



Full wwPDB EM Validation Report ⓘ

Oct 6, 2024 – 12:18 AM JST

PDB ID : 5H0S
EMDB ID : EMD-9565
Title : EM Structure of VP1A and VP1B
Authors : Li, X.; Zhou, N.; Xu, B.; Chen, W.; Zhu, B.; Wang, X.; Wang, J.; Liu, H.;
Cheng, L.
Deposited on : 2016-10-06
Resolution : 3.30 Å(reported)

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<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.dev113
MolProbity : 4.02b-467
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) : 2.39

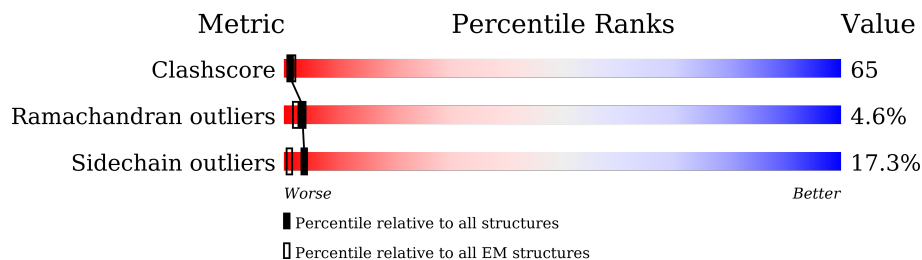
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	1333	<div> <div>21%</div> <div>48%</div> <div>37%</div> <div>14%</div> </div>
1	C	1333	<div> <div>25%</div> <div>19%</div> <div>39%</div> <div>27%</div> <div>8%</div> <div>6%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 18885 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.

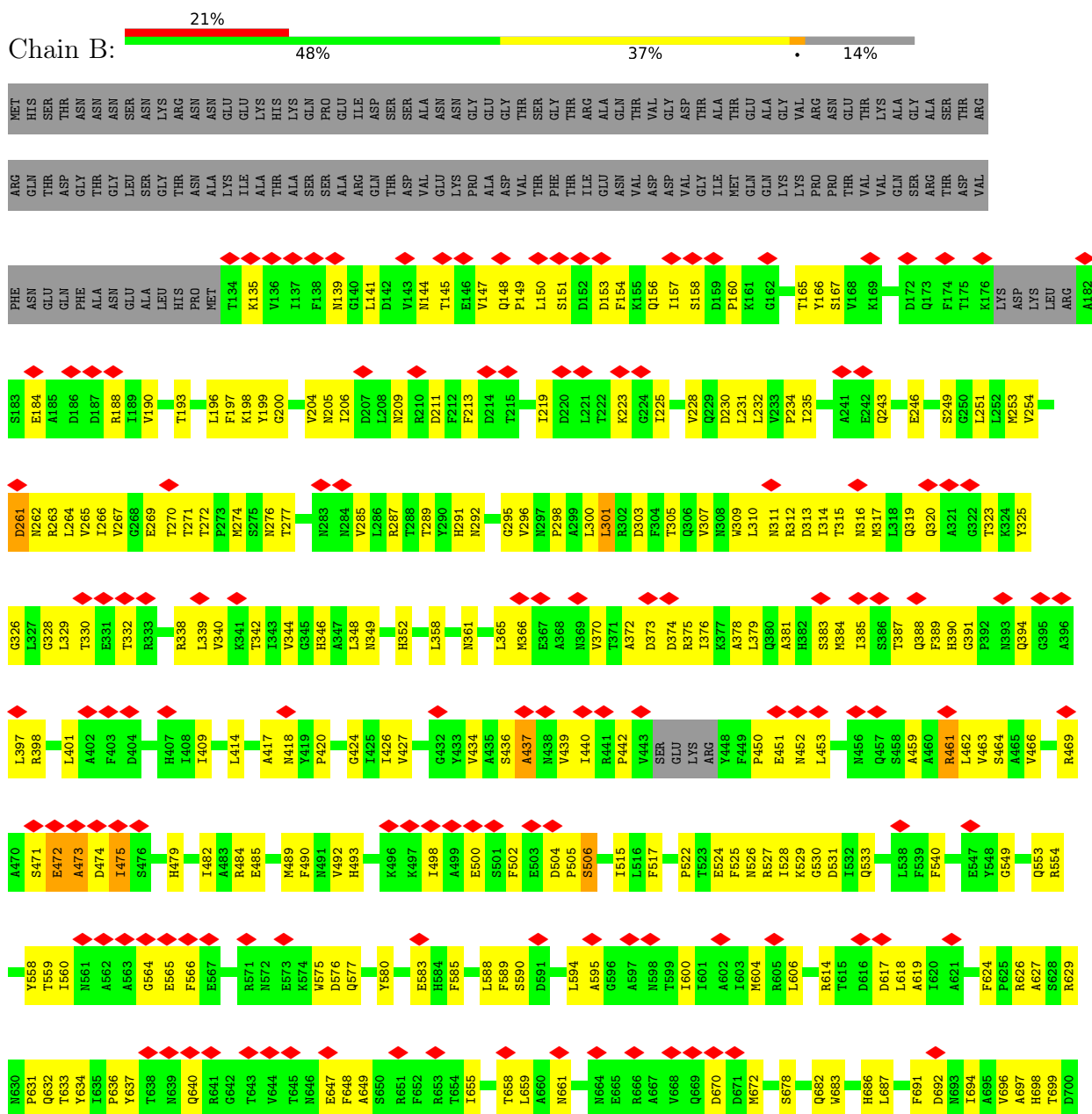
- Molecule 1 is a protein called VP1.

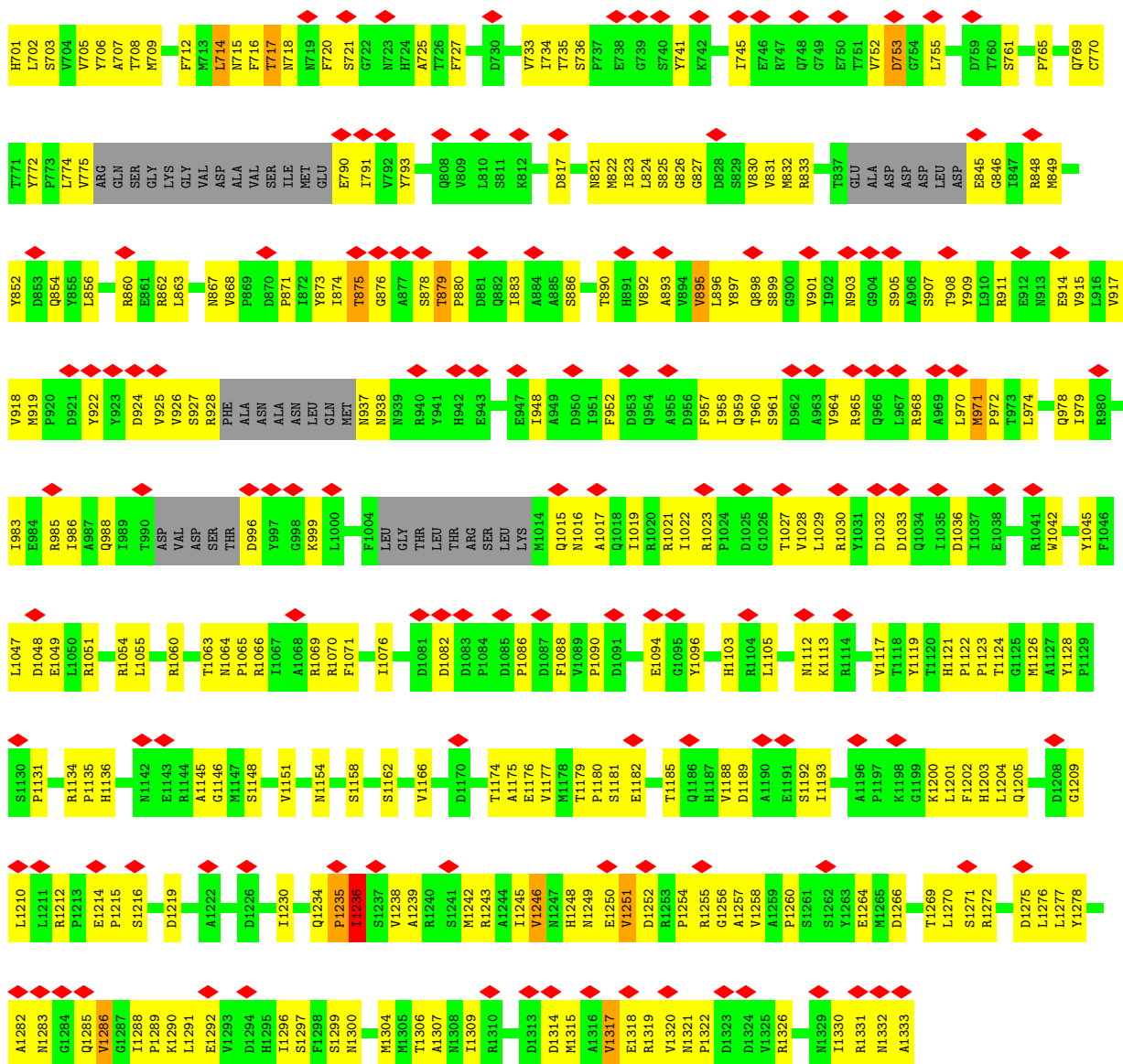
Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	1148	Total	C	N	O	S	0	0
			9058	5731	1574	1718	35		
1	C	1247	Total	C	N	O	S	0	0
			9827	6202	1709	1878	38		

3 Residue-property plots

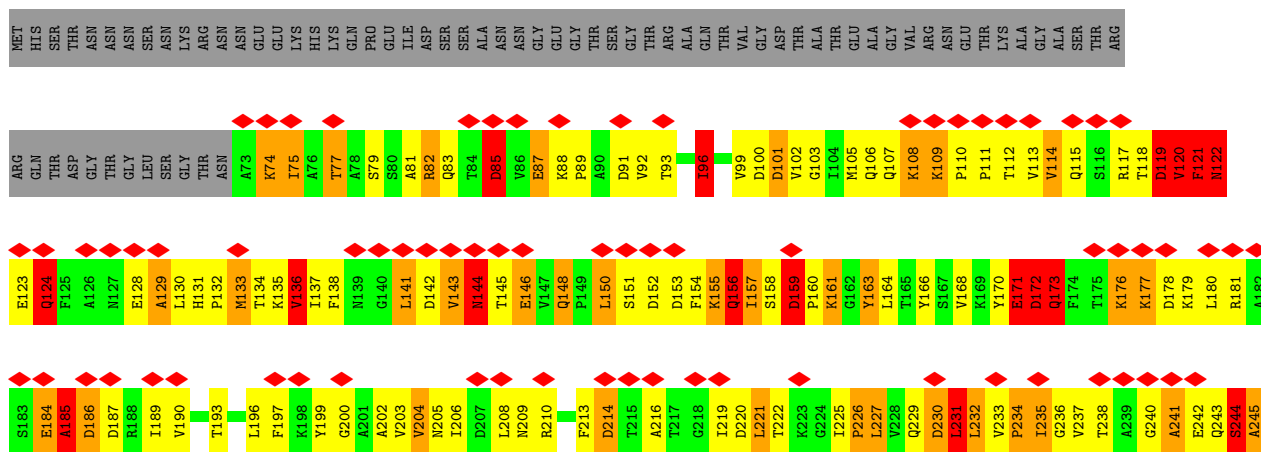
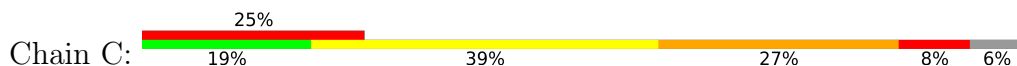
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: VP1





• Molecule 1: VP1



S994	T995	D996	Y997	K998	K999	L1000	L1001	L1002	R1003	F1004	L1005	L1008	L1009	R1010	K1013	M1014	Q1015	N1016	A1017	Q1018	I1019	R1020	R1021	I1022	R1023	P1024	D1025	T1027	V1028	R1029	R1030	Y1031	D1032	D1033	Q1034	I1035	D1036	I1037	E1038	A1039	F1040	R1041	W1042	S1043	R1044	Y1045	F1046	L1047	D1048	E1049	L1050	R1051	L1052	R1053	R1054	L1055				
T874	T875	Q876	A877	S878	T879	P880	D881	Q882	T883	A884	S885	S886	W887	Q888	A889	T890	H891	V892	D893	A893	H894	L895	L896	Y897	Q898	S899	G900	V901	N902	N903	G904	S905	A906	Q907	T908	R909	L910	D911	Q912	Y913	L914	V915	H916	V917	V918	N919	P920	D921	H922	Y923	D924	V925	V926	P927	R928	F929	A930	N931	A932	H933
T814	L815	P816	D817	A818	F819	T820	N821	N822	T823	L824	S825	G826	G827	D828	V829	H830	V831	N832	T833	T834	V835	Q836	T837	E838	A839	D840	D841	D842	L843	D844	E845	G846	T847	R848	N849	T850	T851	H852	D853	Q854	Y855	L856	S857	H858	T859	R860	E861	R862	L863	H864	T865	T866	N867	P868	D869	P870	T871	Y872	Y873	
R685	H686	E687	E688	F691	D692	N693	L694	A695	V696	A697	H698	D700	H701	L702	Y706	A707	T708	W709	S710	W711	F712	W713	L714	W715	F716	T717	W718	W719	F720	S721	G722	F727	K728	P729	D730	Q731	V732	W733	L734	T735	S736	P737	E738	G739	S740	Y741	K742	P743	L744	W745	E746	R747	Q748	G749	E750					
D753	G754	L755	T756	L757	D759	T760	S761	W762	W763	W764	F765	L766	L767	C768	Q769	T770	T771	Y772	F773	L774	W775	ARG	GLN	SER	GLY	LYS	GLY	VAL	ASP	ALA	SER	ILE	NET	GLU	E790	W791	V792	W793	F794	D795	F796	S797	T798	T799	L800	S801	Q802	S803	L804	S805	W806	L810	S811	L812	L813					
T814	L815	P816	D817	A818	F819	T820	N821	N822	T823	L824	S825	G826	G827	D828	V829	H830	V831	N832	T833	T834	V835	Q836	T837	E838	A839	D840	D841	D842	L843	D844	E845	G846	T847	R848	N849	T850	T851	H852	D853	Q854	Y855	L856	S857	H858	T859	R860	E861	R862	L863	H864	T865	T866	N867	P868	D869	P870	T871	Y872	Y873	
T874	T875	Q876	A877	S878	T879	P880	D881	Q882	T883	A884	S885	S886	W887	Q888	A889	T890	H891	V892	D893	A893	H894	L895	L896	Y897	Q898	S899	G900	V901	N902	N903	G904	S905	A906	Q907	T908	R909	L910	D911	Q912	Y913	L914	V915	H916	V917	V918	N919	P920	D921	H922	Y923	D924	V925	V926	P927	R928	F929	A930	N931	A932	H933
L934	D935	N936	N937	N938	N939	N940	Y941	H942	E943	S944	V945	L946	E947	I948	A949	D950	I951	F952	D953	Q954	A955	D956	F957	I958	Q959	T960	S961	D962	A963	V964	R965	Q966	L967	R968	A969	L970	M971	P972	T973	L974	S975	T976	S977	Q978	N979	R980	H981	D982	N983	I984	E1049	L1050	R1051	L1052	R1053	R1054	L1055			
E246	Y247	V248	S249	G250	L251	L252	R253	L254	L255	F256	R257	V258	M259	T260	D261	N262	R263	L264	V265	V267	G268	E269	T270	T271	T272	P273	M274	S275	N276	T277	L278	S279	T280	V281	V282	N283	N284	V285	L286	R287	T288	T289	Y290	H291	N297	P298	A299	L300	L301	R302	D303	F304	T305	Q306	V307	N308	W309			
L310	N311	D312	R313	L314	T315	N316	M317	L318	Q319	Q320	A321	H322	S323	T324	Y325	L327	Q328	L329	T330	E331	P332	R333	L334	D335	Y336	V337	R338	E400	L401	A402	F403	D404	H405	V406	H407	I408	I409	R410	C411	L412	M413	L414	M418	Y419	L422	E423	G424	L425	I426	V427	Q428	L429	M430	T431	V434					
A435	S436	V439	I440	R441	P442	V443	S444	E445	K446	R447	Y448	F449	P450	E451	N452	L453	E454	Q455	N456	Q457	S458	R461	L462	V463	S464	A465	V466	K467	A468	R469	A470	S471	E472	A473	D474	I475	S476	S477	I478	H479	L480	R484	E485	V486	S487	F490	N491	V492	H493	E494	L495	K496	I498	A499						
E500	S501	F502	E503	D504	P505	S506	S507	L508	V509	V510	V511	L512	E513	F514	L515	L516	F517	A518	L519	F520	F521	P522	T523	E524	F525	N526	R527	L528	K529	G530	D531	L532	Q533	N534	V535	L536	L537	L538	F539	S541	R542	W543	Y544	P545	V546	E547	G549	L550	F551	I552	Q553	R554	G555	A556	T557	Y558	T559			
T560	N561	A562	A563	G564	E565	F566	E567	F568	S569	V570	R571	L572	N573	K574	W575	D576	Q577	S578	L579	F580	P581	L581	S582	E583	H584	F585	P586	A587	L588	D591	V592	P593	L594	A595	G596	A597	N598	T599	L600	E601	A602	L603	M604	R605	G606	F607	T608	P609	Q610	G611	P612	L613	R614	T615	D617	L618	A619	L620		
A621	A622	N623	P624	P625	R626	A627	S628	R629	N630	P631	T632	T633	T634	L635	P636	V637	T638	N639	Q640	R641	G642	T643	V644	T645	N646	R651	F652	R653	T654	L655	V656	A657	T658	L659	A660	N661	V662	V663	N664	E665	R666	A667	V668	Q669	D670	D671	N672	K673	A675	T676	R677	T680	K681	Q682	W683	L684				
R685	H686	E687	E688	F691	D692	N693	L694	A695	V696	A697	H698	D700	H701	L702	Y706	A707	T708	W709	S710	W711	F712	W713	L714	W715	F716	T717	W718	W719	F720	S721	G722	F727	K728	P729	D730	Q731	V732	W733	L734	T735	S736	P737	E738	G739	S740	Y741	K742	P743	L744	W745	E746	R747	Q748	G749	E750					
D753	G754	L755	T756	L757	D759	T760	S761	W762	W763	W764	F765	L766	L767	C768	Q769	T770	T771	Y772	F773	L774	W775	ARG	GLN	SER	GLY	LYS	GLY	VAL	ASP	ALA	SER	ILE	NET	GLU	E790	W791	V792	W793	F794	D795	F796	S797	T798	T799	L800	S801	Q802	S803	L804	S805	W806	L810	S811	L812	L813					
T814	L815	P816	D817	A818	F819	T820	N821	N822	T823	L824	S825	G826	G827	D828	V829	H830	V831	N832	T833	T834	V835	Q836	T837	E838	A839	D840	D841	D842	L843	D844	E845	G846	T847	R848	N849	T850	T851	H852	D853	Q854	Y855	L856	S857	H858	T859	R860	E861	R862	L863	H864	T865	T866	N867	P868	D869	P870	T871	Y872	Y873	
T874	T875	Q876	A877	S878	T879	P880	D881	Q882	T883	A884	S885	S886	W887	Q888	A889	T890	H891	V892	D893	A893	H894	L895	L896	Y897	Q898	S899	G900	V901	N902	N903	G904	S905	A906	Q907	T908	R909	L910	D911	Q912	Y913	L914	V915	H916	V917	V918	N919	P920	D921	H922	Y923	D924	V925	V926	P927	R928	F929	A930	N931	A932	H933
L934	D935	N936	N937	N938	N939	N940	Y941	H942	E943	S944	V945	L946	E947	I948	A949	D950	I951	F952	D953	Q954	A955	D956	F957	I958	Q959	T960	S961	D962	A963	V964	R965	Q966	L967	R968	A969	L970	M971	P972	T973	L974	S975	T976	S977	Q978	N979	R980	H981	D982	N983	I984	E1049	L1050	R1051	L1052	R1053	R1054	L1055			

V1302	S1241	T1179	T1118	G1058
S1303	M1242	P1180	Y1119	L1059
M1304	R1243	S1181	T1120	R1060
M1305	I1244	E1182	H1121	L1061
T1306	I1245	G1183	P1122	I1062
A1307	V1246	Y1184	P1123	T1063
N1308	M1247	T1185	T1124	
I1309	H1248	Q1186	G1125	R1066
R1310	N1249	H1187	M1126	I1067
T1311	E1250	V1188	A1127	A1068
G1312	V1251	V1188	Y1128	R1069
D1313	R1252	D1189	P1129	R1070
D1314	R1253	A1190	S1130	F1071
M1315	P1254	E1191	P1131	D1072
A1316	A1257	S1192	T1132	G1073
V1317	V1258	I1193	G1133	V1074
E1318	A1259	M1194	R1134	R1075
R1319	P1260	T1195	P1135	I1076
V1320	S1261		H1136	M1077
N1321	S1262	K1198	V1137	Y1078
P1322	Y1263	G1199	H1138	L1079
D1323	E1264	K1200	M1139	T1080
D1324	M1265	L1201	T1140	D1081
V1325	D1266	F1202	I1141	D1082
R1326	T1267	H1203	N1142	D1083
A1327	G1268	L1204	E1143	P1084
I1328	T1269	Q1205	R1144	D1085
N1329	L1270	F1206	A1145	P1086
I1330	S1271	M1207	G1146	D1087
R1331	R1272	D1208	M1147	F1088
M1332	N1273	G1209	S1148	V1089
A1333	G1274	L1210	K1149	P1090
	D1275	L1211	L1150	D1091
	L1276	R1212	V1151	V1092
	L1277	P1213	A1152	
	Y1278	E1214	D1153	P1093
	S1279	P1215	N1154	E1094
	P1280		I1155	G1095
	V1281	F1218	I1156	Y1096
	A1282	D1219	A1157	V1097
	N1283	P1220	S1158	A1098
	G1284	P1221	V1159	V1099
	Q1285	A1222	I1160	Q1100
	V1286	S1223	K1161	Y1101
	G1287	G1224		A1102
	I1288	E1225	W1164	H1103
	P1289	D1226	V1165	R1104
	K1290	M1227	V1166	L1105
	L1291	R1228	D1167	F1106
	E1292	L1229	I1168	
	V1293	I1230	H1169	S1107
	D1294	Y1231	D1170	S1108
	H1295	P1232	I1171	S1109
	I1296	L1233	E1172	L1110
	S1297	Q1234	Y1173	A1111
	F1298	P1235	T1174	M1112
	S1299	I1236	A1175	K1113
	N1300	S1237	E1176	R1114
	V1301	V1238	V1177	M1115
		A1239	M1178	R1116
		R1240		V1117

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	53.433	Depositor
Minimum map value	-40.259	Depositor
Average map value	0.625	Depositor
Map value standard deviation	5.607	Depositor
Recommended contour level	17	Depositor
Map size (Å)	652.39996, 652.39996, 652.39996	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9319999, 0.9319999, 0.9319999	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	B	0.47	1/9244 (0.0%)	0.65	4/12582 (0.0%)
1	C	1.88	114/10028 (1.1%)	1.75	273/13653 (2.0%)
All	All	1.39	115/19272 (0.6%)	1.34	277/26235 (1.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	9
1	C	0	30
All	All	0	39

All (115) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	543	TRP	CB-CG	-12.16	1.28	1.50
1	C	683	TRP	CB-CG	-11.34	1.29	1.50
1	C	278	LEU	C-N	10.07	1.57	1.34
1	C	449	PHE	C-N	9.81	1.52	1.34
1	C	1167	ASP	CB-CG	-9.25	1.32	1.51
1	C	119	ASP	CB-CG	8.76	1.70	1.51
1	C	543	TRP	CG-CD1	-8.71	1.24	1.36
1	C	325	TYR	CE1-CZ	-8.67	1.27	1.38
1	C	227	LEU	C-N	8.58	1.53	1.34
1	C	244	SER	C-N	7.98	1.52	1.34
1	C	680	THR	CB-CG2	-7.89	1.26	1.52
1	C	764	TRP	CB-CG	-7.63	1.36	1.50
1	C	544	TYR	CB-CG	-7.45	1.40	1.51
1	C	575	TRP	CB-CG	-7.33	1.37	1.50
1	C	803	SER	CB-OG	-7.28	1.32	1.42
1	C	706	TYR	CB-CG	-7.17	1.40	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	683	TRP	CG-CD1	-7.11	1.26	1.36
1	C	741	TYR	CE1-CZ	-6.88	1.29	1.38
1	C	506	SER	CA-CB	-6.82	1.42	1.52
1	C	855	TYR	C-O	-6.75	1.10	1.23
1	C	548	TYR	C-O	-6.64	1.10	1.23
1	C	1158	SER	CB-OG	-6.64	1.33	1.42
1	B	971	MET	C-N	-6.57	1.21	1.34
1	C	1031	TYR	CB-CG	-6.55	1.41	1.51
1	C	1045	TYR	CG-CD1	-6.43	1.30	1.39
1	C	1164	TRP	CG-CD1	-6.29	1.27	1.36
1	C	547	GLU	CD-OE1	-6.25	1.18	1.25
1	C	521	PHE	C-O	-6.22	1.11	1.23
1	C	327	LEU	C-O	-6.14	1.11	1.23
1	C	530	GLY	C-O	-6.12	1.13	1.23
1	C	793	TYR	CE1-CZ	-6.11	1.30	1.38
1	C	585	PHE	C-O	6.10	1.34	1.23
1	C	163	TYR	CE1-CZ	-6.08	1.30	1.38
1	C	637	TYR	CE2-CZ	-6.07	1.30	1.38
1	C	121	PHE	CB-CG	-6.03	1.41	1.51
1	C	1223	SER	CA-CB	-6.01	1.44	1.52
1	C	325	TYR	CZ-OH	-5.99	1.27	1.37
1	C	354	ALA	C-O	-5.98	1.11	1.23
1	C	445	GLU	CG-CD	5.92	1.60	1.51
1	C	1119	TYR	CE1-CZ	-5.92	1.30	1.38
1	C	1045	TYR	CB-CG	-5.90	1.42	1.51
1	C	541	SER	CA-CB	-5.87	1.44	1.52
1	C	857	SER	CB-OG	-5.85	1.34	1.42
1	C	77	THR	C-O	5.83	1.34	1.23
1	C	637	TYR	CG-CD2	-5.82	1.31	1.39
1	C	631	PRO	C-O	-5.81	1.11	1.23
1	C	683	TRP	CD2-CE2	-5.80	1.34	1.41
1	C	75	ILE	C-O	5.79	1.34	1.23
1	C	1101	TYR	CA-C	-5.78	1.38	1.52
1	C	1202	PHE	CB-CG	-5.77	1.41	1.51
1	C	479	HIS	C-O	-5.72	1.12	1.23
1	C	447	ARG	C-N	5.71	1.47	1.34
1	C	1301	VAL	C-O	-5.68	1.12	1.23
1	C	102	VAL	N-CA	-5.67	1.35	1.46
1	C	740	SER	CA-CB	-5.67	1.44	1.52
1	C	956	ASP	CB-CG	5.66	1.63	1.51
1	C	328	GLY	C-O	-5.64	1.14	1.23
1	C	520	PHE	CB-CG	-5.64	1.41	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	544	TYR	CE1-CZ	-5.63	1.31	1.38
1	C	1303	SER	C-O	-5.62	1.12	1.23
1	C	1242	MET	C-O	-5.61	1.12	1.23
1	C	525	PHE	C-O	-5.58	1.12	1.23
1	C	977	SER	CA-CB	-5.56	1.44	1.52
1	C	493	HIS	C-O	-5.53	1.12	1.23
1	C	998	GLY	CA-C	-5.53	1.43	1.51
1	C	346	HIS	N-CA	-5.52	1.35	1.46
1	C	1164	TRP	CD2-CE2	-5.50	1.34	1.41
1	C	430	ASN	CB-CG	-5.47	1.38	1.51
1	C	533	GLN	C-O	-5.46	1.12	1.23
1	C	952	PHE	CB-CG	-5.46	1.42	1.51
1	C	1158	SER	CA-CB	-5.45	1.44	1.52
1	C	1223	SER	CB-OG	-5.44	1.35	1.42
1	C	524	GLU	C-O	-5.43	1.13	1.23
1	C	1077	MET	C-O	-5.42	1.13	1.23
1	C	390	HIS	C-O	-5.40	1.13	1.23
1	C	1201	LEU	CA-C	-5.39	1.39	1.52
1	C	524	GLU	CD-OE1	-5.37	1.19	1.25
1	C	419	TYR	CE1-CZ	-5.35	1.31	1.38
1	C	356	SER	C-O	-5.33	1.13	1.23
1	C	816	PRO	CA-C	-5.32	1.42	1.52
1	C	1231	TYR	CB-CG	-5.32	1.43	1.51
1	C	741	TYR	C-O	-5.32	1.13	1.23
1	C	494	GLU	C-O	-5.30	1.13	1.23
1	C	1076	ILE	C-O	-5.28	1.13	1.23
1	C	547	GLU	CG-CD	-5.27	1.44	1.51
1	C	1042	TRP	CD2-CE2	-5.23	1.35	1.41
1	C	424	GLY	C-O	-5.21	1.15	1.23
1	C	637	TYR	CB-CG	-5.21	1.43	1.51
1	C	691	PHE	C-O	-5.18	1.13	1.23
1	C	938	ASN	N-CA	-5.17	1.36	1.46
1	C	1280	PRO	N-CD	5.17	1.55	1.47
1	C	1071	PHE	C-O	-5.15	1.13	1.23
1	C	769	GLN	N-CA	-5.15	1.36	1.46
1	C	1045	TYR	CE1-CZ	-5.14	1.31	1.38
1	C	1178	MET	C-O	-5.13	1.13	1.23
1	C	683	TRP	C-O	-5.13	1.13	1.23
1	C	735	THR	CA-C	-5.13	1.39	1.52
1	C	74	LYS	C-O	5.13	1.33	1.23
1	C	775	VAL	CA-CB	5.13	1.65	1.54
1	C	1218	PHE	CB-CG	-5.12	1.42	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1164	TRP	CE3-CZ3	-5.12	1.29	1.38
1	C	1165	VAL	C-O	-5.10	1.13	1.23
1	C	490	PHE	C-O	-5.10	1.13	1.23
1	C	506	SER	CB-OG	-5.09	1.35	1.42
1	C	897	TYR	CB-CG	-5.09	1.44	1.51
1	C	580	TYR	CE2-CZ	-5.08	1.31	1.38
1	C	426	ILE	C-O	-5.07	1.13	1.23
1	C	115	GLN	C-O	5.07	1.32	1.23
1	C	706	TYR	CZ-OH	-5.07	1.29	1.37
1	C	1117	VAL	C-O	-5.06	1.13	1.23
1	C	378	ALA	C-O	-5.05	1.13	1.23
1	C	545	PRO	CA-C	-5.04	1.42	1.52
1	C	494	GLU	CD-OE2	-5.03	1.20	1.25
1	C	121	PHE	C-O	-5.02	1.13	1.23
1	C	463	VAL	C-O	-5.00	1.13	1.23

