043 R1044 L1045 R1046 I1047 S1048 S1049 Y1050 V1051 N1052 W1053 I1054 K1055 D1056 H1057 L1058
I1059 K1060 Q1061 G1062 M1063 K1064 A1065 E1066 H1067 A1068 S1069 S1070 L1071 L1072 E1073 L1074 A1075 S1076 T1077 T1078 K1079 C1080 S1081 S1082 V1083 K1084 Y1085 D1086 V1087 E1088 I1089 V1090 E1091 E1092 Y1093 F1094 A1095 R1096 Q1097 I1098 S1099 S1100 F1101 C1102 S1103 I1104 D1105 C1106 T1107 T1108 I1109 L1110 Q1111 L1112 H1113 E1114 I1115 P1116 S1117 L1118
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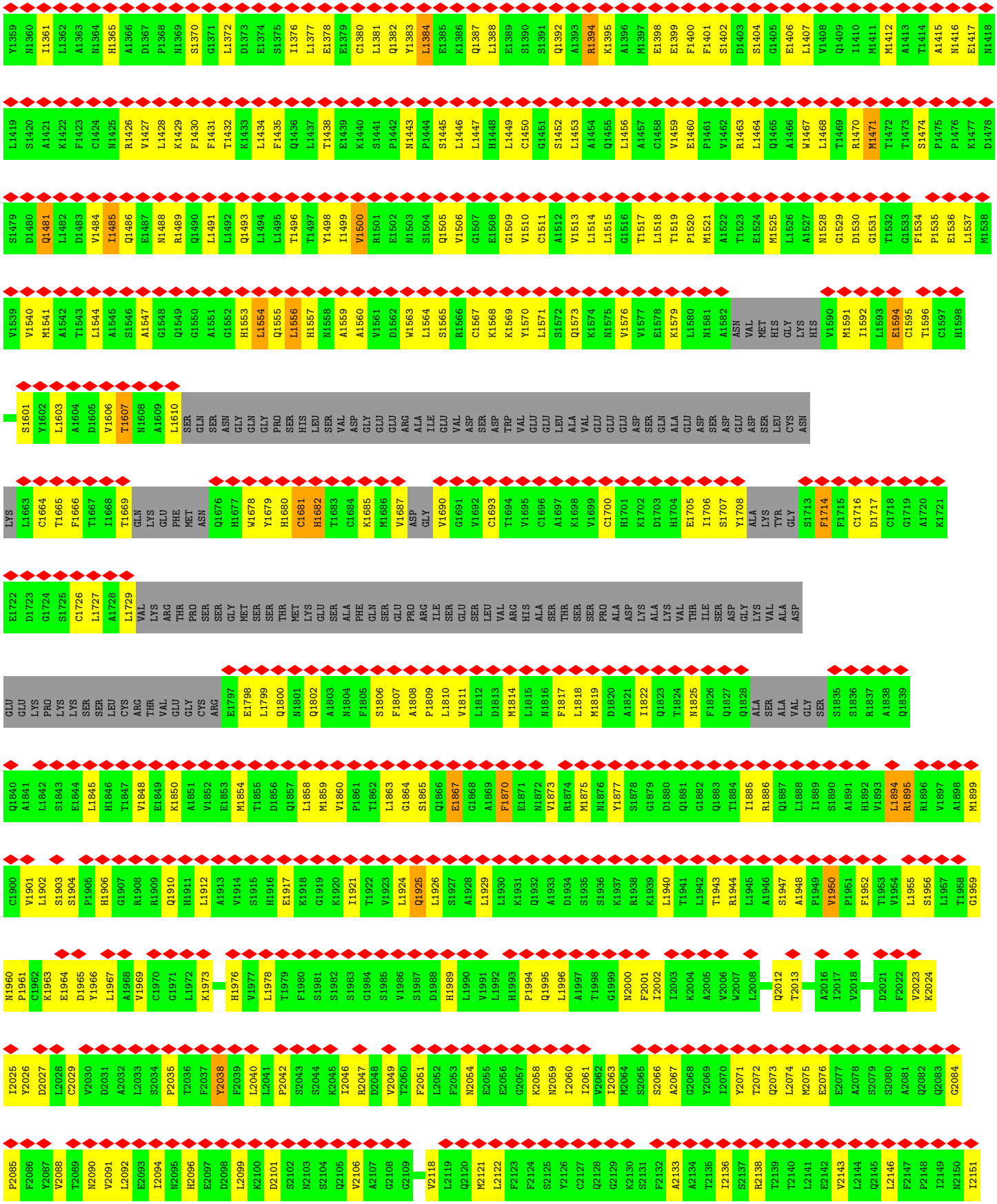
Q1179 N1180 F1181 N1182 E1183 E1184 GLY THR THR GLU LYS P1190 S1191 K1192 E1193 K1194 L1195 Q1196 G1197 F1198 A1199 A1200 V1201 L1202 A1203 I1204 G1205 S1206 S1207 R1208 C1209 K1210 A1211 N1212 T1213 L1214 G1215 P1216 T1217 L1218 V1219 Q1220 N1221 L1222 P1223 S1224 S1225 V1226 Q1227 T1228 V1229 C1230 E1231 S1232 W1233 N1234 N1235 I1236 N1237 T1238
N1239 E1240 F1241 P1242 N1243 I1244 G1245 S1246 W1247 R1248 N1249 A1250 F1251 A1252 N1253 D1254 T1255 I1256 P1257 S1258 E1259 S1260 Y1261 I1262 S1263 A1264 V1265 Q1266 A1267 A1268 H1269 L1270 G1271 T1272 L1273 C1274 S1275 Q1276 S1277 L1278 P1279 L1280 A1281 A1282 S1283 L1284 K1285 H1286 T1287 L1288 L1289 S1290 L1291 V1292 R1293 L1294 T1295 G1296 D1297 L1298
I1299 V1300 W1301 S1302 D1303 E1304 M1305 N1306 P1307 P1308 Q1309 V1310 I1311 R1312 T1313 L1314 L1315 P1316 L1317 L1318 L1319 E1320 S1321 S1322 T1323 E1324 S1325 Y1326 A1327 E1328 I1329 S1330 S1331 N1332 S1333 L1334 E1335 R1336 I1337 L1338 G1339 P1340 A1341 E1342 S1343 D1344 E1345 F1346 L1347 A1348 R1349 V1350 Y1351 E1352 K1353 L1354 I1355 T1356 G1357 C1358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GLU GLU LYS PRO LYS LYS SER SER LEU CYS ARG THR VAL GLU GLY CYS ARG E1797 E1798 L1799 Q1800 N1801 Q1802 A1803 N1804 F1805 S1806 F1807 A1808 P1809 L1810 V1811 L1812 D1813 M1814 L1815 N1816 F1817 L1818 M1819 D1820 A1821 I1822 Q1823 T1824 N1825 F1826 Q1827 Q1828 ALA SER ALA VAL GLY SER S1835 S1836 R1837 A1838 Q1839
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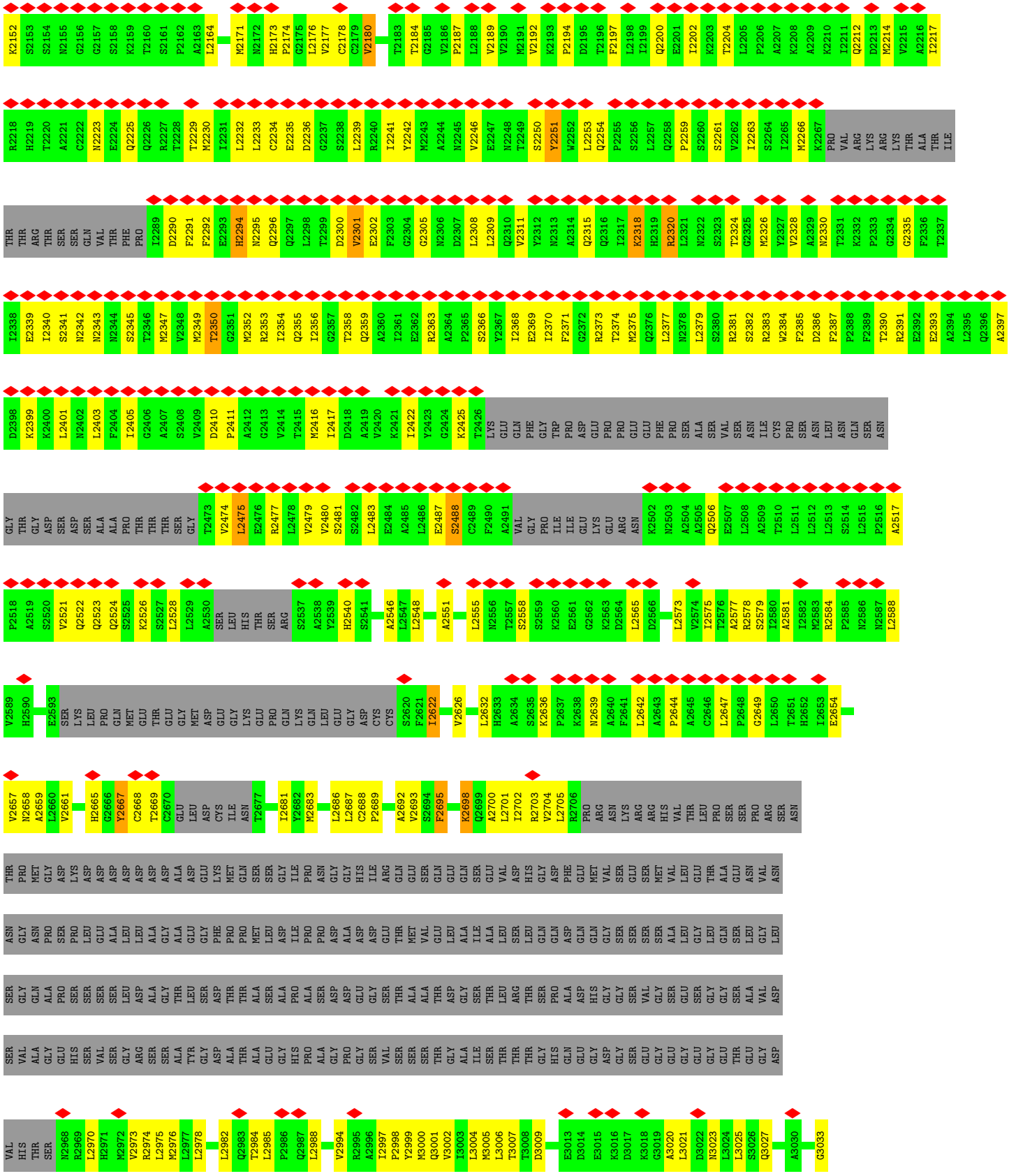
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R2218 H2219 T2220 A2221 C2222 N2223 E2224 Q2225 Q2226 R2227 T2228 T2229 M2230 I2231 L2232 L2233 C2234 E2235 D2236 G2237 S2238 L2239 R2240 I2241 Y2242 M2243 A2244 N2245 V2246 E2247 N2248 T2249 S2250 Y2251 W2252 L2253 Q2254 P2255 S2256 L2257 Q2258 P2259 S2260 S2261 V2262 I2263 S2264 I2265 M2266 K2267 PRO VAL ARG LYS ARG LYS THR ALA THR ILE
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D2398 K2399 K2400 L2401 N2402 L2403 F2404 I2405 G2406 A2407 S2408 V2409 D2410 P2411 A2412 G2413 V2414 T2415 M2416 I2417 D2418 A2419 V2420 K2421 I2422 Y2423 G2424 K2425 T2426 LYS GLU GLN PHE GLY TRP PRO ASP GLU PRO PRO GLU GLU PHE PRO SER ALA SER VAL SER ASN ILE CYS PRO SER ASN LEU ASN GLN SER ASN
GLY THR GLY ASP SER ASP SER ALA ALA PRO THR THR THR SER GLY T2473 V2474 L2475 E2476 R2477 L2478 V2479 V2480 S2481 S2482 L2483 E2484 A2485 L2486 E2487 S2488 C2489 F2490 A2491 VAL GLY PRO ILE ILE GLU LYS GLU ARG ASN K2502 N2503 A2504 A2505 Q2506 E2507 L2508 A2509 T2510 L2511 L2512 L2513 S2514 L2515 P2516 A2517
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THR PRO MET GLY ASP SER LYS ASP ASP ASP ASP ASP ASP ASP ALA ASP GLU GLY LYS MET GLN SER SER GLY ILE ARG GLN GLU SER GLN GLN SER GLU VAL ASP HIS GLY ASP GLU MET VAL SER GLU SER SER MET VAL LEU LEU THR ALA GLU ASN VAL ASN
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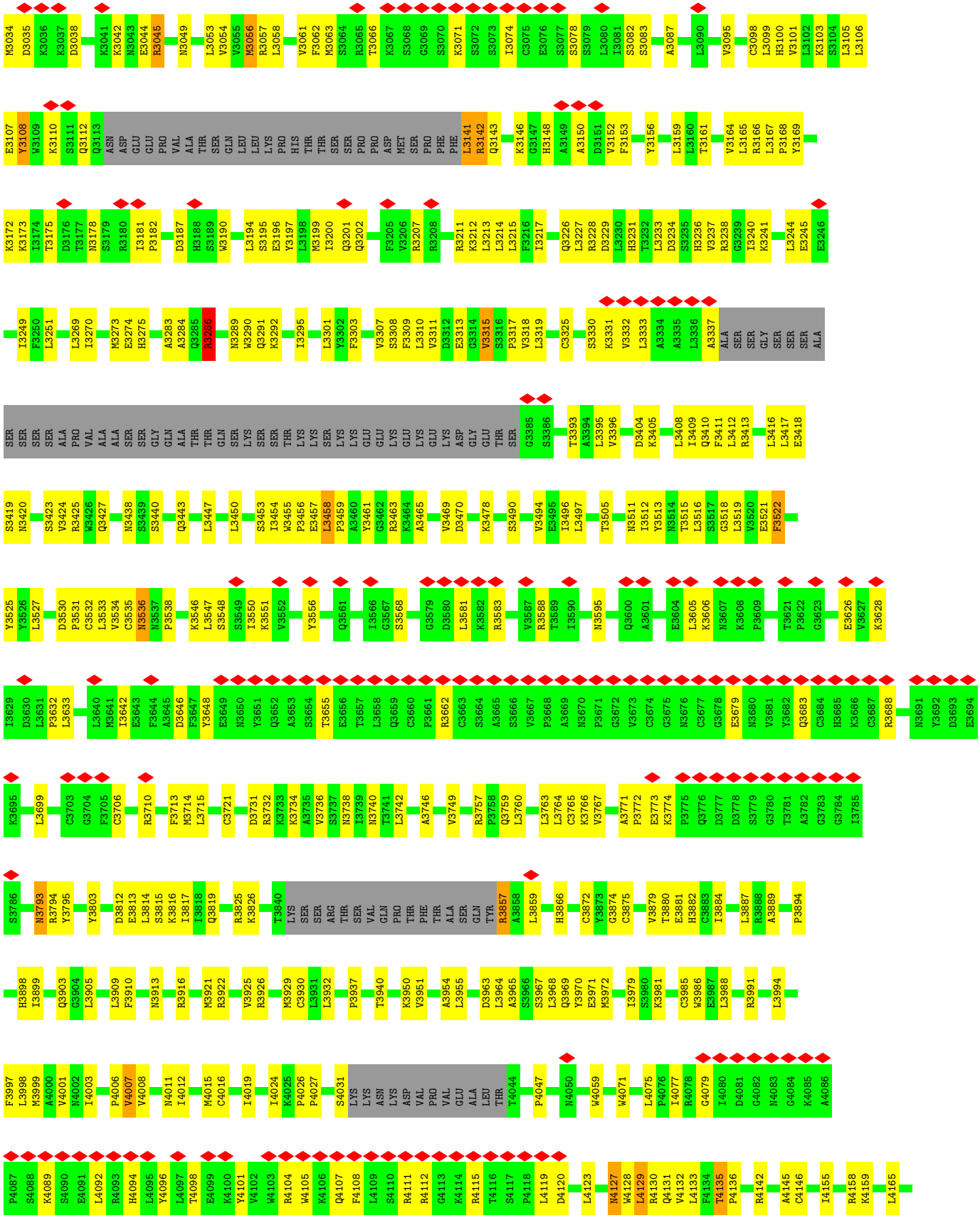

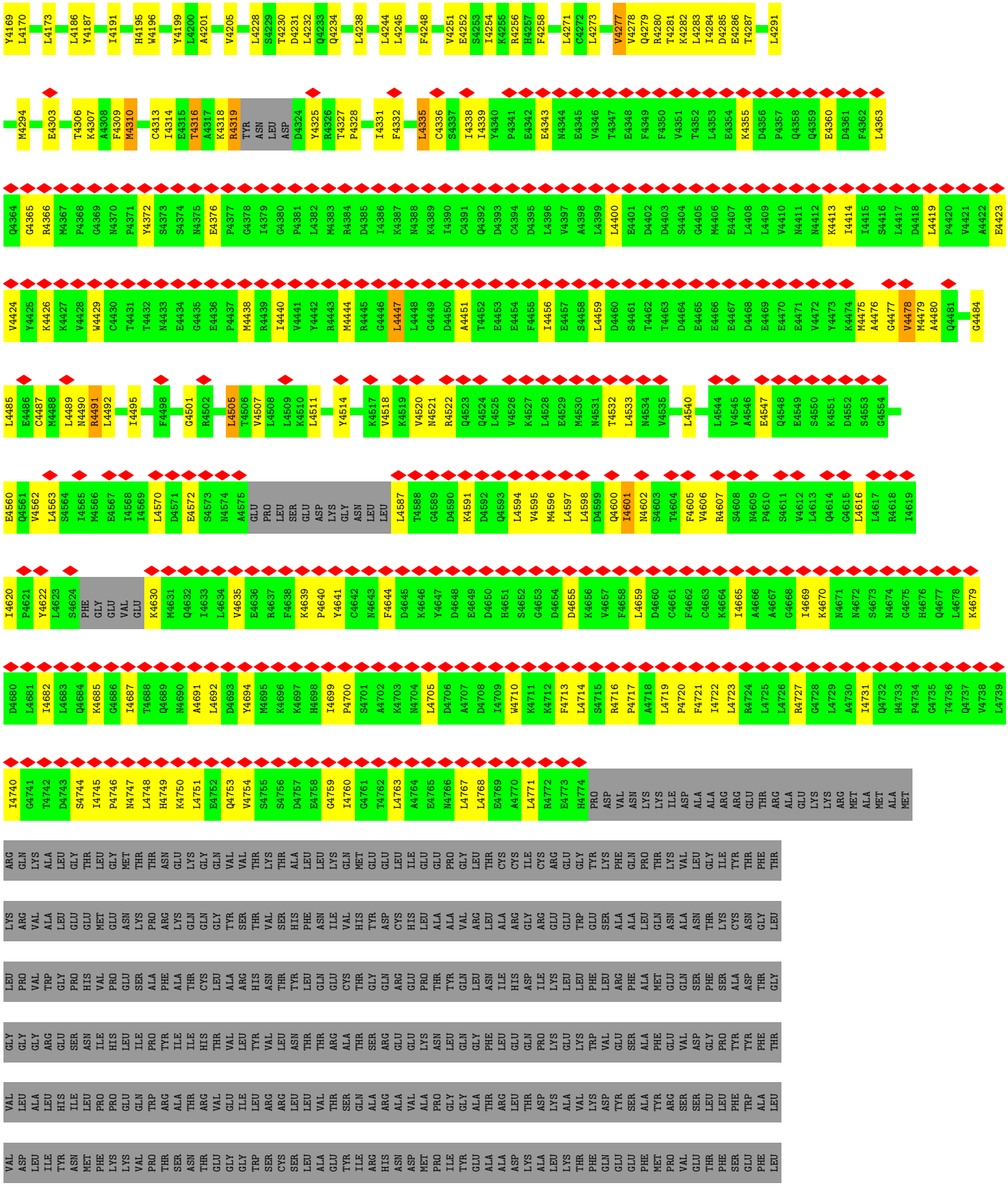
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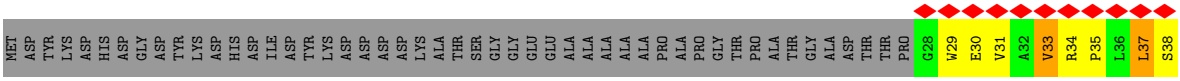
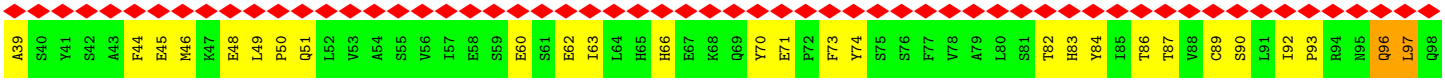
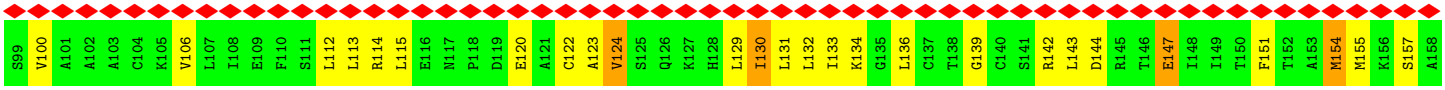
LEU PRO VAL TRP GLY PRO HIS VAL PRO GLU SER ALA PHE ALA THR CYS LEU ALA ARG HIS ASN THR TYR LEU GLN GLU CYS THR GLY GLN ARG GLU PRO THR TYR GLN LEU ASN ILE HIS ASP ILE LYS LEU LEU PHE LEU ARG PHE MET ALA GLU GLN SER PHE SER ALA ASP THR GLY
GLY GLY GLY ARG GLU SER ASN ILE HIS LEU ILE PRO TYR ILE ILE HIS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

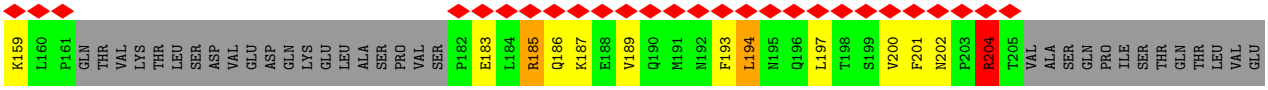
• Molecule 1: UBR4 (endogenously FLAG-tagged at the N-terminus),E3 ubiquitin-protein ligase UBR4,E3 ubiquitin-protein ligase UBR4,E3 ubiquitin-protein ligase UBR4

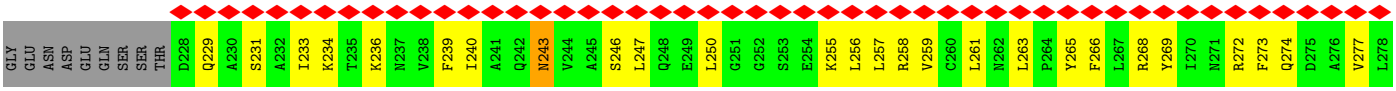
Chain B:

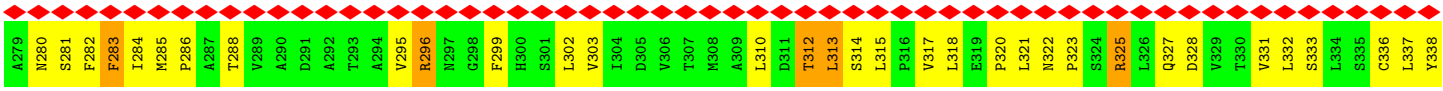


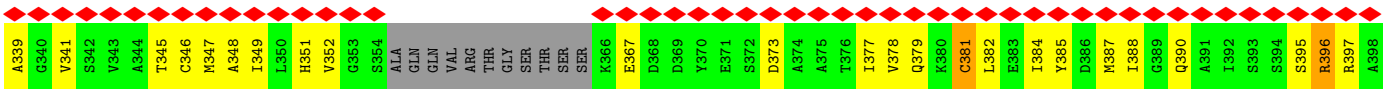


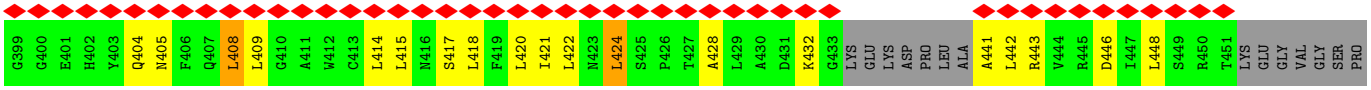


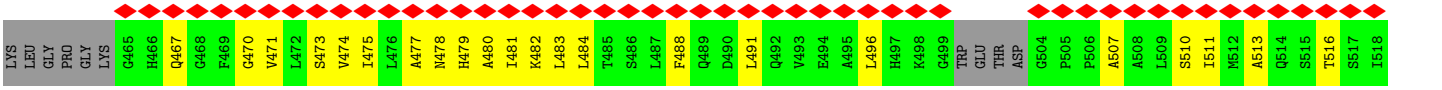


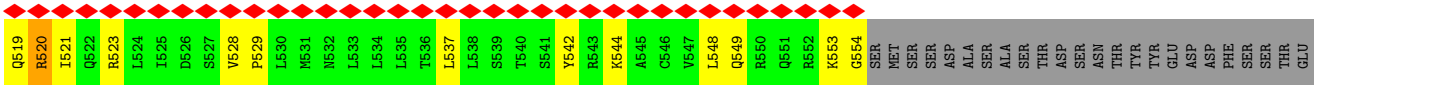


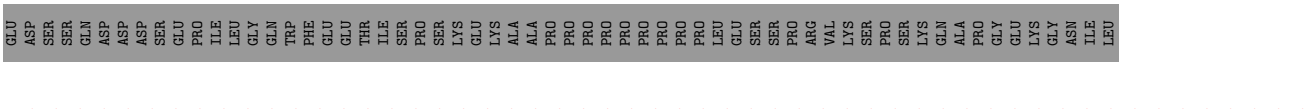


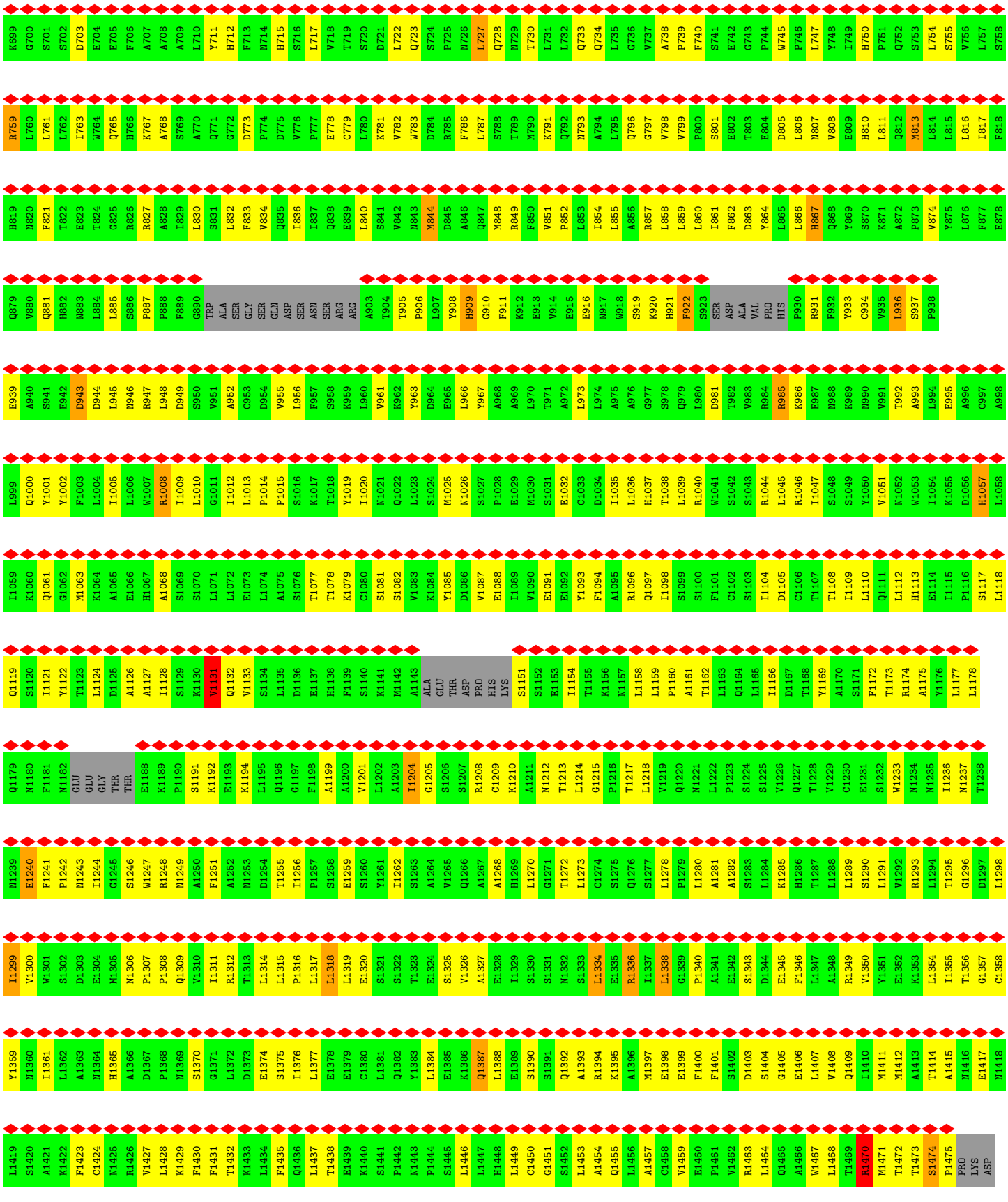








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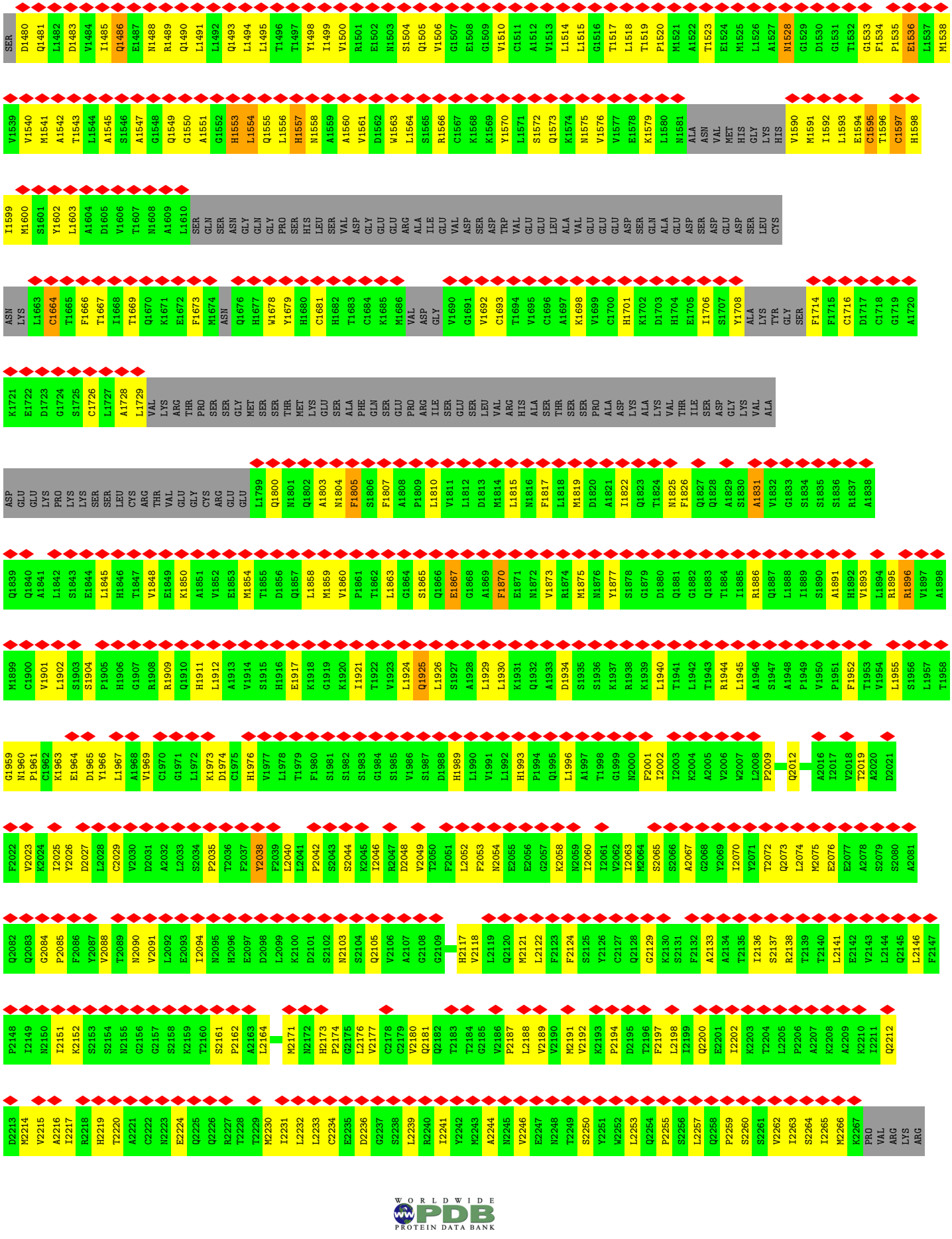
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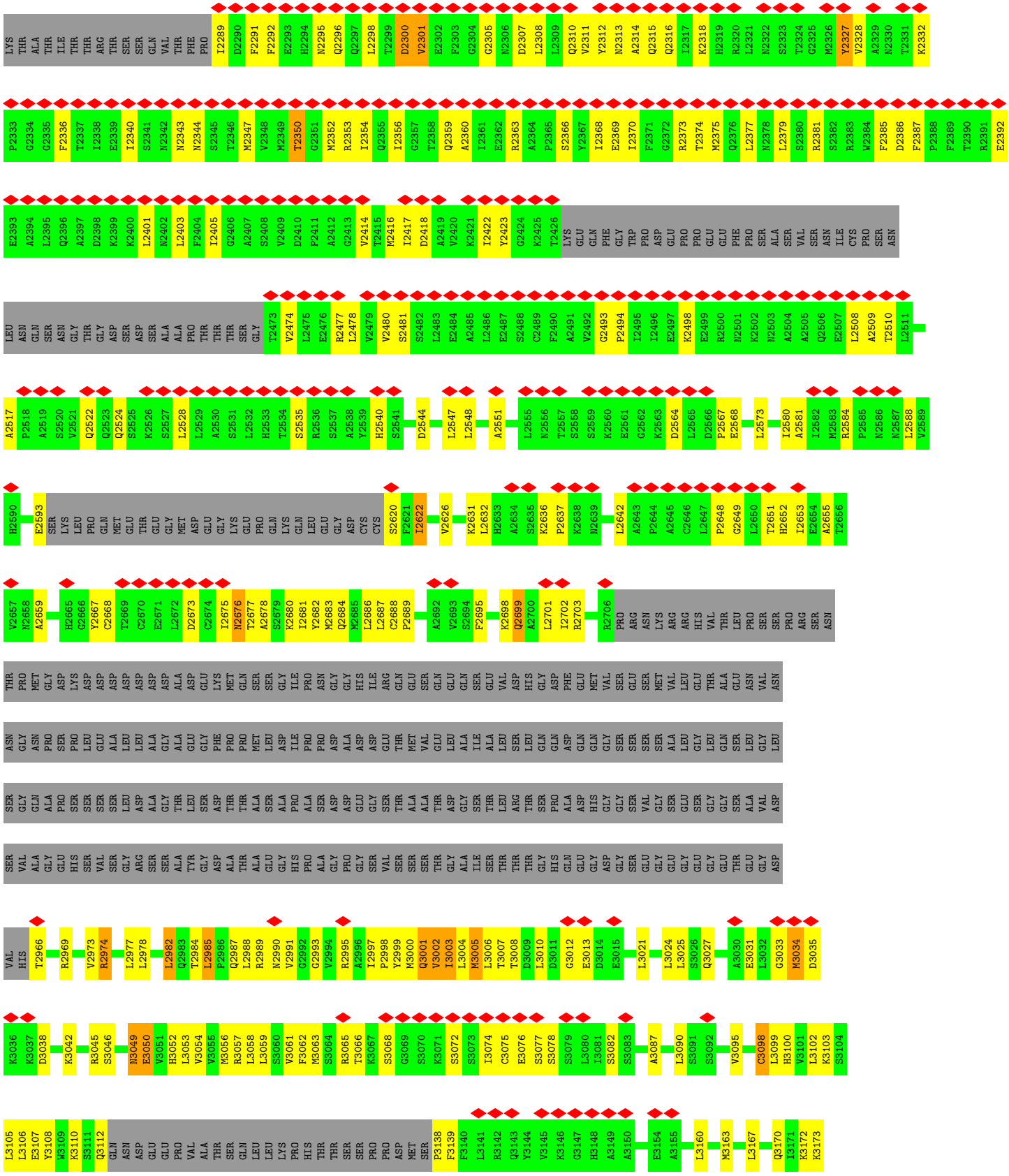
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E2393 A2394 L2395 Q2396 A2397 D2398 K2399 K2400 L2401 N2402 L2403 F2404 I2405 G2406 A2407 S2408 V2409 D2410 P2411 A2412 G2413 V2414 T2415 M2416 I2417 D2418 A2419 V2420 K2421 I2422 Y2423 G2424 K2425 T2426 LYS GLU GLN PHE GLY TRP PRO ASP GLU PRO PRO GLU GLU PHE PRO SER ALA SER VAL SER ASN ILE CYS PRO SER ASN
LEU ASN GLN SER ASN GLY THR GLY ASP SER ASP SER ALA ALA PRO THR THR THR SER GLY T2473 V2474 L2475 E2476 R2477 L2478 V2479 V2480 S2481 S2482 L2483 E2484 A2485 L2486 E2487 S2488 C2489 F2490 A2491 V2492 G2493 P2494 I2495 I2496 E2497 K2498 E2499 R2500 N2501 K2502 N2503 A2504 A2505 Q2506 E2507 L2508 A2509 T2510 L2511
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V2657 M2658 A2659 H2665 G2666 Y2667 C2668 T2669 C2670 E2671 L2672 D2673 C2674 I2675 N2676 T2677 A2678 S2679 K2680 I2681 Y2682 M2683 Q2684 M2685 L2686 L2687 C2688 P2689 A2692 V2693 S2694 F2695 K2698 Q2699 A2700 L2701 I2702 R2703 R2706 PRO ARG ASN LYS ARG ARG HIS VAL THR LEU PRO SER SER PRO ARG SER ASN
THR PRO MET GLY ASP LYS ASP ASP ASP ASP ASP ASP ASP ASP ASP ALA ASP GLU LYS MET GLN SER SER GLY ILE PRO ASN GLY GLY HIS ILE ARG GLN GLU SER GLN GLU GLN SER GLU GLU VAL ASP HIS GLY ASP PHE GLU MET VAL SER GLU SER MET VAL LEU LEU GLU THR ALA GLU ASN VAL ASN
ASN GLY ASN PRO SER PRO LEU GLU ALA LEU LEU ALA GLY ALA GLU GLY PHE PRO PRO MET LEU ASP ILE PRO PRO ASP ALA ASP GLU THR MET VAL GLU LEU ALA ILE ALA LEU SER LEU GLN GLN ASP GLN GLN GLY SER SER SER ALA LEU GLY LEU GLN SER LEU GLY LEU
SER GLY GLN ALA PRO SER SER SER LEU ASP ALA GLY THR LEU SER ASP THR THR ALA SER ALA PRO ALA SER ASP ASP GLU GLY SER THR ALA ALA THR ASP GLY SER THR LEU ARG THR SER PRO ALA ASP HIS GLY GLY SER VAL GLY SER GLU GLY GLY SER GLU GLY GLY SER ALA VAL ASP
SER VAL ALA GLY GLU HIS SER VAL SER GLY ARG SER SER ALA TYR GLY ASP ALA THR ALA GLU GLY HIS PRO ALA GLY PRO GLY SER VAL SER SER SER THR GLY ALA ILE SER THR THR THR GLY HIS GLN GLU GLY ASP GLY SER GLU GLY GLU GLU GLY GLU GLY GLU THR GLU GLY ASP
VAL HIS T2966 R2969 V2973 R2974 L2977 L2978 L2982 Q2983 T2984 L2985 P2986 Q2987 L2988 R2989 N2990 V2991 G2992 G2993 V2994 R2995 A2996 I2997 P2998 Y2999 M3000 Q3001 V3002 I3003 L3004 M3005 L3006 T3007 T3008 D3009 L3010 D3011 G3012 E3013 D3014 E3015 L3021 L3024 L3025 S3026 Q3027 A3030 E3031 L3032 G3033 M3034 D3035
K3036 K3037 D3038 K3042 R3045 S3046 N3049 E3050 V3051 H3052 L3053 V3054 V3055 M3056 R3057 L3058 L3059 S3060 V3061 F3062 M3063 S3064 R3065 T3066 K3067 S3068 G3069 S3070 K3071 S3072 S3073 I3074 C3075 E3076 S3077 S3078 S3079 L3080 I3081 S3082 S3083 A3087 L3090 S3091 S3092 V3095 C3098 L3099 H3100 V3101 L3102 K3103 S3104
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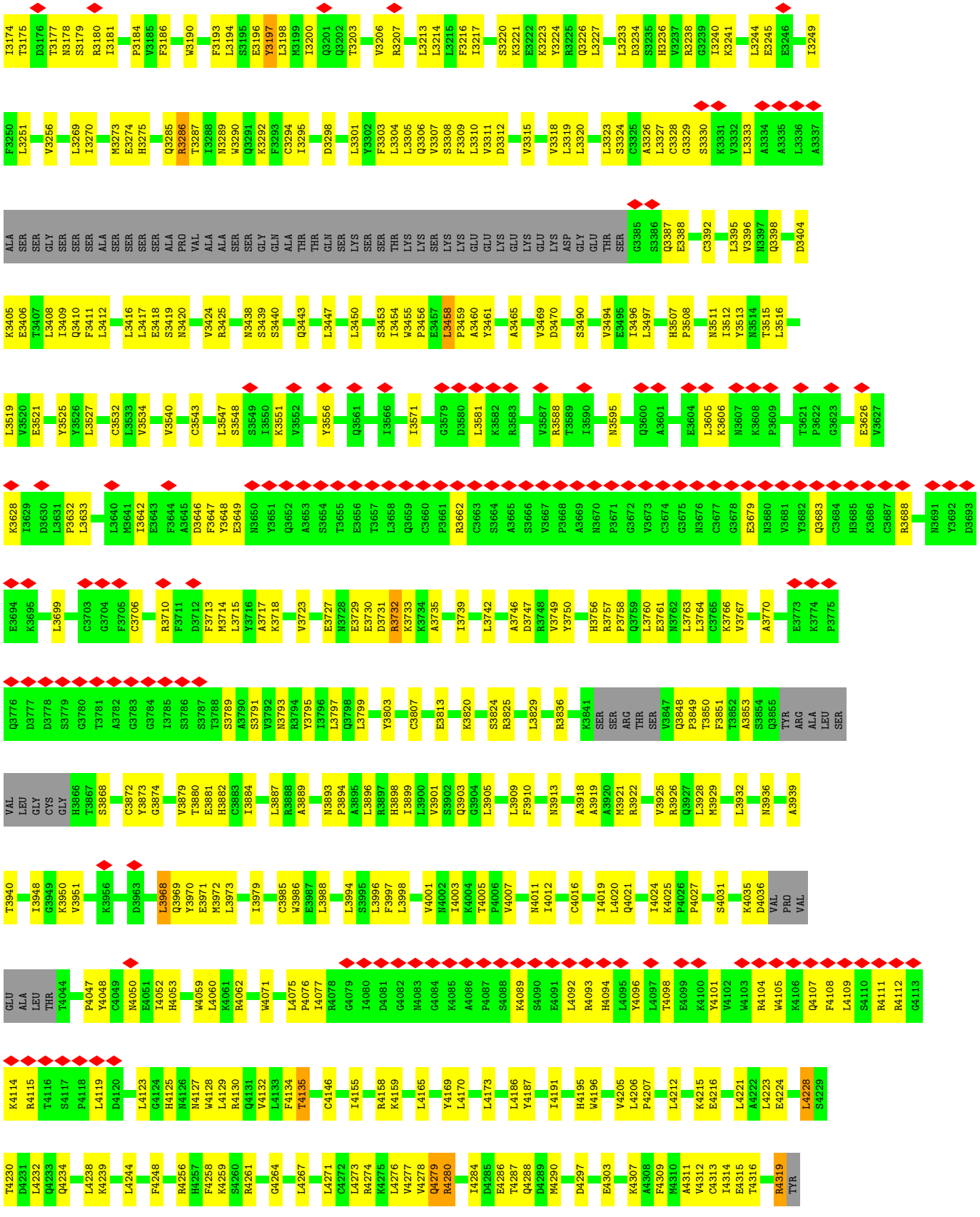
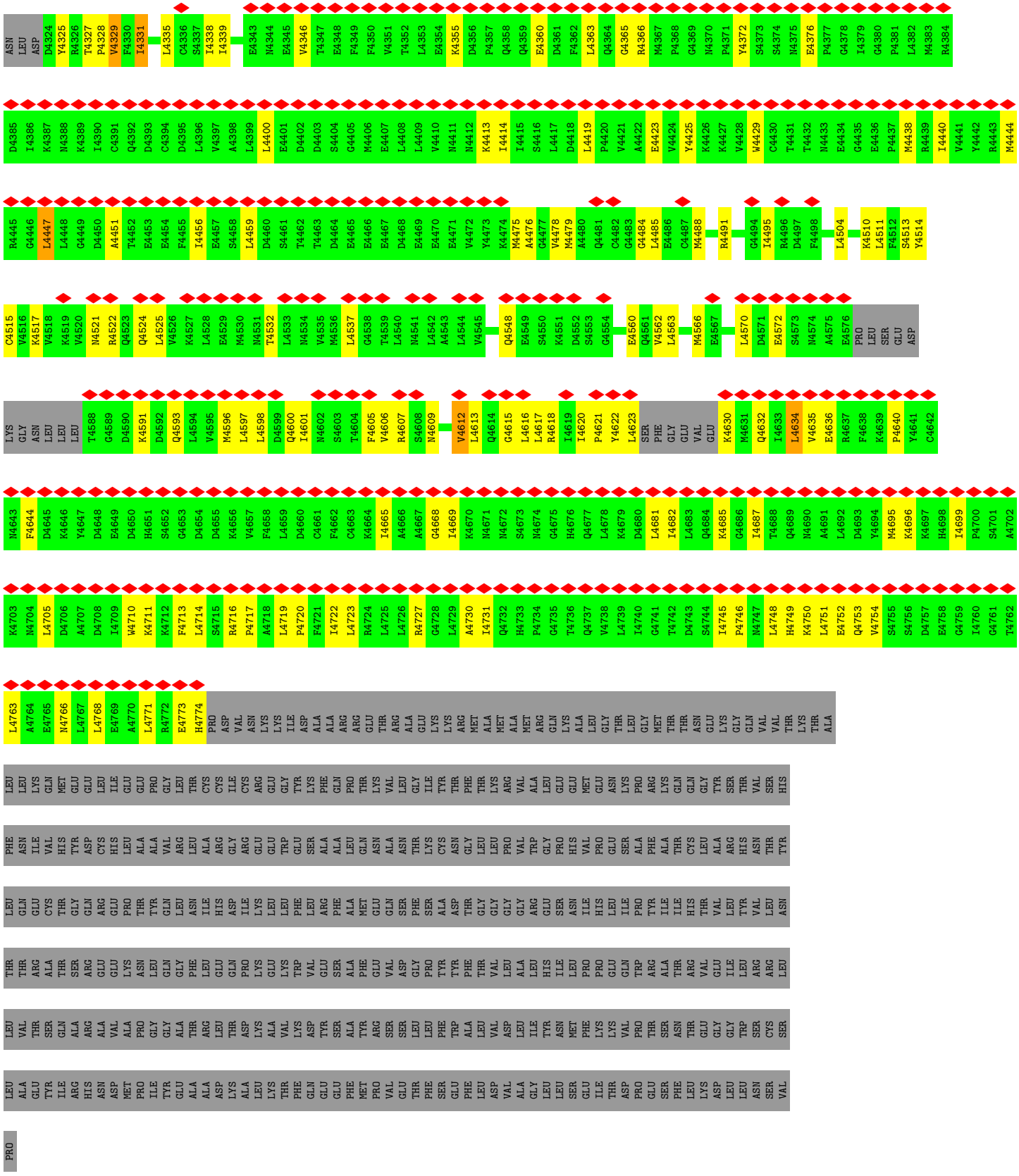
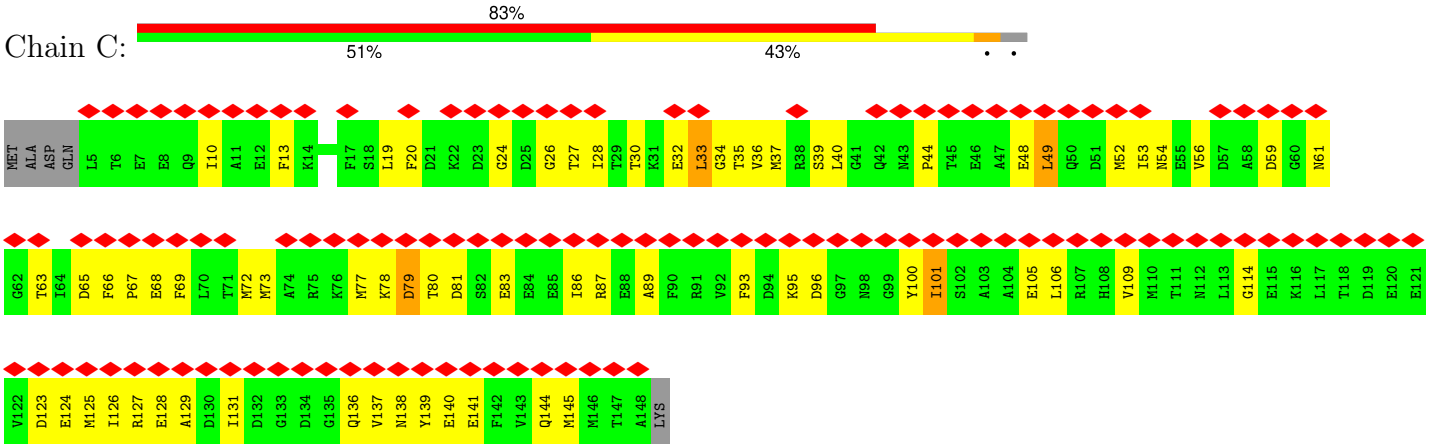




