



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 06:24 PM UTC

PDB ID : 7WOO / pdb_00007woo
EMDB ID : EMD-32653
Title : Cryo-EM structure of the inner ring protomer of the *Saccharomyces cerevisiae* nuclear pore complex
Authors : Li, Z.Q.; Chen, S.J.B.; Zhao, L.; Sui, S.F.
Deposited on : 2022-01-22
Resolution : 3.71 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

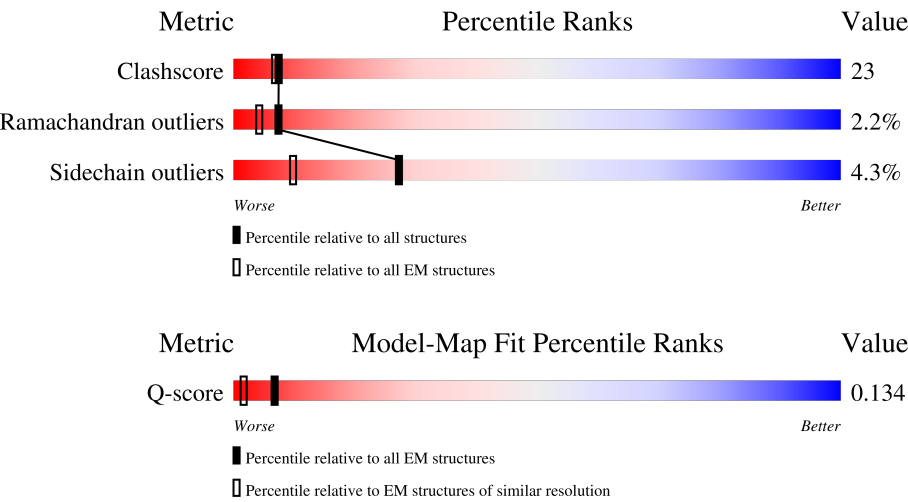
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.71 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10534 (3.21 - 4.21)

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	A	839	83% 53% 32% •• 13%
1	Z	839	53% 52% 29% 6% • 11%
2	C	1391	95% 89% 5% • 5%
3	D	1502	80% 66% 26% • 7%

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Mol	Chain	Length	Quality of chain
4	E	1655	
5	F	1683	
6	G	472	
6	J	472	
7	H	541	
7	K	541	
8	I	823	
8	L	823	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 66949 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Nucleoporin NIC96.

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

- Molecule 2 is a protein called Nucleoporin NUP157.

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

- Molecule 3 is a protein called Nucleoporin NUP170.

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

- Molecule 4 is a protein called Nucleoporin NUP188.

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

- Molecule 5 is a protein called Nucleoporin NUP192.

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

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

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

- Molecule 7 is a protein called Nucleoporin NUP57.

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

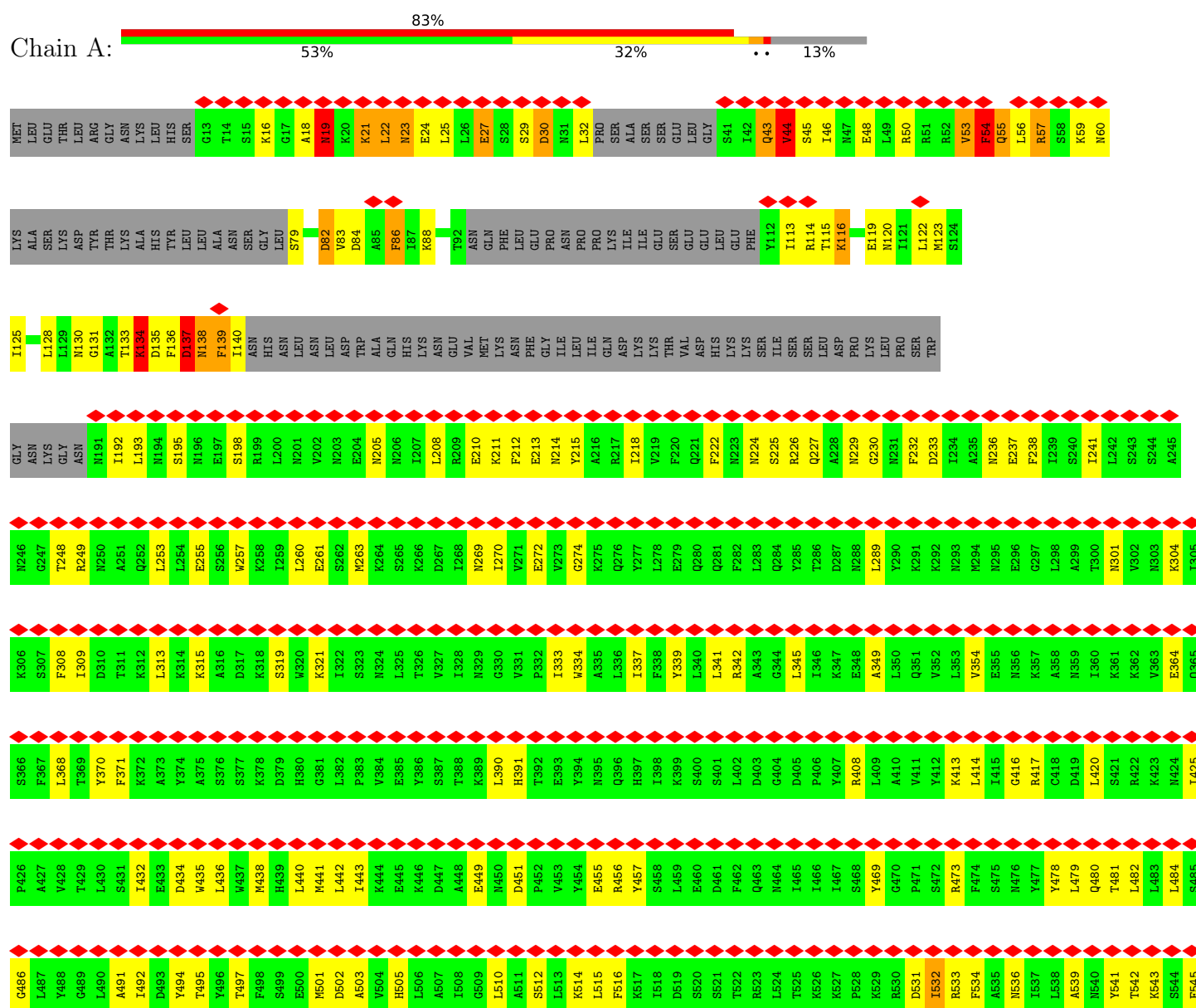
- Molecule 8 is a protein called Nucleoporin NSP1.

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

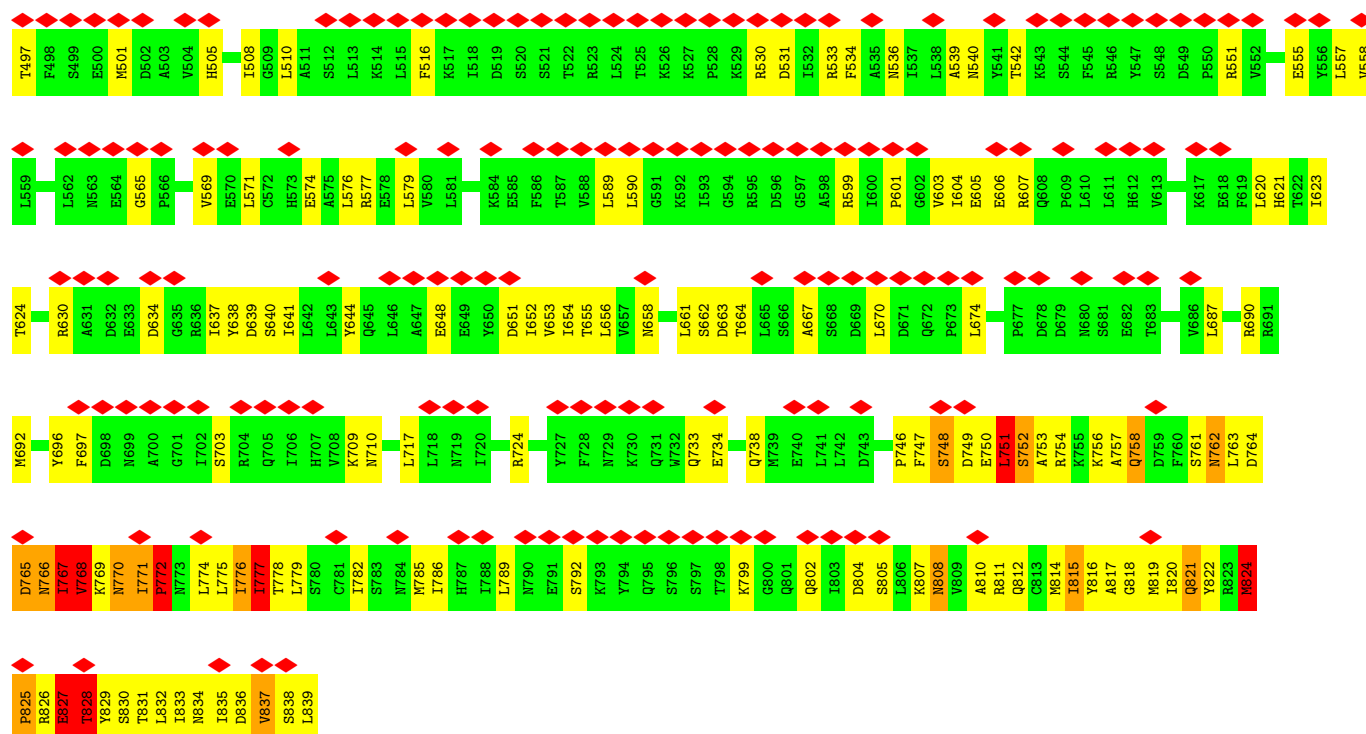
3 Residue-property plots

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

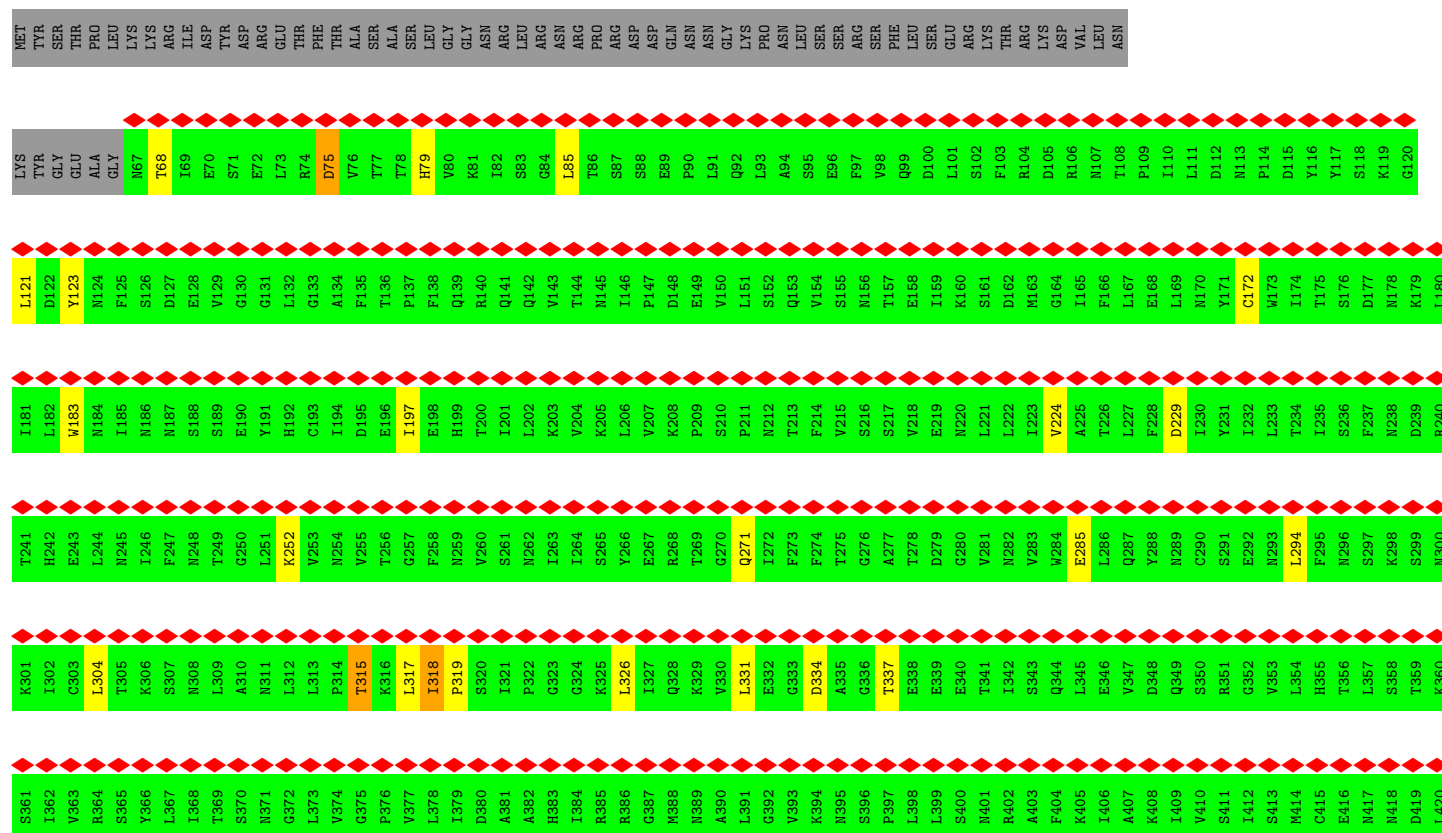
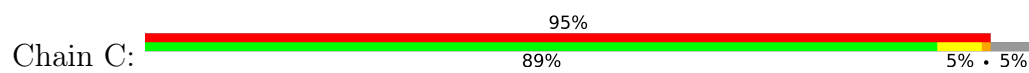
• Molecule 1: Nucleoporin NIC96



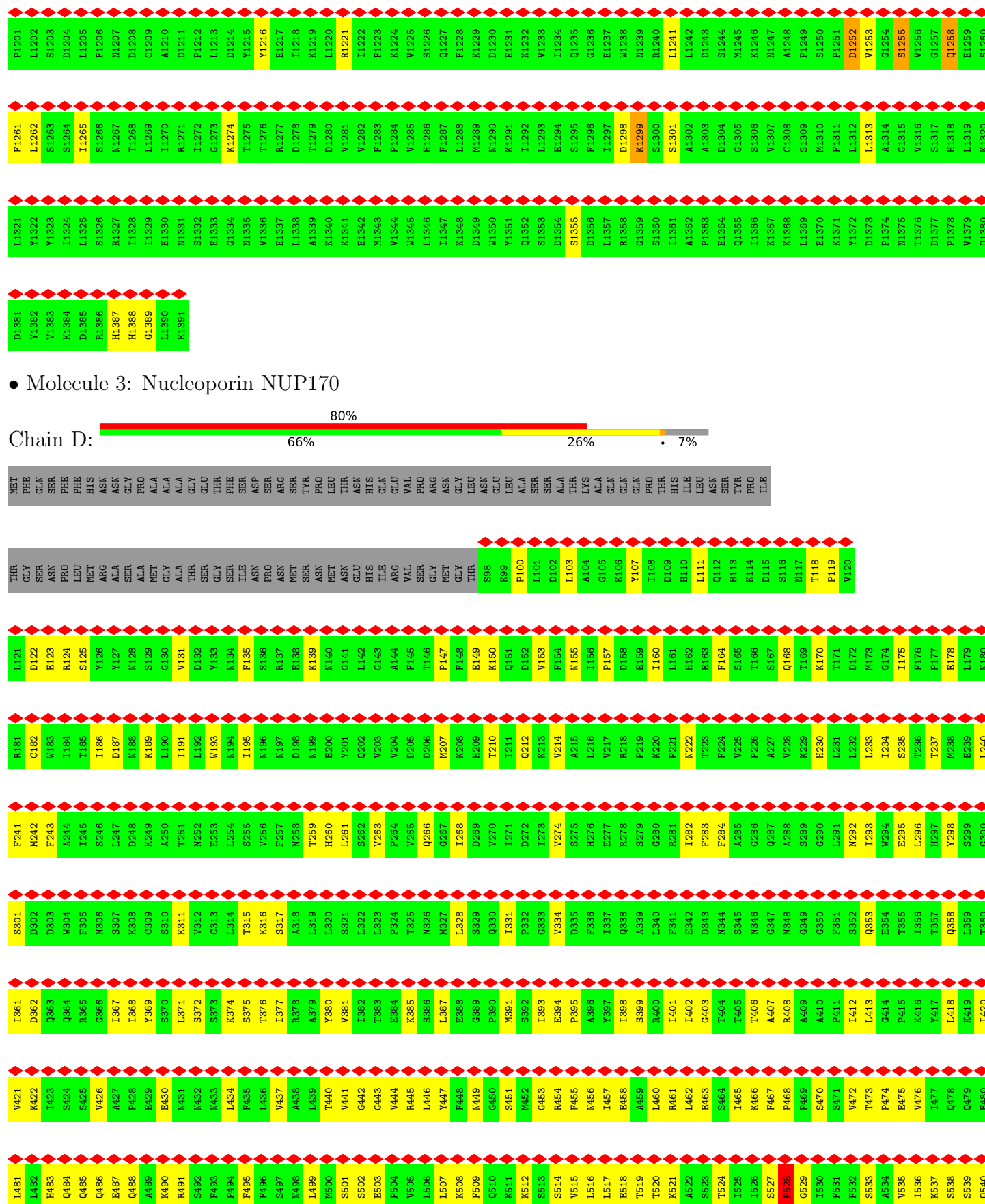




• Molecule 2: Nucleoporin NUP157



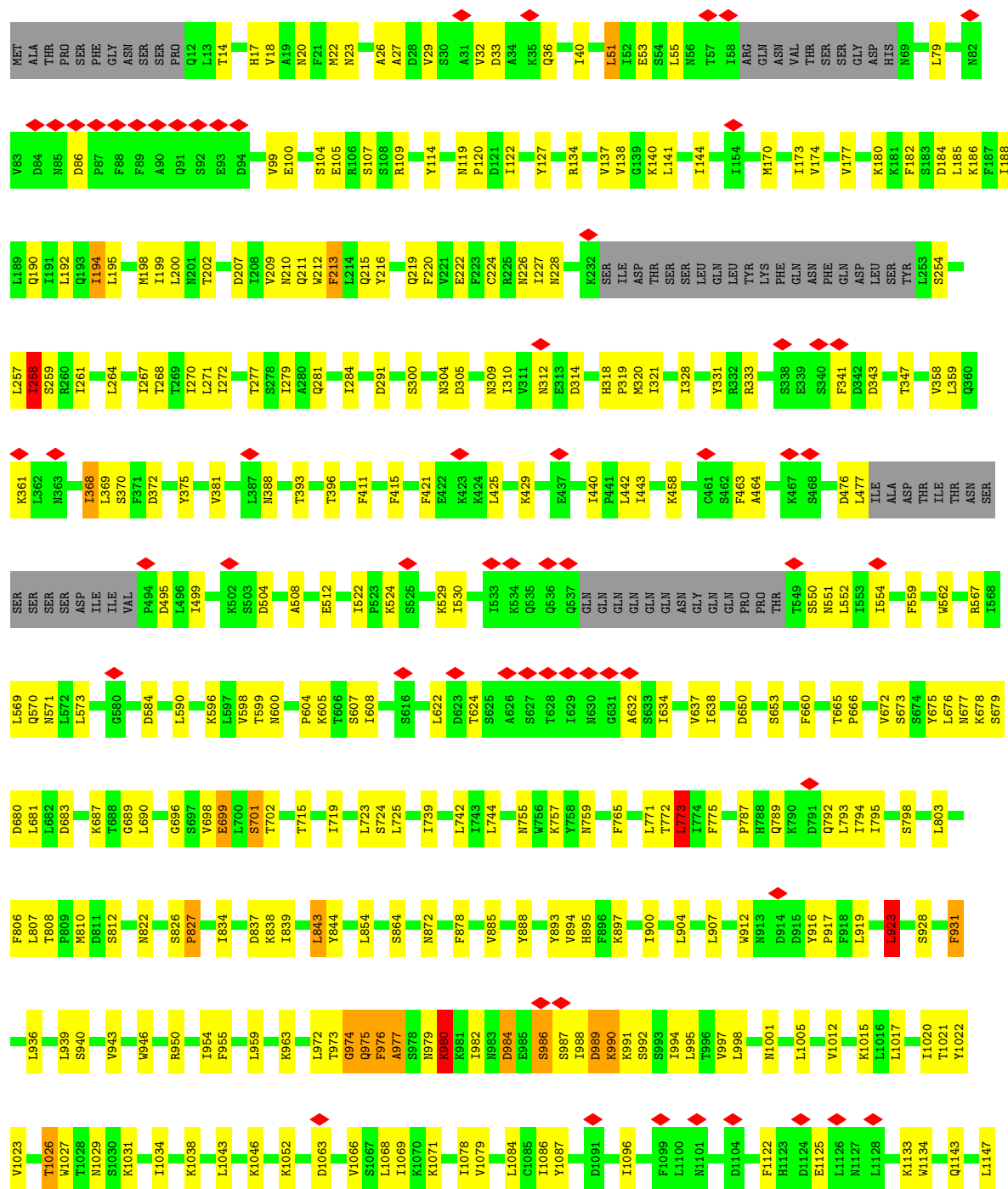
C1141	L1081	I1021	P961	I901	R841	G781	S721	A661	V601	S541	G481	F421
D1142	P1082	E1022	K962	L902	E842	S782	Q722	L662	A602	A542	P482	L422
S1143	Y1083	Q1023	T963	C903	Y843	Y783	I723	A663	V603	P643	L483	A423
S1144	L1084	S1024	V964	Y904	F844	A784	W724	F664	L604	D544	S484	V424
T1145	K1085	P1025	G965	R905	F945	I785	E725	F665	T605	Y455	T485	I425
S1146	E1086	S1026	F966	A906	D846	T786	E726	S666	S606	G546	Q486	T426
F1147	R1087	I1027	L967	G907	L847	A787	R727	A667	N607	I547	K487	T427
L1148	A1088	A1028	L968	E908	K848	S788	W728	G668	A608	L548	A488	T428
Q1149	E1089	M1029	R969	H909	F949	D789	F729	I669	L609	K549	S489	G429
K1150	K1090	I1030	F970	L910	H850	A790	W730	P670	E610	N550	S490	V430
P1151	S1091	S1031	A971	E911	D851	E791	F731	G671	I611	Y551	T491	R431
A1152	L1092	D972	D972	A912	L852	S792	K732	V672	Y612	G552	Y492	L432
L1153	E1093	F1033	K973	A913	F953	I793	R733	G673	C613	K553	I493	Y433
V1154	I1094	S1034	I974	Q914	T854	A794	A734	E674	Y614	Y554	N494	F434
Q1155	D975	P1035	D975	K915	P855	W795	S735	I675	R615	V555	T495	K435
L1156	K976	A1036	K976	F916	N856	W796	K736	K676	T616	E556	T496	G436
S1157	L1097	S1037	G977	E917	A857	A797	T737	P677	P617	N557	C497	S437
E1158	N978	I1038	N978	K918	K858	L798	E738	K678	D618	T558	A498	I438
M1159	Q979	L1039	Q979	I919	T859	I799	K739	S679	E619	A559	S499	S439
I1160	A980	K1040	Q981	D920	K860	L800	M740	S680	V620	L560	T500	R440
H1161	Y1101	K1041	Q981	S921	L861	L801	D741	R681	F621	L561	I501	R441
E1162	L1102	R1042	E982	K922	L862	I802	A742	E682	E622	D562	I502	S442
L1163	F1103	V1043	Y983	I923	I863	N803	F743	S683	S623	T563	S503	I443
F1164	K1104	Y1044	S984	S924	K864	S804	G744	G684	L624	T564	P504	G444
I1165	E1105	S1045	S985	R925	E865	I805	I745	S685	I625	D565	G505	S445
E1166	N986	V1046	R986	N926	I866	K806	S746	V686	E626	E566	I506	L446
A1167	G987	I1047	G987	H927	L867	D807	I747	P687	N627	I567	Y507	K447
S1168	C988	M1048	N988	L928	I868	A808	T748	P688	P628	K568	F508	L448
I1169	N989	M1049	N989	D929	E869	L809	R749	I889	L629	E569	T509	D449
Q1170	E1110	S1050	V970	T930	V670	S810	P750	S690	P630	I570	C510	S450
D1171	A1111	M1051	V671	A931	V671	L811	Q751	Q891	F631	V571	V511	V451
L1172	D992	N1052	N872	I932	N872	I812	V752	N692	I632	P572	R512	K452
L1173	D1113	R1053	A873	D933	A873	N813	E753	L693	H633	L573	K513	F453
L1174	N994	F1054	N874	L934	N874	V614	V754	F694	S634	T574	R514	P454
M1175	L1115	F1055	I875	Y835	I875	F615	V755	D695	Y635	R575	A515	P455
L1176	Y1116	H1056	A876	E936	A876	Y616	L756	K696	G636	S576	N516	T456
F1177	A1117	Y1057	S977	R937	S977	E617	S757	S697	L637	F577	S517	S457
R1178	L1118	C1058	G978	C938	G978	D818	S758	G698	S638	N578	G518	I458
M1179	A1119	F1059	T679	A939	T679	I619	I759	E999	E639	Y579	E519	S459
E1180	S1120	Y1060	S880	E940	S880	D820	S760	C700	A640	T580	L520	S460
T1181	S1121	D1061	A881	N941	A881	A621	V761	D701	C641	S581	S521	S461
R1182	D1122	Y1062	D882	I942	D882	F922	L762	G702	S642	T582	K522	L462
L1183	F1123	L1063	Y883	E943	Y883	K623	A763	I703	T643	P583	G523	E463
D1184	D1124	V1064	I884	L944	I884	S824	V764	W704	A644	Q584	I524	Q464
E1185	L1125	A1065	V885	C945	V885	L825	F765	L705	L645	G585	T525	N465
L1186	T1006	M1066	N886	E946	N886	L826	F766	S706	Y646	Y586	N526	K466
Y1187	L1007	K1067	V887	L947	V887	N627	N767	F707	L647	A587	K527	S467
R1188	S1128	R1068	L888	R948	L888	T628	I768	R708	A648	N588	A528	F468
K1189	E1129	Q1069	K889	R949	K889	L829	H769	F709	C649	V589	L529	I469
Q1190	R1130	E1070	E990	V950	E990	N630	R770	Y710	K650	F590	L530	I470
L1191	I1131	Y1071	R891	V951	R891	G631	F771	G711	F651	A591	E531	G471
T1192	E1132	V1012	F892	D952	F892	A832	S772	S712	N652	S592	N532	H472
L1193	C1133	L1073	G893	I953	G893	G633	F773	A713	K653	Q593	K533	H473
K1194	L1134	R1074	S894	N954	S894	G634	V774	L714	S654	Y594	E534	P474
L1195	A1135	L1075	F955	V955	F955	V635	S775	L715	E555	S595	E535	L475
M1196	R1136	D1076	C956	K956	C956	Y636	F776	I716	H656	A596	H536	N476
K1197	A1137	S1077	H897	L957	H897	D637	T777	T717	I657	E597	K537	T477
R1198	N1138	Q1078	S898	N958	S898	S638	P778	R718	K658	E598	L538	H478
V1199	G1139	F1079	A899	Y959	A899	K639	P779	L719	S659	L599	Y539	D479
L1200	L1140	V1080	D900	Q960	D900	T640	K780	F720	S660	K600	V540	T480

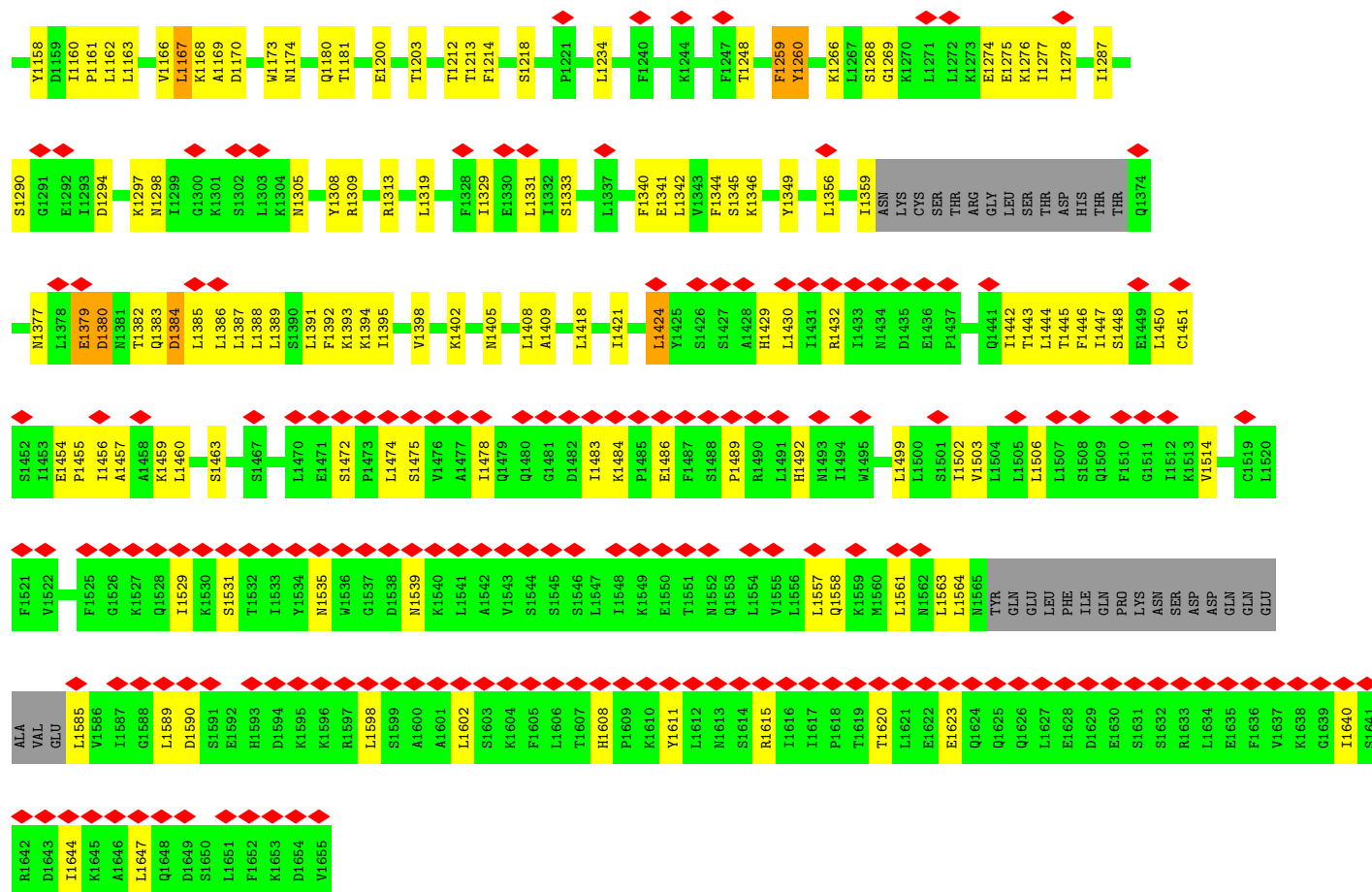


M1362	S1237	Q1143	Y1083	Y1021	S961	Q901	Y841	L781	S721	D661	Q541
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M1365	G1241	S1145	A1085	D1023	L962	S903	Y843	D783	V723	L663	H543
L1366	F1242	Y1146	M1086	L1024	R964	K904	S844	I784	T724	D664	Q544
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K1376	N1244	A1148	F1088	Y1026	I966	G906	I846	G786	S726	P666	E546
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N1377	V1246	L1150	E1090	L1028	L968	S908	L848	H788	L728	P668	K548
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D1380	L1249	M1153	D1093	A1031	I971	N911	E851	T791	K731	L671	S551
S1381	S1250	D1154	R1094	T1032	N972	V912	F852	T792	P732	N672	S552
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C1395	Y1280	V1166	V1104	D1041	E982	F922	Q862	A802	Q742	Q622	S562
M1396	T1281	M1166	Y1105	L1042	E982	D923	I863	F803	Q743	G623	K563
F1397	D1282	M1169	D1106	S1043	Y983	N924	S864	I804	S744	F684	T564
F1398	A1283	R1170	L1107	I1044	T984	Q925	A865	S805	I745	G685	V565
Y1399	R1284	E1171	V1108	E1045	A985	Q925	P866	S806	T746	T686	K566
E1400	I1285	E1172	F1109	K1046	T986	Y926	Y867	S807	G747	E627	Q567
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P1403	F1403	L1175	L1112	E1049	Q989	F929	L869	P809	T749	S689	G569
K1404	K1290	L1176	I1113	A1050	E990	K930	A870	I810	K750	T630	V570
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V1407	I1294	E1178	D1116	S1052	C992	I933	S873	S813	P753	E693	Q573
F1408	I1301	T1179	E1117	M1053	G993	S934	N874	I814	A754	K694	H574
S1409	F1409	P1180	L1118	M1054	S994	S935	G875	N815	N755	E635	K575
G1410	H1333	F1181	A1119	L1055	P995	V936	R876	N816	K756	R696	L576
S1411	K1339	I1182	E1120	S1056	C996	S937	V877	L817	E757	S697	F577
I1412	K1339	L1183	E1207	V1057	S997	S937	I878	K818	D758	N698	V578
V1413	K1339	I1199	K1121	M1058	A998	L938	D879	S819	F759	A699	S579
T1418	F1344	L1200	Q1123	Y1059	S999	D939	K880	D820	D760	L700	V580
A1419	Q1345	S1205	S1124	Y1060	D1000	V940	T881	E821	L761	T701	P681
G1420	S1346	Y1203	S1125	P1061	I1001	Q941	E882	I822	D762	F702	D582
V1421	L1347	Y1204	K1126	K1062	L1002	K942	E883	S823	D763	L703	Y583
S1422	R1348	S1205	T1127	L1064	G1003	D943	V884	Q824	V764	T643	G584
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F1423	E1350	R1207	Q1129	E1065	R1005	V945	A885	N826	I766	T645	I585
M1426	F1351	S1208	Q1130	F1066	A1006	K946	N886	R827	L766	G706	L586
K1429	N1352	K1209	I1131	M1069	I1007	L947	Q887	I828	S767	I707	K587
L1430	L1353	F1210	S1132	I1070	E1008	D948	A888	N829	P768	P708	T588
K1431	T1354	F1211	I1133	A1071	H1009	P949	E889	I829	R769	G709	H589
E1432	G1355	E1212	S1134	M1074	L1010	K950	S890	S830	F770	V710	G590
L1433	K1356	S1213	N1135	D1075	R1011	D951	I891	K831	Y771	V711	K591
I1434	E1358	A1214	D1136	K1076	R1012	L952	A892	V832	G772	D712	Y592
E1435	T1359	E1215	L1367	G1077	A1013	P953	I893	S833	I773	I713	V593
T1436	S1360	Y1218	D1137	K1078	K1014	A954	N894	I834	A774	K714	E594
S1437	M1361	I1227	V1139	L1079	E1015	P955	A895	S835	L775	P715	N595
D1438			L1140	L1079	I1016	N956	M896	K836	L776	V716	A596
			L1141	A1080	G1017	D957	I897	D837	I777	Y717	T597
			R1142	C1081	L1018	T959	K958	C838	T778	N718	F598
				Q1082	R1019	M899	M899	I839	R779	N719	L599
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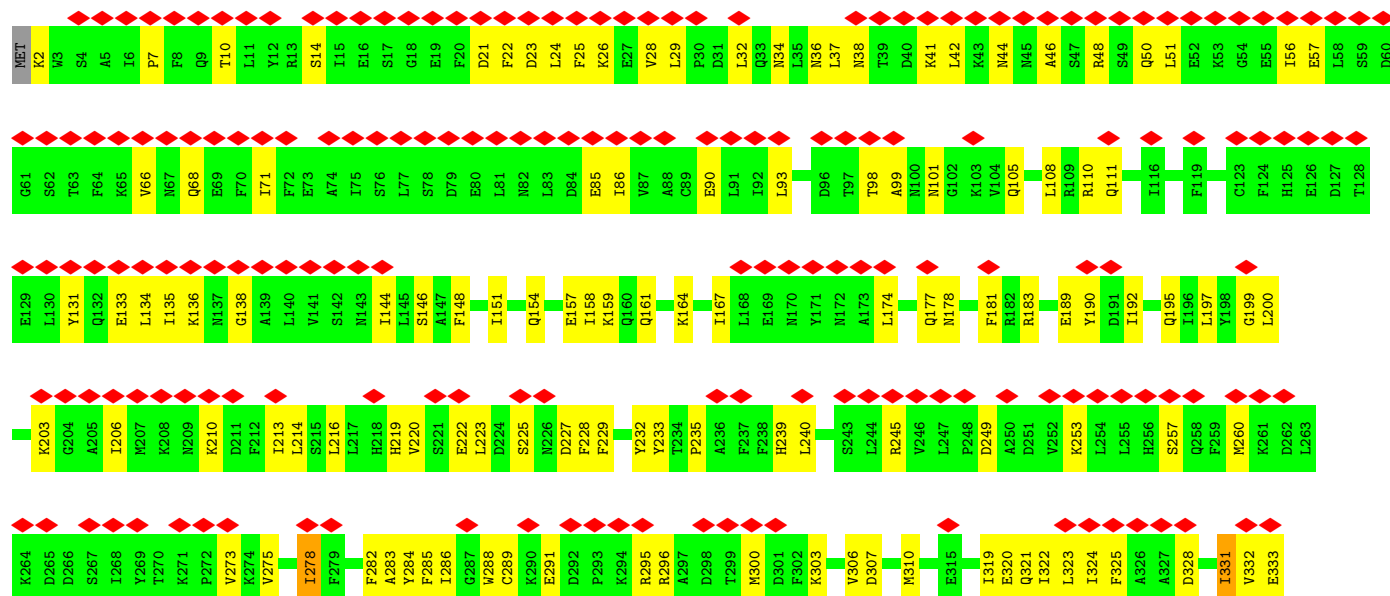