All (277) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	772	TYR	C-N-CD	-26.11	63.15	120.60
1	C	1121	HIS	C-N-CD	-19.15	78.48	120.60
1	C	870	ASP	C-N-CD	-18.50	79.91	120.60
1	C	285	VAL	O-C-N	17.98	151.47	122.70
1	C	173	GLN	O-C-N	-17.55	94.62	122.70
1	C	521	PHE	C-N-CD	-15.71	86.03	120.60
1	C	171	GLU	O-C-N	-15.37	98.10	122.70
1	C	879	THR	C-N-CD	-14.13	89.50	120.60
1	C	285	VAL	CA-C-N	-13.75	86.96	117.20
1	C	279	SER	O-C-N	-13.54	101.03	122.70
1	C	172	ASP	CA-C-N	-13.28	87.98	117.20
1	C	226	PRO	O-C-N	13.07	143.61	122.70
1	C	172	ASP	C-N-CA	-11.88	92.00	121.70
1	C	449	PHE	O-C-N	-11.71	98.85	121.10
1	C	173	GLN	CA-C-N	11.59	142.69	117.20
1	C	285	VAL	C-N-CA	-11.29	93.47	121.70
1	C	119	ASP	CB-CG-OD1	10.98	128.18	118.30
1	C	398	ARG	N-CA-C	10.83	140.24	111.00
1	C	1212	ARG	C-N-CD	-10.53	97.44	120.60
1	C	173	GLN	C-N-CA	10.45	147.83	121.70
1	C	816	PRO	CA-N-CD	-10.39	96.96	111.50
1	C	244	SER	CA-C-N	-10.26	94.63	117.20
1	C	226	PRO	CA-C-N	-10.18	94.81	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1259	ALA	C-N-CD	-9.96	98.69	120.60
1	C	1178	MET	CB-CG-SD	-9.93	82.61	112.40
1	C	449	PHE	C-N-CD	-9.85	98.92	120.60
1	C	1179	THR	C-N-CD	-9.60	99.49	120.60
1	C	448	TYR	O-C-N	-9.55	107.42	122.70
1	C	827	GLY	N-CA-C	-9.39	89.63	113.10
1	C	773	PRO	N-CA-C	-9.24	88.07	112.10
1	C	767	LEU	CA-CB-CG	9.23	136.53	115.30
1	C	278	LEU	O-C-N	9.13	137.30	122.70
1	C	1285	GLN	N-CA-C	9.12	135.62	111.00
1	C	336	TYR	N-CA-C	9.04	135.41	111.00
1	C	793	TYR	C-N-CD	-8.98	100.84	120.60
1	C	721	SER	N-CA-C	-8.89	87.01	111.00
1	C	244	SER	C-N-CA	-8.88	99.50	121.70
1	C	1122	PRO	C-N-CD	-8.88	101.07	120.60
1	C	172	ASP	O-C-N	8.77	136.73	122.70
1	C	1201	LEU	CA-CB-CG	8.70	135.31	115.30
1	C	1281	VAL	CG1-CB-CG2	8.57	124.61	110.90
1	C	1029	LEU	CB-CG-CD1	-8.56	96.45	111.00
1	C	144	ASN	N-CA-CB	8.51	125.91	110.60
1	C	150	LEU	CB-CG-CD2	-8.45	96.64	111.00
1	C	655	ILE	CB-CA-C	-8.44	94.72	111.60
1	C	1307	ALA	N-CA-C	-8.38	88.36	111.00
1	C	1286	VAL	N-CA-C	8.37	133.61	111.00
1	C	350	ILE	CB-CA-C	-8.24	95.12	111.60
1	C	360	ILE	CB-CA-C	-8.22	95.15	111.60
1	C	361	ASN	O-C-N	-8.20	109.58	122.70
1	C	1291	LEU	CB-CG-CD1	-8.15	97.14	111.00
1	C	674	LYS	CD-CE-NZ	-8.10	93.06	111.70
1	C	226	PRO	C-N-CA	-8.09	101.47	121.70
1	C	1300	ASN	N-CA-C	8.09	132.83	111.00
1	C	418	ASN	CB-CA-C	-8.07	94.25	110.40
1	C	813	LEU	CB-CG-CD2	-8.01	97.39	111.00
1	C	1035	ILE	CG1-CB-CG2	-7.99	93.82	111.40
1	C	1199	GLY	N-CA-C	-7.98	93.16	113.10
1	C	866	THR	N-CA-C	-7.83	89.85	111.00
1	C	1042	TRP	N-CA-C	7.83	132.15	111.00
1	C	896	LEU	CB-CG-CD2	-7.81	97.72	111.00
1	C	185	ALA	O-C-N	-7.70	110.38	122.70
1	C	279	SER	CA-C-N	7.68	134.09	117.20
1	C	938	ASN	CB-CA-C	7.67	125.75	110.40
1	C	661	ASN	CA-C-N	-7.63	100.40	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	849	MET	CB-CG-SD	-7.57	89.69	112.40
1	C	279	SER	C-N-CA	7.57	140.61	121.70
1	C	244	SER	O-C-N	7.56	134.80	122.70
1	B	714	LEU	CA-CB-CG	7.53	132.61	115.30
1	C	687	LEU	CB-CG-CD2	-7.49	98.26	111.00
1	C	1230	ILE	CB-CA-C	-7.47	96.66	111.60
1	C	96	ILE	CG1-CB-CG2	-7.42	95.06	111.40
1	C	480	LEU	CB-CG-CD2	-7.33	98.54	111.00
1	C	1291	LEU	CB-CG-CD2	-7.31	98.57	111.00
1	C	635	ILE	N-CA-C	7.31	130.74	111.00
1	C	1331	ARG	NE-CZ-NH1	7.27	123.94	120.30
1	C	946	LEU	CB-CG-CD1	-7.26	98.66	111.00
1	C	1147	MET	N-CA-C	7.25	130.58	111.00
1	C	1313	ASP	CB-CG-OD2	7.19	124.77	118.30
1	C	1043	SER	N-CA-C	7.18	130.39	111.00
1	C	346	HIS	N-CA-CB	-7.13	97.77	110.60
1	C	391	GLY	C-N-CD	-7.08	105.03	120.60
1	C	456	ASN	O-C-N	-7.07	111.39	122.70
1	C	719	ASN	CB-CA-C	-7.05	96.30	110.40
1	C	278	LEU	CA-C-N	-6.99	101.83	117.20
1	C	1031	TYR	CA-C-N	-6.94	101.92	117.20
1	C	638	THR	N-CA-C	6.93	129.71	111.00
1	C	301	LEU	CA-CB-CG	6.92	131.21	115.30
1	C	536	LEU	CB-CG-CD1	-6.92	99.24	111.00
1	C	1033	ASP	CB-CG-OD2	-6.91	112.08	118.30
1	C	1144	ARG	NE-CZ-NH1	6.91	123.75	120.30
1	C	731	GLN	N-CA-C	6.88	129.59	111.00
1	C	1167	ASP	N-CA-CB	-6.88	98.22	110.60
1	C	75	ILE	O-C-N	6.87	133.69	122.70
1	C	775	VAL	CA-CB-CG2	6.85	121.18	110.90
1	C	409	ILE	CG1-CB-CG2	-6.85	96.34	111.40
1	C	688	GLU	CB-CA-C	6.82	124.05	110.40
1	C	124	GLN	N-CA-C	6.82	129.41	111.00
1	C	606	LEU	CB-CG-CD1	-6.82	99.42	111.00
1	C	100	ASP	N-CA-CB	-6.80	98.36	110.60
1	C	828	ASP	CB-CG-OD1	6.80	124.42	118.30
1	C	863	LEU	CB-CG-CD2	-6.78	99.48	111.00
1	C	758	ILE	CB-CA-C	-6.75	98.09	111.60
1	C	954	GLN	N-CA-C	6.71	129.12	111.00
1	C	1330	ILE	CG1-CB-CG2	-6.69	96.68	111.40
1	C	1271	SER	CB-CA-C	-6.67	97.44	110.10
1	C	1025	ASP	CB-CA-C	-6.66	97.08	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	810	LEU	CA-CB-CG	-6.64	100.02	115.30
1	C	120	VAL	N-CA-C	6.62	128.89	111.00
1	C	448	TYR	CA-C-N	-6.60	102.67	117.20
1	C	946	LEU	CA-CB-CG	-6.60	100.12	115.30
1	C	114	VAL	CB-CA-C	-6.52	99.01	111.40
1	C	700	ASP	N-CA-C	6.51	128.59	111.00
1	C	810	LEU	CB-CG-CD1	6.49	122.03	111.00
1	C	891	HIS	N-CA-C	6.47	128.47	111.00
1	C	700	ASP	O-C-N	6.47	133.05	122.70
1	C	475	ILE	N-CA-C	6.42	128.32	111.00
1	C	119	ASP	N-CA-C	-6.41	93.68	111.00
1	C	768	CYS	N-CA-C	6.39	128.26	111.00
1	C	979	ILE	CG1-CB-CG2	-6.38	97.38	111.40
1	C	1159	VAL	CG1-CB-CG2	-6.37	100.71	110.90
1	C	1204	LEU	CB-CG-CD2	-6.37	100.18	111.00
1	C	875	THR	CA-C-N	6.36	128.92	116.20
1	C	824	LEU	CA-CB-CG	6.32	129.84	115.30
1	C	670	ASP	CB-CA-C	-6.31	97.79	110.40
1	C	635	ILE	C-N-CD	-6.30	106.73	120.60
1	C	1304	MET	CB-CG-SD	-6.30	93.49	112.40
1	C	121	PHE	C-N-CA	6.30	137.45	121.70
1	C	702	LEU	CB-CG-CD2	-6.30	100.29	111.00
1	C	1134	ARG	C-N-CD	6.30	141.62	128.40
1	C	1201	LEU	CB-CG-CD2	-6.28	100.33	111.00
1	C	671	ASP	O-C-N	-6.28	112.66	122.70
1	C	525	PHE	CB-CA-C	-6.25	97.90	110.40
1	C	1043	SER	C-N-CA	6.24	137.30	121.70
1	C	1234	GLN	C-N-CD	6.22	141.47	128.40
1	C	314	ILE	CG1-CB-CG2	-6.22	97.71	111.40
1	C	577	GLN	N-CA-CB	6.22	121.80	110.60
1	C	327	LEU	CA-CB-CG	6.19	129.54	115.30
1	C	1128	TYR	C-N-CD	6.13	141.26	128.40
1	C	588	LEU	CB-CG-CD1	-6.12	100.60	111.00
1	C	1032	ASP	CB-CG-OD1	6.11	123.80	118.30
1	C	1188	VAL	CB-CA-C	-6.06	99.89	111.40
1	C	1331	ARG	NE-CZ-NH2	-6.06	117.27	120.30
1	C	272	THR	C-N-CD	6.04	141.08	128.40
1	C	1083	ASP	C-N-CD	6.02	141.05	128.40
1	C	495	LEU	CB-CG-CD1	-6.01	100.78	111.00
1	C	546	VAL	CB-CA-C	-6.01	99.97	111.40
1	C	456	ASN	N-CA-CB	-6.01	99.78	110.60
1	C	401	LEU	CB-CG-CD2	-6.00	100.80	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	767	LEU	CB-CA-C	-5.99	98.83	110.20
1	C	875	THR	C-N-CA	5.97	134.84	122.30
1	C	85	ASP	N-CA-C	5.95	127.05	111.00
1	C	1305	MET	CB-CG-SD	-5.94	94.59	112.40
1	C	1098	ALA	N-CA-C	5.93	127.02	111.00
1	C	864	HIS	CB-CA-C	-5.93	98.53	110.40
1	C	1225	GLU	CA-CB-CG	5.93	126.45	113.40
1	C	329	LEU	CB-CG-CD2	-5.93	100.92	111.00
1	C	1144	ARG	NE-CZ-NH2	-5.89	117.36	120.30
1	C	1221	PRO	N-CA-C	5.89	127.42	112.10
1	C	1225	GLU	N-CA-CB	5.88	121.18	110.60
1	C	159	ASP	CB-CG-OD1	-5.87	113.02	118.30
1	C	715	ASN	N-CA-C	-5.87	95.15	111.00
1	C	461	ARG	N-CA-CB	5.85	121.13	110.60
1	C	661	ASN	C-N-CA	-5.85	107.08	121.70
1	C	1275	ASP	CB-CA-C	-5.83	98.73	110.40
1	C	278	LEU	C-N-CA	-5.80	107.19	121.70
1	C	925	VAL	CB-CA-C	5.80	122.41	111.40
1	C	970	LEU	CB-CG-CD2	-5.79	101.15	111.00
1	C	1191	GLU	O-C-N	5.78	131.95	122.70
1	C	136	VAL	C-N-CA	5.78	136.14	121.70
1	C	630	ASN	N-CA-C	-5.76	95.44	111.00
1	C	730	ASP	CB-CG-OD1	-5.75	113.12	118.30
1	C	1233	LEU	CA-CB-CG	5.75	128.53	115.30
1	C	1168	ILE	CG1-CB-CG2	-5.72	98.81	111.40
1	C	408	ILE	CB-CA-C	-5.72	100.17	111.60
1	C	148	GLN	N-CA-CB	-5.71	100.33	110.60
1	C	1191	GLU	N-CA-C	-5.69	95.64	111.00
1	C	121	PHE	N-CA-CB	-5.68	100.37	110.60
1	B	1317	VAL	C-N-CA	5.65	135.83	121.70
1	C	144	ASN	CB-CA-C	5.65	121.70	110.40
1	C	1286	VAL	CB-CA-C	-5.65	100.67	111.40
1	C	422	LEU	CA-CB-CG	5.64	128.26	115.30
1	C	1070	ARG	N-CA-C	-5.64	95.78	111.00
1	C	1298	PHE	C-N-CA	5.63	135.78	121.70
1	C	1181	SER	C-N-CA	5.62	135.76	121.70
1	C	487	SER	N-CA-CB	-5.62	102.07	110.50
1	C	456	ASN	CA-C-N	5.61	129.54	117.20
1	C	706	TYR	CB-CA-C	-5.60	99.20	110.40
1	C	841	ASP	C-N-CA	5.60	135.71	121.70
1	C	1191	GLU	CA-C-N	-5.59	104.90	117.20
1	C	878	SER	C-N-CA	5.59	135.66	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	82	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	C	413	MET	CB-CG-SD	-5.58	95.67	112.40
1	C	547	GLU	CB-CA-C	-5.57	99.26	110.40
1	C	496	LYS	N-CA-C	-5.56	95.99	111.00
1	C	824	LEU	CB-CG-CD1	-5.56	101.55	111.00
1	C	700	ASP	CA-C-N	-5.51	105.07	117.20
1	C	579	LEU	CB-CG-CD1	-5.51	101.63	111.00
1	C	1230	ILE	N-CA-C	5.50	125.84	111.00
1	C	820	ILE	CG1-CB-CG2	-5.50	99.31	111.40
1	C	156	GLN	CB-CA-C	-5.48	99.43	110.40
1	C	687	LEU	CB-CA-C	5.47	120.59	110.20
1	C	815	LEU	C-N-CD	-5.47	108.57	120.60
1	C	632	GLN	N-CA-C	-5.46	96.25	111.00
1	C	718	ASN	N-CA-C	-5.44	96.31	111.00
1	C	696	VAL	CB-CA-C	-5.41	101.12	111.40
1	C	815	LEU	CB-CG-CD2	-5.39	101.84	111.00
1	C	956	ASP	CB-CA-C	5.39	121.17	110.40
1	C	171	GLU	CA-C-N	5.38	129.04	117.20
1	C	1193	ILE	CG1-CB-CG2	-5.38	99.56	111.40
1	C	844	ASP	N-CA-CB	5.38	120.28	110.60
1	B	1317	VAL	N-CA-C	-5.37	96.50	111.00
1	C	158	SER	N-CA-C	5.35	125.44	111.00
1	C	314	ILE	CB-CA-C	-5.34	100.91	111.60
1	C	1141	ILE	CG1-CB-CG2	-5.34	99.66	111.40
1	C	1253	ARG	C-N-CD	-5.34	108.86	120.60
1	C	447	ARG	O-C-N	5.33	131.23	122.70
1	C	859	ILE	CB-CA-C	5.32	122.23	111.60
1	C	874	ILE	C-N-CA	5.32	134.99	121.70
1	C	1014	MET	N-CA-C	-5.31	96.66	111.00
1	C	654	THR	CB-CA-C	-5.31	97.27	111.60
1	C	299	ALA	N-CA-CB	5.27	117.47	110.10
1	C	956	ASP	CB-CG-OD2	5.27	123.04	118.30
1	C	441	ARG	C-N-CD	-5.26	109.02	120.60
1	C	131	HIS	C-N-CD	-5.26	109.03	120.60
1	C	608	THR	C-N-CD	-5.25	109.04	120.60
1	C	542	ARG	CA-C-N	-5.25	105.66	117.20
1	C	138	PHE	CB-CA-C	-5.24	99.92	110.40
1	C	511	VAL	CB-CA-C	-5.22	101.48	111.40
1	C	928	ARG	CB-CA-C	-5.22	99.96	110.40
1	C	875	THR	N-CA-CB	5.22	120.21	110.30
1	C	458	SER	CA-C-O	5.21	131.05	120.10
1	C	639	ASN	N-CA-CB	5.21	119.97	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	826	GLY	N-CA-C	-5.21	100.08	113.10
1	C	1267	THR	N-CA-C	-5.21	96.94	111.00
1	C	1014	MET	CG-SD-CE	-5.20	91.88	100.20
1	C	1325	VAL	N-CA-C	5.20	125.04	111.00
1	C	534	ASN	CB-CA-C	-5.18	100.04	110.40
1	C	1279	SER	C-N-CD	5.18	139.27	128.40
1	C	1198	LYS	N-CA-C	5.17	124.95	111.00
1	C	543	TRP	N-CA-CB	-5.16	101.31	110.60
1	C	565	GLU	CB-CA-C	5.16	120.72	110.40
1	C	698	HIS	CB-CA-C	-5.15	100.09	110.40
1	B	301	LEU	CA-CB-CG	5.14	127.12	115.30
1	C	96	ILE	CB-CA-C	-5.13	101.34	111.60
1	C	152	ASP	CB-CG-OD2	5.13	122.92	118.30
1	C	1113	LYS	N-CA-C	5.13	124.85	111.00
1	C	152	ASP	N-CA-C	5.12	124.83	111.00
1	C	414	LEU	CB-CG-CD1	-5.12	102.29	111.00
1	C	457	GLN	N-CA-C	5.12	124.83	111.00
1	C	484	ARG	N-CA-C	-5.11	97.19	111.00
1	C	626	ARG	NE-CZ-NH2	-5.11	117.74	120.30
1	C	774	LEU	CA-CB-CG	-5.11	103.55	115.30
1	C	352	HIS	N-CA-C	5.11	124.79	111.00
1	C	645	THR	N-CA-C	5.10	124.77	111.00
1	C	646	ASN	N-CA-C	5.10	124.77	111.00
1	C	495	LEU	CA-CB-CG	5.09	127.02	115.30
1	C	75	ILE	C-N-CA	5.09	134.41	121.70
1	C	922	TYR	N-CA-CB	5.09	119.75	110.60
1	C	537	LEU	CB-CG-CD1	-5.08	102.36	111.00
1	C	1292	GLU	N-CA-CB	5.08	119.75	110.60
1	C	1314	ASP	CB-CG-OD1	5.08	122.87	118.30
1	C	466	VAL	CG1-CB-CG2	-5.07	102.78	110.90
1	C	759	ASP	CB-CG-OD2	5.06	122.85	118.30
1	C	379	LEU	CA-CB-CG	5.05	126.92	115.30
1	C	497	LYS	N-CA-C	5.05	124.63	111.00
1	C	119	ASP	C-N-CA	5.04	134.31	121.70
1	C	1021	ARG	NE-CZ-NH1	-5.04	117.78	120.30
1	C	860	ARG	NE-CZ-NH1	-5.04	117.78	120.30
1	C	700	ASP	CB-CG-OD1	5.04	122.83	118.30
1	C	730	ASP	N-CA-C	5.04	124.59	111.00
1	C	1003	ARG	NE-CZ-NH2	-5.03	117.78	120.30
1	C	709	MET	CB-CG-SD	-5.03	97.32	112.40
1	C	1202	PHE	CB-CG-CD2	-5.02	117.28	120.80
1	C	823	ILE	CG1-CB-CG2	-5.01	100.38	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1166	VAL	CB-CA-C	-5.01	101.88	111.40
1	C	418	ASN	N-CA-C	5.01	124.52	111.00

There are no chirality outliers.

All (39) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	1193	ILE	Peptide
1	B	1235	PRO	Peptide
1	B	1236	ILE	Peptide
1	B	261	ASP	Peptide
1	B	506	SER	Peptide
1	B	717	THR	Peptide
1	B	825	SER	Peptide
1	B	875	THR	Peptide
1	B	895	VAL	Peptide
1	C	1031	TYR	Mainchain
1	C	1068	ALA	Mainchain
1	C	1093	PRO	Mainchain
1	C	121	PHE	Mainchain
1	C	171	GLU	Mainchain
1	C	172	ASP	Mainchain
1	C	173	GLN	Mainchain
1	C	185	ALA	Mainchain
1	C	244	SER	Mainchain
1	C	279	SER	Mainchain
1	C	317	MET	Mainchain
1	C	334	LEU	Mainchain
1	C	351	ASP	Mainchain
1	C	361	ASN	Mainchain
1	C	398	ARG	Peptide
1	C	436	SER	Mainchain
1	C	448	TYR	Mainchain
1	C	449	PHE	Mainchain
1	C	456	ASN	Mainchain
1	C	503	GLU	Mainchain
1	C	519	LEU	Mainchain
1	C	533	GLN	Mainchain
1	C	635	ILE	Peptide,Mainchain
1	C	661	ASN	Mainchain
1	C	662	VAL	Mainchain
1	C	697	ALA	Mainchain

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Mol	Chain	Res	Type	Group
1	C	768	CYS	Mainchain
1	C	897	TYR	Mainchain
1	C	997	TYR	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	9058	0	8964	531	0
1	C	9827	0	9719	1974	0
All	All	18885	0	18683	2459	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 65.