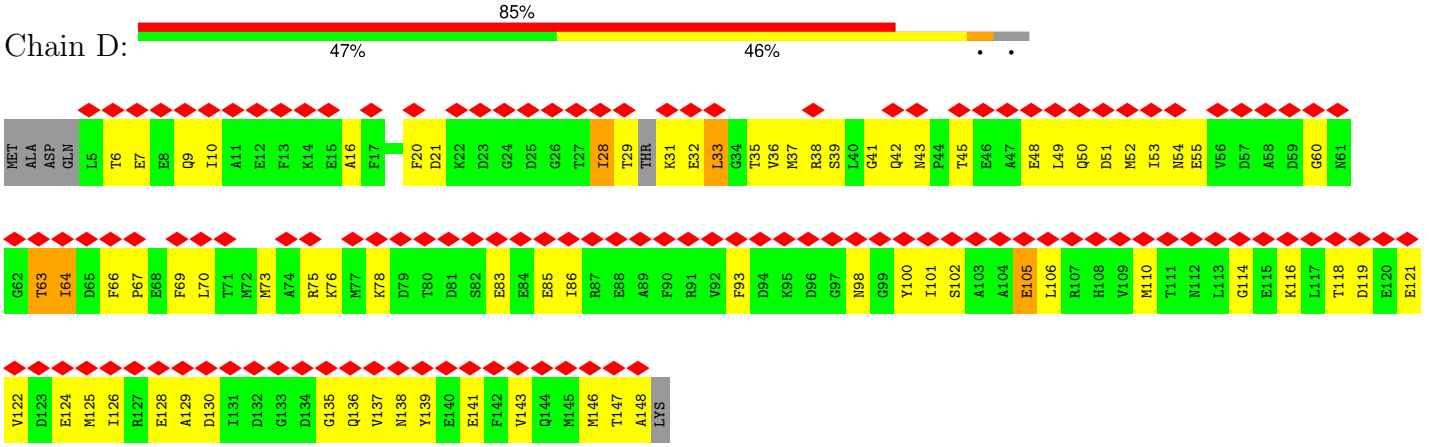
- Molecule 2: Calmodulin-1

Chain C:



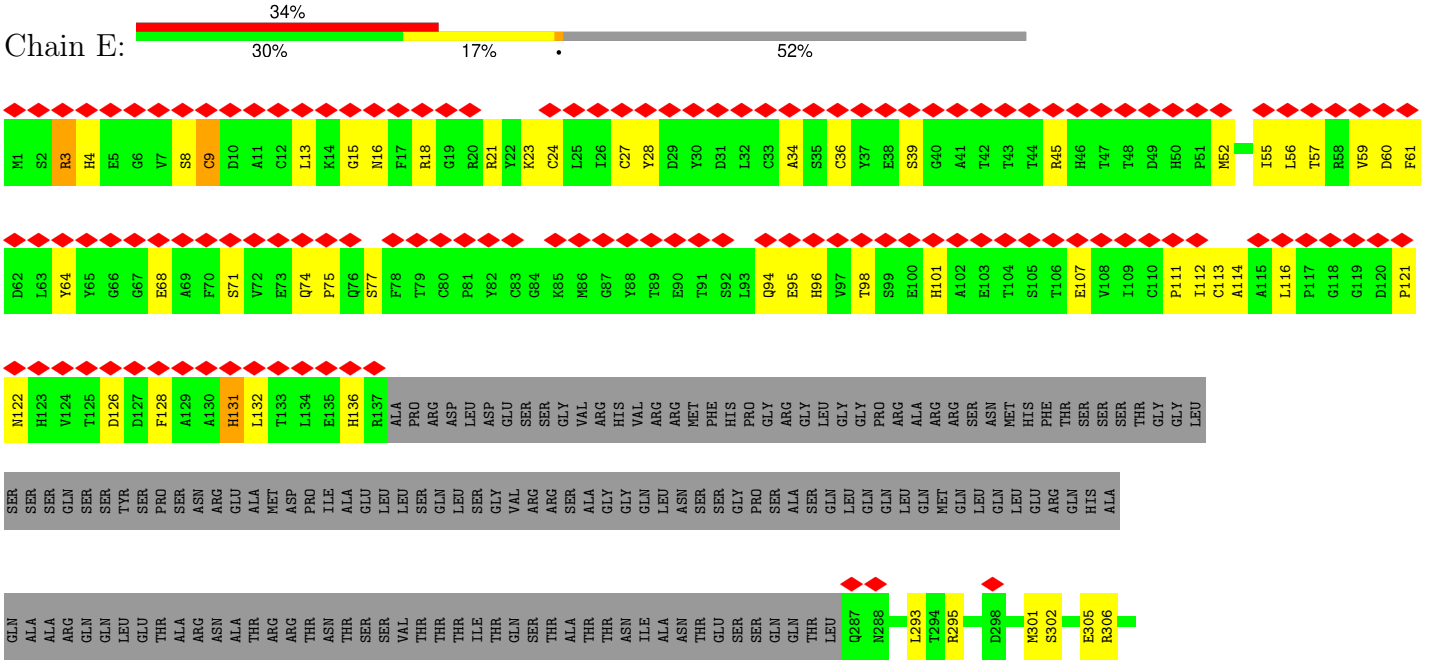
• Molecule 2: Calmodulin-1

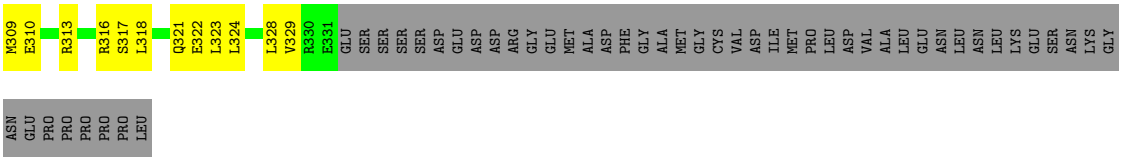
Chain D:



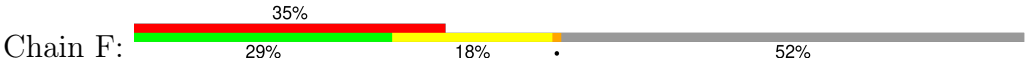
• Molecule 3: E3 ubiquitin-protein ligase KCMF1

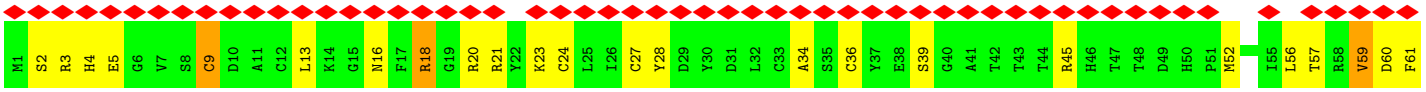
Chain E:

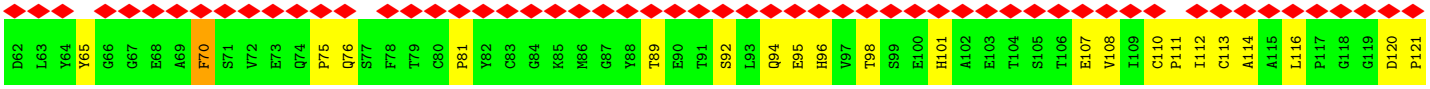


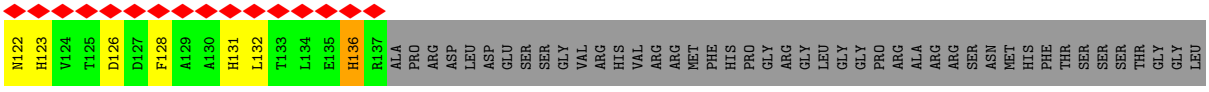


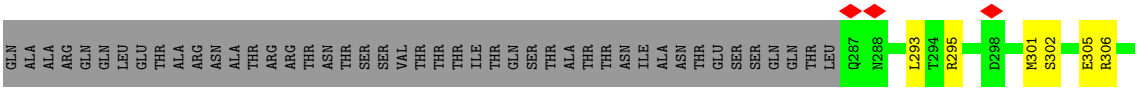
• Molecule 3: E3 ubiquitin-protein ligase KCMF1

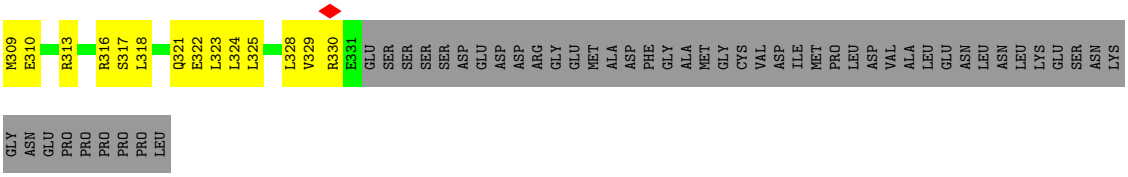












4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	126380	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.255	Depositor
Minimum map value	-0.578	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.13	Depositor
Map size (Å)	440.16, 440.16, 440.16	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.048, 1.048, 1.048	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.88	39/31195 (0.1%)	1.04	1/42247 (0.0%)
1	B	0.91	36/31477 (0.1%)	1.10	2/42619 (0.0%)
2	C	0.97	0/1146	1.24	0/1539
2	D	0.98	0/1138	1.25	0/1526
3	E	1.01	12/1463 (0.8%)	0.99	0/1978
3	F	1.00	13/1463 (0.9%)	1.01	0/1978
All	All	0.91	100/67882 (0.1%)	1.08	3/91887 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	19
1	B	0	25
2	D	0	1
3	E	0	1
3	F	0	2
All	All	0	48

All (100) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1682	HIS	C-N	-10.20	1.20	1.33
1	B	1993	HIS	C-N	8.77	1.43	1.34
1	A	2290	ASP	C-N	-8.62	1.22	1.33
1	B	1865	SER	C-N	8.21	1.44	1.33
1	A	1894	LEU	C-N	-8.11	1.21	1.33
1	A	1717	ASP	C-N	-8.11	1.23	1.33
1	A	1865	SER	C-N	8.01	1.44	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1681	CYS	C-N	-7.75	1.22	1.33
1	B	2318	LYS	C-N	-7.68	1.24	1.33
1	B	2327	TYR	C-N	-7.66	1.22	1.33
1	A	2038	TYR	C-N	7.62	1.44	1.33
1	A	2318	LYS	C-N	-7.62	1.24	1.33
1	A	1860	VAL	C-N	7.60	1.42	1.33
1	B	1860	VAL	C-N	7.54	1.42	1.33
1	B	2038	TYR	C-N	7.51	1.44	1.33
1	B	2076	GLU	C-N	-7.50	1.24	1.33
1	A	2146	LEU	C-N	7.43	1.42	1.33
3	F	9	CYS	C-N	-7.42	1.22	1.33
1	A	2076	GLU	C-N	-7.38	1.24	1.33
3	E	101	HIS	C-N	-7.38	1.24	1.34
1	B	2535	SER	C-N	-7.36	1.24	1.33
1	B	2146	LEU	C-N	7.36	1.42	1.33
3	E	9	CYS	C-N	-7.32	1.22	1.33
3	F	39	SER	C-N	-7.29	1.25	1.33
3	E	59	VAL	C-N	-7.18	1.24	1.34
3	E	39	SER	C-N	-7.18	1.25	1.33
3	F	101	HIS	C-N	-7.12	1.24	1.34
3	E	61	PHE	C-N	-7.06	1.24	1.34
3	F	59	VAL	C-N	-7.05	1.24	1.34
3	F	34	ALA	C-N	-7.03	1.24	1.33
3	F	61	PHE	C-N	-6.96	1.24	1.34
3	E	34	ALA	C-N	-6.84	1.24	1.33
1	A	2251	TYR	C-N	6.75	1.43	1.33
1	A	2294	HIS	C-N	-6.70	1.24	1.33
3	E	98	THR	C-N	-6.70	1.24	1.33
1	B	2026	TYR	C-N	-6.66	1.24	1.33
1	A	2658	ASN	C-N	-6.63	1.25	1.33
3	F	98	THR	C-N	-6.59	1.24	1.33
1	A	1973	LYS	C-N	6.58	1.43	1.33
1	B	1973	LYS	C-N	6.54	1.42	1.33
1	A	2026	TYR	C-N	-6.54	1.24	1.33
1	B	1925	GLN	C-N	6.44	1.43	1.33
1	A	1870	PHE	C-N	-6.26	1.24	1.33
1	B	2392	GLU	C-N	-6.21	1.25	1.33
1	A	2067	ALA	C-N	6.11	1.42	1.33
1	B	1870	PHE	C-N	-6.08	1.25	1.33
1	A	2374	THR	C-N	-6.03	1.25	1.33
1	A	1925	GLN	C-N	6.02	1.43	1.33
1	B	2374	THR	C-N	-5.96	1.25	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2242	TYR	C-N	-5.91	1.25	1.33
1	B	2315	GLN	C-N	-5.89	1.26	1.33
1	B	2067	ALA	C-N	5.88	1.42	1.33
1	A	2315	GLN	C-N	-5.87	1.26	1.33
1	A	2366	SER	C-N	-5.87	1.26	1.33
1	B	2366	SER	C-N	-5.86	1.26	1.33
1	B	2177	VAL	C-N	5.78	1.41	1.33
1	B	2313	ASN	C-N	-5.64	1.26	1.33
1	A	1965	ASP	C-N	-5.61	1.25	1.33
1	B	2510	THR	C-N	-5.58	1.26	1.33
3	F	57	THR	C-N	-5.57	1.26	1.33
3	E	57	THR	C-N	-5.55	1.26	1.33
1	A	2177	VAL	C-N	5.49	1.41	1.33
1	B	2699	GLN	C-N	-5.49	1.26	1.33
3	F	36	CYS	C-N	-5.49	1.26	1.33
1	B	1965	ASP	C-N	-5.48	1.25	1.33
1	B	2350	THR	C-N	-5.42	1.26	1.33
1	B	2084	GLY	C-N	5.39	1.40	1.33
1	B	1825	ASN	C-N	5.38	1.41	1.33
1	A	1895	ARG	C-N	-5.38	1.25	1.33
1	A	2350	THR	C-N	-5.38	1.26	1.33
1	A	2577	ALA	C-N	-5.35	1.27	1.33
3	E	36	CYS	C-N	-5.34	1.27	1.33
1	A	2084	GLY	C-N	5.33	1.40	1.33
1	B	1831	ALA	C-N	5.32	1.39	1.33
3	E	95	GLU	C-N	-5.32	1.27	1.33
3	F	96	HIS	C-N	-5.29	1.27	1.33
1	A	1955	LEU	C-N	5.29	1.40	1.33
1	B	2703	ARG	C-N	-5.27	1.27	1.33
1	A	1867	GLU	C-N	5.24	1.40	1.33
3	E	60	ASP	C-N	-5.23	1.27	1.33
1	B	2234	CYS	C-N	-5.21	1.26	1.34
1	B	2091	VAL	C-N	-5.21	1.26	1.33
3	F	60	ASP	C-N	-5.20	1.27	1.33
3	F	95	GLU	C-N	-5.20	1.27	1.33
3	E	96	HIS	C-N	-5.19	1.27	1.33
1	B	2622	ILE	C-N	-5.17	1.27	1.33
1	A	2234	CYS	C-N	-5.16	1.27	1.34
1	A	1864	GLY	C-N	-5.13	1.25	1.33
3	F	110	CYS	C-N	-5.13	1.27	1.34
1	B	2216	ALA	C-N	5.12	1.40	1.33
1	A	2579	SER	C-N	-5.11	1.27	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1867	GLU	C-N	5.09	1.40	1.33
1	A	2061	ILE	C-N	-5.09	1.27	1.33
1	B	2343	ASN	C-N	-5.09	1.25	1.33
1	B	2035	PRO	C-N	-5.07	1.27	1.33
1	A	2035	PRO	C-N	-5.05	1.27	1.33
1	A	2359	GLN	C-N	-5.03	1.27	1.33
1	A	2558	SER	C-N	-5.02	1.27	1.33
1	A	2622	ILE	C-N	-5.00	1.27	1.33
1	B	2314	ALA	C-N	-5.00	1.27	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1282	ALA	N-CA-C	-6.39	104.32	111.28
1	B	1131	VAL	N-CA-CB	5.70	117.22	110.55
1	B	529	PRO	N-CA-C	-5.06	102.05	112.47

There are no chirality outliers.

All (48) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1008	ARG	Sidechain
1	A	1174	ARG	Sidechain
1	A	1293	ARG	Sidechain
1	A	1394	ARG	Sidechain
1	A	2320	ARG	Sidechain
1	A	2703	ARG	Sidechain
1	A	3045	ARG	Sidechain
1	A	3142	ARG	Sidechain
1	A	3166	ARG	Sidechain
1	A	325	ARG	Sidechain
1	A	3286	ARG	Sidechain
1	A	3732	ARG	Sidechain
1	A	3825	ARG	Sidechain
1	A	3857	ARG	Sidechain
1	A	4319	ARG	Sidechain
1	A	4491	ARG	Sidechain
1	A	849	ARG	Sidechain
1	A	94	ARG	Sidechain
1	A	985	ARG	Sidechain
1	B	1008	ARG	Sidechain
1	B	1312	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	B	1336	ARG	Sidechain
1	B	1470	ARG	Sidechain
1	B	185	ARG	Sidechain
1	B	1896	ARG	Sidechain
1	B	204	ARG	Sidechain
1	B	2381	ARG	Sidechain
1	B	296	ARG	Sidechain
1	B	2974	ARG	Sidechain
1	B	2989	ARG	Sidechain
1	B	3286	ARG	Sidechain
1	B	3732	ARG	Sidechain
1	B	3836	ARG	Sidechain
1	B	396	ARG	Sidechain
1	B	397	ARG	Sidechain
1	B	4115	ARG	Sidechain
1	B	4256	ARG	Sidechain
1	B	4280	ARG	Sidechain
1	B	4319	ARG	Sidechain
1	B	4607	ARG	Sidechain
1	B	520	ARG	Sidechain
1	B	759	ARG	Sidechain
1	B	849	ARG	Sidechain
1	B	985	ARG	Sidechain
2	D	75	ARG	Sidechain
3	E	3	ARG	Sidechain
3	F	18	ARG	Sidechain
3	F	330	ARG	Sidechain

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	30658	0	31020	1288	0
1	B	30933	0	31316	1262	0
2	C	1134	0	1063	68	0
2	D	1127	0	1055	61	0
3	E	1435	0	1344	44	0
3	F	1435	0	1344	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	6	0	0	2	0
4	B	6	0	0	3	0
4	E	4	0	0	0	0
4	F	4	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	2	0
All	All	66746	0	67142	2687	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 20.