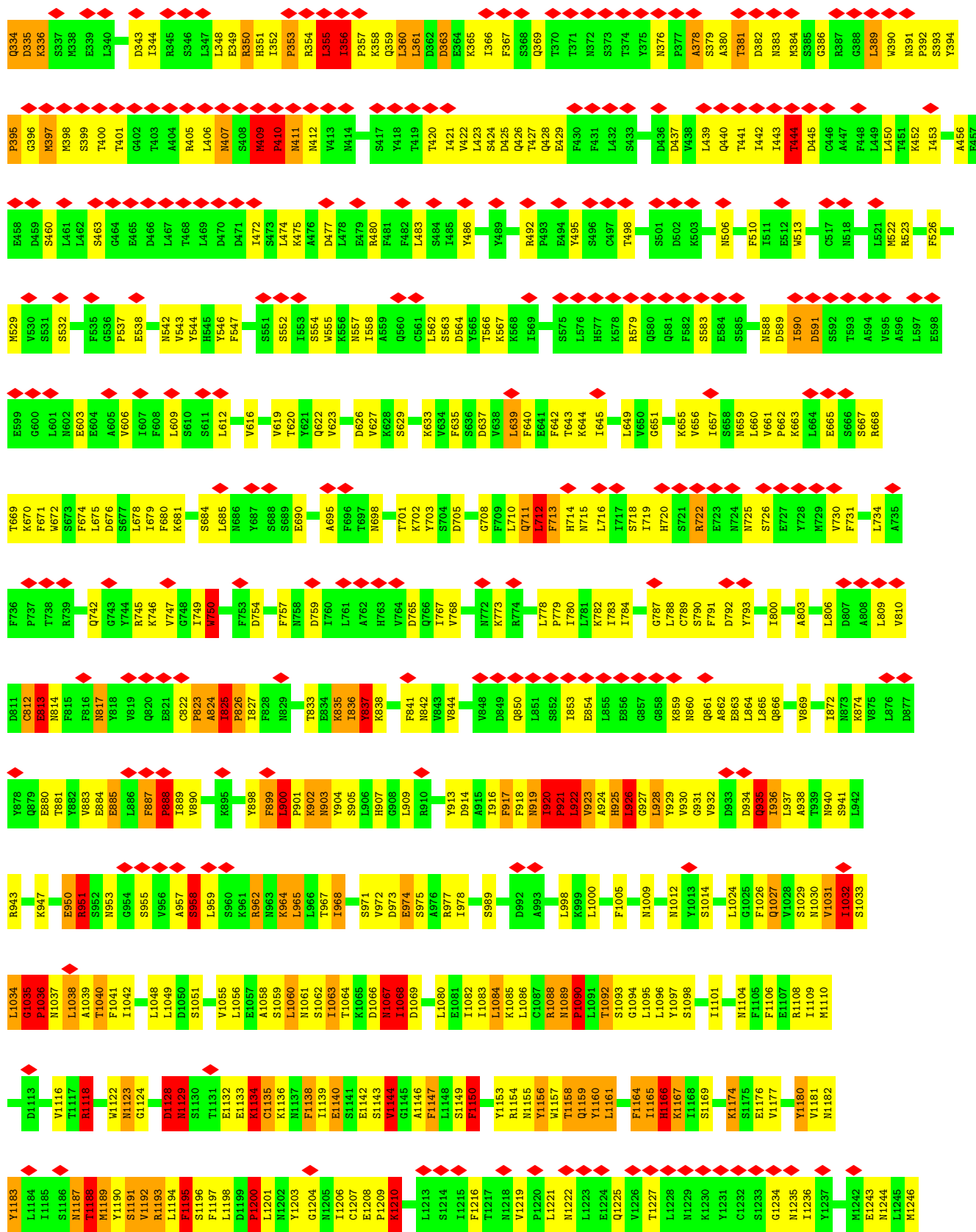
• Molecule 4: Nucleoporin NUP188

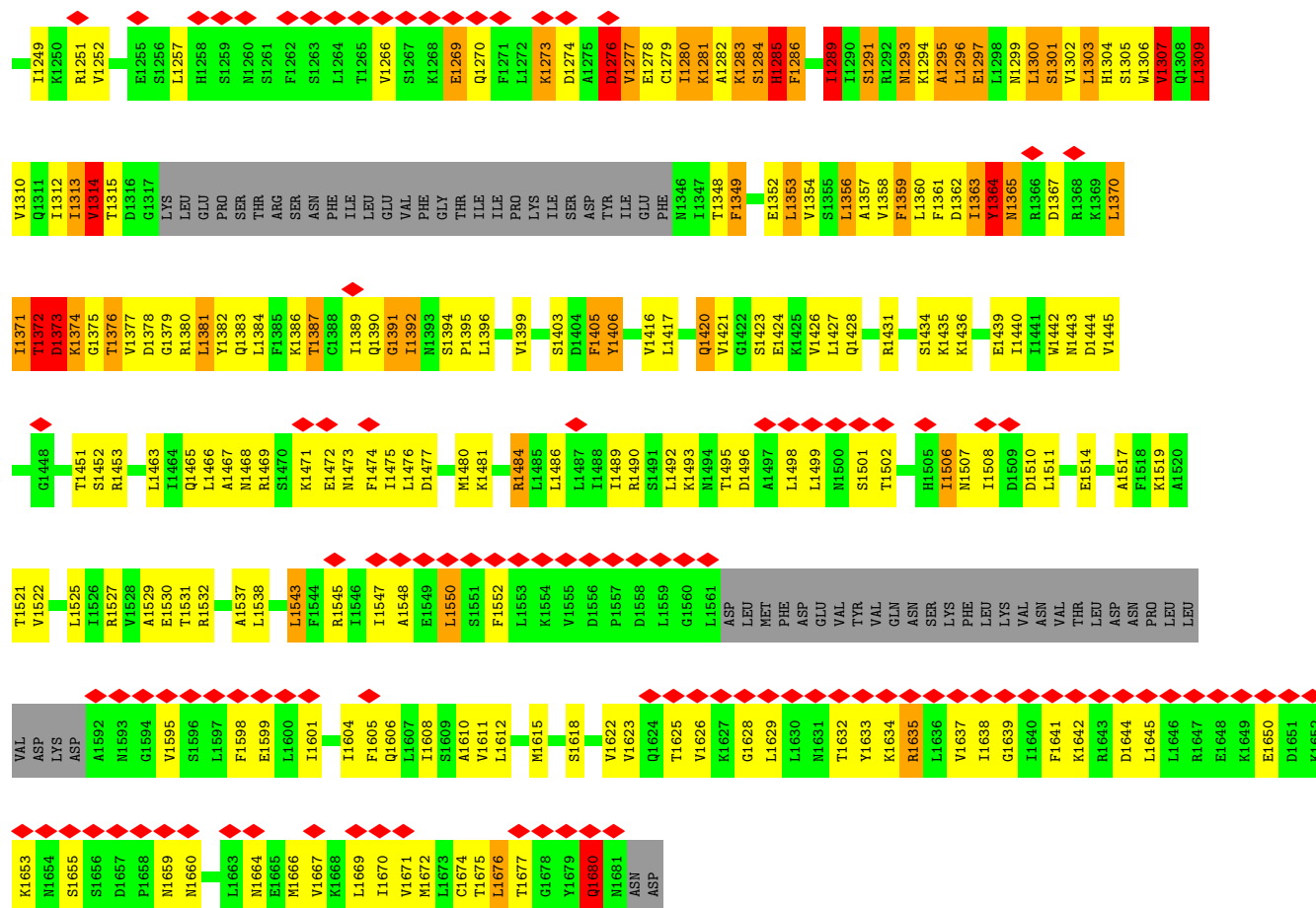




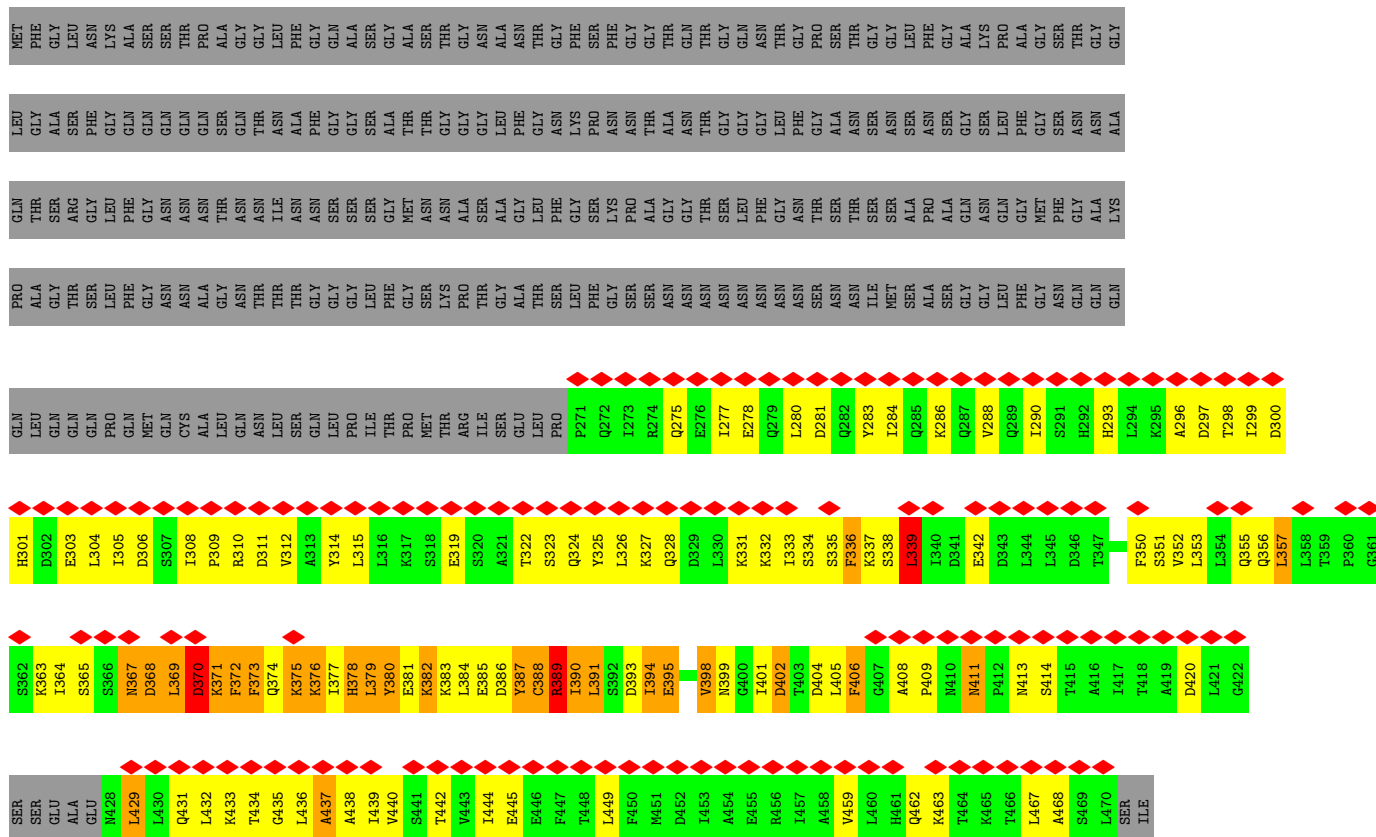
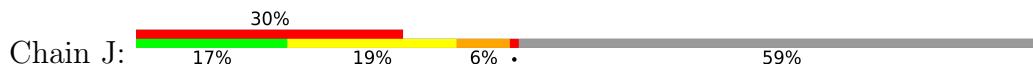
• Molecule 5: Nucleoporin NUP192



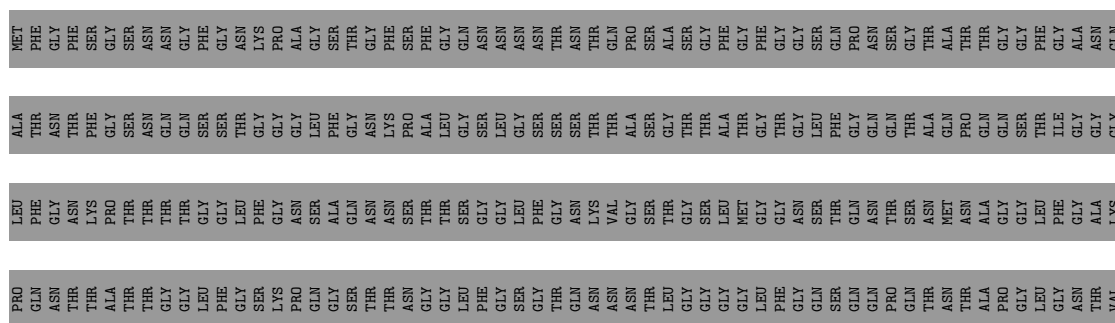


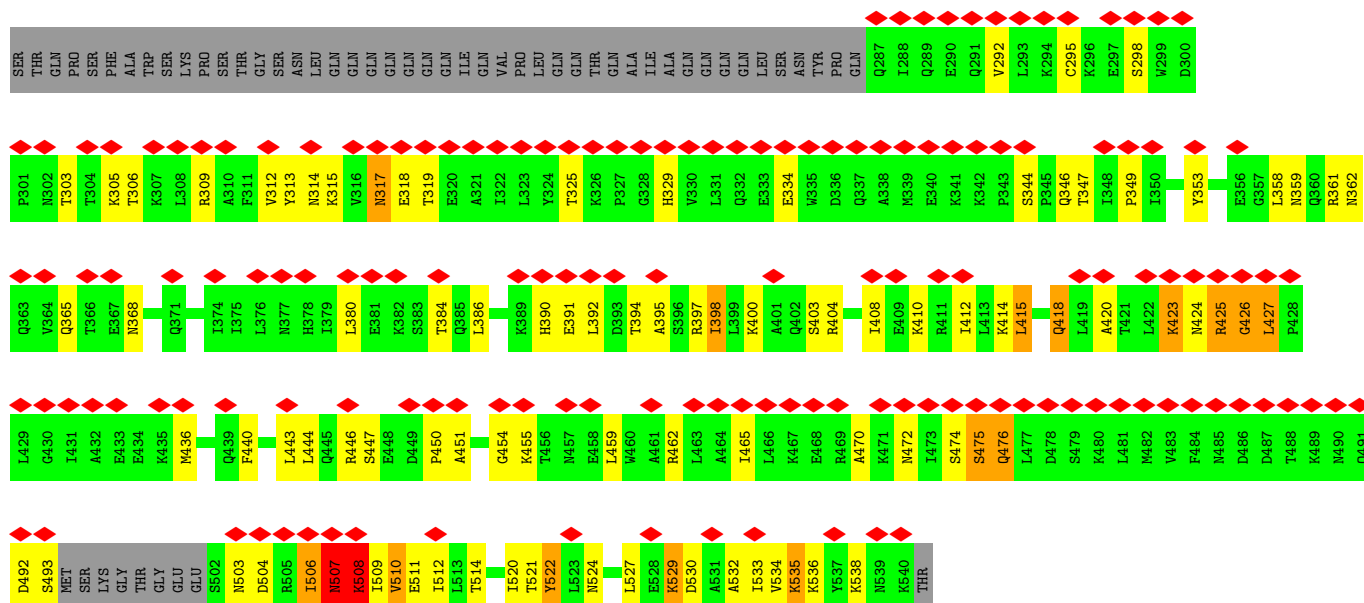


- Molecule 6: Nucleoporin NUP49/NSP49

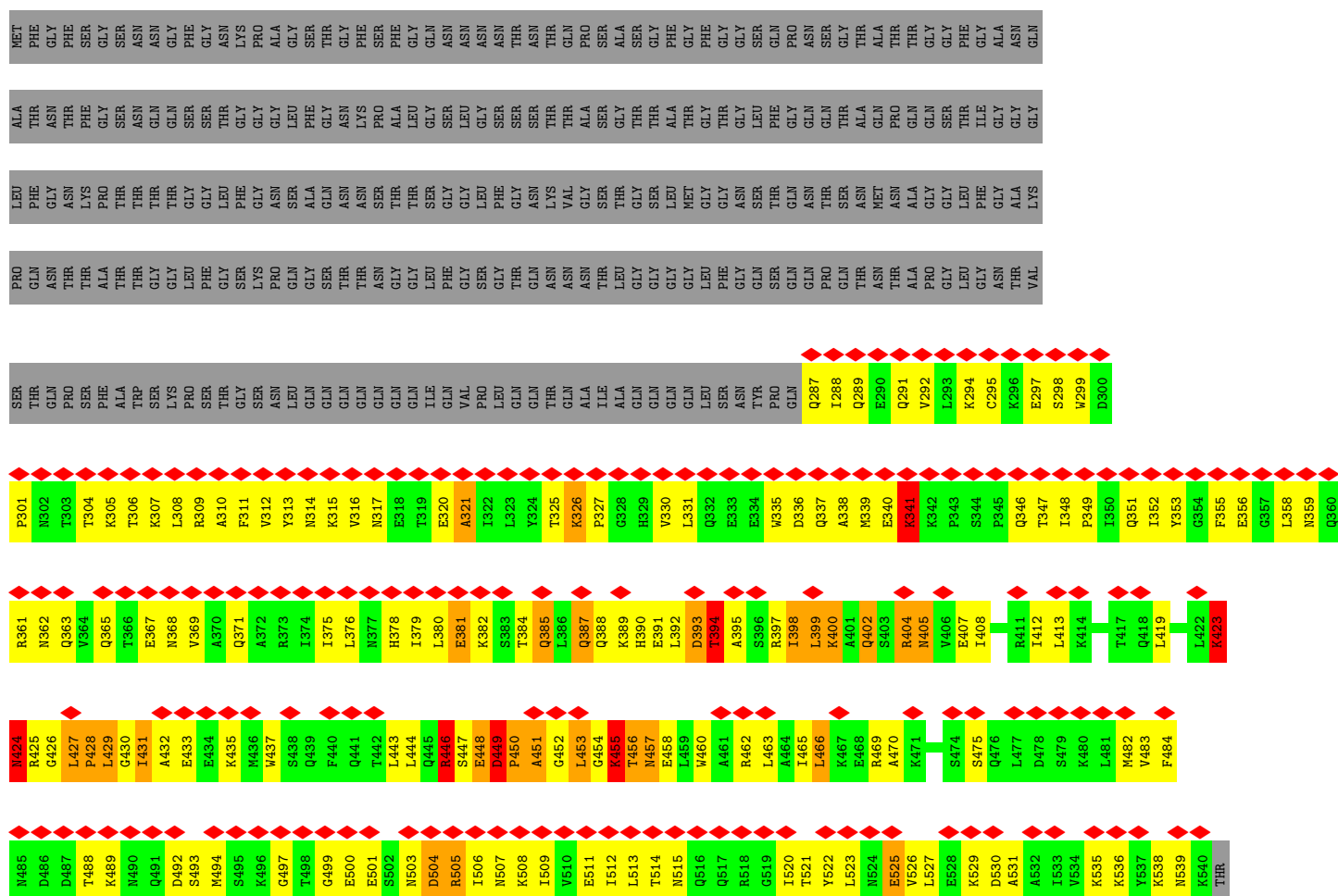
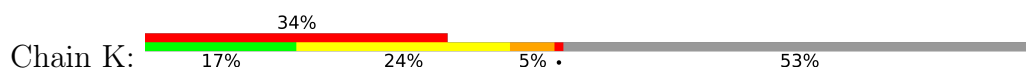


- Molecule 7: Nucleoporin NUP57





• Molecule 7: Nucleoporin NUP57



Chain I: 10% 12% 7% .. 77%





4 Experimental information

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.44	1/5813 (0.0%)	0.79	23/7867 (0.3%)
1	Z	0.57	0/5862	1.08	25/7942 (0.3%)
2	C	0.74	0/10658	1.19	11/14443 (0.1%)
3	D	0.48	0/11192	0.83	9/15173 (0.1%)
4	E	0.43	1/12583 (0.0%)	0.79	19/17054 (0.1%)
5	F	0.77	18/12435 (0.1%)	1.57	241/16887 (1.4%)
6	G	0.38	0/1553	0.83	6/2104 (0.3%)
6	J	0.68	0/1509	1.42	29/2042 (1.4%)
7	H	0.95	5/1832 (0.3%)	1.35	27/2482 (1.1%)
7	K	0.79	2/1829 (0.1%)	1.52	33/2485 (1.3%)
8	I	0.83	7/1431 (0.5%)	1.36	24/1940 (1.2%)
8	L	0.48	0/1378	1.02	5/1873 (0.3%)
All	All	0.62	34/68075 (0.0%)	1.13	452/92292 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	Z	0	1
5	F	0	3
6	G	0	1
7	H	0	1
7	K	0	2
All	All	0	8

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	H	427	LEU	C-N	23.13	1.53	1.33
5	F	1235	ASN	C-N	14.77	1.53	1.33
7	K	326	LYS	C-N	13.71	1.50	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	H	425	ARG	C-N	10.73	1.49	1.33
5	F	1312	ILE	C-O	-9.57	1.14	1.24
5	F	1182	ASN	C-O	8.84	1.35	1.24
5	F	750	TRP	C-N	8.40	1.53	1.33
8	I	737	ASN	N-CA	7.48	1.55	1.46
5	F	1310	VAL	C-O	-7.12	1.14	1.24
5	F	1394	SER	C-N	7.05	1.50	1.33
8	I	737	ASN	CA-C	6.94	1.61	1.52
5	F	409	MET	C-N	6.89	1.50	1.33
7	K	450	PRO	C-O	-6.83	1.15	1.24
5	F	1183	TYR	C-O	6.82	1.32	1.24
5	F	1359	PHE	C-O	-6.75	1.16	1.24
5	F	889	ILE	C-O	-6.53	1.16	1.24
5	F	1313	ILE	C-O	-6.38	1.16	1.24
8	I	737	ASN	C-N	6.31	1.42	1.33
5	F	1154	ARG	C-O	-6.27	1.16	1.24
5	F	356	ILE	C-N	6.14	1.48	1.33
5	F	1314	VAL	CA-C	5.97	1.60	1.52
5	F	1314	VAL	N-CA	5.94	1.53	1.46
7	H	506	ILE	N-CA	5.72	1.53	1.46
8	I	736	ASN	C-N	5.67	1.40	1.33
4	E	1260	TYR	C-O	-5.58	1.16	1.24
7	H	507	ASN	N-CA	5.50	1.53	1.46
5	F	1161	LEU	C-O	-5.48	1.17	1.24
5	F	1164	PHE	C-O	-5.36	1.18	1.24
5	F	1309	LEU	C-O	-5.31	1.17	1.24
8	I	736	ASN	CA-C	5.29	1.59	1.52
1	A	113	ILE	C-O	-5.14	1.17	1.24
8	I	735	ASN	N-CA	5.11	1.52	1.45
7	H	508	LYS	N-CA	5.10	1.52	1.46
8	I	736	ASN	N-CA	5.00	1.52	1.46

All (452) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	1090	PRO	CA-N-CD	-38.16	58.58	112.00
5	F	356	ILE	CA-C-N	19.99	144.83	119.84
5	F	356	ILE	C-N-CA	19.99	144.83	119.84
7	K	326	LYS	CA-C-N	17.29	136.80	120.21
7	K	326	LYS	C-N-CA	17.29	136.80	120.21
5	F	1394	SER	CA-C-N	15.24	138.89	119.84
5	F	1394	SER	C-N-CA	15.24	138.89	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	H	425	ARG	CA-C-N	-13.89	94.18	121.41
7	H	425	ARG	C-N-CA	-13.89	94.18	121.41
5	F	409	MET	CA-C-N	13.68	136.94	119.84
5	F	409	MET	C-N-CA	13.68	136.94	119.84
5	F	644	LYS	CA-C-N	12.77	140.09	122.34
5	F	644	LYS	C-N-CA	12.77	140.09	122.34
6	J	388	CYS	CB-CA-C	-12.76	85.22	109.72
6	J	370	ASP	CA-CB-CG	12.48	125.08	112.60
5	F	1036	PRO	N-CA-CB	12.45	116.32	103.25
5	F	1035	GLY	CA-C-N	11.92	134.74	119.84
5	F	1035	GLY	C-N-CA	11.92	134.74	119.84
5	F	837	TYR	CB-CA-C	11.59	129.22	110.90
5	F	1068	ILE	N-CA-C	-11.55	88.97	106.42
5	F	1234	GLY	O-C-N	11.44	133.63	122.77
5	F	823	PRO	N-CA-C	11.27	135.68	112.47
6	G	424	SER	N-CA-C	-10.77	99.51	111.14
7	K	423	LYS	CA-C-N	10.65	137.20	122.19
7	K	423	LYS	C-N-CA	10.65	137.20	122.19
5	F	833	THR	CA-C-N	10.60	135.79	120.95
5	F	833	THR	C-N-CA	10.60	135.79	120.95
5	F	803	ALA	CA-C-N	-10.53	108.08	122.30
5	F	803	ALA	C-N-CA	-10.53	108.08	122.30
7	K	451	ALA	N-CA-C	10.42	125.30	112.59
1	Z	772	PRO	CA-N-CD	-10.40	97.44	112.00
7	K	450	PRO	N-CA-C	10.22	133.53	112.47
1	A	113	ILE	CA-C-O	-10.07	109.93	120.71
7	H	476	GLN	CB-CA-C	10.06	126.88	111.18
5	F	837	TYR	CA-C-O	-10.02	110.38	120.70
5	F	1067	ASN	CB-CA-C	-9.94	90.65	110.42
5	F	750	TRP	O-C-N	-9.86	109.98	121.32
8	I	800	HIS	CB-CA-C	9.82	130.51	109.99
5	F	1391	GLY	CA-C-N	9.81	139.62	121.97
5	F	1391	GLY	C-N-CA	9.81	139.62	121.97
5	F	1164	PHE	CB-CA-C	-9.51	96.31	110.96
5	F	711	GLN	CB-CA-C	9.36	127.89	110.11
5	F	1235	ASN	CA-C-O	-9.31	101.90	119.32
5	F	935	GLN	CA-C-O	-9.30	107.20	120.51
8	I	734	ALA	N-CA-C	9.22	124.12	111.39
5	F	1225	GLN	CA-C-N	-9.18	111.56	122.95
5	F	1225	GLN	C-N-CA	-9.18	111.56	122.95
5	F	1090	PRO	CA-C-N	-9.10	103.83	121.58
5	F	1090	PRO	C-N-CA	-9.10	103.83	121.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	I	737	ASN	N-CA-C	9.09	121.95	108.14
5	F	1089	ASN	CB-CA-C	9.02	127.94	110.17
6	J	369	LEU	N-CA-C	-8.95	101.47	111.14
1	Z	750	GLU	CA-C-N	8.94	138.62	121.54
1	Z	750	GLU	C-N-CA	8.94	138.62	121.54
7	H	415	LEU	N-CA-C	-8.94	101.50	111.07
5	F	1090	PRO	N-CA-CB	8.85	112.54	103.25
6	J	335	SER	CA-C-N	8.81	137.07	122.54
6	J	335	SER	C-N-CA	8.81	137.07	122.54
1	Z	91	GLN	CB-CA-C	-8.77	92.97	110.42
7	H	476	GLN	N-CA-CB	-8.69	98.94	111.54
5	F	1373	ASP	N-CA-C	-8.66	101.17	112.68
7	K	450	PRO	CB-CA-C	-8.65	97.28	111.56
5	F	1156	TYR	CA-C-O	-8.62	111.82	120.70
5	F	1158	THR	CB-CA-C	8.54	127.03	110.46
5	F	888	PRO	N-CA-C	8.49	129.96	112.47
2	C	693	LEU	CA-C-N	8.49	137.75	121.54
2	C	693	LEU	C-N-CA	8.49	137.75	121.54
5	F	921	PRO	CA-N-CD	-8.47	100.14	112.00
5	F	1088	ARG	O-C-N	8.47	131.83	121.84
4	E	773	LEU	N-CA-C	-8.36	104.22	114.75
1	A	248	THR	CB-CA-C	8.30	119.87	109.16
7	K	452	GLY	CA-C-N	8.23	135.13	122.29
7	K	452	GLY	C-N-CA	8.23	135.13	122.29
6	J	402	ASP	CB-CA-C	-8.18	98.04	110.88
5	F	1222	ASN	CA-C-N	8.18	137.16	121.54
5	F	1222	ASN	C-N-CA	8.18	137.16	121.54
6	G	423	SER	CA-C-N	-8.12	109.39	120.44
6	G	423	SER	C-N-CA	-8.12	109.39	120.44
6	G	422	GLY	O-C-N	-8.12	115.92	123.96
7	K	428	PRO	CA-C-N	8.11	132.74	120.82
7	K	428	PRO	C-N-CA	8.11	132.74	120.82
7	H	475	SER	O-C-N	8.11	132.24	122.27
5	F	812	CYS	CA-C-N	8.06	134.77	121.39
5	F	812	CYS	C-N-CA	8.06	134.77	121.39
5	F	921	PRO	N-CA-CB	-8.06	94.79	103.25
8	I	731	GLY	CA-C-N	8.05	136.92	121.54
8	I	731	GLY	C-N-CA	8.05	136.92	121.54
6	J	335	SER	O-C-N	8.01	135.23	122.41
7	K	341	LYS	N-CA-C	-8.01	93.74	110.80
5	F	1444	ASP	CA-C-N	-8.01	114.12	121.65
5	F	1444	ASP	C-N-CA	-8.01	114.12	121.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	1273	LYS	N-CA-C	-7.96	103.52	113.55
5	F	925	HIS	CA-C-N	7.95	136.72	121.54
5	F	925	HIS	C-N-CA	7.95	136.72	121.54
7	H	520	ILE	CA-C-N	7.94	130.92	120.28
7	H	520	ILE	C-N-CA	7.94	130.92	120.28
8	L	779	THR	CA-C-N	7.93	136.68	121.54
8	L	779	THR	C-N-CA	7.93	136.68	121.54
5	F	1314	VAL	N-CA-C	7.93	125.83	109.34
5	F	935	GLN	N-CA-CB	7.84	123.75	110.49
4	E	212	TRP	O-C-N	7.83	131.08	122.15
1	A	88	LYS	N-CA-C	-7.79	102.87	111.36
4	E	258	ILE	CA-C-O	-7.77	111.71	120.96
7	K	456	THR	N-CA-C	7.76	121.52	109.96
5	F	827	ILE	O-C-N	7.74	130.32	121.96
7	K	431	ILE	CA-C-N	-7.66	108.48	120.88
7	K	431	ILE	C-N-CA	-7.66	108.48	120.88
4	E	759	ASN	CB-CA-C	7.63	125.06	110.27
1	A	43	GLN	CA-C-N	-7.60	108.29	121.97
1	A	43	GLN	C-N-CA	-7.60	108.29	121.97
1	Z	54	PHE	CB-CA-C	-7.59	98.96	110.88
7	H	423	LYS	CA-C-O	-7.58	114.92	119.55
5	F	712	LEU	N-CA-C	-7.56	101.49	111.24
1	A	114	ARG	N-CA-CB	7.55	120.96	110.01
5	F	1140	GLU	N-CA-C	-7.54	102.06	111.11
7	K	489	LYS	N-CA-C	-7.51	104.24	113.41
5	F	917	PHE	N-CA-C	-7.50	102.78	112.23
8	L	793	LEU	N-CA-C	-7.47	99.90	108.49
5	F	1225	GLN	N-CA-C	-7.46	103.48	112.59
7	K	424	ASN	CB-CA-C	7.45	122.31	111.73
4	E	213	PHE	CB-CA-C	7.44	123.19	110.84
5	F	889	ILE	CA-C-O	-7.41	111.52	120.78
5	F	366	ILE	CA-C-N	7.39	135.65	121.54
5	F	366	ILE	C-N-CA	7.39	135.65	121.54
7	H	425	ARG	CA-C-O	-7.37	107.93	122.23
5	F	1090	PRO	CA-CB-CG	-7.35	90.54	104.50
7	K	320	GLU	CA-C-N	7.34	135.56	121.54
7	K	320	GLU	C-N-CA	7.34	135.56	121.54
8	I	736	ASN	CB-CA-C	7.34	125.02	110.42
1	A	137	ASP	CA-CB-CG	7.32	119.92	112.60
5	F	1188	THR	CA-C-N	7.30	135.49	121.54
5	F	1188	THR	C-N-CA	7.30	135.49	121.54
8	I	736	ASN	CA-CB-CG	7.26	119.86	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	899	PHE	CA-C-N	-7.25	115.63	122.37
5	F	899	PHE	C-N-CA	-7.25	115.63	122.37
5	F	827	ILE	CA-C-N	7.24	135.01	122.56
5	F	827	ILE	C-N-CA	7.24	135.01	122.56
8	I	753	GLU	CB-CA-C	-7.18	99.91	110.96
5	F	1128	ASP	CA-CB-CG	7.17	119.77	112.60
7	H	426	GLY	O-C-N	7.17	132.02	122.70
5	F	1378	ASP	CA-C-N	7.16	135.45	121.41
5	F	1378	ASP	C-N-CA	7.16	135.45	121.41
5	F	903	ASN	CA-C-N	7.16	135.22	121.54
5	F	903	ASN	C-N-CA	7.16	135.22	121.54
5	F	1182	ASN	CB-CA-C	-7.12	97.69	110.37
5	F	1061	ASN	CB-CA-C	7.08	122.82	112.05
1	Z	53	VAL	CA-C-O	-7.07	113.60	120.95
5	F	1286	PHE	CB-CA-C	7.05	124.72	109.99
5	F	1180	TYR	CB-CA-C	-7.04	101.51	111.65
6	J	367	ASN	O-C-N	7.03	129.68	122.09
5	F	498	THR	N-CA-C	-6.99	102.49	111.02
7	K	381	GLU	N-CA-C	-6.99	103.67	111.28
5	F	1484	ARG	N-CA-C	-6.98	104.79	113.38
1	Z	827	GLU	N-CA-C	-6.97	103.61	111.07
5	F	887	PHE	CA-C-N	6.95	128.52	119.84
5	F	887	PHE	C-N-CA	6.95	128.52	119.84
5	F	1208	GLU	N-CA-C	-6.91	96.93	109.44
3	D	994	SER	N-CA-C	-6.90	104.45	112.86
1	Z	768	VAL	CA-C-N	-6.88	111.49	120.44
1	Z	768	VAL	C-N-CA	-6.88	111.49	120.44
8	I	737	ASN	CA-C-O	-6.88	113.92	121.28
7	K	465	ILE	N-CA-C	-6.88	105.37	113.42
1	Z	149	ALA	N-CA-C	-6.86	105.04	113.41
5	F	1055	VAL	N-CA-C	-6.86	105.39	113.42
5	F	920	ILE	CA-C-N	6.85	128.40	119.84
5	F	920	ILE	C-N-CA	6.85	128.40	119.84
7	H	506	ILE	CA-C-N	6.84	134.60	121.54
7	H	506	ILE	C-N-CA	6.84	134.60	121.54
7	K	394	THR	CB-CA-C	6.83	117.97	109.16
5	F	644	LYS	O-C-N	6.82	132.09	122.41
4	E	699	GLU	N-CA-C	-6.75	105.33	113.97
5	F	824	ALA	CA-C-O	-6.74	110.87	120.51
5	F	880	GLU	CB-CA-C	-6.72	100.28	110.90
5	F	1035	GLY	O-C-N	6.70	128.47	121.77
8	I	784	ILE	N-CA-C	-6.67	107.37	113.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	1086	LEU	N-CA-C	-6.65	101.39	111.56
6	J	406	PHE	CA-C-O	-6.63	114.04	121.00
6	J	429	LEU	CA-C-N	-6.63	111.38	121.26
6	J	429	LEU	C-N-CA	-6.63	111.38	121.26
5	F	1348	THR	CB-CA-C	6.61	121.38	110.81
7	H	510	VAL	N-CA-C	-6.58	105.72	113.42
6	J	378	HIS	CA-CB-CG	-6.56	107.24	113.80
5	F	1372	THR	CA-CB-OG1	6.55	119.43	109.60
5	F	1378	ASP	CB-CA-C	6.55	123.46	110.42
1	A	43	GLN	O-C-N	-6.51	113.93	122.59
5	F	837	TYR	N-CA-C	-6.51	104.11	111.14
7	K	449	ASP	CA-C-N	6.49	127.95	119.84
7	K	449	ASP	C-N-CA	6.49	127.95	119.84
5	F	900	LEU	N-CA-C	6.47	118.08	108.76
5	F	1379	GLY	CA-C-N	6.47	133.90	121.54
5	F	1379	GLY	C-N-CA	6.47	133.90	121.54
8	I	800	HIS	CA-CB-CG	-6.46	107.34	113.80
5	F	1377	VAL	N-CA-C	-6.45	106.17	111.91
6	G	422	GLY	CA-C-N	-6.44	116.24	123.13
6	G	422	GLY	C-N-CA	-6.44	116.24	123.13
5	F	1134	LYS	N-CA-CB	6.43	121.36	110.49
8	I	736	ASN	CA-C-O	-6.43	111.31	120.51
5	F	1543	LEU	N-CA-C	-6.41	103.79	112.26
7	K	466	LEU	N-CA-CB	-6.37	100.70	110.07
5	F	1405	PHE	CA-C-N	-6.36	109.18	121.58
5	F	1405	PHE	C-N-CA	-6.36	109.18	121.58
3	D	1128	GLN	N-CA-CB	6.36	121.23	110.49
5	F	411	ASN	CA-C-N	6.34	133.64	121.54
5	F	411	ASN	C-N-CA	6.34	133.64	121.54
5	F	1156	TYR	O-C-N	6.34	128.93	122.09
1	Z	815	ILE	N-CA-C	-6.33	104.33	110.72
7	K	431	ILE	CA-C-O	-6.31	112.90	120.78
5	F	590	ILE	CA-C-N	6.31	133.59	121.54
5	F	590	ILE	C-N-CA	6.31	133.59	121.54
1	Z	113	ILE	CA-C-O	-6.30	114.40	120.95
1	A	54	PHE	CB-CA-C	-6.26	99.25	110.70
5	F	1406	TYR	CA-CB-CG	6.24	125.13	113.90
6	J	380	TYR	CB-CA-C	6.19	121.19	110.72
4	E	979	ASN	CB-CA-C	-6.19	100.57	110.84
5	F	1142	GLU	CA-C-N	6.18	131.54	122.08
5	F	1142	GLU	C-N-CA	6.18	131.54	122.08
5	F	1034	LEU	N-CA-CB	-6.18	101.68	110.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	86	PHE	CA-C-N	-6.17	112.63	121.52
1	A	86	PHE	C-N-CA	-6.17	112.63	121.52
5	F	1359	PHE	CA-CB-CG	-6.16	107.64	113.80
5	F	1033	SER	CA-C-O	-6.15	114.81	121.20
5	F	1160	TYR	CA-C-O	-6.14	112.91	119.97
5	F	750	TRP	CA-C-O	-6.13	111.76	120.16
6	J	336	PHE	N-CA-C	-6.11	105.47	113.17
1	Z	832	LEU	N-CA-C	-6.10	104.71	111.36
5	F	793	TYR	CA-CB-CG	6.07	124.83	113.90
1	Z	751	LEU	N-CA-CB	-6.07	100.24	110.49
7	H	427	LEU	CA-C-O	-6.05	111.87	120.16
4	E	212	TRP	CA-C-N	6.04	130.80	121.19
4	E	212	TRP	C-N-CA	6.04	130.80	121.19
5	F	826	PRO	CB-CA-C	-6.04	102.31	111.44
8	I	798	ASN	CA-C-N	6.03	133.06	121.54
8	I	798	ASN	C-N-CA	6.03	133.06	121.54
3	D	1130	GLN	CA-C-N	6.03	129.49	120.69
3	D	1130	GLN	C-N-CA	6.03	129.49	120.69
8	L	780	THR	CB-CA-C	6.03	122.41	110.42
5	F	344	ILE	CA-C-N	6.02	136.79	126.32
5	F	344	ILE	C-N-CA	6.02	136.79	126.32
5	F	1089	ASN	C-N-CD	6.02	149.68	125.00
6	J	387	TYR	N-CA-C	-6.02	104.84	111.82
7	H	520	ILE	CA-C-O	-6.02	114.79	121.17
5	F	1382	TYR	CA-C-O	-6.00	114.58	120.89
5	F	722	ARG	CA-C-N	6.00	130.91	122.08
5	F	722	ARG	C-N-CA	6.00	130.91	122.08
6	J	372	PHE	CA-CB-CG	-5.99	107.81	113.80
4	E	1379	GLU	CA-C-N	5.98	128.61	120.54
4	E	1379	GLU	C-N-CA	5.98	128.61	120.54
5	F	639	LEU	CB-CA-C	5.97	121.67	109.55
7	H	317	ASN	CB-CA-C	5.97	117.14	109.80
3	D	1127	THR	CA-C-N	5.95	132.91	121.54
3	D	1127	THR	C-N-CA	5.95	132.91	121.54
1	A	55	GLN	CB-CA-C	5.94	122.41	109.99
1	Z	750	GLU	N-CA-C	-5.93	104.95	111.82
7	H	504	ASP	CA-C-O	-5.90	116.18	121.67
5	F	1067	ASN	CA-C-N	5.89	128.56	122.96
5	F	1067	ASN	C-N-CA	5.89	128.56	122.96
5	F	921	PRO	CB-CA-C	5.85	121.22	111.56
8	I	797	LEU	N-CA-CB	5.85	118.72	110.12
5	F	336	LYS	CA-C-N	5.85	132.71	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	336	LYS	C-N-CA	5.85	132.71	121.54
5	F	1090	PRO	O-C-N	5.84	130.53	122.64
5	F	1165	ILE	CA-C-O	-5.84	114.88	120.95
5	F	649	LEU	N-CA-C	5.83	117.30	110.41
4	E	1380	ASP	CA-C-O	-5.83	114.66	120.90
5	F	1160	TYR	N-CA-CB	5.83	119.31	110.28
5	F	1090	PRO	N-CD-CG	5.82	111.93	103.20
5	F	1134	LYS	CA-C-N	-5.82	110.42	121.54
5	F	1134	LYS	C-N-CA	-5.82	110.42	121.54
5	F	750	TRP	CA-CB-CG	5.82	124.65	113.60
5	F	1138	PHE	CA-C-N	5.82	132.44	121.97
5	F	1138	PHE	C-N-CA	5.82	132.44	121.97
7	K	463	LEU	N-CA-CB	-5.80	102.00	110.47
5	F	968	ILE	N-CA-C	-5.79	106.85	112.29
5	F	1068	ILE	CA-C-N	5.78	131.23	120.95
5	F	1068	ILE	C-N-CA	5.78	131.23	120.95
5	F	817	ASN	CA-CB-CG	5.77	118.37	112.60
5	F	935	GLN	O-C-N	5.76	130.25	122.59
1	A	532	ILE	N-CA-C	-5.74	106.80	111.91
8	I	795	LYS	N-CA-C	-5.74	104.93	111.07
5	F	1146	ALA	CA-C-N	-5.74	111.59	120.31
5	F	1146	ALA	C-N-CA	-5.74	111.59	120.31
7	K	446	ARG	CG-CD-NE	-5.73	99.40	112.00
1	Z	45	SER	N-CA-C	-5.72	105.05	111.28
7	H	423	LYS	O-C-N	5.71	125.85	120.71
8	I	796	ILE	N-CA-CB	5.70	118.30	110.54
5	F	1306	TRP	CA-C-N	5.70	132.23	121.97
5	F	1306	TRP	C-N-CA	5.70	132.23	121.97
5	F	1376	THR	CA-CB-OG1	-5.70	101.05	109.60
5	F	34	ASN	CA-C-N	5.70	132.43	121.54
5	F	34	ASN	C-N-CA	5.70	132.43	121.54
5	F	1209	PRO	CA-C-N	5.70	132.42	121.54
5	F	1209	PRO	C-N-CA	5.70	132.42	121.54
5	F	1209	PRO	O-C-N	5.70	128.61	122.17
7	K	394	THR	N-CA-C	-5.69	107.58	114.75
1	A	113	ILE	N-CA-C	5.69	117.20	111.00
5	F	833	THR	O-C-N	5.69	132.05	122.21
5	F	1150	PHE	CA-C-N	-5.69	111.67	120.31
5	F	1150	PHE	C-N-CA	-5.69	111.67	120.31
5	F	1061	ASN	CA-C-O	-5.66	115.73	122.13
5	F	1200	PRO	CA-C-N	-5.66	114.74	123.17
5	F	1200	PRO	C-N-CA	-5.66	114.74	123.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	H	530	ASP	CA-C-N	5.66	128.32	120.29
7	H	530	ASP	C-N-CA	5.66	128.32	120.29
5	F	837	TYR	CA-C-N	-5.65	110.49	120.99
5	F	837	TYR	C-N-CA	-5.65	110.49	120.99
5	F	903	ASN	CB-CA-C	5.64	119.52	109.65
6	J	368	ASP	N-CA-C	-5.62	106.13	112.87
6	J	406	PHE	CA-C-N	-5.61	111.09	120.74
6	J	406	PHE	C-N-CA	-5.61	111.09	120.74
8	I	795	LYS	CA-C-O	-5.61	114.93	120.82
6	J	373	PHE	N-CA-CB	5.61	119.70	110.39
1	Z	749	ASP	CA-C-N	5.61	128.84	120.31
1	Z	749	ASP	C-N-CA	5.61	128.84	120.31
6	J	339	LEU	CA-C-N	5.60	129.49	120.30
6	J	339	LEU	C-N-CA	5.60	129.49	120.30
5	F	1040	THR	CB-CA-C	5.60	119.76	109.46
8	I	819	ASN	O-C-N	5.60	129.15	122.27
5	F	1506	ILE	CG1-CB-CG2	-5.59	93.92	110.70
5	F	1348	THR	CA-CB-OG1	-5.59	101.22	109.60
4	E	258	ILE	N-CA-CB	5.58	118.55	110.52
1	A	114	ARG	N-CA-C	-5.57	105.11	111.07
8	I	796	ILE	CA-C-O	-5.57	115.15	120.95
5	F	1166	HIS	CB-CA-C	5.57	120.32	110.85
5	F	1068	ILE	CA-C-O	-5.54	115.21	121.09
2	C	1255	SER	N-CA-C	5.54	122.59	110.80
6	J	389	ARG	CB-CA-C	5.53	119.98	110.79
1	A	44	VAL	N-CA-C	5.52	120.81	109.34
5	F	925	HIS	O-C-N	5.49	129.76	122.95
1	Z	770	ASN	CB-CA-C	5.48	119.89	110.79
5	F	1040	THR	CA-C-O	-5.48	115.17	121.47
5	F	355	LEU	N-CA-C	-5.47	106.68	113.19
8	I	733	ALA	CA-C-N	5.47	130.13	122.36
8	I	733	ALA	C-N-CA	5.47	130.13	122.36
5	F	1386	LYS	CA-C-N	5.47	131.98	121.54
5	F	1386	LYS	C-N-CA	5.47	131.98	121.54
6	J	394	ILE	CA-C-O	-5.46	115.07	120.85
4	E	1380	ASP	O-C-N	5.43	127.74	122.09
3	D	995	PHE	CB-CA-C	5.43	119.15	109.38
4	E	1384	ASP	CB-CA-C	5.43	121.45	110.38
3	D	528	PRO	CA-N-CD	-5.42	104.41	112.00
5	F	884	GLU	CA-C-N	5.42	131.89	121.54
5	F	884	GLU	C-N-CA	5.42	131.89	121.54
2	C	1221	ARG	NE-CZ-NH2	5.40	124.06	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	258	ILE	O-C-N	5.39	128.91	121.90
5	F	410	PRO	CA-C-N	-5.38	112.40	122.73
5	F	410	PRO	C-N-CA	-5.38	112.40	122.73
5	F	1543	LEU	CA-C-N	-5.38	112.49	122.60
5	F	1543	LEU	C-N-CA	-5.38	112.49	122.60
5	F	1359	PHE	CA-C-O	-5.37	114.86	120.55
6	J	379	LEU	CA-C-N	-5.36	114.24	122.60
6	J	379	LEU	C-N-CA	-5.36	114.24	122.60
1	A	825	PRO	CA-C-N	-5.36	112.17	120.31
1	A	825	PRO	C-N-CA	-5.36	112.17	120.31
5	F	1285	HIS	CA-C-O	-5.35	113.47	119.79
5	F	1182	ASN	N-CA-C	5.35	119.44	113.02
5	F	1372	THR	N-CA-CB	5.34	119.52	110.49
5	F	1195	PHE	N-CA-C	5.34	122.18	110.80
5	F	1420	GLN	CA-C-N	5.34	131.58	121.97
5	F	1420	GLN	C-N-CA	5.34	131.58	121.97
7	H	427	LEU	O-C-N	-5.33	115.19	121.32
5	F	1367	ASP	CA-C-N	5.33	129.50	121.40
5	F	1367	ASP	C-N-CA	5.33	129.50	121.40
7	K	428	PRO	N-CA-C	-5.32	108.59	114.92
2	C	475	LEU	CA-C-N	5.32	131.69	121.54
2	C	475	LEU	C-N-CA	5.32	131.69	121.54
5	F	1118	ARG	N-CA-C	-5.32	102.22	109.71
1	Z	145	ASN	CB-CA-C	5.30	119.34	110.92
5	F	749	ILE	O-C-N	5.29	128.83	121.84
5	F	921	PRO	CA-C-N	5.29	131.65	121.54
5	F	921	PRO	C-N-CA	5.29	131.65	121.54
7	H	508	LYS	N-CA-C	5.29	116.24	107.73
5	F	1156	TYR	N-CA-CB	5.29	117.73	110.07
5	F	1174	LYS	CB-CA-C	5.28	119.72	110.64
5	F	712	LEU	CA-C-O	-5.27	115.26	120.80
1	Z	19	ASN	CB-CA-C	5.27	119.81	110.85
5	F	903	ASN	N-CA-C	-5.27	99.36	108.69
5	F	827	ILE	CA-C-O	-5.27	115.93	121.41
1	A	84	ASP	CB-CA-C	-5.27	102.61	110.88
5	F	1289	ILE	N-CA-CB	5.26	116.70	110.55
1	A	19	ASN	CB-CA-C	5.25	119.78	110.85
6	J	382	LYS	CB-CA-C	-5.23	102.10	110.79
4	E	51	LEU	CA-CB-CG	5.23	134.60	116.30
5	F	1377	VAL	CA-C-N	5.23	131.53	121.54
5	F	1377	VAL	C-N-CA	5.23	131.53	121.54
5	F	645	ILE	CA-C-O	-5.23	116.08	121.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	K	388	GLN	N-CA-C	-5.23	105.58	111.28
5	F	925	HIS	CA-C-O	-5.22	114.97	120.92
1	Z	115	THR	CB-CA-C	5.21	120.68	110.67
5	F	1061	ASN	CA-C-N	5.20	131.48	121.54
5	F	1061	ASN	C-N-CA	5.20	131.48	121.54
5	F	395	PRO	CA-C-N	5.20	131.60	121.41
5	F	395	PRO	C-N-CA	5.20	131.60	121.41
5	F	1380	ARG	N-CA-C	-5.20	99.73	110.80
5	F	888	PRO	N-CA-CB	-5.20	97.79	103.25
5	F	889	ILE	CA-C-N	-5.20	114.04	121.52
5	F	889	ILE	C-N-CA	-5.20	114.04	121.52
5	F	1353	LEU	CA-C-N	-5.19	111.78	120.30
5	F	1353	LEU	C-N-CA	-5.19	111.78	120.30
2	C	75	ASP	CA-CB-CG	5.19	117.79	112.60
2	C	914	GLN	OE1-CD-NE2	-5.19	117.41	122.60
5	F	378	ALA	CA-C-O	-5.19	114.65	122.38
5	F	1166	HIS	CA-CB-CG	5.18	118.98	113.80
5	F	1061	ASN	O-C-N	5.18	128.41	122.55
7	H	427	LEU	CA-C-N	5.18	126.11	120.83
7	H	427	LEU	C-N-CA	5.18	126.11	120.83
8	L	703	GLN	CA-C-O	-5.17	115.02	120.55
5	F	916	ILE	O-C-N	5.17	129.03	122.57
3	D	528	PRO	N-CA-CB	-5.16	97.83	103.25
4	E	975	GLN	CB-CA-C	-5.16	101.66	110.95
1	A	86	PHE	CB-CA-C	-5.16	102.78	110.88
7	K	497	GLY	N-CA-C	5.16	119.13	112.83
7	K	525	GLU	N-CA-C	-5.15	105.35	111.69
5	F	1354	VAL	CA-C-O	-5.15	114.91	120.47
5	F	750	TRP	CB-CA-C	5.15	120.31	110.17
5	F	824	ALA	O-C-N	5.15	129.43	122.59
8	I	802	ASP	CA-C-O	-5.14	114.97	120.42
5	F	865	LEU	CA-C-N	-5.14	112.14	121.14
5	F	865	LEU	C-N-CA	-5.14	112.14	121.14
1	A	23	ASN	N-CA-C	-5.12	105.78	111.36
5	F	1033	SER	N-CA-C	5.12	117.01	110.61
5	F	884	GLU	CB-CA-C	5.11	117.48	110.94
1	Z	23	ASN	N-CA-C	-5.11	105.79	111.36
7	H	522	TYR	N-CA-C	-5.11	105.71	111.28
1	Z	51	ARG	CB-CA-C	-5.11	102.86	110.88
1	A	54	PHE	N-CA-C	-5.09	105.43	111.69
5	F	1416	VAL	N-CA-C	-5.09	102.17	108.89
6	J	437	ALA	CA-C-N	5.08	131.24	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	437	ALA	C-N-CA	5.08	131.24	121.54
5	F	1364	TYR	CB-CA-C	5.07	119.62	111.91
5	F	678	LEU	CA-C-N	5.07	131.09	121.97
5	F	678	LEU	C-N-CA	5.07	131.09	121.97
2	C	1258	GLN	OE1-CD-NE2	-5.06	117.54	122.60
5	F	1307	VAL	CA-C-N	-5.06	113.03	122.09
5	F	1307	VAL	C-N-CA	-5.06	113.03	122.09
5	F	822	CYS	CA-C-N	5.06	126.17	119.84
5	F	822	CYS	C-N-CA	5.06	126.17	119.84
5	F	1276	ASP	N-CA-C	-5.06	105.95	111.82
5	F	1376	THR	N-CA-CB	5.06	119.67	111.27
5	F	957	ALA	CA-C-N	5.06	131.20	121.54
5	F	957	ALA	C-N-CA	5.06	131.20	121.54
7	H	535	LYS	CB-CA-C	5.05	120.36	110.67
5	F	1056	LEU	CA-CB-CG	5.04	133.94	116.30
5	F	1144	VAL	N-CA-C	-5.04	105.50	112.50
2	C	271	GLN	OE1-CD-NE2	-5.03	117.57	122.60
5	F	1133	GLU	CA-C-N	5.03	131.14	121.54
5	F	1133	GLU	C-N-CA	5.03	131.14	121.54
5	F	1164	PHE	CA-C-O	-5.03	115.72	121.00
8	I	727	SER	N-CA-C	-5.03	108.42	114.75
1	Z	818	GLY	N-CA-C	-5.02	106.33	113.86
4	E	1380	ASP	CB-CA-C	-5.02	102.78	110.81
2	C	787	ALA	N-CA-C	-5.01	105.34	111.75
5	F	1140	GLU	CB-CA-C	5.01	118.82	110.81