All (2459) 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:C:835:TYR:CE1	1:C:942:HIS:HB3	1.27	1.68
1:C:1278:TYR:CD2	1:C:1288:ILE:HG13	1.23	1.64
1:C:910:LEU:HD23	1:C:915:VAL:CG2	1.27	1.63
1:C:233:VAL:CG2	1:C:234:PRO:HD2	1.28	1.62
1:C:1093:PRO:HG2	1:C:1096:TYR:CE1	1.30	1.61
1:C:233:VAL:HG11	1:C:981:HIS:CE1	1.31	1.60
1:C:829:SER:CB	1:C:965:ARG:HD2	1.15	1.59
1:C:838:GLU:CB	1:C:934:LEU:HB2	1.12	1.55
1:C:1278:TYR:HD2	1:C:1288:ILE:CG1	1.15	1.55
1:C:910:LEU:CD2	1:C:915:VAL:HG23	1.23	1.55
1:C:835:TYR:CE2	1:C:925:VAL:CG2	1.88	1.53
1:C:835:TYR:CE2	1:C:925:VAL:HG21	1.00	1.52
1:C:838:GLU:HB2	1:C:934:LEU:CB	1.42	1.49
1:C:1080:THR:C	1:C:1227:MET:HG2	1.28	1.48
1:C:835:TYR:CD2	1:C:925:VAL:HG21	1.49	1.47
1:C:301:LEU:HD13	1:C:305:THR:CG2	1.41	1.46
1:C:838:GLU:CG	1:C:934:LEU:C	1.81	1.46
1:C:230:ASP:CB	1:C:985:ARG:NE	1.76	1.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:469:ARG:NH1	1:B:498:ILE:CD1	1.78	1.45
1:C:1080:THR:HA	1:C:1227:MET:CG	0.98	1.45
1:C:829:SER:CB	1:C:965:ARG:CD	1.92	1.45
1:C:843:LEU:HD11	1:C:943:GLU:CG	1.01	1.45
1:C:841:ASP:H	1:C:940:ARG:NH1	1.07	1.44
1:C:180:LEU:HD22	1:C:306:GLN:NE2	1.29	1.44
1:C:449:PHE:HB2	1:C:683:TRP:NE1	1.24	1.44
1:C:1080:THR:CA	1:C:1227:MET:HG2	1.22	1.43
1:C:837:THR:O	1:C:934:LEU:CD1	1.67	1.43
1:C:1080:THR:CA	1:C:1227:MET:CG	1.78	1.43
1:C:233:VAL:HG11	1:C:981:HIS:NE2	1.18	1.43
1:C:843:LEU:CD1	1:C:943:GLU:HG3	0.95	1.42
1:B:442:PRO:HB2	1:B:475:ILE:CD1	1.45	1.42
1:C:838:GLU:HG3	1:C:934:LEU:CA	1.50	1.42
1:C:233:VAL:HG22	1:C:234:PRO:CD	1.49	1.41
1:B:389:PHE:CE1	1:B:1319:ARG:HG3	1.54	1.39
1:C:248:VAL:CG1	1:C:970:LEU:HB3	1.53	1.39
1:C:81:ALA:HB2	1:C:170:TYR:CE2	1.59	1.37
1:C:838:GLU:CB	1:C:934:LEU:CB	1.96	1.36
1:C:1093:PRO:CG	1:C:1096:TYR:CE1	2.08	1.36
1:C:449:PHE:CB	1:C:683:TRP:NE1	1.87	1.35
1:C:1214:GLU:CB	1:C:1215:PRO:CD	1.96	1.34
1:C:835:TYR:CD1	1:C:942:HIS:HB3	1.60	1.34
1:C:233:VAL:CG1	1:C:981:HIS:CE1	2.08	1.33
1:C:449:PHE:CB	1:C:683:TRP:HE1	1.39	1.33
1:C:1219:ASP:OD1	1:C:1220:PRO:HD2	1.16	1.33
1:C:835:TYR:CE1	1:C:942:HIS:CB	2.12	1.32
1:C:338:ARG:CG	1:C:342:THR:HG22	1.57	1.32
1:B:135:LYS:CE	1:C:468:ALA:O	1.77	1.32
1:C:383:SER:OG	1:C:796:PRO:CG	1.78	1.32
1:C:233:VAL:CG1	1:C:981:HIS:NE2	1.91	1.31
1:C:230:ASP:HB3	1:C:985:ARG:CD	1.59	1.31
1:C:864:HIS:CE1	1:C:1030:ARG:NH2	2.01	1.29
1:C:1109:SER:OG	1:C:1118:THR:HG21	1.19	1.29
1:C:835:TYR:CZ	1:C:925:VAL:HG21	1.69	1.28
1:C:151:SER:HB3	1:C:400:GLU:OE1	1.24	1.28
1:C:836:GLN:CB	1:C:940:ARG:HG2	1.62	1.27
1:C:230:ASP:CB	1:C:985:ARG:HE	1.36	1.27
1:C:836:GLN:HB2	1:C:940:ARG:CG	1.62	1.27
1:C:838:GLU:HG3	1:C:934:LEU:C	0.90	1.27
1:C:1089:VAL:HG23	1:C:1232:PRO:O	1.30	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1214:GLU:HB3	1:C:1215:PRO:CD	1.59	1.26
1:C:445:GLU:OE2	1:C:447:ARG:HG2	1.27	1.26
1:C:829:SER:HB2	1:C:965:ARG:CD	1.52	1.26
1:C:230:ASP:OD1	1:C:985:ARG:HD3	1.30	1.26
1:B:442:PRO:CB	1:B:475:ILE:HD11	1.66	1.26
1:C:835:TYR:CZ	1:C:925:VAL:CG2	2.20	1.25
1:C:910:LEU:CD2	1:C:915:VAL:CG2	1.96	1.25
1:C:838:GLU:CG	1:C:935:GLN:N	1.98	1.25
1:C:186:ASP:OD1	1:C:279:SER:N	1.69	1.25
1:C:446:LYS:HD3	1:C:448:TYR:OH	1.34	1.25
1:C:659:LEU:O	1:C:662:VAL:HG23	1.27	1.25
1:C:153:ASP:OD2	1:C:401:LEU:HB2	1.10	1.24
1:C:450:PRO:HA	1:C:454:GLU:CG	1.67	1.24
1:C:180:LEU:CD2	1:C:306:GLN:NE2	2.01	1.23
1:C:830:VAL:CG2	1:C:947:GLU:CB	2.15	1.23
1:C:1191:GLU:O	1:C:1195:THR:OG1	1.55	1.23
1:C:225:ILE:HG21	1:C:247:TYR:CD1	1.73	1.22
1:C:230:ASP:CG	1:C:985:ARG:HD3	1.57	1.22
1:B:135:LYS:HE2	1:C:468:ALA:O	1.30	1.22
1:C:372:ALA:HB1	1:C:1315:MET:CE	1.68	1.22
1:C:449:PHE:HB2	1:C:683:TRP:CD1	1.74	1.22
1:C:230:ASP:CG	1:C:985:ARG:CD	2.07	1.22
1:C:660:ALA:O	1:C:662:VAL:N	1.72	1.22
1:C:1119:TYR:O	1:C:1127:ALA:O	1.54	1.22
1:C:230:ASP:C	1:C:985:ARG:HG2	1.58	1.22
1:C:830:VAL:CG2	1:C:947:GLU:HB2	1.68	1.22
1:C:230:ASP:CB	1:C:985:ARG:CD	2.14	1.21
1:C:230:ASP:HB3	1:C:985:ARG:CG	1.68	1.21
1:C:892:VAL:CG1	1:C:894:VAL:CG1	2.19	1.21
1:C:81:ALA:CB	1:C:170:TYR:CE2	2.24	1.20
1:C:446:LYS:CD	1:C:448:TYR:OH	1.88	1.20
1:C:613:LEU:CD2	1:C:632:GLN:HB3	1.71	1.20
1:C:1079:LEU:CD1	1:C:1231:TYR:OH	1.90	1.20
1:C:1214:GLU:CB	1:C:1215:PRO:HD2	1.60	1.19
1:C:845:GLU:OE2	1:C:911:ARG:NE	1.72	1.19
1:C:449:PHE:CA	1:C:683:TRP:HE1	1.54	1.19
1:C:81:ALA:CB	1:C:170:TYR:HE2	1.55	1.19
1:C:225:ILE:CG2	1:C:247:TYR:HD1	1.56	1.18
1:C:654:THR:O	1:C:658:THR:HG22	1.41	1.18
1:C:1263:TYR:CE1	1:C:1278:TYR:CE1	2.32	1.18
1:C:838:GLU:HG3	1:C:935:GLN:N	1.58	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:213:PHE:CB	1:C:219:ILE:HG21	1.74	1.17
1:C:251:LEU:HD23	1:C:1062:ILE:HG13	1.21	1.17
1:C:1292:GLU:O	1:C:1293:VAL:HG23	1.40	1.17
1:C:230:ASP:CG	1:C:985:ARG:NE	1.95	1.17
1:B:388:GLN:HB2	1:B:1320:VAL:HG11	1.18	1.17
1:B:472:GLU:HB3	1:B:761:SER:OG	1.43	1.17
1:C:841:ASP:N	1:C:940:ARG:NH1	1.93	1.17
1:C:835:TYR:O	1:C:846:GLY:HA2	1.42	1.16
1:C:184:GLU:O	1:C:187:ASP:HB3	1.41	1.16
1:C:232:LEU:CD2	1:C:249:SER:HB3	1.74	1.16
1:C:252:LEU:CD1	1:C:971:MET:HE1	1.76	1.16
1:C:232:LEU:HD21	1:C:249:SER:CB	1.75	1.16
1:C:383:SER:OG	1:C:796:PRO:HG3	1.01	1.16
1:C:240:GLY:O	1:C:242:GLU:N	1.79	1.15
1:C:407:HIS:CD2	1:C:1047:LEU:HA	1.80	1.15
1:C:829:SER:OG	1:C:965:ARG:CD	1.74	1.15
1:C:230:ASP:HB3	1:C:985:ARG:NE	1.38	1.15
1:C:406:ASP:OD1	1:C:1039:ALA:HB2	1.41	1.15
1:C:1306:THR:OG1	1:C:1308:ASN:HA	1.47	1.15
1:C:875:THR:OG1	1:C:899:SER:O	1.61	1.15
1:C:338:ARG:HG3	1:C:342:THR:CG2	1.77	1.15
1:C:1072:ASP:O	1:C:1234:GLN:NE2	1.78	1.15
1:C:837:THR:HG22	1:C:934:LEU:CD1	1.77	1.14
1:B:274:MET:CE	1:C:978:GLN:OE1	1.95	1.14
1:C:638:THR:HG21	1:C:1331:ARG:NH2	1.60	1.14
1:C:838:GLU:OE1	1:C:935:GLN:HB2	1.43	1.14
1:B:469:ARG:NH1	1:B:498:ILE:HD12	0.82	1.14
1:C:1219:ASP:OD1	1:C:1220:PRO:CD	1.94	1.14
1:C:1278:TYR:CD2	1:C:1288:ILE:CG1	1.99	1.14
1:C:233:VAL:CG1	1:C:981:HIS:CD2	2.29	1.13
1:C:362:LEU:HD12	1:C:1302:VAL:CG1	1.79	1.13
1:C:843:LEU:HD11	1:C:943:GLU:HG2	1.29	1.13
1:C:901:VAL:HG22	1:C:930:ALA:HB2	1.30	1.13
1:C:838:GLU:OE1	1:C:935:GLN:N	1.80	1.13
1:C:1000:LEU:CD2	1:C:1010:ARG:HH21	1.62	1.13
1:C:248:VAL:HG13	1:C:970:LEU:HB3	1.15	1.13
1:C:671:ASP:O	1:C:672:MET:HB3	1.49	1.13
1:C:451:GLU:OE1	1:C:685:ARG:HG3	1.46	1.13
1:C:383:SER:HG	1:C:796:PRO:CG	1.55	1.12
1:C:613:LEU:HD21	1:C:632:GLN:CB	1.79	1.12
1:C:230:ASP:CG	1:C:985:ARG:HE	1.49	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:668:VAL:CG2	1:C:673:GLN:HB3	1.78	1.12
1:C:1278:TYR:CE2	1:C:1288:ILE:HG13	1.82	1.12
1:C:1079:LEU:HD11	1:C:1231:TYR:OH	0.97	1.12
1:B:472:GLU:O	1:B:761:SER:HB2	1.47	1.11
1:C:144:ASN:HB3	1:C:1318:GLU:OE1	1.47	1.11
1:C:252:LEU:HD13	1:C:971:MET:CE	1.80	1.11
1:C:323:THR:HB	1:C:1266:ASP:HB2	1.27	1.11
1:C:822:MET:HG3	1:C:1044:ARG:HD3	1.25	1.11
1:B:135:LYS:CD	1:C:468:ALA:O	1.97	1.11
1:C:372:ALA:HB1	1:C:1315:MET:HE1	1.26	1.11
1:C:843:LEU:CG	1:C:943:GLU:HG3	1.79	1.11
1:C:157:ILE:HD11	1:C:263:ARG:CG	1.80	1.11
1:C:338:ARG:HG2	1:C:342:THR:N	1.64	1.11
1:C:362:LEU:CD1	1:C:1302:VAL:CG1	2.29	1.11
1:C:660:ALA:C	1:C:662:VAL:H	1.39	1.11
1:C:701:HIS:HE1	1:C:791:ILE:HG23	1.12	1.10
1:C:1093:PRO:HB2	1:C:1096:TYR:CD1	1.86	1.10
1:B:469:ARG:CZ	1:B:498:ILE:HD12	1.81	1.10
1:C:879:THR:H	1:C:880:PRO:CD	1.63	1.10
1:C:1219:ASP:HB2	1:C:1220:PRO:HD3	1.33	1.10
1:C:252:LEU:HD11	1:C:823:ILE:HG21	1.29	1.09
1:C:410:ARG:NH1	1:C:1048:ASP:OD2	1.85	1.09
1:C:830:VAL:HG21	1:C:947:GLU:CB	1.77	1.09
1:C:1084:PRO:O	1:C:1208:ASP:O	1.68	1.09
1:C:478:ILE:CD1	1:C:762:ILE:HD11	1.82	1.09
1:C:841:ASP:H	1:C:940:ARG:CZ	1.65	1.09
1:C:892:VAL:CG1	1:C:894:VAL:HG13	1.80	1.09
1:B:472:GLU:CB	1:B:761:SER:OG	2.00	1.09
1:C:1171:ILE:HD11	1:C:1202:PHE:CZ	1.86	1.09
1:C:334:LEU:HD21	1:C:366:MET:HE3	1.27	1.08
1:C:338:ARG:HG3	1:C:342:THR:HG22	1.14	1.08
1:C:338:ARG:CD	1:C:342:THR:HG22	1.83	1.08
1:C:1047:LEU:HB2	1:C:1051:ARG:HB2	1.34	1.08
1:B:135:LYS:HE3	1:C:470:ALA:H	1.06	1.08
1:C:864:HIS:CE1	1:C:1030:ARG:HH21	1.66	1.08
1:C:342:THR:O	1:C:1305:MET:SD	2.12	1.08
1:C:528:ILE:HG21	1:C:758:ILE:HD11	1.26	1.08
1:C:1263:TYR:CZ	1:C:1278:TYR:OH	2.06	1.08
1:C:301:LEU:CD1	1:C:305:THR:CG2	2.32	1.07
1:C:362:LEU:CD1	1:C:1302:VAL:HG12	1.80	1.07
1:C:633:THR:HG21	1:C:710:SER:OG	1.53	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:656:VAL:HG11	1:C:688:GLU:HB3	1.27	1.07
1:C:225:ILE:HG21	1:C:247:TYR:HD1	0.97	1.07
1:C:611:GLY:O	1:C:634:TYR:CZ	2.06	1.07
1:C:148:GLN:NE2	1:C:375:ARG:HH12	1.51	1.06
1:C:864:HIS:HE1	1:C:1030:ARG:NH2	1.44	1.06
1:C:929:PHE:HB2	1:C:936:MET:HE1	1.37	1.06
1:C:1289:PRO:O	1:C:1293:VAL:HG21	1.53	1.06
1:C:450:PRO:HA	1:C:454:GLU:HG2	1.34	1.06
1:C:1289:PRO:O	1:C:1293:VAL:CG2	2.02	1.06
1:C:892:VAL:HG12	1:C:894:VAL:HG13	1.32	1.06
1:C:606:LEU:HD13	1:C:655:ILE:HG23	1.25	1.05
1:B:472:GLU:HB3	1:B:761:SER:CB	1.84	1.05
1:C:654:THR:HG22	1:C:658:THR:HG21	1.38	1.05
1:C:1263:TYR:CE1	1:C:1278:TYR:CZ	2.43	1.05
1:C:892:VAL:HG12	1:C:894:VAL:CG1	1.84	1.05
1:C:1000:LEU:CD2	1:C:1010:ARG:NH2	2.20	1.05
1:C:1179:THR:OG1	1:C:1180:PRO:HD2	1.54	1.05
1:B:461:ARG:HB2	1:B:461:ARG:HH11	1.20	1.05
1:B:388:GLN:HB2	1:B:1320:VAL:CG1	1.87	1.04
1:C:153:ASP:OD2	1:C:401:LEU:CB	2.03	1.04
1:C:251:LEU:CD2	1:C:1062:ILE:HG13	1.86	1.04
1:C:838:GLU:CG	1:C:934:LEU:HB2	1.86	1.04
1:C:929:PHE:CB	1:C:936:MET:HE1	1.87	1.04
1:B:459:ALA:O	1:B:463:VAL:HG13	1.56	1.04
1:C:1179:THR:OG1	1:C:1180:PRO:CD	2.05	1.04
1:C:1306:THR:CB	1:C:1308:ASN:H	1.63	1.04
1:C:151:SER:CB	1:C:400:GLU:OE1	2.04	1.04
1:C:736:SER:HB2	1:C:1016:ASN:O	1.57	1.04
1:C:835:TYR:CD1	1:C:942:HIS:CB	2.38	1.04
1:C:887:VAL:HG11	1:C:893:ALA:HB2	1.37	1.03
1:C:1089:VAL:HG21	1:C:1233:LEU:HA	1.38	1.03
1:C:838:GLU:CD	1:C:935:GLN:N	2.11	1.03
1:C:701:HIS:CE1	1:C:791:ILE:HG23	1.94	1.03
1:C:830:VAL:CG2	1:C:947:GLU:HB3	1.83	1.03
1:C:837:THR:HG22	1:C:934:LEU:HD11	1.39	1.03
1:C:839:ALA:O	1:C:940:ARG:NH2	1.91	1.03
1:B:388:GLN:O	1:B:1320:VAL:HG12	1.56	1.03
1:C:233:VAL:CG2	1:C:234:PRO:CD	2.22	1.02
1:C:879:THR:H	1:C:880:PRO:HD3	1.22	1.02
1:C:231:LEU:O	1:C:982:ALA:HA	1.59	1.02
1:C:1280:PRO:HB3	1:C:1287:GLY:HA2	1.41	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:157:ILE:HD11	1:C:263:ARG:HG2	1.39	1.02
1:C:668:VAL:HG21	1:C:673:GLN:HB3	1.05	1.02
1:C:874:ILE:HG21	1:C:902:ILE:HD11	1.42	1.02
1:C:1214:GLU:HB2	1:C:1215:PRO:HD2	1.02	1.02
1:C:248:VAL:HG11	1:C:970:LEU:HB3	1.41	1.02
1:C:1093:PRO:CB	1:C:1096:TYR:CE1	2.41	1.02
1:C:157:ILE:CG1	1:C:263:ARG:HG2	1.90	1.01
1:B:135:LYS:HD3	1:C:468:ALA:O	1.59	1.01
1:C:232:LEU:HD21	1:C:249:SER:HB3	1.03	1.01
1:C:450:PRO:HA	1:C:454:GLU:HG3	1.39	1.01
1:C:611:GLY:N	1:C:636:PRO:O	1.93	1.01
1:C:830:VAL:HG22	1:C:947:GLU:HB3	1.40	1.01
1:C:838:GLU:CG	1:C:934:LEU:CA	2.27	1.01
1:B:274:MET:HE3	1:C:978:GLN:OE1	1.57	1.01
1:B:793:TYR:HD2	1:B:1321:ASN:ND2	1.57	1.00
1:B:135:LYS:HE3	1:C:470:ALA:N	1.76	1.00
1:B:469:ARG:HH12	1:B:498:ILE:HD12	1.21	1.00
1:B:469:ARG:HH11	1:B:498:ILE:CD1	1.52	1.00
1:C:839:ALA:C	1:C:940:ARG:NH1	2.14	1.00
1:C:301:LEU:CD1	1:C:305:THR:HG23	1.92	1.00
1:C:924:ASP:OD1	1:C:927:SER:HB2	1.61	0.99
1:C:384:MET:HA	1:C:708:THR:HG21	1.45	0.99
1:C:1171:ILE:HD11	1:C:1202:PHE:CE1	1.96	0.99
1:C:235:ILE:HD11	1:C:978:GLN:NE2	1.76	0.99
1:C:638:THR:HG21	1:C:1331:ARG:HH21	1.24	0.99
1:C:341:LYS:HG3	1:C:1306:THR:HB	1.43	0.99
1:C:362:LEU:HD12	1:C:1302:VAL:HG12	1.00	0.99
1:C:820:ILE:HG21	1:C:983:ILE:CG1	1.93	0.99
1:C:1093:PRO:CG	1:C:1096:TYR:HE1	1.65	0.99
1:B:389:PHE:HE1	1:B:1319:ARG:CG	1.76	0.99
1:C:301:LEU:HD13	1:C:305:THR:HG23	1.01	0.99
1:C:879:THR:N	1:C:880:PRO:HD3	1.77	0.99
1:C:1079:LEU:HD11	1:C:1231:TYR:HH	1.19	0.99
1:C:157:ILE:CD1	1:C:263:ARG:HG2	1.92	0.99
1:C:896:LEU:HD22	1:C:918:VAL:HG21	1.44	0.99
1:C:1219:ASP:CB	1:C:1220:PRO:HD3	1.89	0.99
1:C:1089:VAL:CG2	1:C:1232:PRO:O	2.11	0.98
1:C:835:TYR:HE2	1:C:925:VAL:HG11	1.28	0.98
1:B:274:MET:HE1	1:C:978:GLN:OE1	1.63	0.98
1:C:243:GLN:O	1:C:246:GLU:HB2	1.61	0.98
1:C:440:ILE:HD13	1:C:478:ILE:HG21	1.43	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:301:LEU:HD13	1:C:305:THR:HG21	1.45	0.98
1:C:654:THR:HG22	1:C:658:THR:CG2	1.93	0.98
1:C:254:VAL:CG1	1:C:1062:ILE:HD11	1.93	0.98
1:C:835:TYR:CZ	1:C:925:VAL:HG22	1.95	0.98
1:C:1173:TYR:CD1	1:C:1204:LEU:HD12	1.98	0.98
1:C:242:GLU:HB3	1:C:1200:LYS:HD2	1.46	0.98
1:C:1109:SER:OG	1:C:1118:THR:CG2	2.12	0.98
1:C:261:ASP:O	1:C:1054:ARG:NH2	1.96	0.98
1:C:840:ASP:N	1:C:940:ARG:HH12	1.60	0.98
1:C:1093:PRO:HG2	1:C:1096:TYR:CZ	1.98	0.98
1:C:213:PHE:HB2	1:C:219:ILE:HG21	1.41	0.98
1:C:815:LEU:HB3	1:C:816:PRO:HD2	1.45	0.98
1:C:1000:LEU:HD22	1:C:1010:ARG:NH2	1.78	0.97
1:C:1214:GLU:HB3	1:C:1215:PRO:HD3	0.98	0.97
1:C:180:LEU:HD22	1:C:306:GLN:HE21	1.23	0.97
1:C:509:VAL:HG23	1:C:683:TRP:CZ3	1.99	0.97
1:C:879:THR:N	1:C:880:PRO:CD	2.23	0.97
1:C:148:GLN:HE21	1:C:375:ARG:NH1	1.62	0.97
1:C:554:ARG:HD2	1:C:594:LEU:HD21	1.47	0.97
1:C:451:GLU:OE1	1:C:685:ARG:CG	2.12	0.97
1:C:1137:VAL:O	1:C:1139:MET:N	1.97	0.97
1:C:452:ASN:O	1:C:453:LEU:HB2	1.64	0.97
1:C:668:VAL:HG21	1:C:673:GLN:CB	1.94	0.97
1:C:638:THR:CG2	1:C:1331:ARG:NH2	2.27	0.96
1:C:1155:ILE:CG2	1:C:1166:VAL:HG11	1.94	0.96
1:C:522:PRO:HG2	1:C:636:PRO:HB3	1.47	0.96
1:C:446:LYS:HD3	1:C:448:TYR:HH	1.24	0.96
1:C:1278:TYR:HD2	1:C:1288:ILE:HG12	1.28	0.96
1:C:841:ASP:N	1:C:940:ARG:CZ	2.28	0.96
1:C:450:PRO:CA	1:C:454:GLU:HG2	1.96	0.96
1:C:963:ALA:HB3	1:C:1059:LEU:HG	1.48	0.96
1:C:862:ARG:HB3	1:C:952:PHE:CZ	2.01	0.95
1:C:1031:TYR:HE2	1:C:1041:ARG:NH1	1.63	0.95
1:C:338:ARG:HG3	1:C:342:THR:CB	1.96	0.95
1:C:371:THR:O	1:C:374:ASP:N	1.98	0.95
1:C:837:THR:O	1:C:934:LEU:HD13	0.78	0.95
1:C:184:GLU:O	1:C:187:ASP:CB	2.15	0.95
1:C:372:ALA:CB	1:C:1315:MET:CE	2.43	0.95
1:C:449:PHE:O	1:C:683:TRP:HD1	1.46	0.95
1:C:659:LEU:O	1:C:662:VAL:CG2	2.15	0.95
1:C:1079:LEU:H	1:C:1079:LEU:HD12	1.27	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:85:ASP:OD2	1:C:161:LYS:HG3	1.65	0.95
1:C:1120:THR:O	1:C:1122:PRO:HD3	1.67	0.95
1:C:910:LEU:HD21	1:C:915:VAL:HG23	1.46	0.95
1:C:321:ALA:HB3	1:C:1283:ASN:ND2	1.81	0.95
1:C:815:LEU:HD13	1:C:1051:ARG:NH2	1.81	0.95
1:C:741:TYR:CE2	1:C:1022:ILE:HD11	2.01	0.94
1:C:1093:PRO:HB2	1:C:1096:TYR:CE1	2.02	0.94
1:C:874:ILE:HD11	1:C:883:ILE:CD1	1.97	0.94
1:C:909:TYR:CE1	1:C:913:ASN:OD1	2.20	0.94
1:C:1121:HIS:CD2	1:C:1135:PRO:CG	2.50	0.94
1:C:1310:ARG:CZ	1:C:1310:ARG:HA	1.96	0.94
1:C:248:VAL:HG11	1:C:970:LEU:C	1.88	0.94
1:C:829:SER:HB3	1:C:965:ARG:HD2	1.49	0.94
1:C:1243:ARG:HB3	1:C:1258:VAL:HG22	1.47	0.94
1:C:148:GLN:NE2	1:C:375:ARG:NH1	2.15	0.94
1:C:838:GLU:OE1	1:C:935:GLN:CB	2.15	0.94
1:C:999:LYS:HB2	1:C:1008:LEU:O	1.67	0.94
1:C:1206:PHE:CD2	1:C:1236:ILE:CD1	2.50	0.94
1:C:1292:GLU:O	1:C:1293:VAL:CG2	2.14	0.94
1:B:472:GLU:CB	1:B:761:SER:CB	2.45	0.94
1:C:1081:ASP:N	1:C:1227:MET:HG2	1.82	0.93
1:C:338:ARG:CG	1:C:342:THR:CG2	2.42	0.93
1:C:176:LYS:HG3	1:C:177:LYS:H	1.32	0.93
1:C:887:VAL:CG1	1:C:893:ALA:HB2	1.97	0.93
1:C:317:MET:SD	1:C:1262:SER:HB2	2.08	0.93
1:C:1134:ARG:HB3	1:C:1135:PRO:HD3	1.51	0.93
1:B:262:ASN:O	1:B:361:ASN:ND2	2.02	0.93
1:C:449:PHE:HA	1:C:683:TRP:HE1	1.32	0.93
1:C:838:GLU:CG	1:C:934:LEU:CB	2.42	0.93
1:B:389:PHE:CE1	1:B:1319:ARG:CG	2.50	0.93
1:C:233:VAL:HG13	1:C:981:HIS:CD2	2.05	0.92
1:C:259:MET:HG3	1:C:1055:LEU:HB2	1.49	0.92
1:C:226:PRO:O	1:C:250:GLY:HA3	1.70	0.92
1:C:311:ASN:O	1:C:315:THR:HG23	1.69	0.92
1:C:892:VAL:HG11	1:C:894:VAL:CG1	1.96	0.92
1:C:445:GLU:OE2	1:C:447:ARG:CG	2.17	0.92
1:B:235:ILE:HG13	1:B:978:GLN:HE21	1.33	0.92
1:C:230:ASP:CB	1:C:985:ARG:CG	2.45	0.92
1:C:822:MET:CG	1:C:1044:ARG:HD3	1.99	0.92
1:C:956:ASP:O	1:C:959:GLN:OE1	1.85	0.92
1:C:701:HIS:CE1	1:C:791:ILE:CG2	2.53	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:839:ALA:O	1:C:940:ARG:CZ	2.18	0.92
1:C:843:LEU:HD12	1:C:943:GLU:HG3	1.46	0.92
1:C:845:GLU:CD	1:C:911:ARG:HE	1.73	0.92
1:C:870:ASP:O	1:C:871:PRO:C	2.06	0.92
1:C:213:PHE:HB3	1:C:219:ILE:HG21	1.47	0.92
1:C:478:ILE:HD12	1:C:762:ILE:HD11	1.50	0.92
1:C:1121:HIS:HD2	1:C:1135:PRO:HG3	1.35	0.92
1:C:405:HIS:CD2	1:C:625:PRO:HA	2.03	0.92
1:B:1249:ASN:OD1	1:C:1115:ASN:OD1	1.88	0.92
1:C:230:ASP:HB2	1:C:985:ARG:HE	1.35	0.92
1:C:841:ASP:H	1:C:940:ARG:HH12	0.97	0.92
1:C:1080:THR:C	1:C:1227:MET:CG	2.25	0.91
1:C:225:ILE:CG2	1:C:247:TYR:CD1	2.41	0.91
1:C:935:GLN:HB3	1:C:939:ASN:HB3	1.51	0.91
1:C:528:ILE:HD13	1:C:758:ILE:HD11	1.53	0.91
1:C:701:HIS:HE1	1:C:791:ILE:CG2	1.83	0.91
1:C:1155:ILE:HG21	1:C:1166:VAL:HG11	1.51	0.91
1:C:495:LEU:HD11	1:C:531:ASP:HB3	1.50	0.90
1:C:838:GLU:O	1:C:940:ARG:NH1	2.04	0.90
1:C:1089:VAL:CG2	1:C:1233:LEU:HA	1.98	0.90
1:C:248:VAL:CG1	1:C:970:LEU:CB	2.47	0.90
1:C:452:ASN:O	1:C:453:LEU:CD2	2.18	0.90
1:C:660:ALA:O	1:C:663:VAL:N	2.05	0.90
1:C:1279:SER:N	1:C:1280:PRO:HA	1.87	0.90
1:C:1084:PRO:HD2	1:C:1085:ASP:OD1	1.72	0.90
1:C:870:ASP:O	1:C:871:PRO:O	1.89	0.90
1:C:446:LYS:HD2	1:C:448:TYR:OH	1.71	0.90
1:C:838:GLU:HB3	1:C:934:LEU:CB	2.02	0.90
1:C:1306:THR:OG1	1:C:1308:ASN:CA	2.19	0.90
1:C:87:GLU:HB2	1:C:159:ASP:O	1.72	0.90
1:C:509:VAL:CG2	1:C:683:TRP:CH2	2.55	0.89
1:C:835:TYR:HE1	1:C:942:HIS:HB3	1.17	0.89
1:C:157:ILE:HD11	1:C:263:ARG:CB	2.01	0.89
1:C:1085:ASP:HB2	1:C:1086:PRO:CD	2.02	0.89
1:C:312:ARG:HG3	1:C:312:ARG:HH21	1.38	0.89
1:C:837:THR:C	1:C:934:LEU:HD13	1.91	0.89
1:C:310:LEU:HD21	1:C:1242:MET:HE3	1.55	0.89
1:C:610:GLN:HA	1:C:610:GLN:HE21	1.36	0.89
1:C:892:VAL:CG1	1:C:894:VAL:HG12	2.00	0.89
1:C:1306:THR:OG1	1:C:1308:ASN:N	2.06	0.89
1:C:671:ASP:O	1:C:672:MET:CB	2.14	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:338:ARG:HA	1:C:342:THR:HA	1.52	0.88
1:C:204:VAL:O	1:C:1240:ARG:O	1.90	0.88
1:C:81:ALA:HB2	1:C:170:TYR:HE2	0.75	0.88
1:B:898:GLN:HE21	1:B:917:VAL:HB	1.38	0.88
1:C:323:THR:HA	1:C:1279:SER:OG	1.72	0.88
1:C:389:PHE:CE1	1:C:1319:ARG:HB3	2.08	0.88
1:C:829:SER:OG	1:C:965:ARG:HD3	1.73	0.88
1:C:843:LEU:CD1	1:C:943:GLU:CG	1.86	0.88
1:C:1134:ARG:HB3	1:C:1135:PRO:CD	2.03	0.88
1:B:276:ASN:HD21	1:C:244:SER:HB3	1.39	0.88
1:C:849:MET:HA	1:C:917:VAL:O	1.74	0.88
1:C:323:THR:HB	1:C:1266:ASP:CB	2.04	0.88
1:C:1322:PRO:HB3	1:C:1328:ILE:HD13	1.54	0.88
1:C:924:ASP:OD1	1:C:927:SER:N	2.06	0.88
1:C:129:ALA:HB3	1:C:133:MET:HG2	1.57	0.87
1:C:77:THR:O	1:C:172:ASP:HB2	1.74	0.87
1:C:334:LEU:HD21	1:C:366:MET:CE	2.04	0.87
1:C:1093:PRO:HB2	1:C:1096:TYR:HD1	1.36	0.87
1:C:735:THR:HG21	1:C:1028:VAL:HG21	1.57	0.87
1:C:610:GLN:OE1	1:C:651:ARG:HG2	1.74	0.87
1:C:910:LEU:CD2	1:C:915:VAL:HG21	2.04	0.87
1:C:96:ILE:CD1	1:C:103:GLY:HA2	2.04	0.87
1:C:266:ILE:HD13	1:C:1304:MET:HB2	1.56	0.87
1:C:449:PHE:CA	1:C:683:TRP:NE1	2.22	0.87
1:C:1271:SER:HA	1:C:1277:LEU:HD13	1.56	0.87
1:C:213:PHE:CB	1:C:219:ILE:CG2	2.53	0.87
1:C:213:PHE:HB3	1:C:219:ILE:CG2	2.05	0.87
1:C:830:VAL:HG22	1:C:947:GLU:CB	2.00	0.87
1:C:838:GLU:HG3	1:C:934:LEU:O	1.75	0.87
1:C:503:GLU:OE2	1:C:542:ARG:HD2	1.75	0.86
1:C:874:ILE:HD11	1:C:883:ILE:HD11	1.57	0.86
1:C:886:SER:O	1:C:890:THR:HG22	1.74	0.86
1:C:248:VAL:HG13	1:C:970:LEU:CB	2.03	0.86
1:C:449:PHE:HA	1:C:683:TRP:NE1	1.89	0.86
1:C:841:ASP:N	1:C:940:ARG:HH12	1.63	0.86
1:C:1093:PRO:CB	1:C:1096:TYR:HE1	1.85	0.86
1:C:122:ASN:O	1:C:122:ASN:ND2	2.07	0.86
1:C:265:VAL:HG21	1:C:1301:VAL:HG23	1.57	0.86
1:C:666:ARG:HG2	1:C:666:ARG:HH11	1.40	0.86
1:C:1093:PRO:CB	1:C:1096:TYR:CD1	2.59	0.86
1:C:1211:LEU:HD11	1:C:1246:VAL:HG23	1.55	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:493:HIS:HB2	1:C:756:THR:O	1.74	0.86
1:C:838:GLU:CD	1:C:935:GLN:H	1.76	0.86
1:C:901:VAL:CG2	1:C:930:ALA:HB2	2.06	0.86
1:C:924:ASP:CG	1:C:927:SER:HB2	1.95	0.86
1:C:1121:HIS:CD2	1:C:1135:PRO:HG3	2.08	0.86
1:B:442:PRO:CB	1:B:475:ILE:CD1	2.39	0.86
1:C:1306:THR:C	1:C:1308:ASN:H	1.56	0.86
1:B:461:ARG:HE	1:B:504:ASP:CB	1.89	0.85
1:C:206:ILE:O	1:C:1239:ALA:HB1	1.76	0.85
1:C:323:THR:CB	1:C:1266:ASP:HB2	2.06	0.85
1:C:530:GLY:HA3	1:C:575:TRP:CD1	2.11	0.85
1:C:375:ARG:HG2	1:C:375:ARG:HH11	1.38	0.85
1:C:213:PHE:HB3	1:C:219:ILE:CB	2.05	0.85
1:C:252:LEU:HD13	1:C:971:MET:HE1	0.89	0.85
1:C:1306:THR:C	1:C:1308:ASN:N	2.21	0.85
1:C:199:TYR:OH	1:C:1247:ASN:ND2	2.09	0.85
1:C:462:LEU:O	1:C:462:LEU:HD22	1.76	0.85
1:C:1219:ASP:CB	1:C:1220:PRO:CD	2.54	0.85
1:B:525:PHE:O	1:B:529:LYS:HB3	1.76	0.85
1:C:163:TYR:CE2	1:C:258:VAL:HG23	2.11	0.85
1:C:148:GLN:HE21	1:C:375:ARG:HH12	1.11	0.85
1:C:338:ARG:HG2	1:C:341:LYS:C	1.97	0.85
1:C:1072:ASP:H	1:C:1234:GLN:HE22	1.25	0.85
1:C:820:ILE:HG21	1:C:983:ILE:HG12	1.58	0.84
1:C:371:THR:O	1:C:373:ASP:N	2.09	0.84
1:C:849:MET:HG2	1:C:919:MET:HE3	1.58	0.84
1:C:552:ILE:HD12	1:C:572:ASN:HB2	1.58	0.84
1:C:929:PHE:CB	1:C:936:MET:CE	2.55	0.84
1:B:919:MET:SD	1:B:928:ARG:NH1	2.51	0.84
1:C:334:LEU:HD11	1:C:366:MET:HE1	1.58	0.84
1:C:405:HIS:NE2	1:C:625:PRO:HA	1.90	0.84
1:C:96:ILE:HD12	1:C:103:GLY:HA2	1.57	0.84
1:C:301:LEU:CD1	1:C:305:THR:HG21	2.05	0.84
1:C:454:GLU:O	1:C:455:GLN:HB3	1.76	0.84
1:C:663:VAL:O	1:C:677:ARG:HD2	1.76	0.84
1:B:269:GLU:HB3	1:B:292:ASN:HD22	1.40	0.84
1:B:461:ARG:HH11	1:B:461:ARG:CB	1.89	0.84
1:C:833:ARG:NH1	1:C:942:HIS:NE2	2.26	0.84
1:B:472:GLU:HA	1:B:473:ALA:HB2	1.57	0.84
1:B:1276:LEU:HB3	1:B:1290:LYS:HD3	1.59	0.84
1:C:154:PHE:CE1	1:C:361:ASN:ND2	2.46	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:700:ASP:OD2	1:C:1326:ARG:HG3	1.77	0.84
1:C:733:VAL:HG21	1:C:1022:ILE:HD12	1.60	0.84
1:C:874:ILE:HG13	1:C:895:VAL:CG1	2.08	0.84
1:C:1263:TYR:HE1	1:C:1278:TYR:CE1	1.95	0.84
1:B:459:ALA:O	1:B:463:VAL:CG1	2.26	0.83
1:C:414:LEU:HD23	1:C:814:THR:OG1	1.77	0.83
1:C:1285:GLN:HE21	1:C:1285:GLN:H	1.24	0.83
1:C:495:LEU:H	1:C:495:LEU:HD12	1.43	0.83
1:C:258:VAL:HG11	1:C:1058:GLY:HA2	1.60	0.83
1:C:656:VAL:HG11	1:C:688:GLU:CB	2.08	0.83
1:C:840:ASP:N	1:C:940:ARG:NH1	2.26	0.83
1:C:887:VAL:HG11	1:C:893:ALA:CB	2.07	0.83
1:B:440:ILE:HG12	1:B:772:TYR:CE2	2.13	0.83
1:C:321:ALA:HB3	1:C:1283:ASN:HD21	1.40	0.83
1:C:1021:ARG:HB2	1:C:1021:ARG:HH11	1.43	0.83
1:C:1322:PRO:HB3	1:C:1328:ILE:CD1	2.06	0.83
1:C:660:ALA:C	1:C:662:VAL:N	2.17	0.83
1:C:839:ALA:C	1:C:940:ARG:CZ	2.46	0.83
1:C:550:ILE:HD12	1:C:550:ILE:O	1.78	0.83
1:C:341:LYS:HG3	1:C:1306:THR:CB	2.09	0.83
1:C:865:ILE:HG21	1:C:957:PHE:HE2	1.41	0.83
1:C:874:ILE:CG2	1:C:902:ILE:HD11	2.08	0.83
1:C:1072:ASP:N	1:C:1234:GLN:HE22	1.75	0.83
1:C:107:GLN:OE1	1:C:107:GLN:N	2.11	0.83
1:C:352:HIS:HD2	1:C:1297:SER:H	1.26	0.83
1:C:448:TYR:C	1:C:450:PRO:HD2	1.98	0.83
1:C:1000:LEU:HD22	1:C:1010:ARG:HH21	1.38	0.83
1:C:230:ASP:CA	1:C:985:ARG:HG2	2.07	0.83
1:C:838:GLU:HG3	1:C:934:LEU:CB	2.06	0.83
1:C:865:ILE:CG2	1:C:957:PHE:HE2	1.91	0.83
1:C:1263:TYR:CE1	1:C:1278:TYR:OH	2.27	0.83
1:B:1249:ASN:O	1:C:1109:SER:HA	1.78	0.83
1:C:265:VAL:HG13	1:C:358:LEU:HD13	1.60	0.83
1:C:1210:LEU:O	1:C:1210:LEU:HG	1.78	0.83
1:C:452:ASN:O	1:C:453:LEU:HD23	1.79	0.82
1:C:896:LEU:HA	1:C:918:VAL:CG2	2.09	0.82
1:C:1263:TYR:CD1	1:C:1278:TYR:HE1	1.97	0.82
1:C:509:VAL:CG2	1:C:683:TRP:CZ3	2.61	0.82
1:C:815:LEU:HB3	1:C:816:PRO:CD	2.08	0.82
1:C:449:PHE:CZ	1:C:463:VAL:HG22	2.14	0.82
1:B:461:ARG:HE	1:B:504:ASP:HB2	1.45	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:494:GLU:N	1:C:494:GLU:OE2	2.13	0.82
1:C:1049:GLU:O	1:C:1053:ARG:HG3	1.80	0.82
1:C:1210:LEU:CD2	1:C:1244:ALA:CB	2.58	0.82
1:B:272:THR:HG22	1:B:289:THR:HG22	1.61	0.82
1:C:180:LEU:CD2	1:C:306:GLN:HE22	1.91	0.82
1:C:333:ARG:HE	1:C:1272:ARG:HA	1.44	0.82
1:C:830:VAL:HG23	1:C:947:GLU:HB2	1.60	0.82
1:C:879:THR:H	1:C:880:PRO:HD2	1.44	0.82
1:C:965:ARG:HH11	1:C:968:ARG:NH1	1.78	0.81
1:C:1179:THR:OG1	1:C:1180:PRO:HD3	1.81	0.81
1:B:135:LYS:HE2	1:C:469:ARG:HA	1.61	0.81
1:C:611:GLY:O	1:C:634:TYR:OH	1.98	0.81
1:C:230:ASP:O	1:C:985:ARG:HG2	1.79	0.81
1:C:446:LYS:HB2	1:C:448:TYR:CE1	2.15	0.81
1:C:929:PHE:CG	1:C:936:MET:CE	2.63	0.81
1:C:654:THR:O	1:C:658:THR:CG2	2.26	0.81
1:C:157:ILE:HD11	1:C:263:ARG:HB3	1.59	0.81
1:C:164:LEU:HD11	1:C:353:PHE:HE2	1.42	0.81
1:C:946:LEU:HD21	1:C:965:ARG:HG2	1.63	0.81
1:C:838:GLU:O	1:C:940:ARG:NE	2.11	0.81
1:C:1289:PRO:O	1:C:1293:VAL:HG23	1.80	0.81
1:B:826:GLY:O	1:B:968:ARG:NH2	2.13	0.81
1:C:233:VAL:HG23	1:C:234:PRO:HD2	1.55	0.81
1:C:493:HIS:CB	1:C:756:THR:O	2.28	0.81
1:C:963:ALA:CB	1:C:1059:LEU:HG	2.09	0.81
1:C:230:ASP:O	1:C:985:ARG:CG	2.29	0.81
1:C:656:VAL:CG1	1:C:688:GLU:HG2	2.11	0.81
1:C:1120:THR:O	1:C:1122:PRO:CD	2.28	0.81
1:C:1210:LEU:HD23	1:C:1244:ALA:CB	2.10	0.81
1:C:87:GLU:CB	1:C:159:ASP:O	2.29	0.81
1:C:495:LEU:HD12	1:C:495:LEU:N	1.93	0.81
1:C:741:TYR:HE2	1:C:1022:ILE:HD11	1.42	0.81
1:C:494:GLU:HB3	1:C:577:GLN:NE2	1.96	0.80
1:C:1273:ASN:O	1:C:1273:ASN:ND2	2.14	0.80
1:C:213:PHE:O	1:C:219:ILE:HB	1.80	0.80
1:C:81:ALA:HB3	1:C:170:TYR:CE2	2.16	0.80
1:C:929:PHE:CG	1:C:936:MET:HE2	2.16	0.80
1:C:1306:THR:HG1	1:C:1308:ASN:HA	1.46	0.80
1:C:629:ARG:HB2	1:C:1037:ILE:HG23	1.61	0.80
1:C:452:ASN:O	1:C:453:LEU:CB	2.29	0.80
1:C:1079:LEU:O	1:C:1227:MET:CB	2.29	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1081:ASP:H	1:C:1227:MET:HB3	1.46	0.80
1:B:793:TYR:CD2	1:B:1321:ASN:ND2	2.48	0.80
1:C:144:ASN:CB	1:C:1318:GLU:OE1	2.28	0.80
1:C:835:TYR:CE2	1:C:925:VAL:HG11	2.17	0.80
1:C:685:ARG:HB3	1:C:685:ARG:HH11	1.45	0.80
1:B:394:GLN:HB2	1:C:1005:LEU:HD21	1.63	0.80
1:C:310:LEU:HD21	1:C:1242:MET:CE	2.11	0.80
1:C:528:ILE:HD13	1:C:758:ILE:CD1	2.11	0.80
1:C:837:THR:HG22	1:C:934:LEU:HD12	1.64	0.79
1:C:1134:ARG:HH22	1:C:1154:ASN:HD21	1.30	0.79
1:C:233:VAL:CG1	1:C:981:HIS:CG	2.65	0.79
1:C:1121:HIS:HD2	1:C:1135:PRO:CG	1.91	0.79
1:C:1281:VAL:O	1:C:1283:ASN:N	2.15	0.79
1:C:332:THR:O	1:C:335:ASP:HB2	1.83	0.79
1:C:847:ILE:HG12	1:C:911:ARG:HB2	1.63	0.79
1:C:1214:GLU:HB2	1:C:1215:PRO:CD	1.80	0.79
1:C:659:LEU:O	1:C:659:LEU:HD22	1.83	0.79
1:C:233:VAL:HG12	1:C:981:HIS:CE1	2.17	0.79
1:C:406:ASP:OD1	1:C:1039:ALA:CB	2.29	0.79
1:C:230:ASP:C	1:C:985:ARG:CG	2.47	0.79
1:C:384:MET:HA	1:C:708:THR:CG2	2.13	0.79
1:C:449:PHE:CD1	1:C:450:PRO:HD3	2.18	0.79
1:C:1076:ILE:HB	1:C:1230:ILE:HG22	1.65	0.79
1:C:252:LEU:CD1	1:C:823:ILE:HG21	2.12	0.78
1:C:230:ASP:CB	1:C:985:ARG:HG2	2.13	0.78
1:C:252:LEU:CD1	1:C:971:MET:CE	2.50	0.78
1:C:1109:SER:HG	1:C:1118:THR:HG21	1.45	0.78
1:C:261:ASP:O	1:C:1054:ARG:CZ	2.30	0.78
1:C:924:ASP:OD1	1:C:927:SER:CB	2.30	0.78
1:C:1263:TYR:CD1	1:C:1278:TYR:CE1	2.71	0.78
1:C:441:ARG:HG2	1:C:441:ARG:HH21	1.48	0.78
1:B:342:THR:HB	1:B:1309:ILE:HD11	1.65	0.78
1:C:449:PHE:C	1:C:686:HIS:HD2	1.87	0.78
1:C:685:ARG:HH11	1:C:685:ARG:CB	1.95	0.78
1:C:985:ARG:O	1:C:985:ARG:NH2	2.15	0.78
1:C:1060:ARG:NH1	1:C:1292:GLU:H	1.82	0.78
1:C:1091:ASP:OD1	1:C:1091:ASP:N	2.15	0.78
1:C:1219:ASP:CG	1:C:1220:PRO:CD	2.52	0.78
1:C:434:VAL:HG23	1:C:709:MET:HE1	1.64	0.78
1:C:821:ASN:HA	1:C:824:LEU:HD22	1.66	0.78
1:C:297:ASN:ND2	1:C:298:PRO:HD2	1.99	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:614:ARG:HD3	1:C:635:ILE:HD12	1.64	0.77
1:C:896:LEU:HD22	1:C:918:VAL:CG2	2.14	0.77
1:C:948:ILE:HG13	1:C:962:ASP:HB3	1.65	0.77
1:C:1290:LYS:HZ1	1:C:1299:SER:HB3	1.49	0.77
1:C:1313:ASP:OD1	1:C:1313:ASP:N	2.12	0.77
1:C:449:PHE:CB	1:C:683:TRP:CD1	2.51	0.77
1:C:901:VAL:HA	1:C:928:ARG:O	1.85	0.77
1:C:986:ILE:O	1:C:989:ILE:HG22	1.83	0.77
1:C:77:THR:O	1:C:172:ASP:CB	2.32	0.77
1:C:615:THR:H	1:C:1333:ALA:C	1.87	0.77
1:C:333:ARG:HG2	1:C:333:ARG:HH21	1.49	0.77
1:C:910:LEU:HD23	1:C:915:VAL:HG22	1.61	0.77
1:C:184:GLU:O	1:C:187:ASP:N	2.16	0.77
1:C:338:ARG:CG	1:C:342:THR:N	2.47	0.77
1:C:449:PHE:O	1:C:683:TRP:CD1	2.34	0.77
1:C:830:VAL:HG21	1:C:947:GLU:HB2	1.43	0.77
1:C:835:TYR:CD2	1:C:925:VAL:CG2	2.40	0.77
1:C:946:LEU:N	1:C:946:LEU:HD12	2.00	0.77
1:B:352:HIS:HA	1:B:1300:ASN:HD21	1.50	0.77
1:C:265:VAL:HG21	1:C:1301:VAL:CG2	2.14	0.77
1:C:407:HIS:NE2	1:C:1047:LEU:HD12	2.00	0.77
1:C:484:ARG:CZ	1:C:758:ILE:HG22	2.15	0.77
1:C:896:LEU:CD2	1:C:918:VAL:HG21	2.14	0.77
1:C:1074:VAL:HB	1:C:1173:TYR:HE2	1.50	0.77
1:C:485:GLU:OE1	1:C:486:VAL:HG13	1.85	0.76
1:C:843:LEU:HD21	1:C:943:GLU:CD	2.04	0.76
1:B:1064:ASN:HD21	1:B:1296:ILE:HD11	1.50	0.76
1:C:516:LEU:HB3	1:C:763:VAL:HG11	1.66	0.76
1:C:492:VAL:HG22	1:C:747:ARG:HA	1.66	0.76
1:C:81:ALA:CB	1:C:170:TYR:CZ	2.69	0.76
1:C:339:LEU:HD21	1:C:366:MET:HA	1.68	0.76
1:C:687:LEU:HD23	1:C:687:LEU:C	2.04	0.76
1:C:129:ALA:CB	1:C:133:MET:HG2	2.16	0.76
1:C:232:LEU:CG	1:C:249:SER:HB3	2.14	0.76
1:C:364:ALA:CB	1:C:1050:LEU:HD21	2.15	0.76
1:C:838:GLU:C	1:C:940:ARG:NE	2.38	0.76
1:C:1104:ARG:HG2	1:C:1104:ARG:HH11	1.49	0.76
1:C:838:GLU:O	1:C:940:ARG:CZ	2.34	0.76
1:B:388:GLN:H	1:B:1320:VAL:CG1	1.98	0.76
1:C:835:TYR:CE2	1:C:925:VAL:CB	2.69	0.76
1:C:613:LEU:HD21	1:C:632:GLN:HB3	0.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:874:ILE:HD11	1:C:883:ILE:HD12	1.67	0.76
1:C:897:TYR:CD1	1:C:898:GLN:N	2.54	0.76
1:C:480:LEU:O	1:C:480:LEU:HD23	1.85	0.76
1:C:1044:ARG:HG3	1:C:1044:ARG:HH11	1.51	0.76
1:B:397:LEU:CD2	1:C:1008:LEU:HD11	2.16	0.75
1:C:321:ALA:CB	1:C:1283:ASN:ND2	2.49	0.75
1:C:556:ALA:C	1:C:587:ALA:HB2	2.07	0.75
1:C:734:ILE:HG23	1:C:1017:ALA:HB1	1.68	0.75
1:B:903:ASN:O	1:B:907:SER:CB	2.34	0.75
1:B:793:TYR:HD2	1:B:1321:ASN:HD21	1.31	0.75
1:C:341:LYS:CG	1:C:1306:THR:HB	2.17	0.75
1:C:910:LEU:HD21	1:C:915:VAL:CG2	2.10	0.75
1:C:449:PHE:CG	1:C:466:VAL:HG11	2.22	0.75
1:C:659:LEU:HD22	1:C:662:VAL:HG21	1.67	0.75
1:C:1285:GLN:HE21	1:C:1285:GLN:N	1.85	0.75
1:C:179:LYS:HE3	1:C:181:ARG:HB3	1.67	0.75
1:C:1031:TYR:HE2	1:C:1041:ARG:HH11	1.31	0.75
1:C:254:VAL:HG13	1:C:1062:ILE:CD1	2.17	0.75
1:C:1093:PRO:HG2	1:C:1096:TYR:CD1	2.17	0.75
1:C:1173:TYR:CE1	1:C:1204:LEU:HD12	2.22	0.75
1:C:910:LEU:HG	1:C:915:VAL:HG21	1.69	0.75
1:C:964:VAL:HG13	1:C:1059:LEU:HD21	1.69	0.75
1:B:873:TYR:HB3	1:B:897:TYR:HB2	1.68	0.75
1:C:333:ARG:HG2	1:C:333:ARG:NH2	2.01	0.75
1:B:1185:THR:O	1:B:1205:GLN:NE2	2.20	0.75
1:C:654:THR:CG2	1:C:658:THR:HG21	2.16	0.75
1:C:865:ILE:CG2	1:C:957:PHE:CE2	2.70	0.75
1:C:1085:ASP:HA	1:C:1208:ASP:O	1.87	0.75
1:C:1144:ARG:HD3	1:C:1168:ILE:HG21	1.68	0.75
1:B:436:SER:O	1:B:437:ALA:HB3	1.86	0.74
1:C:233:VAL:HG12	1:C:981:HIS:CG	2.22	0.74
1:C:525:PHE:CE1	1:C:532:ILE:HD12	2.22	0.74
1:C:495:LEU:HD11	1:C:531:ASP:CB	2.17	0.74
1:C:266:ILE:HD13	1:C:1304:MET:CB	2.16	0.74
1:C:451:GLU:HB2	1:C:686:HIS:HB3	1.68	0.74
1:C:611:GLY:CA	1:C:636:PRO:O	2.35	0.74
1:C:1280:PRO:HG3	1:C:1286:VAL:O	1.87	0.74
1:C:87:GLU:OE1	1:C:157:ILE:HG21	1.88	0.74
1:C:449:PHE:CE2	1:C:463:VAL:HG22	2.22	0.74
1:C:404:ASP:O	1:C:408:ILE:HG12	1.87	0.74
1:C:449:PHE:CA	1:C:683:TRP:CD1	2.71	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:838:GLU:OE1	1:C:935:GLN:CA	2.35	0.74
1:C:910:LEU:CG	1:C:915:VAL:CG2	2.65	0.74
1:C:934:LEU:O	1:C:936:MET:N	2.19	0.74
1:B:196:LEU:HD23	1:B:296:VAL:HG11	1.70	0.74
1:B:442:PRO:HB2	1:B:475:ILE:HD11	0.76	0.74
1:C:213:PHE:HB3	1:C:219:ILE:HG13	1.68	0.74
1:C:1296:ILE:O	1:C:1296:ILE:HD13	1.87	0.74
1:B:439:VAL:O	1:B:440:ILE:HG13	1.87	0.74
1:C:87:GLU:HG3	1:C:87:GLU:O	1.87	0.74
1:B:139:ASN:O	1:C:757:ILE:HB	1.88	0.74
1:B:338:ARG:HH12	1:C:1005:LEU:HD22	1.52	0.74
1:B:699:THR:O	1:B:703:SER:OG	2.04	0.74
1:C:372:ALA:CB	1:C:1315:MET:HE3	2.18	0.74
1:C:422:LEU:CD1	1:C:490:PHE:CE2	2.71	0.73
1:C:449:PHE:HB2	1:C:683:TRP:CE2	2.19	0.73
1:C:509:VAL:HG22	1:C:683:TRP:CH2	2.23	0.73
1:C:1280:PRO:CB	1:C:1287:GLY:HA2	2.18	0.73
1:C:259:MET:CG	1:C:1055:LEU:HB2	2.18	0.73
1:C:265:VAL:HG23	1:C:1303:SER:HA	1.70	0.73
1:C:901:VAL:HG22	1:C:930:ALA:CB	2.15	0.73
1:C:1112:ASN:O	1:C:1112:ASN:ND2	2.15	0.73
1:B:442:PRO:HB2	1:B:475:ILE:HD13	1.64	0.73
1:C:108:LYS:HB2	1:C:108:LYS:NZ	2.03	0.73
1:C:1079:LEU:HD11	1:C:1231:TYR:CZ	2.16	0.73
1:C:1104:ARG:HD2	1:C:1104:ARG:O	1.88	0.73
1:C:338:ARG:O	1:C:340:VAL:N	2.20	0.73
1:C:795:ASP:OD1	1:C:795:ASP:N	2.17	0.73
1:C:1278:TYR:CD2	1:C:1288:ILE:CD1	2.71	0.73
1:C:168:VAL:HG23	1:C:204:VAL:HG13	1.70	0.73
1:C:516:LEU:CB	1:C:763:VAL:HG11	2.17	0.73
1:C:338:ARG:O	1:C:341:LYS:O	2.06	0.73
1:B:903:ASN:O	1:B:907:SER:HB2	1.89	0.73
1:C:146:GLU:N	1:C:146:GLU:OE1	2.21	0.73
1:C:254:VAL:HG13	1:C:1062:ILE:HD11	1.70	0.73
1:C:1081:ASP:N	1:C:1227:MET:HB3	2.03	0.73
1:C:247:TYR:CD2	1:C:1070:ARG:HD3	2.24	0.72
1:C:571:ARG:HB3	1:C:571:ARG:HH11	1.53	0.72
1:C:1259:ALA:HB1	1:C:1260:PRO:CD	2.19	0.72
1:C:81:ALA:HB3	1:C:170:TYR:CZ	2.24	0.72
1:C:327:LEU:HD13	1:C:327:LEU:O	1.88	0.72
1:C:985:ARG:NH1	1:C:989:ILE:HD12	2.05	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1231:TYR:HB3	1:C:1232:PRO:HD2	1.72	0.72
1:C:339:LEU:HD13	1:C:397:LEU:CD2	2.19	0.72
1:C:829:SER:HB2	1:C:965:ARG:HD2	0.72	0.72
1:C:1210:LEU:HD23	1:C:1244:ALA:HB2	1.70	0.72
1:C:713:MET:HE1	1:C:804:LEU:HD21	1.71	0.72
1:C:1306:THR:CA	1:C:1308:ASN:H	2.01	0.72
1:C:120:VAL:O	1:C:121:PHE:O	2.07	0.72
1:C:233:VAL:CG1	1:C:981:HIS:ND1	2.52	0.72
1:C:985:ARG:NH2	1:C:988:GLN:HG3	2.03	0.72
1:C:849:MET:CE	1:C:929:PHE:HE2	2.02	0.72
1:C:1168:ILE:HD13	1:C:1168:ILE:N	2.05	0.72
1:C:265:VAL:HG11	1:C:1301:VAL:HG21	1.70	0.72
1:C:362:LEU:HD13	1:C:1302:VAL:CG1	2.19	0.72
1:C:954:GLN:O	1:C:958:ILE:HD11	1.90	0.72
1:B:372:ALA:O	1:B:375:ARG:HG2	1.89	0.72
1:C:666:ARG:HH11	1:C:666:ARG:CG	2.03	0.72
1:C:733:VAL:CG2	1:C:1022:ILE:HD12	2.19	0.72
1:C:835:TYR:CE1	1:C:942:HIS:CG	2.77	0.72
1:B:394:GLN:CB	1:C:1005:LEU:HD21	2.19	0.72
1:C:864:HIS:CE1	1:C:1030:ARG:CZ	2.73	0.72
1:C:874:ILE:HG13	1:C:895:VAL:HG11	1.71	0.72
1:B:1131:PRO:O	1:B:1162:SER:OG	2.07	0.71
1:C:835:TYR:HE2	1:C:925:VAL:CG1	2.01	0.71
1:C:1176:GLU:OE1	1:C:1203:HIS:CE1	2.43	0.71
1:B:533:GLN:HG3	1:B:588:LEU:HD12	1.72	0.71
1:C:213:PHE:HB2	1:C:219:ILE:CG2	2.16	0.71
1:C:829:SER:CB	1:C:965:ARG:HD3	2.12	0.71
1:C:109:LYS:HD2	1:C:110:PRO:HD3	1.72	0.71
1:C:302:ARG:HD2	1:C:318:LEU:HD23	1.70	0.71
1:C:450:PRO:CA	1:C:454:GLU:CG	2.55	0.71
1:C:554:ARG:HG2	1:C:554:ARG:O	1.91	0.71
1:C:935:GLN:CB	1:C:939:ASN:HB3	2.20	0.71
1:C:108:LYS:HB2	1:C:108:LYS:HZ2	1.56	0.71
1:C:235:ILE:HD11	1:C:978:GLN:HE21	1.55	0.71
1:C:1276:LEU:N	1:C:1276:LEU:HD23	2.05	0.71
1:C:339:LEU:HD13	1:C:397:LEU:HD23	1.72	0.71
1:C:1211:LEU:HD11	1:C:1246:VAL:CG2	2.20	0.71
1:B:272:THR:HG23	1:C:235:ILE:HG21	1.72	0.71
1:C:502:PHE:CD1	1:C:507:SER:HB3	2.24	0.71
1:C:1044:ARG:HH11	1:C:1044:ARG:CG	2.03	0.71
1:C:375:ARG:HH11	1:C:375:ARG:CG	2.04	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:613:LEU:O	1:C:613:LEU:HD13	1.90	0.71
1:C:832:MET:HG3	1:C:832:MET:O	1.88	0.71
1:C:841:ASP:N	1:C:940:ARG:NH2	2.37	0.71
1:B:472:GLU:HB2	1:B:761:SER:OG	1.87	0.71
1:C:96:ILE:HD13	1:C:96:ILE:N	2.05	0.71
1:C:606:LEU:HD11	1:C:659:LEU:HB2	1.72	0.71
1:C:511:VAL:HG21	1:C:539:PHE:CE2	2.26	0.71
1:C:1023:ARG:NH2	1:C:1023:ARG:HB3	2.05	0.71
1:C:1250:GLU:C	1:C:1251:VAL:HG23	2.10	0.71
1:B:316:ASN:O	1:B:320:GLN:NE2	2.24	0.71
1:B:903:ASN:O	1:B:907:SER:OG	2.09	0.71
1:C:225:ILE:HD11	1:C:1069:ARG:C	2.11	0.71
1:C:502:PHE:HD1	1:C:507:SER:HB3	1.55	0.71
1:C:366:MET:HG2	1:C:366:MET:O	1.88	0.70
1:C:265:VAL:CG1	1:C:358:LEU:HD13	2.21	0.70
1:C:862:ARG:HH21	1:C:1042:TRP:HZ2	1.38	0.70
1:C:1000:LEU:HD23	1:C:1010:ARG:NE	2.04	0.70
1:C:1076:ILE:O	1:C:1076:ILE:HG12	1.90	0.70
1:B:313:ASP:O	1:B:317:MET:CB	2.39	0.70
1:C:77:THR:O	1:C:172:ASP:CG	2.29	0.70
1:C:210:ARG:HA	1:C:221:LEU:HD11	1.72	0.70
1:C:213:PHE:HB3	1:C:219:ILE:CG1	2.21	0.70
1:C:258:VAL:HG11	1:C:1058:GLY:CA	2.21	0.70
1:C:611:GLY:HA3	1:C:636:PRO:O	1.91	0.70
1:C:850:THR:OG1	1:C:916:LEU:HD22	1.91	0.70
1:C:897:TYR:CZ	1:C:898:GLN:O	2.43	0.70
1:C:301:LEU:HD12	1:C:301:LEU:O	1.91	0.70
1:C:371:THR:C	1:C:373:ASP:N	2.42	0.70
1:C:835:TYR:CE2	1:C:925:VAL:CG1	2.74	0.70
1:C:383:SER:OG	1:C:796:PRO:HG2	1.88	0.70
1:C:656:VAL:CG1	1:C:688:GLU:HB3	2.15	0.70
1:C:910:LEU:CG	1:C:915:VAL:HG21	2.22	0.70
1:C:1259:ALA:HB1	1:C:1260:PRO:HD3	1.73	0.70
1:C:1263:TYR:CZ	1:C:1278:TYR:CZ	2.74	0.70
1:B:875:THR:H	1:B:878:SER:HB3	1.55	0.70
1:B:1282:ALA:HB1	1:B:1283:ASN:HA	1.73	0.70
1:C:713:MET:HE1	1:C:804:LEU:CD2	2.21	0.70
1:C:1292:GLU:C	1:C:1293:VAL:HG23	2.11	0.70
1:C:141:LEU:O	1:C:141:LEU:HG	1.91	0.70
1:C:204:VAL:HG23	1:C:1242:MET:O	1.92	0.70
1:C:230:ASP:HB2	1:C:985:ARG:NE	1.95	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:896:LEU:HD13	1:C:918:VAL:CG2	2.22	0.70
1:C:897:TYR:CG	1:C:898:GLN:N	2.57	0.70
1:C:1261:SER:O	1:C:1263:TYR:N	2.25	0.70
1:C:154:PHE:HE1	1:C:361:ASN:ND2	1.89	0.70
1:C:659:LEU:HD22	1:C:662:VAL:CG2	2.22	0.70
1:C:1031:TYR:CE2	1:C:1041:ARG:NH1	2.55	0.70
1:C:558:TYR:CZ	1:C:585:PHE:HB2	2.27	0.69
1:C:835:TYR:O	1:C:846:GLY:CA	2.32	0.69
1:C:1122:PRO:HB2	1:C:1123:PRO:HD3	1.74	0.69
1:B:472:GLU:CA	1:B:473:ALA:HB2	2.22	0.69
1:C:206:ILE:HD11	1:C:1066:ARG:HD3	1.74	0.69
1:B:606:LEU:HD11	1:B:658:THR:HG21	1.72	0.69
1:C:233:VAL:HG12	1:C:981:HIS:ND1	2.06	0.69
1:C:407:HIS:CD2	1:C:1047:LEU:CA	2.69	0.69
1:C:1270:LEU:O	1:C:1271:SER:O	2.10	0.69
1:B:139:ASN:O	1:C:757:ILE:O	2.10	0.69
1:B:564:GLY:HA2	1:B:565:GLU:HB3	1.73	0.69
1:B:1189:ASP:O	1:B:1192:SER:N	2.21	0.69
1:C:176:LYS:CG	1:C:177:LYS:H	2.05	0.69
1:C:375:ARG:HD3	1:C:398:ARG:NH2	2.07	0.69
1:C:485:GLU:OE1	1:C:706:TYR:CE1	2.46	0.69