All (2687) 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:B:3270:ILE:CD1	1:B:3632:PRO:HG2	1.66	1.25
1:A:3270:ILE:CD1	1:A:3632:PRO:HG2	1.66	1.23
1:B:3087:ALA:CB	1:B:3181:ILE:HG21	1.73	1.19
1:A:73:PHE:CD1	1:A:159:LYS:HA	1.80	1.15
2:D:98:ASN:HB2	5:D:202:CA:CA	1.06	1.15
1:B:3087:ALA:HB2	1:B:3181:ILE:HG21	1.31	1.11
1:A:3270:ILE:HD13	1:A:3632:PRO:HG2	1.25	1.10
1:A:1450:CYS:HB2	1:A:1505:GLN:HB2	1.33	1.09
1:A:1700:CYS:SG	1:A:1726:CYS:HA	1.92	1.09
1:A:2212:GLN:NE2	1:A:2235:GLU:HA	1.65	1.09
1:B:3087:ALA:HB2	1:B:3181:ILE:HD13	1.36	1.08
1:B:910:GLY:HA2	1:B:933:TYR:HA	1.19	1.08
1:B:1205:GLY:HA3	1:B:1215:GLY:CA	1.83	1.08
1:B:3270:ILE:HD13	1:B:3632:PRO:HG2	1.25	1.07
1:A:1500:VAL:HG22	1:A:1547:ALA:HB2	1.33	1.07
1:B:2564:ASP:OD1	1:B:2631:LYS:HB3	1.55	1.06
1:A:1700:CYS:SG	1:A:1727:LEU:N	2.29	1.04
2:C:106:LEU:HD22	2:C:126:ILE:HD11	1.38	1.04
1:A:3269:LEU:HB3	1:A:3633:LEU:CD1	1.89	1.03
1:B:3269:LEU:HB3	1:B:3633:LEU:CD1	1.89	1.02
1:A:2342:ASN:HB3	1:A:2399:LYS:HA	1.40	1.01
1:A:1870:PHE:CZ	1:A:1924:LEU:HD11	1.97	0.99
1:B:1870:PHE:CZ	1:B:1924:LEU:HD11	1.97	0.99
1:B:1205:GLY:HA3	1:B:1215:GLY:HA2	1.43	0.99
1:A:1873:VAL:HG11	1:A:2233:LEU:HD21	1.45	0.99
1:A:3793:ASN:HA	1:B:3521:GLU:HG3	1.43	0.99
1:B:2698:LYS:HD2	1:B:2998:PRO:HA	1.46	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2173:HIS:CD2	1:A:2253:LEU:HD11	1.99	0.98
1:B:1205:GLY:CA	1:B:1215:GLY:HA3	1.94	0.97
1:B:1901:VAL:HG11	1:B:2217:ILE:HD12	1.45	0.96
1:B:3410:GLN:HG3	1:B:3850:THR:HB	1.47	0.96
1:A:53:VAL:HG11	1:A:99:SER:HB3	1.47	0.96
2:D:50:GLN:O	2:D:53:ILE:HG22	1.65	0.96
1:A:1901:VAL:HG11	1:A:2217:ILE:HD12	1.45	0.95
1:A:2294:HIS:O	1:A:2425:LYS:HE2	1.68	0.94
2:D:101:ILE:HB	2:D:137:VAL:HB	1.48	0.93
1:B:1870:PHE:HZ	1:B:1924:LEU:CD1	1.82	0.93
1:A:1438:THR:HA	1:A:1446:LEU:HD13	1.47	0.93
1:A:1870:PHE:HZ	1:A:1924:LEU:CD1	1.82	0.92
1:B:3087:ALA:HB1	1:B:3181:ILE:HG21	1.53	0.91
1:A:690:ILE:HA	1:A:710:LEU:HD21	1.51	0.91
1:B:1438:THR:HA	1:B:1446:LEU:HD13	1.51	0.91
1:B:1394:ARG:HA	1:B:1397:MET:HE2	1.53	0.91
1:B:2564:ASP:CG	1:B:2631:LYS:HB3	1.96	0.90
1:A:1398:GLU:HA	1:A:1449:LEU:HD21	1.50	0.90
1:B:1486:GLN:HA	1:B:1489:ARG:HD2	1.52	0.90
3:F:94:GLN:HA	3:F:132:LEU:HD13	1.53	0.90
1:A:1870:PHE:HE2	1:A:2239:LEU:HD11	1.37	0.90
3:E:94:GLN:HA	3:E:132:LEU:HD13	1.54	0.90
1:B:3003:ILE:HA	1:B:3006:LEU:HD12	1.54	0.89
2:D:98:ASN:CB	5:D:202:CA:CA	1.79	0.89
1:A:1105:ASP:H	1:A:1110:LEU:HD21	1.37	0.89
1:B:3270:ILE:CD1	1:B:3632:PRO:CG	2.51	0.89
1:A:3521:GLU:HG3	1:B:3793:ASN:HA	1.53	0.89
1:B:281:SER:HB2	1:B:443:ARG:HD2	1.56	0.88
1:B:1166:ILE:HG12	1:B:1291:LEU:HB3	1.56	0.88
1:A:3270:ILE:CD1	1:A:3632:PRO:CG	2.51	0.88
1:B:1159:LEU:HA	1:B:1298:LEU:HD13	1.55	0.88
1:B:134:LYS:HA	1:B:315:LEU:HD21	1.54	0.87
1:A:4231:ASP:HB3	1:A:4234:GLN:HB2	1.56	0.87
1:B:1600:MET:HA	1:B:1603:LEU:HD12	1.55	0.87
1:B:2687:LEU:HD22	1:B:2991:VAL:HG21	1.56	0.87
1:A:2027:ASP:OD1	1:A:2029:CYS:SG	2.33	0.87
3:E:114:ALA:HA	3:E:121:PRO:HA	1.56	0.87
1:A:2040:LEU:HD13	1:A:2085:PRO:HB2	1.57	0.87
1:A:3066:THR:HG21	1:A:3082:SER:HB3	1.57	0.86
1:B:1493:GLN:HG2	1:B:1540:VAL:HG22	1.54	0.86
1:A:1401:PHE:HA	1:A:1406:GLU:HG3	1.58	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4306:THR:HG21	1:A:4338:ILE:HG12	1.57	0.86
1:A:3172:LYS:HE3	1:A:3217:ILE:HA	1.57	0.86
1:A:4232:LEU:HD13	1:B:3750:TYR:HB2	1.57	0.86
1:A:1921:ILE:HB	1:A:1948:ALA:HB3	1.57	0.86
2:C:69:PHE:CZ	2:C:73:MET:SD	2.67	0.86
1:A:2040:LEU:CD1	1:A:2085:PRO:HB2	2.06	0.86
1:A:2173:HIS:HD2	1:A:2253:LEU:HD11	1.35	0.86
1:B:2027:ASP:OD1	1:B:2029:CYS:SG	2.33	0.86
2:C:106:LEU:CD2	2:C:126:ILE:HD11	2.05	0.86
1:A:1338:LEU:HD13	1:A:1346:PHE:HA	1.56	0.85
1:A:2375:MET:HG2	1:A:2387:PHE:HE1	1.40	0.85
1:B:2040:LEU:CD1	1:B:2085:PRO:HB2	2.05	0.85
1:A:1112:LEU:HD13	1:A:1179:GLN:HB2	1.57	0.85
1:B:2040:LEU:HD13	1:B:2085:PRO:HB2	1.57	0.85
1:B:3419:SER:O	1:B:3420:ASN:CG	2.19	0.85
1:A:1453:LEU:HB3	1:A:1506:VAL:HG13	1.58	0.85
1:A:687:ALA:HB2	1:A:731:LEU:HD12	1.58	0.85
1:B:1278:LEU:HB3	1:B:1281:ALA:HB2	1.57	0.85
2:C:106:LEU:HD22	2:C:126:ILE:CD1	2.07	0.85
1:A:1960:ASN:HD21	1:A:2012:GLN:HA	1.41	0.85
1:B:4444:MET:HE3	1:B:4447:LEU:HD13	1.58	0.85
1:B:1870:PHE:HZ	1:B:1924:LEU:HD11	1.37	0.84
1:B:910:GLY:CA	1:B:933:TYR:HA	2.04	0.84
1:B:2695:PHE:CE1	1:B:2699:GLN:NE2	2.45	0.84
1:A:1205:GLY:HA2	1:A:1215:GLY:CA	2.07	0.84
1:A:3419:SER:O	1:A:3420:ASN:CG	2.19	0.84
1:B:3419:SER:O	1:B:3420:ASN:OD1	1.96	0.84
3:F:114:ALA:HA	3:F:121:PRO:HA	1.57	0.83
1:A:420:LEU:HD22	1:A:442:LEU:HG	1.61	0.83
1:B:2189:VAL:HG22	1:B:2230:MET:HE1	1.60	0.83
1:B:4705:LEU:HB3	1:B:4754:VAL:HG22	1.60	0.83
1:A:2189:VAL:CG2	1:A:2230:MET:HE1	2.08	0.83
2:C:80:THR:O	2:C:81:ASP:OD1	1.95	0.83
1:B:2189:VAL:CG2	1:B:2230:MET:HE1	2.09	0.83
1:A:73:PHE:HD1	1:A:159:LYS:HA	1.37	0.83
1:A:4444:MET:HE3	1:A:4447:LEU:HD13	1.59	0.83
1:A:3269:LEU:HB3	1:A:3633:LEU:HD11	1.61	0.82
1:A:2189:VAL:HG22	1:A:2230:MET:HE1	1.60	0.82
1:B:1407:LEU:HB3	1:B:1431:PHE:CE1	2.15	0.82
1:B:1407:LEU:HB3	1:B:1431:PHE:HE1	1.45	0.82
1:B:1414:THR:HG23	1:B:1423:PHE:HD2	1.44	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3419:SER:O	1:A:3420:ASN:OD1	1.96	0.82
1:A:4328:PRO:HA	1:A:4331:ILE:HD12	1.61	0.82
1:A:3940:THR:HG21	1:A:3985:CYS:HB3	1.60	0.82
1:B:1475:PRO:HD3	1:B:1485:ILE:HD12	1.61	0.81
1:A:349:ILE:HD12	1:A:429:LEU:HD11	1.62	0.81
1:B:1499:ILE:HG23	1:B:1506:VAL:HB	1.61	0.81
3:E:8:SER:HA	3:E:15:GLY:HA2	1.62	0.81
1:A:1417:GLU:HA	1:A:1470:ARG:HD2	1.62	0.81
1:B:2122:LEU:HD22	1:B:2136:ILE:HD11	1.63	0.81
2:C:49:LEU:C	2:C:49:LEU:HD13	2.06	0.81
1:B:1208:ARG:HD2	1:B:1327:ALA:HB3	1.63	0.81
1:B:3270:ILE:HD13	1:B:3632:PRO:CG	2.11	0.81
1:A:3164:VAL:O	1:A:3168:PRO:HD2	1.81	0.81
1:B:2698:LYS:HE3	1:B:3001:GLN:HB3	1.63	0.81
1:B:3516:LEU:HD22	1:B:3799:LEU:HD21	1.63	0.81
1:A:1700:CYS:SG	1:A:1726:CYS:CA	2.69	0.80
1:B:3269:LEU:HB3	1:B:3633:LEU:HD11	1.61	0.80
1:A:1904:SER:H	1:A:1964:GLU:HB3	1.45	0.80
1:A:2368:ILE:HG23	1:A:2377:LEU:HD11	1.62	0.80
1:A:3997:PHE:HB2	1:A:4016:CYS:HB3	1.63	0.80
1:A:124:VAL:HG12	1:A:129:LEU:HG	1.63	0.80
1:A:352:VAL:HB	1:A:426:PRO:HG3	1.64	0.80
1:B:4713:PHE:HE1	1:B:4751:LEU:HD21	1.46	0.80
1:B:2368:ILE:HD11	1:B:2387:PHE:CZ	2.16	0.80
1:A:659:THR:HA	1:A:663:LEU:HD12	1.63	0.80
1:A:712:HIS:HA	1:A:715:HIS:CD2	2.15	0.79
1:A:3760:LEU:HD11	1:A:3803:TYR:HB2	1.63	0.79
1:B:2122:LEU:CD2	1:B:2136:ILE:HD11	2.13	0.79
1:B:1554:LEU:HG	1:B:1804:ASN:OD1	1.82	0.79
1:B:2375:MET:HG2	1:B:2387:PHE:HE1	1.44	0.79
1:A:1030:MET:HB3	1:A:1034:ASP:HB3	1.62	0.79
1:B:263:LEU:HB2	1:B:266:PHE:HB2	1.65	0.79
1:A:131:LEU:HD11	1:A:142:ARG:HD2	1.64	0.79
1:A:4234:GLN:HE22	1:A:4279:GLN:HB3	1.48	0.79
1:A:4335:LEU:HD22	1:A:4511:LEU:HD11	1.63	0.79
1:B:3588:ARG:HD2	1:B:3646:ASP:OD2	1.83	0.79
1:A:1554:LEU:HG	1:A:1802:GLN:HE22	1.48	0.79
1:A:2122:LEU:HD22	1:A:2136:ILE:HD11	1.63	0.79
1:B:2122:LEU:HD22	1:B:2136:ILE:CD1	2.13	0.79
1:A:3872:CYS:SG	1:A:3875:CYS:HB2	2.23	0.78
1:A:1450:CYS:CB	1:A:1505:GLN:HB2	2.11	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3066:THR:HG21	1:B:3082:SER:HB2	1.65	0.78
1:A:313:LEU:HD13	1:A:388:ILE:HD11	1.65	0.78
1:A:2122:LEU:CD2	1:A:2136:ILE:HD11	2.13	0.78
1:A:3588:ARG:HD2	1:A:3646:ASP:OD2	1.82	0.77
1:B:1408:VAL:HA	1:B:1411:MET:HE2	1.66	0.77
1:A:910:GLY:HA2	1:A:933:TYR:HA	1.66	0.77
1:B:3315:VAL:HG22	1:B:3633:LEU:HD21	1.66	0.77
1:B:1412:MET:HB3	1:B:1463:ARG:NE	1.99	0.77
1:B:3004:LEU:HB2	1:B:3058:LEU:HD11	1.64	0.77
1:A:415:LEU:HD11	1:A:484:LEU:HD21	1.67	0.77
1:A:2122:LEU:HD22	1:A:2136:ILE:CD1	2.13	0.77
1:B:4591:LYS:HB2	1:B:4630:LYS:HE3	1.65	0.77
1:A:4635:VAL:HG11	1:A:4685:LYS:HG3	1.67	0.76
2:D:50:GLN:O	2:D:53:ILE:CG2	2.32	0.76
1:A:3270:ILE:HD13	1:A:3632:PRO:CG	2.11	0.76
1:A:793:ASN:HB2	1:A:854:ILE:HG21	1.66	0.76
1:A:984:ARG:HH11	1:A:984:ARG:HB2	1.51	0.76
1:B:1407:LEU:H	1:B:1407:LEU:HD12	1.50	0.76
1:B:352:VAL:HG22	1:B:467:GLN:HG2	1.67	0.76
1:B:2070:ILE:HD12	1:B:2094:ILE:HD11	1.67	0.76
1:A:656:ASN:HB3	1:B:204:ARG:HD3	1.67	0.76
1:B:1218:LEU:HD22	1:B:1376:ILE:HG23	1.68	0.75
1:B:2637:PRO:HD3	1:B:2648:PRO:HG2	1.67	0.75
1:B:4339:ILE:HG21	1:B:4514:TYR:HB3	1.67	0.75
1:A:3167:LEU:HB3	1:A:3168:PRO:HD3	1.66	0.75
1:B:1545:ALA:HB1	1:B:1553:HIS:HB2	1.68	0.75
1:B:2683:MET:HG3	1:B:2999:TYR:HE2	1.51	0.75
1:A:1870:PHE:HZ	1:A:1924:LEU:HD11	1.37	0.75
1:A:1814:MET:HA	1:A:1817:PHE:CE1	2.21	0.75
1:A:3965:ALA:HA	1:A:4011:ASN:HD21	1.52	0.75
1:B:286:PRO:HB3	1:B:295:VAL:HG21	1.68	0.75
1:B:1201:VAL:HG13	1:B:1218:LEU:HB3	1.67	0.75
1:B:1664:CYS:HB2	1:B:1729:LEU:HA	1.66	0.75
1:B:1489:ARG:NH2	1:B:1533:GLY:HA2	2.01	0.75
1:B:910:GLY:HA2	1:B:933:TYR:CA	2.09	0.74
1:B:1904:SER:H	1:B:1964:GLU:HB3	1.52	0.74
1:A:193:PHE:HB2	1:B:881:GLN:HE21	1.50	0.74
1:B:860:LEU:HB2	1:B:1005:ILE:HD13	1.69	0.74
1:A:1994:PRO:HG3	1:A:2002:ILE:HD11	1.68	0.74
1:A:2192:VAL:HG13	1:A:2197:PHE:HE1	1.52	0.74
1:A:3459:PRO:HA	1:A:3879:VAL:HG21	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4238:LEU:HG	1:B:4287:THR:HG21	1.68	0.74
1:B:112:LEU:HD12	1:B:250:LEU:HD12	1.68	0.74
1:B:2682:TYR:HD2	1:B:2977:LEU:HD11	1.53	0.73
1:A:1314:LEU:HD13	1:A:1317:LEU:HD12	1.69	0.73
1:B:3290:TRP:NE1	1:B:3326:ALA:HB2	2.03	0.73
1:A:1518:LEU:HD22	1:A:1537:LEU:HD11	1.68	0.73
1:B:3203:THR:HB	1:B:3206:VAL:HB	1.69	0.73
1:B:3459:PRO:HA	1:B:3879:VAL:HG21	1.69	0.73
1:B:4621:PRO:HB3	1:B:4668:GLY:HA3	1.69	0.73
1:B:1205:GLY:HA2	1:B:1215:GLY:HA3	1.71	0.73
1:A:4713:PHE:HE1	1:A:4751:LEU:HD21	1.53	0.73
1:B:3749:VAL:HG11	1:B:3813:GLU:HG2	1.70	0.73
1:B:1204:ILE:HG21	1:B:1357:GLY:HA3	1.71	0.73
1:A:200:VAL:HB	1:B:715:HIS:CE1	2.23	0.73
1:A:800:PRO:HD2	1:A:853:LEU:HD23	1.70	0.72
1:A:1205:GLY:HA2	1:A:1215:GLY:HA3	1.70	0.72
1:A:1610:LEU:HD13	1:A:1800:GLN:HA	1.71	0.72
1:A:3240:ILE:HD11	1:A:3275:HIS:HB2	1.70	0.72
1:B:3057:ARG:HB2	1:B:3163:MET:HE1	1.68	0.72
1:B:4105:TRP:HZ2	2:D:129:ALA:HB2	1.55	0.72
1:B:3240:ILE:HD11	1:B:3275:HIS:HB2	1.70	0.72
1:B:3256:VAL:HG23	1:B:3849:PRO:HA	1.71	0.72
1:A:261:LEU:HD21	1:A:332:LEU:HB2	1.72	0.72
1:A:3793:ASN:HA	1:B:3521:GLU:CG	2.20	0.72
1:B:1515:LEU:HD12	1:B:1541:MET:HG3	1.71	0.72
1:B:2305:GLY:HA3	1:B:2308:LEU:HB2	1.71	0.72
1:A:1870:PHE:CE1	1:A:1924:LEU:HD11	2.25	0.72
1:A:2212:GLN:HE21	1:A:2235:GLU:HA	1.54	0.72
1:B:4123:LEU:HD13	1:B:4165:LEU:HD22	1.71	0.72
2:C:69:PHE:CE1	2:C:73:MET:SD	2.82	0.72
3:E:107:GLU:HA	3:E:126:ASP:HA	1.71	0.72
1:A:912:LYS:O	1:A:916:GLU:HG3	1.89	0.72
1:B:1561:VAL:HG22	1:B:1810:LEU:HD22	1.71	0.72
1:B:3090:LEU:HD11	1:B:3184:PRO:HB3	1.72	0.72
1:A:73:PHE:CE1	1:A:159:LYS:HA	2.24	0.72
1:A:97:LEU:HD12	1:A:235:THR:HG23	1.72	0.72
1:A:420:LEU:HD21	1:A:444:VAL:HA	1.71	0.72
1:B:3001:GLN:HB2	1:B:3139:PHE:HE2	1.54	0.72
3:F:107:GLU:HA	3:F:126:ASP:HA	1.71	0.72
1:A:284:ILE:HD12	1:A:442:LEU:HD23	1.70	0.72
1:B:921:HIS:CD2	1:B:993:ALA:HB2	2.25	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2622:ILE:HD11	1:A:2667:TYR:CG	2.25	0.71
1:A:1863:LEU:HB3	1:A:1940:LEU:HD21	1.71	0.71
1:A:3813:GLU:O	1:A:3817:ILE:HG13	1.90	0.71
1:A:471:VAL:HG21	1:A:641:ARG:H	1.55	0.71
1:A:1854:MET:HE1	1:A:2151:ILE:HG23	1.71	0.71
1:A:2151:ILE:HD11	1:A:2164:LEU:HD11	1.72	0.71
1:A:2212:GLN:CD	1:A:2235:GLU:HA	2.14	0.71
1:A:3955:LEU:HD21	1:A:4012:ILE:HD12	1.73	0.71
1:A:3979:ILE:HG21	1:A:4019:ILE:HG23	1.72	0.71
1:B:2987:GLN:HA	1:B:2990:ASN:HD22	1.54	0.71
1:A:1554:LEU:HD11	1:A:1798:GLU:HB2	1.73	0.71
1:B:1870:PHE:CE1	1:B:1924:LEU:HD11	2.25	0.71
1:B:3547:LEU:HD13	1:B:3715:LEU:HD11	1.73	0.71
1:A:2565:LEU:HD21	1:A:2573:LEU:HD12	1.72	0.71
1:B:1117:SER:O	1:B:1121:ILE:HG13	1.91	0.71
1:B:3087:ALA:CB	1:B:3181:ILE:HD13	2.15	0.71
1:B:2626:VAL:HG21	1:B:2681:ILE:HD13	1.73	0.70
1:B:4048:TYR:HE1	1:B:4076:PRO:HD3	1.54	0.70
1:A:1576:VAL:HA	1:A:1579:LYS:HD2	1.73	0.70
1:A:4314:ILE:HG23	1:A:4487:CYS:SG	2.31	0.70
1:A:135:GLY:HA2	1:A:140:CYS:O	1.90	0.70
1:B:4127:ASN:HD21	1:B:4165:LEU:HD21	1.55	0.70
1:A:4477:GLY:HA3	1:A:4518:VAL:HG11	1.72	0.70
1:A:4011:ASN:O	1:A:4015:MET:HG2	1.90	0.70
1:A:1963:LYS:HD3	1:A:1966:TYR:CE2	2.27	0.70
1:A:3066:THR:HA	1:A:3078:SER:HB2	1.72	0.70
1:B:1538:MET:HG2	1:B:1598:HIS:HB3	1.74	0.70
1:B:1438:THR:OG1	1:B:1446:LEU:HB3	1.91	0.70
1:B:3001:GLN:HB2	1:B:3139:PHE:CE2	2.26	0.70
1:A:494:GLU:HB3	1:A:498:LYS:HD3	1.74	0.69
1:A:3955:LEU:HD22	1:A:4003:ILE:HD12	1.74	0.69
1:A:2308:LEU:HD23	1:A:2330:ASN:HD22	1.57	0.69
1:B:1338:LEU:HD13	1:B:1346:PHE:HA	1.74	0.69
1:B:3270:ILE:HD12	1:B:3632:PRO:HG2	1.72	0.69
1:B:1414:THR:HG23	1:B:1423:PHE:CD2	2.27	0.69
1:A:1335:GLU:HA	1:A:1339:GLY:O	1.93	0.69
1:A:1961:PRO:HB3	1:A:2171:MET:HE1	1.75	0.69
1:A:3518:GLY:HA2	1:B:3770:ALA:HB1	1.73	0.69
1:B:4339:ILE:HA	1:B:4475:MET:HB2	1.75	0.69
1:A:73:PHE:HD1	1:A:158:ALA:O	1.75	0.69
1:B:3556:TYR:O	1:B:3606:LYS:HE3	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:VAL:HB	1:B:715:HIS:ND1	2.07	0.69
1:A:3054:VAL:HA	1:A:3057:ARG:HD2	1.75	0.69
1:A:3330:SER:HB3	1:A:3333:LEU:HB3	1.74	0.69
1:A:4705:LEU:HB3	1:A:4754:VAL:HG22	1.73	0.69
1:B:3095:VAL:HG12	1:B:3190:TRP:CZ3	2.27	0.69
1:B:1963:LYS:HD3	1:B:1966:TYR:CE2	2.27	0.69
1:B:4597:LEU:HD11	1:B:4623:LEU:HD12	1.75	0.69
1:B:130:ILE:HG12	1:B:312:THR:HG23	1.74	0.69
1:B:3066:THR:HA	1:B:3078:SER:HB2	1.75	0.69
1:A:2632:LEU:O	1:A:2649:GLY:HA2	1.93	0.68
1:A:193:PHE:HB2	1:B:881:GLN:NE2	2.08	0.68
1:B:1961:PRO:HB3	1:B:2171:MET:HE1	1.75	0.68
1:B:2368:ILE:HG23	1:B:2377:LEU:HD11	1.75	0.68
1:A:797:GLY:HA3	1:A:850:PHE:HB3	1.75	0.68
1:A:3556:TYR:O	1:A:3606:LYS:HE3	1.93	0.68
1:A:329:VAL:HG12	1:A:388:ILE:HG23	1.74	0.68
1:A:1138:HIS:O	1:A:1142:MET:HG2	1.94	0.68
1:A:3812:ASP:O	1:A:3816:LYS:HG3	1.93	0.68
1:A:4238:LEU:HG	1:A:4287:THR:HG21	1.75	0.68
1:B:1191:SER:HB3	1:B:1194:LYS:HG3	1.75	0.68
1:A:845:ASP:HB3	1:A:849:ARG:HH12	1.57	0.68
1:A:286:PRO:HB3	1:A:295:VAL:HG21	1.76	0.68
1:A:1799:LEU:H	1:A:1799:LEU:HD12	1.56	0.68
1:A:2669:THR:HG22	1:A:2970:LEU:HD13	1.76	0.68
1:A:3794:ARG:N	1:B:3521:GLU:OE2	2.20	0.68
1:A:4105:TRP:HZ2	2:C:129:ALA:HB2	1.58	0.68
1:B:1338:LEU:HB3	1:B:1345:GLU:HB2	1.76	0.68
1:A:1142:MET:O	1:A:1143:ALA:C	2.35	0.68
1:A:4335:LEU:HD13	1:A:4511:LEU:HD21	1.75	0.68
1:B:763:ILE:HG22	1:B:767:LYS:HE3	1.74	0.68
1:B:852:PRO:HB2	1:B:855:LEU:HB3	1.76	0.68
1:A:288:THR:HB	1:A:291:ASP:CG	2.19	0.67
1:A:1041:TRP:CZ3	1:A:1044:ARG:HD2	2.28	0.67
1:B:3087:ALA:HA	1:B:3181:ILE:HD12	1.74	0.67
1:A:1047:ILE:HB	1:A:1050:TYR:HD2	1.59	0.67
1:A:1365:HIS:HB3	1:A:1372:LEU:HD12	1.75	0.67
1:A:1173:THR:HG22	1:A:1233:TRP:HZ2	1.60	0.67
1:A:2292:PHE:HE2	1:A:2386:ASP:HB3	1.57	0.67
1:B:4264:GLY:HA2	1:B:4312:VAL:HG11	1.76	0.67
1:A:752:GLN:HE21	1:A:888:PRO:HG3	1.59	0.67
1:A:3143:GLN:HA	1:A:3146:LYS:HE2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1025:MET:HG2	1:B:1026:ASN:N	2.10	0.67
1:B:4522:ARG:HB3	1:B:4572:GLU:HG2	1.77	0.67
1:B:2698:LYS:HE3	1:B:3001:GLN:CB	2.25	0.67
1:B:39:ALA:HB1	1:B:44:PHE:HA	1.76	0.67
1:B:1387:GLN:HG3	1:B:1393:ALA:HB1	1.74	0.67
1:B:1555:GLN:HA	1:B:1558:ASN:HD22	1.59	0.67
1:B:2702:ILE:HD11	1:B:3001:GLN:NE2	2.10	0.67
1:B:3244:LEU:HB3	1:B:3249:ILE:HB	1.76	0.67
1:A:1218:LEU:HD13	1:A:1376:ILE:HG23	1.76	0.67
1:A:2302:GLU:HB2	1:A:2341:SER:HB2	1.76	0.67
1:B:768:ALA:HA	1:B:773:ASP:HB2	1.75	0.67
1:A:1682:HIS:CE1	1:A:2383:ARG:HB2	2.30	0.67
1:A:3244:LEU:HB3	1:A:3249:ILE:HB	1.76	0.67
1:A:3337:ALA:HB1	1:A:3423:SER:HB3	1.77	0.67
1:B:1205:GLY:CA	1:B:1215:GLY:CA	2.56	0.67
1:B:1679:TYR:CD1	1:B:1708:TYR:HA	2.30	0.67
1:A:284:ILE:HG13	1:A:442:LEU:HB3	1.77	0.66
1:A:2013:THR:HG21	1:A:2029:CYS:HB3	1.77	0.66
1:B:265:TYR:HA	1:B:268:ARG:HD3	1.77	0.66
1:B:415:LEU:HD11	1:B:484:LEU:HD21	1.76	0.66
1:B:3241:LYS:O	1:B:3245:GLU:HG2	1.95	0.66
1:B:4094:HIS:O	1:B:4098:THR:HG23	1.95	0.66
1:B:793:ASN:HB2	1:B:854:ILE:HG21	1.78	0.66
1:B:1300:VAL:HG13	1:B:1336:ARG:HD3	1.78	0.66
1:A:2480:VAL:HA	1:A:2524:GLN:CD	2.20	0.66
1:B:1087:VAL:O	1:B:1091:GLU:HG3	1.96	0.66
1:A:4271:LEU:HD22	1:A:4327:THR:HG23	1.77	0.66
1:B:1247:TRP:HA	1:B:1251:PHE:HB2	1.76	0.66
1:B:3994:LEU:HD23	1:B:4060:LEU:HD21	1.78	0.66
1:B:4714:LEU:HD11	1:B:4754:VAL:HG11	1.77	0.66
1:A:763:ILE:HG22	1:A:767:LYS:HE3	1.75	0.66
1:A:1531:GLY:HA3	1:A:1591:MET:HB3	1.77	0.66
1:A:1499:ILE:HG23	1:A:1506:VAL:HB	1.78	0.66
1:A:2636:LYS:HA	1:A:2649:GLY:HA3	1.78	0.66
1:A:3270:ILE:HD12	1:A:3632:PRO:HG2	1.72	0.66
1:B:1863:LEU:HB3	1:B:1940:LEU:HD21	1.76	0.66
1:B:4027:PRO:HD2	3:F:313:ARG:HE	1.59	0.66
1:A:274:GLN:O	1:A:277:VAL:HG22	1.95	0.66
1:A:1428:LEU:HB3	1:A:1491:LEU:HB3	1.78	0.66
1:B:787:LEU:HD12	1:B:832:LEU:HD23	1.78	0.66
1:B:2978:LEU:HD21	1:B:3024:LEU:HD22	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2259:PRO:HG3	1:A:2647:LEU:HD12	1.78	0.65
1:A:3241:LYS:O	1:A:3245:GLU:HG2	1.95	0.65
1:A:1350:VAL:O	1:A:1354:LEU:HG	1.96	0.65
1:B:471:VAL:HG21	1:B:641:ARG:HA	1.76	0.65
1:B:3175:THR:HG21	1:B:3184:PRO:HD3	1.79	0.65
1:A:4094:HIS:O	1:A:4098:THR:HG23	1.96	0.65
1:B:33:VAL:O	1:B:37:LEU:HG	1.95	0.65
1:B:2683:MET:HG3	1:B:2999:TYR:CE2	2.31	0.65
1:A:56:VAL:O	1:A:60:GLU:N	2.28	0.65
1:A:1859:MET:HE2	1:A:2230:MET:HB2	1.78	0.65
1:B:3087:ALA:HB2	1:B:3181:ILE:CD1	2.21	0.65
2:D:93:PHE:CE2	2:D:101:ILE:HA	2.31	0.65
1:A:1361:ILE:HA	1:A:1365:HIS:HB2	1.78	0.65
1:B:1408:VAL:HG11	1:B:1459:VAL:HG11	1.78	0.65
1:A:2054:ASN:HA	1:A:2138:ARG:HB3	1.78	0.65
1:A:3536:ASN:O	1:A:3538:PRO:HD3	1.97	0.65
2:D:83:GLU:HA	2:D:86:ILE:HD12	1.79	0.65
1:A:2345:SER:HA	1:A:2399:LYS:HE2	1.78	0.65
1:A:3408:LEU:HD12	1:A:3411:PHE:HE2	1.62	0.65
1:B:1519:THR:HB	1:B:1520:PRO:HD3	1.78	0.65
3:F:111:PRO:HD2	3:F:128:PHE:CE2	2.32	0.65
1:A:3270:ILE:HD12	1:A:3632:PRO:CG	2.26	0.65
1:A:3447:LEU:HA	1:A:3450:LEU:HD12	1.79	0.65
1:B:1098:ILE:HD11	1:B:1161:ALA:HA	1.78	0.65
1:B:1159:LEU:HB3	1:B:1160:PRO:HD3	1.78	0.65
1:B:1681:CYS:SG	4:B:5202:ZN:ZN	1.86	0.65
1:A:911:PHE:HB3	1:A:914:VAL:HB	1.77	0.64
1:A:2978:LEU:O	1:A:2982:LEU:HG	1.97	0.64
1:A:4495:ILE:HG21	1:A:4505:LEU:HD12	1.80	0.64
3:F:24:CYS:HA	3:F:52:MET:SD	2.37	0.64
1:A:507:ALA:O	1:A:523:ARG:NE	2.30	0.64
1:B:3516:LEU:HD23	1:B:3764:LEU:HD21	1.79	0.64
1:A:1415:ALA:HB2	1:A:1467:TRP:HB2	1.78	0.64
1:B:2054:ASN:HA	1:B:2138:ARG:HB3	1.79	0.64
1:B:3408:LEU:HD12	1:B:3411:PHE:HE2	1.61	0.64
1:A:1104:ILE:HG21	1:A:1168:THR:HG23	1.79	0.64
1:A:1500:VAL:CG2	1:A:1547:ALA:HB2	2.21	0.64
1:B:3063:MET:HG2	1:B:3174:ILE:HD11	1.77	0.64
1:A:1570:TYR:HE2	1:A:1576:VAL:HG21	1.62	0.64
1:A:1681:CYS:SG	4:A:5202:ZN:ZN	1.86	0.64
1:A:3211:ARG:HH21	1:A:3228:ARG:HH22	1.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1859:MET:HE2	1:B:2230:MET:HB2	1.78	0.64
1:A:2040:LEU:CD1	1:A:2085:PRO:CB	2.76	0.64
1:A:4487:CYS:HA	1:A:4490:ASN:HD22	1.62	0.64
1:B:337:LEU:O	1:B:341:VAL:HG13	1.97	0.64
1:A:4522:ARG:HB3	1:A:4572:GLU:HG2	1.79	0.64
1:B:3497:LEU:HD11	1:B:3913:ASN:HD21	1.62	0.64
1:B:3803:TYR:HA	1:B:3807:CYS:HB2	1.80	0.64
1:A:93:PRO:O	1:A:97:LEU:N	2.30	0.64
1:A:98:GLN:HG3	1:A:201:PHE:CE1	2.32	0.64
1:B:4713:PHE:CE1	1:B:4751:LEU:HD21	2.30	0.64
3:F:3:ARG:HG2	3:F:18:ARG:HG2	1.79	0.64
1:A:1054:ILE:O	1:A:1058:LEU:HG	1.98	0.63
1:A:1679:TYR:CD1	1:A:1708:TYR:HA	2.33	0.63
1:B:441:ALA:HB1	1:B:443:ARG:HH22	1.62	0.63
1:B:1499:ILE:HG12	1:B:1506:VAL:HG21	1.80	0.63
3:E:24:CYS:HA	3:E:52:MET:SD	2.39	0.63
1:A:1019:TYR:OH	1:A:1038:THR:HA	1.99	0.63
1:A:1474:SER:HA	1:A:1485:ILE:HD12	1.81	0.63
1:A:1570:TYR:CE2	1:A:1576:VAL:HG21	2.32	0.63
1:A:3463:ARG:HE	1:A:3535:CYS:HA	1.63	0.63
1:B:4127:ASN:HD22	3:F:328:LEU:HD22	1.62	0.63
3:E:71:SER:HB2	3:E:74:GLN:HB2	1.80	0.63
1:A:1708:TYR:HB3	1:A:2353:ARG:CZ	2.28	0.63
1:A:1873:VAL:CG1	1:A:2233:LEU:HD21	2.23	0.63
1:B:510:SER:HB3	1:B:513:ALA:HB2	1.80	0.63
1:B:1214:LEU:HD21	1:B:1354:LEU:HD22	1.81	0.63
1:B:1315:LEU:HB3	1:B:1316:PRO:HD3	1.80	0.63
1:B:2686:LEU:HD21	1:B:3002:VAL:HG21	1.79	0.63
1:B:3447:LEU:HA	1:B:3450:LEU:HD12	1.80	0.63
2:C:13:PHE:HB3	2:C:69:PHE:HE2	1.63	0.63
1:B:3270:ILE:HD12	1:B:3632:PRO:CG	2.26	0.63
1:A:73:PHE:CD1	1:A:159:LYS:CA	2.70	0.63
1:A:2692:ALA:HA	1:A:2695:PHE:HD1	1.63	0.63
1:B:867:HIS:HE1	1:B:1012:ILE:HG21	1.63	0.63
3:E:111:PRO:HD2	3:E:128:PHE:CE2	2.33	0.63
1:A:3148:HIS:CE1	1:A:3150:ALA:HB3	2.33	0.63
1:A:2192:VAL:HG13	1:A:2197:PHE:CE1	2.33	0.62
1:B:1464:LEU:HD23	1:B:1517:THR:HG21	1.81	0.62
1:A:104:CYS:HA	1:A:107:LEU:HD12	1.81	0.62
1:A:516:THR:HB	1:A:519:GLN:HG3	1.80	0.62
1:A:2705:LEU:HG	1:A:3005:MET:HB3	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1104:ILE:HG23	1:A:1110:LEU:HD11	1.82	0.62
1:A:3497:LEU:HD11	1:A:3913:ASN:HD21	1.62	0.62
1:B:46:MET:O	1:B:50:PRO:HD3	1.99	0.62
1:A:136:LEU:HD22	1:A:239:PHE:HZ	1.63	0.62
1:A:790:MET:HE3	1:A:858:LEU:HG	1.81	0.62
1:A:2665:HIS:CD2	1:A:2704:VAL:HB	2.34	0.62
1:B:303:VAL:HG22	1:B:377:ILE:HG13	1.82	0.62
1:B:1318:LEU:HA	1:B:1327:ALA:HB1	1.82	0.62
1:B:4335:LEU:HA	1:B:4338:ILE:HD12	1.81	0.62
2:D:29:THR:HG23	2:D:31:LYS:HB2	1.81	0.62
2:D:122:VAL:O	2:D:126:ILE:HG12	1.99	0.62
1:B:1550:GLY:O	1:B:1553:HIS:HB3	2.00	0.62
1:A:2291:PHE:CZ	1:A:2350:THR:O	2.52	0.62
1:B:1557:HIS:O	1:B:1561:VAL:HG23	1.99	0.62
1:B:1877:TYR:HB2	1:B:1886:ARG:HG3	1.82	0.62
1:B:3099:LEU:HD11	1:B:3193:PHE:HD1	1.65	0.62
1:B:3273:MET:HE1	1:B:3318:VAL:HG21	1.81	0.62
2:D:102:SER:HB2	2:D:105:GLU:CD	2.25	0.62
1:A:1047:ILE:HG13	1:A:1255:THR:HB	1.80	0.62
1:A:1427:VAL:HG13	1:A:1431:PHE:HE2	1.64	0.62
1:B:1178:LEU:HD11	1:B:1199:ALA:HB2	1.81	0.62
1:B:1204:ILE:HG12	1:B:1357:GLY:HA3	1.80	0.62
1:B:1726:CYS:SG	4:B:5206:ZN:ZN	1.88	0.62
1:B:2040:LEU:CD1	1:B:2085:PRO:CB	2.76	0.62
1:A:184:LEU:HD22	1:A:184:LEU:H	1.64	0.61
1:B:2567:PRO:HG3	1:B:2632:LEU:HD22	1.82	0.61
1:A:3007:THR:C	1:A:3009:ASP:H	2.08	0.61
1:B:3763:LEU:HD13	1:B:3799:LEU:HA	1.82	0.61
1:B:4232:LEU:C	1:B:4234:GLN:H	2.08	0.61
1:B:2701:LEU:HD13	1:B:3002:VAL:CG1	2.29	0.61
1:B:3327:LEU:O	1:B:3392:CYS:SG	2.55	0.61
3:E:112:ILE:HD12	3:E:136:HIS:HB3	1.80	0.61
1:A:2626:VAL:HG21	1:A:2681:ILE:HG21	1.81	0.61
1:B:2356:ILE:HD13	1:B:2377:LEU:HD13	1.81	0.61
2:C:33:LEU:CD2	2:C:72:MET:HE1	2.30	0.61
1:A:4591:LYS:HB2	1:A:4630:LYS:HD2	1.82	0.61
1:B:2517:ALA:HB3	1:B:2522:GLN:HE21	1.65	0.61
2:D:33:LEU:HD13	2:D:64:ILE:HG21	1.82	0.61
1:A:1347:LEU:HB3	1:A:1351:TYR:CE2	2.35	0.61
1:A:1681:CYS:HG	4:A:5202:ZN:ZN	1.13	0.61
1:B:414:LEU:HB3	1:B:480:ALA:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1427:VAL:HG13	1:B:1431:PHE:HE2	1.65	0.61
1:B:2698:LYS:HE2	1:B:3001:GLN:HE21	1.64	0.61
1:B:3532:CYS:SG	1:B:3868:SER:HA	2.40	0.61
1:A:252:GLY:HA2	1:A:255:LYS:HD2	1.83	0.61
1:B:1561:VAL:HG22	1:B:1810:LEU:CD2	2.30	0.61
1:B:4027:PRO:HB2	3:F:313:ARG:HH21	1.65	0.61
1:A:263:LEU:HB2	1:A:266:PHE:HB2	1.83	0.61
1:A:497:HIS:O	1:A:498:LYS:C	2.43	0.61
1:A:1564:LEU:HB2	1:A:1603:LEU:HD11	1.82	0.61
1:A:1682:HIS:HB2	1:A:1705:GLU:HB2	1.81	0.61
1:B:4635:VAL:HG11	1:B:4685:LYS:HG3	1.82	0.61
1:A:471:VAL:O	1:A:475:ILE:HG12	1.99	0.61
1:A:1680:HIS:HB3	1:A:1687:VAL:HG12	1.82	0.61
1:A:2698:LYS:HZ3	1:A:3001:GLN:HB3	1.66	0.61
1:B:806:LEU:HD21	1:B:811:LEU:HB2	1.82	0.61
1:B:3053:LEU:HD13	1:B:3160:LEU:HD12	1.81	0.61
1:B:4488:MET:HE3	1:B:4511:LEU:HB3	1.83	0.61
2:C:49:LEU:C	2:C:49:LEU:CD1	2.74	0.61
1:A:104:CYS:HB3	1:A:136:LEU:HD13	1.82	0.60
1:B:740:PHE:HD1	1:B:778:GLU:HG3	1.66	0.60
1:A:1052:ASN:O	1:A:1053:TRP:C	2.45	0.60
1:A:4594:LEU:O	1:A:4598:LEU:HG	2.01	0.60
1:B:1693:CYS:HB3	1:B:1716:CYS:HB2	1.84	0.60
2:D:50:GLN:C	2:D:53:ILE:HG22	2.26	0.60
2:D:137:VAL:HG13	2:D:141:GLU:HB2	1.83	0.60
1:A:1402:SER:HA	1:A:1452:SER:HB2	1.82	0.60
1:B:3057:ARG:HB2	1:B:3163:MET:CE	2.32	0.60
1:B:1119:GLN:HA	1:B:1122:TYR:CE2	2.36	0.60
1:B:1534:PHE:CD2	1:B:1595:CYS:HB2	2.36	0.60
1:B:2308:LEU:HD13	1:B:2328:VAL:HG11	1.84	0.60
1:A:2483:LEU:HD12	1:A:2524:GLN:HB3	1.82	0.60
1:B:851:VAL:HG11	1:B:995:GLU:HG2	1.84	0.60
2:C:33:LEU:HD21	2:C:72:MET:HE1	1.83	0.60
1:A:1594:GLU:HA	1:A:2477:ARG:HH22	1.66	0.60
1:A:2291:PHE:HZ	1:A:2350:THR:O	1.85	0.60
1:B:273:PHE:CD2	1:B:338:TYR:HB2	2.37	0.60
1:B:1124:LEU:O	1:B:1128:ILE:HG12	2.01	0.60
1:B:1290:SER:HA	1:B:1293:ARG:HD3	1.82	0.60
1:A:963:TYR:HE1	1:A:1013:LEU:HD13	1.66	0.60
1:A:3731:ASP:HA	1:A:3734:LYS:HB3	1.83	0.60
1:B:921:HIS:HD2	1:B:993:ALA:HB2	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1340:PRO:HD2	1:B:1343:SER:HB3	1.84	0.60
1:B:3087:ALA:HB2	1:B:3181:ILE:CG2	2.19	0.60
1:A:105:LYS:HG3	1:A:246:SER:HB2	1.83	0.60
1:A:202:ASN:HB3	1:A:204:ARG:NE	2.16	0.60
1:A:2354:ILE:HG12	1:A:2387:PHE:HE2	1.67	0.60
1:A:3187:ASP:H	1:A:3190:TRP:CD1	2.20	0.60
1:A:4278:VAL:O	1:B:3825:ARG:NH1	2.33	0.60
1:A:4594:LEU:HD11	1:A:4620:ILE:HG23	1.83	0.60
1:B:754:LEU:HD22	1:B:807:ASN:HD21	1.65	0.60
1:B:1063:MET:HG2	1:B:1068:ALA:HB2	1.84	0.60
1:B:2368:ILE:HD11	1:B:2387:PHE:CE1	2.37	0.60
1:B:3516:LEU:CD2	1:B:3764:LEU:HD21	2.31	0.60
1:B:4621:PRO:HG3	1:B:4665:ILE:HA	1.82	0.60
1:A:810:HIS:O	1:A:813:MET:HG3	2.01	0.60
1:B:1500:VAL:HG21	1:B:1543:THR:O	2.02	0.60
1:B:1996:LEU:HD11	1:B:2002:ILE:HG13	1.83	0.60
3:F:75:PRO:HD2	3:F:116:LEU:HD23	1.84	0.60
1:A:670:ILE:O	1:A:674:LEU:HG	2.02	0.59
1:A:1519:THR:HB	1:A:1520:PRO:HD3	1.82	0.59
1:A:3273:MET:HE1	1:A:3318:VAL:HG21	1.83	0.59
1:B:1414:THR:HG22	1:B:1424:CYS:SG	2.41	0.59
1:B:2581:ALA:HB2	1:B:2588:LEU:HD22	1.83	0.59
1:A:1171:SER:HA	1:A:1174:ARG:HD2	1.83	0.59
1:B:296:ARG:HH12	1:B:347:MET:HE3	1.67	0.59
1:A:4313:CYS:SG	1:A:4331:ILE:HG12	2.42	0.59
1:B:3894:PRO:O	1:B:3898:HIS:ND1	2.35	0.59
1:A:1607:THR:HB	1:A:2488:SER:HB2	1.84	0.59
1:B:1356:THR:HA	1:B:1400:PHE:CZ	2.36	0.59
1:B:1398:GLU:HA	1:B:1449:LEU:HD21	1.85	0.59
1:B:2682:TYR:CD2	1:B:2977:LEU:HD11	2.36	0.59
1:A:1051:VAL:HG22	1:A:1072:LEU:HD11	1.84	0.59
1:A:2487:GLU:HB2	1:A:2528:LEU:HA	1.84	0.59
1:A:3106:LEU:HG	1:A:3110:LYS:HE3	1.84	0.59
1:B:3723:VAL:HG11	1:B:3824:SER:OG	2.02	0.59
1:B:4682:ILE:HG23	1:B:4687:ILE:HD12	1.84	0.59
2:D:106:LEU:HD11	2:D:110:MET:HE2	1.83	0.59
1:A:1045:LEU:HD12	1:A:1072:LEU:HD11	1.83	0.59
1:A:1429:LYS:O	1:A:1430:PHE:C	2.45	0.59
1:B:4129:LEU:HD23	1:B:4165:LEU:HD23	1.85	0.59
1:B:4314:ILE:HG12	1:B:4484:GLY:HA2	1.85	0.59
1:A:1514:LEU:O	1:A:1518:LEU:HG	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2121:MET:HE2	1:A:2133:ALA:HB1	1.84	0.59
1:A:3201:GLN:HA	1:A:3207:ARG:HH21	1.68	0.59
1:A:4199:TYR:HA	2:C:20:PHE:CZ	2.38	0.59
1:B:151:PHE:HA	1:B:154:MET:HE2	1.84	0.59
1:B:1450:CYS:HB2	1:B:1505:GLN:HB2	1.83	0.59
1:B:2121:MET:HE2	1:B:2133:ALA:HB1	1.84	0.59
1:B:382:LEU:HD12	1:B:475:ILE:HG22	1.83	0.59
1:B:1015:PRO:HB2	1:B:1020:ILE:HD11	1.85	0.59
1:B:1468:LEU:HA	1:B:1471:MET:HE2	1.84	0.59
1:B:2173:HIS:ND1	1:B:2176:LEU:HD22	2.18	0.59
1:B:2698:LYS:HE2	1:B:3001:GLN:NE2	2.17	0.59
1:B:2702:ILE:HG12	1:B:3005:MET:HG2	1.85	0.59
1:B:4271:LEU:HD22	1:B:4274:ARG:HH21	1.67	0.59
1:A:1685:LYS:HA	1:A:2381:ARG:HH22	1.68	0.59
1:B:1515:LEU:CD1	1:B:1541:MET:HG3	2.32	0.59
1:B:1870:PHE:CZ	1:B:1924:LEU:CD1	2.65	0.59
1:A:4316:THR:HA	1:A:4319:ARG:HE	1.67	0.59
1:A:265:TYR:CZ	1:A:301:SER:HB2	2.38	0.58
1:A:2173:HIS:ND1	1:A:2176:LEU:HD22	2.18	0.58
1:B:680:GLU:HB3	1:B:730:THR:HG21	1.84	0.58
1:B:3270:ILE:O	1:B:3274:GLU:HG2	2.03	0.58
1:B:4096:TYR:CE1	2:D:48:GLU:HG2	2.38	0.58
1:B:4620:ILE:HB	1:B:4621:PRO:HD3	1.85	0.58
1:A:688:SER:O	1:A:692:GLU:HG3	2.03	0.58
1:A:2370:ILE:HD11	1:A:2401:LEU:HD11	1.85	0.58
1:B:299:PHE:O	1:B:303:VAL:HG23	2.03	0.58
1:A:1714:PHE:CZ	1:A:1716:CYS:HA	2.38	0.58
1:A:1901:VAL:CG1	1:A:2217:ILE:HD12	2.28	0.58
1:B:3683:GLN:OE1	1:B:3688:ARG:HD2	2.03	0.58
1:B:4325:TYR:HA	1:B:4504:LEU:HD22	1.86	0.58
3:F:302:SER:O	3:F:306:ARG:N	2.34	0.58
1:A:967:TYR:HE2	1:A:1015:PRO:HA	1.66	0.58
1:A:1119:GLN:HA	1:A:1122:TYR:CE2	2.38	0.58
1:A:3240:ILE:HD11	1:A:3275:HIS:CB	2.33	0.58
1:A:3679:GLU:CD	1:A:3683:GLN:HE22	2.11	0.58
1:B:4355:LYS:HE3	1:B:4365:GLY:O	2.04	0.58
1:B:4429:TRP:CE2	1:B:4438:MET:HA	2.38	0.58
1:A:1307:PRO:HB2	1:A:1308:PRO:HD3	1.84	0.58
1:B:3757:ARG:HB3	1:B:3758:PRO:HD3	1.86	0.58
1:A:56:VAL:HA	1:A:59:SER:HB2	1.85	0.58
1:A:1808:ALA:HB3	1:A:1809:PRO:HD3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4089:LYS:HA	1:A:4092:LEU:HD12	1.86	0.58
1:A:1191:SER:HB3	1:A:1194:LYS:HG3	1.85	0.58
1:A:4429:TRP:CE2	1:A:4438:MET:HA	2.38	0.58
1:B:1361:ILE:HA	1:B:1365:HIS:HB2	1.85	0.58
1:B:3679:GLU:CD	1:B:3683:GLN:HE22	2.11	0.58
1:A:3469:VAL:HG21	1:A:3882:HIS:HB3	1.86	0.58
1:B:93:PRO:HB2	1:B:96:GLN:HB2	1.85	0.58
1:B:810:HIS:O	1:B:813:MET:HG3	2.03	0.58
1:B:2978:LEU:HA	1:B:3006:LEU:HD13	1.86	0.58
1:A:53:VAL:O	1:A:57:ILE:HG13	2.03	0.58
1:A:787:LEU:HD12	1:A:832:LEU:HD23	1.85	0.58
1:A:1428:LEU:HD13	1:A:1491:LEU:HB2	1.85	0.58
1:A:2291:PHE:O	1:A:2295:ASN:ND2	2.35	0.58
1:B:1118:LEU:HD12	1:B:1280:LEU:HD23	1.86	0.58
1:B:4221:LEU:O	1:B:4224:GLU:HG3	2.04	0.58
1:A:745:TRP:HE1	1:A:810:HIS:CE1	2.22	0.57
1:A:1090:VAL:HG13	1:A:1127:ALA:HB1	1.85	0.57
1:B:1515:LEU:HD11	1:B:1556:LEU:HD22	1.85	0.57
1:B:2162:PRO:HG2	1:B:2181:GLN:HG2	1.87	0.57
1:B:2548:LEU:HD11	1:B:2580:ILE:HG21	1.85	0.57
1:A:82:THR:HA	1:A:107:LEU:HD13	1.86	0.57
1:A:3683:GLN:OE1	1:A:3688:ARG:HD2	2.03	0.57
1:B:908:TYR:CZ	1:B:931:ARG:HD3	2.39	0.57
1:B:1600:MET:HB3	1:B:2481:SER:HB2	1.84	0.57
1:B:2310:GLN:HG3	1:B:2311:VAL:HG23	1.84	0.57
1:B:4223:LEU:O	1:B:4279:GLN:NE2	2.38	0.57
1:B:4635:VAL:CG1	1:B:4685:LYS:HG3	2.34	0.57
2:C:49:LEU:HD11	2:C:53:ILE:HD12	1.85	0.57
1:A:1203:ALA:HA	1:A:1320:GLU:HG3	1.86	0.57
1:A:1996:LEU:HD13	1:A:2001:PHE:HA	1.86	0.57
1:B:3057:ARG:HD3	1:B:3139:PHE:CD1	2.39	0.57
1:A:1870:PHE:HB3	1:A:1873:VAL:CG2	2.34	0.57
1:A:2657:VAL:HG11	1:A:2693:VAL:O	2.05	0.57
1:A:3547:LEU:HD13	1:A:3715:LEU:HD11	1.84	0.57
1:B:1929:LEU:HD11	1:B:2241:ILE:HD11	1.86	0.57
1:B:3324:SER:O	1:B:3329:GLY:N	2.36	0.57
1:B:39:ALA:CB	1:B:44:PHE:HA	2.35	0.57
1:B:1534:PHE:CE2	1:B:1595:CYS:HB2	2.39	0.57
1:B:3240:ILE:HD11	1:B:3275:HIS:CB	2.33	0.57
1:B:3469:VAL:HG21	1:B:3882:HIS:HB3	1.86	0.57
2:C:95:LYS:HG2	2:C:105:GLU:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:800:PRO:HG3	1:A:854:ILE:HD11	1.85	0.57
1:A:1037:HIS:CE1	1:A:1041:TRP:HE1	2.22	0.57
1:B:1319:LEU:HD21	1:B:1350:VAL:HG13	1.87	0.57
1:B:2354:ILE:HG12	1:B:2387:PHE:HE2	1.68	0.57
1:B:3087:ALA:CA	1:B:3181:ILE:CD1	2.83	0.57
1:A:284:ILE:H	1:A:442:LEU:H	1.52	0.57
1:A:3270:ILE:O	1:A:3274:GLU:HG2	2.03	0.57
1:A:4307:LYS:HD2	1:A:4479:MET:HA	1.85	0.57
1:B:783:TRP:HD1	1:B:821:PHE:HE2	1.53	0.57
1:B:1244:ILE:HG13	1:B:1248:ARG:HB2	1.86	0.57
1:B:1429:LYS:O	1:B:1430:PHE:C	2.45	0.57
1:B:1520:PRO:HA	1:B:1523:THR:HB	1.87	0.57
1:B:2340:ILE:HD13	1:B:2422:ILE:HD11	1.86	0.57
1:A:3894:PRO:O	1:A:3898:HIS:ND1	2.35	0.57
1:B:844:MET:HB3	1:B:848:MET:HE3	1.85	0.57
1:B:1554:LEU:HD12	1:B:1557:HIS:CD2	2.40	0.57
1:B:1681:CYS:HG	4:B:5202:ZN:ZN	1.16	0.57
1:B:3220:SER:HB3	1:B:3223:LYS:HE2	1.87	0.57
1:B:4053:HIS:HB2	1:B:4071:TRP:CD1	2.39	0.57
1:A:189:VAL:HG21	1:B:874:VAL:HG13	1.85	0.57
1:A:1517:THR:O	1:A:1520:PRO:HD2	2.04	0.57
1:B:1268:ALA:O	1:B:1272:THR:HG23	2.05	0.57
1:B:1495:LEU:HA	1:B:1498:TYR:CD2	2.40	0.57
1:B:3087:ALA:CA	1:B:3181:ILE:HD12	2.35	0.57
1:B:4617:LEU:O	1:B:4621:PRO:HD2	2.05	0.57
1:A:1206:SER:HB2	1:A:1319:LEU:HA	1.87	0.57
1:A:1233:TRP:HE3	1:A:1278:LEU:HD13	1.70	0.57
1:A:4355:LYS:HE3	1:A:4365:GLY:O	2.05	0.57
1:B:1133:VAL:HG22	1:B:1246:SER:HB3	1.86	0.57
1:B:1241:PHE:CE1	1:B:1272:THR:HG21	2.39	0.57
1:B:4089:LYS:HA	1:B:4092:LEU:HD12	1.85	0.57
1:A:2308:LEU:HD13	1:A:2328:VAL:HG11	1.86	0.56
1:A:4130:ARG:HB2	1:A:4169:TYR:CE1	2.40	0.56
1:A:4714:LEU:HD11	1:A:4754:VAL:HG11	1.86	0.56
1:B:479:HIS:HA	1:B:482:LYS:HE2	1.87	0.56
1:B:1119:GLN:HA	1:B:1122:TYR:CD2	2.40	0.56
1:A:396:ARG:HH21	1:B:404:GLN:NE2	2.02	0.56
1:A:1101:PHE:CD2	1:A:1168:THR:HG21	2.40	0.56
1:A:1398:GLU:HG3	1:A:1445:SER:HA	1.86	0.56
1:A:3463:ARG:NH2	1:A:3534:VAL:O	2.38	0.56
1:B:516:THR:HB	1:B:519:GLN:HG3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1415:ALA:HB2	1:B:1467:TRP:HB2	1.87	0.56
1:B:2370:ILE:HD11	1:B:2401:LEU:HD11	1.87	0.56
2:D:93:PHE:HE2	2:D:101:ILE:HA	1.69	0.56
3:E:302:SER:O	3:E:306:ARG:N	2.34	0.56
1:A:145:ARG:O	1:A:149:ILE:HG13	2.06	0.56
1:B:470:GLY:H	1:B:473:SER:HB2	1.71	0.56
1:B:4228:LEU:HD22	1:B:4278:VAL:HG11	1.88	0.56
2:C:93:PHE:HB3	2:C:101:ILE:HD12	1.86	0.56
1:A:2027:ASP:CG	1:A:2029:CYS:HG	2.08	0.56
1:A:4598:LEU:O	1:A:4601:ILE:HG23	2.05	0.56
1:B:521:ILE:HG21	1:B:670:ILE:HD11	1.88	0.56
1:A:1169:TYR:HA	1:A:1172:PHE:HD2	1.70	0.56
1:A:1947:SER:C	1:A:3655:THR:HG21	2.30	0.56
1:B:2301:VAL:HG11	1:B:2422:ILE:HG13	1.86	0.56
1:A:1173:THR:HG22	1:A:1233:TRP:CZ2	2.41	0.56
1:A:1481:GLN:HA	1:A:1481:GLN:HE21	1.69	0.56
1:A:1519:THR:HA	1:A:1563:TRP:HZ2	1.69	0.56
1:B:1395:LYS:O	1:B:1399:GLU:HG2	2.06	0.56
1:B:1560:ALA:HA	1:B:1563:TRP:CE3	2.40	0.56
1:B:2977:LEU:HD23	1:B:3006:LEU:HD21	1.88	0.56
1:B:3948:ILE:HA	1:B:3996:LEU:HD21	1.87	0.56
1:A:273:PHE:O	1:A:277:VAL:HG13	2.06	0.56
1:A:2173:HIS:CE1	1:A:2176:LEU:HD22	2.41	0.56
1:A:4699:ILE:HD13	1:A:4747:ASN:HB3	1.87	0.56
1:B:553:LYS:O	1:B:554:GLY:C	2.48	0.56
1:B:3290:TRP:HE1	1:B:3326:ALA:HB2	1.69	0.56
1:B:3951:VAL:HG13	1:B:4012:ILE:HD13	1.87	0.56
1:A:291:ASP:O	1:A:295:VAL:HG23	2.06	0.56
1:A:491:LEU:HD21	1:A:518:ILE:HA	1.88	0.56
1:A:1948:ALA:HB1	1:A:1978:LEU:HD13	1.88	0.56
1:A:2701:LEU:O	1:A:2704:VAL:HG22	2.05	0.56
1:A:1412:MET:HB3	1:A:1463:ARG:CZ	2.36	0.56
1:A:3662:ARG:NH2	1:A:3679:GLU:OE2	2.39	0.56
1:A:4199:TYR:HA	2:C:20:PHE:HZ	1.70	0.56
1:A:4691:ALA:HB1	1:A:4722:ILE:HG23	1.88	0.56
1:B:82:THR:HG23	1:B:136:LEU:HG	1.87	0.56
1:B:4419:LEU:HD13	1:B:4459:LEU:HG	1.87	0.56
2:C:124:GLU:O	2:C:128:GLU:HG2	2.06	0.56
1:A:420:LEU:HD21	1:A:444:VAL:CA	2.35	0.55
1:A:683:MET:SD	1:A:727:LEU:HD23	2.46	0.55
1:A:1159:LEU:HB3	1:A:1160:PRO:HD3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4682:ILE:HG23	1:A:4687:ILE:HD12	1.88	0.55
1:B:2978:LEU:HB2	1:B:3006:LEU:HB3	1.89	0.55
3:E:301:MET:O	3:E:306:ARG:NH1	2.39	0.55
1:A:404:GLN:HE21	1:B:396:ARG:HB2	1.72	0.55
1:A:1058:LEU:HB3	1:A:1063:MET:SD	2.46	0.55
1:A:1899:MET:SD	1:A:2233:LEU:HB2	2.46	0.55
1:A:4489:LEU:HD21	1:A:4532:THR:HG23	1.87	0.55
1:A:4641:TYR:HD1	1:A:4655:ASP:HA	1.71	0.55
1:B:663:LEU:HD23	1:B:674:LEU:CD1	2.36	0.55
1:B:683:MET:HE3	1:B:727:LEU:HD23	1.87	0.55
1:B:827:ARG:HG3	1:B:955:VAL:HG13	1.88	0.55
1:B:967:TYR:CE2	1:B:1015:PRO:HA	2.42	0.55
1:B:1097:GLN:HA	1:B:1097:GLN:HE21	1.71	0.55
1:B:2173:HIS:CE1	1:B:2176:LEU:HD22	2.41	0.55
1:B:3072:SER:C	1:B:3074:ILE:H	2.14	0.55
1:B:3213:LEU:O	1:B:3217:ILE:HG12	2.05	0.55
1:A:183:GLU:H	1:A:183:GLU:CD	2.13	0.55
1:A:2358:THR:HA	1:A:2382:SER:HB2	1.87	0.55
1:B:1572:SER:O	1:B:1573:GLN:C	2.49	0.55
1:B:1603:LEU:HD13	1:B:1807:PHE:CZ	2.41	0.55
1:B:1961:PRO:HB3	1:B:2171:MET:CE	2.37	0.55
1:B:3662:ARG:NH2	1:B:3679:GLU:OE2	2.39	0.55
1:B:3739:ILE:HG12	1:B:3824:SER:HB3	1.88	0.55
1:B:4216:GLU:HG2	1:B:4238:LEU:HB2	1.88	0.55
1:A:1315:LEU:HB3	1:A:1316:PRO:HD3	1.87	0.55
1:A:1556:LEU:HD22	1:A:1559:ALA:HB3	1.89	0.55
1:A:2300:ASP:HA	1:A:2318:LYS:HZ1	1.72	0.55
1:A:2371:PHE:HZ	1:A:2397:ALA:HB2	1.71	0.55
1:B:48:GLU:O	1:B:51:GLN:HB3	2.07	0.55
1:B:284:ILE:H	1:B:441:ALA:HA	1.71	0.55
1:B:1558:ASN:HD21	1:B:1803:ALA:HB1	1.70	0.55
1:B:2263:ILE:HG13	1:B:2266:MET:HE2	1.87	0.55
1:B:2312:TYR:CE2	1:B:2328:VAL:HG13	2.41	0.55
1:B:3729:GLU:HB3	1:B:3733:LYS:HE3	1.88	0.55
1:B:4423:GLU:HB3	1:B:4459:LEU:HD13	1.87	0.55
3:F:28:TYR:CE2	3:F:122:ASN:HB3	2.42	0.55
1:A:204:ARG:O	1:A:205:THR:C	2.50	0.55
1:A:2982:LEU:O	1:A:2985:LEU:HB3	2.06	0.55
1:A:4719:LEU:HB3	1:A:4720:PRO:HD3	1.88	0.55
1:B:1311:ILE:HA	1:B:1334:LEU:HD21	1.87	0.55
1:B:1453:LEU:C	1:B:1455:GLN:H	2.15	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2181:GLN:HG3	1:B:2188:LEU:HD11	1.89	0.55
1:B:4613:LEU:O	1:B:4617:LEU:HG	2.06	0.55
1:A:691:LYS:HD3	1:A:735:LEU:HA	1.88	0.55
1:A:1269:HIS:CE1	1:A:1283:SER:HB3	2.42	0.55
1:B:1088:GLU:HA	1:B:1091:GLU:CD	2.32	0.55
1:B:4313:CYS:SG	1:B:4335:LEU:HD21	2.46	0.55
1:A:674:LEU:O	1:A:678:LEU:HG	2.06	0.55
1:A:1875:MET:SD	1:A:1917:GLU:HA	2.47	0.55
1:A:4024:ILE:HD11	3:E:324:LEU:HD12	1.88	0.55
1:B:1901:VAL:CG1	1:B:2217:ILE:HD12	2.28	0.55
1:B:2212:GLN:N	1:B:2233:LEU:O	2.40	0.55
1:B:4239:LYS:HE2	1:B:4286:GLU:OE1	2.06	0.55
1:B:4771:LEU:O	1:B:4774:HIS:HB3	2.07	0.55
1:A:1118:LEU:HD21	1:A:1269:HIS:HB3	1.87	0.55
1:B:973:LEU:HB3	1:B:1002:TYR:OH	2.06	0.55
1:B:2040:LEU:HD11	1:B:2085:PRO:CB	2.37	0.55
1:B:2966:THR:HA	1:B:2969:ARG:HE	1.72	0.55
1:A:261:LEU:CD2	1:A:332:LEU:HB2	2.36	0.55
1:B:246:SER:O	1:B:250:LEU:HG	2.06	0.55
1:B:3409:ILE:HG12	1:B:3450:LEU:HD22	1.88	0.55
2:C:87:ARG:HG3	2:C:139:TYR:CE1	2.42	0.55
1:B:313:LEU:HD12	1:B:384:ILE:HG23	1.89	0.55
1:A:1529:GLY:HA2	1:A:1592:ILE:HD11	1.89	0.54
1:A:1858:LEU:HB2	1:A:2200:GLN:OE1	2.07	0.54
1:A:4131:GLN:O	1:A:4135:THR:HG23	2.07	0.54
1:B:2360:ALA:HB3	1:B:2363:ARG:HB2	1.88	0.54
1:B:3107:GLU:HA	1:B:3110:LYS:HD2	1.89	0.54
1:A:1348:ALA:O	1:A:1352:GLU:HG3	2.07	0.54
1:A:1961:PRO:HB3	1:A:2171:MET:CE	2.37	0.54
1:A:2474:VAL:HA	1:A:2477:ARG:HE	1.71	0.54
1:A:2654:GLU:HG2	1:A:2692:ALA:HB1	1.88	0.54
1:A:4159:LYS:HZ3	1:A:4196:TRP:CD1	2.25	0.54
1:B:1025:MET:HG2	1:B:1026:ASN:H	1.72	0.54
1:B:3001:GLN:NE2	1:B:3138:PRO:HD3	2.22	0.54
2:D:28:ILE:HD12	2:D:33:LEU:HA	1.88	0.54
2:D:76:LYS:HE2	2:D:76:LYS:HA	1.89	0.54
3:F:301:MET:O	3:F:306:ARG:NH1	2.39	0.54
1:A:35:PRO:HB3	1:A:48:GLU:HB3	1.90	0.54
1:A:4107:GLN:O	1:A:4111:ARG:HG2	2.07	0.54
1:B:808:VAL:HG21	1:B:931:ARG:HD2	1.90	0.54
1:A:183:GLU:O	1:A:187:LYS:HD3	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:545:ALA:O	1:A:644:PRO:HB3	2.07	0.54
1:A:1700:CYS:SG	1:A:1726:CYS:C	2.89	0.54
1:A:3738:ASN:O	1:A:3742:LEU:HG	2.07	0.54
1:A:4476:ALA:C	1:A:4521:ASN:HD21	2.15	0.54
1:B:1545:ALA:HB2	1:B:1556:LEU:HD22	1.89	0.54
1:B:1708:TYR:O	1:B:2353:ARG:NH2	2.40	0.54
1:B:1858:LEU:HB2	1:B:2200:GLN:OE1	2.07	0.54
1:B:3881:GLU:HG2	1:B:3921:MET:HG3	1.88	0.54
2:C:78:LYS:HB2	2:C:80:THR:HG23	1.88	0.54
3:E:75:PRO:HD2	3:E:116:LEU:HD23	1.88	0.54
1:A:1000:GLN:HA	1:A:1270:LEU:HD13	1.89	0.54
1:A:1474:SER:HB2	1:A:1485:ILE:HG21	1.89	0.54
1:A:3568:SER:HB3	1:A:3721:CYS:HA	1.90	0.54
1:B:3406:GLU:HG3	1:B:3850:THR:HG21	1.88	0.54
1:B:4212:LEU:HD23	1:B:4215:LYS:HD2	1.89	0.54
1:A:1047:ILE:HB	1:A:1050:TYR:CD2	2.42	0.54
1:A:1870:PHE:CZ	1:A:1924:LEU:CD1	2.66	0.54
1:A:2040:LEU:HD11	1:A:2085:PRO:CB	2.37	0.54
1:A:3095:VAL:HG12	1:A:3190:TRP:CZ3	2.43	0.54
1:A:4313:CYS:HB3	1:A:4331:ILE:HD13	1.88	0.54
1:B:194:LEU:HD13	1:B:197:LEU:HD12	1.90	0.54
1:B:2701:LEU:HD13	1:B:3002:VAL:HG11	1.90	0.54
1:B:3706:CYS:O	1:B:3710:ARG:NH1	2.41	0.54
1:B:4107:GLN:O	1:B:4111:ARG:HG2	2.07	0.54
1:B:4355:LYS:CE	1:B:4365:GLY:O	2.55	0.54
1:A:299:PHE:HZ	1:A:346:CYS:SG	2.31	0.54
1:A:2266:MET:HE1	1:A:2659:ALA:HB2	1.90	0.54
1:A:3409:ILE:HG12	1:A:3450:LEU:HD22	1.88	0.54
1:B:336:CYS:O	1:B:381:CYS:SG	2.65	0.54
1:B:1306:ASN:HD22	1:B:1309:GLN:HB2	1.72	0.54
1:B:2547:LEU:HD12	1:B:2580:ILE:HD11	1.89	0.54
1:B:2695:PHE:HE1	1:B:2699:GLN:NE2	2.02	0.54
1:B:3172:LYS:HE3	1:B:3217:ILE:HA	1.89	0.54
1:B:3198:LEU:HD22	1:B:3207:ARG:HG3	1.89	0.54
1:A:85:ILE:HA	1:A:88:VAL:HG22	1.90	0.54
1:A:4423:GLU:HB3	1:A:4459:LEU:HD13	1.89	0.54
1:B:49:LEU:C	1:B:51:GLN:N	2.63	0.54
1:B:261:LEU:HD11	1:B:328:ASP:HB3	1.90	0.54
1:B:1394:ARG:NH2	1:B:1437:LEU:HD13	2.23	0.54
1:B:2675:ILE:C	1:B:2677:THR:H	2.15	0.54
1:B:4537:LEU:HD21	1:B:4623:LEU:HD11	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:27:THR:HA	2:C:61:ASN:HA	1.88	0.54
1:A:239:PHE:HA	1:A:242:GLN:OE1	2.08	0.54
1:A:1022:GLN:O	1:A:1026:ASN:N	2.40	0.54
1:A:1435:PHE:CD1	1:A:1498:TYR:HB3	2.43	0.54
1:A:2261:SER:HB2	1:A:2263:ILE:HG22	1.90	0.54
1:A:2668:CYS:O	1:A:2973:VAL:HG21	2.08	0.54
1:A:3881:GLU:HG2	1:A:3921:MET:HG3	1.89	0.54
1:A:4540:LEU:HB2	1:A:4562:VAL:HG11	1.89	0.54
1:B:1875:MET:SD	1:B:1917:GLU:HA	2.47	0.54
1:A:3706:CYS:O	1:A:3710:ARG:NH1	2.41	0.54
1:B:2023:VAL:HG23	1:B:2046:ILE:HD13	1.89	0.54
1:B:2025:ILE:HD12	1:B:2075:MET:HE3	1.90	0.54
1:B:2698:LYS:HD2	1:B:2998:PRO:CA	2.30	0.54
1:A:2180:VAL:HG22	1:A:2214:MET:HE2	1.90	0.53
1:A:2300:ASP:HA	1:A:2318:LYS:NZ	2.23	0.53
1:A:4105:TRP:CZ2	2:C:129:ALA:HB2	2.42	0.53
1:B:44:PHE:CD1	1:B:84:TYR:HB3	2.43	0.53
1:B:231:SER:HA	1:B:234:LYS:HD2	1.89	0.53
1:B:1384:LEU:HD13	1:B:1397:MET:SD	2.48	0.53
1:B:3532:CYS:SG	1:B:3534:VAL:HB	2.48	0.53
1:B:4423:GLU:CB	1:B:4459:LEU:HD13	2.38	0.53
1:A:1407:LEU:HB3	1:A:1431:PHE:HE1	1.72	0.53
1:A:2025:ILE:HD12	1:A:2075:MET:HE3	1.90	0.53
1:B:30:GLU:O	1:B:33:VAL:HG22	2.08	0.53
1:B:63:ILE:HA	1:B:74:TYR:HD2	1.73	0.53
1:B:783:TRP:CD1	1:B:821:PHE:HE2	2.26	0.53
1:B:1044:ARG:C	1:B:1046:ARG:N	2.63	0.53
1:A:1162:THR:O	1:A:1166:ILE:HG13	2.08	0.53
1:A:2051:PHE:HB3	1:A:2059:ASN:HD21	1.73	0.53
1:A:3512:ILE:O	1:A:3516:LEU:HG	2.08	0.53
1:A:3759:GLN:HE21	1:A:3763:LEU:HG	1.74	0.53
1:B:286:PRO:HB2	1:B:346:CYS:HB2	1.89	0.53
1:B:844:MET:HE2	1:B:844:MET:HA	1.90	0.53
1:B:2352:MET:HE1	1:B:2403:LEU:HD13	1.91	0.53
1:A:3169:TYR:HD1	1:A:3213:LEU:HD13	1.74	0.53
1:B:1805:PHE:HD2	1:B:2494:PRO:HD2	1.73	0.53
2:C:87:ARG:HG3	2:C:139:TYR:HE1	1.73	0.53
1:A:552:ARG:NH2	1:A:643:ASP:HA	2.23	0.53
1:A:2096:HIS:HB3	1:A:2099:LEU:HG	1.91	0.53
2:D:138:ASN:CG	2:D:139:TYR:H	2.17	0.53
1:A:392:ILE:O	1:A:399:GLY:HA2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1015:PRO:HG3	1:A:1041:TRP:CD2	2.44	0.53
1:A:3310:LEU:HA	1:A:3859:LEU:HD23	1.90	0.53
1:B:2332:LYS:HA	3:F:20:ARG:HH22	1.74	0.53
1:B:2702:ILE:HG23	1:B:3005:MET:HG2	1.89	0.53