There are no chirality outliers.

All (8) planarity outliers are listed below:

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

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5723	0	5587	299	0
1	Z	5776	0	5607	427	0
2	C	10452	0	10392	49	0
3	D	10976	0	10827	413	0
4	E	12362	0	12566	355	0
5	F	12232	0	11559	848	0
6	G	1533	0	1515	120	0
6	J	1492	0	1465	280	0
7	H	1811	0	1697	148	0
7	K	1808	0	1614	313	0
8	I	1418	0	1293	171	0
8	L	1366	0	1211	166	0
All	All	66949	0	65333	3074	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 23.

All (3074) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:810:ALA:CB	1:Z:836:ASP:HA	1.26	1.59
3:D:955:PRO:CB	3:D:994:SER:CB	1.78	1.59
7:H:522:TYR:CB	1:Z:54:PHE:CB	1.82	1.56
5:F:841:PHE:CD2	5:F:918:PHE:HE1	1.21	1.55
5:F:1357:ALA:HB2	5:F:1381:LEU:CB	1.19	1.53
7:K:538:LYS:HA	8:L:822:LYS:CB	1.10	1.53
6:J:325:TYR:CE2	7:K:390:HIS:HA	1.44	1.52
5:F:376:ASN:CB	5:F:381:THR:CA	1.83	1.51
6:J:383:LYS:NZ	8:L:756:ASN:CA	1.73	1.50
1:Z:753:ALA:HB1	1:Z:815:ILE:C	1.35	1.47
7:H:420:ALA:HB1	8:I:745:TYR:CE1	1.49	1.46
1:A:772:PRO:CB	1:A:828:THR:HG21	1.47	1.44
7:H:418:GLN:NE2	8:I:718:THR:CG2	1.81	1.43
6:J:357:LEU:HB3	7:K:423:LYS:CE	1.46	1.43
7:K:483:VAL:O	7:K:492:ASP:CB	1.66	1.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:321:ALA:CA	7:K:348:ILE:HD11	1.50	1.42
1:Z:757:ALA:CB	1:Z:819:MET:O	1.68	1.41
6:G:404:ASP:CB	6:G:425:GLU:CB	1.97	1.40
8:I:818:ILE:O	8:I:821:ILE:CG2	1.68	1.40
6:J:383:LYS:HZ2	8:L:756:ASN:CG	1.28	1.39
6:J:383:LYS:HZ1	8:L:756:ASN:CA	1.28	1.39
5:F:1353:LEU:CB	5:F:1384:LEU:CB	2.01	1.39
7:K:389:LYS:HA	7:K:393:ASP:CB	1.49	1.39
1:Z:746:PRO:CB	1:Z:753:ALA:HA	1.52	1.39
5:F:1116:VAL:HG11	5:F:1150:PHE:CE2	1.58	1.38
7:K:389:LYS:CA	7:K:393:ASP:HB3	1.49	1.38
5:F:841:PHE:CD2	5:F:918:PHE:CE1	2.11	1.38
7:K:483:VAL:CB	7:K:493:SER:O	1.72	1.37
5:F:334:GLN:NE2	5:F:859:LYS:NZ	1.73	1.36
7:K:538:LYS:CA	8:L:822:LYS:CB	2.01	1.36
4:E:1022:TYR:CE2	4:E:1026:THR:HG21	1.60	1.36
5:F:228:PHE:H	5:F:361:LEU:CB	1.37	1.36
5:F:334:GLN:HE21	5:F:859:LYS:NZ	1.24	1.35
5:F:1227:THR:CB	7:H:475:SER:OG	1.74	1.35
1:Z:810:ALA:CB	1:Z:836:ASP:CA	2.02	1.35
1:A:128:LEU:HD22	4:E:1260:TYR:CE2	1.61	1.35
6:J:383:LYS:NZ	8:L:756:ASN:HA	1.03	1.34
5:F:376:ASN:CB	5:F:381:THR:HA	0.88	1.34
5:F:1357:ALA:CB	5:F:1381:LEU:CB	2.05	1.34
5:F:902:LYS:HE2	7:H:414:LYS:CD	1.58	1.33
6:G:331:LYS:HE2	1:Z:49:LEU:CD1	1.56	1.33
5:F:1633:TYR:CE2	5:F:1635:ARG:HB2	1.63	1.33
1:Z:753:ALA:CB	1:Z:815:ILE:C	2.02	1.32
1:Z:810:ALA:HB1	1:Z:836:ASP:CA	1.57	1.31
1:A:59:LYS:C	8:L:807:LEU:CB	2.03	1.30
7:H:418:GLN:HE21	8:I:718:THR:CG2	1.38	1.30
8:L:775:THR:O	8:L:779:THR:CB	1.78	1.29
5:F:902:LYS:CE	7:H:414:LYS:HD2	1.62	1.29
5:F:1116:VAL:HG11	5:F:1150:PHE:CZ	1.68	1.29
5:F:1084:LEU:HA	5:F:1156:TYR:OH	1.29	1.28
1:A:140:ILE:CG2	4:E:1393:LYS:HD3	1.62	1.28
5:F:334:GLN:HG3	5:F:854:GLU:OE2	1.24	1.28
6:J:357:LEU:CB	7:K:423:LYS:HE3	1.60	1.28
1:A:128:LEU:HD13	4:E:1260:TYR:CZ	1.67	1.28
6:J:333:ILE:O	6:J:336:PHE:CB	1.82	1.27
1:A:43:GLN:O	1:A:44:VAL:CB	1.68	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:675:LEU:O	5:F:679:ILE:HG12	1.13	1.27
7:K:321:ALA:N	7:K:348:ILE:HD11	1.47	1.27
3:D:242:MET:SD	3:D:298:TYR:CE2	2.28	1.27
1:A:128:LEU:HD22	4:E:1260:TYR:CD2	1.67	1.26
7:K:321:ALA:HA	7:K:348:ILE:CG1	1.65	1.25
6:J:405:LEU:O	6:J:409:PRO:CD	1.84	1.25
1:Z:810:ALA:HB3	1:Z:836:ASP:O	1.30	1.24
1:Z:251:ALA:O	1:Z:253:LEU:N	1.70	1.24
5:F:800:ILE:HG12	5:F:885:GLU:OE1	1.37	1.23
1:Z:746:PRO:CB	1:Z:816:TYR:CB	2.16	1.23
1:A:772:PRO:HB3	1:A:828:THR:CG2	1.68	1.22
6:G:431:GLN:HA	7:H:503:ASN:CB	1.67	1.22
1:Z:753:ALA:HB1	1:Z:816:TYR:N	1.54	1.22
6:G:327:LYS:NZ	1:Z:46:ILE:HB	1.54	1.21
7:H:418:GLN:NE2	8:I:718:THR:HG21	1.55	1.21
1:Z:757:ALA:HB2	1:Z:819:MET:C	1.64	1.21
5:F:1129:ASN:ND2	5:F:1132:GLU:HB3	1.56	1.21
6:J:383:LYS:NZ	8:L:756:ASN:CG	1.89	1.20
1:A:814:MET:HG3	1:A:833:ILE:CD1	1.71	1.19
5:F:800:ILE:CG1	5:F:885:GLU:OE1	1.90	1.19
1:Z:824:MET:HG2	1:Z:825:PRO:CD	1.70	1.19
3:D:1244:ASN:CB	1:Z:826:ARG:CB	2.21	1.19
6:J:364:ILE:HA	7:K:424:ASN:ND2	1.55	1.19
1:Z:241:ILE:HG22	1:Z:245:ALA:CB	1.72	1.19
1:Z:807:LYS:HA	1:Z:836:ASP:O	1.41	1.19
4:E:1022:TYR:CD2	4:E:1026:THR:HG21	1.76	1.19
4:E:1022:TYR:CE2	4:E:1026:THR:CG2	2.25	1.19
7:H:425:ARG:C	7:H:427:LEU:H	1.48	1.19
6:G:430:LEU:CB	8:I:780:THR:HA	1.74	1.17
8:I:773:SER:O	8:I:777:ASN:CB	1.90	1.17
7:H:418:GLN:NE2	8:I:718:THR:HG23	1.42	1.16
6:J:383:LYS:NZ	8:L:756:ASN:CB	2.07	1.16
4:E:1309:ARG:O	4:E:1313:ARG:HG3	1.45	1.16
8:I:810:ASN:OD1	1:Z:59:LYS:CB	1.94	1.16
1:Z:810:ALA:HB3	1:Z:836:ASP:C	1.69	1.16
6:J:383:LYS:HZ2	8:L:756:ASN:CB	1.60	1.15
5:F:354:ARG:HB2	5:F:356:ILE:HG22	1.29	1.15
5:F:1529:ALA:HB2	5:F:1611:VAL:HG13	1.22	1.15
1:Z:814:MET:CB	1:Z:833:ILE:HD13	1.76	1.15
5:F:690:GLU:CD	8:I:722:LEU:HD21	1.69	1.15
3:D:1238:ARG:HA	1:Z:830:SER:HB3	1.28	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:444:LEU:O	7:K:447:SER:CB	1.95	1.14
7:K:446:ARG:HH22	7:K:455:LYS:NZ	1.44	1.14
6:J:398:VAL:HG21	7:K:462:ARG:CA	1.78	1.14
6:J:432:LEU:CB	8:L:782:ILE:C	2.20	1.13
1:A:775:LEU:HB3	1:A:832:LEU:CD1	1.79	1.13
7:K:321:ALA:CA	7:K:348:ILE:CD1	2.27	1.12
5:F:675:LEU:O	5:F:679:ILE:CG1	1.96	1.12
7:K:336:ASP:O	7:K:340:GLU:HB2	1.48	1.11
1:Z:810:ALA:CA	1:Z:836:ASP:HA	1.80	1.11
5:F:734:LEU:CD2	5:F:817:ASN:OD1	1.98	1.11
5:F:1203:TYR:CB	5:F:1299:ASN:HD21	1.63	1.11
1:Z:824:MET:CG	1:Z:825:PRO:HD3	1.80	1.11
5:F:922:LEU:HD23	7:H:400:LYS:CE	1.81	1.11
5:F:334:GLN:NE2	5:F:859:LYS:HZ2	1.30	1.11
1:Z:746:PRO:CB	1:Z:753:ALA:CA	2.29	1.11
5:F:841:PHE:HD2	5:F:918:PHE:CE1	1.55	1.10
1:Z:753:ALA:CB	1:Z:816:TYR:N	2.11	1.10
3:D:1493:ASN:HA	5:F:1471:LYS:HD2	1.32	1.10
6:G:289:GLN:HE22	6:J:352:VAL:HG22	0.95	1.10
7:K:321:ALA:HA	7:K:348:ILE:CD1	1.80	1.10
5:F:800:ILE:CD1	5:F:885:GLU:OE1	1.98	1.10
5:F:1550:LEU:CD2	5:F:1552:PHE:CZ	2.34	1.10
6:G:289:GLN:NE2	6:J:352:VAL:HG22	1.67	1.10
6:J:380:TYR:HE2	8:L:751:LEU:HD21	1.09	1.10
5:F:334:GLN:CG	5:F:854:GLU:OE2	1.99	1.10
1:Z:753:ALA:HB1	1:Z:815:ILE:O	1.52	1.10
1:A:783:SER:HA	1:A:839:LEU:HA	1.26	1.09
6:J:432:LEU:CB	8:L:782:ILE:O	2.00	1.09
6:J:431:GLN:HA	7:K:500:GLU:H	1.10	1.09
6:G:327:LYS:HZ3	1:Z:46:ILE:HB	0.96	1.09
1:Z:757:ALA:HB1	1:Z:819:MET:O	1.40	1.08
6:J:405:LEU:O	6:J:409:PRO:HD3	0.93	1.08
1:Z:814:MET:CB	1:Z:833:ILE:CD1	2.32	1.08
5:F:922:LEU:HD23	7:H:400:LYS:NZ	1.68	1.08
5:F:1529:ALA:CB	5:F:1611:VAL:HG13	1.84	1.08
5:F:1550:LEU:CD1	5:F:1604:ILE:HD13	1.84	1.07
1:Z:824:MET:CB	1:Z:825:PRO:HD3	1.85	1.07
1:A:55:GLN:CB	7:K:521:THR:CB	2.32	1.07
5:F:690:GLU:CD	8:I:722:LEU:CD2	2.28	1.07
6:G:331:LYS:HE2	1:Z:49:LEU:HD11	1.29	1.07
7:H:426:GLY:HA2	8:I:736:ASN:N	1.69	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:482:MET:CB	8:L:784:ILE:HA	1.83	1.07
7:K:317:ASN:CB	7:K:346:GLN:HB3	1.83	1.07
5:F:837:TYR:HB2	5:F:918:PHE:CE2	1.90	1.07
1:A:814:MET:HG3	1:A:833:ILE:HD11	1.07	1.06
3:D:242:MET:SD	3:D:298:TYR:CD2	2.48	1.06
5:F:228:PHE:N	5:F:361:LEU:CB	2.18	1.06
7:H:420:ALA:CB	8:I:745:TYR:CE1	2.36	1.06
6:G:430:LEU:CB	8:I:780:THR:HG22	1.83	1.06
7:H:412:ILE:HG23	7:H:415:LEU:HD22	1.38	1.06
7:H:532:ALA:HB2	8:I:818:ILE:HD12	1.34	1.06
4:E:227:ILE:HD11	4:E:258:ILE:HD13	1.37	1.06
7:K:513:LEU:HD21	8:L:800:HIS:CE1	1.90	1.06
5:F:1034:LEU:HD22	5:F:1092:THR:HB	1.37	1.06
7:K:535:LYS:HA	8:L:818:ILE:CB	1.86	1.06
7:H:535:LYS:CB	8:I:821:ILE:HD11	1.86	1.06
7:H:412:ILE:HG23	7:H:415:LEU:CD2	1.86	1.05
1:A:772:PRO:CA	1:A:828:THR:HG21	1.86	1.05
1:A:128:LEU:HD13	4:E:1260:TYR:OH	1.53	1.05
6:J:398:VAL:HG21	7:K:462:ARG:CB	1.86	1.05
1:A:814:MET:CG	1:A:833:ILE:HD11	1.86	1.05
5:F:928:LEU:H	5:F:928:LEU:HD12	1.15	1.05
5:F:841:PHE:CE2	5:F:918:PHE:CE1	2.44	1.05
1:Z:241:ILE:HG22	1:Z:245:ALA:HB1	1.33	1.05
4:E:977:ALA:O	7:K:460:TRP:CB	2.04	1.04
5:F:1203:TYR:CB	5:F:1299:ASN:ND2	2.20	1.04
2:C:1258:GLN:HG2	2:C:1299:LYS:CE	1.86	1.04
1:Z:751:LEU:O	1:Z:753:ALA:N	1.89	1.03
1:A:53:VAL:HG21	8:L:799:SER:OG	1.57	1.03
4:E:1022:TYR:CD2	4:E:1026:THR:CG2	2.40	1.03
6:J:325:TYR:CE2	7:K:390:HIS:CA	2.41	1.03
1:A:140:ILE:HG22	4:E:1393:LYS:NZ	1.73	1.03
2:C:318:ILE:H	2:C:318:ILE:HD12	1.17	1.03
5:F:350:ARG:O	5:F:393:SER:CB	2.06	1.03
4:E:1319:LEU:HD21	4:E:1398:VAL:CG2	1.88	1.02
5:F:159:LYS:HE3	5:F:363:ASP:HA	1.39	1.02
4:E:1394:LYS:O	4:E:1398:VAL:HG23	1.58	1.02
1:Z:753:ALA:HB1	1:Z:816:TYR:CA	1.90	1.02
1:Z:810:ALA:HB3	1:Z:836:ASP:CA	1.86	1.02
5:F:1116:VAL:CG1	5:F:1150:PHE:CE2	2.42	1.02
8:I:739:GLN:O	8:I:741:ARG:N	1.91	1.02
6:J:383:LYS:NZ	8:L:756:ASN:OD1	1.87	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:116:LYS:HB3	1:Z:116:LYS:HZ3	1.19	1.02
1:A:27:GLU:OE2	1:A:30:ASP:HB3	1.58	1.02
1:Z:817:ALA:O	1:Z:821:GLN:N	1.91	1.02
1:A:59:LYS:CB	8:L:807:LEU:CB	2.38	1.01
1:A:814:MET:CG	1:A:833:ILE:CD1	2.37	1.01
5:F:920:ILE:HG21	5:F:924:ALA:O	1.59	1.01
6:G:331:LYS:CE	1:Z:49:LEU:HD11	1.91	1.01
1:Z:27:GLU:OE2	1:Z:30:ASP:HB3	1.58	1.01
1:Z:811:ARG:N	1:Z:836:ASP:CB	2.24	1.01
1:A:140:ILE:HG21	4:E:1393:LYS:HD3	1.05	1.01
7:K:482:MET:CB	8:L:784:ILE:CA	2.38	1.01
3:D:242:MET:SD	3:D:298:TYR:HE2	1.78	1.01
3:D:401:ILE:HG21	3:D:462:LEU:HB3	1.43	1.01
8:I:798:ASN:O	8:I:801:PHE:N	1.92	1.01
5:F:1129:ASN:HD21	5:F:1132:GLU:CB	1.73	1.00
5:F:1550:LEU:CD2	5:F:1552:PHE:CE2	2.44	1.00
4:E:210:ASN:HA	4:E:213:PHE:CB	1.90	1.00
5:F:228:PHE:CD1	5:F:360:LEU:O	2.15	1.00
5:F:909:LEU:CB	7:H:404:ARG:HA	1.91	1.00
7:K:321:ALA:HA	7:K:348:ILE:HG12	1.43	1.00
1:Z:824:MET:HG2	1:Z:825:PRO:HD2	1.36	1.00
4:E:1022:TYR:O	4:E:1026:THR:HG23	1.59	1.00
6:G:431:GLN:CA	7:H:503:ASN:CB	2.39	1.00
3:D:938:LEU:HB2	3:D:940:VAL:HG22	1.41	1.00
5:F:887:PHE:N	5:F:888:PRO:HD2	1.77	1.00
1:Z:810:ALA:C	1:Z:836:ASP:CB	2.35	1.00
5:F:1167:LYS:HA	5:F:1167:LYS:HE3	1.44	0.99
1:A:140:ILE:HG21	4:E:1393:LYS:CD	1.91	0.99
1:Z:810:ALA:HB1	1:Z:836:ASP:HA	1.01	0.99
5:F:228:PHE:CE1	5:F:360:LEU:O	2.15	0.99
5:F:1529:ALA:HB2	5:F:1611:VAL:CG1	1.92	0.99
5:F:1550:LEU:HD22	5:F:1552:PHE:CE2	1.97	0.99
6:G:289:GLN:HE22	6:J:352:VAL:CG2	1.76	0.99
7:H:420:ALA:HB1	8:I:745:TYR:CZ	1.98	0.99
6:J:380:TYR:CE2	8:L:751:LEU:HD21	1.98	0.99
6:G:331:LYS:CE	1:Z:49:LEU:CD1	2.41	0.98
1:Z:757:ALA:HB2	1:Z:819:MET:O	1.46	0.98
6:J:365:SER:H	7:K:424:ASN:ND2	1.60	0.98
7:H:418:GLN:HE21	8:I:718:THR:HG23	0.86	0.98
1:Z:753:ALA:CA	1:Z:816:TYR:HA	1.92	0.98
5:F:1550:LEU:HD21	5:F:1552:PHE:CZ	1.98	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:446:ARG:HH22	7:K:455:LYS:CE	1.76	0.97
7:K:538:LYS:CB	8:L:818:ILE:O	2.13	0.97
3:D:1238:ARG:HA	1:Z:830:SER:CB	1.94	0.97
1:A:128:LEU:CD2	4:E:1260:TYR:CE2	2.47	0.97
1:Z:807:LYS:CA	1:Z:836:ASP:O	2.12	0.97
8:I:818:ILE:C	8:I:821:ILE:HG22	1.87	0.97
6:J:281:ASP:HA	6:J:284:ILE:HD12	1.46	0.97
1:Z:249:ARG:O	1:Z:251:ALA:N	1.98	0.97
1:Z:817:ALA:O	1:Z:821:GLN:CB	2.13	0.97
1:Z:824:MET:HG2	1:Z:825:PRO:HD3	1.43	0.97
1:A:775:LEU:HB3	1:A:832:LEU:HD11	1.44	0.97
5:F:951:ARG:HH21	5:F:953:ASN:H	1.08	0.97
6:G:331:LYS:HE2	1:Z:49:LEU:HD12	1.47	0.97
5:F:968:ILE:HG13	7:H:392:LEU:HD13	1.46	0.97
7:H:493:SER:O	8:I:784:ILE:O	1.83	0.97
5:F:1085:LYS:O	5:F:1089:ASN:CB	2.12	0.96
5:F:1550:LEU:HD22	5:F:1552:PHE:CZ	1.97	0.96
1:Z:133:THR:HG22	1:Z:134:LYS:N	1.77	0.96
7:H:426:GLY:CA	8:I:736:ASN:N	2.27	0.96
8:L:682:ASP:HA	8:L:685:MET:HE3	1.46	0.96
5:F:334:GLN:NE2	5:F:859:LYS:HZ3	1.56	0.96
5:F:1216:PHE:HE2	5:F:1282:ALA:CB	1.77	0.96
5:F:1034:LEU:CD2	5:F:1092:THR:HB	1.95	0.96
7:K:298:SER:HA	7:K:306:THR:HA	1.47	0.96
7:K:526:VAL:O	7:K:530:ASP:HB2	1.66	0.96
6:G:430:LEU:O	7:H:503:ASN:CB	2.13	0.95
6:J:380:TYR:HE2	8:L:751:LEU:CD2	1.79	0.95
6:J:325:TYR:HE2	7:K:390:HIS:HA	1.17	0.95
5:F:1129:ASN:HD21	5:F:1132:GLU:HB3	0.83	0.95
7:H:425:ARG:C	7:H:427:LEU:N	2.21	0.95
1:Z:810:ALA:C	1:Z:836:ASP:HA	1.91	0.95
6:J:431:GLN:HA	7:K:500:GLU:N	1.81	0.95
4:E:227:ILE:HD11	4:E:258:ILE:CD1	1.96	0.95
1:A:751:LEU:HD22	2:C:1313:LEU:HA	1.49	0.95
3:D:528:PRO:HG3	3:D:624:PHE:CE2	2.02	0.95
6:J:383:LYS:CD	8:L:756:ASN:OD1	2.13	0.95
1:Z:824:MET:CG	1:Z:825:PRO:CD	2.43	0.94
7:K:321:ALA:H	7:K:348:ILE:HD11	1.09	0.94
1:Z:824:MET:HB2	1:Z:825:PRO:HD3	1.47	0.94
5:F:920:ILE:CG2	5:F:924:ALA:O	2.15	0.94
6:J:398:VAL:HG21	7:K:462:ARG:HA	1.50	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1550:LEU:HD11	5:F:1604:ILE:HD13	1.48	0.94
8:I:814:LEU:HD21	1:Z:59:LYS:CB	1.97	0.94
5:F:968:ILE:CG1	7:H:392:LEU:HD13	1.97	0.94
6:J:383:LYS:HD2	8:L:756:ASN:OD1	1.68	0.94
5:F:350:ARG:O	5:F:393:SER:HB3	1.68	0.94
6:J:383:LYS:CE	8:L:756:ASN:OD1	2.16	0.94
1:A:772:PRO:HB3	1:A:828:THR:HG21	0.95	0.93
8:I:818:ILE:O	8:I:821:ILE:HG22	0.76	0.93
5:F:1068:ILE:HD12	5:F:1150:PHE:CD2	2.04	0.93
5:F:1038:LEU:C	5:F:1040:THR:H	1.74	0.93
1:Z:753:ALA:HA	1:Z:816:TYR:CB	1.98	0.93
6:G:465:LYS:HB2	1:Z:20:LYS:NZ	1.81	0.93
5:F:354:ARG:CB	5:F:356:ILE:HG22	1.98	0.93
6:J:433:LYS:N	7:K:499:GLY:HA3	1.84	0.93
5:F:1012:ASN:O	8:I:787:GLU:HG2	1.68	0.92
1:Z:241:ILE:CG2	1:Z:245:ALA:HB2	1.99	0.92
3:D:1467:SER:HB2	1:Z:621:HIS:NE2	1.84	0.92
6:G:327:LYS:NZ	1:Z:46:ILE:CB	2.31	0.92
6:G:465:LYS:CB	1:Z:20:LYS:HZ1	1.81	0.92
3:D:515:VAL:HG12	3:D:644:SER:HB3	1.52	0.92
6:J:388:CYS:HB2	7:K:455:LYS:HD2	1.51	0.92
1:A:140:ILE:CG2	4:E:1393:LYS:CD	2.47	0.92
5:F:800:ILE:HD11	5:F:885:GLU:OE1	1.69	0.92
7:K:456:THR:O	7:K:458:GLU:N	2.03	0.92
3:D:483:HIS:HB2	3:D:486:GLN:HG2	1.52	0.91
4:E:1398:VAL:O	4:E:1398:VAL:HG12	1.69	0.91
4:E:687:LYS:CB	5:F:1391:GLY:HA3	2.00	0.91
6:J:388:CYS:O	6:J:388:CYS:SG	2.28	0.91
4:E:989:ASP:O	4:E:991:LYS:N	2.03	0.91
7:K:525:GLU:O	7:K:529:LYS:HB3	1.70	0.91
5:F:334:GLN:HG2	5:F:860:ASN:ND2	1.85	0.91
5:F:837:TYR:HB2	5:F:918:PHE:HE2	1.30	0.91
7:K:321:ALA:H	7:K:348:ILE:CD1	1.83	0.91
3:D:118:THR:HB	3:D:623:GLY:HA2	1.50	0.91
3:D:971:ILE:HD11	3:D:984:THR:HB	1.52	0.91
5:F:711:GLN:OE1	5:F:779:PRO:HA	1.69	0.91
7:K:379:ILE:O	7:K:382:LYS:CB	2.19	0.91
1:Z:362:LYS:O	1:Z:365:GLN:HB2	1.71	0.91
1:A:59:LYS:CA	8:L:807:LEU:CB	2.48	0.90
4:E:1029:ASN:ND2	7:K:475:SER:CB	2.35	0.90
3:D:716:VAL:HG11	3:D:889:GLU:HB2	1.53	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:295:LYS:HG2	6:J:363:LYS:NZ	1.86	0.90
3:D:430:GLU:CD	3:D:528:PRO:HD3	1.95	0.90
6:J:342:GLU:OE1	6:J:375:LYS:NZ	2.04	0.90
1:Z:810:ALA:HB3	1:Z:836:ASP:HA	1.46	0.90
2:C:1258:GLN:HG2	2:C:1299:LYS:NZ	1.87	0.90
7:K:484:PHE:O	7:K:492:ASP:CB	2.20	0.90
1:Z:810:ALA:CB	1:Z:836:ASP:O	2.20	0.90
6:J:364:ILE:CA	7:K:424:ASN:ND2	2.35	0.90
7:K:326:LYS:CB	7:K:327:PRO:HD2	2.02	0.89
1:Z:817:ALA:O	1:Z:821:GLN:CA	2.20	0.89
5:F:887:PHE:H	5:F:888:PRO:HD2	1.37	0.89
5:F:1167:LYS:HA	5:F:1167:LYS:CE	1.99	0.89
7:K:446:ARG:NH1	7:K:446:ARG:O	2.06	0.89
5:F:750:TRP:HZ2	5:F:901:PRO:CB	1.86	0.89
5:F:967:THR:O	7:H:392:LEU:HD21	1.72	0.89
1:Z:753:ALA:CB	1:Z:816:TYR:CA	2.50	0.89
5:F:1672:MET:CB	1:Z:149:ALA:HB2	2.03	0.89
1:Z:127:GLN:HA	1:Z:127:GLN:HE21	1.38	0.89
3:D:499:LEU:HB2	3:D:502:SER:HB3	1.55	0.88
5:F:1116:VAL:HG11	5:F:1150:PHE:HE2	1.32	0.88
5:F:657:ILE:O	5:F:712:LEU:HD12	1.73	0.88
5:F:922:LEU:CD2	7:H:400:LYS:HE3	2.02	0.88
7:K:446:ARG:NH2	7:K:455:LYS:NZ	2.21	0.88
5:F:1134:LYS:C	5:F:1136:LYS:H	1.81	0.88
6:J:387:TYR:HA	8:L:762:LEU:HD22	1.55	0.88
5:F:1187:ASN:CB	5:F:1190:TYR:CB	2.52	0.88
1:A:27:GLU:OE2	1:A:30:ASP:CB	2.21	0.88
1:Z:27:GLU:OE2	1:Z:30:ASP:CB	2.21	0.88
6:G:292:HIS:ND1	6:J:352:VAL:HG11	1.87	0.88
7:H:535:LYS:CB	8:I:821:ILE:CD1	2.51	0.88
6:J:433:LYS:CB	7:K:499:GLY:HA2	2.03	0.88
5:F:968:ILE:HG13	7:H:392:LEU:CD1	2.03	0.88
1:Z:117:LYS:NZ	1:Z:117:LYS:HB3	1.87	0.88
6:J:459:VAL:O	6:J:463:LYS:HB2	1.73	0.88
5:F:1084:LEU:HA	5:F:1156:TYR:CZ	2.09	0.87
5:F:1294:LYS:O	5:F:1295:ALA:O	1.90	0.87
5:F:914:ASP:HA	5:F:917:PHE:CB	2.03	0.87
3:D:175:ILE:HD11	3:D:642:LEU:HB2	1.55	0.87
3:D:944:LEU:HD12	3:D:947:LEU:HD12	1.57	0.87
5:F:935:GLN:O	5:F:938:ALA:N	2.07	0.87
3:D:910:LEU:HD23	3:D:913:LEU:HD12	1.57	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1251:ARG:HH22	5:F:1276:ASP:HB2	1.39	0.87
6:J:429:LEU:CB	6:J:434:THR:OG1	2.23	0.86
4:E:504:ASP:HA	4:E:522:ILE:O	1.73	0.86
3:D:830:SER:HB3	3:D:934:SER:HB3	1.58	0.86
7:H:426:GLY:HA2	8:I:736:ASN:H	1.38	0.86
1:Z:782:ILE:CB	1:Z:839:LEU:C	2.48	0.86
5:F:734:LEU:HD21	5:F:817:ASN:OD1	1.74	0.86
1:Z:241:ILE:CG2	1:Z:245:ALA:CB	2.50	0.86
4:E:182:PHE:CE2	5:F:1189:MET:CB	2.59	0.86
7:K:455:LYS:HD3	7:K:455:LYS:N	1.91	0.86
1:Z:810:ALA:CB	1:Z:836:ASP:C	2.37	0.86
1:Z:811:ARG:CA	1:Z:836:ASP:CB	2.53	0.86
5:F:354:ARG:HB2	5:F:356:ILE:CG2	2.04	0.86
1:Z:746:PRO:O	1:Z:812:GLN:O	1.93	0.86
5:F:389:LEU:H	5:F:389:LEU:HD12	1.41	0.86
5:F:968:ILE:HG23	7:H:392:LEU:HD11	1.56	0.86
7:K:315:LYS:HA	7:K:347:THR:HA	1.58	0.86
1:Z:807:LYS:CB	1:Z:837:VAL:O	2.24	0.85
1:A:751:LEU:CD2	2:C:1313:LEU:HD23	2.04	0.85
5:F:1167:LYS:O	5:F:1167:LYS:HD3	1.76	0.85
1:A:57:ARG:HG2	1:A:57:ARG:HH11	1.38	0.85
1:Z:251:ALA:O	1:Z:252:GLN:C	2.19	0.85
3:D:768:PRO:HA	3:D:771:TYR:HB2	1.57	0.85
5:F:401:THR:CB	5:F:411:ASN:CB	2.53	0.85
7:K:321:ALA:HA	7:K:348:ILE:HD11	1.42	0.85
7:K:404:ARG:HA	7:K:404:ARG:NE	1.88	0.85
6:G:430:LEU:CB	8:I:780:THR:CA	2.53	0.85
1:A:783:SER:CA	1:A:839:LEU:HA	2.06	0.85
5:F:922:LEU:HD23	7:H:400:LYS:HE3	1.58	0.85
6:J:365:SER:N	7:K:424:ASN:ND2	2.25	0.85
5:F:1216:PHE:CE2	5:F:1282:ALA:CB	2.59	0.85
8:I:822:LYS:HZ1	8:I:822:LYS:HA	1.42	0.85
3:D:528:PRO:HG3	3:D:624:PHE:CD2	2.11	0.85
6:J:324:GLN:HA	6:J:327:LYS:HE2	1.56	0.85
6:J:405:LEU:CD2	7:K:469:ARG:HE	1.89	0.85
3:D:537:LYS:HE2	3:D:572:LEU:HD23	1.57	0.84
6:J:371:LYS:O	6:J:371:LYS:NZ	2.10	0.84
6:J:333:ILE:C	6:J:336:PHE:CB	2.50	0.84
6:J:432:LEU:CB	8:L:782:ILE:CA	2.55	0.84
1:A:140:ILE:HG22	4:E:1393:LYS:HZ2	1.41	0.84
1:A:50:ARG:HA	1:A:53:VAL:HG12	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1037:ASN:H	5:F:1040:THR:CB	1.91	0.84
1:Z:49:LEU:O	1:Z:49:LEU:HD22	1.76	0.84
1:Z:242:LEU:HA	1:Z:245:ALA:HB3	1.58	0.84
4:E:687:LYS:CB	5:F:1391:GLY:CA	2.56	0.84
1:A:772:PRO:CB	1:A:828:THR:CG2	2.39	0.84
6:G:295:LYS:CG	6:J:363:LYS:NZ	2.40	0.84
6:J:323:SER:HA	6:J:326:LEU:HD12	1.57	0.84
1:Z:811:ARG:HA	1:Z:836:ASP:CB	2.07	0.84
1:A:787:HIS:CE1	1:A:838:SER:O	2.31	0.83
4:E:1163:LEU:O	4:E:1167:LEU:HB2	1.78	0.83
5:F:1634:LYS:HD2	5:F:1635:ARG:HD3	1.58	0.83
1:Z:747:PHE:HA	1:Z:812:GLN:CB	2.09	0.83
1:Z:756:LYS:CB	1:Z:816:TYR:CB	2.57	0.83
6:G:449:LEU:HD23	1:Z:84:ASP:CG	2.03	0.83
5:F:929:TYR:O	5:F:932:VAL:HG13	1.79	0.83
1:Z:46:ILE:HD12	1:Z:46:ILE:O	1.78	0.83
1:Z:753:ALA:CB	1:Z:816:TYR:HA	2.09	0.82
1:Z:753:ALA:CA	1:Z:816:TYR:CA	2.57	0.82
5:F:690:GLU:CG	8:I:722:LEU:HD21	2.08	0.82
5:F:1084:LEU:HA	5:F:1156:TYR:HH	1.43	0.82
1:A:775:LEU:CB	1:A:832:LEU:CD1	2.57	0.82
6:J:390:ILE:HB	8:L:762:LEU:HD11	1.62	0.82
6:J:333:ILE:O	6:J:336:PHE:CA	2.28	0.82
5:F:1251:ARG:HH22	5:F:1276:ASP:CB	1.92	0.82
6:G:465:LYS:CB	1:Z:20:LYS:NZ	2.42	0.82
5:F:227:ASP:HA	5:F:379:SER:CB	2.10	0.82
5:F:1116:VAL:CG1	5:F:1150:PHE:HE2	1.87	0.82
3:D:1457:LYS:O	1:Z:651:ASP:CB	2.27	0.82
1:A:46:ILE:HA	8:L:792:GLN:H	1.45	0.81
2:C:1258:GLN:HG2	2:C:1299:LYS:HZ1	1.42	0.81
4:E:923:LEU:HD11	4:E:931:PHE:HE2	1.44	0.81
5:F:914:ASP:HA	5:F:917:PHE:HB3	1.59	0.81
6:G:470:LEU:HB2	7:H:538:LYS:HZ3	1.45	0.81
1:Z:753:ALA:HA	1:Z:816:TYR:CA	2.10	0.81
4:E:227:ILE:CD1	4:E:258:ILE:CD1	2.58	0.81