1:C:999:LYS:HE2	1:C:1009:THR:HG22	1.74	0.69
1:C:1047:LEU:HD22	1:C:1051:ARG:HD3	1.71	0.69
1:C:1296:ILE:HD11	1:C:1298:PHE:HE1	1.58	0.69
1:C:180:LEU:CD2	1:C:306:GLN:HE21	1.87	0.69
1:C:429:ILE:C	1:C:429:ILE:HD12	2.13	0.69
1:C:1046:PHE:HD2	1:C:1052:LEU:HD21	1.56	0.69
1:B:388:GLN:CB	1:B:1320:VAL:CG1	2.67	0.69
1:C:449:PHE:C	1:C:686:HIS:CD2	2.65	0.69
1:C:1000:LEU:HD21	1:C:1010:ARG:HH21	1.56	0.69
1:C:1176:GLU:HG2	1:C:1203:HIS:CE1	2.26	0.69
1:B:475:ILE:HD13	1:B:475:ILE:O	1.93	0.69
1:B:640:GLN:HE21	1:B:647:GLU:HB3	1.58	0.69
1:B:1112:ASN:OD1	1:B:1113:LYS:N	2.26	0.69
1:C:371:THR:C	1:C:373:ASP:H	1.94	0.69
1:C:830:VAL:O	1:C:854:GLN:HG2	1.92	0.69
1:C:836:GLN:HB2	1:C:940:ARG:HG2	0.77	0.69
1:C:1322:PRO:CB	1:C:1328:ILE:CD1	2.70	0.69
1:B:469:ARG:HH11	1:B:498:ILE:HD12	0.87	0.69
1:B:926:VAL:HG21	1:B:938:ASN:H	1.56	0.69
1:C:1243:ARG:HG2	1:C:1243:ARG:HH11	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1281:VAL:C	1:C:1283:ASN:H	1.94	0.69
1:B:472:GLU:HB3	1:B:761:SER:HG	1.56	0.69
1:C:77:THR:O	1:C:172:ASP:OD2	2.10	0.69
1:C:251:LEU:HD23	1:C:1062:ILE:CG1	2.12	0.69
1:C:314:ILE:HG22	1:C:318:LEU:CD2	2.22	0.69
1:C:338:ARG:CG	1:C:342:THR:CA	2.70	0.69
1:C:865:ILE:HG21	1:C:957:PHE:CE2	2.26	0.69
1:C:1250:GLU:C	1:C:1251:VAL:CG2	2.61	0.69
1:B:209:ASN:ND2	1:B:211:ASP:OD1	2.25	0.69
1:B:961:SER:HB2	1:B:964:VAL:HG12	1.75	0.69
1:C:333:ARG:O	1:C:335:ASP:N	2.25	0.69
1:C:365:LEU:O	1:C:365:LEU:HD22	1.93	0.69
1:B:699:THR:O	1:B:703:SER:CB	2.41	0.68
1:B:1249:ASN:HB3	1:C:1110:LEU:CB	2.22	0.68
1:C:509:VAL:HG23	1:C:683:TRP:HZ3	1.57	0.68
1:C:837:THR:C	1:C:934:LEU:CD1	2.58	0.68
1:C:232:LEU:HD21	1:C:249:SER:CA	2.23	0.68
1:C:583:GLU:HG3	1:C:583:GLU:O	1.94	0.68
1:C:1085:ASP:OD1	1:C:1085:ASP:N	2.26	0.68
1:C:1173:TYR:CD1	1:C:1204:LEU:CD1	2.74	0.68
1:C:146:GLU:HB2	1:C:1317:VAL:CG1	2.23	0.68
1:C:1093:PRO:CG	1:C:1096:TYR:CD1	2.73	0.68
1:B:1331:ARG:HG2	1:B:1332:ASN:H	1.58	0.68
1:C:180:LEU:HG	1:C:180:LEU:O	1.93	0.68
1:C:320:GLN:O	1:C:321:ALA:HB3	1.93	0.68
1:C:542:ARG:HG3	1:C:542:ARG:O	1.91	0.68
1:C:619:ALA:HB2	1:C:711:ASN:HB2	1.75	0.68
1:C:629:ARG:HG3	1:C:629:ARG:O	1.91	0.68
1:B:472:GLU:HB3	1:B:761:SER:HB2	1.74	0.68
1:C:733:VAL:CB	1:C:1022:ILE:HD12	2.23	0.68
1:C:929:PHE:CG	1:C:936:MET:HE1	2.28	0.68
1:C:1206:PHE:CD2	1:C:1236:ILE:HD11	2.28	0.68
1:B:462:LEU:HD23	1:B:462:LEU:C	2.14	0.68
1:C:168:VAL:HG23	1:C:204:VAL:CG1	2.23	0.68
1:C:448:TYR:C	1:C:450:PRO:CD	2.61	0.68
1:C:168:VAL:HB	1:C:204:VAL:HG12	1.76	0.68
1:C:838:GLU:CB	1:C:934:LEU:HB3	2.16	0.68
1:C:838:GLU:HG2	1:C:935:GLN:C	2.14	0.68
1:C:278:LEU:HD22	1:C:282:VAL:HB	1.76	0.68
1:C:849:MET:CG	1:C:919:MET:CE	2.72	0.68
1:C:1079:LEU:HD12	1:C:1079:LEU:N	2.02	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:259:MET:HG3	1:C:1055:LEU:CB	2.23	0.68
1:C:389:PHE:CE1	1:C:1319:ARG:CB	2.76	0.68
1:C:509:VAL:HG22	1:C:683:TRP:HH2	1.59	0.68
1:C:674:LYS:HB2	1:C:674:LYS:NZ	2.08	0.68
1:C:231:LEU:O	1:C:982:ALA:CA	2.40	0.67
1:C:516:LEU:HB3	1:C:763:VAL:CG1	2.24	0.67
1:C:896:LEU:HD13	1:C:918:VAL:HG21	1.75	0.67
1:C:440:ILE:CD1	1:C:478:ILE:HG21	2.22	0.67
1:C:958:ILE:O	1:C:958:ILE:HG12	1.92	0.67
1:C:1000:LEU:HD23	1:C:1010:ARG:CZ	2.25	0.67
1:B:234:PRO:HB3	1:B:972:PRO:HB3	1.75	0.67
1:B:440:ILE:HG21	1:B:770:CYS:SG	2.34	0.67
1:B:821:ASN:ND2	1:B:1015:GLN:OE1	2.26	0.67
1:C:240:GLY:C	1:C:242:GLU:N	2.47	0.67
1:C:244:SER:C	1:C:246:GLU:N	2.47	0.67
1:C:385:ILE:O	1:C:1328:ILE:HG21	1.95	0.67
1:C:450:PRO:O	1:C:451:GLU:HB3	1.93	0.67
1:C:285:VAL:HG13	1:C:325:TYR:O	1.94	0.67
1:C:791:ILE:HG13	1:C:1325:VAL:CG2	2.25	0.67
1:C:909:TYR:HE1	1:C:913:ASN:OD1	1.77	0.67
1:C:1272:ARG:O	1:C:1272:ARG:HD3	1.93	0.67
1:B:898:GLN:NE2	1:B:917:VAL:HB	2.09	0.67
1:B:409:ILE:HD11	1:B:627:ALA:HA	1.76	0.67
1:C:365:LEU:O	1:C:365:LEU:HD13	1.93	0.67
1:C:820:ILE:CG2	1:C:983:ILE:HG12	2.24	0.67
1:C:1079:LEU:O	1:C:1227:MET:HB2	1.93	0.67
1:C:1149:LYS:O	1:C:1151:VAL:N	2.27	0.67
1:B:397:LEU:O	1:B:398:ARG:NH1	2.24	0.67
1:B:439:VAL:HG23	1:B:440:ILE:H	1.58	0.67
1:C:462:LEU:HD13	1:C:462:LEU:C	2.15	0.67
1:C:702:LEU:HD12	1:C:702:LEU:O	1.93	0.67
1:C:713:MET:CE	1:C:804:LEU:HD23	2.24	0.67
1:C:838:GLU:HB3	1:C:934:LEU:HB3	1.76	0.67
1:C:928:ARG:HH11	1:C:928:ARG:HG3	1.60	0.67
1:B:301:LEU:O	1:B:305:THR:OG1	2.13	0.67
1:C:896:LEU:HA	1:C:918:VAL:HG22	1.76	0.67
1:B:388:GLN:H	1:B:1320:VAL:HG13	1.58	0.67
1:B:388:GLN:C	1:B:1320:VAL:HG12	2.14	0.67
1:B:1119:TYR:HB3	1:B:1134:ARG:HE	1.58	0.67
1:C:607:PHE:O	1:C:608:THR:CG2	2.43	0.66
1:C:659:LEU:C	1:C:659:LEU:HD13	2.15	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:791:ILE:HG13	1:C:1325:VAL:HG21	1.76	0.66
1:C:1105:LEU:H	1:C:1105:LEU:HD12	1.61	0.66
1:C:1206:PHE:HD2	1:C:1236:ILE:CD1	2.04	0.66
1:C:297:ASN:HD22	1:C:298:PRO:HD2	1.58	0.66
1:C:309:TRP:CZ2	1:C:1257:ALA:HB1	2.31	0.66
1:C:394:GLN:HG3	1:C:394:GLN:O	1.96	0.66
1:C:1021:ARG:HH11	1:C:1021:ARG:CB	2.08	0.66
1:C:422:LEU:HD11	1:C:490:PHE:CE2	2.31	0.66
1:C:685:ARG:HB3	1:C:685:ARG:NH1	2.10	0.66
1:B:522:PRO:HG2	1:B:636:PRO:HB3	1.78	0.66
1:C:372:ALA:CB	1:C:1315:MET:HE1	2.12	0.66
1:C:1293:VAL:O	1:C:1294:ASP:HB2	1.95	0.66
1:C:610:GLN:HA	1:C:610:GLN:NE2	2.08	0.66
1:B:147:VAL:HB	1:B:379:LEU:HD22	1.78	0.66
1:B:461:ARG:HB2	1:B:461:ARG:NH1	2.03	0.66
1:B:1066:ARG:HG3	1:B:1239:ALA:HA	1.78	0.66
1:C:822:MET:CE	1:C:1046:PHE:HE2	2.08	0.66
1:C:85:ASP:OD2	1:C:161:LYS:CG	2.41	0.66
1:C:1077:MET:HG3	1:C:1077:MET:O	1.96	0.66
1:C:389:PHE:HZ	1:C:796:PRO:HG2	1.62	0.65
1:C:449:PHE:CG	1:C:450:PRO:N	2.65	0.65
1:B:529:LYS:HB2	1:B:589:PHE:CE2	2.31	0.65
1:B:856:LEU:HD12	1:B:860:ARG:HE	1.60	0.65
1:C:833:ARG:NH1	1:C:942:HIS:CE1	2.63	0.65
1:B:1188:VAL:HG11	1:B:1204:LEU:HD23	1.77	0.65
1:C:179:LYS:HD2	1:C:179:LYS:C	2.16	0.65
1:C:1277:LEU:HD23	1:C:1287:GLY:HA3	1.78	0.65
1:C:225:ILE:HD12	1:C:247:TYR:CE1	2.32	0.65
1:C:766:ILE:HD12	1:C:766:ILE:O	1.97	0.65
1:C:849:MET:CG	1:C:919:MET:HE3	2.27	0.65
1:C:887:VAL:CG1	1:C:893:ALA:CB	2.72	0.65
1:C:1227:MET:O	1:C:1228:ARG:HB3	1.97	0.65
1:C:663:VAL:HG11	1:C:680:THR:HG23	1.77	0.65
1:C:849:MET:HG3	1:C:919:MET:HE2	1.79	0.65
1:C:926:VAL:HG11	1:C:937:ASN:HD22	1.62	0.65
1:B:397:LEU:HD21	1:C:1008:LEU:HD11	1.78	0.65
1:B:1176:GLU:HG2	1:B:1203:HIS:HE1	1.62	0.65
1:C:144:ASN:ND2	1:C:1318:GLU:OE1	2.28	0.65
1:C:157:ILE:HG12	1:C:263:ARG:HG2	1.75	0.65
1:C:317:MET:SD	1:C:1262:SER:CB	2.83	0.65
1:C:612:PHE:HD1	1:C:612:PHE:H	1.45	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:713:MET:CE	1:C:804:LEU:CD2	2.74	0.65
1:C:843:LEU:CD1	1:C:943:GLU:CB	2.73	0.65
1:C:865:ILE:HG22	1:C:957:PHE:CE2	2.30	0.65
1:C:893:ALA:HB1	1:C:915:VAL:HG12	1.77	0.65
1:B:388:GLN:CA	1:B:1320:VAL:HG12	2.27	0.65
1:C:146:GLU:O	1:C:1316:ALA:HA	1.97	0.65
1:C:1060:ARG:HH12	1:C:1292:GLU:H	1.42	0.65
1:B:709:MET:O	1:B:715:ASN:ND2	2.30	0.65
1:C:446:LYS:HD3	1:C:448:TYR:CZ	2.31	0.65
1:C:849:MET:N	1:C:849:MET:SD	2.70	0.65
1:C:180:LEU:HD23	1:C:180:LEU:H	1.62	0.65
1:C:1268:GLY:HA3	1:C:1277:LEU:O	1.97	0.65
1:C:243:GLN:HB2	1:C:246:GLU:HG3	1.77	0.64
1:C:382:HIS:CD2	1:C:800:LEU:HD23	2.31	0.64
1:C:615:THR:HG23	1:C:1333:ALA:C	2.18	0.64
1:C:1074:VAL:CA	1:C:1233:LEU:HD22	2.25	0.64
1:B:588:LEU:HD13	1:B:604:MET:HE3	1.79	0.64
1:C:213:PHE:CZ	1:C:254:VAL:HG23	2.32	0.64
1:C:741:TYR:OH	1:C:1022:ILE:HD13	1.96	0.64
1:C:1135:PRO:HG2	1:C:1137:VAL:HG13	1.78	0.64
1:B:436:SER:O	1:B:437:ALA:CB	2.45	0.64
1:C:117:ARG:HG3	1:C:121:PHE:CZ	2.32	0.64
1:B:1060:ARG:NH1	1:B:1291:LEU:O	2.29	0.64
1:C:840:ASP:CA	1:C:940:ARG:HH12	2.11	0.64
1:C:873:TYR:HD2	1:C:898:GLN:HG3	1.62	0.64
1:C:1127:ALA:O	1:C:1128:TYR:HB2	1.97	0.64
1:C:148:GLN:NE2	1:C:148:GLN:HA	2.12	0.64
1:C:734:ILE:O	1:C:734:ILE:HG22	1.98	0.64
1:C:741:TYR:CE2	1:C:1022:ILE:CD1	2.80	0.64
1:C:1279:SER:HB2	1:C:1280:PRO:O	1.97	0.64
1:C:254:VAL:CG1	1:C:1062:ILE:CD1	2.70	0.64
1:C:547:GLU:HG2	1:C:600:ILE:HG13	1.79	0.64
1:C:750:GLU:HG3	1:C:750:GLU:O	1.96	0.64
1:C:1245:ILE:O	1:C:1245:ILE:HG13	1.98	0.64
1:B:313:ASP:O	1:B:317:MET:HB3	1.97	0.64
1:B:1022:ILE:HG22	1:B:1028:VAL:HA	1.79	0.64
1:C:208:LEU:HB2	1:C:221:LEU:HD22	1.77	0.64
1:C:528:ILE:HG21	1:C:758:ILE:CD1	2.18	0.64
1:C:338:ARG:HG3	1:C:342:THR:CA	2.28	0.64
1:C:362:LEU:HD13	1:C:1302:VAL:HG11	1.79	0.64
1:C:822:MET:HE2	1:C:1046:PHE:HE2	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1020:ARG:NH1	1:C:1041:ARG:O	2.30	0.64
1:C:1210:LEU:CD2	1:C:1244:ALA:HB2	2.28	0.64
1:C:297:ASN:HD22	1:C:298:PRO:CD	2.11	0.64
1:C:753:ASP:N	1:C:753:ASP:OD1	2.30	0.64
1:B:390:HIS:HB2	1:B:1318:GLU:HG2	1.80	0.63
1:C:185:ALA:C	1:C:187:ASP:N	2.50	0.63
1:C:297:ASN:HD22	1:C:297:ASN:C	2.01	0.63
1:C:312:ARG:HH21	1:C:312:ARG:CG	2.09	0.63
1:C:441:ARG:HG2	1:C:441:ARG:NH2	2.12	0.63
1:C:713:MET:HE3	1:C:804:LEU:HD23	1.80	0.63
1:C:909:TYR:CZ	1:C:913:ASN:OD1	2.50	0.63
1:B:135:LYS:CE	1:C:469:ARG:HA	2.28	0.63
1:B:440:ILE:CG2	1:B:770:CYS:SG	2.87	0.63
1:B:1185:THR:H	1:B:1205:GLN:NE2	1.95	0.63
1:C:240:GLY:O	1:C:241:ALA:C	2.37	0.63
1:C:1206:PHE:CE2	1:C:1236:ILE:CD1	2.82	0.63
1:B:1249:ASN:HB3	1:C:1110:LEU:HB2	1.81	0.63
1:C:434:VAL:CG2	1:C:709:MET:HE1	2.29	0.63
1:C:764:TRP:HB2	1:C:765:PRO:HD3	1.79	0.63
1:C:870:ASP:OD1	1:C:870:ASP:N	2.24	0.63
1:C:1080:THR:N	1:C:1227:MET:SD	2.55	0.63
1:B:135:LYS:HE2	1:C:468:ALA:C	2.14	0.63
1:C:258:VAL:CG1	1:C:1058:GLY:CA	2.76	0.63
1:C:1074:VAL:O	1:C:1074:VAL:HG13	1.99	0.63
1:C:1132:THR:O	1:C:1133:GLY:C	2.37	0.63
1:C:422:LEU:HD11	1:C:490:PHE:HE2	1.63	0.63
1:C:616:ASP:OD1	1:C:631:PRO:HB2	1.97	0.63
1:C:836:GLN:O	1:C:838:GLU:N	2.28	0.63
1:C:1137:VAL:CG2	1:C:1164:TRP:CE2	2.81	0.63
1:B:658:THR:HA	1:B:661:ASN:HD22	1.64	0.63
1:C:389:PHE:HD1	1:C:1317:VAL:CG2	2.11	0.63
1:C:655:ILE:O	1:C:659:LEU:HB3	1.98	0.63
1:C:663:VAL:O	1:C:677:ARG:CD	2.45	0.63
1:C:815:LEU:HD13	1:C:1051:ARG:HH21	1.62	0.63
1:C:1049:GLU:O	1:C:1053:ARG:CG	2.46	0.63
1:B:489:MET:SD	1:B:492:VAL:HA	2.39	0.63
1:B:529:LYS:HB2	1:B:589:PHE:HE2	1.64	0.63
1:B:897:TYR:CZ	1:B:899:SER:HB3	2.34	0.63
1:C:1046:PHE:CD2	1:C:1052:LEU:HD21	2.34	0.63
1:C:75:ILE:HG23	1:C:75:ILE:O	1.98	0.63
1:C:154:PHE:CE2	1:C:365:LEU:HB2	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:ASP:O	1:C:985:ARG:HG3	1.98	0.63
1:C:1173:TYR:HB2	1:C:1202:PHE:O	1.99	0.63
1:B:848:ARG:NH1	1:B:914:GLU:O	2.32	0.62
1:B:1048:ASP:OD1	1:B:1049:GLU:N	2.32	0.62
1:C:1054:ARG:CG	1:C:1054:ARG:HH11	2.12	0.62
1:C:143:VAL:HG23	1:C:143:VAL:O	2.00	0.62
1:C:225:ILE:HG23	1:C:226:PRO:HD2	1.81	0.62
1:C:233:VAL:O	1:C:234:PRO:O	2.18	0.62
1:C:259:MET:O	1:C:1054:ARG:NH1	2.31	0.62
1:C:389:PHE:HE1	1:C:1319:ARG:HB3	1.64	0.62
1:B:1047:LEU:HA	1:B:1051:ARG:HH21	1.64	0.62
1:C:156:GLN:NE2	1:C:1309:ILE:HG12	2.13	0.62
1:C:164:LEU:HD11	1:C:353:PHE:CE2	2.31	0.62
1:C:571:ARG:HB3	1:C:571:ARG:NH1	2.14	0.62
1:B:1214:GLU:HG2	1:B:1215:PRO:HD2	1.80	0.62
1:C:81:ALA:CB	1:C:170:TYR:OH	2.47	0.62
1:C:478:ILE:CD1	1:C:762:ILE:CD1	2.68	0.62
1:C:550:ILE:HD12	1:C:550:ILE:C	2.20	0.62
1:C:834:THR:HG22	1:C:848:ARG:HG2	1.81	0.62
1:C:964:VAL:CG1	1:C:1059:LEU:HD21	2.28	0.62
1:C:1173:TYR:CD2	1:C:1204:LEU:HD11	2.35	0.62
1:B:629:ARG:NH2	1:B:1033:ASP:O	2.31	0.62
1:C:333:ARG:HH21	1:C:333:ARG:CG	2.12	0.62
1:C:389:PHE:CD1	1:C:1317:VAL:HG21	2.35	0.62
1:C:428:GLN:OE1	1:C:428:GLN:HA	1.99	0.62
1:C:1135:PRO:HD2	1:C:1164:TRP:HE1	1.64	0.62
1:C:338:ARG:HG2	1:C:342:THR:CA	2.29	0.62
1:C:611:GLY:O	1:C:634:TYR:CE2	2.50	0.62
1:C:827:GLY:HA3	1:C:964:VAL:HG21	1.80	0.62
1:C:830:VAL:HG21	1:C:947:GLU:HB3	1.62	0.62
1:C:985:ARG:NH2	1:C:989:ILE:HB	2.15	0.62
1:B:867:ASN:OD1	1:B:1030:ARG:HD3	2.00	0.62
1:C:656:VAL:HG12	1:C:688:GLU:HG2	1.81	0.62
1:C:945:VAL:C	1:C:946:LEU:HD12	2.20	0.62
1:C:1000:LEU:HD23	1:C:1010:ARG:NH2	2.13	0.62
1:C:1129:PRO:O	1:C:1130:SER:HB3	2.00	0.62
1:C:1296:ILE:HD13	1:C:1296:ILE:C	2.20	0.62
1:C:606:LEU:CD1	1:C:655:ILE:HG23	2.16	0.62
1:C:824:LEU:O	1:C:824:LEU:HD23	1.98	0.62
1:C:849:MET:HE2	1:C:929:PHE:HE2	1.65	0.62
1:C:180:LEU:HD23	1:C:306:GLN:HE22	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:820:ILE:HD13	1:C:820:ILE:O	2.00	0.62
1:C:1060:ARG:HA	1:C:1060:ARG:NE	2.14	0.62
1:B:985:ARG:HH21	1:B:988:GLN:HE21	1.46	0.62
1:C:849:MET:HG3	1:C:919:MET:CE	2.30	0.62
1:B:702:LEU:HA	1:B:705:VAL:HG22	1.82	0.61
1:B:772:TYR:HB2	1:B:775:VAL:HG12	1.81	0.61
1:C:206:ILE:O	1:C:1239:ALA:CB	2.46	0.61
1:C:327:LEU:C	1:C:327:LEU:HD22	2.21	0.61
1:C:733:VAL:HG12	1:C:1020:ARG:O	2.00	0.61
1:C:144:ASN:HD22	1:C:1318:GLU:CD	2.03	0.61
1:C:155:LYS:HD2	1:C:155:LYS:O	2.00	0.61
1:C:718:ASN:OD1	1:C:718:ASN:N	2.29	0.61
1:C:1134:ARG:NH2	1:C:1154:ASN:HD21	1.95	0.61
1:C:1278:TYR:CD2	1:C:1288:ILE:HG12	2.12	0.61
1:B:135:LYS:HE2	1:C:469:ARG:CA	2.30	0.61
1:C:120:VAL:O	1:C:120:VAL:HG22	2.00	0.61
1:C:720:PHE:O	1:C:727:PHE:CE1	2.53	0.61
1:C:1165:VAL:O	1:C:1165:VAL:HG12	2.01	0.61
1:C:1206:PHE:CD2	1:C:1236:ILE:HD12	2.34	0.61
1:C:163:TYR:HE2	1:C:258:VAL:HG23	1.65	0.61
1:C:579:LEU:HB2	1:C:582:SER:OG	2.00	0.61
1:C:1111:ALA:HB2	1:C:1129:PRO:HB2	1.83	0.61
1:C:508:ILE:O	1:C:508:ILE:HG13	2.00	0.61
1:C:820:ILE:CG2	1:C:983:ILE:HD11	2.30	0.61
1:C:1030:ARG:C	1:C:1032:ASP:H	2.02	0.61
1:B:472:GLU:N	1:B:473:ALA:HA	2.16	0.61
1:C:146:GLU:HB2	1:C:1317:VAL:HG12	1.82	0.61
1:C:232:LEU:CD2	1:C:249:SER:CB	2.52	0.61
1:C:674:LYS:HG3	1:C:677:ARG:HH21	1.66	0.61
1:C:1173:TYR:CG	1:C:1204:LEU:HD11	2.36	0.61
1:B:1254:PRO:O	1:B:1256:GLY:N	2.32	0.61
1:C:99:VAL:HG22	1:C:99:VAL:O	2.01	0.61
1:C:255:LEU:HD23	1:C:1058:GLY:C	2.20	0.61
1:C:837:THR:O	1:C:838:GLU:HB2	1.99	0.61
1:C:1036:ASP:OD1	1:C:1036:ASP:N	2.34	0.61
1:C:258:VAL:CG1	1:C:1058:GLY:HA3	2.30	0.61
1:C:849:MET:CE	1:C:929:PHE:CE2	2.84	0.61
1:C:1014:MET:HG3	1:C:1017:ALA:HB2	1.81	0.61
1:C:1277:LEU:O	1:C:1278:TYR:O	2.19	0.61
1:C:348:LEU:CD1	1:C:1301:VAL:HG22	2.30	0.61
1:C:897:TYR:O	1:C:898:GLN:HG2	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:271:THR:HG23	1:C:237:VAL:CG2	2.31	0.61
1:B:629:ARG:NH2	1:B:1036:ASP:O	2.34	0.61
1:C:101:ASP:OD1	1:C:101:ASP:N	2.31	0.61
1:C:309:TRP:CH2	1:C:1257:ALA:HB1	2.36	0.61
1:C:659:LEU:CD2	1:C:662:VAL:HG21	2.31	0.61
1:C:838:GLU:HB2	1:C:934:LEU:CG	2.26	0.61
1:C:965:ARG:NH1	1:C:968:ARG:NH1	2.48	0.61
1:C:1242:MET:SD	1:C:1260:PRO:HG3	2.41	0.61
1:C:114:VAL:HG23	1:C:114:VAL:O	2.00	0.60
1:C:607:PHE:C	1:C:608:THR:HG23	2.20	0.60
1:C:873:TYR:HD2	1:C:898:GLN:CG	2.12	0.60
1:C:1271:SER:HB2	1:C:1275:ASP:O	2.01	0.60
1:B:385:ILE:HG13	1:B:1330:ILE:HG22	1.83	0.60
1:C:466:VAL:HG13	1:C:466:VAL:O	1.99	0.60
1:B:1021:ARG:O	1:B:1029:LEU:HB2	2.01	0.60
1:C:204:VAL:HG21	1:C:1242:MET:HG3	1.81	0.60
1:C:656:VAL:HG13	1:C:656:VAL:O	2.01	0.60
1:C:668:VAL:CG2	1:C:673:GLN:CB	2.66	0.60
1:B:530:GLY:O	1:B:533:GLN:HB3	2.02	0.60
1:B:590:SER:HA	1:B:725:ALA:HB2	1.81	0.60
1:C:843:LEU:HD21	1:C:943:GLU:OE2	2.01	0.60
1:C:1081:ASP:N	1:C:1227:MET:CG	2.57	0.60
1:C:1143:GLU:C	1:C:1145:ALA:H	2.04	0.60
1:C:91:ASP:OD1	1:C:91:ASP:N	2.28	0.60
1:C:123:GLU:O	1:C:123:GLU:HG2	2.00	0.60
1:C:924:ASP:CG	1:C:927:SER:CB	2.69	0.60
1:B:145:THR:HB	1:B:1317:VAL:HG13	1.83	0.60
1:B:453:LEU:HD12	1:B:682:GLN:HE21	1.66	0.60
1:B:1179:THR:OG1	1:B:1181:SER:O	2.18	0.60
1:C:449:PHE:CD1	1:C:450:PRO:CD	2.83	0.60
1:C:874:ILE:HG13	1:C:895:VAL:HG13	1.81	0.60
1:C:1176:GLU:HG3	1:C:1176:GLU:O	2.00	0.60
1:B:427:VAL:HG11	1:B:755:LEU:HD21	1.84	0.60
1:C:184:GLU:O	1:C:187:ASP:CA	2.48	0.60
1:C:929:PHE:CD2	1:C:936:MET:CE	2.84	0.60
1:C:1173:TYR:CG	1:C:1204:LEU:CD1	2.85	0.60
1:C:1271:SER:HB3	1:C:1274:GLY:H	1.66	0.60
1:C:837:THR:CG2	1:C:934:LEU:HD11	2.24	0.60
1:C:874:ILE:CD1	1:C:883:ILE:HD11	2.30	0.60
1:B:475:ILE:O	1:B:475:ILE:HG23	2.01	0.60
1:C:240:GLY:C	1:C:242:GLU:H	2.06	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:446:LYS:CB	1:C:448:TYR:CE1	2.84	0.60
1:B:1234:GLN:HB3	1:B:1235:PRO:HD2	1.82	0.59
1:C:492:VAL:HG23	1:C:492:VAL:O	2.01	0.59
1:C:733:VAL:HG21	1:C:1022:ILE:CD1	2.30	0.59
1:C:862:ARG:HG2	1:C:952:PHE:CE2	2.37	0.59
1:C:929:PHE:CD2	1:C:936:MET:HE2	2.37	0.59
1:B:833:ARG:HD3	1:B:922:TYR:CZ	2.36	0.59
1:B:862:ARG:NH1	1:B:948:ILE:HG21	2.17	0.59
1:C:258:VAL:HG13	1:C:1058:GLY:HA3	1.84	0.59
1:C:980:ARG:O	1:C:984:GLU:HB2	2.02	0.59
1:B:1238:VAL:HG23	1:B:1239:ALA:H	1.67	0.59
1:B:1249:ASN:HB3	1:C:1110:LEU:HB3	1.84	0.59
1:C:1171:ILE:O	1:C:1171:ILE:HG12	2.02	0.59
1:C:1280:PRO:HG3	1:C:1286:VAL:C	2.22	0.59
1:C:146:GLU:HG2	1:C:1317:VAL:HG13	1.84	0.59
1:C:189:ILE:HG12	1:C:286:LEU:CD1	2.32	0.59
1:C:467:LYS:HB3	1:C:467:LYS:NZ	2.16	0.59
1:C:614:ARG:HD3	1:C:635:ILE:CD1	2.32	0.59
1:C:1044:ARG:HG3	1:C:1044:ARG:O	2.02	0.59
1:B:397:LEU:HD21	1:C:1008:LEU:CD1	2.32	0.59
1:C:120:VAL:O	1:C:120:VAL:HG13	2.01	0.59
1:C:176:LYS:HG3	1:C:177:LYS:N	2.11	0.59
1:C:430:ASN:C	1:C:430:ASN:HD22	2.05	0.59
1:C:948:ILE:HG23	1:C:948:ILE:O	2.03	0.59
1:B:637:TYR:HB2	1:B:703:SER:HB3	1.84	0.59
1:C:113:VAL:O	1:C:113:VAL:HG13	2.03	0.59
1:C:154:PHE:HE2	1:C:365:LEU:HB2	1.68	0.59
1:C:208:LEU:CB	1:C:221:LEU:HD22	2.32	0.59
1:C:609:PRO:HB2	1:C:634:TYR:CE2	2.37	0.59
1:C:674:LYS:HB2	1:C:674:LYS:HZ2	1.67	0.59
1:C:989:ILE:HG23	1:C:990:THR:HG23	1.83	0.59
1:C:1094:GLU:HA	1:C:1094:GLU:OE2	2.01	0.59
1:C:1298:PHE:N	1:C:1298:PHE:CD1	2.70	0.59
1:C:1325:VAL:O	1:C:1325:VAL:HG12	2.01	0.59
1:C:493:HIS:HB3	1:C:756:THR:O	2.02	0.59
1:C:494:GLU:O	1:C:494:GLU:HG2	2.02	0.59
1:C:606:LEU:HD13	1:C:655:ILE:CG2	2.17	0.59
1:C:838:GLU:C	1:C:940:ARG:HE	2.01	0.59
1:C:1298:PHE:N	1:C:1298:PHE:HD1	2.00	0.59
1:B:167:SER:OG	1:B:205:ASN:OD1	2.21	0.59
1:B:313:ASP:O	1:B:317:MET:HB2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:128:GLU:OE1	1:C:133:MET:CE	2.51	0.59
1:C:422:LEU:CD1	1:C:490:PHE:HE2	2.12	0.59
1:C:452:ASN:C	1:C:453:LEU:HD22	2.23	0.59
1:C:1280:PRO:HB3	1:C:1287:GLY:CA	2.27	0.59
1:B:1071:PHE:CZ	1:B:1236:ILE:HD13	2.38	0.59
1:C:928:ARG:H	1:C:928:ARG:CD	2.15	0.59
1:B:231:LEU:HB2	1:B:249:SER:HB2	1.85	0.59
1:C:213:PHE:CE1	1:C:254:VAL:HG23	2.37	0.59
1:C:230:ASP:OD2	1:C:985:ARG:NE	2.27	0.59
1:C:244:SER:O	1:C:247:TYR:HB3	2.03	0.59
1:C:1079:LEU:O	1:C:1227:MET:HB3	2.03	0.59
1:C:1104:ARG:HG2	1:C:1104:ARG:NH1	2.18	0.59
1:B:188:ARG:HH22	1:C:237:VAL:CG1	2.16	0.58
1:B:388:GLN:N	1:B:1320:VAL:CG1	2.64	0.58
1:C:108:LYS:HG3	1:C:108:LYS:O	2.02	0.58
1:C:1060:ARG:HA	1:C:1060:ARG:HE	1.68	0.58
1:B:272:THR:CG2	1:C:235:ILE:HG21	2.33	0.58
1:B:472:GLU:HB2	1:B:761:SER:CB	2.33	0.58
1:B:1285:GLN:O	1:B:1286:VAL:HG23	2.03	0.58
1:C:248:VAL:HG11	1:C:970:LEU:CB	2.21	0.58
1:C:389:PHE:CD1	1:C:1319:ARG:HB3	2.37	0.58
1:C:451:GLU:HB2	1:C:686:HIS:CB	2.33	0.58
1:C:1174:THR:HG23	1:C:1174:THR:O	2.03	0.58
1:C:463:VAL:O	1:C:467:LYS:HG3	2.03	0.58
1:C:654:THR:HG22	1:C:658:THR:HG22	1.82	0.58
1:C:756:THR:O	1:C:756:THR:HG22	2.01	0.58
1:C:185:ALA:C	1:C:187:ASP:H	2.07	0.58
1:C:408:ILE:HG22	1:C:408:ILE:O	2.04	0.58
1:C:1070:ARG:O	1:C:1070:ARG:HG2	2.02	0.58
1:C:81:ALA:HB3	1:C:170:TYR:OH	2.02	0.58
1:C:427:VAL:O	1:C:431:THR:HG22	2.03	0.58
1:C:560:ILE:HG23	1:C:560:ILE:O	2.02	0.58
1:C:820:ILE:HG21	1:C:983:ILE:CD1	2.33	0.58
1:C:850:THR:OG1	1:C:916:LEU:CD2	2.52	0.58
1:C:901:VAL:HG13	1:C:901:VAL:O	2.04	0.58
1:C:963:ALA:HB3	1:C:1059:LEU:CG	2.30	0.58
1:C:1135:PRO:O	1:C:1136:HIS:HB2	2.04	0.58
1:C:1276:LEU:HD23	1:C:1276:LEU:H	1.68	0.58
1:C:256:PHE:HD1	1:C:819:PHE:CE2	2.21	0.58
1:B:699:THR:O	1:B:703:SER:HB3	2.04	0.58
1:B:922:TYR:O	1:B:925:VAL:HG13	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:668:VAL:HG23	1:C:673:GLN:HE21	1.68	0.58
1:C:849:MET:CA	1:C:917:VAL:O	2.50	0.58
1:C:892:VAL:HG11	1:C:894:VAL:HG13	1.63	0.58
1:C:935:GLN:HB3	1:C:939:ASN:CB	2.31	0.58
1:C:957:PHE:CD1	1:C:957:PHE:N	2.72	0.58
1:C:1121:HIS:CD2	1:C:1135:PRO:HG2	2.37	0.58
1:C:1055:LEU:O	1:C:1055:LEU:HG	2.01	0.58
1:B:893:ALA:HB1	1:B:915:VAL:HA	1.86	0.58
1:C:360:ILE:HG22	1:C:360:ILE:O	2.03	0.58
1:C:1198:LYS:O	1:C:1198:LYS:HD3	2.03	0.58
1:B:1250:GLU:O	1:B:1251:VAL:HG13	2.04	0.58
1:C:389:PHE:CD1	1:C:1317:VAL:CG2	2.86	0.58
1:C:452:ASN:O	1:C:453:LEU:HD22	2.03	0.58
1:C:644:VAL:HG13	1:C:644:VAL:O	2.03	0.58
1:C:644:VAL:O	1:C:644:VAL:HG22	2.02	0.58
1:C:918:VAL:HG23	1:C:918:VAL:O	2.02	0.58
1:B:824:LEU:HD22	1:B:979:ILE:HD12	1.86	0.57
1:C:1014:MET:CG	1:C:1017:ALA:HB2	2.34	0.57
1:B:461:ARG:HH11	1:B:461:ARG:CG	2.15	0.57
1:B:1076:ILE:HG12	1:B:1230:ILE:HG22	1.85	0.57
1:C:259:MET:HA	1:C:1054:ARG:HB3	1.86	0.57
1:C:439:VAL:HG22	1:C:439:VAL:O	2.03	0.57
1:C:1079:LEU:CD1	1:C:1231:TYR:HH	1.94	0.57
1:C:1085:ASP:HB2	1:C:1086:PRO:HD2	1.83	0.57
1:B:1064:ASN:ND2	1:B:1296:ILE:HD11	2.18	0.57
1:C:314:ILE:HG22	1:C:318:LEU:HD22	1.87	0.57
1:C:656:VAL:CG1	1:C:688:GLU:CG	2.82	0.57
1:C:668:VAL:CG2	1:C:673:GLN:HE21	2.17	0.57
1:C:747:ARG:HG2	1:C:747:ARG:HH11	1.68	0.57
1:C:965:ARG:HH11	1:C:968:ARG:HH12	1.50	0.57
1:C:1121:HIS:CD2	1:C:1135:PRO:CB	2.87	0.57
1:C:154:PHE:HE1	1:C:361:ASN:HD21	1.50	0.57
1:C:405:HIS:CD2	1:C:625:PRO:CA	2.83	0.57
1:C:610:GLN:HE21	1:C:610:GLN:CA	2.12	0.57
1:C:709:MET:O	1:C:715:ASN:ND2	2.37	0.57
1:C:1140:THR:HA	1:C:1167:ASP:HB3	1.86	0.57
1:B:261:ASP:OD2	1:B:263:ARG:NH2	2.37	0.57
1:B:439:VAL:C	1:B:440:ILE:HG13	2.24	0.57
1:B:577:GLN:O	1:B:580:TYR:N	2.37	0.57
1:C:1023:ARG:HB3	1:C:1023:ARG:HH21	1.68	0.57
1:C:1310:ARG:HA	1:C:1310:ARG:NE	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:141:LEU:HD11	1:B:1318:GLU:HG2	1.87	0.57
1:B:874:ILE:HG23	1:B:895:VAL:HG21	1.86	0.57
1:C:403:PHE:CZ	1:C:408:ILE:HG13	2.39	0.57
1:C:342:THR:O	1:C:1305:MET:CE	2.52	0.57
1:C:654:THR:CG2	1:C:658:THR:CG2	2.77	0.57
1:C:635:ILE:HD11	1:C:707:ALA:HA	1.85	0.57
1:C:451:GLU:OE1	1:C:685:ARG:HG2	2.03	0.57
1:C:585:PHE:CE1	1:C:728:LYS:HE2	2.40	0.57
1:C:762:ILE:HD12	1:C:762:ILE:O	2.04	0.57
1:C:1147:MET:HE3	1:C:1152:ALA:HB2	1.87	0.57
1:B:469:ARG:NH1	1:B:498:ILE:CG1	2.61	0.57
1:C:255:LEU:CD2	1:C:1058:GLY:C	2.73	0.57
1:C:389:PHE:HD1	1:C:1317:VAL:HG22	1.70	0.57
1:C:434:VAL:HG23	1:C:709:MET:CE	2.33	0.57
1:C:339:LEU:CD1	1:C:397:LEU:HD23	2.34	0.56
1:C:478:ILE:HD13	1:C:762:ILE:HD11	1.80	0.56
1:C:521:PHE:N	1:C:521:PHE:CD1	2.71	0.56
1:C:668:VAL:CG1	1:C:674:LYS:HD3	2.35	0.56
1:C:820:ILE:HG21	1:C:983:ILE:HG13	1.83	0.56
1:C:915:VAL:HG23	1:C:915:VAL:O	2.04	0.56
1:C:939:ASN:HD22	1:C:939:ASN:C	2.00	0.56
1:C:1231:TYR:N	1:C:1231:TYR:CD1	2.72	0.56
1:B:184:GLU:O	1:B:188:ARG:HG2	2.04	0.56
1:B:793:TYR:HD2	1:B:1321:ASN:CG	2.08	0.56
1:B:831:VAL:H	1:B:854:GLN:HE21	1.52	0.56
1:B:957:PHE:HB2	1:B:1042:TRP:CZ3	2.40	0.56
1:B:383:SER:HB3	1:B:387:THR:HG21	1.86	0.56
1:B:461:ARG:NE	1:B:504:ASP:HB2	2.18	0.56
1:B:472:GLU:O	1:B:761:SER:CB	2.38	0.56
1:C:109:LYS:HB3	1:C:109:LYS:NZ	2.21	0.56
1:C:362:LEU:HD23	1:C:362:LEU:O	2.04	0.56
1:C:446:LYS:HB3	1:C:448:TYR:CZ	2.40	0.56
1:C:471:SER:HB3	1:C:765:PRO:HG2	1.87	0.56
1:C:503:GLU:OE2	1:C:542:ARG:CD	2.50	0.56
1:C:747:ARG:HH11	1:C:747:ARG:CG	2.18	0.56
1:C:890:THR:O	1:C:890:THR:OG1	2.21	0.56
1:C:928:ARG:H	1:C:928:ARG:HD3	1.70	0.56
1:C:1054:ARG:NH1	1:C:1054:ARG:HG2	2.19	0.56
1:C:661:ASN:O	1:C:665:GLU:HB3	2.05	0.56
1:C:1000:LEU:CD2	1:C:1010:ARG:CZ	2.81	0.56
1:B:637:TYR:HB3	1:B:699:THR:HA	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:874:ILE:CG2	1:C:902:ILE:CD1	2.82	0.56
1:C:1135:PRO:HG2	1:C:1137:VAL:CG1	2.34	0.56
1:B:1121:HIS:HD2	1:B:1124:THR:HG22	1.69	0.56
1:C:225:ILE:HD11	1:C:1069:ARG:CB	2.36	0.56
1:B:383:SER:HG	1:B:389:PHE:HZ	1.51	0.56
1:C:498:ILE:CD1	1:C:514:PHE:HZ	2.19	0.56
1:C:582:SER:O	1:C:728:LYS:HD2	2.05	0.56
1:C:1317:VAL:HG13	1:C:1317:VAL:O	2.05	0.56
1:B:338:ARG:NH1	1:C:1005:LEU:HD22	2.21	0.56
1:B:366:MET:HE3	1:B:1309:ILE:HD13	1.86	0.56
1:B:558:TYR:CZ	1:B:590:SER:HB3	2.41	0.56
1:C:96:ILE:HD11	1:C:103:GLY:HA2	1.84	0.56
1:C:449:PHE:HZ	1:C:463:VAL:HG22	1.70	0.56
1:C:556:ALA:O	1:C:587:ALA:HB2	2.04	0.56
1:B:489:MET:SD	1:B:527:ARG:HD2	2.46	0.56
1:C:538:LEU:HD21	1:C:542:ARG:HH21	1.70	0.56
1:C:772:TYR:N	1:C:772:TYR:CD1	2.74	0.56
1:B:310:LEU:O	1:B:314:ILE:HG12	2.05	0.56
1:C:554:ARG:CD	1:C:594:LEU:HD21	2.30	0.56
1:C:1111:ALA:HB2	1:C:1129:PRO:CB	2.36	0.56
1:B:287:ARG:HH11	1:B:330:THR:HB	1.71	0.55
1:B:303:ASP:HA	1:B:311:ASN:HD21	1.71	0.55
1:B:1306:THR:HG22	1:B:1307:ALA:H	1.69	0.55
1:C:758:ILE:HG13	1:C:758:ILE:O	2.06	0.55
1:C:987:ALA:O	1:C:992:VAL:HG13	2.06	0.55
1:C:1081:ASP:N	1:C:1227:MET:CB	2.68	0.55
1:C:1332:ASN:O	1:C:1333:ALA:OXT	2.24	0.55
1:B:264:LEU:HD11	1:B:365:LEU:HD11	1.88	0.55
1:B:414:LEU:HA	1:B:734:ILE:HD11	1.88	0.55
1:B:1290:LYS:HE2	1:B:1300:ASN:HB3	1.87	0.55
1:B:198:LYS:O	1:B:200:GLY:HA2	2.06	0.55
1:C:213:PHE:CZ	1:C:254:VAL:CG2	2.88	0.55
1:C:259:MET:O	1:C:1054:ARG:HG2	2.07	0.55
1:C:348:LEU:HD12	1:C:1301:VAL:HG22	1.88	0.55
1:C:838:GLU:HB2	1:C:934:LEU:CD1	2.36	0.55
1:C:874:ILE:HG22	1:C:874:ILE:O	2.06	0.55
1:C:1175:ALA:HA	1:C:1204:LEU:O	2.07	0.55
1:C:1176:GLU:HG2	1:C:1203:HIS:HE1	1.72	0.55
1:B:924:ASP:OD1	1:B:927:SER:HB2	2.07	0.55
1:C:304:PHE:N	1:C:304:PHE:CD1	2.71	0.55
1:C:387:THR:HG23	1:C:387:THR:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:465:ALA:CB	1:C:506:SER:HB3	2.36	0.55
1:C:838:GLU:HG2	1:C:935:GLN:N	2.14	0.55
1:C:845:GLU:CD	1:C:911:ARG:HH21	2.08	0.55
1:C:1074:VAL:HB	1:C:1173:TYR:CE2	2.37	0.55
1:C:117:ARG:CG	1:C:121:PHE:CZ	2.89	0.55
1:C:461:ARG:HG3	1:C:461:ARG:O	2.06	0.55
1:C:607:PHE:O	1:C:608:THR:HG22	2.06	0.55
1:B:309:TRP:CH2	1:B:1257:ALA:HB1	2.42	0.55
1:B:576:ASP:OD1	1:B:577:GLN:N	2.39	0.55
1:C:225:ILE:HD11	1:C:1069:ARG:CA	2.37	0.55
1:C:230:ASP:HB3	1:C:985:ARG:HG3	1.77	0.55
1:C:446:LYS:CD	1:C:448:TYR:CZ	2.89	0.55
1:C:122:ASN:HD22	1:C:122:ASN:C	2.04	0.55
1:C:180:LEU:HD22	1:C:306:GLN:CD	2.15	0.55
1:C:735:THR:HG21	1:C:1028:VAL:CG2	2.34	0.55
1:C:926:VAL:CG1	1:C:937:ASN:HD22	2.19	0.55
1:C:1000:LEU:HD23	1:C:1010:ARG:HE	1.71	0.55
1:B:276:ASN:OD1	1:C:1199:GLY:HA3	2.07	0.55
1:B:315:THR:O	1:B:319:GLN:HB2	2.06	0.55
1:C:254:VAL:HG13	1:C:1062:ILE:HD13	1.89	0.55
1:C:469:ARG:NH2	1:C:498:ILE:HG23	2.21	0.55
1:B:157:ILE:HD11	1:B:265:VAL:HG22	1.88	0.55
1:B:307:VAL:HG13	1:B:310:LEU:HB3	1.88	0.55
1:C:588:LEU:HG	1:C:604:MET:SD	2.47	0.55
1:C:738:GLU:HB3	1:C:1015:GLN:HG3	1.87	0.55
1:C:822:MET:CE	1:C:1046:PHE:CE2	2.89	0.55
1:C:838:GLU:HA	1:C:940:ARG:HD3	1.89	0.55
1:C:1054:ARG:HH11	1:C:1054:ARG:HG2	1.71	0.55
1:C:1116:ARG:NH1	1:C:1130:SER:HB2	2.22	0.55
1:B:332:THR:HG23	1:B:344:VAL:HG12	1.89	0.55
1:C:547:GLU:HG3	1:C:597:ALA:HA	1.90	0.55
1:C:714:LEU:HD11	1:C:806:VAL:HG12	1.89	0.55
1:C:1044:ARG:CG	1:C:1044:ARG:NH1	2.70	0.55
1:B:1124:THR:HG23	1:B:1126:MET:H	1.72	0.54
1:C:146:GLU:CB	1:C:1317:VAL:CG1	2.85	0.54
1:B:235:ILE:HG13	1:B:978:GLN:NE2	2.14	0.54
1:B:832:MET:SD	1:B:848:ARG:HD2	2.47	0.54
1:C:157:ILE:HG13	1:C:263:ARG:HG2	1.86	0.54
1:C:163:TYR:N	1:C:163:TYR:CD1	2.71	0.54
1:C:498:ILE:H	1:C:498:ILE:HD12	1.72	0.54
1:C:1097:VAL:O	1:C:1097:VAL:HG13	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:875:THR:OG1	1:B:876:GLY:HA2	2.07	0.54
1:C:225:ILE:HG23	1:C:247:TYR:CD1	2.40	0.54
1:C:837:THR:CG2	1:C:934:LEU:CD1	2.68	0.54
1:C:892:VAL:HG12	1:C:894:VAL:H	1.72	0.54
1:C:1171:ILE:CD1	1:C:1202:PHE:CZ	2.78	0.54
1:B:926:VAL:CG2	1:B:938:ASN:H	2.20	0.54
1:B:515:ILE:HG21	1:B:655:ILE:HG21	1.90	0.54
1:C:128:GLU:OE1	1:C:133:MET:HE2	2.08	0.54
1:C:495:LEU:N	1:C:495:LEU:CD1	2.70	0.54
1:C:972:PRO:O	1:C:972:PRO:HG2	2.08	0.54
1:C:1310:ARG:HH21	1:C:1312:GLY:H	1.55	0.54
1:B:291:HIS:CD2	1:B:348:LEU:HD21	2.43	0.54
1:B:1276:LEU:HD22	1:B:1300:ASN:HB2	1.89	0.54
1:C:820:ILE:CG2	1:C:983:ILE:CG1	2.77	0.54
1:C:840:ASP:C	1:C:940:ARG:HH22	2.11	0.54
1:C:1310:ARG:NE	1:C:1310:ARG:CA	2.70	0.54
1:C:1319:ARG:HG3	1:C:1319:ARG:O	2.08	0.54
1:C:511:VAL:HG21	1:C:539:PHE:CZ	2.43	0.54
1:C:887:VAL:HG22	1:C:893:ALA:HA	1.90	0.54
1:C:1134:ARG:HH22	1:C:1154:ASN:ND2	2.04	0.54
1:C:1179:THR:HG23	1:C:1179:THR:O	2.07	0.54
1:C:1193:ILE:HG23	1:C:1193:ILE:O	2.06	0.54
1:B:1314:ASP:N	1:B:1314:ASP:OD1	2.40	0.54
1:C:168:VAL:CG2	1:C:204:VAL:CG1	2.85	0.54
1:C:220:ASP:OD1	1:C:222:THR:HG23	2.08	0.54
1:C:265:VAL:O	1:C:1303:SER:HA	2.08	0.54
1:C:364:ALA:CB	1:C:1050:LEU:CD2	2.85	0.54
1:C:446:LYS:CB	1:C:448:TYR:CZ	2.91	0.54
1:C:467:LYS:HB3	1:C:467:LYS:HZ2	1.72	0.54
1:B:225:ILE:HG23	1:B:1069:ARG:HB2	1.90	0.54
1:C:81:ALA:HB3	1:C:168:VAL:CG1	2.38	0.54
1:C:427:VAL:O	1:C:427:VAL:HG12	2.07	0.54
1:C:458:SER:HB3	1:C:675:ALA:HB1	1.90	0.54
1:C:500:GLU:HA	1:C:500:GLU:OE1	2.08	0.54
1:C:515:ILE:HG21	1:C:655:ILE:HG21	1.89	0.54
1:C:559:THR:HG22	1:C:583:GLU:HG3	1.90	0.54
1:C:612:PHE:N	1:C:612:PHE:CD1	2.73	0.54
1:C:736:SER:CB	1:C:1016:ASN:O	2.46	0.54
1:B:206:ILE:HB	1:B:1066:ARG:HD3	1.90	0.53
1:B:267:VAL:HA	1:B:1304:MET:HE1	1.90	0.53
1:B:434:VAL:O	1:B:439:VAL:HG22	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:258:VAL:CG1	1:C:1058:GLY:HA2	2.34	0.53
1:C:449:PHE:N	1:C:450:PRO:HD3	2.22	0.53
1:C:666:ARG:HG2	1:C:666:ARG:NH1	2.18	0.53
1:C:822:MET:HE3	1:C:1046:PHE:CE2	2.43	0.53
1:C:843:LEU:CD2	1:C:943:GLU:HG3	2.38	0.53
1:C:870:ASP:C	1:C:871:PRO:O	2.44	0.53
1:C:297:ASN:ND2	1:C:298:PRO:CD	2.67	0.53
1:C:385:ILE:O	1:C:1328:ILE:CG2	2.56	0.53
1:C:615:THR:N	1:C:1333:ALA:C	2.59	0.53
1:C:985:ARG:HH22	1:C:989:ILE:HB	1.71	0.53
1:B:139:ASN:O	1:C:757:ILE:CB	2.56	0.53
1:B:1282:ALA:HB1	1:B:1283:ASN:CA	2.39	0.53
1:C:146:GLU:HB2	1:C:1317:VAL:HG13	1.90	0.53
1:C:505:PRO:O	1:C:508:ILE:HG22	2.08	0.53
1:C:741:TYR:CZ	1:C:1022:ILE:CD1	2.91	0.53
1:C:1173:TYR:CE1	1:C:1204:LEU:CD1	2.91	0.53
1:B:1250:GLU:OE1	1:B:1250:GLU:N	2.41	0.53
1:C:259:MET:SD	1:C:1055:LEU:HB2	2.48	0.53
1:C:543:TRP:HD1	1:C:544:TYR:HD1	1.54	0.53
1:C:607:PHE:C	1:C:608:THR:CG2	2.77	0.53
1:C:635:ILE:HG23	1:C:635:ILE:O	2.08	0.53
1:C:849:MET:CG	1:C:919:MET:HG3	2.39	0.53
1:C:352:HIS:CD2	1:C:1297:SER:H	2.17	0.53
1:C:462:LEU:HD22	1:C:462:LEU:C	2.23	0.53
1:C:571:ARG:NH1	1:C:571:ARG:CB	2.71	0.53
1:C:1046:PHE:HB2	1:C:1052:LEU:HD21	1.90	0.53
1:C:1118:THR:HB	1:C:1129:PRO:HA	1.91	0.53
1:C:1322:PRO:CB	1:C:1328:ILE:HD11	2.38	0.53
1:B:1242:MET:SD	1:B:1260:PRO:HG3	2.49	0.53
1:C:157:ILE:CD1	1:C:263:ARG:HB3	2.36	0.53
1:C:206:ILE:HD11	1:C:1066:ARG:CD	2.39	0.53
1:C:652:PHE:HE1	1:C:688:GLU:HB3	1.74	0.53
1:B:1158:SER:O	1:B:1162:SER:HB2	2.09	0.53
1:C:154:PHE:HD1	1:C:262:ASN:HB2	1.73	0.53
1:C:651:ARG:HD2	1:C:651:ARG:O	2.08	0.53
1:C:865:ILE:HD13	1:C:865:ILE:N	2.23	0.53
1:C:1307:ALA:O	1:C:1309:ILE:N	2.39	0.53
1:C:1318:GLU:O	1:C:1318:GLU:HG2	2.08	0.53
1:C:144:ASN:HA	1:C:1318:GLU:HB3	1.91	0.53
1:C:1159:VAL:O	1:C:1159:VAL:HG22	2.09	0.53
1:B:373:ASP:O	1:B:376:ILE:HB	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:422:LEU:C	1:C:422:LEU:HD13	2.29	0.53
1:C:840:ASP:CA	1:C:940:ARG:HH22	2.22	0.53
1:C:1014:MET:HG3	1:C:1017:ALA:CB	2.38	0.53
1:C:1022:ILE:HG12	1:C:1027:THR:O	2.08	0.53
1:C:1231:TYR:HB3	1:C:1232:PRO:CD	2.39	0.53
1:B:388:GLN:N	1:B:1320:VAL:HG12	2.24	0.53
1:B:1148:SER:HB2	1:B:1151:VAL:H	1.74	0.53
1:C:256:PHE:HD1	1:C:819:PHE:CD2	2.26	0.53
1:C:910:LEU:HD23	1:C:915:VAL:HG23	0.57	0.53
1:C:1258:VAL:HG23	1:C:1258:VAL:O	2.07	0.53
1:C:1283:ASN:N	1:C:1283:ASN:OD1	2.41	0.53
1:B:309:TRP:HB3	1:B:1252:ASP:O	2.10	0.52
1:C:434:VAL:O	1:C:434:VAL:HG12	2.09	0.52
1:C:466:VAL:O	1:C:466:VAL:HG22	2.07	0.52
1:C:838:GLU:C	1:C:940:ARG:CZ	2.77	0.52
1:C:1002:LEU:HD13	1:C:1005:LEU:HD13	1.91	0.52
1:B:197:PHE:HD2	1:B:301:LEU:HD22	1.74	0.52
1:B:874:ILE:H	1:B:897:TYR:HB3	1.75	0.52
1:B:1071:PHE:HZ	1:B:1236:ILE:HD13	1.74	0.52
1:C:189:ILE:HG12	1:C:286:LEU:HD12	1.91	0.52
1:C:309:TRP:CD1	1:C:309:TRP:C	2.83	0.52
1:C:498:ILE:HD11	1:C:514:PHE:HZ	1.75	0.52
1:C:736:SER:HB2	1:C:1016:ASN:C	2.28	0.52
1:C:1322:PRO:HB2	1:C:1328:ILE:HD11	1.91	0.52
1:B:144:ASN:H	1:B:1318:GLU:H	1.58	0.52
1:C:168:VAL:CB	1:C:204:VAL:HG12	2.38	0.52
1:C:233:VAL:HG22	1:C:234:PRO:HD2	0.57	0.52
1:C:403:PHE:CE1	1:C:408:ILE:HG13	2.44	0.52
1:C:536:LEU:HD11	1:C:607:PHE:CZ	2.44	0.52
1:B:626:ARG:NH2	1:B:712:PHE:O	2.43	0.52
1:C:285:VAL:HG13	1:C:326:GLY:HA2	1.91	0.52
1:C:607:PHE:O	1:C:608:THR:HG23	2.09	0.52
1:C:1046:PHE:CD2	1:C:1052:LEU:CD2	2.93	0.52
1:B:352:HIS:HD2	1:B:1297:SER:H	1.57	0.52
1:C:855:TYR:CD1	1:C:859:ILE:HB	2.44	0.52
1:C:879:THR:N	1:C:880:PRO:HD2	2.09	0.52
1:B:388:GLN:CA	1:B:1320:VAL:CG1	2.87	0.52
1:B:472:GLU:N	1:B:473:ALA:CA	2.73	0.52
1:B:817:ASP:OD1	1:B:983:ILE:HG21	2.09	0.52
1:C:350:ILE:O	1:C:350:ILE:HG13	2.09	0.52
1:C:397:LEU:H	1:C:397:LEU:HD12	1.72	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:603:ILE:HD13	1:C:659:LEU:HD23	1.91	0.52
1:C:838:GLU:HB2	1:C:934:LEU:HB2	0.53	0.52
1:C:1097:VAL:HG12	1:C:1136:HIS:O	2.10	0.52
1:C:1099:VAL:O	1:C:1139:MET:HA	2.10	0.52
1:C:1105:LEU:HD12	1:C:1105:LEU:N	2.20	0.52
1:B:451:GLU:HG2	1:B:452:ASN:N	2.25	0.52
1:B:472:GLU:C	1:B:761:SER:HB2	2.27	0.52
1:C:157:ILE:HD11	1:C:263:ARG:NE	2.24	0.52
1:C:157:ILE:CD1	1:C:263:ARG:CG	2.61	0.52
1:C:341:LYS:CB	1:C:1306:THR:HB	2.39	0.52
1:C:449:PHE:N	1:C:450:PRO:CD	2.72	0.52
1:C:750:GLU:HA	1:C:756:THR:HG21	1.90	0.52
1:C:937:ASN:N	1:C:937:ASN:OD1	2.41	0.52
1:C:1193:ILE:HG13	1:C:1202:PHE:CZ	2.43	0.52
1:B:878:SER:O	1:B:879:THR:HG23	2.09	0.52
1:C:193:THR:HG21	1:C:300:LEU:HB3	1.91	0.52
1:B:559:THR:HG23	1:B:583:GLU:HG3	1.90	0.52
1:C:285:VAL:CG1	1:C:326:GLY:HA2	2.39	0.52
1:C:830:VAL:HG21	1:C:947:GLU:CG	2.38	0.52
1:C:929:PHE:HB3	1:C:936:MET:CE	2.38	0.52
1:C:967:LEU:HD22	1:C:1062:ILE:HG21	1.92	0.52
1:C:1021:ARG:CB	1:C:1021:ARG:NH1	2.72	0.52
1:B:897:TYR:CE2	1:B:899:SER:HB3	2.44	0.52
1:C:146:GLU:CB	1:C:1317:VAL:HG12	2.40	0.52
1:C:442:PRO:HG2	1:C:442:PRO:O	2.09	0.52
1:C:656:VAL:HG11	1:C:688:GLU:CG	2.39	0.52
1:C:835:TYR:CE1	1:C:942:HIS:CD2	2.98	0.52
1:C:924:ASP:OD1	1:C:927:SER:CA	2.57	0.52
1:C:1230:ILE:O	1:C:1230:ILE:HG13	2.09	0.52
1:C:1247:ASN:HD22	1:C:1247:ASN:N	2.07	0.52
1:B:188:ARG:HH22	1:C:237:VAL:HG13	1.75	0.51
1:B:440:ILE:CG2	1:B:770:CYS:HB2	2.41	0.51
1:B:924:ASP:HB3	1:B:928:ARG:CZ	2.40	0.51
1:C:338:ARG:O	1:C:341:LYS:N	2.42	0.51
1:C:579:LEU:C	1:C:579:LEU:HD12	2.31	0.51
1:C:1081:ASP:O	1:C:1227:MET:HB3	2.10	0.51
1:C:1279:SER:H	1:C:1280:PRO:HA	1.70	0.51
1:C:339:LEU:O	1:C:397:LEU:HD21	2.10	0.51
1:C:511:VAL:CG2	1:C:539:PHE:CE2	2.93	0.51
1:C:612:PHE:CE2	1:C:614:ARG:HB3	2.45	0.51
1:C:613:LEU:HD22	1:C:613:LEU:C	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:694:ILE:C	1:C:694:ILE:HD12	2.31	0.51
1:C:928:ARG:CD	1:C:928:ARG:N	2.73	0.51
1:B:1103:HIS:CE1	1:B:1145:ALA:HB3	2.45	0.51
1:C:210:ARG:HA	1:C:221:LEU:CD1	2.39	0.51
1:C:254:VAL:HG11	1:C:1062:ILE:HD11	1.87	0.51
1:B:1306:THR:HG22	1:B:1307:ALA:N	2.25	0.51
1:B:517:PHE:CE2	1:B:528:ILE:HD11	2.46	0.51
1:C:434:VAL:CG2	1:C:709:MET:CE	2.88	0.51
1:C:484:ARG:O	1:C:485:GLU:C	2.47	0.51
1:C:669:GLN:OE1	1:C:669:GLN:N	2.43	0.51
1:C:815:LEU:CB	1:C:816:PRO:CD	2.81	0.51
1:C:1054:ARG:HH11	1:C:1054:ARG:CB	2.23	0.51
1:C:1259:ALA:HB1	1:C:1260:PRO:HD2	1.91	0.51
1:B:150:LEU:HD21	1:B:378:ALA:HB3	1.93	0.51
1:B:489:MET:SD	1:B:493:HIS:ND1	2.81	0.51
1:B:735:THR:HG21	1:B:1028:VAL:HG11	1.92	0.51
1:B:1128:TYR:HB3	1:B:1134:ARG:HG2	1.93	0.51
1:C:264:LEU:O	1:C:266:ILE:HG12	2.11	0.51
1:C:336:TYR:O	1:C:337:VAL:O	2.29	0.51
1:C:502:PHE:HA	1:C:507:SER:CB	2.41	0.51
1:C:1310:ARG:HG3	1:C:1310:ARG:O	2.11	0.51
1:B:461:ARG:NH1	1:B:461:ARG:CG	2.73	0.51
1:B:531:ASP:OD1	1:B:531:ASP:N	2.37	0.51
1:B:974:LEU:HA	1:B:978:GLN:OE1	2.10	0.51
1:B:1066:ARG:HD2	1:B:1296:ILE:HD13	1.92	0.51
1:C:334:LEU:HD11	1:C:366:MET:CE	2.37	0.51
1:C:409:ILE:HG23	1:C:1040:PHE:CZ	2.44	0.51
1:C:849:MET:HG2	1:C:919:MET:HG3	1.92	0.51
1:C:1222:ALA:O	1:C:1223:SER:HB2	2.10	0.51
1:B:1121:HIS:CD2	1:B:1123:PRO:HD2	2.45	0.51
1:B:1134:ARG:NH1	1:B:1158:SER:OG	2.44	0.51
1:C:285:VAL:O	1:C:327:LEU:N	2.39	0.51
1:C:285:VAL:O	1:C:326:GLY:HA2	2.11	0.51
1:C:320:GLN:O	1:C:321:ALA:CB	2.58	0.51
1:C:516:LEU:HB2	1:C:763:VAL:HG11	1.90	0.51
1:C:668:VAL:CG1	1:C:674:LYS:CD	2.88	0.51
1:B:388:GLN:CB	1:B:1320:VAL:HG11	2.12	0.51
1:C:190:VAL:HG11	1:C:304:PHE:CZ	2.46	0.51
1:C:231:LEU:HD13	1:C:982:ALA:HB1	1.93	0.51
1:C:485:GLU:OE1	1:C:486:VAL:CG1	2.56	0.51
1:B:879:THR:O	1:B:883:ILE:HD12	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:672:MET:SD	1:C:672:MET:C	2.89	0.51
1:C:1101:TYR:OH	1:C:1147:MET:HG2	2.10	0.51
1:B:231:LEU:HD23	1:B:985:ARG:HB3	1.93	0.50
1:B:305:THR:HG22	1:B:307:VAL:HG12	1.92	0.50
1:B:526:ASN:HB2	1:B:721:SER:HB3	1.92	0.50
1:C:337:VAL:HG12	1:C:338:ARG:H	1.76	0.50
1:C:741:TYR:CZ	1:C:1022:ILE:HD11	2.45	0.50
1:C:873:TYR:HA	1:C:896:LEU:O	2.11	0.50
1:C:878:SER:HB3	1:C:903:ASN:CG	2.31	0.50
1:C:887:VAL:O	1:C:887:VAL:HG12	2.10	0.50
1:C:954:GLN:CA	1:C:958:ILE:HD13	2.41	0.50
1:C:986:ILE:C	1:C:989:ILE:HG22	2.32	0.50
1:C:1077:MET:HB2	1:C:1165:VAL:HG22	1.91	0.50
1:C:1206:PHE:CE2	1:C:1236:ILE:HD13	2.46	0.50
1:C:1261:SER:C	1:C:1263:TYR:H	2.12	0.50
1:B:524:GLU:O	1:B:528:ILE:HG13	2.12	0.50
1:C:339:LEU:CD1	1:C:397:LEU:CD2	2.87	0.50
1:C:559:THR:CG2	1:C:583:GLU:HG3	2.41	0.50
1:C:568:PHE:N	1:C:568:PHE:CD1	2.77	0.50
1:C:820:ILE:HG22	1:C:983:ILE:HD11	1.92	0.50
1:C:1202:PHE:CD1	1:C:1202:PHE:C	2.84	0.50
1:C:1259:ALA:CB	1:C:1260:PRO:HD3	2.29	0.50
1:B:490:PHE:HA	1:B:745:ILE:HG12	1.92	0.50