1:B:4636:GLU:O	1:B:4640:PRO:HD3	2.08	0.53
2:C:30:THR:HB	2:C:53:ILE:HG12	1.90	0.53
3:F:23:LYS:HD3	3:F:114:ALA:HB1	1.90	0.53
1:A:834:VAL:HG13	1:A:966:LEU:HD13	1.90	0.53
1:A:1048:SER:HA	1:A:1051:VAL:HB	1.91	0.53
1:A:1877:TYR:CE1	1:A:1885:ILE:HG21	2.43	0.53
1:A:2187:PRO:HB3	1:A:2214:MET:SD	2.48	0.53
1:A:3315:VAL:HG22	1:A:3633:LEU:HD21	1.90	0.53
1:A:4123:LEU:HD13	1:A:4165:LEU:HD22	1.90	0.53
1:A:4355:LYS:CE	1:A:4365:GLY:O	2.57	0.53
1:B:49:LEU:HB3	1:B:50:PRO:HD3	1.89	0.53
1:B:443:ARG:HB2	1:B:446:ASP:CG	2.33	0.53
1:B:909:HIS:NE2	1:B:937:SER:HB2	2.24	0.53
1:B:3106:LEU:HD12	1:B:3200:ILE:HD11	1.89	0.53
2:C:33:LEU:CD1	2:C:72:MET:HE1	2.38	0.53
3:E:27:CYS:SG	3:E:45:ARG:O	2.67	0.53
1:A:103:ALA:O	1:A:107:LEU:HG	2.09	0.53
1:B:1191:SER:H	1:B:1194:LYS:HD3	1.73	0.53
1:B:1387:GLN:CG	1:B:1393:ALA:HB1	2.37	0.53
1:B:1595:CYS:SG	1:B:1596:THR:N	2.82	0.53
1:B:3547:LEU:O	1:B:3551:LYS:HG3	2.09	0.53
1:A:89:CYS:HB2	1:A:239:PHE:CD2	2.44	0.53
1:A:245:ALA:O	1:A:249:GLU:HG3	2.09	0.53
1:A:839:GLU:O	1:A:842:VAL:HG12	2.09	0.53
1:A:2698:LYS:NZ	1:A:3001:GLN:HB3	2.24	0.53
1:A:3547:LEU:O	1:A:3551:LYS:HG3	2.09	0.53
1:A:4096:TYR:CE1	2:C:48:GLU:HG2	2.44	0.53
1:B:4047:PRO:HA	1:B:4075:LEU:CD2	2.39	0.53
1:A:303:VAL:HG22	1:A:377:ILE:HG13	1.90	0.53
1:A:3746:ALA:HA	1:A:3749:VAL:HG22	1.91	0.53
1:B:136:LEU:O	1:B:243:ASN:ND2	2.42	0.53
1:B:1603:LEU:HD13	1:B:1807:PHE:HZ	1.73	0.53
1:B:3512:ILE:O	1:B:3516:LEU:HG	2.08	0.53
2:C:59:ASP:HB3	2:C:63:THR:HB	1.89	0.53
1:A:1306:ASN:HB3	1:A:1309:GLN:HB3	1.92	0.52
1:A:1525:MET:HA	1:A:1530:ASP:HB2	1.91	0.52
1:A:2352:MET:HE1	1:A:2403:LEU:HD13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1010:LEU:HD22	1:B:1037:HIS:CE1	2.44	0.52
1:B:1435:PHE:CD1	1:B:1498:TYR:HB3	2.43	0.52
1:B:1600:MET:HB3	1:B:2481:SER:CB	2.39	0.52
1:B:2698:LYS:CE	1:B:3001:GLN:HE21	2.22	0.52
1:B:3309:PHE:CD2	1:B:3850:THR:HA	2.44	0.52
1:B:3419:SER:HB3	1:B:3425:ARG:HG3	1.92	0.52
1:A:59:SER:HA	1:A:62:GLU:HB2	1.91	0.52
1:A:4665:ILE:O	1:A:4669:ILE:HG13	2.09	0.52
1:B:272:ARG:HD2	1:B:338:TYR:HE1	1.75	0.52
1:B:420:LEU:HD13	1:B:442:LEU:HB2	1.91	0.52
1:B:859:LEU:O	1:B:1009:ILE:HD11	2.09	0.52
1:B:1542:ALA:HB1	1:B:1602:TYR:CG	2.44	0.52
1:B:1930:LEU:HD13	1:B:2219:HIS:HB3	1.91	0.52
1:B:2292:PHE:HA	1:B:2295:ASN:HD22	1.74	0.52
1:B:3997:PHE:HB2	1:B:4016:CYS:HB3	1.90	0.52
1:A:230:ALA:O	1:A:234:LYS:HG3	2.09	0.52
1:A:336:CYS:O	1:A:381:CYS:SG	2.67	0.52
1:A:545:ALA:HB2	1:A:647:PHE:HB2	1.92	0.52
1:A:2073:GLN:HB2	1:A:2088:VAL:HG13	1.91	0.52
1:A:4245:LEU:HD23	1:A:4294:MET:HE1	1.90	0.52
1:A:4644:PHE:HB3	1:A:4722:ILE:HD11	1.90	0.52
1:B:542:TYR:CE2	1:B:689:ILE:HG23	2.44	0.52
1:B:740:PHE:HA	1:B:781:LYS:HG2	1.91	0.52
1:B:1097:GLN:HA	1:B:1097:GLN:NE2	2.24	0.52
1:B:1162:THR:HG22	1:B:1166:ILE:HD11	1.90	0.52
1:B:3042:LYS:HA	1:B:3049:ASN:HB3	1.92	0.52
2:C:138:ASN:HB3	2:C:140:GLU:HG2	1.91	0.52
1:A:1094:PHE:O	1:A:1098:ILE:HG13	2.10	0.52
1:A:1875:MET:HG2	1:A:1877:TYR:CE1	2.44	0.52
1:A:2517:ALA:HB2	1:A:2521:VAL:HB	1.91	0.52
1:B:943:ASP:O	1:B:944:ASP:C	2.52	0.52
1:B:1489:ARG:NH2	1:B:1533:GLY:CA	2.72	0.52
1:B:1845:LEU:HD12	1:B:1850:LYS:HE3	1.92	0.52
1:B:2052:LEU:HG	1:B:2060:ILE:HB	1.91	0.52
1:B:2073:GLN:HB2	1:B:2088:VAL:HG13	1.91	0.52
1:B:2701:LEU:HD12	1:B:3002:VAL:HG21	1.90	0.52
1:B:4195:HIS:CD2	2:D:35:THR:HG21	2.45	0.52
1:A:478:ASN:OD1	1:A:650:LEU:HD13	2.09	0.52
1:A:906:PRO:HG2	1:A:908:TYR:HE2	1.74	0.52
1:B:1819:MET:CE	1:B:2508:LEU:HD12	2.39	0.52
1:B:2291:PHE:HZ	1:B:2350:THR:HB	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1169:TYR:HA	1:A:1172:PHE:CD2	2.44	0.52
1:A:1571:LEU:C	1:A:1573:GLN:N	2.65	0.52
1:A:2292:PHE:CE2	1:A:2386:ASP:HB3	2.40	0.52
1:A:4740:ILE:O	1:A:4744:SER:HB2	2.09	0.52
1:B:4052:ILE:N	1:B:4119:LEU:O	2.43	0.52
2:C:140:GLU:HG3	2:C:141:GLU:HG3	1.91	0.52
1:A:491:LEU:HD23	1:A:517:SER:OG	2.10	0.52
1:A:661:SER:O	1:A:665:SER:HB2	2.09	0.52
1:A:945:LEU:HA	1:A:1053:TRP:CD1	2.45	0.52
1:B:144:ASP:HB2	1:B:147:GLU:HG3	1.91	0.52
1:B:712:HIS:HA	1:B:715:HIS:CD2	2.44	0.52
1:B:3309:PHE:HE1	1:B:3411:PHE:HB3	1.74	0.52
1:B:3408:LEU:HD12	1:B:3411:PHE:CE2	2.44	0.52
1:B:3968:LEU:CD1	1:B:4012:ILE:HD11	2.39	0.52
1:B:4327:THR:HB	1:B:4328:PRO:HD3	1.90	0.52
2:C:100:TYR:CE1	2:C:138:ASN:HB2	2.45	0.52
3:E:4:HIS:O	3:E:16:ASN:HA	2.09	0.52
1:A:844:MET:HA	1:A:844:MET:HE2	1.90	0.52
1:A:2997:ILE:HB	1:A:2998:PRO:HD3	1.90	0.52
1:B:2375:MET:HG2	1:B:2387:PHE:CE1	2.35	0.52
1:B:3513:TYR:CZ	1:B:3525:TYR:HB3	2.44	0.52
1:B:4644:PHE:HB3	1:B:4722:ILE:HD11	1.92	0.52
1:B:4719:LEU:HB3	1:B:4720:PRO:HD3	1.92	0.52
2:C:20:PHE:CD2	2:C:36:VAL:HG22	2.45	0.52
1:A:405:ASN:HB2	1:A:511:ILE:HA	1.92	0.52
1:A:4560:GLU:HA	1:A:4563:LEU:HD12	1.90	0.52
1:A:4723:LEU:HD11	1:A:4760:ILE:HG23	1.91	0.52
1:B:90:SER:HA	1:B:236:LYS:HB2	1.91	0.52
1:B:313:LEU:HD13	1:B:388:ILE:HD11	1.92	0.52
1:B:1542:ALA:HB1	1:B:1602:TYR:CD1	2.45	0.52
1:B:1930:LEU:HB3	1:B:2219:HIS:CD2	2.45	0.52
1:B:2480:VAL:HG13	1:B:2524:GLN:HG3	1.91	0.52
1:B:4077:ILE:HG21	2:D:116:LYS:HE3	1.92	0.52
1:A:345:THR:O	1:A:349:ILE:HG12	2.10	0.52
1:A:470:GLY:O	1:A:474:VAL:HG23	2.10	0.52
1:A:1043:SER:HB3	1:A:1256:ILE:HG21	1.92	0.52
1:A:3950:LYS:HG2	1:A:3971:GLU:OE1	2.10	0.52
1:A:3954:ALA:HB3	1:A:3968:LEU:HD11	1.92	0.52
1:A:4155:ILE:HB	1:A:4158:ARG:HD2	1.92	0.52
1:B:1490:GLN:O	1:B:1494:LEU:HD13	2.09	0.52
1:B:1558:ASN:HD21	1:B:1803:ALA:CB	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3007:THR:HA	1:B:3010:LEU:HG	1.91	0.52
1:B:3793:ASN:OD1	1:B:3795:TYR:HB2	2.10	0.52
1:A:254:GLU:HA	1:A:257:LEU:HD12	1.90	0.51
1:A:1024:SER:HB3	1:A:1074:LEU:HD23	1.92	0.51
1:A:1309:GLN:HA	1:A:1312:ARG:HD2	1.91	0.51
1:A:1499:ILE:HG12	1:A:1506:VAL:HG21	1.92	0.51
1:A:1845:LEU:HD12	1:A:1850:LYS:HE3	1.92	0.51
1:A:3546:LYS:HG2	1:A:3714:MET:SD	2.51	0.51
1:B:723:GLN:HG2	1:B:728:GLN:HG3	1.92	0.51
1:B:1952:PHE:HE1	1:B:1976:HIS:CD2	2.28	0.51
1:B:3936:ASN:HB3	1:B:3939:ALA:HB3	1.92	0.51
1:B:4155:ILE:HB	1:B:4158:ARG:HD2	1.92	0.51
1:B:4224:GLU:HA	1:B:4279:GLN:HE21	1.74	0.51
1:B:4258:PHE:O	1:B:4259:LYS:C	2.51	0.51
2:C:49:LEU:HD13	2:C:49:LEU:O	2.09	0.51
1:A:73:PHE:HB2	1:A:161:PRO:HD3	1.92	0.51
1:A:266:PHE:O	1:A:270:ILE:HG13	2.10	0.51
1:A:3419:SER:HB3	1:A:3425:ARG:HG3	1.92	0.51
1:A:4195:HIS:CD2	2:C:35:THR:HG21	2.44	0.51
1:B:123:ALA:HB1	1:B:154:MET:SD	2.50	0.51
1:B:303:VAL:HG21	1:B:373:ASP:HB3	1.92	0.51
1:B:1214:LEU:O	1:B:1218:LEU:HG	2.10	0.51
1:B:1570:TYR:HA	1:B:1573:GLN:HE21	1.76	0.51
1:B:3063:MET:HG3	1:B:3170:GLN:HB3	1.92	0.51
1:B:3196:GLU:O	1:B:3200:ILE:HG13	2.10	0.51
1:A:80:LEU:HD11	1:A:152:THR:HA	1.92	0.51
1:A:1560:ALA:HA	1:A:1563:TRP:HE3	1.75	0.51
1:A:83:HIS:O	1:A:87:THR:HG23	2.10	0.51
1:A:546:CYS:O	1:A:550:ARG:HG3	2.11	0.51
1:A:549:GLN:O	1:A:553:LYS:HG2	2.09	0.51
1:B:2072:THR:O	1:B:2090:ASN:HB2	2.10	0.51
1:B:3458:LEU:HD11	1:B:3465:ALA:HB1	1.92	0.51
1:B:3766:LYS:HB3	1:B:3795:TYR:CD2	2.45	0.51
2:C:49:LEU:HD11	2:C:53:ILE:CD1	2.40	0.51
3:F:4:HIS:CD2	3:F:21:ARG:HB2	2.44	0.51
1:A:202:ASN:HB3	1:A:204:ARG:CZ	2.41	0.51
1:A:327:GLN:HA	1:A:511:ILE:HD11	1.92	0.51
1:A:539:SER:HB2	1:A:543:ARG:NH1	2.25	0.51
1:A:2094:ILE:HG12	1:A:2143:VAL:HG21	1.93	0.51
1:A:3071:LYS:HD2	1:A:3074:ILE:HB	1.91	0.51
1:A:3404:ASP:OD1	1:A:3404:ASP:N	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:LEU:HD11	1:B:247:LEU:HD12	1.92	0.51
1:A:491:LEU:CD1	1:A:670:ILE:HD11	2.40	0.51
1:A:1159:LEU:HA	1:A:1298:LEU:HD13	1.91	0.51
1:A:1814:MET:HA	1:A:1817:PHE:HE1	1.70	0.51
1:A:3998:LEU:O	1:A:4001:VAL:HG12	2.10	0.51
1:B:663:LEU:HD23	1:B:674:LEU:HD13	1.93	0.51
1:B:712:HIS:HA	1:B:715:HIS:NE2	2.25	0.51
1:B:1169:TYR:HA	1:B:1172:PHE:CD2	2.46	0.51
1:B:1401:PHE:HD2	1:B:1449:LEU:HD22	1.76	0.51
1:B:1558:ASN:O	1:B:1561:VAL:HB	2.11	0.51
1:B:3194:LEU:HB2	1:B:3214:LEU:HD13	1.93	0.51
1:B:3940:THR:HG21	1:B:3985:CYS:HB3	1.90	0.51
1:B:4130:ARG:HB2	1:B:4169:TYR:CE1	2.46	0.51
1:B:4438:MET:HE3	1:B:4440:ILE:HD11	1.93	0.51
1:A:1515:LEU:HA	1:A:1544:LEU:HD13	1.93	0.51
1:A:4423:GLU:CB	1:A:4459:LEU:HD13	2.41	0.51
1:B:31:VAL:O	1:B:35:PRO:HD2	2.11	0.51
1:B:1403:ASP:OD2	1:B:1404:SER:N	2.44	0.51
1:B:3405:LYS:HB2	1:B:3450:LEU:HD21	1.93	0.51
1:B:3519:LEU:HD13	1:B:3767:VAL:HG11	1.92	0.51
1:B:4286:GLU:HB3	1:B:4290:MET:HE3	1.92	0.51
1:B:4548:GLN:HG3	1:B:4605:PHE:HD1	1.75	0.51
2:D:42:GLN:HB2	2:D:78:LYS:HG2	1.92	0.51
1:A:918:TRP:O	1:A:922:PHE:HB2	2.10	0.51
1:A:1010:LEU:HB3	1:A:1037:HIS:CE1	2.45	0.51
1:A:1468:LEU:HD22	1:A:1518:LEU:HD21	1.92	0.51
1:A:1995:GLN:HB2	1:A:2024:LYS:NZ	2.26	0.51
1:A:3233:LEU:HD13	1:A:3290:TRP:HE3	1.76	0.51
1:A:4077:ILE:HG13	1:A:4079:GLY:H	1.75	0.51
1:A:4258:PHE:HE1	2:C:19:LEU:HD21	1.75	0.51
1:B:1893:VAL:HG12	1:B:2001:PHE:HZ	1.76	0.51
1:B:3292:LYS:O	1:B:3295:ILE:HG22	2.11	0.51
1:A:967:TYR:CE2	1:A:1015:PRO:HA	2.44	0.51
1:A:1010:LEU:HB3	1:A:1037:HIS:HE1	1.75	0.51
1:A:3286:ARG:HH21	1:A:3286:ARG:HG3	1.75	0.51
1:B:443:ARG:HB2	1:B:446:ASP:HB2	1.93	0.51
1:B:1473:THR:O	1:B:1485:ILE:HD13	2.10	0.51
1:B:1698:LYS:HG2	1:B:2289:ILE:HD12	1.92	0.51
1:B:3001:GLN:HG2	1:B:3004:LEU:HD23	1.92	0.51
1:A:44:PHE:HE2	1:A:48:GLU:HB2	1.75	0.51
1:A:1019:TYR:CZ	1:A:1023:LEU:HD21	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4679:LYS:NZ	1:A:4731:ILE:O	2.42	0.51
1:B:63:ILE:HA	1:B:74:TYR:CD2	2.46	0.51
1:B:1417:GLU:HA	1:B:1470:ARG:HD2	1.93	0.51
1:B:2359:GLN:HG2	1:B:2418:ASP:OD1	2.11	0.51
1:B:4232:LEU:C	1:B:4234:GLN:N	2.69	0.51
1:A:4282:LYS:O	1:A:4286:GLU:HG2	2.11	0.50
1:B:765:GLN:NE2	1:B:817:ILE:HG23	2.26	0.50
1:B:1091:GLU:HG2	1:B:1158:LEU:HD13	1.92	0.50
1:B:2296:GLN:HE21	1:B:2347:MET:HE1	1.76	0.50
1:A:396:ARG:HH21	1:B:404:GLN:CD	2.18	0.50
1:A:816:LEU:HD21	1:B:193:PHE:CZ	2.46	0.50
1:A:3007:THR:C	1:A:3009:ASP:N	2.65	0.50
1:B:909:HIS:CE1	1:B:937:SER:HB2	2.46	0.50
1:B:1428:LEU:CD1	1:B:1488:ASN:HA	2.42	0.50
1:B:1960:ASN:HD21	1:B:2012:GLN:HA	1.76	0.50
1:B:2023:VAL:HG21	1:B:2049:VAL:HG21	1.93	0.50
1:B:3307:VAL:O	1:B:3311:VAL:HG13	2.12	0.50
1:B:3330:SER:HA	1:B:3333:LEU:HB2	1.93	0.50
2:C:33:LEU:HD11	2:C:72:MET:HE1	1.91	0.50
1:A:548:LEU:HD11	1:A:647:PHE:CE2	2.46	0.50
1:A:1205:GLY:HA2	1:A:1215:GLY:C	2.36	0.50
1:A:1515:LEU:CA	1:A:1544:LEU:HD13	2.42	0.50
1:A:1682:HIS:CE1	1:A:2383:ARG:HD2	2.45	0.50
1:B:31:VAL:O	1:B:34:ARG:HB3	2.12	0.50
1:B:739:PRO:HB3	1:B:782:VAL:HG23	1.94	0.50
1:B:2327:TYR:CD1	1:B:2359:GLN:HG3	2.46	0.50
1:A:3511:ASN:HB2	1:B:4007:VAL:HG22	1.94	0.50
1:B:49:LEU:C	1:B:51:GLN:H	2.19	0.50
1:B:71:GLU:OE1	1:B:122:CYS:HA	2.11	0.50
1:B:143:LEU:HD13	1:B:151:PHE:CE2	2.47	0.50
1:B:808:VAL:HG11	1:B:908:TYR:HB3	1.94	0.50
1:B:834:VAL:HG11	1:B:961:VAL:HG13	1.93	0.50
1:B:3100:HIS:O	1:B:3103:LYS:HG3	2.11	0.50
3:E:324:LEU:O	3:E:328:LEU:HG	2.10	0.50
1:A:650:LEU:O	1:A:654:ILE:HG13	2.11	0.50
1:A:846:ALA:HB1	1:A:850:PHE:CE2	2.47	0.50
1:A:2385:PHE:HB3	1:A:2387:PHE:CZ	2.46	0.50
1:A:3458:LEU:HD11	1:A:3465:ALA:HB1	1.92	0.50
1:A:4597:LEU:O	1:A:4601:ILE:HG22	2.11	0.50
1:B:2009:PRO:HB2	1:B:2642:LEU:HD21	1.94	0.50
1:B:2049:VAL:HG22	1:B:2063:ILE:HG12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:113:CYS:SG	3:E:136:HIS:CE1	3.04	0.50
1:A:3405:LYS:HB2	1:A:3450:LEU:HD21	1.93	0.50
1:B:83:HIS:O	1:B:87:THR:HG23	2.11	0.50
1:B:864:TYR:HA	1:B:936:LEU:HG	1.94	0.50
1:B:3872:CYS:O	1:B:3873:TYR:C	2.55	0.50
1:B:4749:HIS:O	1:B:4753:GLN:HG3	2.11	0.50
2:C:137:VAL:HG13	2:C:141:GLU:HB2	1.93	0.50
1:A:317:VAL:HG12	1:A:318:LEU:N	2.26	0.50
1:A:491:LEU:HD22	1:A:518:ILE:HG12	1.92	0.50
1:A:723:GLN:HG2	1:A:728:GLN:HG3	1.92	0.50
1:A:786:PHE:CE1	1:A:806:LEU:HD13	2.47	0.50
1:A:873:PRO:HG2	1:A:876:LEU:HB2	1.93	0.50
1:A:1050:TYR:HE2	1:A:1255:THR:HG21	1.77	0.50
1:A:1196:GLN:HG2	1:A:1365:HIS:HE1	1.76	0.50
1:A:2340:ILE:HD12	1:A:2401:LEU:HD23	1.93	0.50
1:A:3000:MET:HE2	1:A:3058:LEU:HD13	1.93	0.50
1:A:3200:ILE:HG22	1:A:3202:GLN:H	1.75	0.50
1:A:3408:LEU:HD12	1:A:3411:PHE:CE2	2.44	0.50
1:A:3937:PRO:HA	1:A:3940:THR:HG22	1.94	0.50
1:B:39:ALA:CB	1:B:44:PHE:CD1	2.95	0.50
1:B:2189:VAL:HG21	1:B:2230:MET:HE1	1.93	0.50
1:B:2667:TYR:O	1:B:2668:CYS:SG	2.69	0.50
1:B:2988:LEU:HD21	1:B:2999:TYR:CD1	2.47	0.50
1:B:3003:ILE:O	1:B:3007:THR:HG23	2.12	0.50
1:B:3404:ASP:OD1	1:B:3404:ASP:N	2.41	0.50
1:B:4035:LYS:O	1:B:4036:ASP:C	2.54	0.50
1:B:4077:ILE:HG22	2:D:114:GLY:O	2.11	0.50
1:B:4768:LEU:HA	1:B:4771:LEU:HD12	1.94	0.50
1:A:1058:LEU:HD23	1:A:1061:GLN:HE22	1.75	0.50
1:A:1427:VAL:HG13	1:A:1431:PHE:CE2	2.47	0.50
1:A:2311:VAL:HG13	3:E:56:LEU:HD11	1.94	0.50
1:A:4108:PHE:O	1:A:4112:ARG:HG3	2.12	0.50
1:B:1057:HIS:O	1:B:1061:GLN:HG3	2.12	0.50
1:B:1450:CYS:CB	1:B:1505:GLN:HB2	2.41	0.50
1:B:1453:LEU:C	1:B:1455:GLN:N	2.69	0.50
1:B:1553:HIS:HD2	1:B:1556:LEU:HD23	1.77	0.50
1:B:3273:MET:O	1:B:3273:MET:HE3	2.11	0.50
2:C:44:PRO:HB2	2:C:48:GLU:HB2	1.94	0.50
2:D:124:GLU:O	2:D:128:GLU:HG2	2.12	0.50
1:A:73:PHE:CD1	1:A:158:ALA:O	2.60	0.50
1:A:418:LEU:HD21	1:A:476:LEU:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:683:MET:HE2	1:A:683:MET:HA	1.93	0.50
1:A:881:GLN:HA	1:A:885:LEU:HD12	1.92	0.50
1:A:1156:LYS:HG2	1:A:1304:GLU:HG2	1.94	0.50
1:A:1356:THR:HA	1:A:1400:PHE:HE2	1.77	0.50
1:A:3007:THR:HG21	1:A:3062:PHE:CZ	2.46	0.50
1:B:341:VAL:HB	1:B:417:SER:HB2	1.94	0.50
1:B:834:VAL:HG13	1:B:966:LEU:HD13	1.93	0.50
1:B:852:PRO:CB	1:B:855:LEU:HB3	2.41	0.50
1:B:1044:ARG:C	1:B:1046:ARG:H	2.19	0.50
1:B:1162:THR:O	1:B:1166:ILE:HG13	2.12	0.50
1:B:1359:TYR:CD1	1:B:1406:GLU:HB3	2.47	0.50
1:B:1485:ILE:O	1:B:1489:ARG:HG3	2.12	0.50
1:B:1570:TYR:CE2	1:B:1592:ILE:HG13	2.47	0.50
1:B:2246:VAL:HG13	1:B:2250:SER:HB3	1.94	0.50
1:B:2474:VAL:HG22	1:B:2477:ARG:NH2	2.27	0.50
3:F:27:CYS:SG	3:F:45:ARG:O	2.69	0.50
1:A:85:ILE:CG2	1:A:100:VAL:HG13	2.42	0.49
1:A:662:MET:HB3	1:A:674:LEU:HD11	1.94	0.49
1:A:3273:MET:HE3	1:A:3273:MET:O	2.11	0.49
1:A:3307:VAL:C	1:A:3309:PHE:H	2.19	0.49
1:B:37:LEU:HD12	1:B:38:SER:N	2.26	0.49
1:B:1296:GLY:O	1:B:1300:VAL:HG22	2.12	0.49
1:B:1553:HIS:O	1:B:1553:HIS:CG	2.65	0.49
1:B:2103:ASN:C	1:B:2105:GLN:H	2.19	0.49
1:B:2632:LEU:O	1:B:2649:GLY:HA2	2.12	0.49
1:B:2993:GLY:HA3	1:B:3050:GLU:OE1	2.12	0.49
1:B:4108:PHE:O	1:B:4112:ARG:HG3	2.11	0.49
2:C:24:GLY:HA3	2:C:28:ILE:HD12	1.92	0.49
2:D:86:ILE:HD11	2:D:146:MET:HG2	1.94	0.49
1:A:1233:TRP:HH2	1:A:1281:ALA:HB1	1.77	0.49
1:A:1300:VAL:HA	1:A:1336:ARG:NH1	2.27	0.49
1:A:1565:SER:O	1:A:1569:LYS:HG2	2.11	0.49
1:A:3100:HIS:O	1:A:3103:LYS:HG3	2.11	0.49
1:A:4335:LEU:HD13	1:A:4511:LEU:CD2	2.41	0.49
1:B:3000:MET:HE3	1:B:3054:VAL:HG12	1.92	0.49
1:A:535:LEU:HD12	1:A:682:HIS:CD2	2.46	0.49
1:A:914:VAL:HG11	1:A:1001:TYR:HD1	1.76	0.49
1:A:1101:PHE:HA	1:A:1104:ILE:HD13	1.95	0.49
1:A:2047:ARG:HE	1:A:2066:SER:HB3	1.78	0.49
1:A:2335:GLY:HA3	1:A:2405:ILE:O	2.12	0.49
1:A:3951:VAL:HG13	1:A:4012:ILE:HD13	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4310:MET:HE3	1:A:4335:LEU:HG	1.95	0.49
1:A:4595:VAL:HA	1:A:4598:LEU:HD12	1.94	0.49
1:B:288:THR:HG22	1:B:432:LYS:HB3	1.93	0.49
1:B:786:PHE:HZ	1:B:806:LEU:HD22	1.77	0.49
1:B:1819:MET:CE	1:B:2508:LEU:CD1	2.91	0.49
1:B:1952:PHE:CD1	1:B:1974:ASP:HB2	2.47	0.49
1:B:2070:ILE:HD12	1:B:2094:ILE:CD1	2.40	0.49
1:A:159:LYS:O	1:A:160:LEU:C	2.52	0.49
1:A:244:VAL:O	1:A:248:GLN:HG2	2.12	0.49
1:A:547:VAL:O	1:A:551:GLN:HG3	2.11	0.49
1:A:1929:LEU:HD21	1:A:2241:ILE:HD11	1.94	0.49
1:A:4413:LYS:HD3	1:A:4456:ILE:HD11	1.94	0.49
1:B:477:ALA:O	1:B:481:ILE:HG12	2.11	0.49
3:F:301:MET:SD	3:F:306:ARG:HG3	2.53	0.49
1:A:397:ARG:O	1:A:398:ALA:HB3	2.12	0.49
1:A:1460:GLU:HB2	1:A:1463:ARG:HB3	1.94	0.49
1:A:1510:VAL:O	1:A:1514:LEU:HG	2.13	0.49
1:A:1567:CYS:SG	1:A:1596:THR:HG23	2.52	0.49
1:A:1870:PHE:CE2	1:A:2239:LEU:HD11	2.30	0.49
1:A:2687:LEU:O	1:A:2688:CYS:C	2.55	0.49
1:B:745:TRP:HE1	1:B:810:HIS:CE1	2.31	0.49
1:B:808:VAL:HG22	1:B:933:TYR:CD2	2.48	0.49
1:B:867:HIS:O	1:B:949:ASP:HB2	2.13	0.49
1:B:1451:GLY:O	1:B:1454:ALA:HB3	2.12	0.49
1:B:1848:VAL:O	1:B:1850:LYS:NZ	2.38	0.49
1:B:3588:ARG:HG3	1:B:3648:TYR:CZ	2.47	0.49
1:B:4476:ALA:HB1	1:B:4515:CYS:HA	1.94	0.49
3:E:301:MET:SD	3:E:306:ARG:HG3	2.53	0.49
1:A:686:LEU:O	1:A:690:ILE:HG13	2.12	0.49
1:A:740:PHE:CD1	1:A:778:GLU:HG3	2.48	0.49
1:A:1241:PHE:HE2	1:A:1269:HIS:CD2	2.30	0.49
1:A:1347:LEU:HD22	1:A:1351:TYR:OH	2.13	0.49
1:A:1925:GLN:HB3	1:A:1943:THR:HB	1.95	0.49
1:A:2626:VAL:HG21	1:A:2681:ILE:HD13	1.93	0.49
1:A:4277:VAL:HG21	1:B:3732:ARG:HH22	1.78	0.49
1:B:1300:VAL:CG1	1:B:1336:ARG:HD3	2.43	0.49
1:B:1388:LEU:HG	1:B:1397:MET:HE1	1.95	0.49
1:B:1486:GLN:HG3	1:B:1489:ARG:HH11	1.78	0.49
1:B:3979:ILE:HG21	1:B:4019:ILE:HG23	1.93	0.49
1:B:4560:GLU:HA	1:B:4563:LEU:HD12	1.93	0.49
1:A:31:VAL:O	1:A:35:PRO:HD2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:909:HIS:CD2	1:A:937:SER:HA	2.48	0.49
1:A:1135:LEU:O	1:A:1139:PHE:HD2	1.96	0.49
1:A:1453:LEU:HB3	1:A:1506:VAL:CG1	2.37	0.49
1:A:2356:ILE:HD13	1:A:2377:LEU:HD13	1.94	0.49
1:A:2363:ARG:HH11	1:A:2416:MET:HE1	1.76	0.49
1:A:3988:LEU:H	1:A:3988:LEU:HD12	1.77	0.49
1:B:2292:PHE:CE2	1:B:2386:ASP:HB3	2.47	0.49
1:B:2295:ASN:HB3	1:B:2423:TYR:HB3	1.94	0.49
1:B:3063:MET:HE2	1:B:3170:GLN:HG2	1.95	0.49
1:B:3221:LYS:HD2	1:B:3224:TYR:HD2	1.76	0.49
1:B:4130:ARG:O	1:B:4134:PHE:HD2	1.96	0.49
2:D:60:GLY:HA2	2:D:64:ILE:HG12	1.94	0.49
3:E:309:MET:O	3:E:313:ARG:HG2	2.12	0.49
1:A:129:LEU:HA	1:A:132:LEU:HD12	1.94	0.49
1:A:531:MET:HE1	1:A:535:LEU:HD11	1.94	0.49
1:A:2405:ILE:HD12	1:A:2417:ILE:HD11	1.95	0.49
1:A:2581:ALA:HB2	1:A:2588:LEU:HD22	1.95	0.49
1:A:3412:LEU:HD22	1:A:3454:ILE:HD12	1.95	0.49
1:A:3872:CYS:SG	1:A:3875:CYS:CB	2.93	0.49
1:A:4692:LEU:HD21	1:A:4740:ILE:HG12	1.94	0.49
1:B:1159:LEU:HD13	1:B:1298:LEU:HB2	1.94	0.49
1:B:2040:LEU:HD11	1:B:2085:PRO:HB3	1.95	0.49
1:B:2052:LEU:HD11	1:B:2060:ILE:HD12	1.95	0.49
1:B:3309:PHE:HD2	1:B:3850:THR:HA	1.77	0.49
1:A:396:ARG:HH21	1:B:404:GLN:HE22	1.61	0.49
1:A:1666:PHE:HA	1:A:1669:THR:OG1	2.13	0.49
1:A:2474:VAL:HG13	1:A:2477:ARG:HH21	1.78	0.49
1:A:2548:LEU:HD11	1:A:2588:LEU:HA	1.95	0.49
1:A:2555:LEU:HD23	1:A:2565:LEU:HD22	1.95	0.49
1:A:3410:GLN:HE21	1:A:3857:ARG:HH11	1.60	0.49
1:A:3548:SER:HA	1:A:3551:LYS:HE2	1.95	0.49
1:A:4228:LEU:HD11	1:B:3829:LEU:HD22	1.95	0.49
1:B:1151:SER:O	1:B:1154:ILE:HG12	2.13	0.49
1:B:1930:LEU:HD13	1:B:2219:HIS:CB	2.42	0.49
1:B:2982:LEU:HD11	1:B:3027:GLN:CB	2.43	0.49
1:B:3735:ALA:O	1:B:3739:ILE:HG13	2.13	0.49
3:F:309:MET:O	3:F:313:ARG:HG2	2.12	0.49
1:A:1351:TYR:HA	1:A:1354:LEU:HD12	1.95	0.49
1:A:3307:VAL:C	1:A:3309:PHE:N	2.71	0.49
1:A:4001:VAL:C	1:A:4003:ILE:N	2.69	0.49
1:B:946:ASN:O	1:B:947:ARG:C	2.56	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1673:PHE:HD1	1:B:1714:PHE:HA	1.78	0.49
1:B:3226:GLN:HA	1:B:3289:ASN:ND2	2.28	0.49
2:C:10:ILE:HG13	2:C:66:PHE:HZ	1.76	0.49
2:D:100:TYR:CD1	2:D:136:GLN:HB2	2.48	0.49
1:A:675:SER:HB3	1:A:722:LEU:HD12	1.95	0.48
1:A:1515:LEU:HB2	1:A:1544:LEU:HB3	1.95	0.48
1:A:1895:ARG:NH2	1:A:2180:VAL:HG11	2.27	0.48
1:A:2373:ARG:NH2	1:A:2393:GLU:OE2	2.45	0.48
1:A:4480:ALA:HB2	1:A:4521:ASN:OD1	2.12	0.48
1:B:1355:ILE:HD13	1:B:1397:MET:HG2	1.93	0.48
1:B:2266:MET:HE1	1:B:2659:ALA:HB2	1.93	0.48
1:B:3412:LEU:HD22	1:B:3454:ILE:HD12	1.95	0.48
1:B:4309:PHE:CE1	1:B:4338:ILE:HD11	2.48	0.48
1:B:4314:ILE:HD11	1:B:4479:MET:HE1	1.95	0.48
1:B:4485:LEU:HD12	1:B:4524:GLN:HG2	1.93	0.48
3:E:3:ARG:HG2	3:E:18:ARG:HG2	1.93	0.48
1:A:92:ILE:HD12	1:A:97:LEU:HA	1.94	0.48
1:A:874:VAL:HG13	1:B:189:VAL:HG11	1.94	0.48
1:A:1383:TYR:O	1:A:1387:GLN:HG2	2.13	0.48
1:A:1515:LEU:CD2	1:A:1555:GLN:HG3	2.43	0.48
1:A:3521:GLU:N	1:B:3791:SER:O	2.46	0.48
1:B:272:ARG:HD2	1:B:338:TYR:CE1	2.47	0.48
1:B:313:LEU:HD21	1:B:332:LEU:HD21	1.95	0.48
1:B:1118:LEU:HD13	1:B:1273:LEU:HB2	1.94	0.48
1:B:1374:GLU:O	1:B:1375:SER:C	2.56	0.48
1:B:1536:GLU:O	1:B:1540:VAL:HG23	2.13	0.48
1:B:1859:MET:HE2	1:B:2230:MET:CB	2.44	0.48
1:B:2676:ASN:C	1:B:2678:ALA:N	2.70	0.48
1:B:3410:GLN:NE2	1:B:3853:ALA:HB2	2.28	0.48
2:C:106:LEU:CD2	2:C:126:ILE:CD1	2.80	0.48
2:D:16:ALA:O	2:D:20:PHE:HD2	1.95	0.48
1:A:334:LEU:HD11	1:A:409:LEU:HD13	1.95	0.48
1:A:1682:HIS:HE1	1:A:2383:ARG:HB2	1.76	0.48
1:A:3108:TYR:O	1:A:3112:GLN:HG2	2.13	0.48
1:A:4602:ASN:HA	1:A:4607:ARG:HE	1.77	0.48
1:B:711:TYR:CD2	1:B:887:PRO:HA	2.48	0.48
1:B:811:LEU:HD23	1:B:933:TYR:HE1	1.77	0.48
1:B:857:ARG:O	1:B:861:ILE:HG13	2.13	0.48
1:B:1384:LEU:HB3	1:B:1430:PHE:CE1	2.47	0.48
1:B:1555:GLN:HA	1:B:1558:ASN:ND2	2.26	0.48
1:B:4101:TYR:OH	2:D:85:GLU:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4238:LEU:CG	1:B:4287:THR:HG21	2.38	0.48
1:A:548:LEU:HD13	1:A:642:LYS:C	2.38	0.48
1:A:1190:PRO:HG2	1:A:1195:LEU:HD21	1.95	0.48
1:A:1459:VAL:HG21	1:A:1464:LEU:HD13	1.95	0.48
1:A:1899:MET:CE	1:A:2233:LEU:HB2	2.43	0.48
1:A:2118:VAL:HA	1:A:2644:PRO:HA	1.94	0.48
1:A:3045:ARG:NH2	1:A:3153:PHE:HB2	2.28	0.48
1:A:3226:GLN:HA	1:A:3289:ASN:ND2	2.27	0.48
1:A:4252:GLU:O	1:A:4256:ARG:HG3	2.13	0.48
1:A:4641:TYR:CD1	1:A:4655:ASP:HA	2.48	0.48
1:B:3095:VAL:HG12	1:B:3190:TRP:HZ3	1.76	0.48
1:B:4020:LEU:O	1:B:4024:ILE:HG13	2.13	0.48
1:B:4258:PHE:O	1:B:4261:ARG:N	2.44	0.48
1:B:4696:LYS:O	1:B:4699:ILE:HG22	2.13	0.48
1:A:422:LEU:HD11	1:A:537:LEU:HD23	1.95	0.48
1:A:1665:THR:O	1:A:1669:THR:HG23	2.13	0.48
1:A:2296:GLN:HE21	1:A:2347:MET:HE1	1.77	0.48
1:A:2320:ARG:HH21	3:E:68:GLU:HB3	1.78	0.48
1:A:3212:LYS:HA	1:A:3215:LEU:HG	1.94	0.48
1:A:3922:ARG:NH1	1:A:3970:TYR:OH	2.46	0.48
1:B:2025:ILE:CD1	1:B:2075:MET:HE3	2.44	0.48
1:B:2301:VAL:HG21	1:B:2422:ILE:HG21	1.95	0.48
1:B:2564:ASP:OD1	1:B:2631:LYS:CB	2.45	0.48
1:B:3309:PHE:CE1	1:B:3411:PHE:HB3	2.48	0.48
1:A:411:ALA:O	1:A:412:TRP:C	2.56	0.48
1:A:1030:MET:HE3	1:A:1035:ILE:HD13	1.96	0.48
1:A:1118:LEU:HA	1:A:1121:ILE:HD12	1.95	0.48
1:A:2189:VAL:HG21	1:A:2230:MET:HE1	1.92	0.48
1:A:2480:VAL:HA	1:A:2524:GLN:HG3	1.95	0.48
1:A:2578:ARG:HD2	1:A:2659:ALA:HA	1.96	0.48
1:A:3161:THR:O	1:A:3165:LEU:HG	2.14	0.48
1:A:3418:GLU:HG2	1:A:3461:TYR:CE1	2.49	0.48
1:A:3521:GLU:CG	1:B:3793:ASN:HA	2.37	0.48
1:B:255:LYS:HG2	1:B:258:ARG:NH2	2.29	0.48
1:B:740:PHE:CD1	1:B:778:GLU:HG3	2.48	0.48
1:B:1009:ILE:O	1:B:1013:LEU:HG	2.14	0.48
1:B:1094:PHE:HB3	1:B:1161:ALA:HB1	1.93	0.48
1:B:4311:ALA:O	1:B:4315:GLU:HG2	2.13	0.48
2:D:20:PHE:CD2	2:D:36:VAL:HG22	2.49	0.48
3:F:112:ILE:HG22	3:F:136:HIS:CE1	2.48	0.48
1:A:349:ILE:CD1	1:A:424:LEU:HD13	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1404:SER:HB2	1:A:1406:GLU:HG2	1.95	0.48
1:A:2300:ASP:HB2	1:A:3583:ARG:HH22	1.79	0.48
1:A:3063:MET:HE1	1:A:3167:LEU:HD12	1.95	0.48
1:A:4071:TRP:O	1:A:4075:LEU:HD12	2.13	0.48
1:B:1427:VAL:HG13	1:B:1431:PHE:CE2	2.47	0.48
1:B:1428:LEU:HD13	1:B:1491:LEU:HB2	1.94	0.48
1:B:1428:LEU:HB3	1:B:1491:LEU:HB3	1.95	0.48
1:B:1457:ALA:H	1:B:1510:VAL:HG22	1.78	0.48
1:B:3308:SER:HA	1:B:3319:LEU:HD13	1.96	0.48
1:A:284:ILE:HG22	1:A:286:PRO:HD2	1.96	0.48
1:A:948:LEU:HG	1:A:953:CYS:SG	2.54	0.48
1:A:4325:TYR:CZ	1:A:4495:ILE:HA	2.48	0.48
1:B:286:PRO:HB3	1:B:295:VAL:CG2	2.41	0.48
1:B:1194:LYS:HA	1:B:1370:SER:C	2.38	0.48
1:B:1256:ILE:HG12	1:B:1259:GLU:H	1.78	0.48
1:B:1551:ALA:O	1:B:1554:LEU:HD22	2.14	0.48
1:B:1924:LEU:HD23	1:B:1944:ARG:HA	1.95	0.48
1:B:1925:GLN:HB2	1:B:1945:LEU:HD21	1.96	0.48
1:B:4071:TRP:O	1:B:4075:LEU:HD12	2.13	0.48
2:C:52:MET:O	2:C:56:VAL:HG22	2.13	0.48
1:A:738:ALA:HB3	1:A:741:SER:HB3	1.96	0.48
1:A:857:ARG:O	1:A:861:ILE:HG13	2.14	0.48
1:A:1027:SER:N	1:A:1028:PRO:HD2	2.29	0.48
1:A:1859:MET:HE2	1:A:2230:MET:CB	2.44	0.48
1:A:2405:ILE:CD1	1:A:2417:ILE:HD11	2.44	0.48
1:A:3930:CYS:HB3	1:A:3981:LYS:HG3	1.95	0.48
1:A:4307:LYS:CD	1:A:4479:MET:HA	2.44	0.48
1:A:4438:MET:HE3	1:A:4440:ILE:HD11	1.95	0.48
1:B:836:ILE:O	1:B:840:LEU:HG	2.14	0.48
1:B:1082:SER:HA	1:B:1085:TYR:HB3	1.96	0.48
1:B:1237:ASN:HA	1:B:1285:LYS:HD2	1.96	0.48
2:C:65:ASP:H	2:C:68:GLU:HB3	1.78	0.48
1:A:913:GLU:CD	1:A:913:GLU:H	2.20	0.48
1:A:1022:GLN:C	1:A:1024:SER:N	2.71	0.48
1:A:1434:LEU:CD1	1:A:1449:LEU:HD12	2.44	0.48
1:A:1601:SER:N	1:A:2481:SER:HB3	2.29	0.48
1:A:1902:LEU:HD21	1:A:1967:LEU:HD13	1.96	0.48
1:A:2517:ALA:HB3	1:A:2522:GLN:HG2	1.94	0.48
1:A:2985:LEU:HD12	1:A:2988:LEU:HD13	1.95	0.48
1:A:3226:GLN:OE1	1:A:3227:LEU:HD22	2.14	0.48
1:A:3532:CYS:O	1:A:3536:ASN:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:97:LEU:HD13	1:B:201:PHE:HZ	1.79	0.48
1:B:1278:LEU:HB3	1:B:1281:ALA:CB	2.38	0.48
1:B:1895:ARG:HH22	1:B:2180:VAL:HG11	1.78	0.48
1:B:2220:THR:CG2	1:B:2224:GLU:HA	2.44	0.48
1:B:4021:GLN:HG2	1:B:4025:LYS:HE2	1.96	0.48
1:B:4665:ILE:O	1:B:4669:ILE:HG13	2.14	0.48
1:A:1177:LEU:HG	1:A:1233:TRP:CD2	2.48	0.47
1:A:2040:LEU:HD11	1:A:2085:PRO:HB3	1.95	0.47
1:B:296:ARG:HA	1:B:299:PHE:CD2	2.49	0.47
1:B:1319:LEU:HD22	1:B:1354:LEU:HD21	1.96	0.47
1:B:1921:ILE:HD11	1:B:1969:VAL:HG11	1.96	0.47
1:B:2405:ILE:HG13	1:B:2417:ILE:HD11	1.96	0.47
1:B:3516:LEU:HD11	1:B:3760:LEU:HD21	1.95	0.47
1:A:1693:CYS:HB3	1:A:1716:CYS:HB2	1.95	0.47
1:A:4596:MET:O	1:A:4600:GLN:HG2	2.14	0.47
1:B:303:VAL:HG22	1:B:377:ILE:CG1	2.44	0.47
1:B:347:MET:HE2	1:B:351:HIS:HE1	1.80	0.47
1:B:863:ASP:HB2	1:B:1009:ILE:HG12	1.96	0.47
1:B:908:TYR:CD2	1:B:908:TYR:N	2.81	0.47
1:B:1412:MET:HB3	1:B:1463:ARG:HE	1.78	0.47
1:B:3226:GLN:OE1	1:B:3227:LEU:HD22	2.14	0.47
1:A:92:ILE:HG21	1:A:100:VAL:HG21	1.96	0.47
1:A:273:PHE:HD2	1:A:338:TYR:HB2	1.79	0.47
1:A:786:PHE:HE1	1:A:806:LEU:HD13	1.78	0.47
1:A:864:TYR:HA	1:A:936:LEU:HD21	1.97	0.47
1:A:906:PRO:HG2	1:A:908:TYR:CE2	2.49	0.47
1:A:3142:ARG:O	1:A:3146:LYS:HG3	2.14	0.47
1:A:4119:LEU:HD23	3:E:329:VAL:HG21	1.96	0.47
1:B:1831:ALA:O	1:B:2568:GLU:HG2	2.14	0.47
1:B:2405:ILE:CD1	1:B:2417:ILE:HD11	2.44	0.47
1:B:3440:SER:OG	1:B:3443:GLN:OE1	2.20	0.47
1:B:3747:ASP:O	1:B:3750:TYR:HB3	2.14	0.47
1:A:137:CYS:O	1:A:240:ILE:HG23	2.13	0.47
1:A:799:VAL:HB	1:A:851:VAL:HG11	1.96	0.47
1:A:1023:LEU:HD22	1:A:1038:THR:HG23	1.96	0.47
1:A:1176:TYR:CD1	1:A:1281:ALA:HB3	2.50	0.47
1:A:1570:TYR:C	1:A:1570:TYR:CD2	2.93	0.47
1:A:2025:ILE:CD1	1:A:2075:MET:HE3	2.44	0.47
1:A:2704:VAL:O	1:A:2974:ARG:NH2	2.47	0.47
1:A:3175:THR:HA	1:A:3181:ILE:HG13	1.95	0.47
1:B:1500:VAL:HG13	1:B:1547:ALA:HA	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2181:GLN:HG3	1:B:2188:LEU:CD1	2.44	0.47
1:B:2688:CYS:O	1:B:2689:PRO:C	2.56	0.47
1:B:2982:LEU:HD11	1:B:3027:GLN:HG3	1.96	0.47
1:B:3950:LYS:HG2	1:B:3971:GLU:OE1	2.15	0.47
1:B:4745:ILE:CD1	1:B:4771:LEU:HD13	2.45	0.47
2:C:28:ILE:HG22	2:C:32:GLU:HG2	1.96	0.47
3:F:325:LEU:O	3:F:329:VAL:HG23	2.15	0.47
1:A:29:TRP:CD1	1:A:160:LEU:HD21	2.50	0.47
1:A:984:ARG:HG2	1:A:989:LYS:HB2	1.97	0.47
1:A:1825:ASN:HB3	1:A:2475:LEU:HD23	1.96	0.47
1:A:4413:LYS:CD	1:A:4456:ILE:HD11	2.45	0.47
1:B:239:PHE:O	1:B:243:ASN:ND2	2.48	0.47
1:B:345:THR:O	1:B:349:ILE:HG12	2.14	0.47
1:B:1576:VAL:HA	1:B:1579:LYS:HD2	1.96	0.47
1:B:1909:ARG:HB3	1:B:1911:HIS:CD2	2.49	0.47
1:B:3173:LYS:HA	1:B:3216:PHE:HZ	1.78	0.47
1:B:3418:GLU:HG2	1:B:3461:TYR:CE1	2.49	0.47
1:B:3884:ILE:HD11	1:B:3913:ASN:HD22	1.80	0.47
2:C:49:LEU:CD1	2:C:53:ILE:HD12	2.45	0.47
1:A:3588:ARG:HG3	1:A:3648:TYR:CZ	2.49	0.47
1:A:3772:PRO:HG2	1:B:3918:ALA:HA	1.95	0.47
1:A:4424:VAL:HA	1:A:4459:LEU:HD21	1.96	0.47
1:A:4547:GLU:HG2	1:A:4605:PHE:CE2	2.49	0.47
1:B:694:ASP:CG	1:B:750:HIS:HB3	2.40	0.47
1:B:963:TYR:OH	1:B:1013:LEU:HB3	2.15	0.47
1:B:2368:ILE:CD1	1:B:2387:PHE:CZ	2.93	0.47
1:B:3548:SER:HA	1:B:3551:LYS:HE2	1.95	0.47
1:B:4125:HIS:HA	1:B:4165:LEU:HD12	1.96	0.47
1:A:270:ILE:O	1:A:274:GLN:HG3	2.14	0.47
1:A:327:GLN:NE2	1:A:512:MET:SD	2.88	0.47
1:A:710:LEU:HG	1:A:714:ASN:HD21	1.80	0.47
1:A:860:LEU:HB2	1:A:1005:ILE:HD13	1.96	0.47
1:A:1039:LEU:CD2	1:A:1089:ILE:HD13	2.44	0.47
1:A:1159:LEU:CD2	1:A:1305:MET:HB3	2.45	0.47
1:A:1388:LEU:O	1:A:1394:ARG:NE	2.46	0.47
1:A:1708:TYR:HB3	1:A:2353:ARG:NH2	2.30	0.47
1:A:2356:ILE:HG13	1:A:2379:LEU:HD13	1.95	0.47
1:A:3455:TRP:CZ3	1:A:3458:LEU:HD22	2.50	0.47
1:A:3530:ASP:O	1:A:3531:PRO:C	2.58	0.47
1:A:3884:ILE:HD11	1:A:3913:ASN:HD22	1.79	0.47
1:A:4071:TRP:CE2	1:A:4075:LEU:HD11	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4307:LYS:NZ	1:A:4478:VAL:HB	2.30	0.47
1:A:4533:LEU:HB2	1:A:4587:LEU:HB3	1.96	0.47
1:B:49:LEU:O	1:B:51:GLN:N	2.48	0.47
1:B:544:LYS:O	1:B:548:LEU:HG	2.14	0.47
1:B:549:GLN:O	1:B:553:LYS:HG2	2.14	0.47
1:B:755:SER:O	1:B:759:ARG:HG3	2.14	0.47
1:B:1094:PHE:CE1	1:B:1162:THR:HA	2.50	0.47
1:B:1909:ARG:HB3	1:B:1911:HIS:NE2	2.30	0.47
1:B:3034:MET:SD	1:B:3034:MET:N	2.87	0.47
1:B:3098:CYS:SG	1:B:3167:LEU:HD22	2.55	0.47
1:B:3417:LEU:HD13	1:B:3461:TYR:CD2	2.50	0.47
1:B:3515:THR:O	1:B:3519:LEU:HG	2.15	0.47
1:B:4109:LEU:CD1	1:B:4114:LYS:HB2	2.45	0.47
1:B:4267:LEU:O	1:B:4271:LEU:HG	2.15	0.47
1:B:4413:LYS:HD3	1:B:4456:ILE:HD11	1.97	0.47
1:B:4615:GLY:HA2	1:B:4618:ARG:HD2	1.97	0.47
1:A:310:LEU:HD11	1:A:383:GLU:HG2	1.97	0.47
1:A:793:ASN:O	1:A:797:GLY:N	2.48	0.47
1:B:45:GLU:O	1:B:46:MET:C	2.58	0.47
1:B:283:PHE:HB3	1:B:443:ARG:NH2	2.30	0.47
1:B:1126:ALA:HB1	1:B:1262:ILE:HG23	1.96	0.47
1:B:1896:ARG:HA	1:B:1955:LEU:O	2.15	0.47
1:B:3969:GLN:O	1:B:3973:LEU:HG	2.15	0.47
1:B:4525:LEU:HB3	1:B:4532:THR:HG21	1.97	0.47
2:C:66:PHE:HB3	2:C:67:PRO:HD3	1.97	0.47
3:F:65:TYR:HB3	3:F:70:PHE:HE2	1.80	0.47
1:A:191:MET:N	1:A:191:MET:SD	2.88	0.47
1:A:271:ASN:N	1:A:271:ASN:HD22	2.13	0.47
1:A:292:ALA:HB1	1:A:346:CYS:HB2	1.95	0.47
1:A:315:LEU:O	1:A:317:VAL:HG23	2.15	0.47
1:A:1048:SER:O	1:A:1049:SER:C	2.55	0.47
1:A:1515:LEU:HD11	1:A:1556:LEU:HD23	1.97	0.47
1:A:1594:GLU:HG2	1:A:1595:CYS:N	2.30	0.47
1:A:1921:ILE:HD11	1:A:1969:VAL:HG11	1.96	0.47
1:A:3284:ALA:HA	1:A:3331:LYS:HD2	1.97	0.47
1:B:285:MET:N	1:B:286:PRO:HD2	2.30	0.47
1:B:733:GLN:HA	1:B:738:ALA:HB2	1.96	0.47
1:B:1356:THR:HA	1:B:1400:PHE:CE2	2.50	0.47
1:B:3190:TRP:CD1	1:B:3190:TRP:H	2.33	0.47
1:B:3848:GLN:HE21	1:B:3849:PRO:HD2	1.80	0.47
1:B:4071:TRP:CE2	1:B:4075:LEU:HD11	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:113:CYS:HB3	3:F:120:ASP:O	2.15	0.47
3:F:120:ASP:HB3	3:F:123:HIS:HB2	1.97	0.47
1:A:506:PRO:HG3	1:A:526:ASP:OD2	2.14	0.47
1:A:530:LEU:O	1:A:534:LEU:HG	2.14	0.47
1:A:1570:TYR:CD2	1:A:1592:ILE:HG21	2.50	0.47
1:A:1875:MET:HG2	1:A:1877:TYR:CZ	2.50	0.47
1:A:2122:LEU:HD23	1:A:2136:ILE:HD11	1.96	0.47
1:A:2223:ASN:HB2	1:A:2225:GLN:HG3	1.97	0.47
1:A:2479:VAL:HG21	1:A:2521:VAL:HG13	1.97	0.47
1:A:3292:LYS:O	1:A:3295:ILE:HG22	2.15	0.47
1:A:4006:PRO:HG2	1:B:3507:HIS:O	2.14	0.47
1:A:4135:THR:H	1:A:4142:ARG:HD3	1.79	0.47
1:B:1431:PHE:O	1:B:1435:PHE:HD2	1.98	0.47
1:B:2202:ILE:HG21	1:B:2232:LEU:HD11	1.97	0.47
1:B:2405:ILE:HD12	1:B:2417:ILE:HD11	1.96	0.47
1:B:2701:LEU:HD13	1:B:3002:VAL:HG13	1.95	0.47
1:A:82:THR:HB	1:A:132:LEU:HD22	1.96	0.46
1:A:485:THR:O	1:A:489:GLN:HG2	2.15	0.46
1:A:1233:TRP:HH2	1:A:1281:ALA:CB	2.27	0.46
1:A:1453:LEU:CB	1:A:1506:VAL:HG13	2.38	0.46
1:A:3766:LYS:HB3	1:A:3795:TYR:CE2	2.50	0.46
1:B:3090:LEU:CD1	1:B:3184:PRO:HB3	2.43	0.46
1:B:4112:ARG:NH2	2:D:128:GLU:HB3	2.30	0.46
2:D:70:LEU:O	2:D:73:MET:HG2	2.15	0.46
1:A:260:CYS:O	1:A:263:LEU:HG	2.15	0.46
1:A:317:VAL:O	1:A:318:LEU:HG	2.15	0.46
1:A:318:LEU:HD13	1:A:329:VAL:HG11	1.97	0.46
1:A:1194:LYS:HA	1:A:1370:SER:C	2.41	0.46
1:A:1295:THR:O	1:A:1299:ILE:HG13	2.15	0.46
1:A:1571:LEU:C	1:A:1573:GLN:H	2.23	0.46
1:A:3417:LEU:HD13	1:A:3461:TYR:CD2	2.49	0.46
1:A:3456:PRO:HA	1:A:3496:ILE:HD11	1.96	0.46
1:B:986:LYS:HG3	1:B:1113:HIS:CE1	2.50	0.46
1:B:1963:LYS:HD3	1:B:1966:TYR:CZ	2.50	0.46
1:B:3905:LEU:HD23	1:B:3932:LEU:HD11	1.96	0.46
1:B:4128:TRP:O	1:B:4129:LEU:C	2.57	0.46
1:B:4710:TRP:O	1:B:4714:LEU:HG	2.15	0.46
1:A:1159:LEU:HD23	1:A:1305:MET:HB3	1.98	0.46
1:A:1431:PHE:O	1:A:1435:PHE:HD2	1.98	0.46
1:A:1525:MET:SD	1:A:1534:PHE:HA	2.56	0.46
1:A:2523:GLN:HA	1:A:2526:LYS:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2700:ALA:O	1:A:2704:VAL:HG13	2.14	0.46
1:A:3301:LEU:HD23	1:A:3301:LEU:HA	1.76	0.46
1:A:3419:SER:HB3	1:A:3425:ARG:CG	2.46	0.46
1:A:3749:VAL:HG21	1:A:3817:ILE:HD12	1.97	0.46
1:A:3887:LEU:HD13	1:A:3905:LEU:HD21	1.97	0.46
1:A:4328:PRO:HB2	1:A:4332:PHE:HE2	1.79	0.46
1:B:341:VAL:HB	1:B:417:SER:CB	2.45	0.46
1:B:470:GLY:O	1:B:474:VAL:HG23	2.15	0.46
1:B:765:GLN:HE22	1:B:817:ILE:HG23	1.80	0.46
1:B:1019:TYR:OH	1:B:1038:THR:HA	2.15	0.46
1:B:2053:PHE:O	1:B:2138:ARG:HD2	2.15	0.46
1:B:3456:PRO:HA	1:B:3496:ILE:HD11	1.96	0.46
1:A:273:PHE:CD2	1:A:338:TYR:HB2	2.51	0.46
1:A:471:VAL:HG21	1:A:641:ARG:HG2	1.98	0.46
1:A:847:GLN:HG3	1:A:976:ALA:HB2	1.98	0.46
1:A:1058:LEU:HD23	1:A:1061:GLN:NE2	2.29	0.46
1:A:3527:LEU:HD21	1:A:3757:ARG:HD3	1.97	0.46
1:A:3536:ASN:HD21	1:A:3815:SER:HB2	1.80	0.46
1:A:4101:TYR:HA	1:A:4104:ARG:HB2	1.97	0.46
1:A:4195:HIS:NE2	2:C:35:THR:HG21	2.30	0.46
1:B:274:GLN:O	1:B:277:VAL:HG22	2.16	0.46
1:B:471:VAL:O	1:B:475:ILE:HG12	2.15	0.46
1:B:1159:LEU:CA	1:B:1298:LEU:HD13	2.35	0.46
1:B:2262:VAL:HG13	1:B:2265:ILE:HD12	1.97	0.46
1:B:2509:ALA:HB2	1:B:2528:LEU:HD23	1.97	0.46
1:B:2985:LEU:HD23	1:B:2988:LEU:HD22	1.97	0.46
1:B:3053:LEU:HD13	1:B:3160:LEU:CD1	2.45	0.46
1:B:3419:SER:HB3	1:B:3425:ARG:CG	2.46	0.46
1:B:3455:TRP:CZ3	1:B:3458:LEU:HD22	2.50	0.46
1:B:4128:TRP:CZ2	3:F:328:LEU:HD21	2.51	0.46
1:B:4750:LYS:O	1:B:4754:VAL:HG23	2.15	0.46
1:A:71:GLU:HB2	1:A:72:PRO:HD3	1.97	0.46
1:A:718:VAL:HG12	1:A:763:ILE:HD12	1.97	0.46
1:A:862:PHE:O	1:A:866:LEU:HG	2.15	0.46
1:A:984:ARG:HH11	1:A:984:ARG:CB	2.24	0.46
1:A:1233:TRP:CE3	1:A:1278:LEU:HD13	2.51	0.46
1:A:1963:LYS:HD3	1:A:1966:TYR:CZ	2.50	0.46
1:A:2194:PRO:HG2	1:A:2251:TYR:OH	2.16	0.46
1:B:89:CYS:SG	1:B:239:PHE:CD2	2.97	0.46
1:B:284:ILE:O	1:B:441:ALA:N	2.48	0.46
1:B:387:MET:O	1:B:390:GLN:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:658:ILE:O	1:B:662:MET:HB2	2.16	0.46
1:B:3001:GLN:NE2	1:B:3138:PRO:CD	2.78	0.46
1:B:3021:LEU:HD12	1:B:3024:LEU:HD23	1.97	0.46
1:B:4632:GLN:HA	1:B:4681:LEU:HD21	1.98	0.46
3:E:302:SER:OG	3:E:305:GLU:HB3	2.16	0.46
3:F:324:LEU:O	3:F:328:LEU:HG	2.16	0.46
1:A:104:CYS:SG	1:A:136:LEU:HD22	2.56	0.46
1:A:349:ILE:HG23	1:A:429:LEU:HD11	1.96	0.46
1:A:735:LEU:HD13	1:A:753:SER:HA	1.96	0.46
1:A:847:GLN:HG3	1:A:976:ALA:CB	2.46	0.46
1:A:1203:ALA:O	1:A:1204:ILE:C	2.57	0.46
1:A:1428:LEU:CD1	1:A:1488:ASN:HA	2.46	0.46
1:B:1561:VAL:CG2	1:B:1810:LEU:HD22	2.43	0.46
1:B:2264:SER:HB3	1:B:2652:HIS:CE1	2.51	0.46
1:B:2307:ASP:HB2	1:B:2336:PHE:HB2	1.97	0.46
1:B:2368:ILE:CG2	1:B:2377:LEU:HD11	2.43	0.46
2:D:6:THR:HG23	2:D:9:GLN:H	1.79	0.46
3:E:28:TYR:CE2	3:E:122:ASN:HB3	2.51	0.46
1:A:280:ASN:HD22	1:A:523:ARG:HH11	1.64	0.46
1:A:283:PHE:HA	1:A:442:LEU:O	2.16	0.46
1:A:963:TYR:OH	1:A:1013:LEU:HB3	2.16	0.46
1:A:3910:PHE:HB2	1:A:3929:MET:HE1	1.97	0.46
1:A:4001:VAL:C	1:A:4003:ILE:H	2.22	0.46
1:A:4232:LEU:HD13	1:B:3750:TYR:CB	2.36	0.46
1:A:4325:TYR:HB3	1:A:4501:GLY:HA2	1.98	0.46
1:B:1105:ASP:HB3	1:B:1108:THR:HB	1.98	0.46
1:B:1561:VAL:HG13	1:B:1810:LEU:HD22	1.97	0.46
1:B:2117:HIS:CD2	1:B:2642:LEU:HD22	2.51	0.46
1:B:2677:THR:HA	1:B:2680:LYS:HD2	1.98	0.46
1:B:4206:LEU:HB2	1:B:4207:PRO:HD3	1.98	0.46
1:B:4745:ILE:HB	1:B:4746:PRO:HD3	1.97	0.46
1:A:664:ASN:HD21	1:B:202:ASN:HB3	1.81	0.46
1:A:917:ASN:HA	1:A:920:LYS:HD2	1.98	0.46
1:A:1101:PHE:O	1:A:1104:ILE:HB	2.14	0.46
1:A:1678:TRP:HB3	1:A:1714:PHE:CD1	2.51	0.46
1:A:3313:GLU:O	1:A:3317:PRO:HD3	2.15	0.46
1:A:3880:THR:O	1:A:3884:ILE:HG12	2.16	0.46
1:A:4281:THR:HG22	1:A:4283:LEU:H	1.81	0.46
1:A:4339:ILE:HD13	1:A:4476:ALA:HB2	1.97	0.46
1:B:62:GLU:O	1:B:66:HIS:HB3	2.15	0.46
1:B:327:GLN:O	1:B:331:VAL:HG23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1596:THR:HG22	1:B:2478:LEU:HD13	1.98	0.46
1:B:2291:PHE:CZ	1:B:2350:THR:HB	2.51	0.46
1:B:4101:TYR:HA	1:B:4104:ARG:HB2	1.97	0.46
2:D:51:ASP:HA	2:D:54:ASN:HD22	1.81	0.46
2:D:118:THR:O	2:D:119:ASP:C	2.58	0.46
1:A:110:PHE:CZ	1:A:114:ARG:HD2	2.51	0.46
1:A:506:PRO:HB2	1:A:523:ARG:NH2	2.29	0.46
1:A:1039:LEU:HD22	1:A:1130:LYS:HE2	1.98	0.46
1:A:1515:LEU:HD23	1:A:1555:GLN:HG3	1.98	0.46
1:B:269:TYR:CD1	1:B:339:ALA:HA	2.50	0.46
1:B:484:LEU:O	1:B:488:PHE:HD1	1.99	0.46
1:B:668:ASN:HA	1:B:671:ARG:HB2	1.98	0.46
1:B:1377:LEU:HD12	1:B:1377:LEU:H	1.81	0.46
1:B:2687:LEU:HD13	1:B:2991:VAL:HG11	1.98	0.46
1:B:3046:SER:HB2	1:B:3049:ASN:HD21	1.80	0.46
1:B:3108:TYR:O	1:B:3112:GLN:HG2	2.15	0.46
1:B:4730:ALA:O	1:B:4731:ILE:C	2.59	0.46
2:C:26:GLY:O	2:C:61:ASN:HA	2.16	0.46
1:A:200:VAL:CB	1:B:715:HIS:ND1	2.77	0.46
1:A:511:ILE:HG13	1:A:512:MET:N	2.31	0.46
1:A:1015:PRO:HG3	1:A:1041:TRP:CE2	2.50	0.46
1:A:1132:GLN:HE22	1:A:1293:ARG:HH21	1.62	0.46
1:A:1380:CYS:O	1:A:1380:CYS:SG	2.74	0.46
1:A:1568:LYS:HG2	1:A:1817:PHE:HZ	1.80	0.46
1:A:1877:TYR:HB2	1:A:1886:ARG:HG3	1.98	0.46
1:A:2385:PHE:HB3	1:A:2387:PHE:CE2	2.50	0.46
1:A:2405:ILE:HG13	1:A:2417:ILE:HD11	1.97	0.46
1:B:1345:GLU:CD	1:B:1345:GLU:H	2.24	0.46
1:B:3099:LEU:HB2	1:B:3190:TRP:CZ3	2.51	0.46
1:B:3909:LEU:HD22	1:B:3925:VAL:HG13	1.98	0.46
1:B:4621:PRO:HB3	1:B:4668:GLY:CA	2.44	0.46
1:A:337:LEU:HD11	1:A:414:LEU:HD21	1.98	0.45
1:A:2202:ILE:HG21	1:A:2232:LEU:HD11	1.97	0.45
1:A:3234:ASP:O	1:A:3238:ARG:HG2	2.16	0.45
1:A:3533:LEU:HD12	1:A:3819:GLN:HG2	1.98	0.45
1:B:313:LEU:CD1	1:B:384:ILE:HG23	2.45	0.45
1:B:747:LEU:HB3	1:B:806:LEU:N	2.31	0.45
1:B:858:LEU:HA	1:B:858:LEU:HD23	1.80	0.45
1:B:2356:ILE:HG13	1:B:2379:LEU:HD13	1.98	0.45
2:C:13:PHE:HB3	2:C:69:PHE:CE2	2.47	0.45
2:D:93:PHE:CZ	2:D:101:ILE:HA	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:GLN:O	1:A:193:PHE:HB3	2.16	0.45
1:A:285:MET:N	1:A:286:PRO:CD	2.79	0.45
1:A:1081:SER:HA	1:A:1084:LYS:HD2	1.97	0.45
1:A:1233:TRP:CH2	1:A:1281:ALA:CB	2.99	0.45
1:A:4750:LYS:O	1:A:4754:VAL:HG23	2.17	0.45
1:B:761:LEU:HB3	1:B:779:CYS:SG	2.56	0.45
1:B:1093:TYR:O	1:B:1096:ARG:HG2	2.15	0.45
1:B:1489:ARG:O	1:B:1493:GLN:HG3	2.16	0.45
1:B:3005:MET:HA	1:B:3008:THR:HG23	1.98	0.45
1:A:135:GLY:CA	1:A:140:CYS:O	2.63	0.45
1:A:338:TYR:HA	1:A:341:VAL:HG22	1.97	0.45
1:A:477:ALA:O	1:A:481:ILE:HG12	2.15	0.45
1:A:1023:LEU:CD2	1:A:1038:THR:HG23	2.46	0.45
1:A:1032:GLU:O	1:A:1033:CYS:SG	2.71	0.45
1:A:1087:VAL:O	1:A:1091:GLU:HG3	2.17	0.45
1:A:2101:ASP:HB3	1:A:2106:VAL:HG22	1.98	0.45
1:A:2371:PHE:CZ	1:A:2397:ALA:HB2	2.51	0.45
1:A:4031:SER:N	3:E:310:GLU:OE2	2.50	0.45
1:B:2295:ASN:CB	1:B:2423:TYR:HB3	2.45	0.45
1:B:2626:VAL:HG21	1:B:2681:ILE:HG21	1.98	0.45
1:B:4003:ILE:HG22	1:B:4005:THR:H	1.81	0.45
2:D:20:PHE:HB3	2:D:32:GLU:HB3	1.99	0.45
2:D:39:SER:C	2:D:41:GLY:H	2.25	0.45
2:D:121:GLU:O	2:D:125:MET:HG2	2.16	0.45
1:A:543:ARG:O	1:A:547:VAL:HG23	2.16	0.45
1:A:1959:GLY:O	1:A:1961:PRO:HD3	2.16	0.45
1:A:2092:LEU:HD23	1:A:2094:ILE:HD11	1.97	0.45
1:A:4135:THR:O	1:A:4142:ARG:NH1	2.46	0.45
1:B:827:ARG:NE	1:B:955:VAL:HG22	2.31	0.45
1:B:1240:GLU:CD	1:B:1240:GLU:H	2.24	0.45
1:B:1408:VAL:O	1:B:1412:MET:HG2	2.17	0.45
1:B:1593:LEU:HB3	1:B:2474:VAL:HG11	1.99	0.45
1:B:1902:LEU:HD21	1:B:1967:LEU:HD13	1.98	0.45
1:B:2255:PRO:C	1:B:2257:LEU:N	2.74	0.45
1:B:2636:LYS:HD2	1:B:2653:ILE:HD11	1.98	0.45
1:B:2982:LEU:HD13	1:B:2982:LEU:C	2.41	0.45
3:F:302:SER:OG	3:F:305:GLU:HB3	2.16	0.45
1:A:333:SER:HB2	1:A:388:ILE:CG1	2.46	0.45
1:A:485:THR:HG22	1:A:657:PHE:HD1	1.81	0.45
1:A:1019:TYR:CE2	1:A:1023:LEU:HD11	2.52	0.45
1:A:1039:LEU:HD21	1:A:1089:ILE:HD13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1105:ASP:N	1:A:1110:LEU:HD21	2.18	0.45
1:A:3972:MET:HE3	1:A:3972:MET:HB3	1.73	0.45
1:B:34:ARG:HB3	1:B:35:PRO:HD3	1.99	0.45
1:B:255:LYS:HG2	1:B:258:ARG:HH21	1.80	0.45
1:B:1541:MET:HG2	1:B:1556:LEU:HD11	1.99	0.45
1:B:3410:GLN:HG3	1:B:3850:THR:CB	2.33	0.45
1:B:3910:PHE:HB2	1:B:3929:MET:HE1	1.97	0.45
1:A:144:ASP:O	1:A:148:ILE:HG13	2.17	0.45
1:A:1388:LEU:O	1:A:1394:ARG:HB2	2.17	0.45
1:A:1509:GLY:O	1:A:1513:VAL:HG23	2.17	0.45
1:A:3038:ASP:O	1:A:3042:LYS:HG2	2.17	0.45
1:A:3251:LEU:HD12	1:A:3303:PHE:CD2	2.51	0.45
1:A:3626:GLU:OE1	1:A:3628:LYS:HE3	2.17	0.45
1:A:4745:ILE:HB	1:A:4746:PRO:HD3	1.99	0.45
1:B:908:TYR:O	1:B:908:TYR:CG	2.70	0.45
1:B:985:ARG:HH11	1:B:1280:LEU:HD11	1.81	0.45
1:B:1110:LEU:H	1:B:1175:ALA:CB	2.29	0.45
1:B:1174:ARG:O	1:B:1178:LEU:HG	2.16	0.45
1:B:2698:LYS:HG3	1:B:3002:VAL:HG23	1.98	0.45
1:B:4053:HIS:HB2	1:B:4071:TRP:HD1	1.81	0.45
1:B:4711:LYS:HA	1:B:4714:LEU:HD12	1.99	0.45
1:A:44:PHE:CE2	1:A:48:GLU:HB2	2.51	0.45
1:A:136:LEU:O	1:A:243:ASN:ND2	2.49	0.45
1:A:416:ASN:HD22	1:A:416:ASN:N	2.15	0.45
1:A:680:GLU:HB3	1:A:730:THR:HG21	1.99	0.45
1:A:974:LEU:HD23	1:A:1006:LEU:HD23	1.99	0.45
1:A:1163:LEU:HA	1:A:1166:ILE:HD12	1.98	0.45
1:A:2122:LEU:HB2	1:A:2136:ILE:HD12	1.99	0.45
1:A:4170:LEU:O	1:A:4173:LEU:HB3	2.17	0.45
1:A:4313:CYS:HB3	1:A:4331:ILE:CD1	2.47	0.45
1:B:478:ASN:OD1	1:B:650:LEU:HD13	2.17	0.45
1:B:2122:LEU:HD23	1:B:2136:ILE:HD11	1.96	0.45
1:B:2622:ILE:HD11	1:B:2667:TYR:CG	2.52	0.45
1:B:2702:ILE:CD1	1:B:3001:GLN:NE2	2.79	0.45
1:B:3056:MET:HA	1:B:3059:LEU:HD12	1.99	0.45
1:B:3714:MET:HE3	1:B:3714:MET:HB3	1.78	0.45
1:A:279:ALA:O	1:A:280:ASN:C	2.59	0.45
1:A:284:ILE:O	1:A:442:LEU:N	2.50	0.45
1:A:1456:LEU:HD22	1:A:1510:VAL:HG13	1.98	0.45
1:A:3337:ALA:HB3	1:A:3427:GLN:HE21	1.81	0.45
1:A:3909:LEU:HD22	1:A:3925:VAL:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4098:THR:HB	2:C:109:VAL:HG13	1.99	0.45
1:A:4310:MET:HG2	1:A:4335:LEU:CD1	2.47	0.45
1:A:4419:LEU:HD13	1:A:4459:LEU:HG	1.97	0.45
1:A:4710:TRP:O	1:A:4714:LEU:HG	2.16	0.45
1:B:678:LEU:HB3	1:B:727:LEU:CD2	2.46	0.45
1:B:686:LEU:HA	1:B:686:LEU:HD23	1.73	0.45