5:F:1109:ILE:HD11	5:F:1160:TYR:OH	1.80	0.81
3:D:1377:ASN:ND2	1:Z:758:GLN:HE21	1.76	0.81
1:A:772:PRO:HB3	1:A:828:THR:CB	2.09	0.81
3:D:734:LEU:HB3	3:D:739:THR:HG21	1.60	0.81
5:F:1357:ALA:HB2	5:F:1381:LEU:CA	2.10	0.81
6:G:430:LEU:CB	8:I:780:THR:CG2	2.58	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:483:VAL:CB	7:K:493:SER:C	2.53	0.81
1:Z:810:ALA:C	1:Z:836:ASP:CA	2.54	0.81
4:E:258:ILE:CG2	4:E:261:ILE:HD11	2.10	0.81
7:K:321:ALA:C	7:K:348:ILE:HD11	2.06	0.80
6:G:465:LYS:HB2	1:Z:20:LYS:HZ1	1.40	0.80
6:J:369:LEU:HD13	7:K:419:LEU:HD22	1.62	0.80
1:Z:774:LEU:HA	1:Z:777:ILE:HG22	1.63	0.80
7:K:400:LYS:HD2	7:K:400:LYS:O	1.80	0.80
1:A:128:LEU:CD1	4:E:1260:TYR:CZ	2.60	0.80
5:F:1068:ILE:CD1	5:F:1150:PHE:CD2	2.63	0.80
8:I:814:LEU:CD2	1:Z:59:LYS:CB	2.59	0.80
6:J:386:ASP:HA	6:J:389:ARG:HB2	1.63	0.80
7:K:337:GLN:O	7:K:341:LYS:HE2	1.79	0.80
7:K:446:ARG:NH2	7:K:455:LYS:HZ1	1.79	0.80
8:I:805:ARG:CB	1:Z:88:LYS:NZ	2.45	0.80
1:Z:804:ASP:O	1:Z:808:ASN:HB3	1.81	0.80
5:F:1106:PHE:CD2	5:F:1164:PHE:CE2	2.69	0.80
3:D:160:ILE:HG23	3:D:191:ILE:HG21	1.64	0.80
7:H:412:ILE:CG2	7:H:415:LEU:HD23	2.11	0.80
5:F:1216:PHE:HE2	5:F:1282:ALA:HB2	1.47	0.80
3:D:368:ILE:HB	3:D:380:TYR:HB2	1.63	0.80
8:L:643:LYS:HG3	8:L:647:GLN:HE22	1.47	0.80
1:Z:251:ALA:O	1:Z:254:LEU:N	2.15	0.80
1:Z:779:LEU:CB	1:Z:835:ILE:CB	2.60	0.80
5:F:1068:ILE:CD1	5:F:1150:PHE:HD2	1.95	0.79
7:K:385:GLN:HA	7:K:385:GLN:HE21	1.48	0.79
5:F:935:GLN:O	5:F:937:LEU:N	2.14	0.79
6:J:384:LEU:HD23	6:J:384:LEU:O	1.82	0.79
8:I:822:LYS:HA	8:I:822:LYS:CE	2.12	0.79
2:C:1388:HIS:O	4:E:1331:LEU:CD1	2.31	0.79
4:E:988:ILE:O	4:E:990:LYS:N	2.16	0.79
6:J:353:LEU:HG	7:K:419:LEU:HD11	1.64	0.79
7:K:337:GLN:O	7:K:341:LYS:CE	2.30	0.79
6:J:305:ILE:HD11	8:L:668:VAL:HG12	1.61	0.79
1:Z:824:MET:CB	1:Z:825:PRO:CD	2.60	0.79
3:D:1376:LYS:CB	1:Z:762:ASN:CA	2.60	0.79
7:H:532:ALA:HB2	8:I:818:ILE:CD1	2.12	0.79
5:F:734:LEU:HD22	5:F:817:ASN:OD1	1.81	0.79
1:Z:753:ALA:HB1	1:Z:816:TYR:HA	1.61	0.79
1:Z:753:ALA:HB2	1:Z:815:ILE:C	2.08	0.79
5:F:928:LEU:H	5:F:928:LEU:CD1	1.92	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:325:TYR:CD2	7:K:390:HIS:HA	2.15	0.79
7:H:423:LYS:O	8:I:735:ASN:CB	2.31	0.78
7:K:314:ASN:HB2	7:K:361:ARG:HH12	1.46	0.78
3:D:515:VAL:HB	3:D:604:PRO:HG3	1.66	0.78
3:D:1376:LYS:CB	1:Z:762:ASN:HA	2.13	0.78
5:F:1436:LYS:O	5:F:1440:ILE:HB	1.83	0.78
7:K:310:ALA:HB3	7:K:352:ILE:HB	1.64	0.78
5:F:922:LEU:CD2	7:H:400:LYS:CE	2.58	0.78
5:F:1134:LYS:O	5:F:1136:LYS:N	2.16	0.78
1:Z:133:THR:CG2	1:Z:134:LYS:N	2.46	0.78
6:G:295:LYS:HG2	6:J:363:LYS:HZ1	1.47	0.78
1:Z:663:ASP:O	1:Z:667:ALA:HB3	1.84	0.78
1:A:775:LEU:CB	1:A:832:LEU:HD11	2.13	0.78
5:F:1035:GLY:O	5:F:1042:ILE:CB	2.32	0.78
6:J:333:ILE:HA	6:J:336:PHE:CB	2.13	0.78
4:E:182:PHE:HE2	5:F:1189:MET:CB	1.96	0.78
5:F:1633:TYR:CZ	5:F:1635:ARG:HB2	2.19	0.78
7:K:358:LEU:HD22	8:L:662:ILE:HD13	1.64	0.78
1:A:82:ASP:OD1	1:A:82:ASP:N	2.14	0.77
3:D:445:ARG:HB2	3:D:466:LYS:HB2	1.67	0.77
1:A:53:VAL:CG2	8:L:799:SER:OG	2.31	0.77
1:A:253:LEU:HD22	1:A:502:ASP:HB3	1.67	0.77
5:F:1606:GLN:O	5:F:1610:ALA:HB2	1.83	0.77
6:J:319:GLU:HA	6:J:322:THR:HG22	1.66	0.77
3:D:263:VAL:HB	3:D:311:LYS:HE3	1.65	0.77
5:F:1139:ILE:HG12	5:F:1291:SER:OG	1.84	0.77
1:Z:91:GLN:O	1:Z:93:ASN:N	2.18	0.77
1:A:779:LEU:CB	1:A:835:ILE:CB	2.61	0.77
2:C:1258:GLN:CG	2:C:1299:LYS:CE	2.62	0.77
3:D:395:PRO:HB3	3:D:418:LEU:HD23	1.65	0.77
1:Z:768:VAL:HA	1:Z:771:ILE:HD12	1.66	0.77
3:D:1468:TYR:H	1:Z:621:HIS:CE1	2.02	0.77
5:F:968:ILE:HG23	7:H:392:LEU:CD1	2.14	0.77
5:F:1435:LYS:NZ	5:F:1484:ARG:NH2	2.32	0.77
3:D:744:SER:HA	3:D:758:ASP:HB2	1.67	0.77
3:D:1238:ARG:HG2	1:Z:830:SER:HB2	1.66	0.77
8:I:737:ASN:OD1	8:I:738:ASP:OD1	2.01	0.77
4:E:973:THR:OG1	4:E:974:GLY:N	2.14	0.77
5:F:1038:LEU:O	5:F:1040:THR:N	2.18	0.77
6:J:383:LYS:HZ3	8:L:756:ASN:CG	1.88	0.77
4:E:1022:TYR:CE2	4:E:1026:THR:HG22	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:753:ALA:C	1:Z:816:TYR:HA	2.09	0.77
1:Z:810:ALA:HB2	1:Z:839:LEU:CA	2.15	0.77
1:Z:810:ALA:HB1	1:Z:835:ILE:O	1.84	0.76
4:E:1359:ILE:HG21	1:Z:453:VAL:HG11	1.67	0.76
6:G:327:LYS:HZ2	1:Z:46:ILE:HA	1.50	0.76
7:H:412:ILE:CG2	7:H:415:LEU:CD2	2.62	0.76
8:I:822:LYS:HA	8:I:822:LYS:NZ	1.99	0.76
1:A:128:LEU:HD13	4:E:1260:TYR:CE2	2.20	0.76
4:E:1319:LEU:HD21	4:E:1398:VAL:HG23	1.67	0.76
5:F:1216:PHE:HE2	5:F:1282:ALA:HB1	1.48	0.76
5:F:1370:LEU:O	5:F:1371:ILE:HG12	1.86	0.76
5:F:1357:ALA:CA	5:F:1381:LEU:CB	2.63	0.76
6:J:387:TYR:CB	8:L:759:SER:OG	2.33	0.76
1:Z:146:LEU:O	1:Z:146:LEU:HD12	1.85	0.76
5:F:506:ASN:O	5:F:510:PHE:HB2	1.84	0.76
5:F:1606:GLN:HB3	1:Z:141:ASN:HD22	1.50	0.76
6:J:398:VAL:HB	7:K:462:ARG:O	1.85	0.76
3:D:509:PHE:HA	3:D:517:LEU:HG	1.68	0.76
1:Z:810:ALA:HB2	1:Z:839:LEU:HA	1.68	0.76
3:D:298:TYR:CE1	3:D:311:LYS:HE2	2.21	0.75
8:I:805:ARG:CB	1:Z:88:LYS:CE	2.64	0.75
7:K:359:ASN:HA	7:K:362:ASN:HD22	1.49	0.75
1:Z:746:PRO:CB	1:Z:752:SER:C	2.60	0.75
1:A:120:ASN:OD1	6:J:413:ASN:ND2	2.20	0.75
3:D:1249:LEU:CB	5:F:1502:THR:O	2.34	0.75
5:F:159:LYS:NZ	5:F:363:ASP:CB	2.49	0.75
7:K:313:TYR:HA	7:K:349:PRO:HB3	1.68	0.75
6:J:376:LYS:NZ	8:L:756:ASN:HD22	1.84	0.75
7:K:538:LYS:CB	8:L:821:ILE:CG2	2.64	0.75
5:F:1442:TRP:CE2	5:F:1484:ARG:HB3	2.21	0.75
7:K:446:ARG:HH22	7:K:455:LYS:HZ1	1.30	0.75
1:A:16:LYS:HE2	6:J:467:LEU:O	1.86	0.75
1:A:226:ARG:NH2	1:A:230:GLY:O	2.20	0.75
3:D:508:LYS:HG3	3:D:517:LEU:H	1.50	0.75
5:F:1034:LEU:O	5:F:1095:LEU:HD11	1.85	0.75
7:K:538:LYS:CB	8:L:821:ILE:HG23	2.16	0.75
4:E:923:LEU:HD11	4:E:931:PHE:CE2	2.21	0.75
1:Z:133:THR:HG22	1:Z:134:LYS:H	1.48	0.75
3:D:402:ILE:HG21	3:D:406:THR:H	1.51	0.75
3:D:576:LEU:HD22	3:D:601:THR:HB	1.69	0.75
5:F:227:ASP:CB	5:F:361:LEU:CB	2.65	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:446:ARG:NH2	7:K:455:LYS:CE	2.50	0.75
1:A:128:LEU:CD2	4:E:1260:TYR:CD2	2.62	0.75
5:F:900:LEU:C	5:F:900:LEU:HD12	2.12	0.75
7:H:420:ALA:HB1	8:I:745:TYR:HE1	1.48	0.75
5:F:1294:LYS:O	5:F:1295:ALA:C	2.28	0.74
1:A:137:ASP:HB2	4:E:1386:LEU:HA	1.69	0.74
1:A:233:ASP:OD2	1:A:236:ASN:ND2	2.21	0.74
7:H:412:ILE:HA	7:H:415:LEU:HB2	1.67	0.74
6:J:365:SER:H	7:K:424:ASN:HD21	1.33	0.74
1:Z:116:LYS:HE2	1:Z:116:LYS:O	1.88	0.74
1:Z:44:VAL:CB	1:Z:47:ASN:ND2	2.50	0.74
1:A:192:ILE:HD12	1:A:571:LEU:HD11	1.68	0.74
5:F:1216:PHE:CZ	5:F:1282:ALA:HA	2.21	0.74
1:Z:753:ALA:HB2	1:Z:816:TYR:N	2.02	0.74
1:Z:810:ALA:HB1	1:Z:836:ASP:N	2.03	0.74
1:A:783:SER:HA	1:A:839:LEU:CA	2.12	0.74
3:D:490:LYS:HE2	3:D:533:SER:HB3	1.70	0.74
3:D:1241:GLY:HA2	1:Z:826:ARG:O	1.87	0.74
5:F:750:TRP:CZ2	5:F:901:PRO:CB	2.70	0.74
7:K:287:GLN:O	7:K:291:GLN:N	2.18	0.74
1:Z:117:LYS:HB3	1:Z:117:LYS:HZ1	1.52	0.74
5:F:1274:ASP:HA	5:F:1277:VAL:HB	1.68	0.74
5:F:1550:LEU:HD21	5:F:1552:PHE:CE2	2.19	0.74
6:G:431:GLN:CB	7:H:503:ASN:N	2.51	0.74
6:J:350:PHE:CD1	7:K:419:LEU:HD12	2.23	0.74
7:K:513:LEU:CD2	8:L:800:HIS:CE1	2.69	0.74
6:G:357:LEU:O	8:I:732:ALA:O	2.06	0.74
6:J:364:ILE:HA	7:K:424:ASN:HD22	1.52	0.73
7:K:379:ILE:O	7:K:382:LYS:N	2.20	0.73
7:K:387:GLN:HA	7:K:387:GLN:HE21	1.51	0.73
4:E:224:CYS:O	4:E:228:ASN:HB2	1.87	0.73
5:F:922:LEU:HD23	7:H:400:LYS:HZ1	1.50	0.73
5:F:376:ASN:CB	5:F:381:THR:C	2.59	0.73
5:F:951:ARG:HH21	5:F:953:ASN:N	1.84	0.73
3:D:1238:ARG:CA	1:Z:830:SER:HB3	2.13	0.73
4:E:1359:ILE:CG2	1:Z:453:VAL:HG11	2.18	0.73
5:F:1635:ARG:O	5:F:1639:GLY:HA3	1.89	0.73
8:I:821:ILE:HD13	8:I:821:ILE:C	2.13	0.73
1:Z:810:ALA:HB1	1:Z:835:ILE:C	2.12	0.73
3:D:413:LEU:HD11	3:D:444:VAL:HG11	1.69	0.73
3:D:472:VAL:HG23	3:D:474:PRO:HD2	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1216:PHE:CE2	5:F:1282:ALA:HB2	2.23	0.73
1:Z:365:GLN:O	1:Z:368:LEU:HB2	1.87	0.73
1:A:128:LEU:HB3	4:E:1260:TYR:HE2	1.54	0.73
2:C:1258:GLN:HG2	2:C:1299:LYS:HE2	1.69	0.73
4:E:182:PHE:CZ	5:F:1189:MET:CB	2.71	0.73
5:F:968:ILE:CG1	7:H:392:LEU:CD1	2.65	0.73
5:F:1669:LEU:CB	1:Z:145:ASN:CB	2.67	0.73
1:Z:822:TYR:O	1:Z:828:THR:HG23	1.88	0.73
6:J:398:VAL:CG2	7:K:462:ARG:HA	2.19	0.73
1:Z:754:ARG:HA	1:Z:819:MET:CB	2.17	0.73
1:A:60:ASN:N	8:L:807:LEU:CB	2.52	0.73
3:D:155:ASN:HA	3:D:646:SER:HB3	1.71	0.73
5:F:951:ARG:NH2	5:F:953:ASN:H	1.84	0.73
7:K:312:VAL:HG23	7:K:352:ILE:HG13	1.71	0.73
7:K:483:VAL:H	7:K:493:SER:C	1.96	0.73
5:F:424:SER:O	5:F:428:GLN:NE2	2.21	0.72
5:F:1283:LYS:HA	5:F:1283:LYS:CE	2.17	0.72
6:G:430:LEU:C	7:H:503:ASN:CB	2.61	0.72
3:D:750:LYS:HB2	3:D:751:PRO:HD3	1.71	0.72
1:Z:771:ILE:HG22	1:Z:772:PRO:CD	2.19	0.72
5:F:159:LYS:HE3	5:F:363:ASP:CA	2.15	0.72
1:Z:822:TYR:O	1:Z:828:THR:CG2	2.37	0.72
6:J:432:LEU:CB	8:L:782:ILE:HA	2.19	0.72
1:Z:49:LEU:HD22	1:Z:49:LEU:C	2.15	0.72
1:Z:774:LEU:HD23	1:Z:774:LEU:C	2.14	0.72
6:J:433:LYS:H	7:K:499:GLY:HA3	1.52	0.72
7:K:404:ARG:HA	7:K:404:ARG:HE	1.55	0.72
7:K:520:ILE:HA	7:K:523:LEU:HB2	1.71	0.72
1:A:634:ASP:O	1:A:636:ARG:NH1	2.22	0.72
7:K:429:LEU:C	7:K:429:LEU:HD12	2.15	0.72
8:L:637:LEU:HD21	8:L:640:LEU:HD23	1.72	0.72
4:E:984:ASP:N	4:E:984:ASP:OD1	2.17	0.72
5:F:354:ARG:CZ	5:F:354:ARG:HB3	2.20	0.72
5:F:1363:ILE:HG22	1:Z:125:ILE:CD1	2.19	0.72
1:Z:127:GLN:HE21	1:Z:127:GLN:CA	2.01	0.72
4:E:258:ILE:HG23	4:E:261:ILE:HD11	1.70	0.72
1:Z:746:PRO:O	1:Z:812:GLN:C	2.33	0.72
1:A:315:LYS:HE3	1:A:321:LYS:HA	1.72	0.72
7:H:425:ARG:O	7:H:427:LEU:N	2.19	0.72
3:D:915:GLU:OE1	3:D:980:SER:HB3	1.90	0.71
6:G:465:LYS:HE3	1:Z:20:LYS:HZ3	1.54	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:389:ARG:O	6:J:389:ARG:NH1	2.23	0.71
1:Z:116:LYS:HB3	1:Z:116:LYS:NZ	1.95	0.71
5:F:334:GLN:HE22	5:F:859:LYS:NZ	1.83	0.71
6:J:303:GLU:HG2	6:J:304:LEU:HD12	1.70	0.71
7:K:448:GLU:HA	7:K:448:GLU:OE2	1.89	0.71
5:F:1027:GLN:HG2	5:F:1036:PRO:HA	1.71	0.71
6:G:470:LEU:CB	7:H:538:LYS:NZ	2.50	0.71
1:A:775:LEU:HB3	1:A:832:LEU:HD12	1.72	0.71
3:D:268:ILE:HG21	3:D:284:PHE:HE2	1.54	0.71
5:F:837:TYR:CB	5:F:918:PHE:CE2	2.71	0.71
5:F:1435:LYS:CE	5:F:1484:ARG:NH2	2.53	0.71
6:G:295:LYS:C	6:J:363:LYS:NZ	2.48	0.71
6:J:376:LYS:O	6:J:376:LYS:HD2	1.89	0.71
7:K:378:HIS:O	7:K:381:GLU:CB	2.38	0.71
3:D:451:SER:H	3:D:458:GLU:HB3	1.55	0.71
8:I:724:ASP:O	8:I:727:SER:HB2	1.89	0.71
8:I:822:LYS:HA	8:I:822:LYS:HE3	1.70	0.71
6:G:470:LEU:HB2	7:H:538:LYS:NZ	2.05	0.71
7:K:538:LYS:C	8:L:822:LYS:CB	2.64	0.71
1:Z:746:PRO:CB	1:Z:753:ALA:N	2.53	0.71
3:D:935:PHE:HD2	3:D:936:VAL:HG22	1.55	0.71
5:F:1134:LYS:C	5:F:1136:LYS:N	2.45	0.71
5:F:376:ASN:CB	5:F:382:ASP:H	2.04	0.71
5:F:1550:LEU:CD1	5:F:1604:ILE:CD1	2.68	0.71
7:H:527:LEU:HD23	7:H:527:LEU:C	2.15	0.71
5:F:926:LEU:C	5:F:926:LEU:HD12	2.15	0.71
4:E:227:ILE:CD1	4:E:258:ILE:HD13	2.17	0.71
5:F:1080:LEU:HG	5:F:1156:TYR:HD2	1.56	0.71
1:A:59:LYS:O	8:L:807:LEU:CB	2.39	0.70
3:D:528:PRO:CG	3:D:624:PHE:CE2	2.74	0.70
6:G:296:ALA:HB2	6:J:363:LYS:HD2	1.71	0.70
8:L:800:HIS:O	8:L:804:LEU:HB3	1.91	0.70
1:A:140:ILE:HG22	4:E:1393:LYS:HZ3	1.56	0.70
8:I:795:LYS:C	8:I:795:LYS:HZ2	1.99	0.70
6:J:383:LYS:HE3	8:L:759:SER:HB2	1.73	0.70
1:Z:753:ALA:O	1:Z:816:TYR:HA	1.92	0.70
7:K:321:ALA:O	7:K:339:MET:HE1	1.91	0.70
1:Z:601:PRO:HB3	1:Z:605:GLU:HB2	1.74	0.70
5:F:887:PHE:N	5:F:888:PRO:CD	2.54	0.70
7:K:317:ASN:CA	7:K:346:GLN:HB3	2.21	0.70
4:E:1309:ARG:O	4:E:1313:ARG:CG	2.35	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:295:LYS:CD	6:J:363:LYS:HZ3	2.05	0.70
1:Z:44:VAL:O	1:Z:47:ASN:HB2	1.91	0.70
5:F:1088:ARG:HH11	5:F:1088:ARG:HG3	1.56	0.70
6:J:429:LEU:HA	6:J:434:THR:H	1.57	0.70
1:A:16:LYS:HA	1:A:19:ASN:HD22	1.57	0.70
2:C:318:ILE:H	2:C:318:ILE:CD1	1.96	0.70
3:D:937:SER:HB3	3:D:941:GLN:HB2	1.73	0.70
5:F:841:PHE:CE2	5:F:918:PHE:CD1	2.79	0.70
7:K:505:ARG:HA	7:K:508:LYS:HB3	1.73	0.70
5:F:1216:PHE:HZ	5:F:1282:ALA:HA	1.55	0.70
1:Z:116:LYS:HE2	1:Z:116:LYS:C	2.17	0.70
4:E:1029:ASN:HD21	7:K:475:SER:CB	2.04	0.70
7:H:412:ILE:O	7:H:415:LEU:HB3	1.92	0.70
3:D:475:GLU:O	3:D:486:GLN:NE2	2.24	0.69
5:F:328:ASP:HB3	5:F:331:ILE:HD11	1.74	0.69
5:F:1024:LEU:HA	5:F:1048:LEU:HB3	1.73	0.69
1:A:301:ASN:HB3	1:A:345:LEU:HD13	1.74	0.69
3:D:545:GLN:HG3	3:D:572:LEU:HD13	1.74	0.69
4:E:1356:LEU:HB2	1:Z:453:VAL:CG2	2.21	0.69
7:H:426:GLY:CA	8:I:736:ASN:H	1.98	0.69
7:H:508:LYS:HG3	7:H:510:VAL:HG13	1.74	0.69
1:Z:29:SER:HA	1:Z:32:LEU:HG	1.74	0.69
3:D:222:ASN:H	3:D:301:SER:HB2	1.57	0.69
3:D:763:ASP:HB3	3:D:765:ILE:HD11	1.74	0.69
5:F:333:GLU:O	5:F:335:ASP:N	2.23	0.69
5:F:914:ASP:OD1	5:F:917:PHE:HB2	1.91	0.69
1:Z:767:ILE:O	1:Z:771:ILE:N	2.20	0.69
3:D:617:ALA:HA	3:D:630:THR:HG21	1.73	0.69
7:K:310:ALA:O	7:K:352:ILE:N	2.25	0.69
7:K:426:GLY:HA2	8:L:738:ASP:HB3	1.72	0.69
1:Z:146:LEU:HD12	1:Z:146:LEU:C	2.17	0.69
1:A:29:SER:HA	1:A:32:LEU:HG	1.75	0.69
5:F:1157:TRP:CD1	5:F:1160:TYR:CE1	2.81	0.69
3:D:860:ILE:HG21	3:D:893:ILE:HG13	1.72	0.69
1:Z:16:LYS:HA	1:Z:19:ASN:HD22	1.57	0.69
1:Z:748:SER:OG	1:Z:752:SER:HB3	1.92	0.69
1:A:669:ASP:O	1:A:724:ARG:NH2	2.25	0.69
1:A:682:GLU:HG2	1:A:691:ARG:HH22	1.58	0.69
1:A:775:LEU:HD13	1:A:832:LEU:HD11	1.75	0.69
2:C:1388:HIS:O	4:E:1331:LEU:HD11	1.92	0.69
5:F:376:ASN:CB	5:F:382:ASP:N	2.55	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1283:LYS:O	5:F:1284:SER:C	2.32	0.69
6:G:327:LYS:NZ	1:Z:46:ILE:HA	2.08	0.69
1:Z:782:ILE:CB	1:Z:839:LEU:O	2.41	0.69
1:A:775:LEU:HD13	1:A:832:LEU:CD1	2.23	0.69
5:F:1129:ASN:CG	5:F:1132:GLU:HB3	2.17	0.69
8:I:731:GLY:C	8:I:733:ALA:H	2.01	0.69
1:A:814:MET:HG2	1:A:833:ILE:HG12	1.75	0.69
5:F:376:ASN:CB	5:F:381:THR:N	2.55	0.69
5:F:1543:LEU:C	5:F:1543:LEU:HD12	2.18	0.69
5:F:1036:PRO:CB	5:F:1042:ILE:CB	2.70	0.68
6:J:376:LYS:HZ1	8:L:756:ASN:HD22	1.41	0.68
1:A:133:THR:O	1:A:136:PHE:N	2.25	0.68
1:A:816:TYR:HA	1:A:819:MET:HG2	1.75	0.68
3:D:828:ILE:HD13	3:D:925:GLN:HA	1.73	0.68
5:F:968:ILE:HG12	7:H:392:LEU:HD13	1.74	0.68
5:F:1633:TYR:HE2	5:F:1635:ARG:HB2	1.47	0.68
5:F:926:LEU:HD12	5:F:926:LEU:O	1.93	0.68
5:F:967:THR:O	7:H:392:LEU:CD2	2.40	0.68
6:J:383:LYS:HZ3	8:L:756:ASN:CB	2.05	0.68
5:F:1116:VAL:HG11	5:F:1150:PHE:HZ	1.51	0.68
8:I:738:ASP:HB2	8:I:740:LYS:HE2	1.74	0.68
3:D:421:VAL:HG21	3:D:490:LYS:HB3	1.74	0.68
5:F:1303:LEU:O	5:F:1303:LEU:HD13	1.94	0.68
6:G:396:THR:CB	1:Z:89:ASP:OD2	2.41	0.68
1:Z:251:ALA:C	1:Z:253:LEU:N	2.51	0.68
5:F:320:GLU:OE1	5:F:351:HIS:CE1	2.47	0.68
8:L:728:THR:HB	8:L:734:ALA:HB2	1.76	0.68
1:A:364:GLU:OE1	1:A:408:ARG:NH1	2.26	0.68
5:F:661:VAL:HG11	5:F:712:LEU:CD1	2.23	0.68
6:J:297:ASP:OD2	7:K:362:ASN:ND2	2.27	0.68
5:F:334:GLN:CB	5:F:860:ASN:CG	2.59	0.67
5:F:750:TRP:HE1	5:F:754:ASP:HB2	1.59	0.67
6:G:289:GLN:OE1	6:J:352:VAL:HA	1.94	0.67
5:F:249:ASP:OD2	5:F:295:ARG:NH1	2.27	0.67
5:F:334:GLN:HE21	5:F:859:LYS:HZ2	0.83	0.67
5:F:1359:PHE:CE1	5:F:1363:ILE:HG23	2.29	0.67
1:Z:133:THR:O	1:Z:136:PHE:N	2.25	0.67
1:Z:249:ARG:C	1:Z:251:ALA:H	2.02	0.67
1:A:57:ARG:HG2	1:A:57:ARG:NH1	2.01	0.67
1:A:249:ARG:NH1	1:A:494:TYR:OH	2.27	0.67
7:H:412:ILE:O	7:H:415:LEU:CB	2.42	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:333:ILE:O	6:J:336:PHE:C	2.37	0.67
7:K:451:ALA:HB3	7:K:453:LEU:HD12	1.76	0.67
7:K:513:LEU:CD2	8:L:800:HIS:HE1	2.07	0.67
1:Z:724:ARG:NH1	1:Z:724:ARG:O	2.27	0.67
5:F:1363:ILE:C	5:F:1363:ILE:HD12	2.19	0.67
6:G:327:LYS:NZ	1:Z:46:ILE:CA	2.57	0.67
6:J:365:SER:N	7:K:424:ASN:HD22	1.91	0.67
3:D:235:SER:HB2	3:D:240:LEU:HD13	1.77	0.67
3:D:261:LEU:HD13	3:D:311:LYS:HB2	1.75	0.67
5:F:667:SER:HA	5:F:670:LYS:HB3	1.77	0.67
6:J:405:LEU:HA	6:J:408:ALA:HB3	1.76	0.67
2:C:784:ALA:HB3	3:D:1357:LYS:H	1.59	0.67
5:F:860:ASN:HD22	5:F:861:GLN:HG3	1.60	0.67
7:H:532:ALA:CB	8:I:818:ILE:HD12	2.20	0.67
6:J:357:LEU:CB	7:K:423:LYS:CE	2.43	0.67
7:K:308:LEU:HD13	7:K:355:PHE:HE2	1.58	0.67
1:Z:810:ALA:HB2	1:Z:839:LEU:CB	2.24	0.67
1:A:218:ILE:HD11	1:A:241:ILE:HD12	1.77	0.66
7:K:326:LYS:CB	7:K:327:PRO:CD	2.72	0.66
3:D:753:PRO:HD2	3:D:756:LYS:HD2	1.77	0.66
5:F:690:GLU:CD	8:I:722:LEU:HD23	2.19	0.66
5:F:1305:SER:C	5:F:1307:VAL:H	2.03	0.66
5:F:1642:LYS:HA	5:F:1645:LEU:HD23	1.77	0.66
6:J:380:TYR:CE2	8:L:751:LEU:CD2	2.68	0.66
4:E:440:ILE:HG12	4:E:590:LEU:HD13	1.77	0.66
5:F:159:LYS:HZ2	5:F:363:ASP:CB	2.07	0.66
5:F:334:GLN:HG3	5:F:854:GLU:CD	2.18	0.66
7:K:513:LEU:HD21	8:L:800:HIS:HE1	1.53	0.66
5:F:690:GLU:OE1	8:I:722:LEU:HD23	1.95	0.66
5:F:883:VAL:O	8:I:761:ASN:ND2	2.28	0.66
6:G:331:LYS:HE2	1:Z:49:LEU:CG	2.25	0.66
3:D:292:ASN:ND2	3:D:380:TYR:OH	2.28	0.66
3:D:583:TYR:HE2	3:D:628:PHE:HB2	1.59	0.66
4:E:1398:VAL:O	4:E:1398:VAL:CG1	2.42	0.66
5:F:711:GLN:OE1	5:F:779:PRO:CA	2.44	0.66
5:F:1116:VAL:CG1	5:F:1150:PHE:CZ	2.64	0.66
6:G:295:LYS:CG	6:J:363:LYS:HZ3	2.07	0.66
6:J:404:ASP:O	6:J:408:ALA:N	2.29	0.66
6:J:405:LEU:CD2	7:K:469:ARG:NE	2.59	0.66
1:Z:746:PRO:CB	1:Z:752:SER:O	2.44	0.66
4:E:209:VAL:O	4:E:213:PHE:CB	2.44	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:456:THR:C	7:K:458:GLU:H	2.03	0.66
1:Z:87:ILE:HD13	1:Z:87:ILE:N	2.10	0.66
5:F:1303:LEU:O	5:F:1303:LEU:HD22	1.96	0.66
3:D:260:HIS:CG	3:D:261:LEU:HA	2.31	0.65
7:K:399:LEU:HD12	7:K:399:LEU:O	1.96	0.65
5:F:809:LEU:HG	5:F:810:VAL:HG13	1.77	0.65
5:F:837:TYR:CB	5:F:918:PHE:HE2	2.04	0.65
8:I:739:GLN:C	8:I:741:ARG:H	1.97	0.65
1:Z:46:ILE:HD12	1:Z:46:ILE:C	2.21	0.65
3:D:863:ILE:HG21	3:D:887:GLN:HA	1.79	0.65
6:J:370:ASP:HA	6:J:373:PHE:HB2	1.78	0.65
7:K:352:ILE:HG21	7:K:358:LEU:HG	1.78	0.65
7:K:404:ARG:HG3	8:L:704:GLN:NE2	2.11	0.65
3:D:580:VAL:O	3:D:595:ASN:N	2.29	0.65
3:D:611:LEU:HD11	3:D:640:ALA:HB2	1.78	0.65
5:F:690:GLU:OE2	8:I:722:LEU:HD21	1.96	0.65
6:G:449:LEU:HD21	1:Z:84:ASP:O	1.97	0.65
7:K:387:GLN:HA	7:K:387:GLN:NE2	2.11	0.65
1:A:192:ILE:HA	1:A:195:SER:HB3	1.79	0.65
3:D:943:ASP:O	3:D:947:LEU:HG	1.96	0.65
5:F:1442:TRP:CD2	5:F:1484:ARG:HD2	2.31	0.65
6:J:339:LEU:CB	7:K:405:ASN:OD1	2.44	0.65
7:K:291:GLN:HA	7:K:294:LYS:HB2	1.79	0.65
1:Z:644:TYR:HB3	1:Z:653:VAL:HG22	1.77	0.65
3:D:362:ASP:HB2	3:D:369:TYR:HE2	1.61	0.65
5:F:1128:ASP:OD2	5:F:1206:ILE:HG23	1.96	0.65
5:F:1314:VAL:HG11	5:F:1373:ASP:HB3	1.78	0.65
7:H:404:ARG:O	7:H:408:ILE:HB	1.96	0.65
8:I:792:GLN:HB2	8:I:795:LYS:HG3	1.79	0.65
1:Z:827:GLU:HA	1:Z:827:GLU:OE2	1.97	0.65
3:D:449:ASN:HD22	3:D:463:GLU:HG2	1.61	0.65
3:D:971:ILE:HD11	3:D:984:THR:CB	2.26	0.65
4:E:1405:ASN:HB3	4:E:1455:PRO:HG2	1.78	0.65
5:F:389:LEU:C	5:F:389:LEU:HD13	2.22	0.65
5:F:900:LEU:HD12	5:F:900:LEU:O	1.97	0.65
5:F:920:ILE:HB	5:F:924:ALA:C	2.21	0.65
6:G:350:PHE:CE2	7:H:418:GLN:NE2	2.65	0.65
6:J:333:ILE:CA	6:J:336:PHE:CB	2.74	0.65
3:D:454:ARG:HB3	3:D:455:PHE:HD1	1.62	0.65
5:F:336:LYS:NZ	5:F:703:TYR:OH	2.29	0.65
5:F:382:ASP:HB3	5:F:386:GLY:H	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:355:LEU:N	5:F:355:LEU:HD12	2.11	0.65
5:F:844:VAL:HG22	5:F:862:ALA:HA	1.79	0.65
5:F:1633:TYR:CE2	5:F:1635:ARG:CB	2.59	0.65
6:G:465:LYS:HB2	1:Z:20:LYS:HZ3	1.59	0.65
7:K:311:PHE:CD2	7:K:341:LYS:NZ	2.58	0.65
7:K:527:LEU:O	7:K:531:ALA:CB	2.45	0.65
1:Z:804:ASP:O	1:Z:808:ASN:CB	2.45	0.65
3:D:915:GLU:OE1	3:D:980:SER:CB	2.44	0.65
4:E:1022:TYR:O	4:E:1026:THR:CG2	2.41	0.65
5:F:22:PHE:O	5:F:26:LYS:NZ	2.30	0.65
5:F:249:ASP:O	5:F:253:LYS:HB2	1.97	0.65
5:F:555:TRP:HB2	5:F:633:LYS:HD3	1.77	0.65
6:G:296:ALA:HA	6:J:363:LYS:HE3	1.79	0.65
6:G:327:LYS:HZ3	1:Z:46:ILE:CB	1.88	0.65
6:G:430:LEU:CB	8:I:780:THR:CB	2.75	0.65
8:I:643:LYS:HG3	8:I:647:GLN:HE22	1.62	0.65