1:B:735:THR:O	1:B:1017:ALA:HA	2.11	0.50
1:C:1078:TYR:HD2	1:C:1229:LEU:CD1	2.25	0.50
1:C:638:THR:HG22	1:C:638:THR:O	2.11	0.50
1:C:836:GLN:HB2	1:C:940:ARG:CB	2.38	0.50
1:C:947:GLU:O	1:C:947:GLU:HG3	2.11	0.50
1:C:1119:TYR:HE2	1:C:1135:PRO:HG3	1.76	0.50
1:C:614:ARG:HG3	1:C:614:ARG:O	2.10	0.50
1:C:617:ASP:HA	1:C:620:ILE:HG22	1.93	0.50
1:C:652:PHE:HZ	1:C:687:LEU:HD21	1.76	0.50
1:C:835:TYR:CE1	1:C:925:VAL:CG2	2.89	0.50
1:C:1248:HIS:HB3	1:C:1252:ASP:O	2.11	0.50
1:C:157:ILE:HD11	1:C:263:ARG:CD	2.41	0.50
1:C:204:VAL:CG2	1:C:1242:MET:O	2.58	0.50
1:C:255:LEU:HD23	1:C:1058:GLY:O	2.10	0.50
1:C:338:ARG:HG3	1:C:342:THR:HB	1.88	0.50
1:C:405:HIS:CD2	1:C:624:PHE:O	2.64	0.50
1:C:409:ILE:HD13	1:C:409:ILE:O	2.12	0.50
1:C:881:ASP:O	1:C:884:ALA:HB3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:987:ALA:O	1:C:992:VAL:CG1	2.60	0.50
1:C:1206:PHE:CD2	1:C:1236:ILE:HD13	2.45	0.50
1:B:683:TRP:CH2	1:B:687:LEU:HD11	2.46	0.50
1:C:235:ILE:HG22	1:C:236:GLY:N	2.27	0.50
1:C:304:PHE:N	1:C:304:PHE:HD1	2.10	0.50
1:C:551:PHE:CD1	1:C:551:PHE:C	2.85	0.50
1:C:1071:PHE:HB3	1:C:1234:GLN:OE1	2.12	0.50
1:C:1122:PRO:CB	1:C:1123:PRO:HD3	2.41	0.50
1:C:232:LEU:HD11	1:C:245:ALA:O	2.11	0.50
1:C:251:LEU:HD21	1:C:1062:ILE:HG13	1.87	0.50
1:C:338:ARG:HD3	1:C:342:THR:HG22	1.83	0.50
1:C:109:LYS:HD2	1:C:110:PRO:CD	2.39	0.50
1:C:449:PHE:HA	1:C:683:TRP:CD1	2.45	0.50
1:C:485:GLU:OE1	1:C:706:TYR:CD1	2.65	0.50
1:C:1031:TYR:CE2	1:C:1041:ARG:HG3	2.47	0.50
1:C:1247:ASN:ND2	1:C:1247:ASN:N	2.58	0.50
1:B:461:ARG:NE	1:B:504:ASP:CB	2.69	0.49
1:B:1021:ARG:HH22	1:B:1032:ASP:HB2	1.77	0.49
1:C:176:LYS:CG	1:C:177:LYS:N	2.73	0.49
1:C:270:THR:HG22	1:C:291:HIS:HA	1.94	0.49
1:C:462:LEU:HD23	1:C:506:SER:OG	2.11	0.49
1:C:887:VAL:CG2	1:C:893:ALA:HA	2.42	0.49
1:C:1085:ASP:CB	1:C:1086:PRO:CD	2.79	0.49
1:C:248:VAL:HG11	1:C:970:LEU:O	2.12	0.49
1:C:547:GLU:CD	1:C:599:THR:HG23	2.32	0.49
1:C:1088:PHE:CG	1:C:1088:PHE:O	2.65	0.49
1:B:269:GLU:HB3	1:B:292:ASN:ND2	2.20	0.49
1:C:446:LYS:HE2	1:C:472:GLU:OE2	2.12	0.49
1:C:686:HIS:ND1	1:C:686:HIS:O	2.45	0.49
1:B:526:ASN:HD21	1:B:727:PHE:HD2	1.60	0.49
1:B:1245:ILE:O	1:B:1246:VAL:HG13	2.12	0.49
1:C:157:ILE:CD1	1:C:263:ARG:NE	2.75	0.49
1:C:314:ILE:N	1:C:314:ILE:HD13	2.28	0.49
1:C:347:ALA:CB	1:C:1300:ASN:HB3	2.43	0.49
1:C:820:ILE:CG2	1:C:983:ILE:CD1	2.90	0.49
1:C:1250:GLU:O	1:C:1251:VAL:CG2	2.60	0.49
1:B:206:ILE:O	1:B:1239:ALA:HB1	2.12	0.49
1:C:268:GLY:O	1:C:269:GLU:HB2	2.11	0.49
1:C:409:ILE:HD12	1:C:1040:PHE:CZ	2.47	0.49
1:C:467:LYS:NZ	1:C:467:LYS:CB	2.72	0.49
1:C:606:LEU:HD22	1:C:655:ILE:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:853:ASP:OD1	1:C:854:GLN:N	2.46	0.49
1:C:199:TYR:CZ	1:C:1246:VAL:HG12	2.47	0.49
1:B:427:VAL:HG11	1:B:755:LEU:CD2	2.42	0.49
1:B:845:GLU:N	1:B:846:GLY:HA2	2.26	0.49
1:B:1269:THR:HG22	1:B:1270:LEU:H	1.78	0.49
1:C:555:GLY:HA2	1:C:570:GLY:HA2	1.95	0.49
1:C:639:ASN:HB3	1:C:1330:ILE:CD1	2.43	0.49
1:C:862:ARG:HB3	1:C:952:PHE:HZ	1.70	0.49
1:B:243:GLN:O	1:B:246:GLU:HB2	2.13	0.49
1:B:437:ALA:O	1:B:701:HIS:CE1	2.66	0.49
1:C:441:ARG:NH2	1:C:441:ARG:CG	2.73	0.49
1:C:494:GLU:HB2	1:C:531:ASP:OD2	2.13	0.49
1:C:912:GLU:O	1:C:912:GLU:HG2	2.12	0.49
1:B:271:THR:HG23	1:C:237:VAL:HG23	1.94	0.49
1:C:339:LEU:HD13	1:C:397:LEU:HD21	1.91	0.49
1:B:631:PRO:HA	1:B:718:ASN:HD21	1.78	0.49
1:B:649:ALA:HB1	1:B:692:ASP:OD1	2.12	0.49
1:B:996:ASP:HB2	1:B:999:LYS:HG3	1.94	0.49
1:B:1210:LEU:HD11	1:B:1256:GLY:HA3	1.95	0.49
1:C:225:ILE:HD12	1:C:247:TYR:HE1	1.76	0.49
1:C:312:ARG:CG	1:C:312:ARG:NH2	2.71	0.49
1:C:558:TYR:CZ	1:C:585:PHE:CB	2.96	0.49
1:B:558:TYR:CE1	1:B:590:SER:HB3	2.48	0.48
1:B:893:ALA:HB1	1:B:915:VAL:HG12	1.94	0.48
1:C:1101:TYR:CD1	1:C:1101:TYR:O	2.66	0.48
1:C:1297:SER:C	1:C:1298:PHE:HD1	2.16	0.48
1:B:150:LEU:HD12	1:B:150:LEU:O	2.12	0.48
1:C:565:GLU:HG2	1:C:566:PHE:N	2.29	0.48
1:C:1281:VAL:C	1:C:1283:ASN:N	2.58	0.48
1:B:276:ASN:OD1	1:C:1199:GLY:CA	2.62	0.48
1:B:970:LEU:HD21	1:B:1070:ARG:HH21	1.79	0.48
1:C:348:LEU:HD11	1:C:1301:VAL:HG22	1.95	0.48
1:C:445:GLU:CD	1:C:447:ARG:HG2	2.22	0.48
1:C:833:ARG:HH11	1:C:942:HIS:CE1	2.27	0.48
1:C:892:VAL:HG11	1:C:894:VAL:HG11	1.90	0.48
1:C:987:ALA:O	1:C:992:VAL:O	2.31	0.48
1:C:1186:GLN:H	1:C:1205:GLN:HE22	1.60	0.48
1:C:1290:LYS:NZ	1:C:1299:SER:HB3	2.22	0.48
1:B:439:VAL:HG23	1:B:440:ILE:N	2.27	0.48
1:C:96:ILE:HD12	1:C:96:ILE:HG23	1.62	0.48
1:C:820:ILE:HG21	1:C:983:ILE:HD11	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:836:GLN:C	1:C:838:GLU:H	2.14	0.48
1:C:1210:LEU:HD23	1:C:1244:ALA:HB1	1.92	0.48
1:B:361:ASN:OD1	1:B:1054:ARG:NH2	2.36	0.48
1:C:128:GLU:OE1	1:C:133:MET:HE1	2.13	0.48
1:C:492:VAL:CG1	1:C:580:TYR:HD2	2.26	0.48
1:C:605:ARG:HG3	1:C:605:ARG:O	2.13	0.48
1:C:741:TYR:OH	1:C:1022:ILE:CD1	2.61	0.48
1:C:828:ASP:N	1:C:828:ASP:OD1	2.45	0.48
1:C:849:MET:HG2	1:C:919:MET:CE	2.30	0.48
1:C:985:ARG:NH2	1:C:988:GLN:CG	2.76	0.48
1:C:1276:LEU:HB3	1:C:1290:LYS:HG3	1.95	0.48
1:B:505:PRO:HG3	1:B:670:ASP:OD2	2.14	0.48
1:B:560:ILE:HG23	1:B:564:GLY:HA3	1.96	0.48
1:B:862:ARG:NH1	1:B:948:ILE:HD13	2.29	0.48
1:B:1103:HIS:NE2	1:B:1146:GLY:O	2.46	0.48
1:B:1117:VAL:HB	1:B:1154:ASN:HD22	1.78	0.48
1:C:302:ARG:CD	1:C:318:LEU:HD23	2.43	0.48
1:C:840:ASP:HA	1:C:940:ARG:HH22	1.77	0.48
1:C:1137:VAL:HG22	1:C:1164:TRP:NE1	2.28	0.48
1:C:1259:ALA:CB	1:C:1260:PRO:CD	2.76	0.48
1:B:157:ILE:O	1:B:158:SER:OG	2.26	0.48
1:B:614:ARG:NH1	1:B:707:ALA:HB1	2.29	0.48
1:B:1088:PHE:CE2	1:B:1090:PRO:HG3	2.48	0.48
1:C:592:VAL:HG13	1:C:593:PRO:HD2	1.95	0.48
1:C:843:LEU:HD12	1:C:943:GLU:CG	2.15	0.48
1:C:878:SER:HB2	1:C:880:PRO:HD3	1.95	0.48
1:C:1066:ARG:HG2	1:C:1238:VAL:O	2.14	0.48
1:C:339:LEU:HD12	1:C:399:PRO:HB3	1.94	0.48
1:C:539:PHE:O	1:C:543:TRP:HB3	2.12	0.48
1:B:434:VAL:O	1:B:439:VAL:CG2	2.62	0.48
1:B:549:GLY:O	1:B:553:GLN:HG2	2.14	0.48
1:B:634:TYR:HB2	1:B:720:PHE:HD1	1.79	0.48
1:C:824:LEU:HA	1:C:968:ARG:HD2	1.96	0.48
1:C:892:VAL:HG12	1:C:894:VAL:HG12	1.69	0.48
1:C:1137:VAL:HG21	1:C:1164:TRP:CE2	2.48	0.48
1:B:157:ILE:HG21	1:B:263:ARG:HD2	1.95	0.48
1:B:426:ILE:HG12	1:B:714:LEU:HD21	1.95	0.48
1:C:189:ILE:HG12	1:C:286:LEU:HD11	1.96	0.48
1:C:290:TYR:HA	1:C:328:GLY:HA2	1.96	0.48
1:C:530:GLY:HA3	1:C:575:TRP:NE1	2.29	0.48
1:C:629:ARG:HB2	1:C:1037:ILE:CG2	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1104:ARG:NH1	1:C:1104:ARG:CG	2.71	0.48
1:C:1243:ARG:HG2	1:C:1243:ARG:NH1	2.24	0.48
1:B:868:VAL:HB	1:B:890:THR:HA	1.96	0.47
1:C:408:ILE:N	1:C:408:ILE:HD13	2.29	0.47
1:C:560:ILE:HG22	1:C:585:PHE:HE2	1.79	0.47
1:C:671:ASP:HA	1:C:674:LYS:HZ1	1.78	0.47
1:C:730:ASP:OD1	1:C:731:GLN:N	2.46	0.47
1:C:838:GLU:HG2	1:C:934:LEU:C	2.13	0.47
1:C:1116:ARG:NH1	1:C:1130:SER:CB	2.77	0.47
1:B:199:TYR:CE1	1:B:1246:VAL:HA	2.48	0.47
1:C:82:ARG:HH22	1:C:209:ASN:HD22	1.62	0.47
1:C:121:PHE:HB3	1:C:122:ASN:H	1.34	0.47
1:C:144:ASN:HB3	1:C:1318:GLU:CD	2.27	0.47
1:C:450:PRO:O	1:C:451:GLU:CB	2.60	0.47
1:C:451:GLU:CB	1:C:686:HIS:CB	2.92	0.47
1:C:713:MET:CE	1:C:804:LEU:HD21	2.41	0.47
1:C:1075:ARG:O	1:C:1075:ARG:HG3	2.14	0.47
1:B:148:GLN:HB2	1:B:149:PRO:HD2	1.96	0.47
1:C:247:TYR:CG	1:C:1070:ARG:HD3	2.48	0.47
1:C:259:MET:O	1:C:1054:ARG:HB3	2.14	0.47
1:C:312:ARG:HG3	1:C:312:ARG:NH2	2.18	0.47
1:C:382:HIS:NE2	1:C:800:LEU:HD23	2.28	0.47
1:C:822:MET:C	1:C:822:MET:SD	2.92	0.47
1:C:835:TYR:CD1	1:C:942:HIS:HB2	2.44	0.47
1:C:1105:LEU:HD12	1:C:1105:LEU:C	2.35	0.47
1:C:1250:GLU:O	1:C:1251:VAL:HG22	2.14	0.47
1:B:426:ILE:HG12	1:B:714:LEU:CD2	2.44	0.47
1:B:558:TYR:CZ	1:B:585:PHE:HB2	2.48	0.47
1:C:514:PHE:HE2	1:C:535:VAL:HG13	1.80	0.47
1:C:838:GLU:O	1:C:839:ALA:HB3	2.14	0.47
1:C:1046:PHE:HD2	1:C:1052:LEU:CD2	2.22	0.47
1:C:1155:ILE:CG2	1:C:1166:VAL:CG1	2.81	0.47
1:B:139:ASN:O	1:C:757:ILE:CG2	2.63	0.47
1:B:863:LEU:HD21	1:B:871:PRO:HD3	1.95	0.47
1:B:1131:PRO:HA	1:B:1134:ARG:NH1	2.29	0.47
1:C:227:LEU:HD23	1:C:246:GLU:O	2.14	0.47
1:C:338:ARG:NE	1:C:342:THR:HG22	2.26	0.47
1:C:370:VAL:CG1	1:C:398:ARG:HB2	2.44	0.47
1:C:543:TRP:CD1	1:C:543:TRP:C	2.86	0.47
1:C:1021:ARG:HB2	1:C:1021:ARG:NH1	2.22	0.47
1:C:1105:LEU:O	1:C:1105:LEU:HD13	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:156:GLN:HG2	1:B:266:ILE:HD11	1.96	0.47
1:B:204:VAL:CG1	1:B:1242:MET:HB2	2.45	0.47
1:B:752:VAL:O	1:B:753:ASP:HB2	2.15	0.47
1:B:971:MET:HA	1:B:972:PRO:HD3	1.60	0.47
1:B:1023:ARG:NE	1:B:1027:THR:OG1	2.48	0.47
1:C:498:ILE:HD11	1:C:514:PHE:CZ	2.50	0.47
1:C:516:LEU:HA	1:C:516:LEU:HD23	1.72	0.47
1:C:552:ILE:CD1	1:C:572:ASN:HB2	2.39	0.47
1:C:826:GLY:H	1:C:968:ARG:CD	2.27	0.47
1:C:896:LEU:CD1	1:C:918:VAL:HG21	2.42	0.47
1:C:928:ARG:HG3	1:C:928:ARG:NH1	2.29	0.47
1:B:154:PHE:CG	1:B:264:LEU:HG	2.50	0.47
1:B:383:SER:O	1:B:708:THR:HG23	2.15	0.47
1:B:528:ILE:HG13	1:B:528:ILE:H	1.56	0.47
1:B:697:ALA:HA	1:B:774:LEU:HD12	1.97	0.47
1:B:1200:LYS:HD3	1:B:1202:PHE:HE1	1.79	0.47
1:C:118:THR:O	1:C:119:ASP:C	2.52	0.47
1:C:203:VAL:HG12	1:C:1243:ARG:HD2	1.97	0.47
1:C:579:LEU:HD12	1:C:579:LEU:O	2.15	0.47
1:C:686:HIS:ND1	1:C:686:HIS:C	2.68	0.47
1:C:843:LEU:HD12	1:C:943:GLU:CB	2.44	0.47
1:B:298:PRO:O	1:B:301:LEU:HB3	2.15	0.47
1:B:694:ILE:HG22	1:B:698:HIS:ND1	2.30	0.47
1:B:733:VAL:HG21	1:B:741:TYR:CD1	2.50	0.47
1:B:960:THR:HG23	1:B:965:ARG:NH1	2.30	0.47
1:B:1066:ARG:HH21	1:B:1296:ILE:HD12	1.79	0.47
1:C:200:GLY:HA2	1:C:1246:VAL:HG22	1.95	0.47
1:C:323:THR:CG2	1:C:1266:ASP:HB2	2.44	0.47
1:C:835:TYR:HE1	1:C:942:HIS:CD2	2.33	0.47
1:C:1206:PHE:HD2	1:C:1236:ILE:HD11	1.73	0.47
1:B:231:LEU:HB2	1:B:249:SER:CB	2.45	0.47
1:B:323:THR:HA	1:B:1266:ASP:OD1	2.15	0.47
1:B:329:LEU:HD21	1:B:332:THR:OG1	2.14	0.47
1:B:482:ILE:HG23	1:B:706:TYR:CE1	2.50	0.47
1:B:530:GLY:HA3	1:B:575:TRP:CD1	2.49	0.47
1:C:153:ASP:OD1	1:C:153:ASP:N	2.48	0.47
1:C:379:LEU:O	1:C:380:GLN:C	2.51	0.47
1:C:525:PHE:O	1:C:525:PHE:CG	2.68	0.47
1:C:1228:ARG:HG3	1:C:1228:ARG:O	2.15	0.47
1:B:154:PHE:HA	1:B:262:ASN:OD1	2.15	0.47
1:B:232:LEU:HD22	1:B:974:LEU:HD21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:265:VAL:HG21	1:B:358:LEU:HD13	1.97	0.47
1:B:957:PHE:CD2	1:B:958:ILE:HG13	2.50	0.47
1:C:652:PHE:HB3	1:C:691:PHE:CD2	2.50	0.47
1:C:1021:ARG:O	1:C:1029:LEU:HB2	2.15	0.47
1:C:1031:TYR:O	1:C:1031:TYR:CG	2.68	0.47
1:C:1062:ILE:HG23	1:C:1062:ILE:O	2.15	0.47
1:C:1205:GLN:O	1:C:1205:GLN:HG3	2.15	0.47
1:C:1254:PRO:HG2	1:C:1257:ALA:HB2	1.97	0.47
1:C:1270:LEU:O	1:C:1271:SER:C	2.52	0.47
1:C:237:VAL:HG12	1:C:238:THR:H	1.80	0.46
1:C:560:ILE:CG2	1:C:585:PHE:HE2	2.28	0.46
1:C:733:VAL:HB	1:C:1022:ILE:HD12	1.94	0.46
1:C:804:LEU:HD23	1:C:804:LEU:HA	1.66	0.46
1:C:873:TYR:CD2	1:C:898:GLN:HG3	2.48	0.46
1:C:946:LEU:N	1:C:946:LEU:CD1	2.73	0.46
1:C:1112:ASN:HD22	1:C:1112:ASN:C	2.01	0.46
1:B:274:MET:HB2	1:B:277:THR:HG23	1.97	0.46
1:B:424:GLY:HA2	1:B:427:VAL:HG12	1.98	0.46
1:B:701:HIS:CD2	1:B:791:ILE:HD11	2.50	0.46
1:C:451:GLU:OE1	1:C:686:HIS:N	2.49	0.46
1:C:451:GLU:OE2	1:C:682:GLN:CB	2.64	0.46
1:C:741:TYR:O	1:C:741:TYR:CD1	2.68	0.46
1:C:1176:GLU:OE1	1:C:1203:HIS:HE1	1.96	0.46
1:B:617:ASP:OD1	1:B:618:LEU:N	2.48	0.46
1:B:880:PRO:HB3	1:B:909:TYR:HB2	1.96	0.46
1:B:1210:LEU:HD13	1:B:1243:ARG:NH1	2.30	0.46
1:B:1271:SER:HB3	1:B:1275:ASP:OD2	2.15	0.46
1:C:163:TYR:CE2	1:C:258:VAL:CG2	2.93	0.46
1:C:171:GLU:OE2	1:C:1179:THR:OG1	2.21	0.46
1:C:370:VAL:HG13	1:C:398:ARG:H	1.79	0.46
1:C:492:VAL:HG22	1:C:747:ARG:CA	2.41	0.46
1:C:838:GLU:CG	1:C:934:LEU:O	2.47	0.46
1:B:793:TYR:CD2	1:B:1321:ASN:CG	2.87	0.46
1:C:841:ASP:N	1:C:940:ARG:HH22	2.13	0.46
1:C:962:ASP:O	1:C:965:ARG:HB3	2.15	0.46
1:B:1064:ASN:OD1	1:B:1065:PRO:HD2	2.16	0.46
1:B:1269:THR:HG22	1:B:1270:LEU:N	2.30	0.46
1:B:1278:TYR:CE2	1:B:1290:LYS:HA	2.50	0.46
1:C:450:PRO:C	1:C:454:GLU:HG2	2.35	0.46
1:C:947:GLU:HA	1:C:947:GLU:OE2	2.16	0.46
1:B:482:ILE:O	1:B:485:GLU:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:926:VAL:HG21	1:B:937:ASN:N	2.30	0.46
1:B:1174:THR:HG23	1:B:1201:LEU:HD21	1.97	0.46
1:C:820:ILE:HD12	1:C:820:ILE:HG23	1.58	0.46
1:C:901:VAL:CG2	1:C:930:ALA:CB	2.85	0.46
1:C:997:TYR:C	1:C:999:LYS:N	2.67	0.46
1:B:219:ILE:HA	1:B:228:VAL:HG22	1.98	0.46
1:C:652:PHE:HE1	1:C:688:GLU:CB	2.29	0.46
1:C:663:VAL:HG11	1:C:680:THR:CG2	2.46	0.46
1:B:231:LEU:HD12	1:B:249:SER:HB2	1.97	0.46
1:B:285:VAL:HG21	1:B:325:TYR:CE2	2.50	0.46
1:C:338:ARG:CG	1:C:342:THR:HA	2.44	0.46
1:C:747:ARG:CG	1:C:747:ARG:NH1	2.72	0.46
1:C:1155:ILE:O	1:C:1155:ILE:HG22	2.16	0.46
1:B:919:MET:SD	1:B:925:VAL:HG12	2.56	0.46
1:B:1216:SER:O	1:B:1219:ASP:HB2	2.16	0.46
1:C:178:ASP:O	1:C:306:GLN:OE1	2.34	0.46
1:C:329:LEU:HA	1:C:329:LEU:HD23	1.67	0.46
1:C:514:PHE:CD2	1:C:532:ILE:HG23	2.51	0.46
1:C:716:PHE:CD1	1:C:716:PHE:C	2.88	0.46
1:C:716:PHE:CD1	1:C:716:PHE:O	2.69	0.46
1:C:872:ILE:HD12	1:C:873:TYR:H	1.81	0.46
1:C:887:VAL:HG13	1:C:893:ALA:HA	1.98	0.46
1:C:1233:LEU:C	1:C:1234:GLN:HG3	2.37	0.46
1:B:822:MET:HG3	1:B:1045:TYR:CD1	2.51	0.46
1:B:845:GLU:HG2	1:B:911:ARG:HD2	1.98	0.46
1:C:81:ALA:HB3	1:C:168:VAL:HG13	1.98	0.46
1:C:322:GLY:O	1:C:1279:SER:CB	2.64	0.46
1:C:455:GLN:HG2	1:C:455:GLN:O	2.15	0.46
1:C:525:PHE:CE1	1:C:532:ILE:CD1	2.96	0.46
1:C:543:TRP:CD1	1:C:543:TRP:O	2.69	0.46
1:C:558:TYR:CE1	1:C:585:PHE:HB2	2.51	0.46
1:C:579:LEU:CB	1:C:582:SER:OG	2.63	0.46
1:C:585:PHE:HA	1:C:586:PRO:HD3	1.56	0.46
1:C:825:SER:O	1:C:825:SER:OG	2.34	0.46
1:C:1078:TYR:O	1:C:1078:TYR:CD1	2.68	0.46
1:C:1132:THR:O	1:C:1133:GLY:O	2.33	0.46
1:C:1275:ASP:OD1	1:C:1275:ASP:N	2.34	0.46
1:B:342:THR:HB	1:B:1309:ILE:CD1	2.42	0.45
1:B:793:TYR:CD2	1:B:1322:PRO:HD2	2.51	0.45
1:B:1204:LEU:HD21	1:B:1230:ILE:HD11	1.98	0.45
1:C:262:ASN:HA	1:C:361:ASN:OD1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:696:VAL:O	1:C:696:VAL:HG12	2.15	0.45
1:C:720:PHE:O	1:C:720:PHE:CD1	2.70	0.45
1:C:1047:LEU:HB2	1:C:1051:ARG:HD3	1.98	0.45
1:C:1105:LEU:C	1:C:1105:LEU:CD1	2.85	0.45
1:B:165:THR:HG22	1:B:166:TYR:N	2.30	0.45
1:B:230:ASP:OD1	1:B:230:ASP:N	2.49	0.45
1:B:231:LEU:CD2	1:B:986:ILE:HG13	2.46	0.45
1:B:554:ARG:CZ	1:B:594:LEU:HD12	2.46	0.45
1:B:1122:PRO:HB2	1:B:1123:PRO:HD3	1.98	0.45
1:C:439:VAL:O	1:C:439:VAL:HG13	2.16	0.45
1:C:603:ILE:HD13	1:C:659:LEU:CD2	2.46	0.45
1:C:874:ILE:HG21	1:C:902:ILE:CD1	2.29	0.45
1:C:928:ARG:HH11	1:C:928:ARG:CG	2.23	0.45
1:B:329:LEU:HD12	1:B:346:HIS:CE1	2.51	0.45
1:B:504:ASP:O	1:B:506:SER:HA	2.16	0.45
1:C:96:ILE:HD13	1:C:96:ILE:H	1.76	0.45
1:C:108:LYS:NZ	1:C:108:LYS:CB	2.72	0.45
1:C:497:LYS:H	1:C:497:LYS:HG2	1.49	0.45
1:C:1127:ALA:O	1:C:1128:TYR:CB	2.64	0.45
1:C:1206:PHE:CE2	1:C:1236:ILE:HD12	2.51	0.45
1:C:1219:ASP:CG	1:C:1220:PRO:HD2	2.08	0.45
1:B:479:HIS:O	1:B:482:ILE:N	2.50	0.45
1:B:1238:VAL:HG23	1:B:1239:ALA:N	2.31	0.45
1:C:160:PRO:HG3	1:C:265:VAL:HG12	1.98	0.45
1:C:213:PHE:HB3	1:C:219:ILE:HB	1.92	0.45
1:C:525:PHE:HE1	1:C:532:ILE:CD1	2.30	0.45
1:C:629:ARG:CB	1:C:1037:ILE:HG23	2.41	0.45
1:C:643:THR:HG22	1:C:644:VAL:HG12	1.97	0.45
1:C:674:LYS:NZ	1:C:674:LYS:CB	2.73	0.45
1:C:1062:ILE:HD12	1:C:1062:ILE:HA	1.53	0.45
1:C:1078:TYR:HB2	1:C:1229:LEU:CD1	2.47	0.45
1:B:307:VAL:HG11	1:B:1245:ILE:HG23	1.98	0.45
1:B:370:VAL:HG23	1:B:374:ASP:OD2	2.17	0.45
1:B:1278:TYR:HD2	1:B:1288:ILE:HG23	1.82	0.45
1:C:285:VAL:O	1:C:326:GLY:CA	2.65	0.45
1:C:341:LYS:HB2	1:C:1306:THR:HB	1.98	0.45
1:C:375:ARG:NH1	1:C:375:ARG:CG	2.69	0.45
1:C:376:ILE:HA	1:C:376:ILE:HD12	1.62	0.45
1:C:407:HIS:HD2	1:C:1047:LEU:HA	1.63	0.45
1:C:407:HIS:CE1	1:C:1047:LEU:HD12	2.52	0.45
1:C:441:ARG:O	1:C:770:CYS:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:742:LYS:HA	1:C:743:PRO:HD3	1.84	0.45
1:C:986:ILE:HA	1:C:989:ILE:HG22	1.97	0.45
1:B:166:TYR:OH	1:B:1264:GLU:OE2	2.31	0.45
1:B:340:VAL:HG21	1:C:1008:LEU:HB3	1.98	0.45
1:B:696:VAL:HG21	1:B:1326:ARG:HH12	1.81	0.45
1:B:716:PHE:O	1:B:717:THR:HB	2.16	0.45
1:C:377:LYS:HE2	1:C:621:ALA:O	2.16	0.45
1:C:746:GLU:N	1:C:746:GLU:OE2	2.49	0.45
1:C:838:GLU:CG	1:C:934:LEU:HA	2.36	0.45
1:C:838:GLU:CG	1:C:935:GLN:CA	2.89	0.45
1:C:1168:ILE:N	1:C:1168:ILE:CD1	2.73	0.45
1:C:1285:GLN:CA	1:C:1285:GLN:NE2	2.80	0.45
1:B:147:VAL:HG13	1:B:375:ARG:HD2	1.99	0.45
1:B:270:THR:HG23	1:B:289:THR:HB	1.99	0.45
1:B:461:ARG:HE	1:B:504:ASP:HB3	1.75	0.45
1:C:484:ARG:NE	1:C:758:ILE:HG22	2.31	0.45
1:C:517:PHE:CE1	1:C:521:PHE:CD2	3.04	0.45
1:C:674:LYS:HB2	1:C:674:LYS:HZ3	1.80	0.45
1:C:829:SER:O	1:C:965:ARG:NH2	2.49	0.45
1:C:240:GLY:O	1:C:242:GLU:CA	2.59	0.45
1:C:270:THR:HB	1:C:289:THR:CG2	2.47	0.45
1:C:849:MET:CG	1:C:919:MET:CG	2.94	0.45
1:C:853:ASP:HA	1:C:856:LEU:HB2	1.98	0.45
1:C:1060:ARG:NH1	1:C:1292:GLU:N	2.59	0.45
1:B:231:LEU:HD21	1:B:986:ILE:HG13	1.99	0.45
1:B:301:LEU:HG	1:B:305:THR:OG1	2.17	0.45
1:B:875:THR:OG1	1:B:901:VAL:O	2.34	0.45
1:B:1096:TYR:CE1	1:B:1136:HIS:HB3	2.51	0.45
1:B:1181:SER:O	1:B:1182:GLU:HB3	2.17	0.45
1:C:180:LEU:HD11	1:C:304:PHE:O	2.16	0.45
1:C:208:LEU:HB3	1:C:221:LEU:CD2	2.47	0.45
1:C:310:LEU:CD2	1:C:1242:MET:HE3	2.37	0.45
1:C:407:HIS:NE2	1:C:1047:LEU:HA	2.22	0.45
1:C:541:SER:C	1:C:543:TRP:H	2.17	0.45
1:C:1212:ARG:HA	1:C:1213:PRO:HD3	1.73	0.45
1:C:1297:SER:C	1:C:1298:PHE:CD1	2.91	0.45
1:B:1176:GLU:HG2	1:B:1203:HIS:CE1	2.46	0.45
1:C:737:PRO:HD2	1:C:1016:ASN:O	2.17	0.45
1:C:840:ASP:C	1:C:940:ARG:HH12	2.18	0.45
1:B:338:ARG:O	1:B:339:LEU:HB2	2.17	0.44
1:B:594:LEU:HD23	1:B:595:ALA:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:863:LEU:HD21	1:B:871:PRO:CD	2.47	0.44
1:C:109:LYS:HB3	1:C:110:PRO:CD	2.48	0.44
1:C:225:ILE:O	1:C:227:LEU:N	2.50	0.44
1:C:504:ASP:OD2	1:C:506:SER:HB2	2.16	0.44
1:C:738:GLU:HG3	1:C:738:GLU:O	2.17	0.44
1:C:839:ALA:CA	1:C:940:ARG:NH1	2.80	0.44
1:C:905:SER:O	1:C:908:THR:HG22	2.16	0.44
1:C:1034:GLN:OE1	1:C:1034:GLN:HA	2.17	0.44
1:C:1111:ALA:HB2	1:C:1129:PRO:CG	2.47	0.44
1:B:462:LEU:HD23	1:B:462:LEU:O	2.17	0.44
1:B:484:ARG:O	1:B:527:ARG:NH1	2.51	0.44
1:B:588:LEU:HD22	1:B:604:MET:HE2	1.99	0.44
1:C:362:LEU:C	1:C:362:LEU:CD2	2.85	0.44
1:C:492:VAL:CG2	1:C:747:ARG:HA	2.42	0.44
1:C:564:GLY:O	1:C:565:GLU:HB3	2.17	0.44
1:C:654:THR:C	1:C:658:THR:HG22	2.25	0.44
1:C:720:PHE:C	1:C:722:GLY:N	2.68	0.44
1:B:1332:ASN:HA	1:B:1333:ALA:HA	1.58	0.44
1:C:310:LEU:HD21	1:C:1242:MET:HE1	1.97	0.44
1:C:449:PHE:C	1:C:683:TRP:CD1	2.89	0.44
1:C:1219:ASP:CG	1:C:1220:PRO:HD3	2.25	0.44
1:C:1263:TYR:CE2	1:C:1278:TYR:OH	2.55	0.44
1:C:1294:ASP:O	1:C:1295:HIS:CG	2.71	0.44
1:B:135:LYS:CE	1:C:469:ARG:CA	2.93	0.44
1:B:575:TRP:CG	1:B:576:ASP:N	2.85	0.44
1:C:252:LEU:HD11	1:C:823:ILE:CG2	2.22	0.44
1:C:429:ILE:HD12	1:C:429:ILE:O	2.16	0.44
1:C:543:TRP:HD1	1:C:544:TYR:CD1	2.34	0.44
1:C:883:ILE:HG23	1:C:895:VAL:HG21	2.00	0.44
1:C:1101:TYR:CD1	1:C:1101:TYR:C	2.91	0.44
1:C:1250:GLU:O	1:C:1250:GLU:HG3	2.18	0.44
1:B:1242:MET:HA	1:B:1258:VAL:O	2.17	0.44
1:C:81:ALA:O	1:C:168:VAL:HG12	2.17	0.44
1:C:176:LYS:HA	1:C:176:LYS:HD3	1.81	0.44
1:C:204:VAL:CG2	1:C:1242:MET:HB2	2.48	0.44
1:C:449:PHE:CE2	1:C:454:GLU:HG3	2.53	0.44
1:C:451:GLU:OE2	1:C:682:GLN:HB3	2.18	0.44
1:C:540:PHE:HE2	1:C:604:MET:HE3	1.82	0.44
1:C:713:MET:HE3	1:C:804:LEU:CD2	2.44	0.44
1:C:836:GLN:O	1:C:940:ARG:HB3	2.17	0.44
1:C:954:GLN:HG2	1:C:957:PHE:CD1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1099:VAL:O	1:C:1099:VAL:CG2	2.66	0.44
1:C:1144:ARG:HE	1:C:1144:ARG:HB3	1.49	0.44
1:B:261:ASP:HA	1:B:262:ASN:HB3	1.99	0.44
1:B:540:PHE:CD1	1:B:600:ILE:HG12	2.53	0.44
1:C:259:MET:HG3	1:C:1055:LEU:CA	2.46	0.44
1:C:375:ARG:HA	1:C:375:ARG:HD2	1.74	0.44
1:C:985:ARG:HH22	1:C:989:ILE:CA	2.31	0.44
1:C:1143:GLU:C	1:C:1145:ALA:N	2.69	0.44
1:B:157:ILE:HD13	1:B:263:ARG:HD2	1.98	0.44
1:B:349:ASN:HA	1:B:1299:SER:HA	1.99	0.44
1:C:146:GLU:CB	1:C:1317:VAL:HG13	2.47	0.44
1:C:256:PHE:CD1	1:C:819:PHE:CD2	3.06	0.44
1:B:733:VAL:HG22	1:B:734:ILE:N	2.33	0.44
1:B:886:SER:O	1:B:890:THR:HG22	2.17	0.44
1:B:1082:ASP:CG	1:B:1212:ARG:HH12	2.21	0.44
1:C:161:LYS:HB2	1:C:161:LYS:HE2	1.79	0.44
1:C:168:VAL:CG2	1:C:204:VAL:HG12	2.47	0.44
1:C:176:LYS:HB2	1:C:199:TYR:CD2	2.53	0.44
1:C:738:GLU:O	1:C:738:GLU:CG	2.66	0.44
1:C:865:ILE:HG22	1:C:865:ILE:O	2.17	0.44
1:C:1073:GLY:HA3	1:C:1233:LEU:HD21	1.78	0.44
1:B:312:ARG:HA	1:B:315:THR:HG22	1.99	0.44
1:B:387:THR:HG22	1:B:1322:PRO:HD3	2.00	0.44
1:B:389:PHE:CD1	1:B:1319:ARG:HG3	2.34	0.44
1:B:895:VAL:HG22	1:B:896:LEU:H	1.83	0.44
1:B:1076:ILE:HB	1:B:1166:VAL:HG13	2.00	0.44
1:C:233:VAL:HG23	1:C:234:PRO:CD	2.28	0.44
1:C:302:ARG:HH11	1:C:302:ARG:CG	2.31	0.44
1:C:426:ILE:HG21	1:C:426:ILE:HD13	1.74	0.44
1:C:714:LEU:HA	1:C:714:LEU:HD23	1.58	0.44
1:C:970:LEU:HA	1:C:970:LEU:HD23	1.64	0.44
1:C:979:ILE:HD13	1:C:979:ILE:HG21	1.77	0.44
1:C:1014:MET:O	1:C:1014:MET:HG2	2.17	0.44
1:C:1138:HIS:CG	1:C:1138:HIS:O	2.68	0.44
1:B:272:THR:HG21	1:C:235:ILE:HD13	1.63	0.43
1:B:833:ARG:O	1:B:849:MET:N	2.49	0.43
1:C:556:ALA:O	1:C:587:ALA:CB	2.64	0.43
1:C:849:MET:CG	1:C:919:MET:HE2	2.40	0.43
1:C:1122:PRO:N	1:C:1123:PRO:CD	2.81	0.43
1:B:285:VAL:HG23	1:B:326:GLY:HA2	1.99	0.43
1:C:314:ILE:HG23	1:C:314:ILE:HD12	1.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1023:ARG:NH1	1:C:1029:LEU:HD21	2.33	0.43
1:C:1050:LEU:HA	1:C:1050:LEU:HD13	1.72	0.43
1:C:1094:GLU:OE2	1:C:1094:GLU:CA	2.66	0.43
1:C:1137:VAL:HG22	1:C:1164:TRP:CE2	2.52	0.43
1:C:1310:ARG:HA	1:C:1310:ARG:NH1	2.31	0.43
1:B:1180:PRO:HB3	1:B:1212:ARG:HB3	1.99	0.43
1:C:144:ASN:CG	1:C:1318:GLU:OE1	2.56	0.43
1:C:153:ASP:OD2	1:C:401:LEU:HD22	2.17	0.43
1:C:614:ARG:O	1:C:614:ARG:CG	2.66	0.43
1:C:652:PHE:CB	1:C:691:PHE:CE2	3.01	0.43
1:C:1078:TYR:HB2	1:C:1229:LEU:HD11	2.00	0.43
1:C:1176:GLU:OE1	1:C:1203:HIS:NE2	2.51	0.43
1:C:1263:TYR:O	1:C:1297:SER:HB2	2.18	0.43
1:B:251:LEU:HA	1:B:254:VAL:HG22	2.01	0.43
1:B:823:ILE:HG23	1:B:964:VAL:HG23	2.00	0.43
1:B:849:MET:SD	1:B:917:VAL:HG23	2.59	0.43
1:B:908:THR:HG23	1:B:911:ARG:NH1	2.33	0.43
1:C:733:VAL:HG23	1:C:743:PRO:HA	2.01	0.43
1:C:880:PRO:HB3	1:C:906:ALA:HA	1.66	0.43
1:B:381:ALA:HB3	1:B:624:PHE:HE2	1.82	0.43
1:B:388:GLN:OE1	1:B:1320:VAL:CG1	2.66	0.43
1:B:515:ILE:HD12	1:B:659:LEU:HD11	2.01	0.43
1:B:733:VAL:HG22	1:B:734:ILE:H	1.84	0.43
1:B:895:VAL:HG12	1:B:917:VAL:HG12	2.00	0.43
1:B:1121:HIS:CD2	1:B:1124:THR:HG22	2.51	0.43
1:C:237:VAL:HG12	1:C:238:THR:N	2.34	0.43
1:C:310:LEU:HA	1:C:310:LEU:HD12	1.51	0.43
1:C:635:ILE:O	1:C:635:ILE:CG2	2.67	0.43
1:C:928:ARG:N	1:C:928:ARG:HD2	2.34	0.43
1:C:954:GLN:HG2	1:C:957:PHE:HD1	1.83	0.43
1:C:1075:ARG:O	1:C:1075:ARG:CG	2.64	0.43
1:C:1120:THR:O	1:C:1122:PRO:HD2	2.12	0.43
1:C:1290:LYS:NZ	1:C:1297:SER:OG	2.44	0.43
1:B:922:TYR:HD1	1:B:925:VAL:HG11	1.82	0.43
1:C:144:ASN:HB3	1:C:1318:GLU:H	1.83	0.43
1:C:674:LYS:CB	1:C:674:LYS:HZ3	2.32	0.43
1:C:716:PHE:O	1:C:716:PHE:HD1	2.00	0.43
1:C:760:THR:O	1:C:760:THR:OG1	2.29	0.43
1:C:923:TYR:N	1:C:923:TYR:CD1	2.86	0.43
1:C:971:MET:HE2	1:C:971:MET:HB3	1.64	0.43
1:C:1023:ARG:HG2	1:C:1024:PRO:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1029:LEU:HA	1:C:1029:LEU:HD23	1.71	0.43
1:C:1202:PHE:O	1:C:1202:PHE:HD1	2.01	0.43
1:B:213:PHE:HB3	1:B:219:ILE:HD12	1.99	0.43
1:B:895:VAL:O	1:B:918:VAL:HG12	2.18	0.43
1:B:1175:ALA:HA	1:B:1204:LEU:O	2.18	0.43
1:B:1209:GLY:O	1:B:1212:ARG:HG2	2.18	0.43
1:C:156:GLN:HE22	1:C:1309:ILE:HG12	1.79	0.43
1:C:548:TYR:CZ	1:C:552:ILE:HG13	2.53	0.43
1:C:1156:ILE:O	1:C:1156:ILE:HG22	2.17	0.43
1:C:1159:VAL:HG23	1:C:1164:TRP:O	2.18	0.43
1:C:1186:GLN:H	1:C:1205:GLN:NE2	2.16	0.43
1:C:1310:ARG:NE	1:C:1310:ARG:C	2.72	0.43
1:B:188:ARG:HH22	1:C:237:VAL:HG11	1.84	0.43
1:B:442:PRO:HB3	1:B:770:CYS:HB3	1.99	0.43
1:C:343:ILE:HD13	1:C:343:ILE:HG21	1.73	0.43
1:C:494:GLU:N	1:C:494:GLU:CD	2.72	0.43
1:C:614:ARG:CD	1:C:635:ILE:HD12	2.42	0.43
1:C:639:ASN:HB3	1:C:1330:ILE:HD13	2.01	0.43
1:C:672:MET:O	1:C:672:MET:HG2	2.18	0.43
1:C:830:VAL:HA	1:C:854:GLN:HG2	2.00	0.43
1:C:1099:VAL:HG11	1:C:1119:TYR:OH	2.19	0.43
1:B:417:ALA:HB3	1:B:734:ILE:HD12	2.00	0.43
1:B:619:ALA:HA	1:B:624:PHE:HD2	1.84	0.43
1:C:233:VAL:HG13	1:C:981:HIS:NE2	2.04	0.43
1:C:550:ILE:HD11	1:C:594:LEU:CD1	2.48	0.43
1:C:1050:LEU:HD12	1:C:1054:ARG:CZ	2.48	0.43
1:C:1060:ARG:HH12	1:C:1292:GLU:N	2.14	0.43
1:C:1074:VAL:HG12	1:C:1171:ILE:CG2	2.48	0.43
1:B:450:PRO:HG3	1:B:686:HIS:HB2	2.00	0.43
1:B:505:PRO:HG2	1:B:672:MET:CE	2.49	0.43
1:B:1236:ILE:HD12	1:B:1238:VAL:N	2.34	0.43
1:C:136:VAL:O	1:C:136:VAL:HG13	2.19	0.43
1:C:601:ILE:HD12	1:C:601:ILE:HG23	1.70	0.43
1:C:887:VAL:HG13	1:C:893:ALA:CA	2.49	0.43
1:C:896:LEU:HD22	1:C:896:LEU:HA	1.76	0.43
1:C:1072:ASP:HB3	1:C:1172:GLU:HG2	2.01	0.43
1:C:1193:ILE:HG13	1:C:1202:PHE:CE2	2.54	0.43
1:C:1193:ILE:HG21	1:C:1193:ILE:HD13	1.65	0.43
1:B:505:PRO:HA	1:B:506:SER:HA	1.59	0.42
1:B:873:TYR:HD1	1:B:896:LEU:HB2	1.83	0.42
1:B:880:PRO:HG3	1:B:905:SER:C	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:151:SER:N	1:C:400:GLU:OE1	2.50	0.42
1:C:186:ASP:CG	1:C:279:SER:N	2.62	0.42
1:C:265:VAL:O	1:C:1303:SER:CA	2.67	0.42
1:C:357:VAL:HG22	1:C:1054:ARG:HD2	2.01	0.42
1:C:469:ARG:HD3	1:C:513:GLU:OE1	2.18	0.42
1:C:810:LEU:HD23	1:C:810:LEU:HA	1.42	0.42
1:C:833:ARG:HH11	1:C:942:HIS:CD2	2.37	0.42
1:C:1074:VAL:O	1:C:1074:VAL:CG1	2.67	0.42
1:C:1085:ASP:HB3	1:C:1243:ARG:NH2	2.34	0.42
1:C:1270:LEU:HA	1:C:1270:LEU:HD23	1.57	0.42
1:C:1276:LEU:CB	1:C:1290:LYS:HG3	2.49	0.42
1:B:153:ASP:OD2	1:B:401:LEU:HD21	2.19	0.42
1:B:701:HIS:NE2	1:B:791:ILE:HD11	2.34	0.42
1:B:952:PHE:HB2	1:B:958:ILE:HD12	2.02	0.42
1:B:1128:TYR:CE2	1:B:1135:PRO:HD3	2.53	0.42
1:C:155:LYS:O	1:C:155:LYS:CG	2.67	0.42
1:C:448:TYR:HB2	1:C:449:PHE:H	1.10	0.42
1:C:936:MET:O	1:C:936:MET:SD	2.77	0.42
1:C:1013:LYS:HE3	1:C:1015:GLN:NE2	2.34	0.42
1:C:1022:ILE:O	1:C:1022:ILE:HG22	2.17	0.42
1:C:1059:LEU:HD12	1:C:1059:LEU:HA	1.80	0.42
1:C:1134:ARG:CB	1:C:1135:PRO:CD	2.85	0.42
1:B:228:VAL:HG11	1:B:253:MET:HG3	2.01	0.42
1:B:1066:ARG:HH21	1:B:1296:ILE:CD1	2.32	0.42
1:B:1236:ILE:CD1	1:B:1238:VAL:HG22	2.49	0.42
1:C:197:PHE:HE1	1:C:1242:MET:HG3	1.83	0.42
1:C:225:ILE:CG2	1:C:226:PRO:HD2	2.48	0.42
1:C:454:GLU:OE2	1:C:454:GLU:HA	2.19	0.42
1:C:612:PHE:O	1:C:612:PHE:CG	2.70	0.42
1:C:720:PHE:O	1:C:720:PHE:CG	2.69	0.42
1:C:791:ILE:HG21	1:C:1325:VAL:HG21	2.01	0.42
1:C:845:GLU:HB3	1:C:846:GLY:H	1.54	0.42
1:C:1014:MET:CG	1:C:1014:MET:O	2.67	0.42
1:C:1137:VAL:CG2	1:C:1164:TRP:CD2	3.03	0.42
1:C:1177:VAL:O	1:C:1177:VAL:CG2	2.66	0.42
1:C:1178:MET:HG3	1:C:1178:MET:O	2.20	0.42
1:B:372:ALA:HB3	1:B:1315:MET:CE	2.49	0.42
1:B:500:GLU:CD	1:B:502:PHE:H	2.22	0.42
1:B:720:PHE:HD2	1:B:727:PHE:CD1	2.36	0.42
1:B:1051:ARG:O	1:B:1055:LEU:HB2	2.20	0.42
1:C:267:VAL:HG21	1:C:344:VAL:CG2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:409:ILE:HG23	1:C:409:ILE:HD12	1.58	0.42
1:C:494:GLU:HB3	1:C:577:GLN:HE22	1.79	0.42
1:C:504:ASP:N	1:C:504:ASP:OD1	2.52	0.42
1:C:892:VAL:HG13	1:C:894:VAL:HG12	1.94	0.42
1:C:941:TYR:HD1	1:C:941:TYR:HA	1.72	0.42
1:C:954:GLN:C	1:C:958:ILE:CD1	2.88	0.42
1:C:1193:ILE:HG13	1:C:1202:PHE:HZ	1.84	0.42
1:C:1273:ASN:ND2	1:C:1273:ASN:C	2.72	0.42
1:C:1321:ASN:HB3	1:C:1322:PRO:HD2	2.01	0.42
1:B:188:ARG:NH2	1:C:237:VAL:HG11	2.35	0.42
1:B:287:ARG:HB2	1:B:328:GLY:HA3	2.00	0.42
1:B:434:VAL:HB	1:B:439:VAL:HG11	2.01	0.42
1:B:734:ILE:HG12	1:B:1019:ILE:HD13	2.01	0.42
1:C:144:ASN:CA	1:C:1318:GLU:HB3	2.49	0.42
1:C:389:PHE:CZ	1:C:796:PRO:HG2	2.50	0.42
1:C:560:ILE:HG22	1:C:585:PHE:CE2	2.54	0.42
1:C:830:VAL:HA	1:C:854:GLN:CG	2.50	0.42
1:C:985:ARG:HH21	1:C:988:GLN:HG3	1.79	0.42
1:C:1205:GLN:O	1:C:1205:GLN:CG	2.67	0.42
1:C:1330:ILE:H	1:C:1330:ILE:HD12	1.85	0.42
1:B:135:LYS:CE	1:C:470:ALA:N	2.65	0.42
1:B:139:ASN:O	1:C:757:ILE:HG22	2.20	0.42
1:B:190:VAL:HG12	1:B:300:LEU:HB3	2.01	0.42
1:B:193:THR:HA	1:B:296:VAL:HG13	2.01	0.42
1:C:314:ILE:O	1:C:318:LEU:HD22	2.18	0.42
1:C:519:LEU:HA	1:C:519:LEU:HD23	1.51	0.42
1:C:520:PHE:CZ	1:C:691:PHE:HE1	2.38	0.42
1:C:1079:LEU:O	1:C:1079:LEU:HD13	2.19	0.42
1:C:1084:PRO:O	1:C:1209:GLY:C	2.58	0.42
1:C:1089:VAL:O	1:C:1089:VAL:CG1	2.68	0.42
1:B:390:HIS:HB2	1:B:1318:GLU:CG	2.47	0.42
1:B:440:ILE:CG2	1:B:770:CYS:CB	2.98	0.42
1:C:455:GLN:O	1:C:455:GLN:CG	2.68	0.42
1:C:1046:PHE:C	1:C:1048:ASP:N	2.73	0.42
1:C:1078:TYR:O	1:C:1078:TYR:HD1	2.02	0.42
1:C:1159:VAL:O	1:C:1159:VAL:CG2	2.67	0.42
1:B:265:VAL:HG12	1:B:1304:MET:HE2	2.01	0.42
1:C:208:LEU:CB	1:C:221:LEU:CD2	2.98	0.42
1:C:333:ARG:NE	1:C:1272:ARG:HA	2.24	0.42
1:C:613:LEU:HD22	1:C:614:ARG:N	2.35	0.42
1:C:965:ARG:NH1	1:C:968:ARG:CZ	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:986:ILE:HA	1:C:989:ILE:CG2	2.49	0.42
1:C:1034:GLN:N	1:C:1034:GLN:CD	2.72	0.42
1:C:1278:TYR:CE2	1:C:1288:ILE:CD1	3.01	0.42
1:B:614:ARG:O	1:B:633:THR:HG22	2.19	0.42
1:B:712:PHE:HB2	1:B:715:ASN:ND2	2.34	0.42
1:B:1060:ARG:HA	1:B:1063:THR:HG22	2.02	0.42
1:C:124:GLN:OE1	1:C:124:GLN:CA	2.68	0.42
1:C:923:TYR:N	1:C:923:TYR:HD1	2.17	0.42
1:B:274:MET:O	1:B:277:THR:N	2.49	0.42
1:B:852:TYR:CE2	1:B:856:LEU:HD22	2.54	0.42
1:B:1105:LEU:HD11	1:B:1122:PRO:HD3	2.01	0.42
1:B:1248:HIS:HB2	1:B:1251:VAL:HG22	2.01	0.42
1:C:365:LEU:HD13	1:C:365:LEU:C	2.38	0.42
1:C:839:ALA:C	1:C:940:ARG:NH2	2.66	0.42
1:C:1247:ASN:ND2	1:C:1247:ASN:O	2.51	0.42
1:C:1282:ALA:C	1:C:1284:GLY:N	2.73	0.42
1:B:588:LEU:HD13	1:B:604:MET:CE	2.47	0.41
1:B:632:GLN:H	1:B:718:ASN:ND2	2.18	0.41
1:B:649:ALA:HA	1:B:691:PHE:HE1	1.85	0.41
1:B:1289:PRO:HG2	1:B:1292:GLU:HG2	2.00	0.41
1:C:385:ILE:H	1:C:708:THR:HG22	1.85	0.41
1:C:430:ASN:C	1:C:430:ASN:ND2	2.73	0.41
1:C:503:GLU:OE2	1:C:542:ARG:CG	2.68	0.41
1:C:913:ASN:HD22	1:C:913:ASN:HA	1.72	0.41
1:C:1149:LYS:O	1:C:1150:LEU:C	2.59	0.41
1:C:1212:ARG:O	1:C:1212:ARG:HG3	2.20	0.41
1:B:472:GLU:CB	1:B:761:SER:HB3	2.42	0.41
1:B:1276:LEU:HD13	1:B:1300:ASN:ND2	2.35	0.41
1:C:179:LYS:HD2	1:C:180:LEU:N	2.35	0.41
1:C:480:LEU:C	1:C:480:LEU:CD2	2.88	0.41
1:C:656:VAL:CG1	1:C:688:GLU:CB	2.85	0.41
1:C:743:PRO:HD2	1:C:743:PRO:O	2.19	0.41
1:C:870:ASP:CB	1:C:871:PRO:HD2	2.47	0.41
1:C:1137:VAL:HG22	1:C:1164:TRP:CD1	2.55	0.41
1:C:1278:TYR:CD2	1:C:1288:ILE:HD11	2.53	0.41
1:C:1288:ILE:HG12	1:C:1288:ILE:H	1.55	0.41
1:B:303:ASP:O	1:C:1103:HIS:HE1	2.03	0.41
1:B:451:GLU:HG2	1:B:452:ASN:H	1.85	0.41
1:B:479:HIS:ND1	1:B:479:HIS:N	2.67	0.41
1:B:683:TRP:O	1:B:686:HIS:HB3	2.19	0.41
1:B:862:ARG:HH12	1:B:948:ILE:HG21	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:892:VAL:HG21	1:B:952:PHE:CE1	2.56	0.41
1:B:985:ARG:NH2	1:B:988:GLN:HE21	2.14	0.41
1:B:1119:TYR:HB3	1:B:1134:ARG:NE	2.31	0.41
1:B:1300:ASN:OD1	1:B:1300:ASN:N	2.52	0.41
1:C:202:ALA:O	1:C:1244:ALA:N	2.38	0.41
1:C:289:THR:O	1:C:329:LEU:N	2.54	0.41
1:C:371:THR:O	1:C:372:ALA:C	2.56	0.41
1:C:418:ASN:OD1	1:C:418:ASN:N	2.53	0.41
1:C:676:THR:O	1:C:676:THR:HG22	2.20	0.41
1:C:721:SER:O	1:C:721:SER:OG	2.10	0.41
1:C:1207:MET:HE2	1:C:1207:MET:HB2	1.80	0.41
1:B:305:THR:CG2	1:B:307:VAL:HG12	2.51	0.41
1:B:694:ILE:HD12	1:B:772:TYR:CE1	2.55	0.41
1:C:133:MET:SD	1:C:133:MET:O	2.78	0.41
1:C:136:VAL:O	1:C:136:VAL:CG1	2.68	0.41
1:C:362:LEU:O	1:C:362:LEU:CD2	2.68	0.41
1:C:383:SER:HG	1:C:796:PRO:HG3	0.58	0.41
1:C:385:ILE:HG12	1:C:708:THR:HG22	2.00	0.41
1:C:612:PHE:HE2	1:C:614:ARG:HB3	1.85	0.41
1:C:700:ASP:CG	1:C:1326:ARG:HG3	2.38	0.41
1:C:734:ILE:HD13	1:C:734:ILE:HG21	1.74	0.41
1:C:865:ILE:CG2	1:C:865:ILE:O	2.68	0.41
1:C:883:ILE:HD12	1:C:883:ILE:HG23	1.76	0.41
1:C:77:THR:C	1:C:172:ASP:OD2	2.58	0.41
1:C:214:ASP:C	1:C:216:ALA:N	2.73	0.41
1:C:236:GLY:C	1:C:237:VAL:CG2	2.88	0.41
1:C:407:HIS:HD2	1:C:1047:LEU:CA	2.28	0.41
1:C:427:VAL:O	1:C:427:VAL:CG1	2.69	0.41
1:C:449:PHE:HB3	1:C:683:TRP:HE1	1.61	0.41
1:C:536:LEU:HD23	1:C:536:LEU:HA	1.56	0.41
1:C:934:LEU:H	1:C:934:LEU:HG	1.66	0.41
1:C:971:MET:HB2	1:C:972:PRO:HD2	2.03	0.41
1:C:1072:ASP:N	1:C:1072:ASP:OD1	2.52	0.41
1:C:1078:TYR:HB3	1:C:1159:VAL:O	2.20	0.41
1:C:1215:PRO:CD	1:C:1215:PRO:O	2.68	0.41
1:C:1251:VAL:O	1:C:1251:VAL:HG12	2.21	0.41
1:B:390:HIS:O	1:B:1317:VAL:HG23	2.20	0.41
1:B:437:ALA:O	1:B:701:HIS:HE1	2.04	0.41
1:B:1271:SER:OG	1:B:1272:ARG:N	2.53	0.41
1:C:298:PRO:CG	1:C:298:PRO:O	2.68	0.41
1:C:485:GLU:HB3	1:C:706:TYR:HE1	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:520:PHE:C	1:C:521:PHE:CD1	2.94	0.41
1:C:651:ARG:HD2	1:C:655:ILE:HG12	2.02	0.41
1:C:729:PRO:O	1:C:731:GLN:N	2.53	0.41
1:C:928:ARG:NH1	1:C:928:ARG:CG	2.77	0.41
1:C:1019:ILE:O	1:C:1019:ILE:HG13	2.19	0.41
1:C:1191:GLU:O	1:C:1191:GLU:HG3	2.16	0.41
1:B:560:ILE:HG12	1:B:566:PHE:CD1	2.56	0.41
1:B:733:VAL:HG21	1:B:741:TYR:HD1	1.86	0.41
1:B:873:TYR:CB	1:B:897:TYR:HB2	2.43	0.41
1:B:1236:ILE:HD13	1:B:1238:VAL:HG22	2.02	0.41
1:C:265:VAL:HG23	1:C:1302:VAL:O	2.21	0.41
1:C:287:ARG:CB	1:C:329:LEU:O	2.68	0.41
1:C:370:VAL:HG13	1:C:370:VAL:O	2.21	0.41
1:C:548:TYR:CE2	1:C:552:ILE:HG13	2.55	0.41
1:C:1014:MET:HE3	1:C:1014:MET:HB3	1.96	0.41
1:C:1037:ILE:HD11	1:C:1040:PHE:CD2	2.56	0.41
1:B:765:PRO:O	1:B:769:GLN:HB2	2.20	0.41
1:C:77:THR:OG1	1:C:172:ASP:OD2	2.37	0.41
1:C:367:GLU:OE1	1:C:367:GLU:HA	2.21	0.41
1:C:571:ARG:HH11	1:C:571:ARG:CB	2.26	0.41
1:C:585:PHE:CE1	1:C:728:LYS:HG2	2.56	0.41
1:C:742:LYS:HE2	1:C:742:LYS:HB3	1.32	0.41
1:C:897:TYR:CD1	1:C:897:TYR:C	2.94	0.41
1:C:974:LEU:HA	1:C:974:LEU:HD23	1.83	0.41
1:C:1099:VAL:HG21	1:C:1119:TYR:OH	2.20	0.41
1:B:141:LEU:HD21	1:B:391:GLY:HA2	2.02	0.41
1:B:223:LYS:HD2	1:B:1203:HIS:ND1	2.35	0.41
1:B:262:ASN:H	1:B:1054:ARG:CZ	2.34	0.41
1:B:418:ASN:O	1:B:420:PRO:HD3	2.21	0.41
1:B:694:ILE:HG23	1:B:772:TYR:CE1	2.56	0.41
1:B:752:VAL:O	1:B:752:VAL:HG12	2.20	0.41
1:B:791:ILE:HD12	1:B:791:ILE:HA	1.82	0.41
1:B:826:GLY:HA2	1:B:827:GLY:HA3	1.50	0.41
1:B:890:THR:C	1:B:892:VAL:H	2.24	0.41
1:C:110:PRO:CB	1:C:111:PRO:CD	2.98	0.41
1:C:236:GLY:O	1:C:237:VAL:HG22	2.21	0.41
1:C:429:ILE:HD13	1:C:799:THR:HG22	2.01	0.41
1:C:501:SER:O	1:C:501:SER:OG	2.23	0.41
1:C:601:ILE:N	1:C:601:ILE:HD13	2.36	0.41
1:C:731:GLN:O	1:C:731:GLN:CG	2.69	0.41
1:C:835:TYR:HE1	1:C:942:HIS:CG	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:990:THR:OG1	1:C:992:VAL:HG12	2.20	0.41
1:C:1085:ASP:HB2	1:C:1086:PRO:HD3	1.98	0.41
1:C:1262:SER:O	1:C:1262:SER:OG	2.30	0.41
1:C:1280:PRO:HB2	1:C:1281:VAL:H	1.62	0.41
1:B:157:ILE:HG12	1:B:264:LEU:O	2.21	0.41
1:B:157:ILE:HD12	1:B:160:PRO:HA	2.02	0.41
1:B:648:PHE:CE2	1:B:691:PHE:HZ	2.39	0.41
1:B:1096:TYR:CD1	1:B:1136:HIS:HB3	2.55	0.41
1:C:364:ALA:HB1	1:C:1050:LEU:HD21	2.01	0.41
1:C:471:SER:O	1:C:765:PRO:HG3	2.20	0.41
1:C:837:THR:HA	1:C:936:MET:CG	2.51	0.41
1:C:865:ILE:HD11	1:C:1020:ARG:NH2	2.36	0.41
1:B:261:ASP:OD1	1:B:263:ARG:HB2	2.21	0.40
1:B:394:GLN:O	1:B:394:GLN:HG2	2.21	0.40
1:B:958:ILE:HG22	1:B:959:GLN:N	2.35	0.40
1:C:101:ASP:O	1:C:103:GLY:N	2.54	0.40
1:C:110:PRO:HB2	1:C:111:PRO:HD2	2.03	0.40
1:C:225:ILE:O	1:C:227:LEU:HG	2.21	0.40
1:C:399:PRO:O	1:C:399:PRO:CG	2.69	0.40
1:C:579:LEU:O	1:C:579:LEU:CD1	2.69	0.40
1:C:743:PRO:O	1:C:743:PRO:CD	2.69	0.40
1:C:762:ILE:CD1	1:C:762:ILE:O	2.69	0.40
1:C:979:ILE:O	1:C:983:ILE:HG13	2.21	0.40
1:C:1022:ILE:O	1:C:1022:ILE:CG2	2.68	0.40
1:C:360:ILE:O	1:C:360:ILE:CG2	2.68	0.40
1:C:408:ILE:HG22	1:C:412:LEU:HD12	2.02	0.40
1:C:730:ASP:O	1:C:731:GLN:HG2	2.22	0.40
1:C:897:TYR:OH	1:C:928:ARG:HG3	2.21	0.40
1:C:909:TYR:OH	1:C:913:ASN:OD1	2.32	0.40
1:C:978:GLN:HE21	1:C:978:GLN:HB2	1.75	0.40
1:C:1253:ARG:HA	1:C:1254:PRO:HD3	1.87	0.40
1:B:295:GLY:N	1:B:349:ASN:OD1	2.54	0.40
1:B:558:TYR:CE1	1:B:585:PHE:HB2	2.57	0.40
1:B:736:SER:HA	1:B:1016:ASN:O	2.21	0.40
1:B:830:VAL:HA	1:B:854:GLN:HE21	1.85	0.40
1:B:924:ASP:HB3	1:B:928:ARG:NH2	2.36	0.40
1:C:146:GLU:CG	1:C:1317:VAL:HG13	2.49	0.40
1:C:164:LEU:HD13	1:C:1296:ILE:HG13	2.03	0.40
1:C:166:TYR:HE1	1:C:1298:PHE:CZ	2.38	0.40
1:C:451:GLU:CB	1:C:686:HIS:HB2	2.51	0.40
1:C:750:GLU:HB3	1:C:757:ILE:HG13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1000:LEU:O	1:C:1000:LEU:CG	2.69	0.40
1:C:1185:THR:OG1	1:C:1186:GLN:N	2.55	0.40
1:C:1278:TYR:HB3	1:C:1279:SER:H	1.68	0.40
1:B:678:SER:O	1:B:682:GLN:HG2	2.21	0.40
1:B:1086:PRO:HB3	1:B:1177:VAL:HG22	2.02	0.40
1:B:1277:LEU:HA	1:B:1289:PRO:HA	2.02	0.40
1:C:554:ARG:CZ	1:C:594:LEU:CD2	2.99	0.40
1:C:985:ARG:HH22	1:C:989:ILE:CB	2.33	0.40
1:C:1033:ASP:HB3	1:C:1034:GLN:NE2	2.37	0.40
1:C:1245:ILE:HG21	1:C:1245:ILE:HD13	1.62	0.40
1:C:1254:PRO:O	1:C:1254:PRO:CD	2.69	0.40
1:C:1292:GLU:O	1:C:1292:GLU:CG	2.69	0.40
1:B:462:LEU:O	1:B:466:VAL:HG23	2.22	0.40
1:B:606:LEU:HD21	1:B:658:THR:HG23	2.02	0.40
1:B:874:ILE:HG23	1:B:895:VAL:CG2	2.50	0.40
1:B:898:GLN:O	1:B:928:ARG:HD3	2.21	0.40
1:C:322:GLY:O	1:C:1279:SER:HB2	2.20	0.40
1:C:391:GLY:HA3	1:C:392:PRO:HD3	1.90	0.40
1:C:407:HIS:HE2	1:C:1047:LEU:HD12	1.79	0.40
1:C:841:ASP:CA	1:C:940:ARG:CZ	2.98	0.40
1:C:1034:GLN:OE1	1:C:1034:GLN:CA	2.69	0.40
1:C:1105:LEU:O	1:C:1105:LEU:CD1	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	1132/1333 (85%)	999 (88%)	121 (11%)	12 (1%)	12	40
1	C	1243/1333 (93%)	937 (75%)	209 (17%)	97 (8%)	1	5
All	All	2375/2666 (89%)	1936 (82%)	330 (14%)	109 (5%)	3	13