1:B:1077:THR:HA	1:B:1082:SER:HB2	1.98	0.45
1:B:1407:LEU:H	1:B:1407:LEU:CD1	2.25	0.45
1:B:3301:LEU:HD23	1:B:3301:LEU:HA	1.76	0.45
1:B:3461:TYR:O	1:B:3534:VAL:HG11	2.17	0.45
2:D:7:GLU:HA	2:D:10:ILE:HG22	1.99	0.45
1:A:55:SER:O	1:A:59:SER:N	2.36	0.45
1:A:1090:VAL:HG11	1:A:1131:VAL:HG22	1.99	0.45
1:A:1468:LEU:HA	1:A:1471:MET:HE2	1.99	0.45
1:A:1515:LEU:CD1	1:A:1541:MET:HG3	2.47	0.45
1:A:1570:TYR:CG	1:A:1592:ILE:HG21	2.52	0.45
1:A:1807:PHE:O	1:A:1810:LEU:HB3	2.17	0.45
1:A:1924:LEU:HD23	1:A:1944:ARG:HA	1.99	0.45
1:A:2390:THR:O	1:A:2391:ARG:C	2.59	0.45
1:A:2480:VAL:HA	1:A:2524:GLN:CG	2.46	0.45
1:A:2978:LEU:HB2	1:A:3006:LEU:HD13	1.99	0.45
1:A:3194:LEU:HD13	1:A:3214:LEU:HD21	1.97	0.45
1:A:3478:LYS:HD2	1:A:3478:LYS:HA	1.83	0.45
1:B:1204:ILE:CG2	1:B:1357:GLY:HA3	2.43	0.45
1:B:1831:ALA:HB2	1:B:2260:SER:HB3	1.97	0.45
1:B:3887:LEU:HD13	1:B:3905:LEU:HD21	1.98	0.45
1:B:4052:ILE:HG23	3:F:322:GLU:HB3	1.99	0.45
3:E:317:SER:O	3:E:321:GLN:HG3	2.17	0.45
1:A:31:VAL:O	1:A:34:ARG:HB3	2.17	0.45
1:A:488:PHE:HE2	1:A:670:ILE:HD12	1.82	0.45
1:A:1557:HIS:HB2	1:A:1799:LEU:HD23	1.97	0.45
1:A:1610:LEU:HD21	1:A:1799:LEU:HB2	1.99	0.45
1:A:1807:PHE:O	1:A:1811:VAL:HG23	2.17	0.45
1:A:1950:VAL:HG11	1:A:1969:VAL:HG11	1.98	0.45
1:A:2375:MET:HG2	1:A:2387:PHE:CE1	2.32	0.45
1:A:2540:HIS:HB3	1:A:2584:ARG:NE	2.32	0.45
1:A:3148:HIS:CE1	1:A:3152:VAL:H	2.34	0.45
1:A:3229:ASP:HB2	1:A:3289:ASN:HD22	1.82	0.45
1:A:3905:LEU:HD23	1:A:3932:LEU:HD11	1.99	0.45
1:A:4026:PRO:O	1:A:4027:PRO:C	2.59	0.45
1:A:4595:VAL:CG2	1:A:4630:LYS:HA	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:283:PHE:HB3	1:B:443:ARG:CZ	2.47	0.45
1:B:1047:ILE:O	1:B:1051:VAL:HG23	2.17	0.45
1:B:1498:TYR:O	1:B:1504:SER:HB2	2.17	0.45
1:B:1959:GLY:O	1:B:1961:PRO:HD3	2.16	0.45
1:B:2978:LEU:HD23	1:B:3010:LEU:HD11	1.98	0.45
1:B:3012:GLY:H	1:B:3077:SER:HB2	1.80	0.45
1:B:3226:GLN:HA	1:B:3289:ASN:HD22	1.81	0.45
1:B:3756:HIS:HB2	1:B:3807:CYS:SG	2.57	0.45
1:B:4050:ASN:OD1	2:D:38:ARG:NH2	2.50	0.45
1:A:97:LEU:HD23	1:A:98:GLN:N	2.32	0.44
1:A:3033:GLY:O	1:A:3034:MET:C	2.61	0.44
1:A:3642:ILE:HD13	1:A:3713:PHE:CE1	2.52	0.44
1:A:4570:LEU:HD13	1:A:4622:TYR:CB	2.47	0.44
1:A:4639:LYS:HB3	1:A:4640:PRO:HD3	1.99	0.44
1:B:414:LEU:O	1:B:418:LEU:HG	2.17	0.44
1:B:722:LEU:H	1:B:722:LEU:HD12	1.82	0.44
1:B:1564:LEU:HD13	1:B:1596:THR:HG23	1.98	0.44
1:B:1728:ALA:O	1:B:1729:LEU:C	2.60	0.44
1:B:2695:PHE:CZ	1:B:2699:GLN:NE2	2.84	0.44
1:B:3234:ASP:O	1:B:3238:ARG:HG2	2.16	0.44
1:A:94:ARG:H	1:A:94:ARG:HD2	1.81	0.44
1:A:252:GLY:O	1:A:256:LEU:HG	2.18	0.44
1:A:471:VAL:CG2	1:A:641:ARG:H	2.26	0.44
1:A:738:ALA:O	1:A:785:ARG:NH1	2.50	0.44
1:A:1346:PHE:O	1:A:1350:VAL:HG23	2.17	0.44
1:A:1903:SER:HB2	1:A:1910:GLN:HA	1.99	0.44
1:A:2622:ILE:HD11	1:A:2667:TYR:CB	2.47	0.44
1:A:4120:ASP:OD1	1:A:4120:ASP:N	2.46	0.44
1:A:4332:PHE:HB2	1:A:4507:VAL:HG12	2.00	0.44
1:B:418:LEU:HD11	1:B:477:ALA:HA	1.98	0.44
1:B:1174:ARG:HG2	1:B:1320:GLU:OE2	2.16	0.44
1:B:2122:LEU:HB2	1:B:2136:ILE:HD12	1.99	0.44
1:B:3058:LEU:HD12	1:B:3058:LEU:HA	1.82	0.44
1:B:3099:LEU:HD11	1:B:3193:PHE:CD1	2.51	0.44
1:B:4170:LEU:O	1:B:4173:LEU:HB3	2.17	0.44
1:B:4313:CYS:HB3	1:B:4331:ILE:HG23	1.99	0.44
3:F:24:CYS:CA	3:F:52:MET:SD	3.05	0.44
1:A:202:ASN:CG	1:A:204:ARG:HG3	2.43	0.44
1:A:288:THR:HG22	1:A:290:ALA:H	1.81	0.44
1:A:1180:ASN:O	1:A:1181:PHE:C	2.58	0.44
1:B:115:LEU:HD13	1:B:130:ILE:HG13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:333:SER:OG	1:B:385:TYR:HA	2.18	0.44
1:B:674:LEU:O	1:B:678:LEU:HG	2.18	0.44
1:B:813:MET:HB2	1:B:813:MET:HE3	1.68	0.44
1:B:1295:THR:HG22	1:B:1299:ILE:HD13	2.00	0.44
1:B:3058:LEU:HG	1:B:3062:PHE:CZ	2.52	0.44
1:B:3642:ILE:HD13	1:B:3713:PHE:CE1	2.52	0.44
1:B:3880:THR:O	1:B:3884:ILE:HG12	2.16	0.44
1:B:4705:LEU:CD1	1:B:4753:GLN:HB2	2.47	0.44
3:E:24:CYS:CA	3:E:52:MET:SD	3.06	0.44
1:A:264:PRO:HG2	1:A:305:ASP:OD2	2.18	0.44
1:A:1381:LEU:HB3	1:A:1426:ARG:NH2	2.32	0.44
1:A:3513:TYR:CD1	1:A:3525:TYR:HD1	2.35	0.44
1:A:3525:TYR:CE2	1:A:3874:GLY:HA2	2.53	0.44
1:A:4746:PRO:O	1:A:4750:LYS:HG3	2.16	0.44
1:B:1664:CYS:HB3	1:B:1667:THR:HG23	1.99	0.44
1:B:2300:ASP:OD2	1:B:2344:ASN:ND2	2.50	0.44
1:B:4093:ARG:NH2	2:D:51:ASP:OD2	2.51	0.44
2:D:60:GLY:H	2:D:63:THR:HB	1.82	0.44
2:D:93:PHE:CE2	2:D:101:ILE:HG12	2.52	0.44
1:A:59:SER:O	1:A:63:ILE:HG13	2.17	0.44
1:A:844:MET:HB3	1:A:848:MET:HE3	1.98	0.44
1:A:1534:PHE:N	1:A:1535:PRO:HD2	2.32	0.44
1:A:1899:MET:HE2	1:A:2233:LEU:HB3	2.00	0.44
1:A:2349:MET:HB2	1:A:2397:ALA:O	2.18	0.44
1:A:3004:LEU:HD22	1:A:3061:VAL:HG11	2.00	0.44
1:A:3273:MET:HG3	1:A:3633:LEU:CD2	2.48	0.44
1:B:382:LEU:HD23	1:B:382:LEU:HA	1.82	0.44
1:B:443:ARG:HB2	1:B:446:ASP:CB	2.47	0.44
1:B:909:HIS:ND1	1:B:934:CYS:O	2.49	0.44
1:B:1859:MET:SD	1:B:2244:ALA:HA	2.58	0.44
1:B:1891:ALA:HB3	1:B:1893:VAL:HG23	1.98	0.44
1:B:1976:HIS:ND1	1:B:1989:HIS:NE2	2.57	0.44
1:B:2129:GLY:HA3	1:B:2161:SER:O	2.17	0.44
1:B:3004:LEU:O	1:B:3008:THR:HG23	2.18	0.44
2:C:13:PHE:CD1	2:C:40:LEU:HD13	2.52	0.44
1:A:284:ILE:HG22	1:A:286:PRO:CD	2.47	0.44
1:A:718:VAL:HG13	1:A:760:LEU:HD23	1.98	0.44
1:A:911:PHE:HD2	1:A:1001:TYR:CD1	2.35	0.44
1:A:1434:LEU:HD11	1:A:1449:LEU:HD12	2.00	0.44
1:A:2309:LEU:O	3:E:77:SER:OG	2.34	0.44
1:A:2522:GLN:O	1:A:2526:LYS:HG3	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2692:ALA:HA	1:A:2695:PHE:CD1	2.49	0.44
1:A:3291:GLN:HA	1:A:3395:LEU:HD11	1.99	0.44
1:A:3412:LEU:O	1:A:3416:LEU:HB2	2.18	0.44
1:A:4047:PRO:HA	1:A:4075:LEU:HD23	1.99	0.44
1:B:1414:THR:HG21	1:B:1424:CYS:HA	1.99	0.44
1:B:2048:ASP:OD1	1:B:2049:VAL:N	2.51	0.44
1:B:2215:VAL:HG23	1:B:2231:ILE:HB	1.99	0.44
1:B:2264:SER:HB3	1:B:2652:HIS:NE2	2.32	0.44
1:B:2540:HIS:HB3	1:B:2584:ARG:CZ	2.48	0.44
1:B:2985:LEU:O	1:B:2988:LEU:HB2	2.17	0.44
1:B:3273:MET:HG3	1:B:3633:LEU:CD2	2.48	0.44
1:B:4234:GLN:HE22	1:B:4279:GLN:HB3	1.83	0.44
1:A:405:ASN:ND2	1:A:513:ALA:O	2.51	0.44
1:A:1489:ARG:O	1:A:1493:GLN:HG3	2.18	0.44
1:A:1680:HIS:O	1:A:1706:ILE:HA	2.17	0.44
1:A:1867:GLU:HG2	1:A:2236:ASP:OD2	2.18	0.44
1:A:3087:ALA:HB2	1:A:3181:ILE:HG21	2.00	0.44
1:A:3963:ASP:O	1:A:3964:LEU:C	2.60	0.44
1:B:115:LEU:HD12	1:B:133:ILE:HD12	1.99	0.44
1:B:302:LEU:O	1:B:303:VAL:C	2.61	0.44
1:B:1191:SER:O	1:B:1192:LYS:C	2.61	0.44
1:B:1952:PHE:CZ	1:B:1969:VAL:HG12	2.53	0.44
1:B:2060:ILE:HG12	1:B:2074:LEU:HD12	2.00	0.44
1:B:3251:LEU:HD12	1:B:3303:PHE:CD2	2.52	0.44
1:B:3626:GLU:OE1	1:B:3628:LYS:HE3	2.17	0.44
1:B:3998:LEU:O	1:B:4001:VAL:HG12	2.18	0.44
2:D:86:ILE:CD1	2:D:146:MET:HG2	2.48	0.44
1:A:867:HIS:CD2	1:A:947:ARG:HD2	2.52	0.44
1:A:1098:ILE:O	1:A:1101:PHE:HB2	2.18	0.44
1:A:1378:GLU:HG2	1:A:1426:ARG:HG3	2.00	0.44
1:A:2973:VAL:O	1:A:2976:MET:HG3	2.17	0.44
1:A:3889:ALA:HB2	3:E:293:LEU:HD13	2.00	0.44
1:B:185:ARG:HA	1:B:185:ARG:HE	1.83	0.44
1:B:648:LEU:HD23	1:B:648:LEU:HA	1.69	0.44
1:B:1429:LYS:O	1:B:1432:THR:N	2.51	0.44
1:B:1480:ASP:HB3	1:B:1483:ASP:HB2	2.00	0.44
1:B:2151:ILE:HD12	1:B:2162:PRO:HD2	1.99	0.44
1:B:3087:ALA:CA	1:B:3181:ILE:HD13	2.47	0.44
1:B:3269:LEU:HB3	1:B:3633:LEU:HD12	1.92	0.44
1:B:3305:LEU:HB2	1:B:3323:LEU:HD21	1.99	0.44
1:B:3571:ILE:HG12	1:B:3717:ALA:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4606:VAL:HG13	1:B:4612:VAL:HG12	1.99	0.44
2:D:147:THR:O	2:D:148:ALA:C	2.60	0.44
3:E:301:MET:HE1	3:E:305:GLU:HG2	2.00	0.44
1:A:1039:LEU:HD22	1:A:1130:LYS:CD	2.48	0.44
1:A:1048:SER:O	1:A:1051:VAL:HB	2.18	0.44
1:A:1130:LYS:O	1:A:1131:VAL:C	2.59	0.44
1:A:1299:ILE:HG22	1:A:1336:ARG:HH11	1.83	0.44
1:A:1474:SER:CB	1:A:1485:ILE:HG21	2.48	0.44
1:A:1571:LEU:O	1:A:1573:GLN:N	2.51	0.44
1:A:4115:ARG:NH2	2:C:125:MET:SD	2.91	0.44
1:B:155:MET:C	1:B:157:SER:N	2.74	0.44
1:B:1077:THR:C	1:B:1078:THR:HG1	2.26	0.44
1:B:1355:ILE:HD13	1:B:1397:MET:CG	2.47	0.44
1:B:1468:LEU:O	1:B:1472:THR:HG23	2.17	0.44
1:B:2973:VAL:O	1:B:2977:LEU:HB2	2.18	0.44
1:B:3899:ILE:O	1:B:3903:GLN:HG2	2.18	0.44
1:B:3922:ARG:NH1	1:B:3970:TYR:OH	2.50	0.44
2:C:145:MET:HE3	2:C:145:MET:HB3	1.90	0.44
3:F:301:MET:HE1	3:F:305:GLU:HG2	2.00	0.44
1:A:34:ARG:HB3	1:A:35:PRO:HD3	2.00	0.43
1:A:261:LEU:HD23	1:A:332:LEU:HD13	1.99	0.43
1:A:321:LEU:HD23	1:A:321:LEU:HA	1.86	0.43
1:A:1197:GLY:C	1:A:1372:LEU:HD21	2.43	0.43
1:A:2072:THR:O	1:A:2090:ASN:HB2	2.18	0.43
1:A:2194:PRO:HD3	1:A:2251:TYR:CE1	2.52	0.43
1:A:4101:TYR:CD2	2:C:89:ALA:HB2	2.53	0.43
1:A:4159:LYS:HE2	1:A:4159:LYS:HB3	1.84	0.43
1:B:1000:GLN:HG3	1:B:1270:LEU:HD13	2.00	0.43
1:B:1815:LEU:HD12	1:B:2508:LEU:HD21	1.99	0.43
1:B:1854:MET:HE2	1:B:2152:LYS:N	2.32	0.43
1:B:4127:ASN:ND2	3:F:328:LEU:HD22	2.31	0.43
2:D:37:MET:HG2	2:D:69:PHE:HE1	1.83	0.43
2:D:101:ILE:N	2:D:137:VAL:O	2.48	0.43
1:A:539:SER:O	1:A:543:ARG:HD3	2.18	0.43
1:A:853:LEU:O	1:A:857:ARG:HG2	2.18	0.43
1:A:3083:SER:HB3	1:A:3178:ASN:HD22	1.84	0.43
1:A:3826:LYS:HE2	1:A:3826:LYS:HB3	1.84	0.43
1:A:4419:LEU:HD22	1:A:4459:LEU:HD12	1.99	0.43
1:B:1534:PHE:N	1:B:1535:PRO:HD2	2.33	0.43
1:B:3412:LEU:O	1:B:3416:LEU:HB2	2.18	0.43
1:B:3490:SER:O	1:B:3494:VAL:HG23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3746:ALA:HA	1:B:3749:VAL:HG22	1.99	0.43
1:B:3764:LEU:HD23	1:B:3764:LEU:HA	1.83	0.43
1:B:3972:MET:HG3	1:B:4011:ASN:O	2.18	0.43
1:B:4125:HIS:HA	1:B:4165:LEU:CD1	2.48	0.43
1:A:98:GLN:HG3	1:A:201:PHE:CZ	2.54	0.43
1:A:765:GLN:NE2	1:A:817:ILE:HG23	2.33	0.43
1:A:1811:VAL:HA	1:A:1814:MET:HE2	2.00	0.43
1:A:3308:SER:HA	1:A:3319:LEU:HD13	2.00	0.43
1:A:3317:PRO:HG3	1:A:3424:VAL:CG2	2.48	0.43
1:A:4146:CYS:HA	1:A:4186:LEU:HD22	2.00	0.43
1:A:4310:MET:HE3	1:A:4335:LEU:CD2	2.49	0.43
1:A:4360:GLU:CD	1:A:4366:ARG:HH21	2.26	0.43
1:B:280:ASN:HB3	1:B:283:PHE:HE1	1.84	0.43
1:B:3068:SER:HA	1:B:3075:CYS:HB2	2.00	0.43
1:B:4413:LYS:CD	1:B:4456:ILE:HD11	2.48	0.43
3:E:9:CYS:O	3:E:13:LEU:HA	2.18	0.43
3:E:23:LYS:HD3	3:E:114:ALA:HB1	2.00	0.43
1:A:110:PHE:O	1:A:114:ARG:HG2	2.18	0.43
1:A:197:LEU:HD23	1:A:197:LEU:HA	1.84	0.43
1:A:1178:LEU:HD21	1:A:1202:LEU:HD21	2.00	0.43
1:A:1192:LYS:HA	1:A:1195:LEU:HB2	2.00	0.43
1:A:2698:LYS:NZ	1:A:2998:PRO:O	2.52	0.43
1:A:3505:THR:OG1	1:A:3916:ARG:NH1	2.37	0.43
1:A:3595:ASN:HD21	1:A:3605:LEU:HD13	1.83	0.43
1:A:4278:VAL:O	1:B:3825:ARG:HD3	2.18	0.43
1:B:124:VAL:HG21	1:B:129:LEU:HD21	1.99	0.43
1:B:855:LEU:HD23	1:B:1002:TYR:HE2	1.82	0.43
1:B:1177:LEU:HD21	1:B:1233:TRP:HB2	1.99	0.43
1:B:1209:CYS:SG	1:B:1210:LYS:N	2.91	0.43
1:B:1244:ILE:HG12	1:B:1249:ASN:HB3	2.01	0.43
1:B:2675:ILE:C	1:B:2677:THR:N	2.75	0.43
1:B:2997:ILE:HB	1:B:2998:PRO:HD3	2.00	0.43
1:B:3301:LEU:HD21	1:B:3326:ALA:HB3	1.99	0.43
1:B:3889:ALA:HB2	3:F:293:LEU:HD13	1.99	0.43
1:B:4746:PRO:O	1:B:4750:LYS:HG3	2.18	0.43
2:D:130:ASP:OD2	2:D:135:GLY:N	2.48	0.43
3:E:21:ARG:HB3	3:E:55:ILE:HB	2.01	0.43
1:A:34:ARG:O	1:A:35:PRO:C	2.61	0.43
1:A:516:THR:HG22	1:A:518:ILE:H	1.84	0.43
1:A:864:TYR:HA	1:A:936:LEU:CD2	2.48	0.43
1:A:1021:ASN:OD1	1:A:1071:LEU:HD21	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2578:ARG:HD2	1:A:2659:ALA:CB	2.48	0.43
1:A:3173:LYS:HB3	1:A:3173:LYS:HE2	1.76	0.43
1:A:3773:GLU:HB3	1:A:3794:ARG:HE	1.83	0.43
1:A:3899:ILE:O	1:A:3903:GLN:HG2	2.19	0.43
1:A:3986:TRP:CZ2	3:E:316:ARG:HG2	2.54	0.43
1:A:4007:VAL:HG22	1:B:3511:ASN:HB2	2.00	0.43
1:A:4749:HIS:O	1:A:4753:GLN:HG3	2.18	0.43
1:B:428:ALA:O	1:B:432:LYS:HG2	2.18	0.43
1:B:796:GLN:HB2	1:B:798:VAL:HG23	2.00	0.43
1:B:1289:LEU:HD11	1:B:1325:SER:HB2	2.00	0.43
1:B:2038:TYR:C	1:B:2038:TYR:CD2	2.96	0.43
1:B:2984:THR:O	1:B:2987:GLN:N	2.51	0.43
1:B:3033:GLY:C	1:B:3035:ASP:N	2.76	0.43
1:B:3727:GLU:H	1:B:3731:ASP:HB2	1.82	0.43
1:B:4146:CYS:HA	1:B:4186:LEU:HD22	2.01	0.43
1:B:4159:LYS:HZ3	1:B:4196:TRP:CD1	2.36	0.43
2:C:54:ASN:C	2:C:56:VAL:N	2.77	0.43
1:A:773:ASP:HB3	1:A:774:PRO:HD2	1.99	0.43
1:A:872:ALA:O	1:B:186:GLN:NE2	2.52	0.43
1:A:1429:LYS:O	1:A:1432:THR:N	2.51	0.43
1:A:1707:SER:O	1:A:1708:TYR:C	2.62	0.43
1:A:4136:PRO:HB2	1:B:3508:PRO:HB3	2.00	0.43
1:A:4273:LEU:HD12	1:A:4291:LEU:HD12	2.00	0.43
1:B:793:ASN:O	1:B:797:GLY:N	2.52	0.43
1:B:1345:GLU:O	1:B:1349:ARG:HG2	2.18	0.43
1:B:1996:LEU:HD22	1:B:2019:THR:HG21	2.00	0.43
1:B:2683:MET:HE2	1:B:2999:TYR:OH	2.19	0.43
1:B:3001:GLN:HG3	1:B:3139:PHE:CZ	2.54	0.43
1:B:3301:LEU:HD21	1:B:3326:ALA:CB	2.48	0.43
2:C:100:TYR:CD1	2:C:136:GLN:HB3	2.54	0.43
1:A:270:ILE:HG12	1:A:335:SER:CB	2.48	0.43
1:A:317:VAL:HG12	1:A:318:LEU:H	1.82	0.43
1:A:420:LEU:O	1:A:424:LEU:HG	2.19	0.43
1:A:1332:ASN:HA	1:A:1335:GLU:CD	2.44	0.43
1:A:1521:MET:HB2	1:A:1537:LEU:HD21	1.99	0.43
1:A:1606:VAL:O	1:A:1610:LEU:HG	2.19	0.43
1:A:2305:GLY:HA2	1:A:2339:GLU:H	1.83	0.43
1:A:2340:ILE:HD13	1:A:2422:ILE:HD11	2.00	0.43
1:A:2363:ARG:NH1	1:A:2416:MET:HE1	2.34	0.43
1:A:2698:LYS:NZ	1:A:3002:VAL:HG23	2.33	0.43
1:A:3057:ARG:HG3	1:A:3141:LEU:HG	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4128:TRP:HA	1:A:4131:GLN:HG2	2.01	0.43
1:A:4318:LYS:HA	1:A:4491:ARG:HH22	1.83	0.43
1:A:4491:ARG:O	1:A:4495:ILE:HG13	2.19	0.43
1:B:66:HIS:NE2	1:B:71:GLU:HG2	2.33	0.43
1:B:257:LEU:HD23	1:B:257:LEU:HA	1.59	0.43
1:B:1038:THR:O	1:B:1039:LEU:C	2.61	0.43
1:B:1077:THR:HG23	1:B:1082:SER:H	1.84	0.43
1:B:1191:SER:N	1:B:1194:LYS:HD3	2.32	0.43
1:B:1388:LEU:C	1:B:1390:SER:H	2.26	0.43
1:B:3540:VAL:HB	1:B:3718:LYS:HD2	1.99	0.43
1:B:4024:ILE:HD11	3:F:324:LEU:HD12	2.00	0.43
1:B:4414:ILE:HD11	1:B:4451:ALA:HB1	2.01	0.43
1:B:4601:ILE:HD11	1:B:4620:ILE:CD1	2.49	0.43
1:A:124:VAL:HG11	1:A:129:LEU:CD2	2.48	0.43
1:A:296:ARG:HA	1:A:299:PHE:CE2	2.54	0.43
1:A:404:GLN:OE1	1:A:404:GLN:HA	2.17	0.43
1:A:659:THR:HA	1:A:663:LEU:CD1	2.40	0.43
1:A:817:ILE:HG22	1:A:821:PHE:CE2	2.53	0.43
1:A:1281:ALA:HA	1:A:1284:LEU:CG	2.49	0.43
1:A:1394:ARG:HH11	1:A:1443:ASN:HD21	1.65	0.43
1:A:2661:VAL:HG11	1:A:2701:LEU:HG	2.01	0.43
1:A:2688:CYS:O	1:A:2689:PRO:C	2.61	0.43
1:A:3207:ARG:O	1:A:3211:ARG:HG3	2.18	0.43
1:B:321:LEU:HD12	1:B:395:SER:CB	2.49	0.43
1:B:862:PHE:CE1	1:B:866:LEU:HD11	2.53	0.43
1:B:2493:GLY:O	1:B:2498:LYS:HE3	2.19	0.43
1:B:2544:ASP:HA	1:B:2580:ILE:HD12	2.00	0.43
1:B:2564:ASP:OD2	1:B:2631:LYS:O	2.37	0.43
1:B:3095:VAL:HG11	1:B:3186:PHE:HE1	1.84	0.43
2:D:38:ARG:HD2	2:D:43:ASN:HA	2.00	0.43
1:A:255:LYS:O	1:A:259:VAL:HG23	2.19	0.43
1:A:732:LEU:HD21	1:A:760:LEU:HD12	2.00	0.43
1:A:1298:LEU:HA	1:A:1301:TRP:NE1	2.34	0.43
1:A:2023:VAL:HG21	1:A:2049:VAL:HG21	2.01	0.43
1:A:2368:ILE:HD11	1:A:2387:PHE:CZ	2.54	0.43
1:A:3490:SER:O	1:A:3494:VAL:HG23	2.18	0.43
1:A:4600:GLN:O	1:A:4601:ILE:C	2.62	0.43
1:B:282:PHE:HB3	1:B:420:LEU:HD11	1.99	0.43
1:B:1359:TYR:CE1	1:B:1406:GLU:HB3	2.53	0.43
1:B:1407:LEU:HB3	1:B:1431:PHE:CZ	2.51	0.43
1:B:1560:ALA:HB1	1:B:1599:ILE:HG23	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2027:ASP:CG	1:B:2029:CYS:SG	3.00	0.43
1:B:2622:ILE:HD11	1:B:2667:TYR:CB	2.47	0.43
1:B:3310:LEU:HG	1:B:3851:PHE:HB3	2.01	0.43
1:B:3409:ILE:HD13	1:B:3454:ILE:HD11	2.01	0.43
1:B:3460:ALA:O	1:B:3868:SER:N	2.40	0.43
1:B:3525:TYR:HE2	1:B:3874:GLY:HA2	1.84	0.43
3:F:317:SER:O	3:F:321:GLN:HG3	2.17	0.43
1:A:329:VAL:CG1	1:A:388:ILE:HD12	2.49	0.43
1:A:547:VAL:HA	1:A:550:ARG:HH11	1.83	0.43
1:A:811:LEU:HD23	1:A:933:TYR:HE1	1.84	0.43
1:A:852:PRO:O	1:A:853:LEU:C	2.61	0.43
1:A:1281:ALA:HB2	1:A:1284:LEU:HD12	2.01	0.43
1:A:2683:MET:HE3	1:A:2683:MET:HB2	1.90	0.43
1:A:2698:LYS:O	1:A:2702:ILE:HG13	2.19	0.43
1:A:3007:THR:O	1:A:3009:ASP:N	2.52	0.43
1:A:4477:GLY:CA	1:A:4518:VAL:HG11	2.46	0.43
1:B:29:TRP:CE3	1:B:73:PHE:HZ	2.37	0.43
1:B:194:LEU:HD13	1:B:194:LEU:HA	1.89	0.43
1:B:405:ASN:O	1:B:409:LEU:HG	2.19	0.43
1:B:801:SER:O	1:B:805:ASP:N	2.52	0.43
1:B:1514:LEU:O	1:B:1518:LEU:HG	2.19	0.43
1:B:2263:ILE:HG12	1:B:2655:ALA:HB1	2.00	0.43
1:B:3294:CYS:HB3	1:B:3301:LEU:HG	1.99	0.43
1:B:3295:ILE:HD12	1:B:3295:ILE:HA	1.93	0.43
1:B:4598:LEU:HD11	1:B:4634:LEU:HB2	2.00	0.43
1:B:4606:VAL:HG11	1:B:4616:LEU:HD22	2.00	0.43
1:B:4751:LEU:HD23	1:B:4751:LEU:HA	1.77	0.43
1:A:248:GLN:HB3	1:B:496:LEU:HD11	2.01	0.42
1:A:280:ASN:HB2	1:A:412:TRP:HE1	1.84	0.42
1:A:405:ASN:CB	1:A:511:ILE:HA	2.49	0.42
1:A:484:LEU:O	1:A:488:PHE:HD1	2.02	0.42
1:A:864:TYR:HD2	1:A:865:LEU:HD23	1.84	0.42
1:A:973:LEU:HD23	1:A:973:LEU:HA	1.85	0.42
1:A:1345:GLU:H	1:A:1345:GLU:CD	2.27	0.42
1:A:1859:MET:N	1:A:2200:GLN:OE1	2.43	0.42
1:A:2698:LYS:HG2	1:A:2998:PRO:HA	2.00	0.42
1:A:3021:LEU:O	1:A:3025:LEU:HG	2.18	0.42
1:A:3699:LEU:HD23	1:A:3706:CYS:HB2	2.01	0.42
1:A:4101:TYR:CE2	2:C:89:ALA:HB2	2.54	0.42
1:A:4622:TYR:HA	1:A:4670:LYS:HE3	2.00	0.42
1:B:256:LEU:HD12	1:B:317:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:265:TYR:HB3	1:B:302:LEU:HD13	2.01	0.42
1:B:654:ILE:O	1:B:658:ILE:HG13	2.19	0.42
1:B:881:GLN:HA	1:B:885:LEU:HD12	2.00	0.42
1:B:1032:GLU:O	1:B:1035:ILE:HB	2.19	0.42
1:B:1405:GLY:O	1:B:1409:GLN:HG2	2.18	0.42
1:B:2192:VAL:HG13	1:B:2197:PHE:HE1	1.82	0.42
1:B:3396:VAL:HG11	1:B:3438:ASN:CB	2.49	0.42
1:B:3986:TRP:CZ2	3:F:316:ARG:HG2	2.54	0.42
1:A:666:ARG:HA	1:A:671:ARG:HE	1.84	0.42
1:A:1269:HIS:ND1	1:A:1283:SER:HB3	2.35	0.42
1:A:1288:LEU:O	1:A:1292:VAL:HG23	2.18	0.42
1:A:1324:GLU:HA	1:A:1327:ALA:HB2	2.01	0.42
1:A:3440:SER:OG	1:A:3443:GLN:OE1	2.20	0.42
1:A:4003:ILE:HB	1:A:4008:VAL:HG11	2.01	0.42
1:A:4199:TYR:HE1	2:C:39:SER:HA	1.84	0.42
1:A:4727:ARG:O	1:A:4731:ILE:HG13	2.19	0.42
1:A:4744:SER:O	1:A:4748:LEU:HG	2.19	0.42
1:B:474:VAL:HG11	1:B:646:LEU:HG	1.99	0.42
1:B:866:LEU:HD13	1:B:1013:LEU:HD21	2.01	0.42
1:B:1177:LEU:HD23	1:B:1177:LEU:HA	1.84	0.42
1:B:1387:GLN:HB3	1:B:1397:MET:SD	2.59	0.42
1:B:1701:HIS:HB2	1:B:1706:ILE:HD11	2.01	0.42
1:B:3021:LEU:O	1:B:3025:LEU:HG	2.19	0.42
1:B:3525:TYR:CE2	1:B:3874:GLY:HA2	2.54	0.42
1:B:4360:GLU:CD	1:B:4366:ARG:HH21	2.25	0.42
2:D:45:THR:OG1	2:D:48:GLU:HG3	2.19	0.42
3:F:2:SER:H	3:F:59:VAL:HG21	1.84	0.42
1:A:718:VAL:HG13	1:A:760:LEU:CD2	2.49	0.42
1:A:1377:LEU:H	1:A:1377:LEU:HD12	1.84	0.42
1:A:2023:VAL:HG23	1:A:2046:ILE:HD13	2.02	0.42
1:A:3095:VAL:HG12	1:A:3190:TRP:CH2	2.54	0.42
1:A:3515:THR:HG21	1:A:3764:LEU:HD22	2.01	0.42
1:A:3736:VAL:HG12	1:A:3740:ASN:HD21	1.85	0.42
1:A:4570:LEU:HD13	1:A:4622:TYR:HB2	2.01	0.42
1:B:1097:GLN:HE21	1:B:1097:GLN:CA	2.31	0.42
1:B:1560:ALA:HB1	1:B:1599:ILE:CG2	2.49	0.42
1:B:1575:ASN:O	1:B:1579:LYS:HG3	2.20	0.42
1:B:2151:ILE:HD11	1:B:2164:LEU:HD21	2.01	0.42
1:B:2379:LEU:HD23	1:B:2379:LEU:H	1.84	0.42
1:B:3527:LEU:HD11	1:B:3757:ARG:HB2	2.00	0.42
1:B:3647:PHE:HB2	1:B:3649:GLU:HG3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:318:LEU:O	3:E:322:GLU:HG2	2.20	0.42
1:A:240:ILE:O	1:A:244:VAL:HG23	2.19	0.42
1:A:296:ARG:HA	1:A:299:PHE:CZ	2.54	0.42
1:A:317:VAL:C	1:A:318:LEU:HG	2.44	0.42
1:A:699:LYS:O	1:A:703:ASP:HB2	2.19	0.42
1:A:1556:LEU:HD21	1:A:1563:TRP:CZ3	2.54	0.42
1:A:2071:TYR:CE1	1:A:2091:VAL:HG22	2.55	0.42
1:A:2355:GLN:HB2	1:A:2384:TRP:CE2	2.55	0.42
1:A:2695:PHE:O	1:A:2698:LYS:HB3	2.19	0.42
1:A:3023:ASN:O	1:A:3027:GLN:HG2	2.19	0.42
1:A:4281:THR:HB	1:A:4284:ILE:HG12	2.00	0.42
1:A:4484:GLY:O	1:A:4485:LEU:C	2.62	0.42
1:B:154:MET:O	1:B:157:SER:OG	2.34	0.42
1:B:183:GLU:O	1:B:187:LYS:HG2	2.19	0.42
1:B:488:PHE:HE2	1:B:670:ILE:HD12	1.84	0.42
1:B:881:GLN:HA	1:B:885:LEU:HB2	2.01	0.42
1:B:1014:PRO:HB3	1:B:1057:HIS:CD2	2.55	0.42
1:B:1110:LEU:O	1:B:1175:ALA:HB1	2.20	0.42
1:B:1912:LEU:HB2	1:B:1926:LEU:HD11	2.02	0.42
1:B:2192:VAL:HG13	1:B:2197:PHE:CE1	2.54	0.42
1:B:3595:ASN:HD21	1:B:3605:LEU:HD13	1.83	0.42
1:B:4372:TYR:HD1	1:B:4376:GLU:OE2	2.02	0.42
2:D:66:PHE:HB3	2:D:67:PRO:HD3	2.01	0.42
1:A:856:ALA:HB1	1:A:1001:TYR:HD2	1.85	0.42
1:A:1057:HIS:HA	1:A:1060:LYS:HD2	2.01	0.42
1:A:1176:TYR:CZ	1:A:1280:LEU:HB2	2.55	0.42
1:A:1817:PHE:CE2	1:A:1818:LEU:HG	2.55	0.42
1:A:1854:MET:HE2	1:A:2152:LYS:H	1.83	0.42
1:A:3409:ILE:HD13	1:A:3454:ILE:HD11	2.01	0.42
1:A:4659:LEU:HG	1:A:4721:PHE:HB3	2.01	0.42
1:A:4716:ARG:HA	1:A:4717:PRO:HD3	1.94	0.42
1:B:1473:THR:O	1:B:1485:ILE:HG21	2.19	0.42
1:B:1867:GLU:HG2	1:B:2236:ASP:OD2	2.18	0.42
1:B:2009:PRO:CB	1:B:2642:LEU:HD21	2.50	0.42
1:B:4513:SER:O	1:B:4517:LYS:HG2	2.19	0.42
3:E:4:HIS:CD2	3:E:21:ARG:HB2	2.55	0.42
3:E:113:CYS:SG	3:E:131:HIS:CE1	3.13	0.42
1:A:926:ALA:O	1:A:928:PRO:HD3	2.19	0.42
1:A:2178:CYS:HB3	1:A:2214:MET:HE1	2.02	0.42
1:A:3195:SER:HG	1:A:3231:HIS:CE1	2.34	0.42
1:A:3997:PHE:HZ	1:A:4128:TRP:CE3	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:136:LEU:HD23	1:B:136:LEU:HA	1.82	0.42
1:B:313:LEU:HD21	1:B:332:LEU:CD2	2.49	0.42
1:B:352:VAL:HG21	1:B:424:LEU:HD13	2.02	0.42
1:B:1545:ALA:HB2	1:B:1556:LEU:CD2	2.48	0.42
1:B:1597:CYS:SG	1:B:2477:ARG:HB2	2.59	0.42
1:B:2405:ILE:CG1	1:B:2417:ILE:HD11	2.49	0.42
1:B:4119:LEU:HD11	3:F:329:VAL:HG11	2.00	0.42
1:B:4346:VAL:HG21	1:B:4425:TYR:CD1	2.55	0.42
3:E:111:PRO:HD2	3:E:128:PHE:CZ	2.54	0.42
3:E:295:ARG:HG2	3:E:295:ARG:O	2.19	0.42
3:F:295:ARG:HG2	3:F:295:ARG:O	2.19	0.42
3:F:318:LEU:O	3:F:322:GLU:HG2	2.20	0.42
1:A:112:LEU:HD13	1:A:252:GLY:HA3	2.02	0.42
1:A:273:PHE:CE1	1:A:334:LEU:HB3	2.54	0.42
1:A:415:LEU:HD21	1:A:484:LEU:HD11	2.01	0.42
1:A:1219:VAL:O	1:A:1227:GLN:NE2	2.53	0.42
1:A:1233:TRP:CH2	1:A:1281:ALA:HB1	2.54	0.42
1:A:1345:GLU:O	1:A:1349:ARG:HG2	2.19	0.42
1:A:2263:ILE:HA	1:A:2575:ILE:HD11	2.02	0.42
1:A:2266:MET:SD	1:A:2575:ILE:HG12	2.60	0.42
1:A:3295:ILE:HD12	1:A:3295:ILE:HA	1.84	0.42
1:A:3550:ILE:HD11	1:A:3715:LEU:HD12	2.01	0.42
1:A:3884:ILE:HD11	1:A:3913:ASN:ND2	2.34	0.42
1:B:30:GLU:H	1:B:30:GLU:HG3	1.66	0.42
1:B:131:LEU:HD11	1:B:142:ARG:HG3	2.01	0.42
1:B:2137:SER:O	1:B:2141:LEU:N	2.51	0.42
1:B:3269:LEU:HB3	1:B:3633:LEU:HD13	1.90	0.42
1:B:4491:ARG:O	1:B:4495:ILE:HG13	2.20	0.42
2:C:123:ASP:O	2:C:127:ARG:HG2	2.20	0.42
3:F:111:PRO:HD2	3:F:128:PHE:CZ	2.55	0.42
1:A:1090:VAL:HG21	1:A:1131:VAL:HG13	2.02	0.42
1:A:1138:HIS:HA	1:A:1141:LYS:HD3	2.02	0.42
1:A:1912:LEU:HB2	1:A:1926:LEU:HD11	2.02	0.42
1:A:2049:VAL:HG22	1:A:2063:ILE:HG12	2.01	0.42
1:A:2551:ALA:HA	1:A:2573:LEU:HD22	2.01	0.42
1:A:4414:ILE:HD11	1:A:4451:ALA:HB1	2.02	0.42
1:B:115:LEU:CD1	1:B:130:ILE:HG13	2.50	0.42
1:B:255:LYS:O	1:B:259:VAL:HG23	2.20	0.42
1:B:919:SER:HA	1:B:922:PHE:CD2	2.54	0.42
1:B:943:ASP:OD2	1:B:943:ASP:N	2.52	0.42
1:B:2300:ASP:OD1	1:B:2300:ASP:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2701:LEU:HD12	1:B:3002:VAL:CG2	2.50	0.42
2:C:34:GLY:HA2	2:C:37:MET:HE2	2.01	0.42
2:C:95:LYS:HE2	2:C:109:VAL:HG23	2.02	0.42
1:A:94:ARG:O	1:A:97:LEU:HB3	2.19	0.42
1:A:130:ILE:HD12	1:A:308:MET:HG3	2.02	0.42
1:A:150:THR:O	1:A:154:MET:HG3	2.20	0.42
1:A:1848:VAL:O	1:A:1850:LYS:NZ	2.38	0.42
1:A:2042:PRO:HD3	1:A:2088:VAL:O	2.20	0.42
1:A:3749:VAL:HG23	1:A:3814:LEU:HD13	2.02	0.42
1:A:3773:GLU:O	1:A:3774:LYS:C	2.63	0.42
1:B:414:LEU:HD12	1:B:483:LEU:HD12	2.01	0.42
1:B:1591:MET:O	1:B:1594:GLU:HG2	2.20	0.42
1:B:1693:CYS:N	1:B:1716:CYS:SG	2.92	0.42
1:B:2551:ALA:HA	1:B:2573:LEU:HD22	2.01	0.42
1:B:2686:LEU:HD11	1:B:3002:VAL:HG11	2.02	0.42
1:B:3050:GLU:O	1:B:3054:VAL:HG23	2.19	0.42
1:B:3061:VAL:O	1:B:3065:ARG:N	2.44	0.42
1:B:3076:GLU:H	1:B:3076:GLU:HG3	1.73	0.42
1:B:3233:LEU:HD13	1:B:3290:TRP:HE3	1.85	0.42
1:B:3699:LEU:HD23	1:B:3706:CYS:HB2	2.01	0.42
1:B:3922:ARG:O	1:B:3926:ARG:HG3	2.20	0.42
1:B:4224:GLU:HA	1:B:4279:GLN:NE2	2.35	0.42
1:B:4510:LYS:HE2	1:B:4514:TYR:OH	2.19	0.42
2:D:28:ILE:H	2:D:28:ILE:HG12	1.48	0.42
3:E:3:ARG:HG2	3:E:18:ARG:CG	2.50	0.42
1:A:124:VAL:HG11	1:A:129:LEU:HD23	2.02	0.42
1:A:336:CYS:SG	1:A:384:ILE:HD12	2.59	0.42
1:A:699:LYS:O	1:A:704:GLU:HG3	2.20	0.42
1:A:2405:ILE:CG1	1:A:2417:ILE:HD11	2.50	0.42
1:A:3269:LEU:HB3	1:A:3633:LEU:HD13	1.91	0.42
1:A:4328:PRO:O	1:A:4331:ILE:HB	2.19	0.42
1:A:4372:TYR:HD1	1:A:4376:GLU:OE2	2.02	0.42
1:A:4748:LEU:HB2	1:A:4768:LEU:HD21	2.02	0.42
1:B:159:LYS:HA	1:B:159:LYS:HD2	1.85	0.42
1:B:321:LEU:HD23	1:B:321:LEU:HA	1.87	0.42
1:B:1307:PRO:HB2	1:B:1308:PRO:HD3	2.01	0.42
1:B:1486:GLN:HG3	1:B:1489:ARG:NH1	2.35	0.42
1:B:1554:LEU:HA	1:B:1557:HIS:CD2	2.54	0.42
1:B:1563:TRP:HD1	1:B:1566:ARG:HH11	1.68	0.42
1:B:2369:GLU:HA	1:B:2373:ARG:O	2.20	0.42
1:B:2379:LEU:HB3	1:B:2385:PHE:HZ	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3054:VAL:HG13	1:B:3057:ARG:HD2	2.02	0.42
1:B:4273:LEU:HD22	1:B:4284:ILE:CG2	2.49	0.42
1:A:184:LEU:HD22	1:A:184:LEU:N	2.32	0.41
1:A:1046:ARG:HD2	1:A:1046:ARG:HA	1.88	0.41
1:A:3453:SER:O	1:A:3456:PRO:HD2	2.20	0.41
1:B:100:VAL:HG12	1:B:239:PHE:HE1	1.85	0.41
1:B:3988:LEU:HD12	1:B:3988:LEU:H	1.85	0.41
1:B:4309:PHE:CD1	1:B:4338:ILE:HD11	2.54	0.41
2:C:73:MET:O	2:C:77:MET:N	2.46	0.41
3:F:9:CYS:O	3:F:13:LEU:HA	2.19	0.41
3:F:81:PRO:HB2	3:F:108:VAL:HB	2.02	0.41
1:A:29:TRP:HA	1:A:32:ALA:HB3	2.01	0.41
1:A:292:ALA:O	1:A:296:ARG:HG3	2.19	0.41
1:A:643:ASP:HA	1:A:644:PRO:HD2	1.96	0.41
1:A:768:ALA:HA	1:A:773:ASP:HB2	2.01	0.41
1:A:853:LEU:HD13	1:A:998:ALA:HB2	2.02	0.41
1:A:1382:GLN:N	1:A:1426:ARG:HH21	2.18	0.41
1:A:1682:HIS:HA	1:A:2381:ARG:NH2	2.35	0.41
1:A:2038:TYR:C	1:A:2038:TYR:CD2	2.96	0.41
1:A:2118:VAL:HG11	1:A:2174:PRO:HB3	2.03	0.41
1:A:3167:LEU:HB3	1:A:3168:PRO:CD	2.43	0.41
1:A:3396:VAL:HG11	1:A:3438:ASN:CB	2.49	0.41
1:A:3771:ALA:HB1	1:B:3919:ALA:HB2	2.02	0.41
1:A:3922:ARG:O	1:A:3926:ARG:HG3	2.20	0.41
1:A:4492:LEU:HD23	1:A:4492:LEU:HA	1.87	0.41
1:A:4710:TRP:HZ3	1:A:4751:LEU:HD23	1.86	0.41
1:B:943:ASP:HB3	1:B:1255:THR:HG21	2.01	0.41
1:B:1679:TYR:HB2	1:B:1692:VAL:HG22	2.02	0.41
1:B:1805:PHE:CD2	1:B:2494:PRO:HD2	2.52	0.41
1:B:2046:ILE:HG23	1:B:2063:ILE:HG23	2.01	0.41
1:B:2118:VAL:HG11	1:B:2174:PRO:HB3	2.02	0.41
1:B:2259:PRO:HB2	1:B:2651:THR:HG21	2.00	0.41
1:B:2593:GLU:HG3	1:B:2667:TYR:OH	2.20	0.41
1:B:3729:GLU:HA	1:B:3732:ARG:HB3	2.02	0.41
1:B:3884:ILE:HD11	1:B:3913:ASN:ND2	2.34	0.41
1:B:4307:LYS:HG2	1:B:4478:VAL:CG1	2.50	0.41
1:B:4695:MET:HE1	1:B:4748:LEU:HD21	2.01	0.41
1:A:73:PHE:HD2	1:A:74:TYR:HD1	1.67	0.41
1:A:366:LYS:HA	1:A:369:ASP:CG	2.45	0.41
1:A:694:ASP:CB	1:A:750:HIS:HB3	2.50	0.41
1:A:995:GLU:O	1:A:999:LEU:HG	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1060:LYS:O	1:A:1061:GLN:C	2.63	0.41
1:A:1194:LYS:HA	1:A:1370:SER:O	2.20	0.41
1:A:1201:VAL:HG13	1:A:1218:LEU:HB3	2.02	0.41
1:A:2639:ASN:HB3	1:A:2642:LEU:HG	2.01	0.41
1:A:3053:LEU:HA	1:A:3056:MET:HE2	2.01	0.41
1:A:3099:LEU:HD22	1:A:3190:TRP:CE2	2.55	0.41
1:A:3470:ASP:OD1	3:E:293:LEU:HG	2.21	0.41
1:A:3964:LEU:HA	1:A:3967:SER:HB2	2.02	0.41
1:A:3991:ARG:HA	1:A:4059:TRP:CZ3	2.55	0.41
1:A:4699:ILE:HA	1:A:4700:PRO:HD3	1.94	0.41
1:B:320:PRO:O	1:B:325:ARG:NH1	2.49	0.41
1:B:321:LEU:HD12	1:B:395:SER:HB2	2.03	0.41
1:B:655:LEU:HD23	1:B:655:LEU:HA	1.75	0.41
1:B:1243:ASN:OD1	1:B:1243:ASN:N	2.53	0.41
1:B:1678:TRP:CD1	1:B:1678:TRP:H	2.39	0.41
1:B:1859:MET:N	1:B:2200:GLN:OE1	2.43	0.41
1:B:2187:PRO:HB3	1:B:2214:MET:SD	2.59	0.41
1:B:3320:LEU:HD23	1:B:3320:LEU:HA	1.92	0.41
1:B:3387:GLN:HG2	1:B:3388:GLU:N	2.35	0.41
1:B:4108:PHE:HA	1:B:4111:ARG:CG	2.50	0.41
1:B:4363:LEU:HD21	1:B:4444:MET:HG3	2.00	0.41
2:C:10:ILE:HG13	2:C:66:PHE:CZ	2.55	0.41
3:F:5:GLU:HA	3:F:16:ASN:OD1	2.21	0.41
1:A:29:TRP:O	1:A:33:VAL:HG13	2.19	0.41
1:A:1204:ILE:HD11	1:A:1357:GLY:CA	2.50	0.41
1:A:1232:SER:O	1:A:1236:ILE:HG13	2.21	0.41
1:A:1679:TYR:CE1	1:A:1708:TYR:HA	2.55	0.41
1:A:2479:VAL:HG21	1:A:2521:VAL:HG22	2.02	0.41
1:A:2517:ALA:CB	1:A:2521:VAL:HB	2.50	0.41
1:A:3181:ILE:HA	1:A:3182:PRO:HD3	1.88	0.41
1:A:3311:VAL:HB	1:A:3315:VAL:HB	2.03	0.41
1:A:4132:VAL:CG1	1:A:4145:ALA:HB2	2.50	0.41
1:A:4244:LEU:O	1:A:4248:PHE:HD1	2.03	0.41
1:B:139:GLY:HA2	1:B:240:ILE:HD11	2.02	0.41
1:B:310:LEU:HA	1:B:313:LEU:HB2	2.03	0.41
1:B:310:LEU:O	1:B:314:SER:N	2.50	0.41
1:B:422:LEU:HD11	1:B:537:LEU:HG	2.02	0.41
1:B:1132:GLN:HE22	1:B:1293:ARG:HH21	1.69	0.41
1:B:1244:ILE:HG21	1:B:1249:ASN:HB3	2.01	0.41
1:B:1428:LEU:HB3	1:B:1491:LEU:CB	2.51	0.41
1:B:1600:MET:HG2	1:B:2478:LEU:HD12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2025:ILE:HD13	1:B:2075:MET:CE	2.50	0.41
1:B:3102:LEU:O	1:B:3197:TYR:OH	2.31	0.41
1:B:4129:LEU:HD12	1:B:4129:LEU:HA	1.85	0.41
1:B:4187:TYR:O	1:B:4191:ILE:HG12	2.21	0.41
1:B:4331:ILE:O	1:B:4335:LEU:HG	2.21	0.41
2:C:131:ILE:HD11	2:C:144:GLN:HG2	2.03	0.41
1:A:108:ILE:O	1:A:112:LEU:HG	2.20	0.41
1:A:418:LEU:O	1:A:422:LEU:HG	2.21	0.41
1:A:1178:LEU:CD2	1:A:1202:LEU:HD21	2.50	0.41
1:A:1294:LEU:O	1:A:1298:LEU:HG	2.20	0.41
1:A:2025:ILE:HD13	1:A:2075:MET:CE	2.50	0.41
1:A:3142:ARG:HA	1:A:3142:ARG:HD3	1.85	0.41
1:A:4767:LEU:O	1:A:4771:LEU:HG	2.21	0.41
1:B:114:ARG:HD3	1:B:114:ARG:HA	1.68	0.41
1:B:694:ASP:OD2	1:B:750:HIS:HB3	2.20	0.41
1:B:808:VAL:HG11	1:B:908:TYR:CB	2.49	0.41
1:B:936:LEU:HD13	1:B:1008:ARG:NH2	2.35	0.41
1:B:1374:GLU:OE1	1:B:1423:PHE:HB2	2.21	0.41
1:B:2058:LYS:HB2	1:B:2074:LEU:HD11	2.01	0.41
1:B:2564:ASP:OD1	1:B:2631:LYS:HD3	2.20	0.41
1:B:2985:LEU:HA	1:B:2988:LEU:HD13	2.02	0.41
1:B:3311:VAL:HG23	1:B:3312:ASP:O	2.20	0.41
1:B:3396:VAL:HG11	1:B:3438:ASN:HB3	2.02	0.41
1:B:3512:ILE:HD11	1:B:3761:GLU:HG2	2.02	0.41
1:B:3901:VAL:HG11	1:B:3939:ALA:HB2	2.02	0.41
1:B:4244:LEU:O	1:B:4248:PHE:HD1	2.03	0.41
1:B:4727:ARG:NE	1:B:4766:ASN:HB3	2.35	0.41
1:A:418:LEU:HD11	1:A:477:ALA:HA	2.01	0.41
1:A:481:ILE:O	1:A:485:THR:HG23	2.20	0.41
1:A:548:LEU:HD22	1:A:642:LYS:HA	2.02	0.41
1:A:693:VAL:HG21	1:A:710:LEU:HD22	2.02	0.41
1:A:834:VAL:HG11	1:A:961:VAL:HG13	2.03	0.41
1:A:921:HIS:HB2	1:A:993:ALA:HB2	2.03	0.41
1:A:1178:LEU:HA	1:A:1181:PHE:CE2	2.55	0.41
1:A:1255:THR:OG1	1:A:1256:ILE:N	2.54	0.41
1:A:1536:GLU:O	1:A:1540:VAL:HG23	2.20	0.41
1:A:1556:LEU:HD13	1:A:1560:ALA:HB2	2.01	0.41
1:A:2054:ASN:HB3	1:A:2060:ILE:HD11	2.02	0.41
1:A:3053:LEU:HD22	1:A:3156:TYR:CD1	2.55	0.41
1:A:3463:ARG:NH2	1:A:3538:PRO:HA	2.35	0.41
1:A:3519:LEU:CD1	1:A:3767:VAL:HG11	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4108:PHE:HA	1:A:4111:ARG:CG	2.50	0.41
1:A:4694:TYR:CD1	1:A:4694:TYR:C	2.98	0.41
1:B:229:GLN:O	1:B:233:ILE:HG13	2.20	0.41
1:B:916:GLU:O	1:B:920:LYS:HG3	2.20	0.41
1:B:1388:LEU:HD23	1:B:1394:ARG:HG3	2.02	0.41
1:B:1475:PRO:HG2	1:B:1481:GLN:HB2	2.01	0.41
1:B:1590:VAL:HA	1:B:1593:LEU:HD13	2.01	0.41
1:B:2414:VAL:HG11	1:B:2416:MET:HE3	2.02	0.41
1:B:3087:ALA:CB	1:B:3181:ILE:CD1	2.89	0.41
1:A:325:ARG:O	1:A:326:LEU:C	2.64	0.41
1:A:414:LEU:HD12	1:A:483:LEU:HD12	2.01	0.41
1:A:942:GLU:HB3	1:A:947:ARG:NE	2.35	0.41
1:A:1268:ALA:O	1:A:1272:THR:HG23	2.20	0.41
1:A:1384:LEU:HD22	1:A:1384:LEU:HA	1.95	0.41
1:A:1729:LEU:HD23	1:A:1729:LEU:HA	1.90	0.41
1:A:1798:GLU:H	1:A:1798:GLU:CD	2.28	0.41
1:A:2311:VAL:HG11	3:E:64:TYR:CD1	2.56	0.41
1:A:3049:ASN:HB3	1:A:3156:TYR:OH	2.19	0.41
1:A:3283:ALA:HB1	1:A:3325:CYS:CB	2.50	0.41
1:A:4303:GLU:HB2	1:A:4475:MET:SD	2.60	0.41
1:A:4336:CYS:HB3	1:A:4514:TYR:HE2	1.85	0.41
1:A:4713:PHE:CE1	1:A:4751:LEU:HD21	2.44	0.41
1:B:1486:GLN:O	1:B:1490:GLN:HG3	2.20	0.41
1:B:1859:MET:CE	1:B:2230:MET:HB2	2.50	0.41
1:B:2094:ILE:HD13	1:B:2124:PHE:CZ	2.56	0.41
1:B:2687:LEU:O	1:B:2688:CYS:C	2.63	0.41
1:B:3003:ILE:O	1:B:3006:LEU:HB2	2.21	0.41
1:B:3105:LEU:HB2	1:B:3197:TYR:OH	2.21	0.41
1:B:3287:THR:OG1	1:B:3330:SER:HB3	2.20	0.41
1:B:3306:GLN:O	1:B:3309:PHE:HB2	2.21	0.41
1:B:3928:LEU:O	1:B:3932:LEU:HG	2.21	0.41
1:B:4562:VAL:O	1:B:4566:MET:HG3	2.20	0.41
1:B:4616:LEU:O	1:B:4620:ILE:HG13	2.21	0.41
2:C:83:GLU:HA	2:C:86:ILE:HB	2.03	0.41
1:A:108:ILE:HD11	1:A:243:ASN:HB3	2.03	0.41
1:A:925:ASP:N	1:A:925:ASP:OD1	2.54	0.41
1:A:1001:TYR:O	1:A:1005:ILE:HG13	2.21	0.41
1:A:1395:LYS:O	1:A:1399:GLU:HG2	2.21	0.41
1:A:1976:HIS:ND1	1:A:1989:HIS:NE2	2.57	0.41
1:A:2246:VAL:O	1:A:2250:SER:OG	2.37	0.41
1:A:2686:LEU:HD13	1:A:2999:TYR:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2975:LEU:HD11	1:A:3020:ALA:CB	2.51	0.41
1:A:3107:GLU:HA	1:A:3110:LYS:HD2	2.02	0.41
1:A:3450:LEU:O	1:A:3454:ILE:HG13	2.21	0.41
1:A:3522:PHE:HD1	1:A:3522:PHE:H	1.67	0.41
1:A:4759:GLY:O	1:A:4763:LEU:HG	2.21	0.41
1:B:132:LEU:HD21	1:B:143:LEU:CD1	2.50	0.41
1:B:1001:TYR:CE2	1:B:1005:ILE:HD11	2.56	0.41
1:B:1169:TYR:O	1:B:1173:THR:HG23	2.21	0.41
1:B:2044:SER:OG	1:B:2065:SER:HB2	2.20	0.41
1:B:2298:LEU:N	1:B:2422:ILE:O	2.43	0.41
1:B:3236:HIS:O	1:B:3240:ILE:HG12	2.21	0.41
1:B:3320:LEU:HD12	1:B:3424:VAL:HG13	2.03	0.41
1:B:4570:LEU:HD13	1:B:4622:TYR:HB3	2.03	0.41
2:D:121:GLU:O	2:D:122:VAL:C	2.60	0.41
3:F:89:THR:N	3:F:92:SER:OG	2.50	0.41
1:A:86:THR:CG2	1:A:141:SER:HB3	2.51	0.41
1:A:469:PHE:CZ	1:A:474:VAL:HG22	2.55	0.41
1:A:884:LEU:C	1:A:886:SER:H	2.29	0.41
1:A:1039:LEU:HB3	1:A:1130:LYS:HD2	2.03	0.41
1:A:1041:TRP:HA	1:A:1044:ARG:HG3	2.03	0.41
1:A:1133:VAL:HG22	1:A:1247:TRP:CE2	2.56	0.41
1:A:1210:LYS:HE3	1:A:1210:LYS:HB2	1.93	0.41
1:A:1515:LEU:HD11	1:A:1556:LEU:CD2	2.50	0.41
1:A:1952:PHE:HE1	1:A:1976:HIS:CD2	2.39	0.41
1:A:2229:THR:CG2	1:A:2241:ILE:HG23	2.51	0.41
1:A:2250:SER:O	1:A:2254:GLN:HG3	2.21	0.41
1:A:2301:VAL:HG13	1:A:2340:ILE:HG23	2.02	0.41
1:A:2311:VAL:HG11	3:E:64:TYR:CG	2.56	0.41
1:A:2324:THR:C	1:A:2326:MET:H	2.29	0.41
1:A:2506:GLN:HG3	1:A:2546:ALA:HB1	2.02	0.41
1:A:3053:LEU:HD22	1:A:3156:TYR:CE1	2.56	0.41
1:A:3098:CYS:O	1:A:3101:VAL:HG12	2.21	0.41
1:A:3105:LEU:HB2	1:A:3197:TYR:OH	2.21	0.41
1:A:3236:HIS:O	1:A:3240:ILE:HG12	2.21	0.41
1:A:3413:ARG:NH1	1:A:3457:GLU:OE1	2.41	0.41
1:A:3951:VAL:HA	1:A:3968:LEU:HD22	2.03	0.41
1:A:4077:ILE:HG22	2:C:114:GLY:O	2.21	0.41
1:A:4717:PRO:O	1:A:4720:PRO:HD2	2.21	0.41
1:B:120:GLU:H	1:B:120:GLU:HG3	1.59	0.41
1:B:348:ALA:CB	1:B:421:ILE:HG23	2.51	0.41
1:B:945:LEU:HG	1:B:946:ASN:OD1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1213:THR:O	1:B:1217:THR:HG23	2.20	0.41
1:B:2173:HIS:HE2	1:B:2253:LEU:HD11	1.86	0.41
1:B:2255:PRO:C	1:B:2257:LEU:H	2.29	0.41
1:B:2620:SER:C	1:B:2622:ILE:N	2.78	0.41
1:B:3031:GLU:O	1:B:3052:HIS:NE2	2.54	0.41
1:B:3453:SER:O	1:B:3456:PRO:HD2	2.20	0.41
1:B:4205:VAL:HG11	1:B:4248:PHE:CE2	2.56	0.41
1:B:4476:ALA:C	1:B:4521:ASN:HD21	2.25	0.41
2:D:106:LEU:O	2:D:110:MET:HG2	2.21	0.41
3:F:3:ARG:HG2	3:F:18:ARG:CG	2.49	0.41
3:F:94:GLN:HG3	3:F:132:LEU:HB3	2.03	0.41
1:A:478:ASN:O	1:A:482:LYS:HG3	2.20	0.41
1:A:659:THR:O	1:A:663:LEU:HB2	2.21	0.41
1:A:740:PHE:CD2	1:A:781:LYS:HG2	2.56	0.41
1:A:1051:VAL:HG13	1:A:1072:LEU:HG	2.02	0.41
1:A:1218:LEU:HD22	1:A:1376:ILE:HA	2.02	0.41
1:A:1240:GLU:H	1:A:1240:GLU:CD	2.29	0.41
1:A:1428:LEU:HD12	1:A:1488:ASN:HA	2.01	0.41
1:A:1664:CYS:SG	1:A:1666:PHE:HB3	2.61	0.41
1:A:1929:LEU:HD11	1:A:2241:ILE:HD11	2.02	0.41
1:A:2054:ASN:OD1	1:A:2058:LYS:N	2.53	0.41
1:A:4132:VAL:O	1:A:4133:LEU:C	2.64	0.41
1:A:4343:GLU:HB3	1:A:4426:LYS:NZ	2.36	0.41
1:B:268:ARG:HB3	1:B:272:ARG:HH21	1.85	0.41
1:B:1035:ILE:HD13	1:B:1035:ILE:HA	1.91	0.41
1:B:1870:PHE:HE2	1:B:2239:LEU:HD11	1.86	0.41
1:B:2191:MET:HB3	1:B:2198:LEU:HB2	2.03	0.41
1:B:2198:LEU:HD23	1:B:2198:LEU:HA	1.88	0.41
1:B:3000:MET:HE2	1:B:3000:MET:HB2	1.79	0.41
1:B:3095:VAL:HG11	1:B:3186:PHE:CE1	2.56	0.41
1:B:3439:SER:HB3	1:B:3443:GLN:HB2	2.03	0.41
1:B:3450:LEU:O	1:B:3454:ILE:HG13	2.21	0.41
1:B:3470:ASP:OD1	3:F:293:LEU:HG	2.20	0.41
1:B:3729:GLU:O	1:B:3730:GLU:C	2.64	0.41
1:B:4723:LEU:HD13	1:B:4763:LEU:HB2	2.01	0.41
2:C:79:ASP:OD1	2:C:79:ASP:N	2.54	0.41
1:A:73:PHE:CE1	1:A:155:MET:SD	3.14	0.40
1:A:484:LEU:HD22	1:A:530:LEU:HD11	2.03	0.40
1:A:1118:LEU:HD13	1:A:1273:LEU:HG	2.03	0.40
1:A:1499:ILE:HG22	1:A:1511:CYS:SG	2.60	0.40
1:A:1819:MET:HA	1:A:1822:ILE:HB	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2173:HIS:CD2	1:A:2253:LEU:CD1	2.87	0.40
1:A:2410:ASP:HA	1:A:2411:PRO:HD3	1.94	0.40
1:A:3044:GLU:O	1:A:3049:ASN:ND2	2.53	0.40
1:A:3968:LEU:O	1:A:3969:GLN:C	2.63	0.40
1:A:4195:HIS:NE2	2:C:35:THR:CG2	2.85	0.40
1:A:4714:LEU:HD11	1:A:4754:VAL:CG1	2.49	0.40
1:B:129:LEU:HD23	1:B:129:LEU:HA	1.88	0.40
1:B:337:LEU:HD12	1:B:337:LEU:HA	1.94	0.40
1:B:484:LEU:HB3	1:B:657:PHE:CZ	2.56	0.40
1:B:491:LEU:HD13	1:B:521:ILE:HG13	2.03	0.40
1:B:1104:ILE:HG23	1:B:1110:LEU:CD1	2.51	0.40
1:B:1236:ILE:CG2	1:B:1282:ALA:HB2	2.51	0.40
1:B:1845:LEU:HA	1:B:2194:PRO:HA	2.02	0.40
1:B:2316:GLN:HE22	3:F:76:GLN:CD	2.29	0.40
1:B:3179:SER:O	1:B:3180:ARG:C	2.65	0.40
1:B:3298:ASP:HB3	1:B:3398:GLN:CD	2.45	0.40
1:B:4031:SER:HB3	3:F:310:GLU:OE2	2.21	0.40
1:B:4059:TRP:CE3	3:F:323:LEU:HD21	2.56	0.40
1:B:4307:LYS:HG2	1:B:4478:VAL:HG13	2.01	0.40
1:A:112:LEU:HD11	1:A:247:LEU:HD12	2.04	0.40
1:A:234:LYS:O	1:A:238:VAL:HG23	2.21	0.40
1:A:317:VAL:O	1:A:318:LEU:C	2.63	0.40
1:A:671:ARG:HB3	1:A:722:LEU:HD11	2.03	0.40
1:A:741:SER:OG	1:A:785:ARG:NH1	2.54	0.40
1:A:1025:MET:HE2	1:A:1025:MET:HB3	1.88	0.40
1:A:1137:GLU:HG2	1:A:1141:LYS:HD2	2.04	0.40
1:A:1204:ILE:HG21	1:A:1218:LEU:HD12	2.03	0.40
1:A:1392:GLN:CD	1:A:1392:GLN:H	2.28	0.40
1:A:1996:LEU:HB3	1:A:2000:ASN:HB3	2.03	0.40
1:A:2060:ILE:HG12	1:A:2074:LEU:HD12	2.03	0.40
1:A:2369:GLU:HA	1:A:2373:ARG:O	2.20	0.40
1:A:4059:TRP:CE3	3:E:323:LEU:HD21	2.56	0.40
1:A:4127:ASN:C	1:A:4129:LEU:N	2.78	0.40
1:A:4187:TYR:O	1:A:4191:ILE:HG12	2.21	0.40
1:A:4201:ALA:HA	1:A:4205:VAL:HG12	2.03	0.40
1:A:4280:ARG:NH1	1:A:4285:ASP:OD2	2.52	0.40
1:A:4363:LEU:HD21	1:A:4444:MET:HG3	2.02	0.40
1:B:322:ASN:O	1:B:323:PRO:C	2.63	0.40
1:B:336:CYS:O	1:B:337:LEU:C	2.63	0.40
1:B:684:ALA:HA	1:B:734:GLN:HG3	2.03	0.40
1:B:905:THR:HG22	1:B:906:PRO:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1079:LYS:C	1:B:1081:SER:H	2.28	0.40
1:B:2042:PRO:HD3	1:B:2088:VAL:O	2.21	0.40
1:B:2220:THR:HG23	1:B:2224:GLU:HA	2.02	0.40
1:B:3289:ASN:HA	1:B:3292:LYS:NZ	2.36	0.40
1:B:3295:ILE:HD13	1:B:3395:LEU:HD23	2.03	0.40
1:B:3742:LEU:HD13	1:B:3820:LYS:HG2	2.03	0.40
1:B:4273:LEU:O	1:B:4280:ARG:NH2	2.53	0.40
1:B:4716:ARG:HA	1:B:4717:PRO:HD3	1.92	0.40
2:D:50:GLN:HA	2:D:53:ILE:HG22	2.03	0.40
3:F:65:TYR:HB3	3:F:70:PHE:CE2	2.56	0.40
1:A:81:SER:O	1:A:85:ILE:HG13	2.21	0.40
1:A:793:ASN:HB3	1:A:854:ILE:HG13	2.02	0.40
1:A:864:TYR:C	1:A:866:LEU:H	2.30	0.40
1:A:1055:LYS:O	1:A:1059:ILE:HG13	2.22	0.40
1:A:1063:MET:SD	1:A:1068:ALA:HB2	2.62	0.40
1:A:1806:SER:C	1:A:1809:PRO:HD2	2.47	0.40
1:A:3196:GLU:HA	1:A:3199:MET:HG2	2.02	0.40
1:A:4325:TYR:CE1	1:A:4495:ILE:HA	2.56	0.40
1:B:507:ALA:O	1:B:523:ARG:NE	2.51	0.40
1:B:791:LYS:HD3	1:B:836:ILE:HG12	2.03	0.40
1:B:833:PHE:HE1	1:B:858:LEU:HD22	1.87	0.40
1:B:855:LEU:CD2	1:B:1002:TYR:HE2	2.34	0.40
1:B:1110:LEU:H	1:B:1175:ALA:HB2	1.86	0.40
1:B:1242:PRO:HB2	1:B:1251:PHE:HZ	1.87	0.40
1:B:1528:ASN:HD22	1:B:1528:ASN:H	1.68	0.40
1:B:1822:ILE:CG2	1:B:1826:PHE:CE2	3.04	0.40
1:B:2702:ILE:HA	1:B:3005:MET:HG2	2.03	0.40
1:B:3013:GLU:HG2	1:B:3077:SER:HB3	2.03	0.40
1:B:3106:LEU:HG	1:B:3110:LYS:HE3	2.02	0.40
1:B:3177:THR:OG1	1:B:3178:ASN:N	2.55	0.40
1:B:3304:LEU:HD23	1:B:3304:LEU:HA	1.93	0.40
1:B:4132:VAL:HA	1:B:4135:THR:HG23	2.02	0.40
1:B:4596:MET:O	1:B:4600:GLN:HG2	2.21	0.40
1:A:193:PHE:CZ	1:B:816:LEU:HD21	2.56	0.40
1:A:545:ALA:HB1	1:A:648:LEU:HG	2.04	0.40
1:A:718:VAL:HG13	1:A:760:LEU:HG	2.03	0.40
1:A:918:TRP:HA	1:A:918:TRP:CE3	2.56	0.40
1:A:1176:TYR:CD1	1:A:1281:ALA:CB	3.05	0.40
1:A:1219:VAL:O	1:A:1222:LEU:HB2	2.20	0.40
1:A:1312:ARG:O	1:A:1316:PRO:HD3	2.21	0.40
1:A:1447:LEU:HA	1:A:1505:GLN:HG3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2302:GLU:HG3	1:A:2343:ASN:HD21	1.86	0.40
1:A:4251:VAL:HB	1:A:4254:ILE:HD12	2.02	0.40
1:B:408:LEU:HD13	1:B:520:ARG:HB3	2.04	0.40
1:B:952:ALA:O	1:B:956:LEU:HG	2.21	0.40
1:B:1109:ILE:HG23	1:B:1178:LEU:HD12	2.03	0.40
1:B:1127:ALA:O	1:B:1131:VAL:HG22	2.21	0.40
1:B:1314:LEU:HA	1:B:1317:LEU:HD12	2.02	0.40
1:B:1474:SER:HA	1:B:1485:ILE:CD1	2.51	0.40
1:B:2680:LYS:O	1:B:2684:GLN:HG3	2.22	0.40
1:B:2702:ILE:HD11	1:B:3001:GLN:CD	2.46	0.40
1:B:3556:TYR:O	1:B:3606:LYS:CE	2.67	0.40
1:B:3893:ASN:HB3	1:B:3896:LEU:HB2	2.03	0.40
1:B:4274:ARG:HB2	1:B:4288:GLN:HE22	1.86	0.40
1:B:4303:GLU:O	1:B:4307:LYS:HG3	2.21	0.40
1:B:4325:TYR:O	1:B:4329:VAL:HG23	2.22	0.40
1:B:4609:ASN:HB3	1:B:4612:VAL:HB	2.02	0.40
2:D:52:MET:O	2:D:55:GLU:HB3	2.21	0.40
1:A:268:ARG:O	1:A:272:ARG:HG3	2.22	0.40
1:A:659:THR:HA	1:A:663:LEU:HB2	2.02	0.40
1:A:1416:ASN:O	1:A:1470:ARG:NH1	2.52	0.40
1:A:3034:MET:HG2	1:A:3035:ASP:N	2.36	0.40
1:A:3393:THR:HA	1:A:3396:VAL:HG12	2.04	0.40
1:A:4601:ILE:HA	1:A:4606:VAL:HG11	2.02	0.40
1:B:31:VAL:O	1:B:35:PRO:CD	2.69	0.40
1:B:60:GLU:HG3	1:B:106:VAL:HG13	2.02	0.40
1:B:747:LEU:HD11	1:B:793:ASN:ND2	2.37	0.40
1:B:1424:CYS:O	1:B:1428:LEU:HG	2.21	0.40
1:B:1666:PHE:HA	1:B:1669:THR:OG1	2.21	0.40
1:B:2311:VAL:HG13	3:F:56:LEU:HD11	2.02	0.40
1:B:2686:LEU:CD2	1:B:3002:VAL:HG21	2.49	0.40
1:B:3789:SER:O	1:B:3797:LEU:HD11	2.21	0.40
1:B:4062:ARG:HB2	1:B:4062:ARG:NH1	2.37	0.40
1:B:4316:THR:O	1:B:4319:ARG:HB2	2.21	0.40
2:D:67:PRO:HA	2:D:70:LEU:HB3	2.04	0.40
2:D:137:VAL:CG1	2:D:141:GLU:HB2	2.50	0.40
2:D:143:VAL:O	2:D:147:THR:HG23	2.22	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	3853/5205 (74%)	3738 (97%)	115 (3%)	0	100	100
1	B	3884/5205 (75%)	3762 (97%)	122 (3%)	0	100	100
2	C	142/149 (95%)	136 (96%)	6 (4%)	0	100	100
2	D	139/149 (93%)	132 (95%)	7 (5%)	0	100	100
3	E	178/381 (47%)	175 (98%)	3 (2%)	0	100	100
3	F	178/381 (47%)	170 (96%)	8 (4%)	0	100	100
All	All	8374/11470 (73%)	8113 (97%)	261 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	3438/4542 (76%)	3329 (97%)	109 (3%)	34	59
1	B	3474/4542 (76%)	3347 (96%)	127 (4%)	29	54
2	C	123/127 (97%)	118 (96%)	5 (4%)	26	51
2	D	122/127 (96%)	115 (94%)	7 (6%)	17	43
3	E	162/330 (49%)	161 (99%)	1 (1%)	84	90
3	F	162/330 (49%)	159 (98%)	3 (2%)	52	71
All	All	7481/9998 (75%)	7229 (97%)	252 (3%)	34	57