1:Z:410:ALA:HB2	1:Z:428:VAL:HG11	1.79	0.65
1:Z:751:LEU:C	1:Z:753:ALA:H	2.03	0.65
1:A:449:GLU:O	1:A:456:ARG:NH2	2.31	0.64
5:F:914:ASP:CA	5:F:917:PHE:HB3	2.27	0.64
6:G:331:LYS:CE	1:Z:49:LEU:HD12	2.20	0.64
3:D:1376:LYS:CB	1:Z:762:ASN:N	2.60	0.64
4:E:1319:LEU:HD21	4:E:1398:VAL:HG22	1.79	0.64
5:F:1424:GLU:O	5:F:1428:GLN:HB2	1.97	0.64
8:I:786:ASN:O	8:I:786:ASN:ND2	2.29	0.64
5:F:690:GLU:OE1	8:I:722:LEU:CD2	2.44	0.64
3:D:919:VAL:HG21	3:D:927:LEU:H	1.62	0.64
4:E:687:LYS:CB	5:F:1391:GLY:HA2	2.27	0.64
5:F:633:LYS:HZ2	5:F:635:PHE:HB2	1.61	0.64
5:F:1084:LEU:CA	5:F:1156:TYR:OH	2.25	0.64
1:A:776:ILE:HG23	1:A:831:THR:HG22	1.79	0.64
3:D:260:HIS:CD2	3:D:261:LEU:HD23	2.33	0.64
5:F:310:MET:HE2	5:F:453:ILE:HG22	1.78	0.64
5:F:718:SER:O	5:F:722:ARG:NH2	2.30	0.64
1:Z:590:LEU:HD23	1:Z:604:ILE:HG21	1.79	0.64
1:A:772:PRO:CA	1:A:828:THR:CG2	2.72	0.64
5:F:1088:ARG:HG3	5:F:1088:ARG:NH1	2.12	0.64
1:Z:821:GLN:CB	1:Z:829:TYR:CB	2.76	0.64
3:D:529:GLY:O	3:D:581:PRO:HD3	1.98	0.64
1:Z:824:MET:SD	1:Z:824:MET:N	2.70	0.64
5:F:1435:LYS:HZ3	5:F:1484:ARG:NH2	1.94	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:377:ILE:HG22	6:J:378:HIS:HD2	1.62	0.64
5:F:177:GLN:NE2	5:F:178:ASN:OD1	2.31	0.64
5:F:350:ARG:O	5:F:393:SER:HB2	1.94	0.64
5:F:442:ILE:HG23	5:F:443:ILE:HG13	1.80	0.64
6:J:322:THR:O	6:J:326:LEU:HG	1.98	0.64
7:K:355:PHE:HD1	7:K:358:LEU:HD12	1.61	0.64
1:Z:45:SER:O	1:Z:48:GLU:N	2.31	0.64
1:A:128:LEU:HD13	4:E:1260:TYR:HH	1.63	0.63
1:A:210:GLU:O	1:A:213:GLU:N	2.31	0.63
2:C:885:VAL:HG13	2:C:901:ILE:HG23	1.79	0.63
5:F:1216:PHE:CE2	5:F:1282:ALA:HB1	2.29	0.63
3:D:581:PRO:HA	3:D:594:GLU:HA	1.79	0.63
3:D:1494:ASN:O	5:F:1471:LYS:HE2	1.98	0.63
4:E:1377:ASN:CB	4:E:1380:ASP:CB	2.76	0.63
5:F:389:LEU:HD12	5:F:389:LEU:N	2.11	0.63
5:F:1110:MET:HE2	5:F:1157:TRP:CZ2	2.34	0.63
5:F:1363:ILE:CG2	1:Z:125:ILE:HD12	2.28	0.63
6:J:334:SER:O	6:J:337:LYS:N	2.27	0.63
1:Z:577:ARG:HH21	1:Z:630:ARG:HE	1.46	0.63
5:F:1309:LEU:O	5:F:1309:LEU:HD22	1.98	0.63
4:E:258:ILE:HG22	4:E:261:ILE:CG1	2.28	0.63
5:F:321:GLN:HA	5:F:324:ILE:HG12	1.81	0.63
5:F:1303:LEU:HD22	5:F:1303:LEU:C	2.23	0.63
5:F:1406:TYR:HH	5:F:1452:SER:HG	1.43	0.63
6:J:389:ARG:HG2	6:J:389:ARG:HH11	1.63	0.63
4:E:1418:LEU:HG	4:E:1421:ILE:HD12	1.81	0.63
5:F:36:ASN:HD22	5:F:110:ARG:HH11	1.46	0.63
5:F:101:ASN:OD1	5:F:105:GLN:NE2	2.31	0.63
5:F:841:PHE:HD2	5:F:918:PHE:HE1	0.69	0.63
7:K:321:ALA:C	7:K:348:ILE:CD1	2.69	0.63
8:L:703:GLN:HA	8:L:706:GLU:OE1	1.98	0.63
5:F:656:VAL:HG13	5:F:657:ILE:HG13	1.80	0.63
5:F:883:VAL:O	8:I:761:ASN:CG	2.41	0.63
6:J:357:LEU:HB3	7:K:423:LYS:HE2	1.68	0.63
7:K:505:ARG:O	7:K:509:ILE:N	2.28	0.63
5:F:1297:GLU:OE1	5:F:1297:GLU:HA	1.96	0.63
1:Z:92:THR:O	1:Z:92:THR:OG1	2.15	0.63
1:Z:751:LEU:C	1:Z:753:ALA:N	2.57	0.63
3:D:412:ILE:HG13	3:D:413:LEU:HD12	1.79	0.63
7:H:511:GLU:CB	8:I:800:HIS:CE1	2.82	0.63
3:D:377:ILE:HD11	3:D:420:ILE:HD13	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:971:SER:HB3	7:H:392:LEU:HD21	1.80	0.63
8:I:778:LYS:O	8:I:778:LYS:HD3	1.98	0.63
6:J:315:LEU:HD23	8:L:679:LEU:HG	1.81	0.63
8:L:640:LEU:HA	8:L:643:LYS:HB3	1.80	0.63
4:E:421:PHE:O	4:E:425:LEU:HB2	1.99	0.62
2:C:811:LEU:CD1	2:C:867:LEU:HD21	2.30	0.62
3:D:557:THR:HG21	3:D:571:THR:HG21	1.81	0.62
3:D:932:ILE:HG23	3:D:933:ILE:HG13	1.82	0.62
5:F:334:GLN:CG	5:F:854:GLU:CD	2.72	0.62
7:K:419:LEU:HD23	7:K:419:LEU:O	1.97	0.62
1:Z:422:ARG:HE	1:Z:424:ASN:H	1.48	0.62
5:F:657:ILE:HG23	5:F:660:LEU:HB3	1.80	0.62
5:F:1635:ARG:O	5:F:1639:GLY:CA	2.46	0.62
6:J:390:ILE:HG12	8:L:766:ILE:HD12	1.80	0.62
7:K:338:ALA:HA	7:K:341:LYS:HE2	1.80	0.62
1:Z:196:ASN:HD21	1:Z:530:ARG:HE	1.44	0.62
3:D:242:MET:SD	3:D:298:TYR:HD2	2.17	0.62
3:D:412:ILE:HB	3:D:476:VAL:HG21	1.82	0.62
4:E:1640:ILE:O	4:E:1644:ILE:HB	1.99	0.62
7:K:400:LYS:HD2	7:K:400:LYS:C	2.20	0.62
1:Z:44:VAL:O	1:Z:47:ASN:CB	2.46	0.62
7:H:521:THR:HA	7:H:524:ASN:HB2	1.82	0.62
8:L:643:LYS:O	8:L:647:GLN:NE2	2.33	0.62
8:L:685:MET:HA	8:L:688:HIS:ND1	2.14	0.62
1:A:123:MET:O	6:J:414:SER:HB2	2.00	0.62
1:A:654:ILE:HD11	1:A:696:TYR:HD2	1.63	0.62
4:E:1143:GLN:HA	4:E:1158:TYR:HA	1.81	0.62
5:F:603:GLU:HA	5:F:606:VAL:HG12	1.82	0.62
1:A:337:ILE:HG23	1:A:349:ALA:HB1	1.81	0.62
1:A:775:LEU:CB	1:A:832:LEU:HD12	2.27	0.62
4:E:258:ILE:HG22	4:E:261:ILE:HG13	1.81	0.62
5:F:1399:VAL:O	5:F:1399:VAL:HG12	2.00	0.62
7:H:426:GLY:HA2	8:I:736:ASN:CA	2.30	0.62
1:Z:814:MET:CB	1:Z:833:ILE:HD12	2.28	0.62
1:A:56:LEU:CB	8:L:804:LEU:HD13	2.30	0.62
1:A:60:ASN:CB	8:L:803:ALA:O	2.47	0.62
3:D:850:ASN:HD22	3:D:904:LYS:HD3	1.64	0.62
8:I:737:ASN:OD1	8:I:738:ASP:CG	2.41	0.62
6:J:293:HIS:HB3	7:K:359:ASN:HD21	1.63	0.62
7:K:365:GLN:HB3	8:L:669:LEU:HD13	1.81	0.62
8:L:682:ASP:O	8:L:685:MET:HG2	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:LEU:HD11	1:A:339:TYR:HE2	1.64	0.62
4:E:980:LYS:O	4:E:980:LYS:HD2	2.00	0.62
5:F:1469:ARG:HH12	5:F:1530:GLU:HG2	1.65	0.62
6:J:371:LYS:HZ2	6:J:371:LYS:C	2.06	0.62
7:K:295:CYS:O	7:K:299:TRP:HB2	2.00	0.62
1:A:23:ASN:C	1:A:25:LEU:H	2.08	0.62
1:A:742:LEU:HD13	1:A:744:LEU:HD12	1.82	0.62
5:F:38:ASN:HD22	5:F:41:LYS:HB2	1.63	0.62
5:F:334:GLN:HE22	5:F:859:LYS:CD	2.13	0.62
5:F:1314:VAL:HG11	5:F:1373:ASP:CB	2.29	0.62
5:F:1314:VAL:HG23	5:F:1314:VAL:O	1.98	0.62
6:J:301:HIS:CE1	8:L:665:TRP:HB3	2.35	0.62
7:K:359:ASN:O	7:K:363:GLN:HG2	2.00	0.62
8:L:637:LEU:HD23	8:L:640:LEU:H	1.65	0.62
1:Z:753:ALA:HA	1:Z:816:TYR:HA	1.72	0.62
1:A:542:THR:HA	1:A:545:PHE:CE1	2.35	0.61
6:G:452:ASP:CB	1:Z:84:ASP:OD2	2.48	0.61
7:K:527:LEU:O	7:K:531:ALA:HB2	2.00	0.61
3:D:929:PHE:O	3:D:932:ILE:HG22	1.99	0.61
3:D:518:GLU:HA	3:D:536:ILE:HD12	1.82	0.61
3:D:971:ILE:CD1	3:D:984:THR:HB	2.29	0.61
4:E:567:ARG:O	4:E:571:ASN:ND2	2.33	0.61
5:F:1156:TYR:O	5:F:1159:GLN:N	2.33	0.61
7:K:317:ASN:HA	7:K:346:GLN:HB3	1.82	0.61
1:Z:23:ASN:C	1:Z:25:LEU:H	2.08	0.61
1:Z:310:ASP:HA	1:Z:314:LYS:HB3	1.80	0.61
3:D:483:HIS:HB2	3:D:486:GLN:CG	2.28	0.61
5:F:138:GLY:H	5:F:206:ILE:HD11	1.64	0.61
5:F:195:GLN:NE2	5:F:232:TYR:O	2.33	0.61
6:J:325:TYR:HE2	7:K:390:HIS:CA	1.96	0.61
1:Z:822:TYR:HB3	1:Z:824:MET:HE1	1.81	0.61
1:A:137:ASP:CB	4:E:1386:LEU:HG	2.30	0.61
3:D:470:SER:HB3	3:D:475:GLU:HG2	1.82	0.61
6:G:427:GLU:CB	8:I:779:THR:HG21	2.31	0.61
6:J:383:LYS:HZ2	8:L:756:ASN:CA	1.67	0.61
1:Z:814:MET:HA	1:Z:817:ALA:HB3	1.82	0.61
1:A:557:LEU:HG	1:A:579:LEU:HD11	1.83	0.61
2:C:867:LEU:HD22	2:C:888:LEU:HD21	1.82	0.61
4:E:982:ILE:HG22	4:E:982:ILE:O	2.00	0.61
6:J:357:LEU:HB3	7:K:423:LYS:HE3	0.67	0.61
3:D:147:PRO:HB2	3:D:580:VAL:HG21	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:22:MET:HE1	4:E:122:ILE:HG21	1.81	0.61
4:E:215:GLN:NE2	4:E:219:GLN:OE1	2.34	0.61
6:G:431:GLN:CB	7:H:503:ASN:CB	2.78	0.61
3:D:421:VAL:HG22	3:D:491:ARG:HB3	1.82	0.61
5:F:303:LYS:O	5:F:307:ASP:HB2	2.00	0.61
3:D:927:LEU:HD13	3:D:973:ARG:HH22	1.66	0.61
5:F:690:GLU:HG3	8:I:722:LEU:HG	1.82	0.61
6:J:327:LYS:O	6:J:331:LYS:HG3	2.01	0.61
7:K:312:VAL:HG12	7:K:361:ARG:HH21	1.66	0.61
1:Z:459:LEU:O	1:Z:463:GLN:HB2	2.01	0.61
5:F:1435:LYS:HE2	5:F:1484:ARG:HH21	1.65	0.61
5:F:1653:LYS:HG2	5:F:1655:SER:H	1.66	0.61
7:H:386:LEU:O	8:I:690:GLN:NE2	2.33	0.61
4:E:673:SER:O	4:E:677:ASN:ND2	2.33	0.60
5:F:922:LEU:H	5:F:922:LEU:HD12	1.65	0.60
2:C:1388:HIS:C	4:E:1331:LEU:HD11	2.26	0.60
3:D:1241:GLY:CA	1:Z:826:ARG:O	2.48	0.60
5:F:398:MET:O	5:F:400:THR:HG23	2.01	0.60
7:K:308:LEU:HB3	7:K:355:PHE:CE2	2.36	0.60
3:D:454:ARG:HB3	3:D:455:PHE:CD1	2.37	0.60
6:J:308:ILE:HD11	7:K:369:VAL:HG13	1.83	0.60
1:Z:56:LEU:HD22	1:Z:60:ASN:HD21	1.65	0.60
1:Z:207:ILE:HB	1:Z:246:ASN:CB	2.31	0.60
1:A:779:LEU:C	1:A:835:ILE:CB	2.74	0.60
3:D:237:THR:O	3:D:266:GLN:HA	2.01	0.60
4:E:987:SER:OG	4:E:987:SER:O	2.15	0.60
4:E:1620:THR:HB	4:E:1623:GLU:HB2	1.83	0.60
5:F:759:ASP:O	5:F:773:LYS:NZ	2.34	0.60
5:F:1118:ARG:HG2	5:F:1118:ARG:HH11	1.66	0.60
5:F:1157:TRP:CD1	5:F:1160:TYR:HE1	2.19	0.60
7:H:450:PRO:O	7:H:454:GLY:N	2.35	0.60
3:D:298:TYR:CD1	3:D:311:LYS:HE2	2.37	0.60
7:H:436:MET:O	7:H:440:PHE:HB3	2.02	0.60
8:I:778:LYS:HD3	8:I:778:LYS:C	2.26	0.60
6:J:432:LEU:CA	8:L:782:ILE:O	2.50	0.60
6:J:433:LYS:N	7:K:499:GLY:CA	2.63	0.60
7:K:385:GLN:HE21	7:K:385:GLN:CA	2.12	0.60
1:Z:218:ILE:HD11	1:Z:241:ILE:HD12	1.84	0.60
1:A:57:ARG:HH11	1:A:57:ARG:CG	2.08	0.60
1:A:590:LEU:HD23	1:A:604:ILE:HG21	1.84	0.60
7:K:523:LEU:O	7:K:527:LEU:CB	2.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:777:ILE:HG23	1:Z:777:ILE:O	2.00	0.60
1:A:208:LEU:O	1:A:212:PHE:HB2	2.02	0.60
5:F:29:LEU:HD13	5:F:134:LEU:HG	1.84	0.60
6:G:449:LEU:HA	1:Z:84:ASP:CG	2.26	0.60
6:J:371:LYS:O	6:J:371:LYS:HD2	2.01	0.60
6:J:384:LEU:HD23	6:J:384:LEU:C	2.26	0.60
1:A:510:LEU:HD22	1:A:515:LEU:HD22	1.82	0.60
3:D:789:VAL:HG11	3:D:952:LEU:HD11	1.84	0.60
3:D:1467:SER:HA	1:Z:621:HIS:HE1	1.67	0.60
3:D:1493:ASN:OD1	5:F:1471:LYS:HG2	2.02	0.60
5:F:668:ARG:HH22	5:F:719:ILE:HA	1.66	0.60
5:F:1349:PHE:N	5:F:1349:PHE:CD1	2.70	0.60
6:G:357:LEU:O	8:I:732:ALA:C	2.44	0.60
6:J:364:ILE:CA	7:K:424:ASN:HD22	2.07	0.60
5:F:332:VAL:HG13	5:F:335:ASP:HA	1.84	0.60
7:H:361:ARG:NH2	8:I:666:ASP:OD2	2.35	0.60
8:L:776:PHE:HA	8:L:779:THR:CB	2.32	0.60
1:Z:753:ALA:CB	1:Z:815:ILE:O	2.29	0.60
1:A:613:VAL:HG11	1:A:619:PHE:HB2	1.84	0.60
3:D:449:ASN:HD21	3:D:461:ARG:HB2	1.65	0.60
3:D:989:GLN:HA	3:D:998:ALA:HA	1.82	0.60
7:K:444:LEU:HA	7:K:447:SER:CB	2.32	0.60
1:Z:287:ASP:HA	1:Z:290:TYR:HB3	1.83	0.60
1:Z:766:ASN:C	1:Z:770:ASN:HD22	2.09	0.60
1:A:193:LEU:HA	1:A:539:ALA:HB1	1.84	0.59
3:D:863:ILE:CG2	3:D:887:GLN:HA	2.32	0.59
5:F:1084:LEU:CA	5:F:1156:TYR:CZ	2.85	0.59
5:F:334:GLN:NE2	5:F:859:LYS:CD	2.65	0.59
5:F:661:VAL:O	5:F:667:SER:OG	2.21	0.59
5:F:1032:ILE:HG22	5:F:1032:ILE:O	2.01	0.59
8:L:702:ARG:O	8:L:706:GLU:OE1	2.20	0.59
5:F:1139:ILE:CG1	5:F:1291:SER:OG	2.49	0.59
6:J:398:VAL:HG21	7:K:462:ARG:C	2.28	0.59
7:K:298:SER:CA	7:K:306:THR:HA	2.27	0.59
1:Z:393:GLU:HA	1:Z:396:GLN:HG2	1.84	0.59
1:Z:766:ASN:O	1:Z:769:LYS:CB	2.50	0.59
1:A:128:LEU:CG	4:E:1260:TYR:CE2	2.86	0.59
2:C:318:ILE:HD12	2:C:318:ILE:N	2.01	0.59
2:C:811:LEU:HD11	2:C:867:LEU:HD21	1.83	0.59
3:D:268:ILE:HG21	3:D:284:PHE:CE2	2.36	0.59
5:F:405:ARG:NH1	5:F:407:ASN:HB3	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1309:LEU:HD22	5:F:1309:LEU:C	2.27	0.59
6:J:324:GLN:OE1	6:J:328:GLN:NE2	2.35	0.59
6:J:351:SER:O	6:J:355:GLN:NE2	2.36	0.59
6:J:334:SER:C	6:J:337:LYS:H	2.09	0.59
1:Z:531:ASP:OD2	1:Z:540:ASN:ND2	2.36	0.59
1:A:814:MET:CG	1:A:833:ILE:CG1	2.81	0.59
1:A:814:MET:HG2	1:A:833:ILE:CD1	2.28	0.59
3:D:641:VAL:HB	3:D:648:GLU:HG2	1.83	0.59
5:F:725:ASN:ND2	5:F:789:CYS:SG	2.76	0.59
8:I:795:LYS:C	8:I:795:LYS:HD3	2.28	0.59
1:Z:501:MET:O	1:Z:505:HIS:ND1	2.34	0.59
1:Z:771:ILE:HB	1:Z:772:PRO:HD2	1.83	0.59
1:A:16:LYS:HD3	6:J:468:ALA:HA	1.84	0.59
1:A:775:LEU:CG	1:A:832:LEU:HD11	2.33	0.59
3:D:713:ILE:HD12	3:D:769:ARG:HD3	1.83	0.59
3:D:744:SER:HA	3:D:758:ASP:CB	2.33	0.59
4:E:757:LYS:HG3	5:F:1195:PHE:HB2	1.85	0.59
5:F:235:PRO:O	5:F:239:HIS:ND1	2.35	0.59
2:C:786:THR:CB	2:C:789:ASP:OD2	2.50	0.59
3:D:1377:ASN:CG	1:Z:758:GLN:HE21	2.11	0.59
4:E:258:ILE:HG22	4:E:261:ILE:HD11	1.84	0.59
5:F:323:LEU:HD11	5:F:483:LEU:HD23	1.84	0.59
5:F:353:PRO:HA	5:F:393:SER:HA	1.85	0.59
5:F:837:TYR:CG	5:F:918:PHE:CE2	2.90	0.59
5:F:935:GLN:CB	5:F:998:LEU:HD23	2.33	0.59
7:K:379:ILE:HG21	8:L:680:TYR:CE1	2.38	0.59
1:Z:227:GLN:NE2	1:Z:606:GLU:O	2.30	0.59
1:A:123:MET:CB	6:J:413:ASN:HB3	2.32	0.59
4:E:1031:LYS:NZ	4:E:1084:LEU:O	2.36	0.59
5:F:510:PHE:HA	5:F:513:TRP:HB3	1.85	0.59
5:F:51:LEU:HD23	5:F:71:ILE:HG13	1.84	0.59
6:G:292:HIS:ND1	6:J:352:VAL:CG1	2.63	0.59
6:G:295:LYS:CB	6:J:363:LYS:NZ	2.65	0.59
7:H:412:ILE:HG23	7:H:415:LEU:HD23	1.67	0.59
4:E:793:LEU:HD11	4:E:1162:LEU:HD21	1.83	0.58
6:G:401:ILE:O	6:G:405:LEU:HB2	2.03	0.58
1:A:589:LEU:HA	1:A:603:VAL:HG22	1.84	0.58
3:D:353:GLN:HB3	3:D:372:SER:HB2	1.84	0.58
5:F:1434:SER:OG	5:F:1435:LYS:N	2.36	0.58
7:K:312:VAL:CG2	7:K:352:ILE:HG13	2.33	0.58
1:Z:531:ASP:OD1	1:Z:531:ASP:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:767:ILE:O	1:Z:770:ASN:N	2.36	0.58
1:A:440:LEU:HA	1:A:443:ILE:HD12	1.85	0.58
5:F:1093:SER:O	5:F:1096:LEU:CB	2.51	0.58
5:F:1116:VAL:HG21	5:F:1150:PHE:HZ	1.67	0.58
5:F:1246:MET:CB	5:F:1279:CYS:CB	2.81	0.58
5:F:1468:ASN:ND2	5:F:1530:GLU:OE1	2.36	0.58
4:E:267:ILE:HA	4:E:270:ILE:HD12	1.85	0.58
5:F:679:ILE:O	5:F:679:ILE:HG22	2.03	0.58
5:F:746:LYS:HD2	5:F:898:TYR:H	1.68	0.58
5:F:1031:VAL:CB	6:G:314:TYR:HB3	2.34	0.58
5:F:1538:LEU:HD11	5:F:1543:LEU:HD23	1.84	0.58
1:A:22:LEU:O	1:A:25:LEU:HB3	2.04	0.58
3:D:491:ARG:HG3	3:D:521:LYS:HB2	1.86	0.58
5:F:2:LYS:HG2	5:F:7:PRO:HG2	1.84	0.58
1:Z:22:LEU:O	1:Z:25:LEU:HB3	2.04	0.58
1:A:46:ILE:HA	8:L:792:GLN:N	2.16	0.58
5:F:492:ARG:HH12	5:F:495:TYR:H	1.51	0.58
6:G:465:LYS:HE3	1:Z:20:LYS:NZ	2.18	0.58
8:L:774:ASN:HD22	8:L:777:ASN:HD22	1.51	0.58
8:L:793:LEU:O	8:L:796:ILE:N	2.36	0.58
3:D:860:ILE:CG2	3:D:893:ILE:HG13	2.33	0.58
3:D:1467:SER:HA	1:Z:621:HIS:CE1	2.38	0.58
4:E:1022:TYR:CZ	4:E:1026:THR:HG22	2.37	0.58
5:F:199:GLY:O	5:F:203:LYS:NZ	2.37	0.58
5:F:227:ASP:CA	5:F:379:SER:CB	2.79	0.58
5:F:333:GLU:C	5:F:335:ASP:N	2.61	0.58
5:F:1473:ASN:HB2	5:F:1475:ILE:H	1.69	0.58
5:F:1508:ILE:HA	5:F:1511:LEU:HB3	1.85	0.58
7:H:426:GLY:HA3	8:I:735:ASN:C	2.27	0.58
1:Z:133:THR:O	1:Z:135:ASP:N	2.37	0.58
1:A:236:ASN:ND2	1:A:261:GLU:OE1	2.35	0.58
3:D:119:PRO:HB3	3:D:739:THR:HG22	1.84	0.58
3:D:298:TYR:HE1	3:D:311:LYS:CE	2.17	0.58
3:D:507:LEU:HG	3:D:512:LYS:HB3	1.85	0.58
6:J:332:LYS:HE3	7:K:402:GLN:HG3	1.86	0.58
7:K:429:LEU:HD12	7:K:429:LEU:O	2.03	0.58
2:C:121:LEU:HD23	2:C:123:TYR:CZ	2.38	0.58
5:F:1005:PHE:O	5:F:1009:ASN:HB2	2.03	0.58
5:F:1129:ASN:OD1	5:F:1132:GLU:N	2.36	0.58
5:F:1492:LEU:O	5:F:1495:THR:OG1	2.22	0.58
6:G:295:LYS:C	6:J:363:LYS:HZ2	2.11	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:449:LEU:HA	1:Z:84:ASP:OD2	2.03	0.58
7:H:426:GLY:HA3	8:I:736:ASN:N	2.18	0.58
1:Z:421:SER:O	1:Z:423:LYS:NZ	2.37	0.58
1:A:133:THR:O	1:A:135:ASP:N	2.37	0.58
5:F:909:LEU:O	7:H:403:SER:C	2.47	0.58
5:F:914:ASP:CB	5:F:917:PHE:HB3	2.34	0.58
6:G:295:LYS:HB3	6:J:363:LYS:HZ2	1.68	0.58
3:D:799:THR:HA	3:D:803:PHE:HB2	1.85	0.57
4:E:1259:PHE:CD1	4:E:1259:PHE:C	2.82	0.57
5:F:333:GLU:C	5:F:335:ASP:H	2.11	0.57
1:Z:44:VAL:O	1:Z:47:ASN:N	2.37	0.57
3:D:853:PHE:CE2	3:D:900:VAL:HG21	2.39	0.57
7:H:397:ARG:NH2	8:I:698:GLN:OE1	2.37	0.57
8:I:785:ASN:CB	1:Z:112:TYR:HA	2.34	0.57
8:I:823:LYS:HD2	8:I:823:LYS:O	2.04	0.57
7:K:313:TYR:HD1	7:K:349:PRO:HB3	1.68	0.57
5:F:1014:SER:H	8:I:788:ASP:H	1.49	0.57
5:F:1435:LYS:NZ	5:F:1484:ARG:HH22	2.00	0.57
7:K:444:LEU:O	7:K:447:SER:N	2.38	0.57
7:K:513:LEU:HD11	8:L:800:HIS:ND1	2.20	0.57
8:L:765:LEU:O	8:L:769:ILE:HB	2.03	0.57
1:A:706:ILE:HB	1:A:711:LYS:HE2	1.86	0.57
3:D:298:TYR:CE1	3:D:311:LYS:CE	2.87	0.57
5:F:579:ARG:HH11	5:F:698:ASN:HB3	1.69	0.57
5:F:841:PHE:CD2	5:F:918:PHE:CD1	2.89	0.57
6:J:308:ILE:HB	6:J:309:PRO:HD3	1.86	0.57
1:Z:810:ALA:CB	1:Z:835:ILE:O	2.51	0.57
3:D:328:LEU:HD11	3:D:334:VAL:HG22	1.86	0.57
3:D:515:VAL:HB	3:D:604:PRO:CG	2.35	0.57
3:D:753:PRO:HG2	3:D:756:LYS:HE3	1.87	0.57
5:F:712:LEU:HG	5:F:716:LEU:HD23	1.86	0.57
5:F:1063:ILE:HG22	5:F:1063:ILE:O	2.05	0.57
5:F:1467:ALA:HB1	5:F:1473:ASN:HB3	1.84	0.57
4:E:888:TYR:O	4:E:897:LYS:NZ	2.37	0.57
5:F:354:ARG:HB3	5:F:354:ARG:NH1	2.20	0.57
5:F:1118:ARG:HG2	5:F:1118:ARG:NH1	2.19	0.57
5:F:1650:GLU:OE1	5:F:1659:ASN:ND2	2.37	0.57
1:A:417:ARG:NH2	1:A:442:LEU:O	2.38	0.57
1:A:559:LEU:HA	1:A:562:LEU:HD13	1.86	0.57
3:D:853:PHE:HE2	3:D:900:VAL:HG21	1.70	0.57
5:F:702:LYS:HA	5:F:767:ILE:HD11	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1110:MET:HE1	5:F:1161:LEU:HD11	1.86	0.57
7:H:397:ARG:HB2	8:I:697:LEU:HD21	1.86	0.57
1:A:751:LEU:HD22	2:C:1313:LEU:HD23	1.86	0.57
4:E:1005:LEU:HD13	4:E:1046:LYS:HZ1	1.68	0.57
5:F:397:MET:N	5:F:397:MET:SD	2.77	0.57
5:F:590:ILE:HG13	5:F:591:ASP:H	1.69	0.57
5:F:712:LEU:HG	5:F:716:LEU:CD2	2.35	0.57
8:L:799:SER:O	8:L:803:ALA:HB3	2.05	0.57
4:E:1484:LYS:HZ2	4:E:1486:GLU:HB2	1.69	0.57
1:A:435:TRP:HA	1:A:438:MET:SD	2.44	0.57
1:A:775:LEU:HB3	1:A:832:LEU:CG	2.34	0.57
4:E:812:SER:O	4:E:872:ASN:ND2	2.38	0.57
4:E:837:ASP:HB3	4:E:839:ILE:H	1.69	0.57
6:J:398:VAL:CB	7:K:462:ARG:O	2.53	0.57
1:Z:824:MET:HB2	1:Z:825:PRO:CD	2.30	0.57
3:D:832:VAL:H	3:D:929:PHE:HE2	1.52	0.56
4:E:216:TYR:HD1	4:E:220:PHE:HB2	1.70	0.56
4:E:997:VAL:O	4:E:1001:ASN:ND2	2.38	0.56
5:F:28:VAL:O	5:F:32:LEU:N	2.30	0.56
5:F:353:PRO:O	5:F:356:ILE:CG2	2.53	0.56
5:F:620:THR:HG23	5:F:627:VAL:HG21	1.87	0.56
5:F:750:TRP:NE1	5:F:754:ASP:HB2	2.20	0.56
5:F:1360:LEU:C	5:F:1362:ASP:H	2.13	0.56
6:G:465:LYS:HB3	1:Z:20:LYS:HZ1	1.66	0.56
7:H:522:TYR:CB	1:Z:54:PHE:C	2.77	0.56
8:I:818:ILE:HD13	8:I:818:ILE:N	2.20	0.56
7:K:321:ALA:N	7:K:348:ILE:CD1	2.39	0.56
7:K:427:LEU:N	7:K:428:PRO:HD3	2.20	0.56
3:D:186:ILE:HG22	3:D:189:LYS:HB2	1.87	0.56
3:D:481:LEU:HD23	3:D:488:GLN:HB3	1.86	0.56
3:D:485:GLN:HA	3:D:577:PHE:CZ	2.40	0.56
3:D:527:SER:HB3	3:D:528:PRO:HD2	1.87	0.56
3:D:970:ILE:HG23	3:D:975:ILE:HD12	1.87	0.56
4:E:358:VAL:HG13	4:E:359:LEU:HG	1.87	0.56
5:F:1123:ASN:HB3	5:F:1143:SER:OG	2.05	0.56
7:H:358:LEU:O	7:H:362:ASN:ND2	2.38	0.56
8:I:778:LYS:HZ2	8:I:778:LYS:HA	1.70	0.56
6:J:398:VAL:HG23	7:K:466:LEU:HD11	1.87	0.56
3:D:242:MET:CE	3:D:298:TYR:CD2	2.88	0.56
3:D:535:VAL:HB	3:D:575:LYS:HB2	1.87	0.56
3:D:773:ILE:O	3:D:777:ILE:HG12	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:986:SER:O	4:E:986:SER:OG	2.22	0.56
4:E:1319:LEU:CD2	4:E:1398:VAL:CG2	2.76	0.56
4:E:1443:THR:O	4:E:1446:PHE:HB2	2.06	0.56
4:E:1611:TYR:O	4:E:1615:ARG:HB2	2.04	0.56
5:F:909:LEU:O	7:H:403:SER:HB2	2.05	0.56
5:F:1118:ARG:HH11	5:F:1118:ARG:CG	2.18	0.56
5:F:1270:GLN:O	5:F:1274:ASP:HB2	2.06	0.56
5:F:1435:LYS:O	5:F:1439:GLU:N	2.28	0.56
5:F:1666:MET:O	5:F:1670:ILE:HB	2.05	0.56
6:G:295:LYS:CB	6:J:363:LYS:HZ2	2.19	0.56
7:K:444:LEU:C	7:K:447:SER:CB	2.75	0.56
1:Z:277:TYR:O	1:Z:280:GLN:NE2	2.37	0.56
1:Z:638:TYR:HA	1:Z:641:ILE:HG22	1.88	0.56
5:F:668:ARG:HD2	5:F:716:LEU:HD13	1.88	0.56
5:F:1431:ARG:HD2	5:F:1474:PHE:H	1.70	0.56
6:G:402:ASP:OD2	7:H:462:ARG:NH1	2.38	0.56
6:J:309:PRO:HA	6:J:312:VAL:CG2	2.35	0.56
6:J:391:LEU:HD13	7:K:455:LYS:HA	1.86	0.56
6:J:405:LEU:HD22	7:K:469:ARG:HE	1.67	0.56
6:J:405:LEU:HD23	7:K:469:ARG:HE	1.66	0.56
1:Z:241:ILE:CG2	1:Z:245:ALA:HB1	2.22	0.56
3:D:611:LEU:CD1	3:D:640:ALA:HB2	2.35	0.56
4:E:1644:ILE:HD13	4:E:1647:LEU:HD21	1.86	0.56
5:F:661:VAL:HG11	5:F:712:LEU:HD12	1.87	0.56
5:F:825:ILE:HG22	5:F:890:VAL:HG13	1.87	0.56
5:F:1150:PHE:CD1	5:F:1150:PHE:C	2.83	0.56
5:F:1501:SER:OG	5:F:1502:THR:N	2.38	0.56
6:G:295:LYS:C	6:J:363:LYS:HZ1	2.12	0.56
6:J:296:ALA:O	6:J:299:ILE:HG12	2.06	0.56
1:Z:80:PHE:CD1	1:Z:80:PHE:N	2.73	0.56
3:D:398:ILE:O	3:D:402:ILE:HG12	2.06	0.56
3:D:985:ALA:O	3:D:988:LEU:CB	2.54	0.56
4:E:679:SER:OG	4:E:680:ASP:N	2.34	0.56
4:E:972:LEU:HD23	4:E:995:LEU:HD11	1.86	0.56
5:F:537:PRO:HA	5:F:622:GLN:HB3	1.86	0.56
5:F:1038:LEU:C	5:F:1040:THR:N	2.45	0.56
5:F:1550:LEU:HD13	5:F:1552:PHE:CE1	2.40	0.56
8:I:822:LYS:HZ1	8:I:822:LYS:CA	2.18	0.56