All (109) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	120	VAL
1	C	121	PHE
1	C	122	ASN
1	C	129	ALA
1	C	144	ASN
1	C	186	ASP
1	C	234	PRO
1	C	241	ALA
1	C	280	THR
1	C	299	ALA
1	C	337	VAL
1	C	338	ARG
1	C	372	ALA
1	C	450	PRO
1	C	455	GLN
1	C	475	ILE
1	C	661	ASN
1	C	730	ASP
1	C	772	TYR
1	C	773	PRO
1	C	871	PRO
1	C	875	THR
1	C	879	THR
1	C	880	PRO
1	C	891	HIS
1	C	935	GLN
1	C	1024	PRO
1	C	1130	SER
1	C	1134	ARG
1	C	1138	HIS
1	C	1147	MET
1	C	1150	LEU
1	C	1182	GLU
1	C	1213	PRO
1	C	1221	PRO
1	C	1262	SER
1	C	1271	SER
1	C	1278	TYR
1	C	1282	ALA
1	C	1293	VAL
1	C	1308	ASN
1	B	437	ALA

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Mol	Chain	Res	Type
1	B	473	ALA
1	B	1251	VAL
1	B	1255	ARG
1	B	1286	VAL
1	C	130	LEU
1	C	184	GLU
1	C	339	LEU
1	C	403	PHE
1	C	453	LEU
1	C	565	GLU
1	C	639	ASN
1	C	837	THR
1	C	842	ASP
1	C	948	ILE
1	C	1049	GLU
1	C	1067	ILE
1	C	1190	ALA
1	C	1228	ARG
1	C	1251	VAL
1	C	1280	PRO
1	C	1295	HIS
1	C	1325	VAL
1	C	1329	ASN
1	C	1332	ASN
1	B	151	SER
1	B	753	ASP
1	C	231	LEU
1	C	235	ILE
1	C	442	PRO
1	C	448	TYR
1	C	522	PRO
1	C	1045	TYR
1	C	1129	PRO
1	C	1222	ALA
1	C	1294	ASP
1	C	265	VAL
1	C	646	ASN
1	C	731	GLN
1	C	1093	PRO
1	C	1136	HIS
1	C	1144	ARG
1	C	1191	GLU