All (252) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	VAL
1	A	44	PHE
1	A	69	GLN
1	A	92	ILE
1	A	94	ARG
1	A	97	LEU
1	A	100	VAL
1	A	191	MET
1	A	277	VAL
1	A	284	ILE
1	A	318	LEU
1	A	347	MET
1	A	401	GLU
1	A	444	VAL
1	A	530	LEU
1	A	686	LEU
1	A	722	LEU
1	A	771	GLN
1	A	799	VAL
1	A	807	ASN
1	A	813	MET
1	A	830	LEU
1	A	909	HIS
1	A	911	PHE
1	A	913	GLU
1	A	937	SER
1	A	984	ARG
1	A	1040	ARG
1	A	1045	LEU
1	A	1046	ARG
1	A	1061	GLN
1	A	1063	MET
1	A	1072	LEU
1	A	1113	HIS
1	A	1131	VAL
1	A	1154	ILE
1	A	1159	LEU
1	A	1173	THR
1	A	1177	LEU
1	A	1214	LEU
1	A	1244	ILE
1	A	1301	TRP

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Mol	Chain	Res	Type
1	A	1303	ASP
1	A	1318	LEU
1	A	1384	LEU
1	A	1471	MET
1	A	1481	GLN
1	A	1484	VAL
1	A	1485	ILE
1	A	1486	GLN
1	A	1496	THR
1	A	1500	VAL
1	A	1528	ASN
1	A	1553	HIS
1	A	1554	LEU
1	A	1556	LEU
1	A	1594	GLU
1	A	1607	THR
1	A	1690	VAL
1	A	1714	PHE
1	A	1894	LEU
1	A	1906	HIS
1	A	1950	VAL
1	A	1956	SER
1	A	2180	VAL
1	A	2184	THR
1	A	2204	THR
1	A	2301	VAL
1	A	2475	LEU
1	A	2488	SER
1	A	2667	TYR
1	A	2695	PHE
1	A	2698	LYS
1	A	2984	THR
1	A	2994	VAL
1	A	3056	MET
1	A	3108	TYR
1	A	3141	LEU
1	A	3159	LEU
1	A	3237	VAL
1	A	3286	ARG
1	A	3315	VAL
1	A	3332	VAL
1	A	3458	LEU