7:K:389:LYS:CB	7:K:393:ASP:HB3	2.32	0.56
1:Z:409:LEU:O	1:Z:413:LYS:HB2	2.04	0.56
1:A:16:LYS:HG2	6:J:468:ALA:HA	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:765:PHE:HB3	4:E:843:LEU:HD22	1.88	0.56
7:H:418:GLN:HE22	8:I:718:THR:CG2	2.03	0.56
1:Z:139:PHE:CD1	1:Z:139:PHE:C	2.84	0.56
1:Z:334:TRP:HA	1:Z:337:ILE:HD12	1.87	0.56
1:Z:692:MET:O	1:Z:696:TYR:HB2	2.06	0.56
3:D:449:ASN:HB3	3:D:463:GLU:HG2	1.86	0.56
4:E:928:SER:HA	4:E:931:PHE:HB2	1.88	0.56
5:F:552:SER:O	5:F:557:ASN:ND2	2.37	0.56
5:F:690:GLU:CG	8:I:722:LEU:CD2	2.80	0.56
6:J:319:GLU:HA	6:J:322:THR:CG2	2.36	0.56
7:K:404:ARG:O	7:K:407:GLU:N	2.37	0.56
7:K:446:ARG:HH22	7:K:455:LYS:HZ3	1.48	0.56
1:A:139:PHE:CD1	1:A:139:PHE:C	2.84	0.56
5:F:1251:ARG:NH2	5:F:1276:ASP:CB	2.66	0.56
5:F:1595:VAL:O	5:F:1599:GLU:HB2	2.06	0.56
6:G:351:SER:O	6:G:355:GLN:NE2	2.39	0.56
7:K:297:GLU:HB3	7:K:304:THR:OG1	2.04	0.56
7:K:538:LYS:O	8:L:822:LYS:CB	2.54	0.56
8:L:658:TYR:O	8:L:662:ILE:HG22	2.06	0.56
3:D:545:GLN:HG3	3:D:572:LEU:CD1	2.36	0.56
3:D:710:VAL:HG22	3:D:711:VAL:H	1.71	0.56
5:F:333:GLU:HA	5:F:420:THR:CB	2.36	0.56
5:F:679:ILE:O	5:F:745:ARG:NH1	2.39	0.56
5:F:869:VAL:HA	5:F:872:ILE:HD12	1.86	0.56
5:F:1403:SER:OG	5:F:1451:THR:O	2.22	0.56
5:F:1598:PHE:HA	5:F:1601:ILE:HB	1.86	0.56
6:J:388:CYS:HA	6:J:391:LEU:HB2	1.89	0.56
1:Z:289:LEU:HD21	1:Z:312:LYS:HG2	1.88	0.56
1:Z:652:ILE:HA	1:Z:655:THR:HG22	1.87	0.56
1:A:46:ILE:HA	8:L:792:GLN:CB	2.36	0.55
5:F:637:ASP:HA	5:F:640:PHE:HD2	1.71	0.55
5:F:1176:GLU:OE1	5:F:1176:GLU:N	2.39	0.55
7:H:418:GLN:CD	8:I:718:THR:HG21	2.26	0.55
3:D:441:VAL:HA	3:D:490:LYS:HB2	1.87	0.55
4:E:134:ARG:NH2	4:E:198:MET:O	2.39	0.55
5:F:885:GLU:HG3	5:F:885:GLU:O	2.07	0.55
5:F:1300:LEU:HD23	5:F:1300:LEU:C	2.31	0.55
6:G:391:LEU:O	6:G:395:GLU:HB2	2.06	0.55
1:A:776:ILE:HD11	1:A:828:THR:HA	1.88	0.55
2:C:1258:GLN:CD	2:C:1299:LYS:HE3	2.31	0.55
3:D:222:ASN:O	3:D:301:SER:N	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:277:THR:HG22	4:E:381:VAL:HG21	1.88	0.55
4:E:331:TYR:OH	4:E:388:ASN:ND2	2.40	0.55
4:E:1450:LEU:HD22	4:E:1456:ILE:HG21	1.88	0.55
7:H:533:ILE:HA	7:H:536:LYS:HB2	1.87	0.55
1:A:607:ARG:HD2	1:A:610:LEU:HD12	1.87	0.55
3:D:654:THR:HB	3:D:655:PRO:HD2	1.87	0.55
3:D:1237:SER:CB	1:Z:829:TYR:CB	2.84	0.55
4:E:312:ASN:ND2	4:E:314:ASP:O	2.39	0.55
5:F:657:ILE:HG12	5:F:660:LEU:HD13	1.87	0.55
5:F:902:LYS:HD3	5:F:903:ASN:H	1.71	0.55
5:F:1063:ILE:HB	5:F:1066:ASP:HB3	1.87	0.55
1:Z:23:ASN:C	1:Z:25:LEU:N	2.64	0.55
3:D:508:LYS:HB3	3:D:516:LEU:HA	1.87	0.55
4:E:264:LEU:O	4:E:268:THR:OG1	2.23	0.55
5:F:1243:GLU:HB3	5:F:1283:LYS:HD2	1.89	0.55
5:F:1435:LYS:CE	5:F:1484:ARG:HH21	2.18	0.55
6:G:411:ASN:OD1	6:G:411:ASN:N	2.37	0.55
6:J:309:PRO:HA	6:J:312:VAL:HB	1.88	0.55
1:Z:589:LEU:HA	1:Z:603:VAL:HG22	1.88	0.55
1:A:814:MET:CG	1:A:833:ILE:HG12	2.35	0.55
3:D:139:LYS:HE3	3:D:600:GLU:HB2	1.88	0.55
3:D:484:GLN:HG2	3:D:568:GLN:OE1	2.07	0.55
3:D:911:ASN:HA	3:D:914:TYR:CD2	2.42	0.55
4:E:318:HIS:H	4:E:321:ILE:HD11	1.71	0.55
4:E:1309:ARG:HH21	4:E:1313:ARG:HH12	1.55	0.55
4:E:1585:LEU:N	4:E:1590:ASP:OD2	2.40	0.55
5:F:1606:GLN:HB3	1:Z:141:ASN:ND2	2.19	0.55
5:F:1674:CYS:HA	5:F:1677:THR:OG1	2.07	0.55
6:J:405:LEU:HD11	7:K:470:ALA:HA	1.87	0.55
8:L:640:LEU:HD13	8:L:643:LYS:HG2	1.88	0.55
8:L:672:GLY:HA2	8:L:675:GLN:HG2	1.87	0.55
1:A:309:ILE:HG23	1:A:313:LEU:HD12	1.89	0.55
1:A:492:ILE:HD11	1:A:510:LEU:HD12	1.89	0.55
1:A:642:LEU:HA	1:A:645:GLN:NE2	2.22	0.55
3:D:175:ILE:HG12	3:D:182:CYS:SG	2.47	0.55
3:D:903:ILE:HG23	3:D:953:PHE:CE1	2.42	0.55
3:D:956:ASN:O	3:D:960:LYS:N	2.37	0.55
5:F:355:LEU:H	5:F:355:LEU:CD1	2.20	0.55
5:F:554:SER:OG	5:F:555:TRP:N	2.39	0.55
5:F:1068:ILE:HG22	5:F:1068:ILE:O	2.05	0.55
5:F:1376:THR:O	5:F:1376:THR:OG1	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:324:GLN:OE1	6:J:327:LYS:HE3	2.06	0.55
1:Z:25:LEU:O	1:Z:25:LEU:HD23	2.07	0.55
3:D:155:ASN:HA	3:D:646:SER:CB	2.36	0.55
3:D:475:GLU:OE2	3:D:487:GLU:N	2.40	0.55
3:D:507:LEU:HG	3:D:512:LYS:CB	2.37	0.55
4:E:258:ILE:HG22	4:E:261:ILE:CD1	2.37	0.55
4:E:1356:LEU:HB2	1:Z:453:VAL:HG21	1.88	0.55
5:F:227:ASP:CB	5:F:379:SER:CB	2.84	0.55
5:F:788:LEU:HD12	5:F:874:LYS:HE2	1.88	0.55
5:F:928:LEU:HD12	5:F:928:LEU:N	2.01	0.55
5:F:1040:THR:O	5:F:1042:ILE:N	2.40	0.55
5:F:1167:LYS:HD3	5:F:1167:LYS:C	2.30	0.55
5:F:1356:LEU:O	5:F:1356:LEU:HG	2.03	0.55
7:K:431:ILE:O	7:K:435:LYS:CB	2.55	0.55
7:K:456:THR:C	7:K:458:GLU:N	2.64	0.55
8:L:792:GLN:HA	8:L:796:ILE:HB	1.88	0.55
1:Z:288:ASN:O	1:Z:292:LYS:HB2	2.06	0.55
5:F:334:GLN:NE2	5:F:859:LYS:CE	2.68	0.55
5:F:1067:ASN:HD22	5:F:1069:ASP:HB2	1.71	0.55
5:F:1674:CYS:C	5:F:1676:LEU:H	2.13	0.55
8:I:674:GLU:OE1	8:I:675:GLN:NE2	2.40	0.55
6:J:364:ILE:C	7:K:424:ASN:HD22	2.15	0.55
3:D:467:PHE:CG	3:D:473:THR:HG23	2.42	0.55
4:E:20:ASN:ND2	4:E:894:VAL:O	2.40	0.55
4:E:137:VAL:HA	4:E:140:LYS:HG2	1.88	0.55
5:F:1088:ARG:HH12	8:I:785:ASN:HA	1.72	0.55
5:F:1362:ASP:CB	1:Z:125:ILE:HG21	2.37	0.55
5:F:1674:CYS:C	5:F:1676:LEU:N	2.65	0.55
7:H:529:LYS:HB2	8:I:814:LEU:HD11	1.88	0.55
1:A:128:LEU:CD1	4:E:1260:TYR:CE2	2.88	0.54
1:A:660:LEU:HG	1:A:685:PRO:HB3	1.88	0.54
3:D:187:ASP:O	3:D:210:THR:HA	2.07	0.54
5:F:1286:PHE:O	5:F:1286:PHE:HD1	1.89	0.54
6:G:281:ASP:HA	6:G:284:ILE:HD12	1.89	0.54
8:I:751:LEU:HA	8:I:754:ASN:HD22	1.72	0.54
1:Z:439:HIS:HD1	1:Z:457:TYR:HH	1.55	0.54
1:A:25:LEU:HD23	1:A:25:LEU:O	2.07	0.54
1:A:215:TYR:HB3	1:A:505:HIS:NE2	2.23	0.54
3:D:1238:ARG:HA	1:Z:830:SER:HB2	1.87	0.54
4:E:14:THR:HB	4:E:17:HIS:HB2	1.88	0.54
5:F:10:THR:O	5:F:14:SER:HB3	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:837:TYR:CG	5:F:918:PHE:HE2	2.25	0.54
5:F:1200:PRO:O	5:F:1299:ASN:OD1	2.26	0.54
5:F:1445:VAL:HG12	5:F:1453:ARG:HG3	1.89	0.54
5:F:1473:ASN:OD1	5:F:1476:LEU:N	2.34	0.54
8:I:752:ASP:OD1	8:I:756:ASN:ND2	2.40	0.54
1:Z:197:GLU:O	1:Z:530:ARG:NH2	2.40	0.54
1:A:501:MET:HA	1:A:541:TYR:CE1	2.41	0.54
1:A:814:MET:CG	1:A:833:ILE:HD13	2.35	0.54
3:D:164:PHE:HA	3:D:186:ILE:HD12	1.88	0.54
3:D:528:PRO:HG3	3:D:624:PHE:HE2	1.67	0.54
3:D:691:LYS:O	3:D:696:ARG:NH2	2.41	0.54
4:E:723:LEU:HD23	4:E:794:ILE:HD12	1.88	0.54
5:F:788:LEU:HA	5:F:791:PHE:HB3	1.88	0.54
5:F:837:TYR:CD2	5:F:918:PHE:HE2	2.26	0.54
6:G:465:LYS:HE3	1:Z:20:LYS:CE	2.37	0.54
8:I:739:GLN:C	8:I:741:ARG:N	2.61	0.54
7:K:352:ILE:HG21	7:K:358:LEU:CG	2.38	0.54
7:K:402:GLN:HE21	7:K:402:GLN:C	2.14	0.54
1:Z:136:PHE:C	1:Z:136:PHE:CD1	2.85	0.54
1:Z:661:LEU:HB2	1:Z:717:LEU:HD13	1.89	0.54
3:D:402:ILE:HG13	3:D:406:THR:HB	1.88	0.54
5:F:225:SER:HA	5:F:383:ASN:HD21	1.73	0.54
5:F:273:VAL:HB	5:F:384:MET:HE1	1.89	0.54
5:F:579:ARG:HH22	5:F:701:THR:HG21	1.71	0.54
5:F:1364:TYR:HD1	5:F:1364:TYR:O	1.90	0.54
6:J:305:ILE:HD11	8:L:668:VAL:CG1	2.35	0.54
6:J:398:VAL:CG2	7:K:462:ARG:CB	2.76	0.54
7:K:379:ILE:O	7:K:382:LYS:CA	2.55	0.54
1:A:775:LEU:CD1	1:A:832:LEU:HD11	2.37	0.54
3:D:605:VAL:HG13	3:D:641:VAL:HG13	1.88	0.54
4:E:227:ILE:CD1	4:E:258:ILE:HD11	2.36	0.54
4:E:1022:TYR:CZ	4:E:1026:THR:CG2	2.89	0.54
5:F:46:ALA:O	5:F:50:GLN:HB3	2.07	0.54
5:F:133:GLU:HA	5:F:136:LYS:HD3	1.88	0.54
5:F:349:GLU:O	5:F:480:ARG:NH2	2.40	0.54
1:Z:25:LEU:HD23	1:Z:25:LEU:C	2.33	0.54
1:Z:262:SER:O	1:Z:266:LYS:NZ	2.41	0.54
1:Z:462:PHE:HA	1:Z:465:ILE:HD12	1.89	0.54
1:Z:463:GLN:HE21	1:Z:487:LEU:HD11	1.72	0.54
1:A:116:LYS:O	1:A:116:LYS:HD3	2.08	0.54
1:A:814:MET:HG2	1:A:833:ILE:CG1	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:103:LEU:HG	3:D:107:TYR:CE2	2.41	0.54
3:D:443:GLY:HA2	3:D:490:LYS:HG3	1.90	0.54
4:E:210:ASN:CA	4:E:213:PHE:CB	2.76	0.54
4:E:333:ARG:NH1	4:E:341:PHE:O	2.40	0.54
5:F:389:LEU:H	5:F:389:LEU:CD1	2.16	0.54
8:L:645:THR:O	8:L:649:THR:HG23	2.08	0.54
2:C:786:THR:H	2:C:789:ASP:HB2	1.72	0.54
2:C:1258:GLN:CG	2:C:1299:LYS:HE3	2.36	0.54
3:D:784:ILE:O	3:D:949:PHE:HB2	2.08	0.54
5:F:354:ARG:CB	5:F:354:ARG:CZ	2.86	0.54
6:J:405:LEU:CD1	7:K:470:ALA:HA	2.38	0.54
1:Z:779:LEU:CB	1:Z:835:ILE:HA	2.37	0.54
1:Z:820:ILE:O	1:Z:821:GLN:C	2.49	0.54
1:A:391:HIS:NE2	1:A:416:GLY:O	2.33	0.54
3:D:403:GLY:O	3:D:408:ARG:NE	2.37	0.54
4:E:180:LYS:NZ	4:E:184:ASP:OD1	2.40	0.54
5:F:1498:LEU:HG	5:F:1514:GLU:HB3	1.88	0.54
1:Z:789:LEU:HB3	1:Z:799:LYS:HD2	1.90	0.54
1:A:23:ASN:C	1:A:25:LEU:N	2.64	0.54
1:A:691:ARG:O	1:A:695:ILE:HG12	2.07	0.54
3:D:222:ASN:HB3	3:D:301:SER:HA	1.90	0.54
3:D:662:LEU:HB3	3:D:667:LEU:HD13	1.90	0.54
4:E:885:VAL:HG21	4:E:923:LEU:HD21	1.90	0.54
5:F:1550:LEU:CD1	5:F:1604:ILE:HG21	2.38	0.54
5:F:1635:ARG:O	5:F:1639:GLY:N	2.40	0.54
7:H:298:SER:HA	7:H:306:THR:HA	1.90	0.54
6:J:382:LYS:HE2	6:J:382:LYS:N	2.22	0.54
7:K:433:GLU:HB2	8:L:741:ARG:HH11	1.73	0.54
1:A:25:LEU:HD23	1:A:25:LEU:C	2.33	0.54
3:D:284:PHE:CE1	3:D:296:LEU:HG	2.42	0.54
4:E:1259:PHE:C	4:E:1259:PHE:HD1	2.16	0.54
1:A:545:PHE:HD2	1:A:549:ASP:HB2	1.74	0.53
4:E:463:PHE:O	4:E:554:ILE:HA	2.07	0.53
5:F:1363:ILE:HG23	1:Z:125:ILE:HD12	1.89	0.53
5:F:1363:ILE:CG2	1:Z:125:ILE:CD1	2.85	0.53
6:G:295:LYS:HD3	6:J:363:LYS:HZ3	1.72	0.53
8:I:814:LEU:HD21	1:Z:59:LYS:CA	2.38	0.53
7:K:430:GLY:C	7:K:432:ALA:N	2.65	0.53
1:A:642:LEU:HA	1:A:645:GLN:CD	2.33	0.53
1:A:814:MET:HG3	1:A:833:ILE:HD13	1.79	0.53
4:E:757:LYS:HA	5:F:1195:PHE:CD2	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:1290:SER:OG	4:E:1297:LYS:NZ	2.40	0.53
4:E:1319:LEU:HD22	4:E:1394:LYS:HB3	1.90	0.53
5:F:1283:LYS:CE	5:F:1283:LYS:CA	2.84	0.53
8:I:785:ASN:CB	1:Z:112:TYR:CB	2.85	0.53
1:Z:674:LEU:HD21	1:Z:724:ARG:HG3	1.90	0.53
2:C:197:ILE:HD13	2:C:224:VAL:HG11	1.91	0.53
3:D:440:THR:OG1	3:D:444:VAL:HG12	2.07	0.53
5:F:44:ASN:OD1	5:F:44:ASN:N	2.40	0.53
6:J:364:ILE:C	7:K:424:ASN:ND2	2.65	0.53
1:A:255:GLU:OE2	1:A:480:GLN:NE2	2.40	0.53
2:C:172:CYS:HB2	2:C:183:TRP:CE2	2.44	0.53
2:C:786:THR:N	2:C:789:ASP:HB2	2.24	0.53
4:E:29:VAL:HG12	4:E:32:VAL:HG11	1.91	0.53
4:E:170:MET:HA	4:E:173:ILE:HG22	1.89	0.53
5:F:1014:SER:N	8:I:788:ASP:O	2.41	0.53
7:K:321:ALA:HA	7:K:348:ILE:HG13	1.76	0.53
7:K:337:GLN:O	7:K:341:LYS:CD	2.56	0.53
4:E:826:SER:OG	4:E:844:TYR:OH	2.26	0.53
4:E:1531:SER:O	4:E:1535:ASN:ND2	2.42	0.53
5:F:286:ILE:HA	5:F:289:CYS:HB2	1.91	0.53
5:F:824:ALA:O	5:F:826:PRO:N	2.41	0.53
5:F:1024:LEU:HD22	5:F:1049:LEU:HD23	1.90	0.53
6:G:296:ALA:HA	6:J:363:LYS:CE	2.39	0.53
1:Z:127:GLN:HA	1:Z:127:GLN:NE2	2.16	0.53
1:Z:761:SER:C	1:Z:763:LEU:H	2.15	0.53
3:D:585:ILE:HG21	3:D:593:VAL:HB	1.90	0.53
4:E:1341:GLU:OE1	4:E:1346:LYS:NZ	2.42	0.53
5:F:427:THR:OG1	5:F:428:GLN:NE2	2.41	0.53
5:F:835:LYS:O	5:F:838:LYS:N	2.42	0.53
5:F:917:PHE:CE2	5:F:922:LEU:HD21	2.43	0.53
7:K:367:GLU:O	7:K:371:GLN:HG3	2.09	0.53
8:L:751:LEU:HA	8:L:755:LEU:HD13	1.90	0.53
1:A:625:GLU:OE1	1:A:629:ARG:NH2	2.33	0.53
3:D:606:GLN:N	3:D:642:LEU:O	2.36	0.53
4:E:607:SER:OG	4:E:608:ILE:N	2.40	0.53
4:E:715:THR:HB	4:E:742:LEU:HD22	1.90	0.53
4:E:1234:LEU:HD12	4:E:1287:ILE:HG13	1.90	0.53
4:E:1382:THR:OG1	4:E:1383:GLN:NE2	2.41	0.53
5:F:159:LYS:CE	5:F:363:ASP:HA	2.26	0.53
5:F:936:ILE:O	5:F:940:ASN:ND2	2.42	0.53
5:F:1634:LYS:O	5:F:1638:ILE:N	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:327:LYS:HZ2	1:Z:46:ILE:CA	2.18	0.53
7:K:394:THR:HB	7:K:398:ILE:HG13	1.90	0.53
7:K:427:LEU:N	7:K:428:PRO:CD	2.72	0.53
1:A:767:ILE:O	1:A:771:ILE:HG12	2.08	0.53
3:D:515:VAL:CG1	3:D:644:SER:HB3	2.32	0.53
3:D:576:LEU:HD13	3:D:601:THR:O	2.08	0.53
5:F:320:GLU:OE1	5:F:351:HIS:HE1	1.92	0.53
6:J:389:ARG:CB	6:J:389:ARG:CZ	2.84	0.53
6:J:429:LEU:HA	6:J:434:THR:N	2.24	0.53
6:J:433:LYS:CB	7:K:499:GLY:CA	2.81	0.53
3:D:150:LYS:HD3	3:D:153:VAL:CG2	2.39	0.53
4:E:258:ILE:O	4:E:261:ILE:N	2.41	0.53
5:F:1370:LEU:O	5:F:1371:ILE:CG1	2.56	0.53
8:I:752:ASP:O	8:I:756:ASN:ND2	2.42	0.53
7:K:483:VAL:H	7:K:494:MET:N	2.07	0.53
1:Z:87:ILE:N	1:Z:87:ILE:CD1	2.72	0.53
1:Z:623:ILE:HG23	1:Z:624:THR:HG23	1.91	0.53
1:A:289:LEU:HD22	1:A:308:PHE:HA	1.91	0.53
1:A:451:ASP:O	1:A:456:ARG:NE	2.38	0.53
1:A:681:SER:HB2	1:A:691:ARG:HD3	1.91	0.53
1:A:829:TYR:CD1	1:A:829:TYR:C	2.85	0.53
4:E:107:SER:HB2	4:E:190:GLN:HE22	1.74	0.53
5:F:902:LYS:CE	7:H:414:LYS:CD	2.46	0.53
6:J:310:ARG:HG2	6:J:314:TYR:CZ	2.44	0.53
6:J:390:ILE:N	6:J:390:ILE:CD1	2.72	0.53
7:K:511:GLU:O	7:K:515:ASN:ND2	2.42	0.53
1:Z:127:GLN:CA	1:Z:127:GLN:NE2	2.72	0.53
1:Z:799:LYS:HA	1:Z:802:GLN:HE21	1.73	0.53
1:A:83:VAL:HA	1:A:86:PHE:CD2	2.43	0.52
1:A:812:GLN:HA	1:A:815:ILE:HD12	1.91	0.52
3:D:470:SER:HB3	3:D:475:GLU:CG	2.39	0.52
3:D:775:LEU:O	3:D:779:ARG:HG3	2.08	0.52
4:E:864:SER:OG	4:E:1147:LEU:O	2.24	0.52
5:F:320:GLU:CD	5:F:351:HIS:CE1	2.87	0.52
5:F:929:TYR:C	5:F:931:GLY:H	2.17	0.52
5:F:1037:ASN:N	5:F:1040:THR:CB	2.69	0.52
5:F:1058:ALA:C	5:F:1060:LEU:H	2.16	0.52
5:F:1058:ALA:C	5:F:1060:LEU:N	2.67	0.52
5:F:1098:SER:O	5:F:1101:ILE:HB	2.09	0.52
5:F:1672:MET:CB	1:Z:149:ALA:CB	2.84	0.52
6:G:427:GLU:HG2	8:I:779:THR:HG21	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:385:GLN:CA	7:K:385:GLN:NE2	2.72	0.52
1:Z:289:LEU:HD23	1:Z:308:PHE:HA	1.91	0.52
1:Z:807:LYS:O	1:Z:836:ASP:O	2.27	0.52
1:A:48:GLU:O	7:K:514:THR:HG23	2.09	0.52
1:A:590:LEU:HD13	1:A:624:THR:HG23	1.92	0.52
1:A:772:PRO:HA	1:A:828:THR:HG21	1.87	0.52
2:C:693:LEU:HB3	2:C:694:PHE:HD1	1.74	0.52
4:E:368:ILE:HG22	4:E:369:LEU:HD12	1.92	0.52
4:E:1170:ASP:O	4:E:1174:ASN:ND2	2.42	0.52
5:F:812:CYS:SG	5:F:813:GLU:N	2.83	0.52
5:F:1147:PHE:CD1	5:F:1147:PHE:C	2.85	0.52
5:F:1360:LEU:CD1	5:F:1360:LEU:N	2.73	0.52
7:H:303:THR:OG1	7:H:329:HIS:O	2.22	0.52
7:H:426:GLY:CA	8:I:735:ASN:C	2.83	0.52
6:J:384:LEU:HD21	7:K:455:LYS:HG2	1.91	0.52
6:J:388:CYS:CB	7:K:455:LYS:HD2	2.32	0.52
1:A:643:LEU:O	1:A:647:ALA:N	2.38	0.52
2:C:1261:PHE:CZ	2:C:1265:ILE:HD11	2.43	0.52
4:E:584:ASP:N	4:E:584:ASP:OD1	2.38	0.52
4:E:739:ILE:HG21	4:E:795:ILE:HG22	1.92	0.52
4:E:789:GLN:OE1	4:E:792:GLN:NE2	2.40	0.52
4:E:954:ILE:HG12	4:E:1015:LYS:HG2	1.92	0.52
4:E:1563:LEU:HD12	4:E:1564:LEU:HG	1.92	0.52
5:F:920:ILE:HG13	5:F:924:ALA:HA	1.89	0.52
5:F:1522:VAL:HA	5:F:1525:LEU:HD12	1.91	0.52
8:I:778:LYS:HG2	8:I:794:ILE:CB	2.39	0.52
6:J:311:ASP:HA	6:J:314:TYR:CD2	2.43	0.52
6:J:324:GLN:O	6:J:328:GLN:HG2	2.09	0.52
1:Z:536:ASN:O	1:Z:540:ASN:ND2	2.42	0.52
3:D:421:VAL:HG13	3:D:491:ARG:CB	2.40	0.52
3:D:664:ASP:O	3:D:667:LEU:N	2.42	0.52
4:E:989:ASP:O	4:E:992:SER:N	2.36	0.52
4:E:1409:ALA:HB1	4:E:1459:LYS:HG3	1.90	0.52
5:F:210:LYS:HG2	5:F:214:LEU:HD13	1.92	0.52
5:F:922:LEU:N	5:F:922:LEU:CD1	2.72	0.52
5:F:1048:LEU:O	5:F:1051:SER:OG	2.26	0.52
5:F:1392:ILE:CB	5:F:1405:PHE:CE2	2.93	0.52
5:F:1634:LYS:HD3	5:F:1638:ILE:HD12	1.91	0.52
1:Z:123:MET:SD	1:Z:123:MET:C	2.93	0.52
1:A:274:GLY:HA2	1:A:484:LEU:HD22	1.91	0.52
3:D:1467:SER:HB2	1:Z:621:HIS:CE1	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:724:SER:HA	4:E:1166:VAL:HA	1.90	0.52
5:F:1094:GLY:O	5:F:1098:SER:N	2.42	0.52
5:F:1370:LEU:C	5:F:1371:ILE:HG12	2.33	0.52
5:F:1529:ALA:HB1	5:F:1611:VAL:HG13	1.83	0.52
6:J:406:PHE:O	6:J:409:PRO:HD2	2.09	0.52
3:D:186:ILE:CG2	3:D:189:LYS:HB2	2.40	0.52
3:D:662:LEU:HB3	3:D:667:LEU:CD1	2.40	0.52
4:E:33:ASP:OD1	4:E:33:ASP:N	2.42	0.52
5:F:154:GLN:HA	5:F:157:GLU:HG3	1.92	0.52
5:F:757:PHE:HD1	5:F:780:ILE:HD11	1.74	0.52
5:F:1027:GLN:CG	5:F:1036:PRO:HA	2.37	0.52
5:F:1251:ARG:NH2	5:F:1276:ASP:HB3	2.25	0.52
8:I:781:ASN:HD22	8:I:781:ASN:N	2.08	0.52
8:I:814:LEU:HD23	1:Z:59:LYS:CB	2.39	0.52
6:J:364:ILE:HG22	6:J:367:ASN:HD21	1.75	0.52
6:J:432:LEU:HA	8:L:782:ILE:O	2.10	0.52
7:K:352:ILE:HG21	7:K:358:LEU:CD2	2.40	0.52
8:L:692:LYS:HD2	8:L:695:GLN:HE21	1.75	0.52
1:Z:391:HIS:NE2	1:Z:417:ARG:O	2.42	0.52
1:A:140:ILE:CG2	4:E:1393:LYS:NZ	2.61	0.52
3:D:944:LEU:O	3:D:947:LEU:HB2	2.10	0.52
5:F:389:LEU:N	5:F:389:LEU:CD1	2.72	0.52
5:F:1605:PHE:HA	5:F:1608:ILE:HG12	1.91	0.52
6:J:332:LYS:HG2	7:K:398:ILE:HG21	1.91	0.52
7:K:309:ARG:HG3	7:K:353:TYR:CZ	2.44	0.52
4:E:141:LEU:HA	4:E:144:ILE:HD12	1.92	0.52
4:E:827:PRO:HB3	4:E:893:TYR:CZ	2.44	0.52
5:F:690:GLU:HG2	8:I:722:LEU:HD21	1.92	0.52
5:F:711:GLN:HG2	5:F:779:PRO:HB3	1.92	0.52
5:F:900:LEU:C	5:F:900:LEU:CD1	2.82	0.52
5:F:1664:ASN:HA	5:F:1667:VAL:HG12	1.92	0.52
8:I:795:LYS:CA	8:I:795:LYS:NZ	2.73	0.52
8:L:692:LYS:HD2	8:L:695:GLN:NE2	2.25	0.52
1:Z:414:LEU:HD11	1:Z:438:MET:HB2	1.92	0.52
1:A:133:THR:O	1:A:134:LYS:C	2.52	0.52
1:A:687:LEU:HD23	1:A:690:ARG:HH11	1.74	0.52
3:D:233:LEU:HD11	3:D:282:ILE:HD13	1.92	0.52
3:D:969:SER:O	3:D:972:ASN:HB2	2.10	0.52
4:E:976:PHE:CZ	7:K:457:ASN:HB3	2.44	0.52
5:F:583:SER:O	5:F:583:SER:OG	2.28	0.52
5:F:837:TYR:CD2	5:F:918:PHE:CE2	2.97	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1227:THR:HA	7:H:472:ASN:HB3	1.92	0.52
6:G:465:LYS:HB3	1:Z:20:LYS:NZ	2.20	0.52
7:H:314:ASN:HB2	7:H:361:ARG:HH12	1.75	0.52
6:J:376:LYS:HD2	6:J:376:LYS:C	2.33	0.52
7:K:387:GLN:NE2	7:K:387:GLN:CA	2.73	0.52
1:Z:133:THR:O	1:Z:134:LYS:C	2.52	0.52
3:D:792:THR:HA	3:D:830:SER:HB2	1.92	0.52
4:E:1268:SER:OG	4:E:1269:GLY:N	2.42	0.52
5:F:639:LEU:HA	5:F:642:PHE:HB3	1.91	0.52
5:F:836:ILE:N	5:F:836:ILE:CD1	2.72	0.52
5:F:958:SER:HB3	5:F:962:ARG:HA	1.91	0.52
7:H:391:GLU:O	7:H:395:ALA:HB3	2.10	0.52
6:J:442:THR:CB	7:K:509:ILE:CD1	2.88	0.52
7:K:446:ARG:C	7:K:446:ARG:HD3	2.34	0.52
1:Z:215:TYR:HA	1:Z:218:ILE:HD12	1.92	0.52
1:Z:817:ALA:C	1:Z:821:GLN:H	2.13	0.52
3:D:160:ILE:CG2	3:D:191:ILE:HG21	2.37	0.51
4:E:681:LEU:HA	4:E:690:LEU:CB	2.40	0.51
5:F:177:GLN:O	5:F:181:PHE:HB2	2.10	0.51
5:F:328:ASP:O	5:F:331:ILE:HD11	2.09	0.51
5:F:543:VAL:HA	5:F:546:TYR:HB2	1.91	0.51
5:F:690:GLU:HG3	8:I:722:LEU:CG	2.40	0.51
6:G:387:TYR:HA	6:G:390:ILE:HB	1.92	0.51
8:I:818:ILE:CD1	8:I:818:ILE:N	2.72	0.51
1:Z:482:LEU:O	1:Z:487:LEU:N	2.43	0.51
1:Z:767:ILE:HD12	1:Z:768:VAL:H	1.74	0.51
1:A:641:ILE:HG23	1:A:653:VAL:HG13	1.91	0.51
3:D:263:VAL:HB	3:D:311:LYS:CE	2.37	0.51
3:D:501:SER:O	3:D:508:LYS:NZ	2.41	0.51
4:E:1380:ASP:C	4:E:1382:THR:N	2.68	0.51
7:H:309:ARG:NE	7:H:353:TYR:OH	2.37	0.51
6:J:433:LYS:CA	7:K:499:GLY:CA	2.88	0.51
7:K:337:GLN:O	7:K:341:LYS:HD3	2.10	0.51
8:L:675:GLN:O	8:L:679:LEU:HD13	2.10	0.51
1:Z:138:ASN:C	1:Z:138:ASN:HD22	2.19	0.51
1:Z:431:SER:OG	1:Z:432:ILE:N	2.42	0.51
1:A:128:LEU:HB3	4:E:1260:TYR:CE2	2.40	0.51
3:D:915:GLU:OE2	3:D:980:SER:OG	2.23	0.51
5:F:157:GLU:OE1	5:F:183:ARG:NH1	2.42	0.51
5:F:355:LEU:N	5:F:355:LEU:CD1	2.72	0.51
5:F:809:LEU:HD13	5:F:1252:VAL:HG23	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1427:LEU:HD22	5:F:1466:LEU:HG	1.91	0.51
5:F:1496:ASP:HA	5:F:1499:LEU:HG	1.93	0.51
5:F:1550:LEU:HD12	5:F:1604:ILE:HD13	1.87	0.51
6:J:383:LYS:CE	8:L:756:ASN:HA	2.23	0.51
6:J:390:ILE:CG1	8:L:766:ILE:HD12	2.40	0.51
1:Z:670:LEU:HD13	1:Z:724:ARG:HD3	1.92	0.51
2:C:885:VAL:CG1	2:C:901:ILE:HG23	2.39	0.51
3:D:240:LEU:HB3	3:D:263:VAL:CG1	2.40	0.51
3:D:484:GLN:HG3	3:D:564:THR:O	2.10	0.51
3:D:484:GLN:NE2	3:D:565:VAL:HA	2.24	0.51
5:F:343:ASP:OD2	5:F:702:LYS:NZ	2.38	0.51
5:F:1177:VAL:HA	5:F:1180:TYR:CB	2.41	0.51
5:F:1363:ILE:HD12	5:F:1364:TYR:N	2.25	0.51
7:H:397:ARG:NH1	8:I:701:GLU:OE1	2.43	0.51
8:I:682:ASP:HA	8:I:685:MET:HE3	1.90	0.51
1:A:817:ALA:HB2	1:A:832:LEU:HD13	1.92	0.51
3:D:863:ILE:HD12	3:D:887:GLN:HG3	1.92	0.51
4:E:86:ASP:OD1	4:E:86:ASP:N	2.44	0.51
4:E:508:ALA:HB1	4:E:512:GLU:HG2	1.93	0.51
5:F:929:TYR:O	5:F:931:GLY:N	2.43	0.51