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Mol	Chain	Res	Type
1	C	1223	SER
1	C	1235	PRO
1	B	384	MET
1	B	1094	GLU
1	C	336	TYR
1	C	577	GLN
1	C	898	GLN
1	C	942	HIS
1	C	958	ILE
1	C	1260	PRO
1	B	879	THR
1	C	245	ALA
1	C	644	VAL
1	C	794	PRO
1	C	1109	SER
1	C	1234	GLN
1	C	1137	VAL
1	B	1236	ILE
1	C	273	PRO
1	C	635	ILE
1	B	1246	VAL
1	C	1128	TYR
1	C	1236	ILE
1	C	1274	GLY
1	C	1286	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	1000/1155 (87%)	993 (99%)	7 (1%)	81	88
1	C	1087/1155 (94%)	733 (67%)	354 (33%)	0	1
All	All	2087/2310 (90%)	1726 (83%)	361 (17%)	3	7

All (361) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	461	ARG
1	B	464	SER
1	B	471	SER
1	B	472	GLU
1	B	474	ASP
1	B	475	ILE
1	B	790	GLU
1	C	74	LYS
1	C	79	SER
1	C	83	GLN
1	C	85	ASP
1	C	87	GLU
1	C	88	LYS
1	C	89	PRO
1	C	92	VAL
1	C	93	THR
1	C	96	ILE
1	C	101	ASP
1	C	105	MET
1	C	106	GLN
1	C	108	LYS
1	C	109	LYS
1	C	112	THR
1	C	119	ASP
1	C	120	VAL
1	C	122	ASN
1	C	124	GLN
1	C	132	PRO
1	C	133	MET
1	C	134	THR
1	C	135	LYS
1	C	136	VAL
1	C	137	ILE
1	C	141	LEU
1	C	142	ASP
1	C	143	VAL
1	C	145	THR
1	C	146	GLU
1	C	150	LEU
1	C	155	LYS
1	C	156	GLN
1	C	157	ILE
1	C	159	ASP