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Mol	Chain	Res	Type
1	A	3522	PHE
1	A	3536	ASN
1	A	3581	LEU
1	A	3765	CYS
1	A	3793	ASN
1	A	3866	HIS
1	A	3994	LEU
1	A	3999	MET
1	A	4007	VAL
1	A	4127	ASN
1	A	4129	LEU
1	A	4135	THR
1	A	4230	THR
1	A	4277	VAL
1	A	4309	PHE
1	A	4310	MET
1	A	4316	THR
1	A	4335	LEU
1	A	4400	LEU
1	A	4447	LEU
1	A	4478	VAL
1	A	4505	LEU
1	A	4520	VAL
1	A	4601	ILE
1	A	4616	LEU
1	B	33	VAL
1	B	37	LEU
1	B	70	TYR
1	B	86	THR
1	B	92	ILE
1	B	96	GLN
1	B	97	LEU
1	B	113	LEU
1	B	124	VAL
1	B	130	ILE
1	B	147	GLU
1	B	154	MET
1	B	194	LEU
1	B	200	VAL
1	B	204	ARG
1	B	243	ASN
1	B	283	PHE

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Mol	Chain	Res	Type
1	B	312	THR
1	B	313	LEU
1	B	318	LEU
1	B	325	ARG
1	B	367	GLU
1	B	378	VAL
1	B	379	GLN
1	B	381	CYS
1	B	408	LEU
1	B	424	LEU
1	B	448	LEU
1	B	511	ILE
1	B	528	VAL
1	B	677	SER
1	B	680	GLU
1	B	686	LEU
1	B	698	LEU
1	B	703	ASP
1	B	717	LEU
1	B	727	LEU
1	B	799	VAL
1	B	813	MET
1	B	830	LEU
1	B	844	MET
1	B	867	HIS
1	B	909	HIS
1	B	911	PHE
1	B	922	PHE
1	B	936	LEU
1	B	939	GLU
1	B	943	ASP
1	B	948	LEU
1	B	981	ASP
1	B	992	THR
1	B	1036	LEU
1	B	1040	ARG
1	B	1045	LEU
1	B	1057	HIS
1	B	1112	LEU
1	B	1131	VAL
1	B	1204	ILE
1	B	1212	ASN

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Mol	Chain	Res	Type
1	B	1240	GLU
1	B	1299	ILE
1	B	1318	LEU
1	B	1326	VAL
1	B	1334	LEU
1	B	1338	LEU
1	B	1358	CYS
1	B	1387	GLN
1	B	1392	GLN
1	B	1470	ARG
1	B	1474	SER
1	B	1486	GLN
1	B	1528	ASN
1	B	1536	GLU
1	B	1549	GLN
1	B	1553	HIS
1	B	1554	LEU
1	B	1557	HIS
1	B	1595	CYS
1	B	1597	CYS
1	B	1664	CYS
1	B	1800	GLN
1	B	1805	PHE
1	B	1817	PHE
1	B	1873	VAL
1	B	1934	ASP
1	B	2300	ASP
1	B	2301	VAL
1	B	2673	ASP
1	B	2676	ASN
1	B	2974	ARG
1	B	2982	LEU
1	B	2985	LEU
1	B	2995	ARG
1	B	3001	GLN
1	B	3002	VAL
1	B	3003	ILE
1	B	3005	MET
1	B	3034	MET
1	B	3038	ASP
1	B	3045	ARG
1	B	3049	ASN

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Mol	Chain	Res	Type
1	B	3050	GLU
1	B	3098	CYS
1	B	3197	TYR
1	B	3285	GLN
1	B	3286	ARG
1	B	3328	CYS
1	B	3458	LEU
1	B	3543	CYS
1	B	3581	LEU
1	B	3968	LEU
1	B	4135	THR
1	B	4228	LEU
1	B	4230	THR
1	B	4276	LEU
1	B	4277	VAL
1	B	4279	GLN
1	B	4297	ASP
1	B	4329	VAL
1	B	4331	ILE
1	B	4400	LEU
1	B	4447	LEU
1	B	4593	GLN
1	B	4612	VAL
1	B	4634	LEU
1	B	4752	GLU
1	B	4773	GLU
2	C	33	LEU
2	C	49	LEU
2	C	79	ASP
2	C	96	ASP
2	C	101	ILE
2	D	21	ASP
2	D	28	ILE
2	D	33	LEU
2	D	49	LEU
2	D	63	THR
2	D	64	ILE
2	D	105	GLU
3	E	131	HIS
3	F	70	PHE
3	F	131	HIS
3	F	136	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (140) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	GLN
1	A	98	GLN
1	A	196	GLN
1	A	229	GLN
1	A	243	ASN
1	A	271	ASN
1	A	274	GLN
1	A	327	GLN
1	A	402	HIS
1	A	407	GLN
1	A	466	HIS
1	A	479	HIS
1	A	664	ASN
1	A	712	HIS
1	A	714	ASN
1	A	729	ASN
1	A	792	GLN
1	A	867	HIS
1	A	868	GLN
1	A	879	GLN
1	A	881	GLN
1	A	917	ASN
1	A	1067	HIS
1	A	1182	ASN
1	A	1227	GLN
1	A	1253	ASN
1	A	1364	ASN
1	A	1365	HIS
1	A	1418	ASN
1	A	1481	GLN
1	A	1486	GLN
1	A	1493	GLN
1	A	1553	HIS
1	A	1598	HIS
1	A	1682	HIS
1	A	1802	GLN
1	A	1892	HIS
1	A	1916	HIS
1	A	2296	GLN
1	A	2343	ASN
1	A	2990	ASN

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Mol	Chain	Res	Type
1	A	3023	ASN
1	A	3148	HIS
1	A	3178	ASN
1	A	3321	GLN
1	A	3397	ASN
1	A	3410	GLN
1	A	3491	GLN
1	A	3536	ASN
1	A	3591	ASN
1	A	3639	ASN
1	A	3683	GLN
1	A	3740	ASN
1	A	3759	GLN
1	A	3835	GLN
1	A	4011	ASN
1	A	4127	ASN
1	A	4161	GLN
1	A	4234	GLN
1	A	4279	GLN
1	A	4490	ASN
1	A	4602	ASN
1	B	69	GLN
1	B	83	HIS
1	B	98	GLN
1	B	192	ASN
1	B	229	GLN
1	B	243	ASN
1	B	262	ASN
1	B	274	GLN
1	B	379	GLN
1	B	407	GLN
1	B	656	ASN
1	B	729	ASN
1	B	867	HIS
1	B	881	GLN
1	B	882	HIS
1	B	921	HIS
1	B	979	GLN
1	B	1022	GLN
1	B	1097	GLN
1	B	1111	GLN
1	B	1113	HIS

Continued on next page...