5:F:1132:GLU:HG3	5:F:1135:CYS:HB2	1.93	0.51
5:F:1439:GLU:HA	5:F:1442:TRP:HB3	1.93	0.51
6:J:382:LYS:N	6:J:382:LYS:CE	2.73	0.51
7:K:321:ALA:HB2	7:K:346:GLN:HA	1.92	0.51
1:Z:734:GLU:OE2	1:Z:738:GLN:NE2	2.43	0.51
1:A:48:GLU:HA	7:K:514:THR:HG21	1.93	0.51
3:D:377:ILE:HB	3:D:393:ILE:HB	1.93	0.51
4:E:1340:PHE:O	4:E:1344:PHE:HB2	2.11	0.51
4:E:1342:LEU:HA	4:E:1346:LYS:HD3	1.92	0.51
5:F:544:TYR:HA	5:F:547:PHE:HD2	1.76	0.51
5:F:920:ILE:HB	5:F:924:ALA:CA	2.41	0.51
5:F:950:GLU:N	5:F:950:GLU:OE2	2.43	0.51
1:A:760:PHE:CZ	1:A:768:VAL:HG13	2.45	0.51
3:D:832:VAL:HG23	3:D:929:PHE:CE2	2.46	0.51
4:E:550:SER:OG	4:E:551:ASN:N	2.44	0.51
5:F:378:ALA:O	5:F:383:ASN:HA	2.11	0.51
8:I:742:GLN:HB3	8:I:746:LYS:HZ2	1.75	0.51
7:K:308:LEU:HB3	7:K:355:PHE:CZ	2.46	0.51
1:A:621:HIS:ND1	1:A:625:GLU:OE2	2.32	0.51
3:D:170:LYS:NZ	3:D:212:GLN:O	2.37	0.51
3:D:242:MET:O	3:D:259:THR:OG1	2.21	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:568:GLN:HE21	3:D:573:GLN:HG2	1.76	0.51
3:D:790:PHE:HB3	3:D:933:ILE:HG21	1.92	0.51
3:D:887:GLN:OE1	3:D:887:GLN:N	2.43	0.51
5:F:332:VAL:CG1	5:F:335:ASP:HA	2.40	0.51
5:F:838:LYS:HA	5:F:841:PHE:HB2	1.92	0.51
5:F:1012:ASN:O	8:I:787:GLU:CG	2.52	0.51
8:I:805:ARG:CB	1:Z:88:LYS:HZ1	2.24	0.51
6:J:371:LYS:C	6:J:371:LYS:CE	2.84	0.51
6:J:406:PHE:CD1	6:J:406:PHE:C	2.85	0.51
6:J:437:ALA:O	6:J:439:ILE:N	2.44	0.51
7:K:379:ILE:C	7:K:382:LYS:H	2.19	0.51
8:L:643:LYS:HG3	8:L:647:GLN:NE2	2.22	0.51
1:Z:807:LYS:CB	1:Z:837:VAL:C	2.84	0.51
2:C:229:ASP:CG	2:C:252:LYS:HE2	2.36	0.51
3:D:421:VAL:HG13	3:D:491:ARG:HB3	1.92	0.51
5:F:841:PHE:HZ	5:F:922:LEU:HD22	1.75	0.51
5:F:914:ASP:HA	5:F:917:PHE:H	1.76	0.51
5:F:1517:ALA:O	5:F:1521:THR:OG1	2.24	0.51
7:K:389:LYS:CB	7:K:393:ASP:CB	2.88	0.51
7:K:399:LEU:HD12	7:K:399:LEU:C	2.35	0.51
1:A:123:MET:O	6:J:414:SER:CB	2.59	0.51
3:D:528:PRO:CG	3:D:624:PHE:HE2	2.21	0.51
4:E:182:PHE:HZ	5:F:1189:MET:CB	2.23	0.51
5:F:320:GLU:CD	5:F:351:HIS:HD1	2.19	0.51
5:F:334:GLN:NE2	5:F:859:LYS:HD2	2.26	0.51
5:F:452:LYS:HE3	5:F:456:ALA:HB2	1.92	0.51
5:F:1510:ASP:N	5:F:1510:ASP:OD1	2.42	0.51
5:F:1532:ARG:NH1	5:F:1615:MET:SD	2.84	0.51
8:I:794:ILE:HA	8:I:797:LEU:HD13	1.93	0.51
6:J:431:GLN:C	7:K:499:GLY:H	2.19	0.51
7:K:365:GLN:HA	7:K:368:ASN:HD22	1.76	0.51
1:A:193:LEU:HB3	1:A:546:ARG:HH12	1.76	0.50
1:A:837:VAL:HG11	2:C:1142:ASP:HB2	1.93	0.50
4:E:757:LYS:HA	5:F:1195:PHE:HD2	1.76	0.50
4:E:810:MET:SD	4:E:810:MET:N	2.84	0.50
4:E:1402:LYS:NZ	4:E:1454:GLU:OE1	2.43	0.50
5:F:726:SER:O	5:F:726:SER:OG	2.27	0.50
5:F:836:ILE:N	5:F:836:ILE:HD12	2.26	0.50
6:G:350:PHE:CZ	7:H:418:GLN:NE2	2.79	0.50
8:I:643:LYS:O	8:I:647:GLN:NE2	2.44	0.50
1:Z:278:LEU:HD22	1:Z:437:TRP:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:787:HIS:HE1	1:A:838:SER:O	1.90	0.50
2:C:229:ASP:CG	2:C:252:LYS:CE	2.85	0.50
2:C:970:PHE:CE2	2:C:974:ILE:HD11	2.46	0.50
3:D:353:GLN:OE1	3:D:374:LYS:HB2	2.11	0.50
3:D:970:ILE:HG23	3:D:975:ILE:CD1	2.40	0.50
5:F:713:PHE:HA	5:F:716:LEU:HB2	1.93	0.50
5:F:1370:LEU:O	5:F:1371:ILE:CB	2.59	0.50
5:F:1618:SER:HB2	1:Z:634:ASP:O	2.10	0.50
6:J:310:ARG:NE	6:J:314:TYR:OH	2.44	0.50
6:J:404:ASP:O	6:J:408:ALA:HB2	2.11	0.50
6:J:462:GLN:HE22	8:L:812:THR:HG23	1.76	0.50
7:K:535:LYS:CA	8:L:818:ILE:CB	2.75	0.50
1:A:224:ASN:OD1	1:A:607:ARG:NH2	2.41	0.50
1:A:414:LEU:HD21	1:A:438:MET:HB2	1.94	0.50
2:C:317:LEU:HB2	2:C:318:ILE:HD12	1.92	0.50
3:D:507:LEU:HA	3:D:512:LYS:O	2.12	0.50
5:F:355:LEU:HD12	5:F:355:LEU:H	1.74	0.50
5:F:681:LYS:HE3	5:F:685:LEU:HA	1.93	0.50
5:F:968:ILE:CG2	7:H:392:LEU:HD11	2.36	0.50
7:K:355:PHE:CD1	7:K:358:LEU:HD12	2.45	0.50
8:L:647:GLN:HA	8:L:650:GLU:HG2	1.93	0.50
8:L:671:LYS:O	8:L:675:GLN:HG2	2.10	0.50
1:Z:116:LYS:C	1:Z:116:LYS:CE	2.85	0.50
1:Z:251:ALA:O	1:Z:253:LEU:CA	2.54	0.50
1:Z:639:ASP:OD1	1:Z:639:ASP:N	2.43	0.50
1:Z:757:ALA:CB	1:Z:819:MET:C	2.39	0.50
1:A:626:GLN:O	1:A:630:ARG:HG2	2.11	0.50
3:D:586:LEU:HD21	3:D:592:TYR:HD1	1.76	0.50
3:D:665:ASN:CG	3:D:666:PRO:HD3	2.36	0.50
3:D:828:ILE:CD1	3:D:925:GLN:HA	2.41	0.50
3:D:873:SER:CB	3:D:877:VAL:HB	2.42	0.50
4:E:1259:PHE:HD1	4:E:1259:PHE:O	1.94	0.50
4:E:1294:ASP:O	4:E:1298:ASN:N	2.42	0.50
5:F:253:LYS:NZ	5:F:257:SER:OG	2.44	0.50
5:F:1088:ARG:NH1	5:F:1088:ARG:CG	2.73	0.50
5:F:1285:HIS:C	5:F:1285:HIS:ND1	2.70	0.50
5:F:1363:ILE:C	5:F:1363:ILE:CD1	2.85	0.50
5:F:1373:ASP:O	5:F:1376:THR:N	2.28	0.50
8:L:637:LEU:HD22	8:L:640:LEU:HB2	1.92	0.50
1:A:27:GLU:OE2	1:A:30:ASP:HB2	2.11	0.50
1:A:684:ASN:HB3	1:A:687:LEU:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:518:GLU:HA	3:D:536:ILE:CD1	2.41	0.50
4:E:270:ILE:HD11	4:E:320:MET:HE3	1.94	0.50
5:F:665:GLU:HB2	5:F:720:HIS:NE2	2.25	0.50
5:F:1067:ASN:N	5:F:1067:ASN:OD1	2.42	0.50
5:F:1472:GLU:OE1	5:F:1531:THR:OG1	2.25	0.50
5:F:1502:THR:H	5:F:1510:ASP:HB2	1.77	0.50
6:G:465:LYS:HB3	1:Z:20:LYS:CE	2.42	0.50
6:J:389:ARG:NH1	6:J:389:ARG:CG	2.72	0.50
6:J:390:ILE:N	6:J:390:ILE:HD12	2.26	0.50
7:K:313:TYR:CD1	7:K:349:PRO:HB3	2.45	0.50
7:K:336:ASP:HB3	7:K:340:GLU:OE1	2.11	0.50
7:K:375:ILE:O	7:K:379:ILE:HG22	2.11	0.50
1:A:599:ARG:NH1	1:A:605:GLU:OE2	2.44	0.50
3:D:358:GLN:OE1	3:D:422:LYS:HG3	2.11	0.50
4:E:1275:GLU:HA	4:E:1278:ILE:HD12	1.93	0.50
5:F:562:LEU:O	5:F:566:THR:OG1	2.23	0.50
7:H:359:ASN:HA	7:H:362:ASN:HD22	1.75	0.50
7:H:412:ILE:HG22	7:H:415:LEU:HD23	1.94	0.50
6:J:281:ASP:O	6:J:284:ILE:HB	2.11	0.50
7:K:536:LYS:HA	7:K:539:ASN:HB2	1.94	0.50
1:A:138:ASN:HD22	1:A:138:ASN:C	2.19	0.50
5:F:544:TYR:OH	5:F:629:SER:OG	2.29	0.50
5:F:838:LYS:O	5:F:842:ASN:HB2	2.12	0.50
1:A:137:ASP:OD2	4:E:1385:LEU:HD12	2.11	0.50
4:E:200:LEU:HD13	4:E:271:LEU:HD22	1.94	0.50
5:F:1157:TRP:O	5:F:1158:THR:C	2.55	0.50
7:H:317:ASN:HA	7:H:346:GLN:HB3	1.94	0.50
8:L:650:GLU:HG3	8:L:651:SER:N	2.27	0.50
1:Z:440:LEU:HA	1:Z:443:ILE:HG12	1.94	0.50
1:Z:771:ILE:CB	1:Z:772:PRO:HD2	2.42	0.50
1:A:516:PHE:HZ	1:A:532:ILE:HG22	1.76	0.50
1:A:814:MET:HB2	1:A:836:ASP:OD2	2.11	0.50
4:E:185:LEU:HD23	4:E:188:ILE:HD11	1.94	0.50
4:E:207:ASP:OD1	4:E:207:ASP:N	2.40	0.50
5:F:900:LEU:HD22	5:F:904:TYR:CZ	2.47	0.50
8:I:750:THR:O	8:I:753:GLU:HB3	2.11	0.50
6:J:277:ILE:CD1	6:J:280:LEU:HD23	2.42	0.50
7:K:289:GLN:O	7:K:292:VAL:HB	2.11	0.50
8:L:667:GLN:NE2	8:L:668:VAL:HG23	2.26	0.50
1:Z:239:ILE:O	1:Z:243:SER:OG	2.30	0.50
1:Z:533:ARG:HH21	1:Z:534:PHE:HB3	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:771:ILE:HG22	1:Z:772:PRO:HD3	1.94	0.50
4:E:411:PHE:O	4:E:415:PHE:HB3	2.11	0.49
4:E:1429:HIS:HD2	4:E:1474:LEU:HD22	1.77	0.49
5:F:669:THR:HA	5:F:672:TRP:HB2	1.94	0.49
5:F:1138:PHE:C	5:F:1140:GLU:H	2.20	0.49
5:F:1370:LEU:O	5:F:1371:ILE:HB	2.12	0.49
7:H:443:LEU:HA	7:H:446:ARG:HB2	1.94	0.49
8:I:822:LYS:CE	8:I:822:LYS:CA	2.84	0.49
6:J:370:ASP:HA	6:J:373:PHE:CB	2.40	0.49
6:J:384:LEU:C	6:J:384:LEU:CD2	2.85	0.49
7:K:429:LEU:HB2	8:L:741:ARG:CZ	2.42	0.49
8:L:637:LEU:CD2	8:L:640:LEU:H	2.24	0.49
8:L:692:LYS:O	8:L:695:GLN:HG3	2.11	0.49
1:Z:576:LEU:HA	1:Z:579:LEU:HB2	1.94	0.49
3:D:449:ASN:HB3	3:D:463:GLU:CG	2.41	0.49
3:D:932:ILE:CG2	3:D:933:ILE:HG13	2.41	0.49
4:E:477:LEU:HA	4:E:499:ILE:HA	1.94	0.49
4:E:725:LEU:HD23	4:E:1167:LEU:HA	1.93	0.49
5:F:50:GLN:NE2	5:F:57:GLU:OE2	2.45	0.49
5:F:616:VAL:HG12	5:F:656:VAL:HG21	1.92	0.49
5:F:684:SER:HB3	5:F:695:ALA:HB2	1.94	0.49
5:F:1166:HIS:ND1	5:F:1166:HIS:C	2.70	0.49
5:F:1529:ALA:HB2	5:F:1611:VAL:CG2	2.42	0.49
7:H:527:LEU:C	7:H:527:LEU:CD2	2.85	0.49
8:I:740:LYS:O	8:I:743:GLN:NE2	2.45	0.49
6:J:309:PRO:O	6:J:312:VAL:HB	2.12	0.49
3:D:412:ILE:HG22	3:D:476:VAL:HB	1.93	0.49
5:F:555:TRP:HA	5:F:558:ILE:HG12	1.94	0.49
5:F:668:ARG:O	5:F:672:TRP:HB2	2.12	0.49
5:F:1543:LEU:O	5:F:1547:ILE:HG22	2.12	0.49
6:G:427:GLU:CG	8:I:779:THR:HG21	2.41	0.49
6:G:431:GLN:CB	7:H:503:ASN:H	2.22	0.49
8:I:795:LYS:HE3	8:I:799:SER:HB3	1.94	0.49
8:L:696:SER:O	8:L:699:TYR:HB2	2.11	0.49
1:Z:242:LEU:CA	1:Z:245:ALA:HB3	2.18	0.49
1:A:764:ASP:O	1:A:768:VAL:HG23	2.12	0.49
1:A:818:GLY:O	1:A:821:GLN:NE2	2.40	0.49
3:D:119:PRO:HB3	3:D:739:THR:CG2	2.42	0.49
3:D:442:GLY:HA2	3:D:488:GLN:HG2	1.94	0.49
4:E:114:TYR:HB2	4:E:194:ILE:HD11	1.93	0.49
4:E:476:ASP:OD1	4:E:476:ASP:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:806:LEU:O	5:F:814:ASN:CB	2.60	0.49
5:F:1357:ALA:HA	5:F:1381:LEU:CB	2.42	0.49
5:F:1469:ARG:HH22	5:F:1530:GLU:HB3	1.76	0.49
5:F:1667:VAL:HA	5:F:1670:ILE:HG22	1.95	0.49
8:I:822:LYS:NZ	8:I:822:LYS:CA	2.73	0.49
6:J:433:LYS:CA	7:K:499:GLY:HA3	2.42	0.49
7:K:315:LYS:HA	7:K:347:THR:CA	2.38	0.49
1:Z:637:ILE:O	1:Z:640:SER:OG	2.28	0.49
1:A:205:ASN:OD1	1:A:208:LEU:HB2	2.12	0.49
1:A:505:HIS:HE1	1:A:541:TYR:OH	1.96	0.49
1:A:558:VAL:HG22	1:A:611:LEU:HD21	1.93	0.49
3:D:375:SER:HB3	3:D:420:ILE:HG13	1.94	0.49
4:E:1017:LEU:O	4:E:1021:THR:OG1	2.26	0.49
5:F:900:LEU:HD13	5:F:904:TYR:CE1	2.47	0.49
5:F:913:TYR:O	5:F:917:PHE:N	2.46	0.49
5:F:1092:THR:O	5:F:1092:THR:OG1	2.23	0.49
5:F:1139:ILE:HG12	5:F:1291:SER:CB	2.42	0.49
5:F:1628:GLY:O	5:F:1632:THR:HB	2.13	0.49
8:I:816:LYS:HE2	8:I:816:LYS:N	2.28	0.49
7:K:335:TRP:CH2	7:K:339:MET:HE2	2.47	0.49
3:D:491:ARG:CB	3:D:520:THR:HB	2.42	0.49
3:D:631:GLN:NE2	3:D:656:ASP:OD2	2.44	0.49
3:D:653:ARG:HG3	3:D:657:GLU:HB2	1.93	0.49
4:E:27:ALA:O	4:E:119:ASN:ND2	2.45	0.49
4:E:186:LYS:HE2	4:E:834:ILE:HG23	1.95	0.49
4:E:822:ASN:O	4:E:826:SER:HB3	2.13	0.49
4:E:995:LEU:HA	4:E:998:LEU:HB2	1.95	0.49
5:F:973:ASP:O	5:F:975:SER:N	2.44	0.49
5:F:1477:ASP:O	5:F:1481:LYS:N	2.45	0.49
5:F:1550:LEU:HD21	5:F:1552:PHE:HZ	1.66	0.49
5:F:1641:PHE:HA	5:F:1644:ASP:HB2	1.95	0.49
6:G:289:GLN:CD	6:J:352:VAL:HG22	2.32	0.49
7:H:309:ARG:NH2	7:H:334:GLU:OE2	2.45	0.49
7:H:390:HIS:O	7:H:394:THR:OG1	2.24	0.49
7:H:511:GLU:CB	8:I:800:HIS:HE1	2.24	0.49
7:H:522:TYR:CB	1:Z:55:GLN:N	2.75	0.49
6:J:398:VAL:CG2	7:K:462:ARG:CA	2.69	0.49
7:K:310:ALA:CB	7:K:352:ILE:HB	2.38	0.49
7:K:504:ASP:O	7:K:507:ASN:N	2.44	0.49
1:Z:771:ILE:CG2	1:Z:772:PRO:HD2	2.42	0.49
1:A:54:PHE:HA	1:A:57:ARG:HD3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:334:GLN:HG2	5:F:860:ASN:HD21	1.73	0.49
5:F:472:ILE:HG23	5:F:474:LEU:H	1.76	0.49
5:F:665:GLU:HA	5:F:668:ARG:HG2	1.94	0.49
5:F:959:LEU:CB	6:G:325:TYR:HB2	2.43	0.49
7:H:344:SER:O	7:H:347:THR:OG1	2.31	0.49
8:I:805:ARG:CB	1:Z:88:LYS:HZ3	2.23	0.49
6:J:389:ARG:NH1	6:J:389:ARG:C	2.71	0.49
3:D:175:ILE:CD1	3:D:642:LEU:HB2	2.36	0.49
3:D:499:LEU:CB	3:D:502:SER:HB3	2.35	0.49
3:D:586:LEU:HD11	3:D:592:TYR:HA	1.94	0.49
3:D:753:PRO:HD2	3:D:756:LYS:CD	2.40	0.49
3:D:896:MET:O	3:D:900:VAL:HG23	2.13	0.49
3:D:971:ILE:HD11	3:D:984:THR:CG2	2.43	0.49
3:D:1494:ASN:O	5:F:1471:LYS:CE	2.59	0.49
5:F:288:TRP:O	5:F:295:ARG:NH2	2.45	0.49
5:F:334:GLN:HE22	5:F:859:LYS:HZ3	1.46	0.49
5:F:1269:GLU:O	5:F:1273:LYS:HB3	2.13	0.49
6:G:449:LEU:HD23	1:Z:84:ASP:OD1	2.12	0.49
6:J:350:PHE:HD1	7:K:419:LEU:HD12	1.73	0.49
6:J:372:PHE:CD2	6:J:372:PHE:C	2.89	0.49
6:J:389:ARG:CZ	6:J:389:ARG:C	2.85	0.49
8:L:774:ASN:HA	8:L:777:ASN:HB2	1.95	0.49
4:E:1460:LEU:O	4:E:1463:SER:OG	2.31	0.49
5:F:159:LYS:CE	5:F:363:ASP:CA	2.88	0.49
5:F:914:ASP:HA	5:F:917:PHE:HB2	1.93	0.49
7:H:315:LYS:HA	7:H:347:THR:HA	1.95	0.49
6:J:376:LYS:NZ	8:L:756:ASN:ND2	2.57	0.49
6:J:383:LYS:HZ3	8:L:756:ASN:CA	2.09	0.49
1:Z:140:ILE:HA	1:Z:143:ASN:HB3	1.93	0.49
1:Z:807:LYS:C	1:Z:836:ASP:O	2.56	0.49
1:A:270:ILE:HD13	1:A:486:GLY:HA3	1.95	0.49
3:D:1468:TYR:N	1:Z:621:HIS:CE1	2.77	0.49
4:E:994:ILE:HG13	4:E:995:LEU:HD12	1.95	0.49
5:F:161:GLN:HA	5:F:164:LYS:HG3	1.94	0.49
5:F:914:ASP:CA	5:F:917:PHE:CB	2.85	0.49
5:F:1373:ASP:O	5:F:1375:GLY:N	2.45	0.49
5:F:1671:VAL:HG13	1:Z:149:ALA:HB1	1.94	0.49
6:G:395:GLU:HA	6:G:398:VAL:HB	1.95	0.49
6:G:436:LEU:HD13	7:H:503:ASN:CB	2.43	0.49
7:K:430:GLY:C	7:K:432:ALA:H	2.20	0.49
1:Z:211:LYS:CB	1:Z:246:ASN:O	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:449:ASN:ND2	3:D:461:ARG:HB2	2.27	0.48
3:D:578:VAL:O	3:D:596:ALA:HA	2.12	0.48
3:D:745:ILE:HG13	3:D:746:THR:H	1.77	0.48
3:D:836:LYS:HB2	3:D:914:TYR:CD1	2.47	0.48
5:F:463:SER:O	5:F:463:SER:OG	2.31	0.48
5:F:835:LYS:HD3	5:F:835:LYS:N	2.28	0.48
5:F:1305:SER:C	5:F:1307:VAL:N	2.69	0.48
5:F:1465:GLN:HG3	5:F:1527:ARG:NH2	2.28	0.48
6:J:380:TYR:O	6:J:380:TYR:CD1	2.66	0.48
7:K:538:LYS:CB	8:L:821:ILE:HG22	2.42	0.48
1:Z:223:ASN:ND2	1:Z:555:GLU:OE2	2.35	0.48
1:Z:275:LYS:NZ	1:Z:441:MET:SD	2.81	0.48
1:A:341:LEU:HD21	1:A:371:PHE:HZ	1.78	0.48
3:D:421:VAL:HG21	3:D:490:LYS:CB	2.41	0.48
3:D:453:GLY:O	3:D:456:ASN:N	2.45	0.48
3:D:539:SER:HA	3:D:545:GLN:NE2	2.29	0.48
4:E:1598:LEU:O	4:E:1602:LEU:HB2	2.13	0.48
5:F:866:GLN:HA	5:F:869:VAL:HG12	1.95	0.48
5:F:923:VAL:HG23	5:F:925:HIS:H	1.77	0.48
6:G:428:ASN:HD21	6:G:432:LEU:HD23	1.78	0.48
8:I:778:LYS:C	8:I:778:LYS:CD	2.85	0.48
8:L:638:ASP:HA	8:L:641:VAL:CG2	2.42	0.48
2:C:914:GLN:HE21	2:C:953:ILE:HG23	1.78	0.48
3:D:503:GLU:OE1	3:D:508:LYS:HD3	2.14	0.48
3:D:919:VAL:CG2	3:D:927:LEU:H	2.26	0.48
4:E:570:GLN:HE21	4:E:622:LEU:HB3	1.78	0.48
5:F:389:LEU:C	5:F:389:LEU:CD1	2.86	0.48
5:F:1304:HIS:CG	5:F:1304:HIS:O	2.66	0.48
6:G:449:LEU:HD23	1:Z:84:ASP:CB	2.42	0.48
8:I:795:LYS:CE	8:I:799:SER:HB3	2.43	0.48
6:J:370:ASP:HA	6:J:373:PHE:CG	2.48	0.48
1:Z:305:ILE:HG21	1:Z:336:LEU:HA	1.94	0.48
1:A:315:LYS:HD2	1:A:319:SER:OG	2.13	0.48
1:A:571:LEU:O	1:A:574:GLU:HG3	2.13	0.48
3:D:539:SER:HA	3:D:545:GLN:HE22	1.78	0.48
4:E:573:LEU:HD22	4:E:637:VAL:HG13	1.96	0.48
4:E:1063:ASP:N	4:E:1063:ASP:OD1	2.44	0.48
5:F:922:LEU:HD12	5:F:922:LEU:N	2.23	0.48
5:F:935:GLN:C	5:F:937:LEU:N	2.71	0.48
5:F:951:ARG:NE	5:F:951:ARG:CA	2.76	0.48
5:F:989:SER:O	5:F:989:SER:OG	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:ILE:HG22	4:E:1393:LYS:CE	2.43	0.48
1:A:413:LYS:HD2	1:A:425:ILE:HD11	1.94	0.48
3:D:927:LEU:HD13	3:D:973:ARG:NH2	2.29	0.48
4:E:134:ARG:NH1	4:E:198:MET:SD	2.87	0.48
4:E:1384:ASP:HA	4:E:1388:LEU:HB2	1.96	0.48
5:F:291:GLU:HG3	5:F:295:ARG:HG2	1.95	0.48
5:F:1463:LEU:HD12	5:F:1463:LEU:HA	1.73	0.48
6:J:324:GLN:HA	6:J:327:LYS:CE	2.35	0.48
6:J:389:ARG:CZ	6:J:389:ARG:HB3	2.44	0.48
1:Z:494:TYR:O	1:Z:497:THR:OG1	2.27	0.48
1:A:749:ASP:O	1:A:752:SER:OG	2.29	0.48
3:D:481:LEU:CD2	3:D:488:GLN:HB3	2.43	0.48
4:E:936:LEU:O	4:E:940:SER:OG	2.26	0.48
5:F:971:SER:OG	5:F:972:VAL:N	2.46	0.48
7:H:292:VAL:HG22	8:I:644:TRP:HZ3	1.79	0.48
8:I:795:LYS:C	8:I:795:LYS:CD	2.85	0.48
7:K:535:LYS:O	7:K:539:ASN:N	2.43	0.48
3:D:491:ARG:HA	3:D:520:THR:HB	1.96	0.48
3:D:976:THR:CB	3:D:981:ILE:CB	2.91	0.48
5:F:927:GLY:HA3	5:F:978:ILE:HD11	1.95	0.48
6:J:283:TYR:O	6:J:286:LYS:HG2	2.14	0.48
6:J:383:LYS:CD	8:L:756:ASN:CG	2.85	0.48
6:J:445:GLU:O	6:J:449:LEU:HB2	2.13	0.48
3:D:503:GLU:HB2	3:D:507:LEU:N	2.29	0.48
4:E:675:TYR:HA	4:E:678:LYS:HG2	1.96	0.48
4:E:795:ILE:O	4:E:798:SER:OG	2.29	0.48
5:F:260:MET:HE3	5:F:306:VAL:HB	1.94	0.48
5:F:837:TYR:CG	5:F:918:PHE:CZ	3.02	0.48
5:F:1529:ALA:HB2	5:F:1611:VAL:HG22	1.95	0.48
6:G:465:LYS:HE3	1:Z:20:LYS:HE2	1.94	0.48
8:I:750:THR:O	8:I:754:ASN:ND2	2.46	0.48
8:I:814:LEU:HD21	1:Z:59:LYS:HA	1.96	0.48
6:J:390:ILE:HG23	6:J:394:ILE:HG23	1.94	0.48
7:K:433:GLU:HB3	7:K:437:TRP:CZ3	2.49	0.48
7:K:513:LEU:HD11	8:L:800:HIS:HD1	1.78	0.48
1:Z:341:LEU:HD22	1:Z:415:ILE:HD11	1.96	0.48
1:Z:753:ALA:HB2	1:Z:815:ILE:CB	2.43	0.48
1:Z:767:ILE:HD12	1:Z:768:VAL:HG23	1.95	0.48
1:A:18:ALA:HA	1:A:21:LYS:HB2	1.96	0.48
1:A:128:LEU:CD1	4:E:1260:TYR:OH	2.44	0.48
1:A:342:ARG:NE	1:A:434:ASP:OD1	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:723:ILE:HG23	1:A:735:THR:HG23	1.96	0.48
2:C:1216:TYR:HB2	2:C:1241:LEU:HD13	1.95	0.48
3:D:585:ILE:HG12	3:D:591:LYS:HB2	1.94	0.48
3:D:628:PHE:O	3:D:779:ARG:HD2	2.14	0.48
3:D:986:THR:C	3:D:988:LEU:H	2.20	0.48
4:E:878:PHE:HZ	4:E:917:PRO:HB3	1.77	0.48
5:F:275:VAL:HA	5:F:278:ILE:HB	1.96	0.48
5:F:320:GLU:CD	5:F:351:HIS:ND1	2.72	0.48
5:F:965:LEU:O	5:F:965:LEU:HG	2.13	0.48
5:F:1031:VAL:CB	6:G:314:TYR:O	2.61	0.48
5:F:1300:LEU:HD23	5:F:1301:SER:HA	1.96	0.48
6:G:294:LEU:O	6:G:298:THR:OG1	2.22	0.48
6:G:452:ASP:CB	1:Z:84:ASP:CG	2.87	0.48
6:J:384:LEU:CD2	7:K:455:LYS:HG2	2.43	0.48
6:J:398:VAL:CG2	7:K:462:ARG:O	2.62	0.48
7:K:314:ASN:H	7:K:349:PRO:HA	1.79	0.48
8:L:774:ASN:HB3	8:L:795:LYS:HE2	1.96	0.48
8:L:777:ASN:HD22	8:L:795:LYS:HA	1.79	0.48
3:D:538:SER:OG	3:D:545:GLN:HB2	2.14	0.48
3:D:910:LEU:HA	3:D:913:LEU:HD12	1.96	0.48
3:D:1238:ARG:CG	1:Z:830:SER:HB2	2.40	0.48
4:E:1022:TYR:CD2	4:E:1026:THR:HG22	2.38	0.48
4:E:1499:LEU:HA	4:E:1502:ILE:HG12	1.95	0.48
5:F:925:HIS:HA	5:F:928:LEU:CD1	2.44	0.48
5:F:1027:GLN:HG3	5:F:1027:GLN:O	2.13	0.48
5:F:1493:LYS:HD2	5:F:1493:LYS:HA	1.66	0.48
6:G:380:TYR:HA	6:G:383:LYS:HE3	1.95	0.48
8:I:778:LYS:HA	8:I:778:LYS:NZ	2.29	0.48
1:Z:18:ALA:HA	1:Z:21:LYS:HB2	1.95	0.48
1:Z:641:ILE:HD13	1:Z:656:LEU:HD12	1.96	0.48
1:Z:771:ILE:HG22	1:Z:772:PRO:HD2	1.94	0.48
1:A:255:GLU:HB3	1:A:480:GLN:HE21	1.79	0.47
3:D:315:THR:HG22	3:D:317:SER:H	1.79	0.47
3:D:426:VAL:CG2	3:D:437:VAL:HG23	2.44	0.47
4:E:18:VAL:HA	4:E:40:ILE:HD11	1.96	0.47
4:E:1345:SER:O	4:E:1349:TYR:HB2	2.14	0.47
5:F:1289:ILE:HD12	5:F:1289:ILE:HA	1.64	0.47
8:I:731:GLY:C	8:I:733:ALA:N	2.71	0.47
7:K:313:TYR:HA	7:K:349:PRO:CB	2.40	0.47
1:Z:138:ASN:C	1:Z:138:ASN:ND2	2.72	0.47
1:A:138:ASN:C	1:A:138:ASN:ND2	2.72	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:301:ASN:HA	1:A:304:LYS:HE3	1.96	0.47
3:D:442:GLY:O	3:D:468:PRO:HG3	2.15	0.47
4:E:1163:LEU:HB3	4:E:1173:TRP:HH2	1.78	0.47
5:F:1439:GLU:O	5:F:1443:ASN:N	2.34	0.47
5:F:1550:LEU:CD1	5:F:1552:PHE:CZ	2.97	0.47
6:G:315:LEU:HD23	8:I:679:LEU:HD23	1.95	0.47
6:J:334:SER:C	6:J:336:PHE:H	2.15	0.47
7:K:429:LEU:C	7:K:429:LEU:CD1	2.85	0.47
8:L:769:ILE:HA	8:L:772:VAL:HG12	1.95	0.47
1:Z:116:LYS:HE2	1:Z:116:LYS:CA	2.44	0.47
1:Z:271:VAL:HG22	1:Z:459:LEU:HD22	1.96	0.47
1:Z:786:ILE:CD1	1:Z:838:SER:HA	2.44	0.47
3:D:517:LEU:HB2	3:D:540:GLN:OE1	2.14	0.47
3:D:789:VAL:HG11	3:D:952:LEU:CD1	2.44	0.47
3:D:917:SER:OG	3:D:975:ILE:HA	2.15	0.47
4:E:1260:TYR:O	4:E:1260:TYR:CD1	2.67	0.47
5:F:421:ILE:C	5:F:423:LEU:N	2.72	0.47
5:F:951:ARG:NE	5:F:951:ARG:HA	2.29	0.47
6:J:300:ASP:HA	6:J:303:GLU:OE1	2.14	0.47
7:K:427:LEU:H	7:K:428:PRO:HD3	1.79	0.47
7:K:454:GLY:C	7:K:456:THR:H	2.22	0.47
7:K:538:LYS:CB	8:L:822:LYS:CB	2.85	0.47
3:D:445:ARG:HH11	3:D:466:LYS:HB3	1.79	0.47
4:E:105:GLU:O	4:E:109:ARG:N	2.47	0.47
4:E:725:LEU:HG	4:E:1169:ALA:HB3	1.97	0.47
4:E:954:ILE:HD11	4:E:1015:LYS:HE3	1.97	0.47
4:E:1031:LYS:HB2	4:E:1034:ILE:HG12	1.96	0.47
5:F:161:GLN:HB2	5:F:183:ARG:HH12	1.79	0.47
5:F:609:LEU:HA	5:F:612:LEU:HB2	1.96	0.47
5:F:616:VAL:O	5:F:620:THR:OG1	2.24	0.47
8:I:821:ILE:CD1	8:I:821:ILE:C	2.85	0.47
6:J:311:ASP:CG	7:K:376:LEU:HD21	2.39	0.47
6:J:326:LEU:HD22	8:L:689:SER:OG	2.14	0.47
2:C:888:LEU:HA	2:C:892:PHE:CD2	2.49	0.47
3:D:182:CYS:SG	3:D:195:ILE:HD11	2.55	0.47
3:D:893:ILE:O	3:D:897:ILE:HG13	2.15	0.47
5:F:710:LEU:HA	5:F:713:PHE:HB3	1.96	0.47
5:F:900:LEU:HD22	5:F:904:TYR:CE2	2.49	0.47
5:F:1486:LEU:HA	5:F:1489:ILE:HB	1.96	0.47
6:G:353:LEU:HD11	6:G:365:SER:HB2	1.97	0.47
7:H:380:LEU:O	7:H:384:THR:OG1	2.25	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:492:ASP:O	7:H:493:SER:CB	2.62	0.47
6:J:311:ASP:HA	6:J:314:TYR:CG	2.48	0.47