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Mol	Chain	Res	Type
1	C	161	LYS
1	C	173	GLN
1	C	176	LYS
1	C	177	LYS
1	C	196	LEU
1	C	204	VAL
1	C	205	ASN
1	C	214	ASP
1	C	221	LEU
1	C	229	GLN
1	C	230	ASP
1	C	231	LEU
1	C	232	LEU
1	C	251	LEU
1	C	255	LEU
1	C	265	VAL
1	C	283	ASN
1	C	287	ARG
1	C	297	ASN
1	C	300	LEU
1	C	302	ARG
1	C	304	PHE
1	C	306	GLN
1	C	309	TRP
1	C	312	ARG
1	C	315	THR
1	C	316	ASN
1	C	318	LEU
1	C	319	GLN
1	C	320	GLN
1	C	327	LEU
1	C	330	THR
1	C	333	ARG
1	C	338	ARG
1	C	339	LEU
1	C	342	THR
1	C	346	HIS
1	C	350	ILE
1	C	351	ASP
1	C	356	SER
1	C	361	ASN
1	C	362	LEU

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Mol	Chain	Res	Type
1	C	363	ARG
1	C	366	MET
1	C	375	ARG
1	C	376	ILE
1	C	377	LYS
1	C	384	MET
1	C	386	SER
1	C	397	LEU
1	C	409	ILE
1	C	422	LEU
1	C	429	ILE
1	C	430	ASN
1	C	439	VAL
1	C	440	ILE
1	C	441	ARG
1	C	445	GLU
1	C	446	LYS
1	C	448	TYR
1	C	452	ASN
1	C	454	GLU
1	C	455	GLN
1	C	466	VAL
1	C	467	LYS
1	C	472	GLU
1	C	480	LEU
1	C	494	GLU
1	C	495	LEU
1	C	497	LYS
1	C	498	ILE
1	C	505	PRO
1	C	513	GLU
1	C	521	PHE
1	C	522	PRO
1	C	523	THR
1	C	524	GLU
1	C	526	ASN
1	C	529	LYS
1	C	538	LEU
1	C	547	GLU
1	C	550	ILE
1	C	552	ILE
1	C	553	GLN

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Mol	Chain	Res	Type
1	C	554	ARG
1	C	560	ILE
1	C	565	GLU
1	C	571	ARG
1	C	572	ASN
1	C	574	LYS
1	C	576	ASP
1	C	578	SER
1	C	581	LEU
1	C	583	GLU
1	C	584	HIS
1	C	591	ASP
1	C	594	LEU
1	C	599	THR
1	C	605	ARG
1	C	607	PHE
1	C	613	LEU
1	C	614	ARG
1	C	615	THR
1	C	617	ASP
1	C	628	SER
1	C	629	ARG
1	C	633	THR
1	C	635	ILE
1	C	637	TYR
1	C	639	ASN
1	C	641	ARG
1	C	643	THR
1	C	646	ASN
1	C	651	ARG
1	C	656	VAL
1	C	658	THR
1	C	659	LEU
1	C	666	ARG
1	C	669	GLN
1	C	674	LYS
1	C	685	ARG
1	C	686	HIS
1	C	698	HIS
1	C	708	THR
1	C	717	THR
1	C	720	PHE

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Mol	Chain	Res	Type
1	C	729	PRO
1	C	736	SER
1	C	742	LYS
1	C	744	ILE
1	C	746	GLU
1	C	747	ARG
1	C	748	GLN
1	C	755	LEU
1	C	765	PRO
1	C	766	ILE
1	C	767	LEU
1	C	770	CYS
1	C	792	VAL
1	C	795	ASP
1	C	797	SER
1	C	799	THR
1	C	800	LEU
1	C	802	GLN
1	C	806	VAL
1	C	812	LYS
1	C	813	LEU
1	C	814	THR
1	C	816	PRO
1	C	817	ASP
1	C	820	ILE
1	C	823	ILE
1	C	824	LEU
1	C	828	ASP
1	C	829	SER
1	C	840	ASP
1	C	842	ASP
1	C	843	LEU
1	C	848	ARG
1	C	849	MET
1	C	850	THR
1	C	851	THR
1	C	856	LEU
1	C	860	ARG
1	C	865	ILE
1	C	866	THR
1	C	867	ASN
1	C	870	ASP

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Mol	Chain	Res	Type
1	C	874	ILE
1	C	888	GLN
1	C	896	LEU
1	C	897	TYR
1	C	898	GLN
1	C	902	ILE
1	C	907	SER
1	C	910	LEU
1	C	911	ARG
1	C	913	ASN
1	C	916	LEU
1	C	917	VAL
1	C	921	ASP
1	C	922	TYR
1	C	928	ARG
1	C	931	ASN
1	C	934	LEU
1	C	935	GLN
1	C	939	ASN
1	C	940	ARG
1	C	941	TYR
1	C	945	VAL
1	C	948	ILE
1	C	951	ILE
1	C	954	GLN
1	C	957	PHE
1	C	958	ILE
1	C	962	ASP
1	C	965	ARG
1	C	966	GLN
1	C	967	LEU
1	C	973	THR
1	C	976	THR
1	C	978	GLN
1	C	988	GLN
1	C	989	ILE
1	C	991	ASP
1	C	1003	ARG
1	C	1014	MET
1	C	1021	ARG
1	C	1022	ILE
1	C	1023	ARG

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Mol	Chain	Res	Type
1	C	1024	PRO
1	C	1034	GLN
1	C	1036	ASP
1	C	1038	GLU
1	C	1043	SER
1	C	1044	ARG
1	C	1049	GLU
1	C	1050	LEU
1	C	1051	ARG
1	C	1053	ARG
1	C	1054	ARG
1	C	1059	LEU
1	C	1061	LEU
1	C	1062	ILE
1	C	1063	THR
1	C	1070	ARG
1	C	1072	ASP
1	C	1075	ARG
1	C	1076	ILE
1	C	1077	MET
1	C	1079	LEU
1	C	1080	THR
1	C	1082	ASP
1	C	1083	ASP
1	C	1088	PHE
1	C	1089	VAL
1	C	1092	VAL
1	C	1099	VAL
1	C	1104	ARG
1	C	1105	LEU
1	C	1106	PHE
1	C	1110	LEU
1	C	1112	ASN
1	C	1114	ARG
1	C	1118	THR
1	C	1122	PRO
1	C	1123	PRO
1	C	1124	THR
1	C	1126	MET
1	C	1132	THR
1	C	1140	THR
1	C	1141	ILE

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Mol	Chain	Res	Type
1	C	1147	MET
1	C	1149	LYS
1	C	1158	SER
1	C	1161	LYS
1	C	1168	ILE
1	C	1169	HIS
1	C	1170	ASP
1	C	1171	ILE
1	C	1177	VAL
1	C	1182	GLU
1	C	1185	THR
1	C	1186	GLN
1	C	1187	HIS
1	C	1191	GLU
1	C	1192	SER
1	C	1195	THR
1	C	1200	LYS
1	C	1201	LEU
1	C	1202	PHE
1	C	1204	LEU
1	C	1207	MET
1	C	1208	ASP
1	C	1210	LEU
1	C	1211	LEU
1	C	1212	ARG
1	C	1213	PRO
1	C	1214	GLU
1	C	1219	ASP
1	C	1221	PRO
1	C	1227	MET
1	C	1236	ILE
1	C	1237	SER
1	C	1240	ARG
1	C	1242	MET
1	C	1243	ARG
1	C	1246	VAL
1	C	1247	ASN
1	C	1250	GLU
1	C	1253	ARG
1	C	1262	SER
1	C	1263	TYR
1	C	1264	GLU

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Mol	Chain	Res	Type
1	C	1272	ARG
1	C	1273	ASN
1	C	1276	LEU
1	C	1277	LEU
1	C	1283	ASN
1	C	1285	GLN
1	C	1286	VAL
1	C	1288	ILE
1	C	1290	LYS
1	C	1292	GLU
1	C	1296	ILE
1	C	1298	PHE
1	C	1305	MET
1	C	1309	ILE
1	C	1310	ARG
1	C	1313	ASP
1	C	1319	ARG
1	C	1320	VAL
1	C	1323	ASP
1	C	1325	VAL
1	C	1326	ARG
1	C	1328	ILE
1	C	1331	ARG
1	C	1332	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (62) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	139	ASN
1	B	148	GLN
1	B	291	HIS
1	B	292	ASN
1	B	311	ASN
1	B	346	HIS
1	B	438	ASN
1	B	661	ASN
1	B	682	GLN
1	B	693	ASN
1	B	698	HIS
1	B	701	HIS
1	B	718	ASN
1	B	748	GLN

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Mol	Chain	Res	Type
1	B	854	GLN
1	B	898	GLN
1	B	913	ASN
1	B	942	HIS
1	B	988	GLN
1	B	1064	ASN
1	B	1169	HIS
1	B	1205	GLN
1	B	1300	ASN
1	C	106	GLN
1	C	115	GLN
1	C	144	ASN
1	C	148	GLN
1	C	173	GLN
1	C	195	ASN
1	C	205	ASN
1	C	209	ASN
1	C	229	GLN
1	C	297	ASN
1	C	306	GLN
1	C	311	ASN
1	C	352	HIS
1	C	369	ASN
1	C	430	ASN
1	C	455	GLN
1	C	577	GLN
1	C	610	GLN
1	C	646	ASN
1	C	673	GLN
1	C	690	GLN
1	C	693	ASN
1	C	701	HIS
1	C	748	GLN
1	C	802	GLN
1	C	854	GLN
1	C	864	HIS
1	C	882	GLN
1	C	959	GLN
1	C	966	GLN
1	C	1103	HIS
1	C	1121	HIS
1	C	1154	ASN

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Mol	Chain	Res	Type
1	C	1186	GLN
1	C	1203	HIS
1	C	1205	GLN
1	C	1247	ASN
1	C	1285	GLN
1	C	1308	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

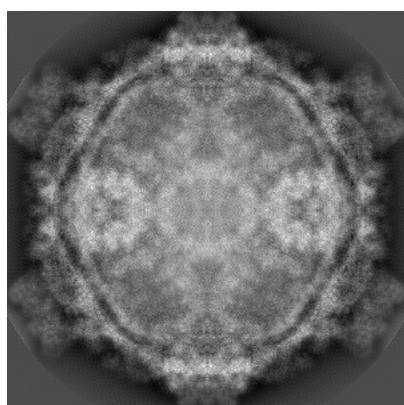
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9565. These allow visual inspection of the internal detail of the map and identification of artifacts.

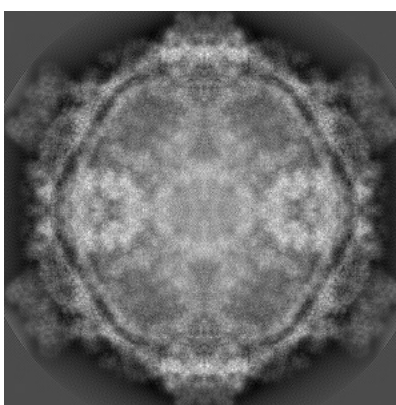
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

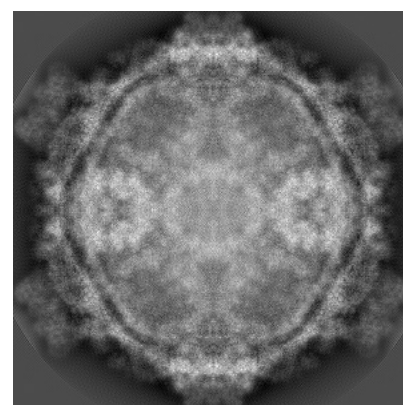
6.1.1 Primary map



X



Y

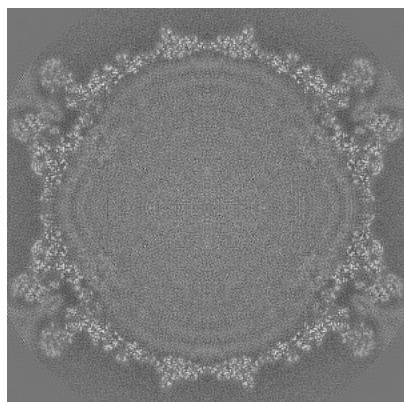


Z

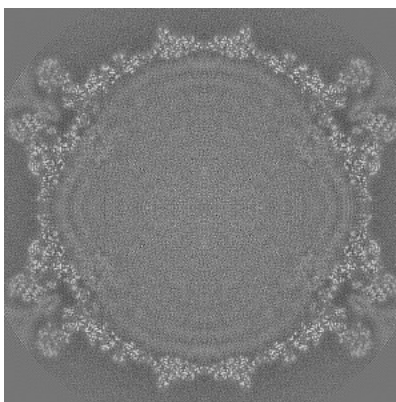
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

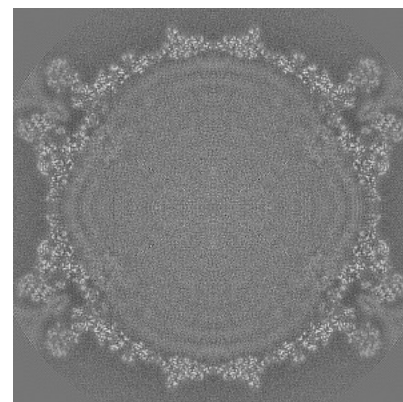
6.2.1 Primary map



X Index: 350



Y Index: 350

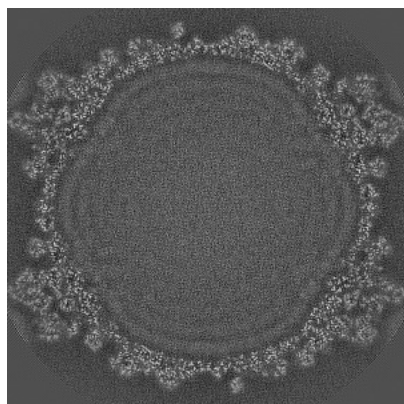


Z Index: 350

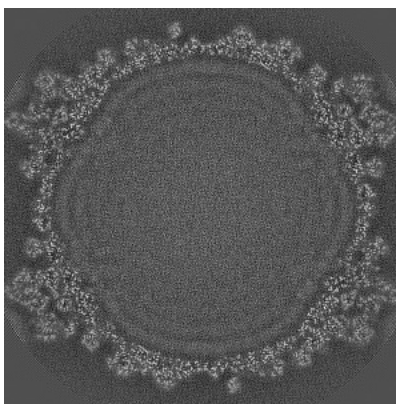
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

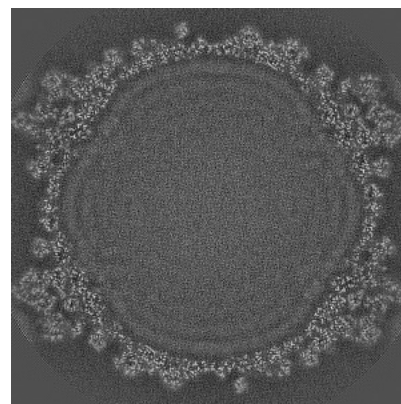
6.3.1 Primary map



X Index: 320



Y Index: 320

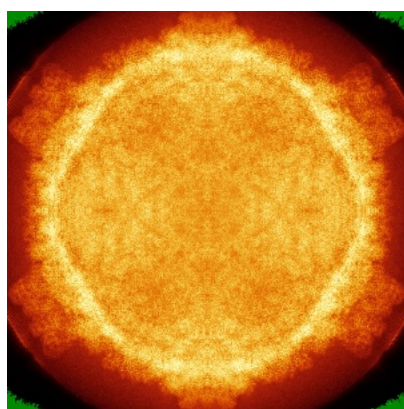


Z Index: 320

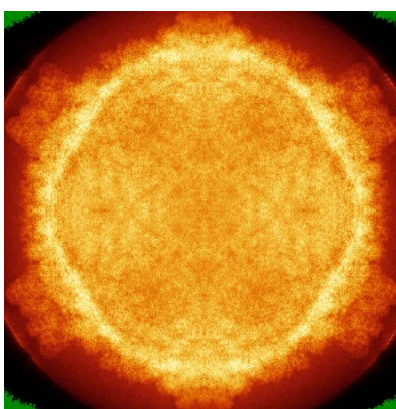
The images above show the largest variance slices of the map in three orthogonal directions.

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

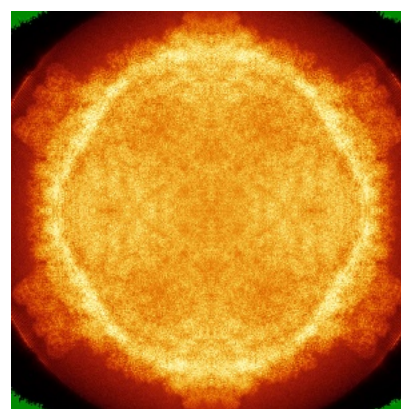
6.4.1 Primary map



X



Y

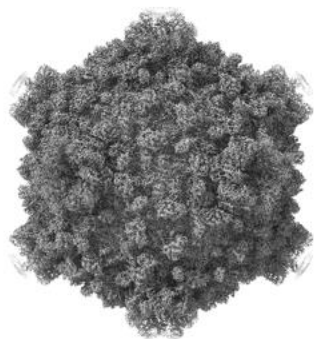


Z

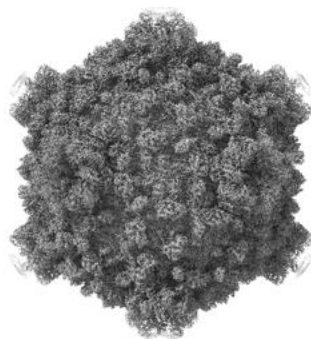
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

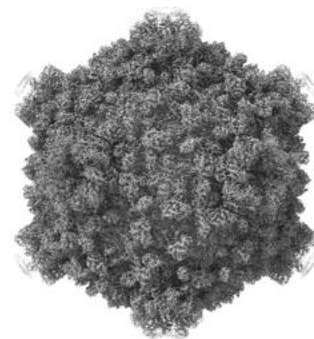
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 17.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

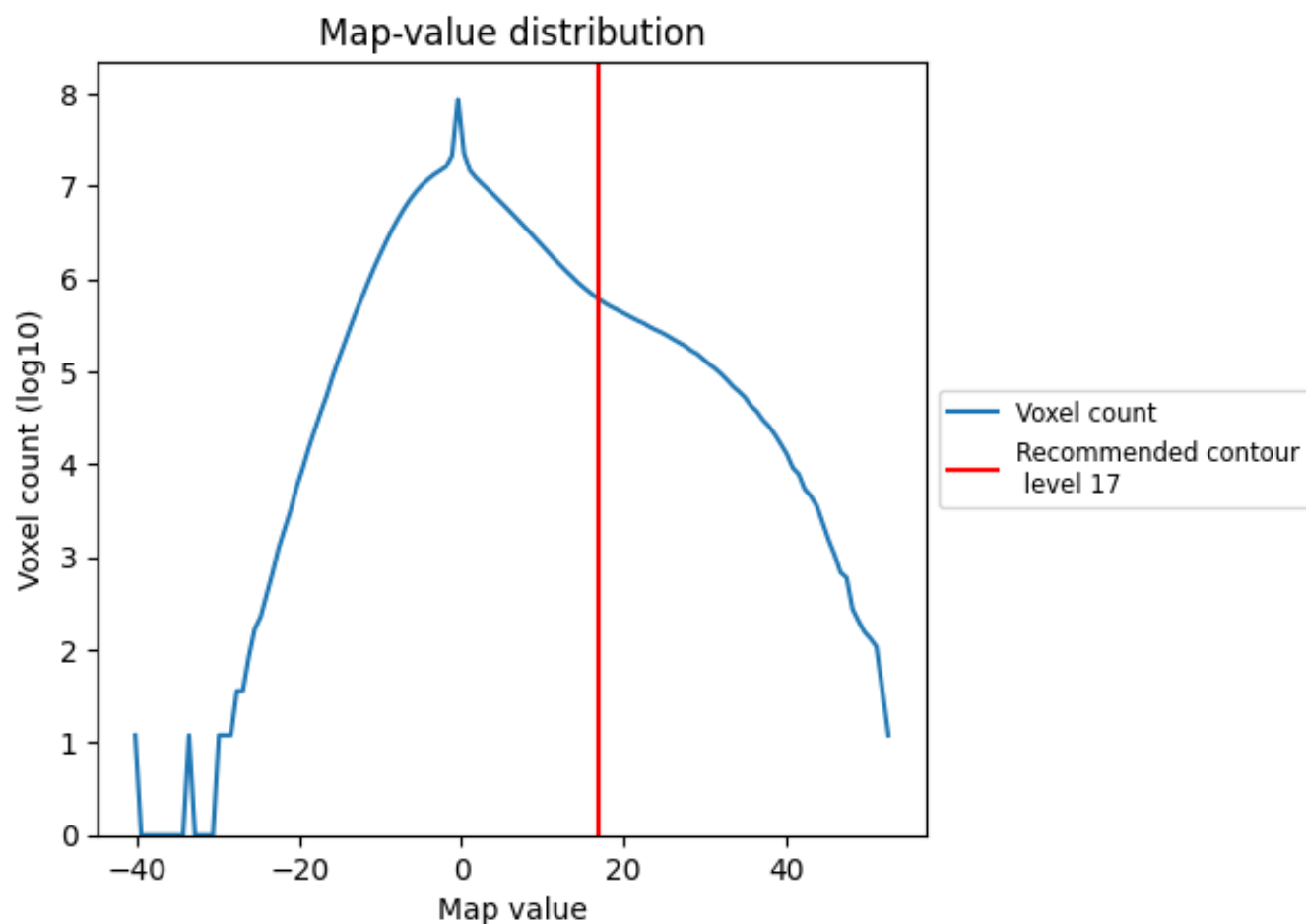
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

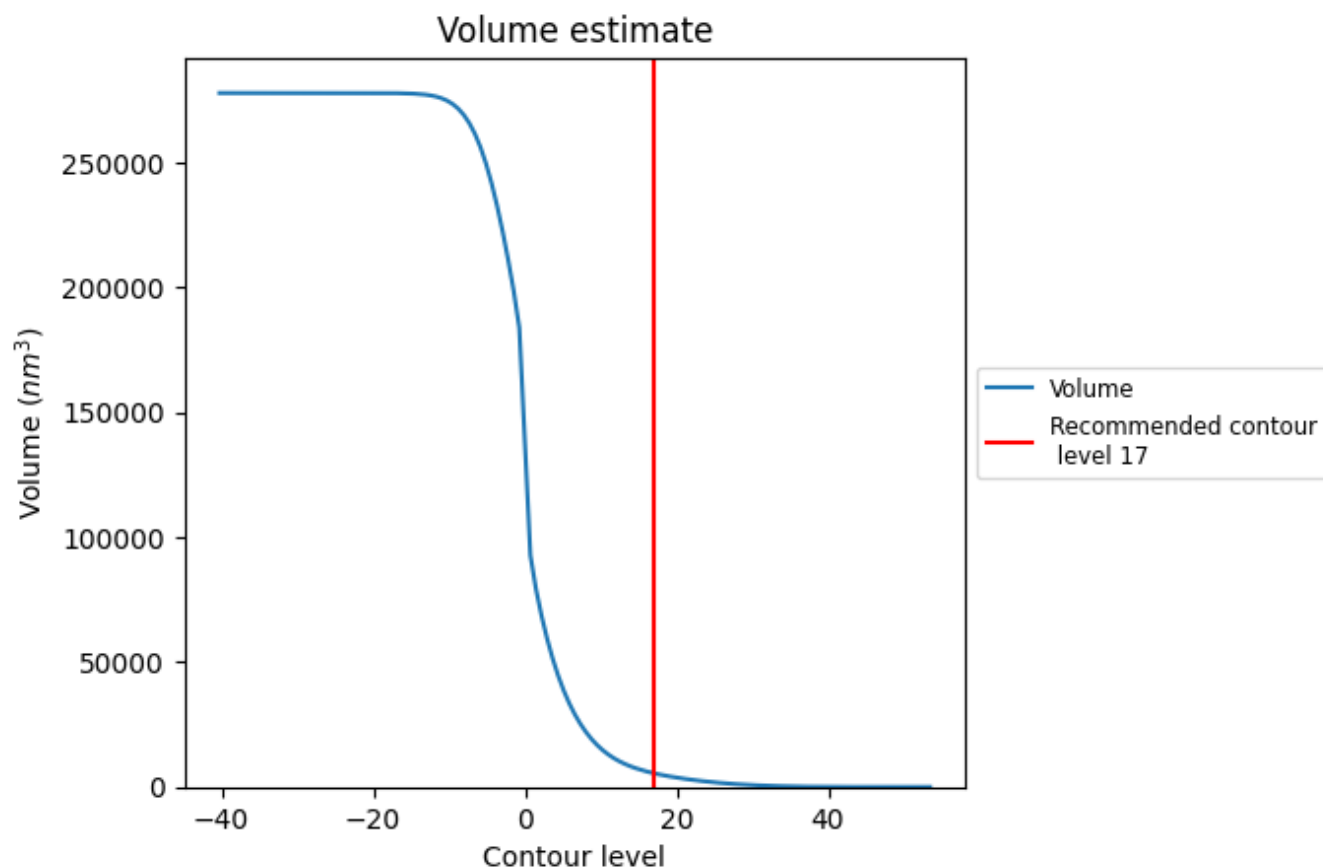
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

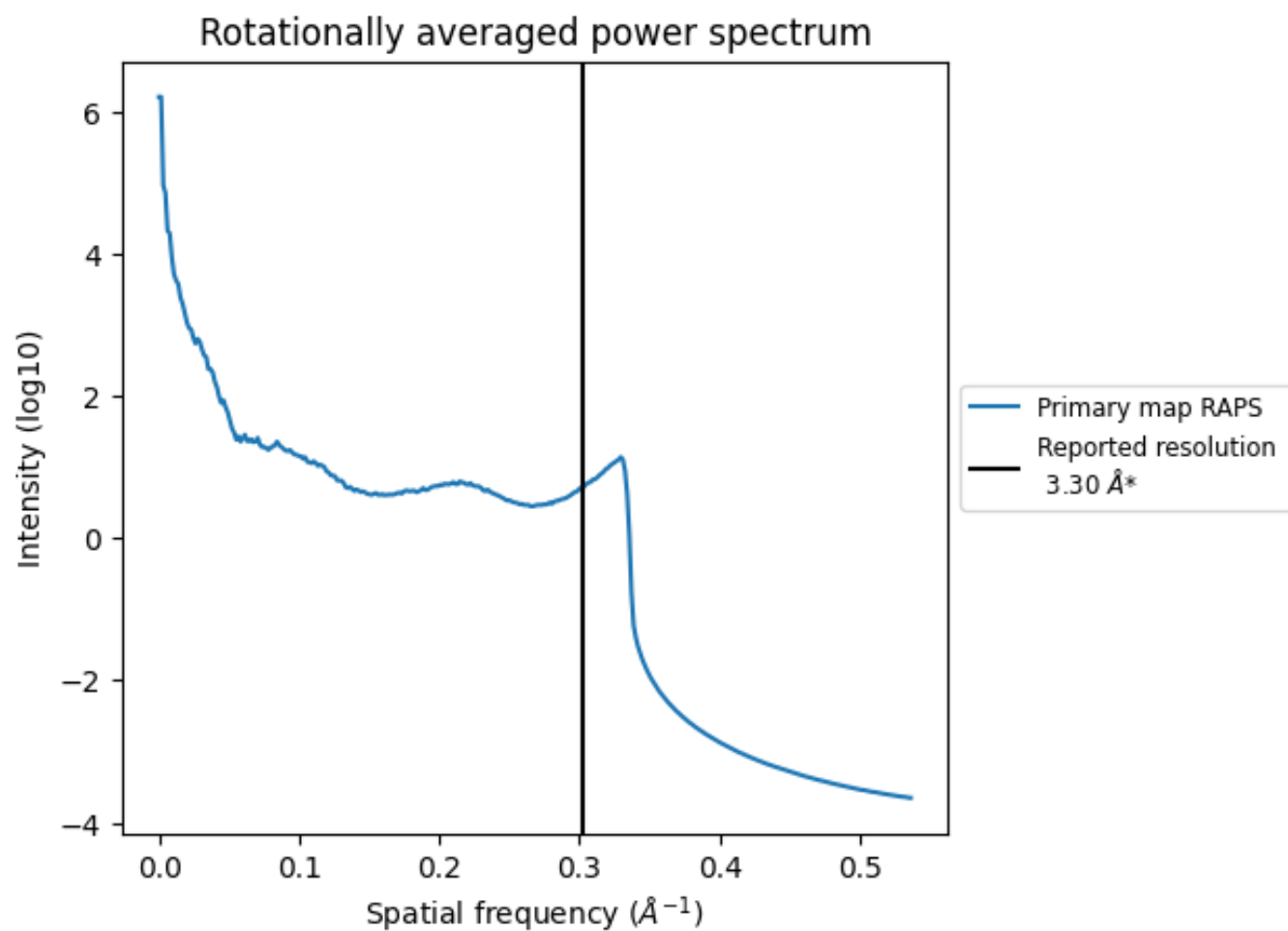
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5491 nm^3 ; this corresponds to an approximate mass of 4961 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

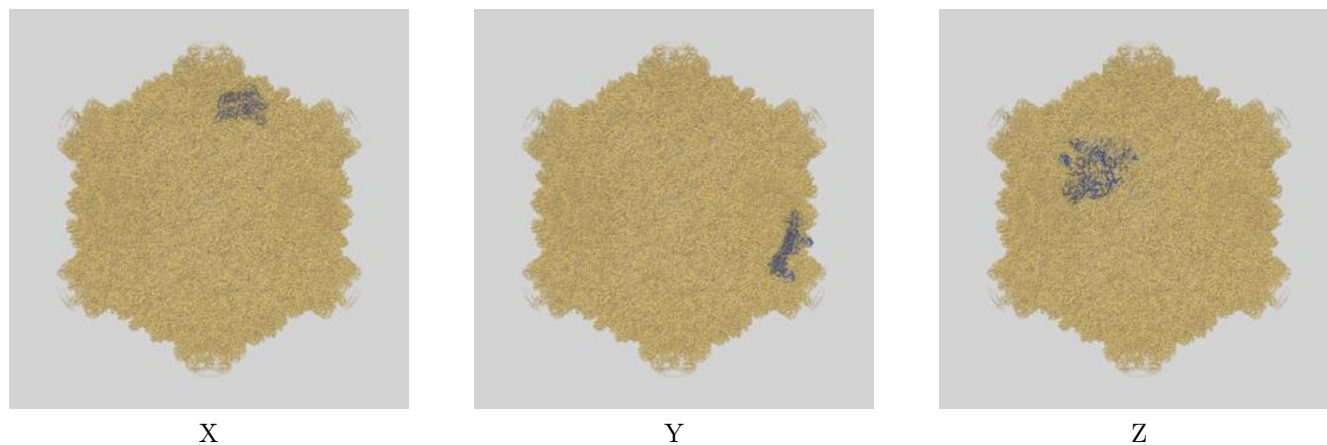
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

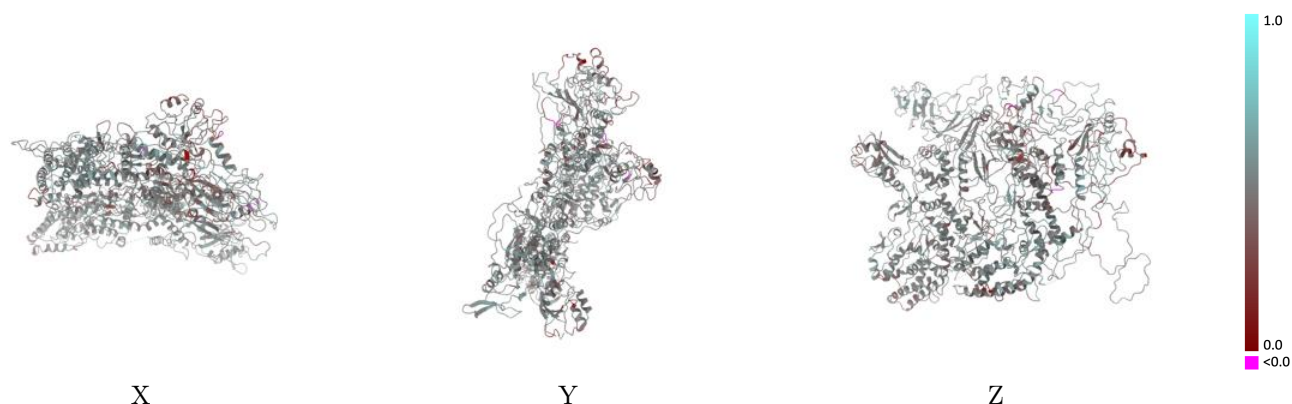
This section contains information regarding the fit between EMDB map EMD-9565 and PDB model 5H0S. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



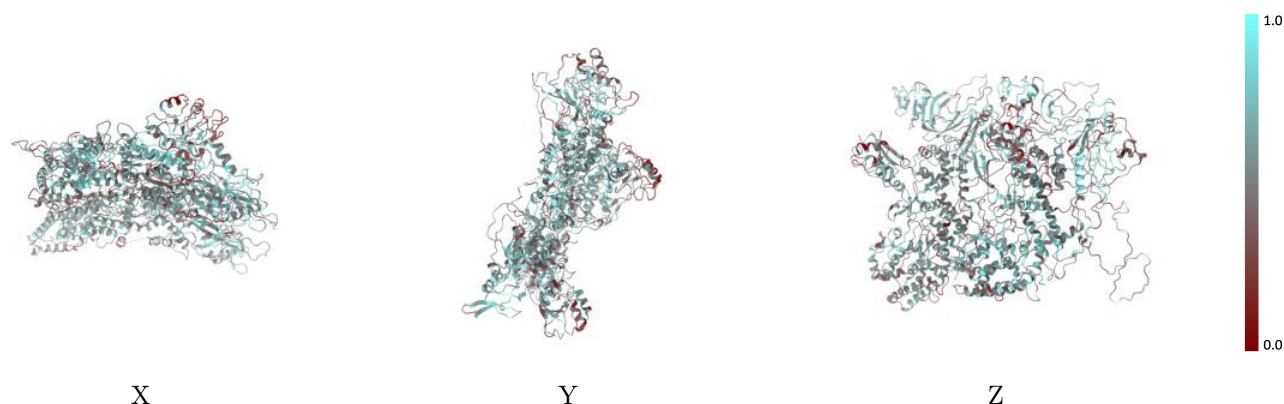
The images above show the 3D surface view of the map at the recommended contour level 17.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



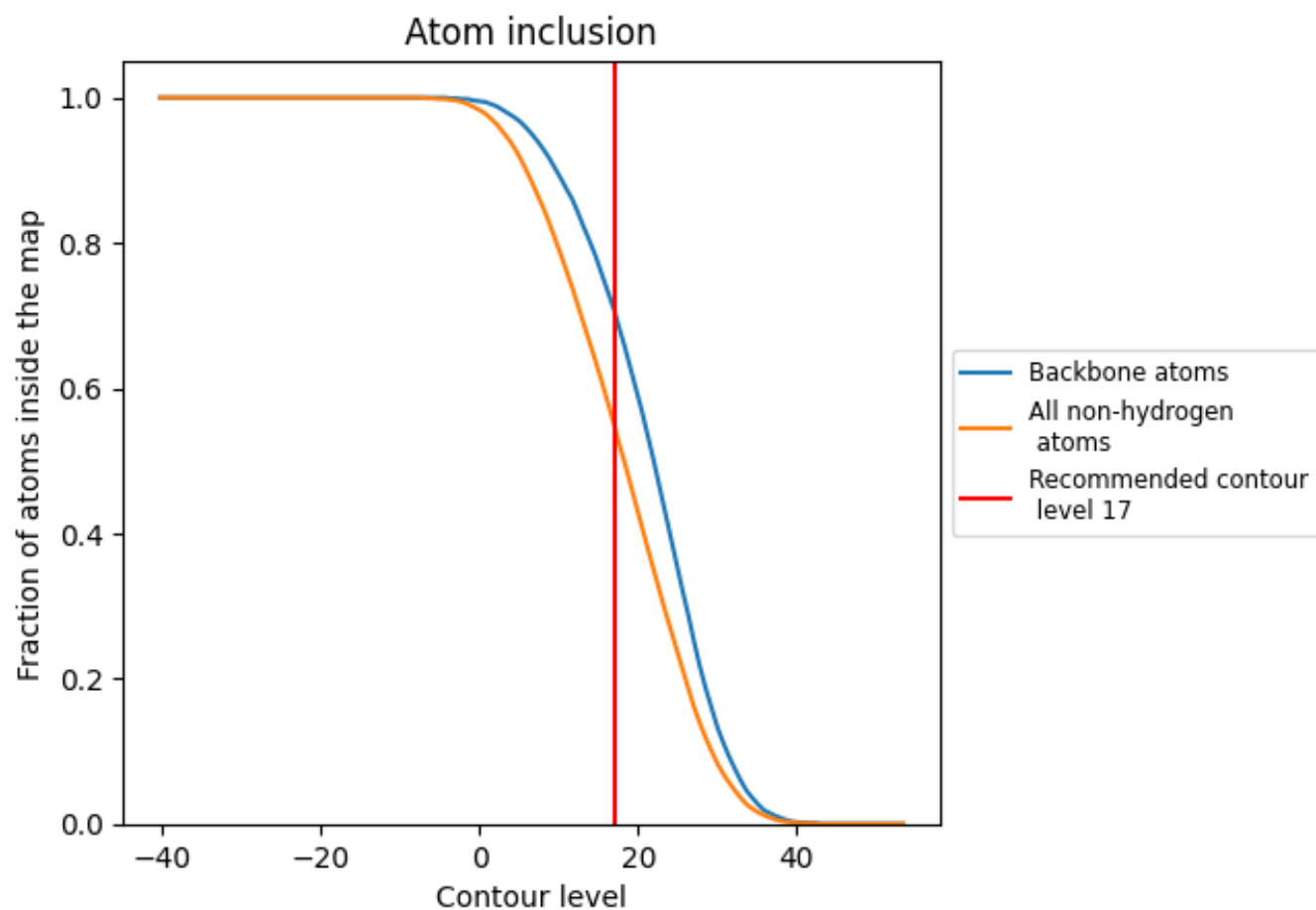
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (17).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 55% 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 (17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5490	<div></div> 0.4770
B	<div></div> 0.5460	<div></div> 0.4780
C	<div></div> 0.5520	<div></div> 0.4760