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Mol	Chain	Res	Type
1	B	1132	GLN
1	B	1227	GLN
1	B	1234	ASN
1	B	1266	GLN
1	B	1306	ASN
1	B	1309	GLN
1	B	1364	ASN
1	B	1387	GLN
1	B	1418	ASN
1	B	1486	GLN
1	B	1493	GLN
1	B	1528	ASN
1	B	1553	HIS
1	B	1558	ASN
1	B	1573	GLN
1	B	1800	GLN
1	B	1925	GLN
1	B	2182	GLN
1	B	2219	HIS
1	B	2258	GLN
1	B	2294	HIS
1	B	2296	GLN
1	B	2316	GLN
1	B	2319	HIS
1	B	2522	GLN
1	B	2524	GLN
1	B	2699	GLN
1	B	2983	GLN
1	B	2990	ASN
1	B	3001	GLN
1	B	3049	ASN
1	B	3209	GLN
1	B	3397	ASN
1	B	3438	ASN
1	B	3491	GLN
1	B	3591	ASN
1	B	3639	ASN
1	B	3683	GLN
1	B	3740	ASN
1	B	3756	HIS
1	B	3835	GLN
1	B	3848	GLN

Continued on next page...

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Mol	Chain	Res	Type
1	B	4002	ASN
1	B	4021	GLN
1	B	4233	GLN
1	B	4490	ASN
1	B	4602	ASN
1	B	4766	ASN
2	C	43	ASN
2	C	54	ASN
2	C	98	ASN
2	C	138	ASN
2	D	54	ASN
2	D	61	ASN
2	D	98	ASN
3	F	74	GLN
3	F	76	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 24 ligands modelled in this entry, 24 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

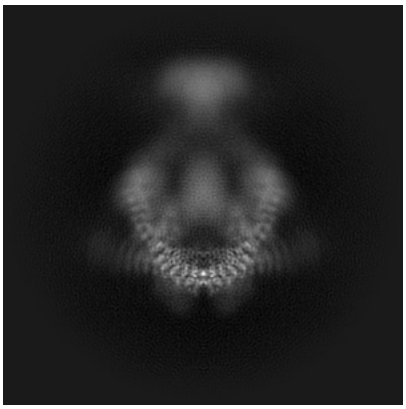
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-46686. These allow visual inspection of the internal detail of the map and identification of artifacts.

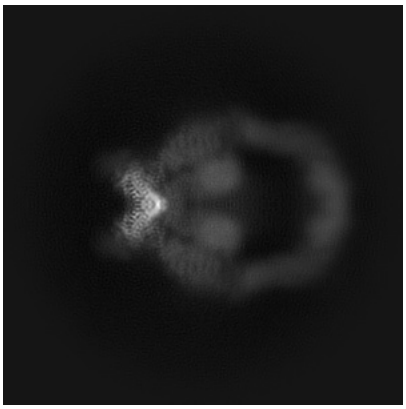
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

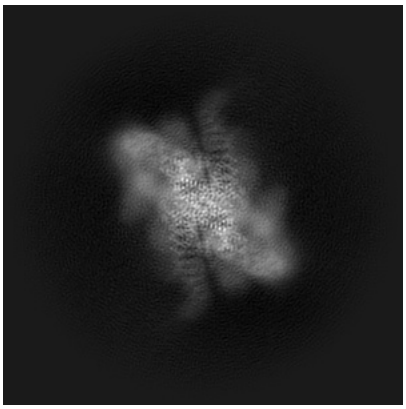
6.1.1 Primary map



X

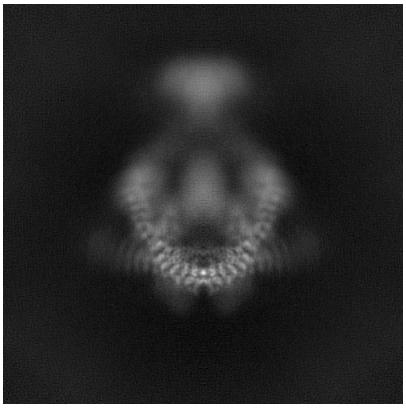


Y

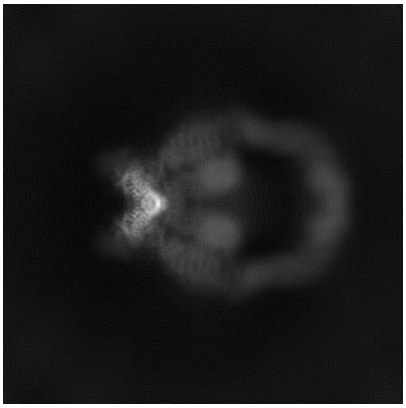


Z

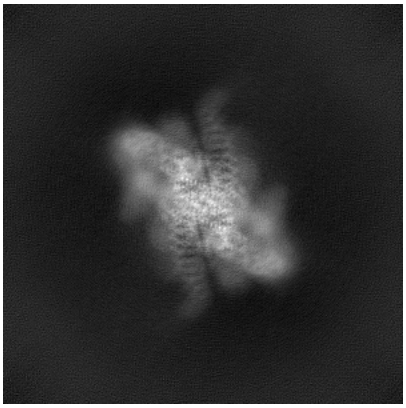
6.1.2 Raw map



X



Y

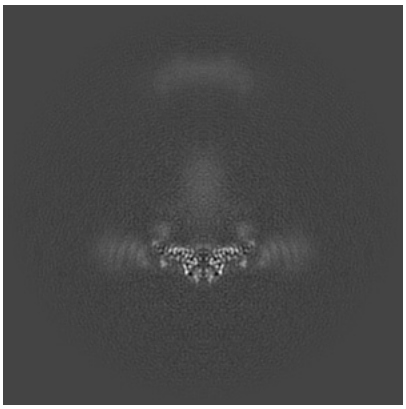


Z

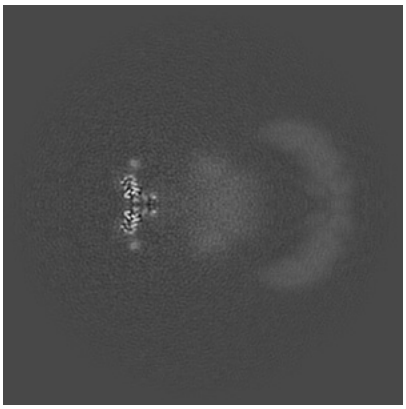
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

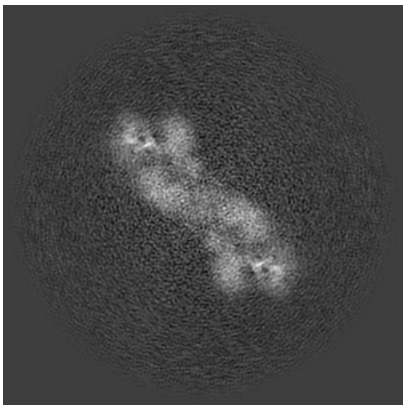
6.2.1 Primary map



X Index: 210



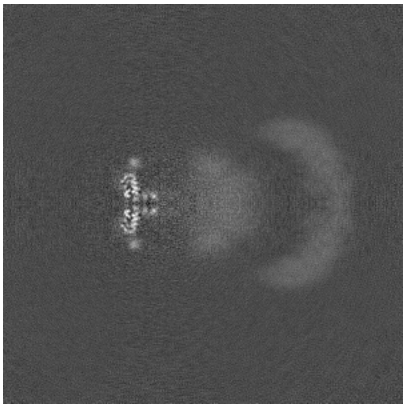
Y Index: 210



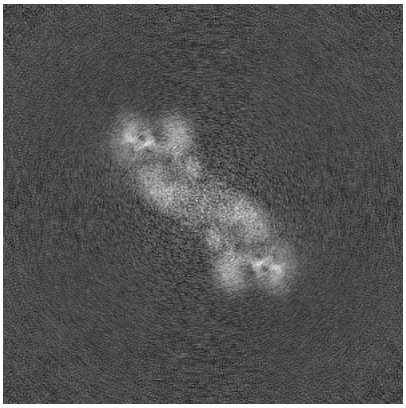
Z Index: 210

6.2.2 Raw map

X Index: 210



Y Index: 210



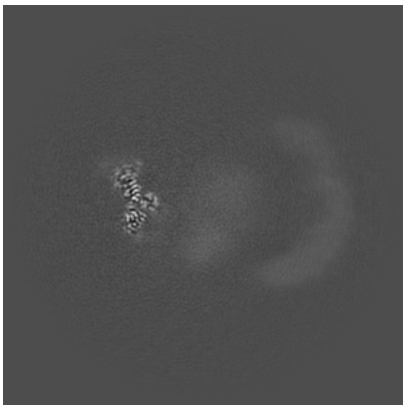
Z Index: 210

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

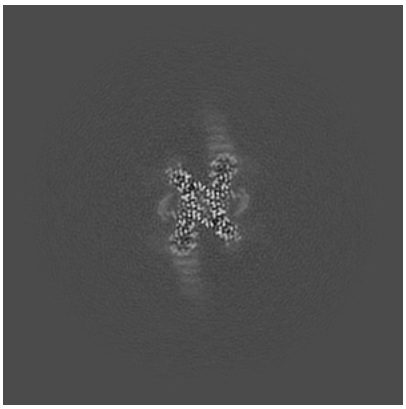
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 193

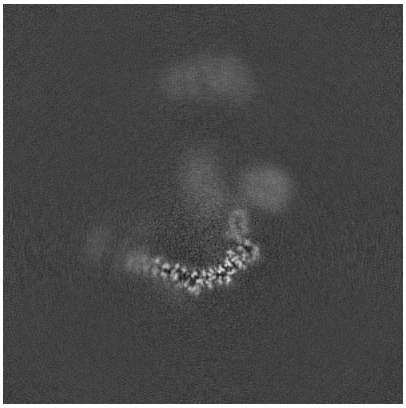


Y Index: 221

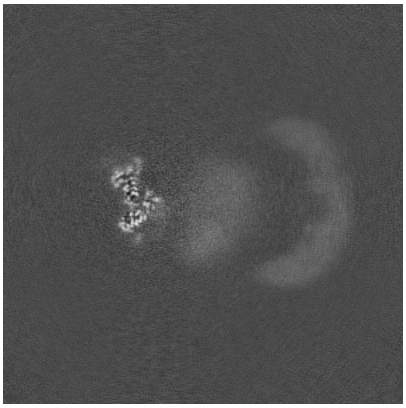


Z Index: 140

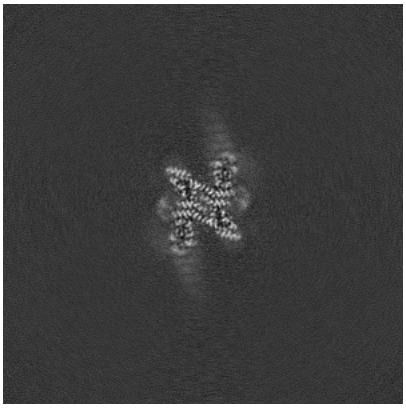
6.3.2 Raw map



X Index: 188



Y Index: 218

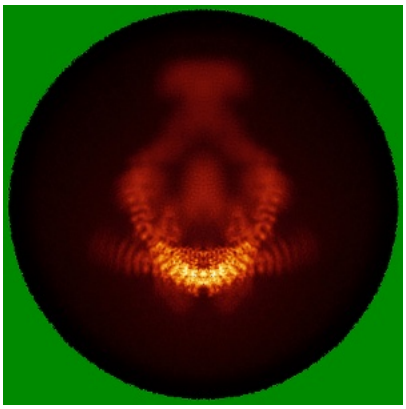


Z Index: 138

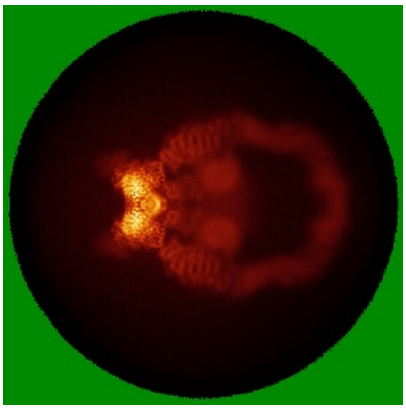
The images above show the largest variance slices of the map in three orthogonal directions.

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

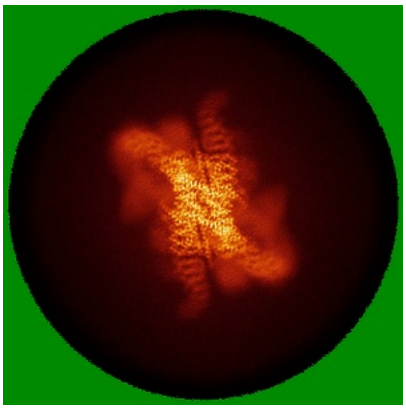
6.4.1 Primary map



X

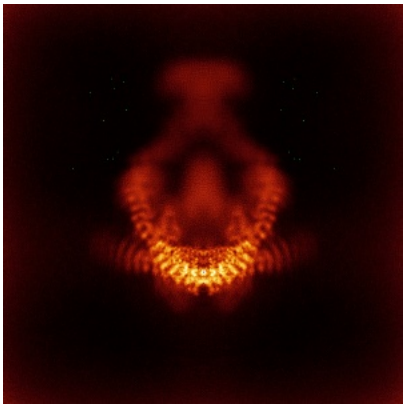


Y

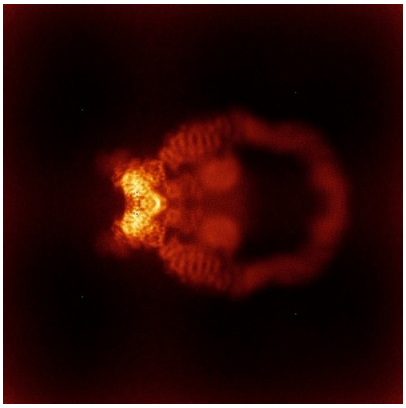


Z

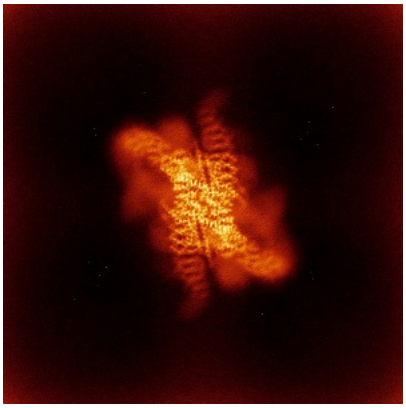
6.4.2 Raw map



X



Y

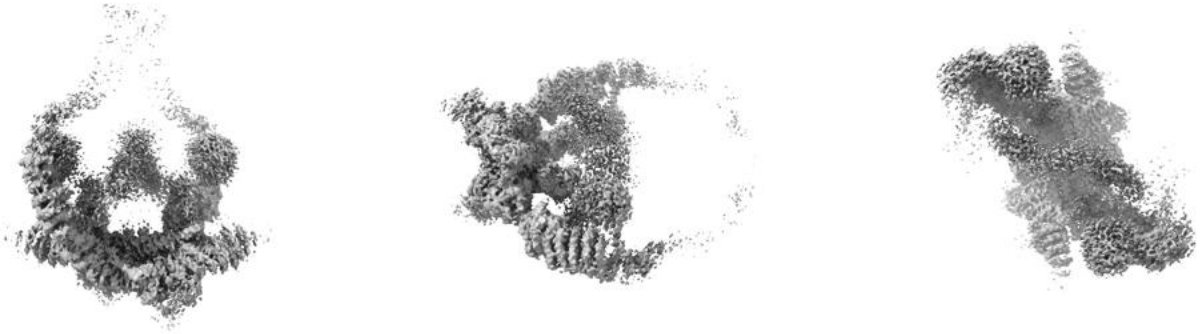


Z

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

6.5 Orthogonal surface views (i)

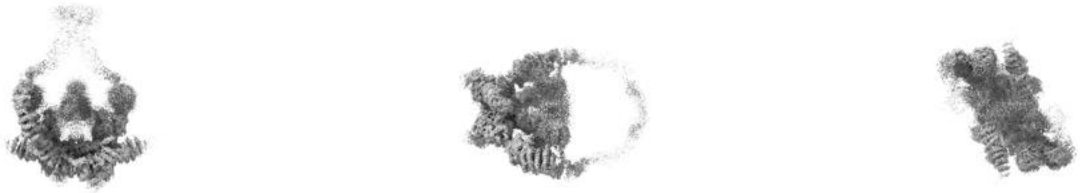
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

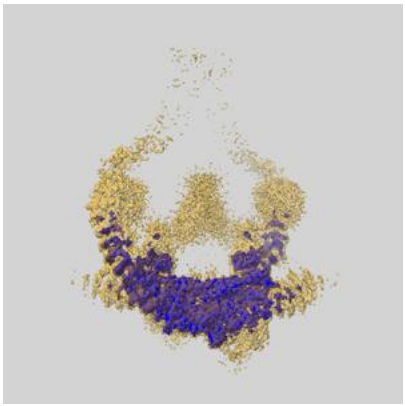
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

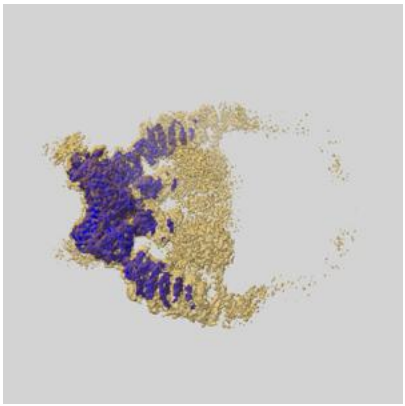
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

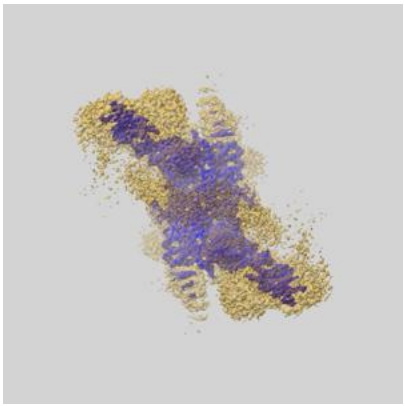
6.6.1 emd_46686_msk_1.map (i)



X



Y

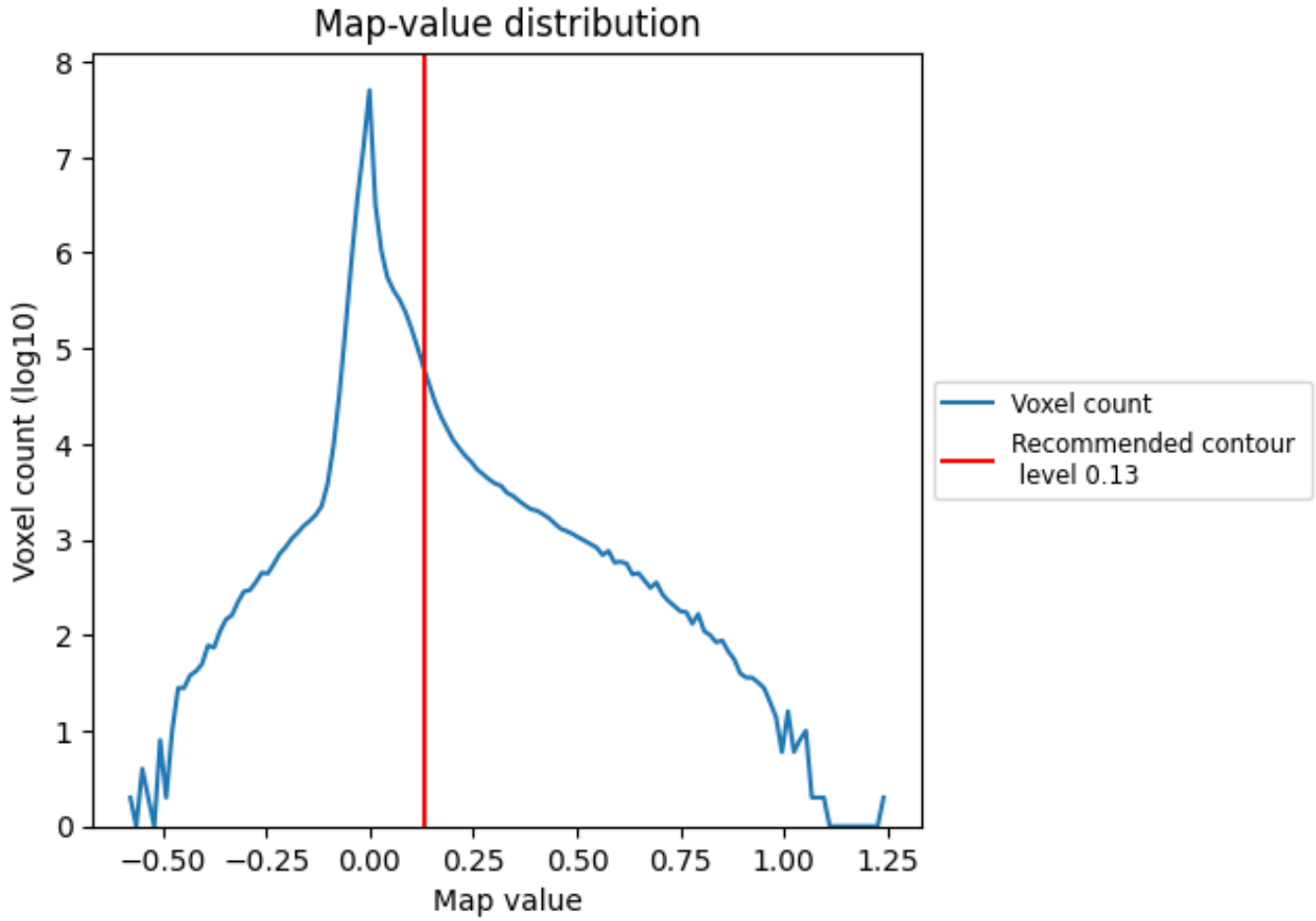


Z

7 Map analysis

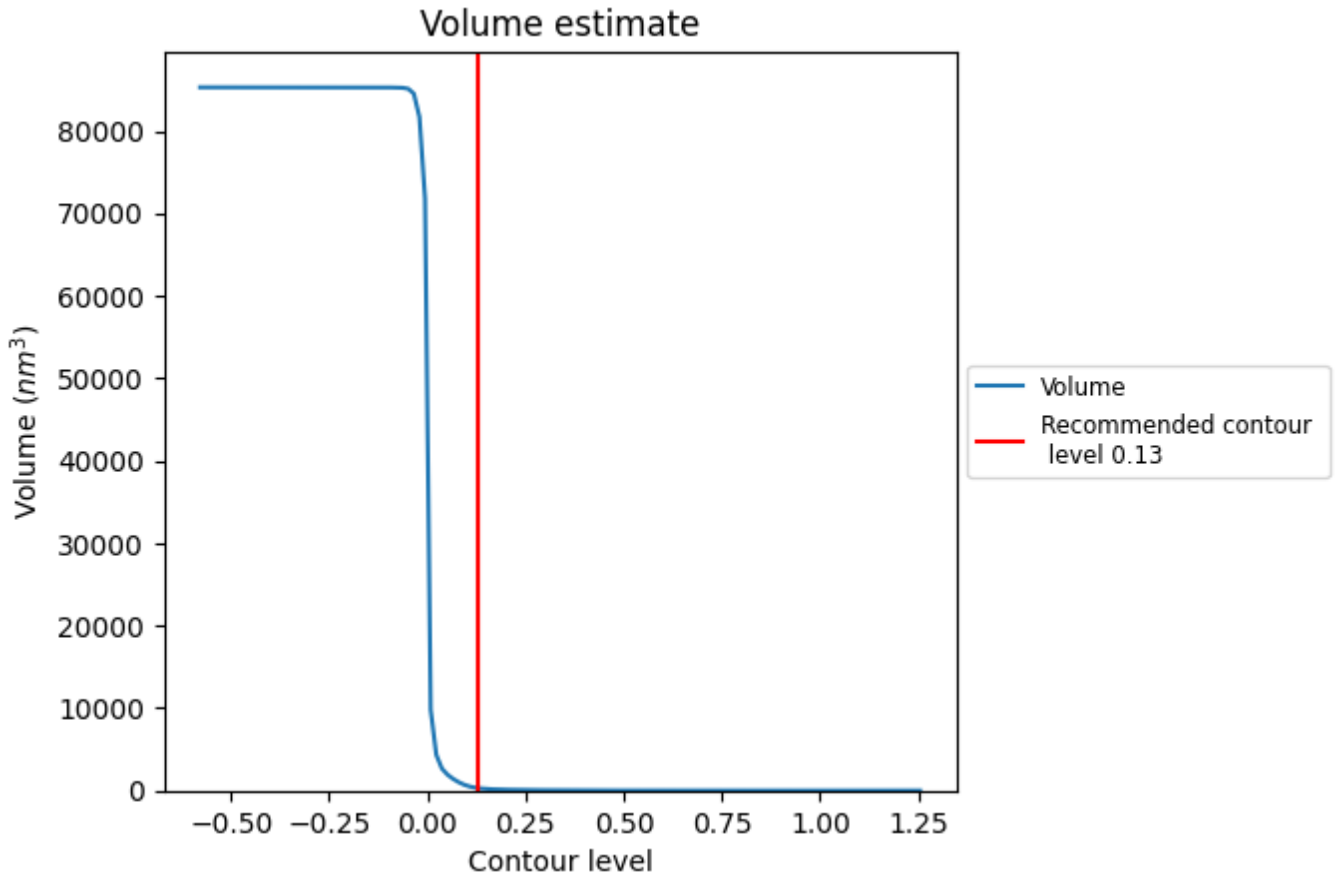
This section contains the results of statistical analysis of the map.

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.

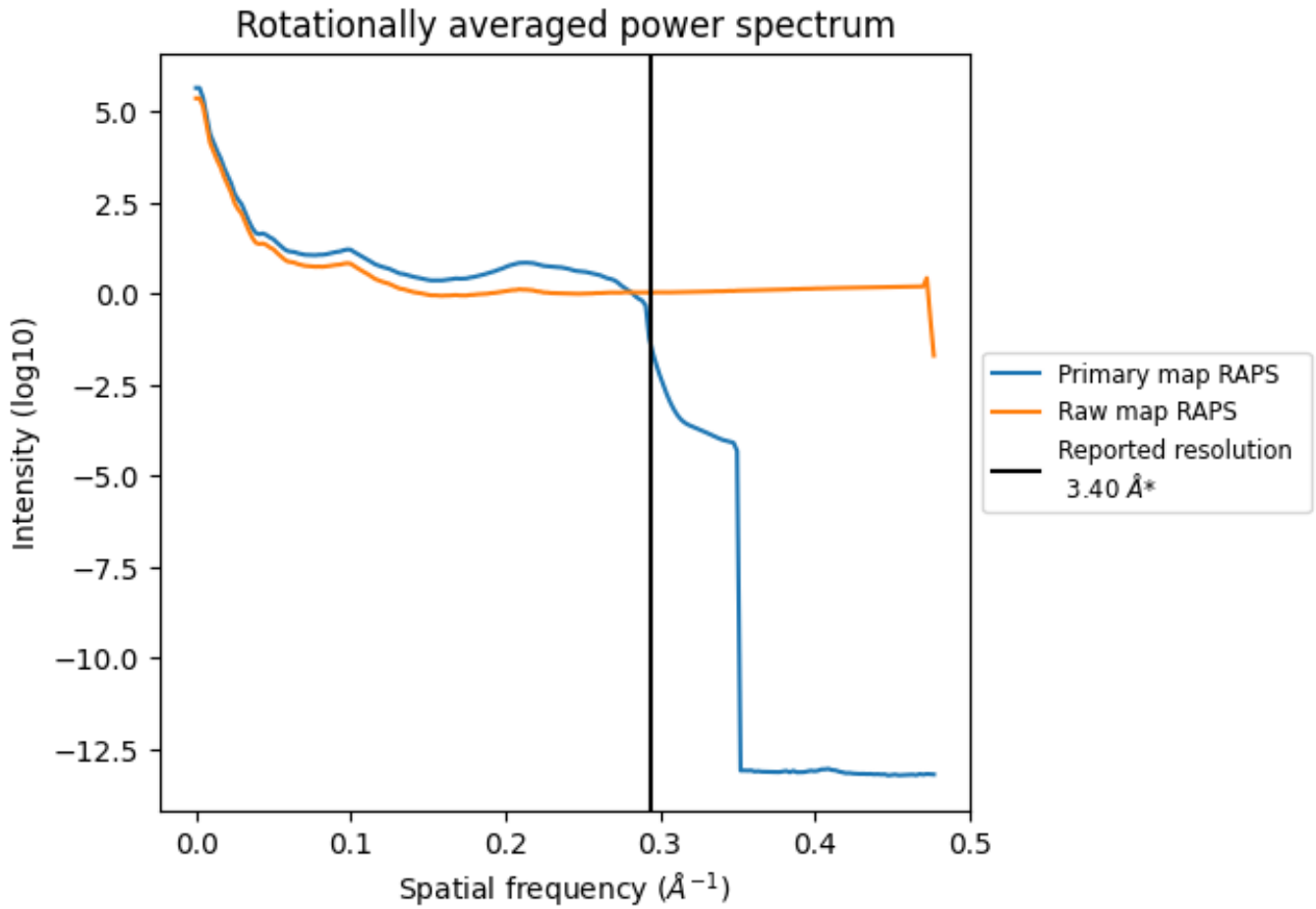
7.2 Volume estimate



The volume at the recommended contour level is 296 nm^3; this corresponds to an approximate mass of 268 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)

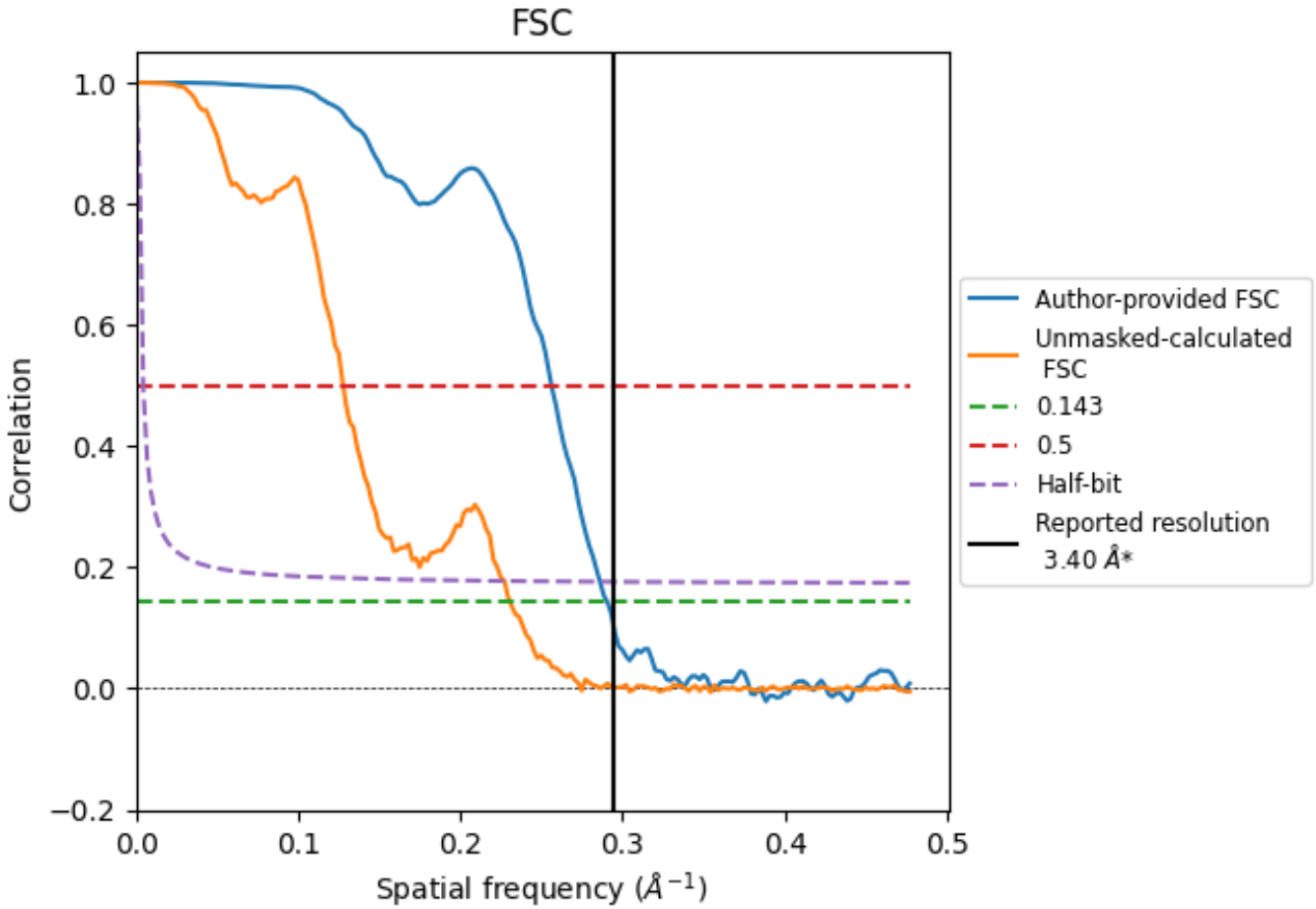


*Reported resolution corresponds to spatial frequency of 0.294 $Å^{-1}$

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8.2 Resolution estimates (i)

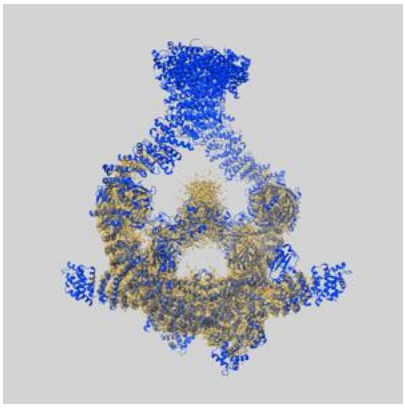
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.44	3.90	3.50
Unmasked-calculated*	4.34	7.83	4.40

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.34 differs from the reported value 3.4 by more than 10 %

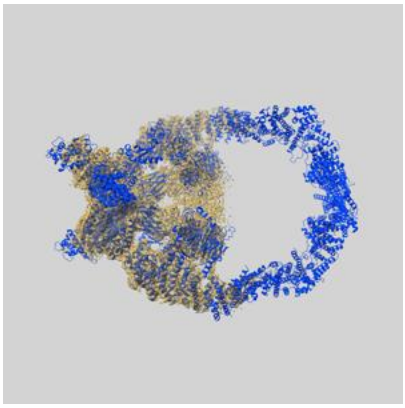
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-46686 and PDB model 9D9Z. Per-residue inclusion information can be found in section 3 on page 6.

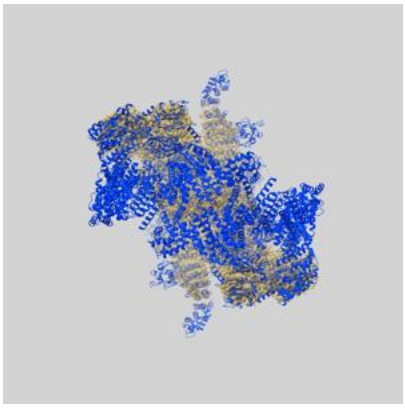
9.1 Map-model overlay



X



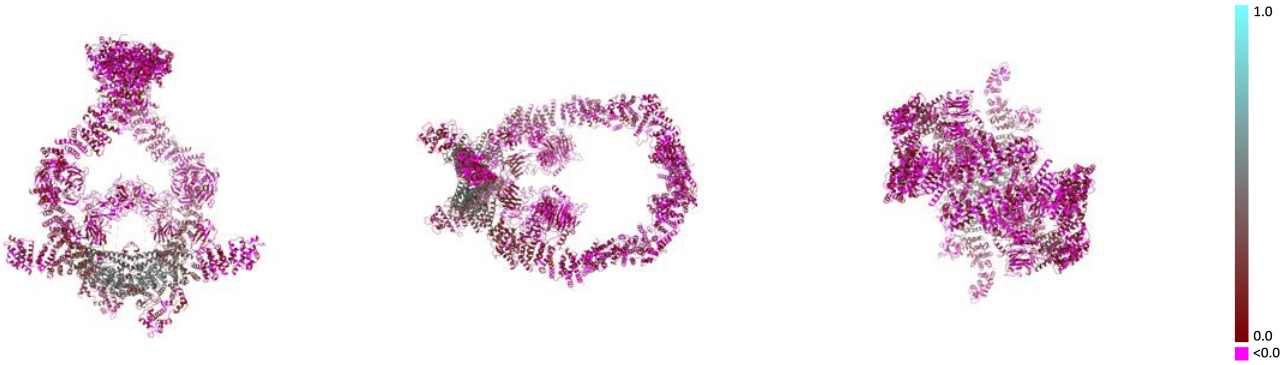
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.13 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.

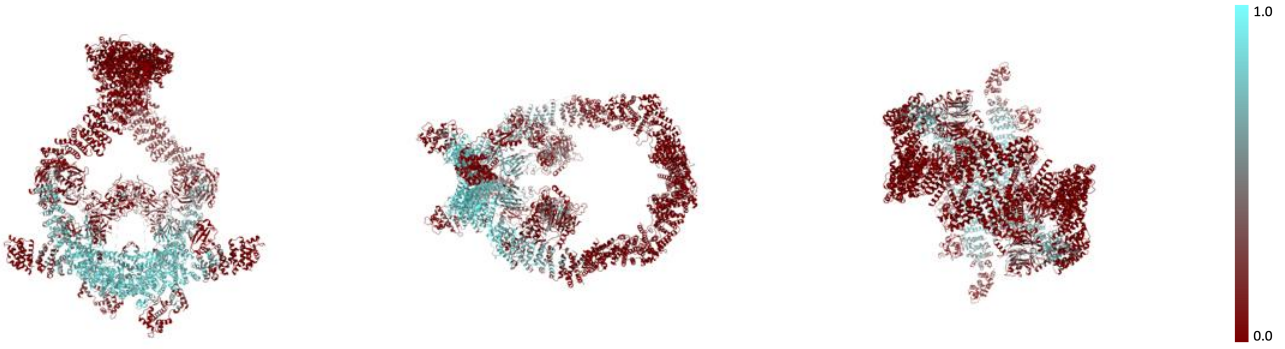
9.2 Q-score mapped to coordinate model



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.

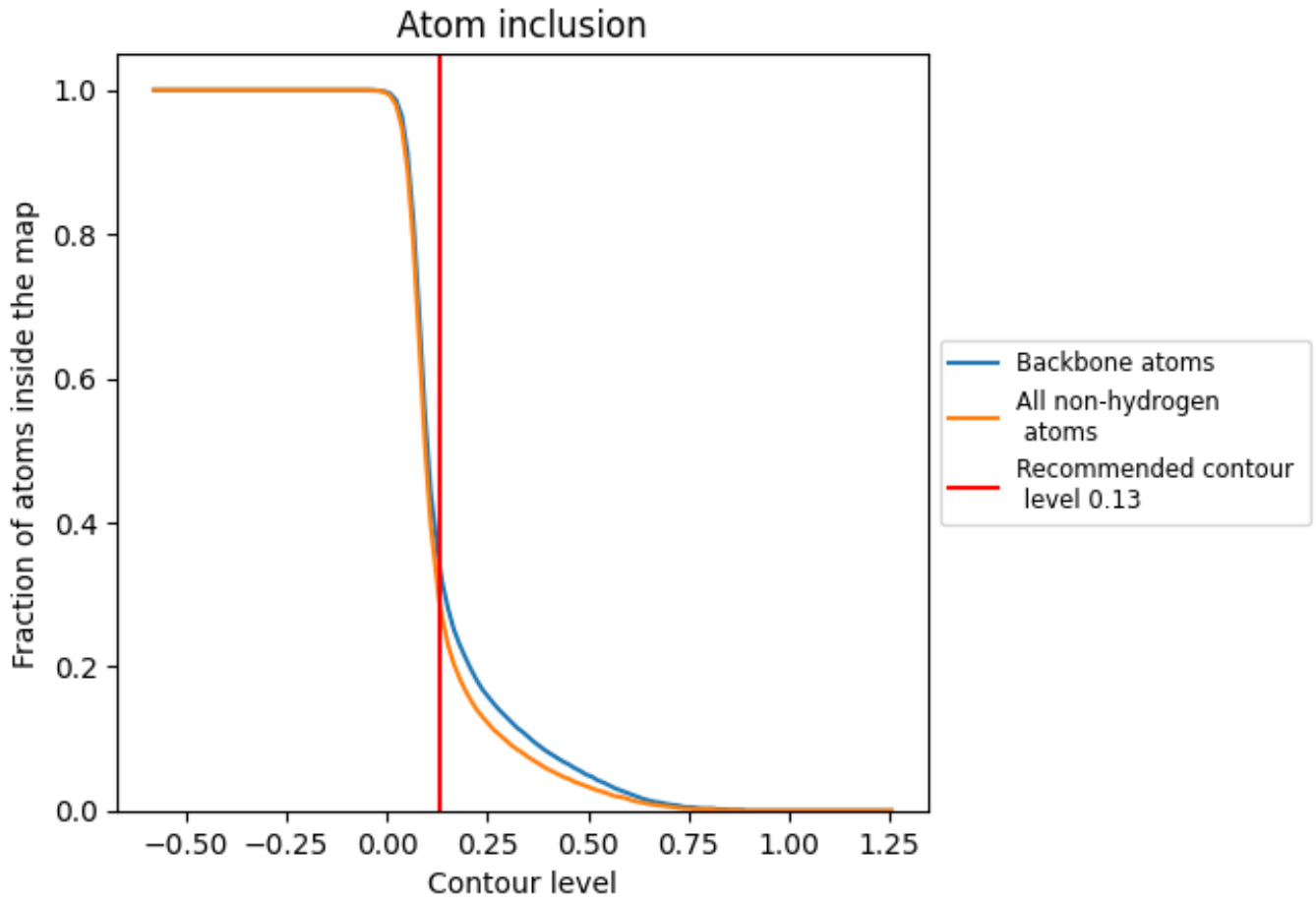
9.3 Atom inclusion mapped to coordinate model



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 (0.13).

9.4 Atom inclusion (i)



At the recommended contour level, 34% of all backbone atoms, 29% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.2930	0.1100
A	0.3000	0.1120
B	0.2990	0.1130
C	0.1500	0.0740
D	0.1350	0.0820
E	0.2720	0.0850
F	0.2740	0.0890