6:J:371:LYS:C	6:J:371:LYS:CD	2.88	0.47
8:L:818:ILE:HA	8:L:821:ILE:HG22	1.97	0.47
1:Z:710:ASN:OD1	1:Z:710:ASN:N	2.48	0.47
1:A:687:LEU:HA	1:A:690:ARG:HG2	1.96	0.47
3:D:1376:LYS:CB	1:Z:762:ASN:CB	2.93	0.47
4:E:803:LEU:HG	4:E:807:LEU:HD12	1.96	0.47
4:E:1200:GLU:HA	4:E:1203:THR:HG22	1.97	0.47
5:F:110:ARG:NH2	5:F:190:TYR:OH	2.47	0.47
5:F:1392:ILE:CB	5:F:1405:PHE:HE2	2.28	0.47
8:I:738:ASP:O	8:I:740:LYS:HG3	2.14	0.47
7:K:402:GLN:C	7:K:402:GLN:NE2	2.72	0.47
2:C:285:GLU:HB2	2:C:304:LEU:HD11	1.96	0.47
3:D:412:ILE:HG13	3:D:413:LEU:CD1	2.43	0.47
3:D:568:GLN:NE2	3:D:573:GLN:HG2	2.30	0.47
3:D:911:ASN:HA	3:D:914:TYR:CE2	2.49	0.47
4:E:51:LEU:HA	4:E:109:ARG:HD3	1.97	0.47
4:E:141:LEU:HD11	4:E:195:LEU:HD13	1.97	0.47
4:E:604:PRO:HG3	4:E:666:PRO:HG2	1.95	0.47
4:E:989:ASP:C	4:E:991:LYS:N	2.72	0.47
4:E:1166:VAL:HG23	4:E:1167:LEU:HD23	1.96	0.47
4:E:1442:ILE:O	4:E:1445:THR:OG1	2.26	0.47
4:E:1608:HIS:HB3	4:E:1611:TYR:HB3	1.97	0.47
5:F:46:ALA:O	5:F:50:GLN:CB	2.62	0.47
5:F:219:HIS:NE2	5:F:222:GLU:OE2	2.48	0.47
5:F:665:GLU:HG2	5:F:668:ARG:HG3	1.97	0.47
5:F:850:GLN:HA	5:F:853:ILE:HD12	1.97	0.47
5:F:907:HIS:CB	7:H:410:LYS:HD3	2.44	0.47
5:F:938:ALA:O	5:F:941:SER:OG	2.22	0.47
5:F:1506:ILE:HG22	5:F:1507:ASN:H	1.79	0.47
6:G:404:ASP:CB	6:G:425:GLU:O	2.63	0.47
7:H:472:ASN:O	7:H:476:GLN:CB	2.63	0.47
8:I:792:GLN:O	8:I:794:ILE:N	2.46	0.47
6:J:277:ILE:HD12	6:J:280:LEU:HD23	1.97	0.47
6:J:389:ARG:HH11	6:J:389:ARG:CG	2.23	0.47
7:K:483:VAL:N	7:K:493:SER:C	2.70	0.47
8:L:661:LYS:HE2	8:L:665:TRP:CH2	2.50	0.47
1:Z:539:ALA:HA	1:Z:542:THR:HG22	1.97	0.47
1:Z:551:ARG:HH12	1:Z:607:ARG:HH12	1.63	0.47
1:Z:807:LYS:CB	1:Z:836:ASP:O	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:LEU:HB3	1:A:546:ARG:NH1	2.30	0.47
1:A:615:ASP:HB2	1:A:618:GLU:HG3	1.97	0.47
1:A:688:LEU:O	1:A:692:MET:HG2	2.14	0.47
3:D:295:GLU:CD	3:D:316:LYS:HE3	2.40	0.47
3:D:447:TYR:O	3:D:462:LEU:HD12	2.15	0.47
3:D:1465:ILE:HG23	3:D:1487:TYR:CZ	2.49	0.47
5:F:21:ASP:HB2	5:F:24:LEU:HB2	1.97	0.47
5:F:711:GLN:NE2	5:F:714:HIS:HB2	2.29	0.47
5:F:1423:SER:HA	5:F:1426:VAL:HG12	1.97	0.47
6:G:295:LYS:NZ	6:J:363:LYS:HZ3	2.12	0.47
7:K:358:LEU:O	7:K:362:ASN:ND2	2.48	0.47
8:L:643:LYS:CG	8:L:647:GLN:HE22	2.23	0.47
2:C:1389:GLY:HA2	4:E:1331:LEU:CD1	2.45	0.47
3:D:149:GLU:OE2	3:D:653:ARG:NH1	2.37	0.47
3:D:903:ILE:HG12	3:D:953:PHE:CG	2.50	0.47
4:E:33:ASP:OD2	4:E:946:TRP:NE1	2.40	0.47
5:F:623:VAL:HG11	5:F:626:ASP:HB2	1.97	0.47
5:F:1622:VAL:HA	5:F:1625:THR:HG22	1.97	0.47
8:I:694:ASP:OD2	8:I:698:GLN:NE2	2.37	0.47
7:K:312:VAL:CG1	7:K:361:ARG:HH21	2.27	0.47
1:Z:574:GLU:HA	1:Z:577:ARG:HB2	1.96	0.47
1:A:16:LYS:CD	6:J:468:ALA:HA	2.45	0.47
1:A:817:ALA:CB	1:A:832:LEU:HD13	2.45	0.47
3:D:830:SER:CB	3:D:934:SER:HB3	2.38	0.47
5:F:655:LYS:HG3	5:F:708:GLY:HA2	1.95	0.47
5:F:1210:LYS:HB2	5:F:1289:ILE:HD11	1.96	0.47
5:F:1249:ILE:HA	5:F:1252:VAL:HG12	1.95	0.47
6:G:470:LEU:CB	7:H:538:LYS:HZ1	2.06	0.47
4:E:1052:LYS:HZ2	4:E:1068:LEU:HD23	1.79	0.46
4:E:1558:GLN:NE2	4:E:1590:ASP:OD1	2.48	0.46
5:F:228:PHE:CE2	5:F:359:GLN:HA	2.50	0.46
5:F:657:ILE:O	5:F:712:LEU:CD1	2.56	0.46
5:F:929:TYR:C	5:F:931:GLY:N	2.73	0.46
5:F:1104:ASN:O	5:F:1108:ARG:NH1	2.48	0.46
5:F:1281:LYS:HD2	5:F:1281:LYS:HA	1.54	0.46
5:F:1635:ARG:HA	5:F:1635:ARG:HD2	1.55	0.46
6:J:432:LEU:CA	8:L:782:ILE:HA	2.45	0.46
7:K:402:GLN:NE2	7:K:402:GLN:CA	2.76	0.46
7:K:413:LEU:HG	8:L:749:GLN:HE21	1.80	0.46
3:D:260:HIS:NE2	3:D:261:LEU:HD23	2.30	0.46
3:D:361:ILE:HD12	3:D:368:ILE:HG12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:611:LEU:CG	3:D:640:ALA:HB2	2.45	0.46
3:D:797:ARG:NH2	3:D:799:THR:OG1	2.49	0.46
5:F:10:THR:O	5:F:14:SER:CB	2.63	0.46
5:F:975:SER:HA	5:F:978:ILE:HG22	1.97	0.46
5:F:1014:SER:N	8:I:788:ASP:H	2.12	0.46
5:F:1167:LYS:HE3	5:F:1167:LYS:CA	2.27	0.46
5:F:1283:LYS:NZ	5:F:1286:PHE:HB3	2.30	0.46
5:F:1293:ASN:ND2	5:F:1293:ASN:C	2.73	0.46
7:H:312:VAL:HG12	7:H:361:ARG:HH21	1.80	0.46
8:I:788:ASP:N	8:I:788:ASP:OD1	2.49	0.46
6:J:293:HIS:CB	7:K:359:ASN:HD21	2.27	0.46
6:J:433:LYS:CA	7:K:499:GLY:HA2	2.44	0.46
7:K:310:ALA:HB3	7:K:352:ILE:CB	2.40	0.46
8:L:664:SER:HA	8:L:667:GLN:HE21	1.80	0.46
1:Z:776:ILE:C	1:Z:778:THR:H	2.23	0.46
1:A:269:ASN:HB3	1:A:272:GLU:HB2	1.96	0.46
1:A:420:LEU:HD13	1:A:457:TYR:HB2	1.97	0.46
3:D:125:SER:OG	3:D:734:LEU:HD13	2.15	0.46
4:E:207:ASP:O	4:E:211:GLN:HB2	2.15	0.46
4:E:284:ILE:HD11	4:E:328:ILE:HD12	1.96	0.46
4:E:1160:ILE:HG13	4:E:1161:PRO:HD3	1.98	0.46
5:F:425:ASP:OD1	5:F:425:ASP:N	2.48	0.46
5:F:538:GLU:O	5:F:542:ASN:ND2	2.49	0.46
5:F:640:PHE:O	5:F:643:THR:C	2.58	0.46
5:F:902:LYS:HE2	7:H:414:LYS:HD2	0.67	0.46
5:F:1177:VAL:C	5:F:1180:TYR:CB	2.88	0.46
8:I:821:ILE:HD13	8:I:821:ILE:O	2.16	0.46
1:Z:192:ILE:HG22	1:Z:539:ALA:HB3	1.97	0.46
1:Z:210:GLU:O	1:Z:214:ASN:ND2	2.49	0.46
1:Z:306:LYS:HE2	1:Z:331:VAL:HG22	1.97	0.46
1:A:810:ALA:HB1	1:A:836:ASP:OD1	2.15	0.46
3:D:495:PHE:O	3:D:499:LEU:HG	2.16	0.46
4:E:458:LYS:HG3	4:E:562:TRP:HE1	1.81	0.46
4:E:923:LEU:C	4:E:923:LEU:CD2	2.87	0.46
4:E:1503:VAL:HA	4:E:1506:LEU:HG	1.96	0.46
5:F:322:ILE:HA	5:F:325:PHE:HB3	1.97	0.46
5:F:750:TRP:CG	5:F:750:TRP:O	2.68	0.46
5:F:1364:TYR:O	5:F:1364:TYR:CD1	2.68	0.46
6:G:310:ARG:NE	6:G:314:TYR:OH	2.49	0.46
6:J:281:ASP:HA	6:J:284:ILE:CD1	2.31	0.46
6:J:434:THR:OG1	6:J:435:GLY:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:538:LYS:CB	8:L:818:ILE:C	2.88	0.46
3:D:430:GLU:HA	3:D:624:PHE:CD2	2.50	0.46
3:D:608:ILE:CD1	3:D:641:VAL:HG22	2.46	0.46
3:D:713:ILE:HD12	3:D:769:ARG:CG	2.46	0.46
4:E:596:LYS:O	4:E:600:ASN:ND2	2.49	0.46
5:F:154:GLN:HG3	5:F:190:TYR:HE2	1.81	0.46
5:F:439:LEU:HA	5:F:442:ILE:HG22	1.97	0.46
5:F:1406:TYR:OH	5:F:1452:SER:O	2.33	0.46
5:F:1543:LEU:C	5:F:1543:LEU:CD1	2.88	0.46
8:I:822:LYS:HG3	8:I:822:LYS:O	2.15	0.46
6:J:353:LEU:HD12	7:K:423:LYS:HG2	1.98	0.46
7:K:301:PRO:HB3	7:K:353:TYR:O	2.16	0.46
7:K:447:SER:CB	8:L:751:LEU:CD1	2.94	0.46
1:Z:697:PHE:HA	1:Z:703:SER:HB3	1.96	0.46
3:D:234:ILE:HD12	3:D:243:PHE:CE2	2.51	0.46
3:D:430:GLU:OE2	3:D:528:PRO:HA	2.16	0.46
4:E:1029:ASN:HD22	7:K:475:SER:CB	2.26	0.46
4:E:1086:ILE:HD11	4:E:1096:ILE:HB	1.97	0.46
5:F:319:ILE:HD11	5:F:477:ASP:HB2	1.97	0.46
5:F:526:PHE:HA	5:F:529:MET:HB3	1.97	0.46
1:Z:768:VAL:HA	1:Z:771:ILE:CD1	2.41	0.46
1:A:563:ASN:O	1:A:564:GLU:HG3	2.15	0.46
3:D:503:GLU:OE1	3:D:503:GLU:N	2.45	0.46
3:D:519:THR:HG21	3:D:605:VAL:N	2.31	0.46
3:D:863:ILE:CD1	3:D:887:GLN:HG3	2.46	0.46
4:E:100:GLU:O	4:E:104:SER:OG	2.26	0.46
5:F:303:LYS:HA	5:F:306:VAL:HG22	1.96	0.46
5:F:334:GLN:HE21	5:F:859:LYS:HZ3	1.26	0.46
5:F:750:TRP:O	5:F:750:TRP:CD1	2.69	0.46
5:F:1110:MET:CE	5:F:1157:TRP:CZ2	2.99	0.46
5:F:1136:LYS:CB	5:F:1207:CYS:HA	2.45	0.46
7:H:386:LEU:HG	8:I:690:GLN:HE21	1.81	0.46
6:J:371:LYS:NZ	6:J:371:LYS:C	2.70	0.46
1:Z:820:ILE:O	1:Z:822:TYR:N	2.48	0.46
1:A:238:PHE:HZ	1:A:505:HIS:CD2	2.34	0.46
3:D:462:LEU:HD21	3:D:465:ILE:CG2	2.46	0.46
4:E:559:PHE:HZ	4:E:567:ARG:HH22	1.64	0.46
5:F:671:PHE:HA	5:F:674:PHE:HB2	1.96	0.46
5:F:1067:ASN:ND2	5:F:1069:ASP:HB2	2.31	0.46
5:F:1139:ILE:HD12	5:F:1139:ILE:H	1.80	0.46
6:J:357:LEU:CD2	7:K:423:LYS:HE3	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:314:ASN:O	7:K:348:ILE:N	2.48	0.46
1:Z:49:LEU:C	1:Z:49:LEU:HD13	2.40	0.46
1:A:761:SER:CB	2:C:1355:SER:OG	2.64	0.46
3:D:207:MET:HE1	3:D:241:PHE:CD2	2.51	0.46
3:D:515:VAL:HA	3:D:644:SER:HB3	1.97	0.46
4:E:1134:TRP:NE1	4:E:1170:ASP:OD2	2.40	0.46
5:F:98:THR:HG22	5:F:99:ALA:H	1.81	0.46
5:F:917:PHE:CD1	5:F:917:PHE:O	2.69	0.46
5:F:1480:MET:HG2	5:F:1537:ALA:HB1	1.98	0.46
7:K:483:VAL:O	7:K:493:SER:N	2.48	0.46
1:Z:86:PHE:N	1:Z:86:PHE:CD1	2.79	0.46
1:Z:555:GLU:HA	1:Z:607:ARG:HH21	1.81	0.46
3:D:1000:ASP:N	3:D:1000:ASP:OD1	2.49	0.46
4:E:393:THR:H	4:E:396:THR:HG22	1.80	0.46
5:F:564:ASP:N	5:F:564:ASP:OD1	2.49	0.46
8:I:778:LYS:HB2	8:I:794:ILE:CB	2.46	0.46
7:K:288:ILE:O	7:K:292:VAL:HG23	2.16	0.46
7:K:426:GLY:CA	8:L:738:ASP:HB3	2.45	0.46
7:K:429:LEU:HB2	8:L:741:ARG:NH2	2.31	0.46
1:Z:390:LEU:HD21	1:Z:416:GLY:HA2	1.96	0.46
1:A:140:ILE:CG2	4:E:1393:LYS:CE	2.94	0.45
1:A:210:GLU:OE2	1:A:214:ASN:ND2	2.49	0.45
1:A:469:TYR:HB3	1:A:473:ARG:HB2	1.97	0.45
2:C:914:GLN:HE21	2:C:953:ILE:CG2	2.29	0.45
3:D:1494:ASN:O	5:F:1471:LYS:NZ	2.49	0.45
4:E:1038:LYS:HD2	4:E:1038:LYS:HA	1.78	0.45
5:F:159:LYS:CE	5:F:363:ASP:CB	2.93	0.45
5:F:1080:LEU:HG	5:F:1156:TYR:CD2	2.45	0.45
5:F:1608:ILE:HA	5:F:1612:LEU:HD13	1.98	0.45
7:H:318:GLU:CB	7:H:346:GLN:HA	2.46	0.45
6:J:405:LEU:HD22	7:K:469:ARG:NE	2.26	0.45
7:K:444:LEU:O	7:K:447:SER:CA	2.61	0.45
7:K:522:TYR:HA	7:K:525:GLU:HG2	1.98	0.45
1:Z:774:LEU:HD23	1:Z:774:LEU:O	2.14	0.45
1:A:354:VAL:HA	1:A:368:LEU:HD11	1.98	0.45
3:D:111:LEU:HD22	3:D:775:LEU:HD21	1.97	0.45
4:E:23:ASN:HD22	4:E:838:LYS:HD2	1.81	0.45
5:F:56:ILE:HD13	5:F:86:ILE:HD13	1.97	0.45
5:F:1034:LEU:HD22	5:F:1092:THR:CB	2.28	0.45
5:F:1036:PRO:CB	5:F:1042:ILE:H	2.30	0.45
7:H:314:ASN:HB2	7:H:361:ARG:HH22	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:412:ILE:CA	7:H:415:LEU:HB2	2.42	0.45
8:I:793:LEU:HA	8:I:796:ILE:HG13	1.97	0.45
6:J:275:GLN:NE2	6:J:278:GLU:OE1	2.49	0.45
7:K:315:LYS:CG	7:K:347:THR:HG22	2.46	0.45
8:L:684:VAL:HA	8:L:687:GLU:OE1	2.16	0.45
1:Z:249:ARG:C	1:Z:251:ALA:N	2.65	0.45
1:A:545:PHE:CD2	1:A:549:ASP:HB2	2.50	0.45
1:A:739:MET:O	1:A:742:LEU:HB2	2.16	0.45
3:D:789:VAL:HG21	3:D:952:LEU:CD1	2.47	0.45
4:E:279:ILE:HG23	4:E:281:GLN:HG2	1.97	0.45
4:E:624:THR:HG23	4:E:632:ALA:HB2	1.97	0.45
5:F:444:THR:HB	5:F:445:ASP:H	1.53	0.45
5:F:672:TRP:CD1	5:F:675:LEU:HD22	2.51	0.45
5:F:1090:PRO:HD3	5:F:1093:SER:OG	2.16	0.45
7:K:330:VAL:C	7:K:331:LEU:HD12	2.41	0.45
1:Z:88:LYS:O	1:Z:92:THR:HG23	2.15	0.45
1:A:679:ASP:HB3	1:A:684:ASN:HB2	1.99	0.45
4:E:174:VAL:HA	4:E:177:VAL:HG12	1.97	0.45
5:F:334:GLN:HB3	5:F:860:ASN:CG	2.37	0.45
5:F:914:ASP:CG	5:F:917:PHE:CB	2.89	0.45
6:J:380:TYR:CD1	6:J:383:LYS:HD3	2.51	0.45
7:K:315:LYS:HB2	8:L:670:VAL:HB	1.99	0.45
7:K:404:ARG:CG	8:L:704:GLN:NE2	2.80	0.45
1:Z:555:GLU:OE1	1:Z:607:ARG:NH2	2.49	0.45
3:D:641:VAL:HB	3:D:648:GLU:CG	2.45	0.45
4:E:650:ASP:OD2	4:E:653:SER:OG	2.28	0.45
4:E:982:ILE:HD12	4:E:982:ILE:N	2.31	0.45
5:F:690:GLU:CG	8:I:722:LEU:CG	2.95	0.45
5:F:922:LEU:CD2	7:H:400:LYS:HZ1	2.23	0.45
6:G:289:GLN:OE1	6:J:352:VAL:HG13	2.16	0.45
7:H:295:CYS:HA	7:H:298:SER:HB2	1.99	0.45
8:I:778:LYS:CG	8:I:794:ILE:CB	2.94	0.45
8:I:794:ILE:HA	8:I:797:LEU:CD1	2.46	0.45
7:K:466:LEU:O	7:K:470:ALA:N	2.40	0.45
1:Z:831:THR:HA	1:Z:834:ASN:HB2	1.98	0.45
1:A:48:GLU:CA	7:K:514:THR:HG21	2.47	0.45
1:A:195:SER:OG	1:A:536:ASN:OD1	2.34	0.45
1:A:630:ARG:O	1:A:634:ASP:N	2.41	0.45
1:A:654:ILE:HG13	1:A:706:ILE:HG21	1.98	0.45
3:D:100:PRO:HG2	3:D:898:LYS:NZ	2.32	0.45
3:D:393:ILE:HD11	3:D:460:LEU:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:504:ASP:OD1	4:E:524:LYS:NZ	2.49	0.45
4:E:696:GLY:HA2	5:F:1383:GLN:CB	2.47	0.45
4:E:772:THR:HA	4:E:775:PHE:HB2	1.99	0.45
4:E:1472:SER:HB2	4:E:1475:SER:H	1.81	0.45
5:F:1680:GLN:OE1	5:F:1680:GLN:HA	2.12	0.45
8:I:685:MET:O	8:I:688:HIS:ND1	2.44	0.45
7:K:316:VAL:H	7:K:347:THR:HA	1.81	0.45
7:K:466:LEU:O	7:K:469:ARG:N	2.49	0.45
1:Z:239:ILE:HD12	1:Z:258:LYS:HD3	1.99	0.45
1:A:128:LEU:CB	4:E:1260:TYR:HE2	2.26	0.45
1:A:494:TYR:O	1:A:497:THR:OG1	2.31	0.45
3:D:434:LEU:HD22	3:D:447:TYR:HB3	1.99	0.45
3:D:437:VAL:HA	3:D:446:LEU:O	2.16	0.45
3:D:476:VAL:HG13	3:D:488:GLN:HG3	1.99	0.45
3:D:763:ASP:O	3:D:765:ILE:HG12	2.17	0.45
3:D:789:VAL:HA	3:D:949:PHE:CE1	2.51	0.45
3:D:873:SER:OG	3:D:877:VAL:HB	2.17	0.45
4:E:912:TRP:CD1	4:E:917:PRO:HD3	2.52	0.45
4:E:1356:LEU:CB	1:Z:453:VAL:CG2	2.94	0.45
4:E:1380:ASP:C	4:E:1382:THR:H	2.24	0.45
5:F:859:LYS:HD2	5:F:860:ASN:H	1.81	0.45
5:F:920:ILE:HB	5:F:924:ALA:HA	1.97	0.45
5:F:1110:MET:CE	5:F:1157:TRP:HZ2	2.29	0.45
5:F:1219:VAL:O	5:F:1221:LEU:N	2.44	0.45
7:H:470:ALA:O	7:H:474:SER:HB2	2.17	0.45
7:H:508:LYS:HD2	7:H:508:LYS:HA	1.43	0.45
1:Z:658:ASN:O	1:Z:662:SER:HB2	2.17	0.45
1:Z:767:ILE:H	1:Z:767:ILE:HG13	1.47	0.45
1:Z:771:ILE:CG2	1:Z:772:PRO:CD	2.93	0.45
4:E:53:GLU:HB2	4:E:140:LYS:HD2	1.98	0.45
5:F:359:GLN:CB	5:F:421:ILE:HA	2.47	0.45
5:F:588:ASN:HB3	5:F:768:VAL:HG12	1.98	0.45
5:F:792:ASP:OD2	5:F:1244:ASN:ND2	2.43	0.45
6:J:284:ILE:O	6:J:288:VAL:HG23	2.17	0.45
1:Z:599:ARG:NE	1:Z:605:GLU:OE1	2.39	0.45
3:D:654:THR:O	3:D:658:ILE:HG13	2.16	0.45
4:E:1180:GLN:NE2	4:E:1181:THR:O	2.40	0.45
5:F:1472:GLU:OE2	5:F:1473:ASN:ND2	2.50	0.45
5:F:1638:ILE:HA	5:F:1641:PHE:CD2	2.52	0.45
6:J:389:ARG:NH1	6:J:389:ARG:CA	2.79	0.45
7:K:389:LYS:CA	7:K:393:ASP:CB	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L:802:ASP:O	8:L:806:SER:CB	2.65	0.45
1:Z:542:THR:HG21	1:Z:557:LEU:HD21	1.99	0.45
1:A:775:LEU:HD22	1:A:832:LEU:HD11	1.99	0.45
3:D:615:PHE:CE2	3:D:627:GLU:HG2	2.52	0.45
5:F:320:GLU:OE2	5:F:351:HIS:ND1	2.50	0.45
6:J:404:ASP:O	6:J:408:ALA:CB	2.65	0.45
7:K:395:ALA:O	7:K:399:LEU:HB3	2.17	0.45
1:A:137:ASP:HB2	4:E:1386:LEU:HG	1.98	0.44
1:A:679:ASP:CG	1:A:684:ASN:HD22	2.24	0.44
3:D:234:ILE:O	3:D:240:LEU:HD12	2.16	0.44
3:D:735:SER:O	3:D:739:THR:OG1	2.32	0.44
4:E:755:ASN:CB	5:F:1376:THR:OG1	2.64	0.44
4:E:955:PHE:O	4:E:959:LEU:HB2	2.17	0.44
4:E:963:LYS:HB2	4:E:963:LYS:HE3	1.84	0.44
4:E:1395:ILE:HD12	4:E:1398:VAL:HB	2.00	0.44
4:E:1421:ILE:HA	4:E:1424:LEU:HD23	1.99	0.44
5:F:23:ASP:OD1	5:F:23:ASP:N	2.47	0.44
5:F:943:ARG:HB3	5:F:947:LYS:NZ	2.32	0.44
5:F:1495:THR:HA	5:F:1498:LEU:HB2	1.97	0.44
6:G:427:GLU:HB3	8:I:779:THR:HG21	1.99	0.44
7:H:451:ALA:O	7:H:455:LYS:N	2.45	0.44
6:J:286:LYS:O	6:J:290:ILE:HG12	2.18	0.44
6:J:372:PHE:O	6:J:372:PHE:CD1	2.69	0.44
7:K:389:LYS:HA	7:K:393:ASP:HB3	0.61	0.44
1:Z:27:GLU:OE2	1:Z:30:ASP:HB2	2.11	0.44
1:Z:54:PHE:HA	1:Z:57:ARG:CZ	2.47	0.44
1:Z:661:LEU:HA	1:Z:664:THR:HG22	1.99	0.44
1:A:54:PHE:HA	1:A:57:ARG:CD	2.47	0.44
1:A:123:MET:CB	6:J:413:ASN:CB	2.95	0.44
1:A:125:ILE:CB	4:E:1212:THR:OG1	2.65	0.44
1:A:128:LEU:CB	4:E:1260:TYR:CE2	3.00	0.44
1:A:212:PHE:CE2	1:A:541:TYR:CZ	3.05	0.44
1:A:675:VAL:HA	1:A:684:ASN:HD21	1.81	0.44
3:D:123:GLU:HG2	3:D:124:ARG:H	1.82	0.44
3:D:910:LEU:HD23	3:D:913:LEU:CD1	2.38	0.44
3:D:937:SER:HB3	3:D:941:GLN:CB	2.43	0.44
4:E:495:ASP:HB2	4:E:529:LYS:HG3	1.99	0.44
6:J:364:ILE:HG23	7:K:424:ASN:HB3	1.99	0.44
1:Z:12:SER:O	1:Z:12:SER:OG	2.31	0.44
1:A:739:MET:SD	1:A:778:THR:OG1	2.63	0.44
3:D:399:SER:O	3:D:407:ALA:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:445:ARG:O	3:D:465:ILE:HA	2.18	0.44
3:D:527:SER:HB2	3:D:614:LEU:HD22	1.99	0.44
4:E:1071:LYS:HD3	4:E:1071:LYS:HA	1.82	0.44
5:F:159:LYS:HE3	5:F:363:ASP:CB	2.45	0.44
5:F:378:ALA:O	5:F:383:ASN:OD1	2.35	0.44
5:F:1118:ARG:NH1	5:F:1118:ARG:CG	2.80	0.44
5:F:1285:HIS:O	5:F:1285:HIS:CG	2.70	0.44
8:L:638:ASP:HA	8:L:641:VAL:HG23	1.99	0.44
1:Z:766:ASN:O	1:Z:769:LYS:N	2.50	0.44
1:Z:792:SER:OG	1:Z:799:LYS:NZ	2.43	0.44
1:A:16:LYS:CG	6:J:468:ALA:HA	2.47	0.44
1:A:333:ILE:HG13	1:A:334:TRP:N	2.33	0.44
1:A:644:TYR:O	1:A:648:GLU:N	2.51	0.44
3:D:716:VAL:HB	3:D:885:ALA:HB1	1.99	0.44
3:D:878:ILE:HG22	3:D:879:ASP:H	1.83	0.44
3:D:908:SER:O	3:D:911:ASN:HB3	2.17	0.44
4:E:300:SER:O	4:E:304:ASN:HB2	2.16	0.44
4:E:1020:ILE:HA	4:E:1023:VAL:HG12	1.98	0.44
5:F:48:ARG:NH1	5:F:85:GLU:OE2	2.48	0.44
5:F:210:LYS:HE2	5:F:210:LYS:HB3	1.78	0.44
5:F:336:LYS:HZ1	5:F:778:LEU:HD12	1.82	0.44
5:F:841:PHE:HE2	5:F:918:PHE:CE1	2.22	0.44
5:F:1084:LEU:CB	5:F:1156:TYR:CE1	3.00	0.44
5:F:1359:PHE:O	5:F:1359:PHE:CG	2.69	0.44
7:H:313:TYR:HD1	7:H:349:PRO:HB3	1.82	0.44
7:H:455:LYS:O	7:H:459:LEU:HB2	2.17	0.44
6:J:300:ASP:O	6:J:304:LEU:HD13	2.17	0.44
6:J:374:GLN:CD	6:J:374:GLN:C	2.85	0.44
1:A:260:LEU:HA	1:A:263:MET:HE2	1.99	0.44
1:A:589:LEU:O	1:A:604:ILE:HG22	2.17	0.44
1:A:749:ASP:HB2	2:C:1274:LYS:HZ3	1.82	0.44
4:E:442:LEU:HD23	4:E:442:LEU:HA	1.86	0.44
5:F:148:PHE:HA	5:F:151:ILE:HG12	1.99	0.44
5:F:365:LYS:HA	5:F:369:GLN:CB	2.47	0.44
5:F:663:LYS:HA	5:F:720:HIS:CE1	2.53	0.44
5:F:905:SER:CB	8:I:753:GLU:HB2	2.48	0.44
5:F:1026:PHE:HD2	5:F:1034:LEU:HD11	1.83	0.44
5:F:1026:PHE:HE1	5:F:1049:LEU:HD11	1.83	0.44
5:F:1084:LEU:CB	5:F:1156:TYR:CZ	3.00	0.44
5:F:1606:GLN:O	5:F:1610:ALA:CB	2.60	0.44
6:J:395:GLU:C	6:J:395:GLU:CD	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:484:PHE:C	7:K:492:ASP:CB	2.88	0.44
1:Z:357:LYS:HA	1:Z:360:ILE:HB	2.00	0.44
3:D:617:ALA:HB1	3:D:782:ARG:HH22	1.82	0.44
4:E:1122:PHE:HA	4:E:1125:GLU:HG2	1.99	0.44
4:E:1379:GLU:OE1	4:E:1383:GLN:NE2	2.50	0.44
5:F:56:ILE:HG13	5:F:66:VAL:HG21	2.00	0.44
5:F:351:HIS:O	5:F:351:HIS:CG	2.70	0.44
5:F:881:THR:HA	5:F:885:GLU:HB3	2.00	0.44
5:F:1068:ILE:CD1	5:F:1150:PHE:CE2	3.00	0.44
5:F:1191:SER:HB3	5:F:1192:VAL:H	1.51	0.44
5:F:1286:PHE:O	5:F:1286:PHE:CD1	2.70	0.44
7:H:298:SER:OG	7:H:305:LYS:O	2.25	0.44
1:Z:733:GLN:HA	1:Z:785:MET:HE3	1.99	0.44
1:A:193:LEU:CD1	1:A:578:GLU:HG3	2.48	0.44
1:A:628:ALA:HB1	1:A:644:TYR:CE2	2.53	0.44
3:D:331:ILE:O	3:D:334:VAL:HG23	2.18	0.44
3:D:445:ARG:NH1	3:D:466:LYS:HB3	2.32	0.44
4:E:22:MET:HA	4:E:26:ALA:HB3	1.99	0.44
4:E:119:ASN:N	4:E:119:ASN:OD1	2.50	0.44
4:E:1087:TYR:HB2	4:E:1213:THR:HG21	2.00	0.44
4:E:1359:ILE:HD12	4:E:1430:LEU:HD23	2.00	0.44
5:F:148:PHE:HE2	5:F:216:LEU:HD11	1.83	0.44
5:F:1543:LEU:HD12	5:F:1543:LEU:O	2.18	0.44
5:F:1623:VAL:HA	5:F:1626:VAL:HG22	2.00	0.44
7:K:315:LYS:CD	7:K:347:THR:HG22	2.48	0.44
7:K:413:LEU:HD21	8:L:749:GLN:HB3	2.00	0.44
3:D:353:GLN:HG2	3:D:374:LYS:H	1.82	0.44
3:D:929:PHE:HA	3:D:932:ILE:HG22	1.99	0.44
3:D:1494:ASN:N	5:F:1471:LYS:HE2	2.32	0.44
4:E:773:LEU:O	4:E:773:LEU:HD22	2.18	0.44
4:E:1214:PHE:O	4:E:1218:SER:OG	2.33	0.44
4:E:1305:ASN:OD1	4:E:1305:ASN:N	2.51	0.44
4:E:1475:SER:HA	4:E:1478:ILE:HD12	2.00	0.44
5:F:452:LYS:HA	5:F:452:LYS:HD2	1.70	0.44
5:F:1309:LEU:C	5:F:1309:LEU:CD2	2.86	0.44
5:F:1490:ARG:HE	5:F:1493:LYS:HB3	1.83	0.44
8:I:795:LYS:C	8:I:795:LYS:NZ	2.72	0.44
6:J:377:ILE:HG22	6:J:378:HIS:CD2	2.47	0.44
6:J:389:ARG:HH22	6:J:393:ASP:HB2	1.82	0.44
7:K:444:LEU:CA	7:K:447:SER:CB	2.95	0.44
8:L:637:LEU:O	8:L:641:VAL:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:757:ALA:HA	1:Z:820:ILE:CB	2.47	0.44
1:A:137:ASP:OD2	4:E:1386:LEU:HG	2.16	0.44
1:A:341:LEU:HD21	1:A:371:PHE:CZ	2.53	0.44
5:F:1363:ILE:HG22	1:Z:125:ILE:HD11	1.97	0.44
6:J:277:ILE:HG12	8:L:641:VAL:HG22	1.99	0.44
6:J:391:LEU:CD1	7:K:455:LYS:HA	2.48	0.44
1:A:222:PHE:HD1	1:A:232:PHE:HB3	1.83	0.43
1:A:253:LEU:HG	1:A:257:TRP:CD1	2.53	0.43
1:A:760:PHE:HD2	1:A:823:ARG:HH11	1.66	0.43
3:D:713:ILE:CD1	3:D:769:ARG:HD3	2.48	0.43
3:D:936:VAL:O	3:D:936:VAL:HG12	2.18	0.43
4:E:773:LEU:HD23	4:E:773:LEU:HA	1.50	0.43
4:E:806:PHE:HE2	4:E:854:LEU:HD21	1.82	0.43
4:E:1430:LEU:O	4:E:1432:ARG:NH1	2.51	0.43
5:F:174:LEU:C	5:F:177:GLN:HE22	2.26	0.43
5:F:662:PRO:HA	5:F:668:ARG:HE	1.83	0.43
5:F:672:TRP:CE2	5:F:716:LEU:HD12	2.53	0.43
5:F:1227:THR:HA	7:H:472:ASN:CB	2.47	0.43
6:G:436:LEU:CD1	7:H:503:ASN:CB	2.96	0.43
7:H:394:THR:HA	8:I:697:LEU:HD22	2.00	0.43
7:H:511:GLU:HA	7:H:514:THR:CB	2.48	0.43
7:K:385:GLN:HA	7:K:385:GLN:NE2	2.23	0.43
1:Z:196:ASN:HD21	1:Z:530:ARG:NE	2.13	0.43
3:D:585:ILE:O	3:D:589:HIS:HB2	2.17	0.43
5:F:1349:PHE:N	5:F:1349:PHE:HD1	2.15	0.43
1:Z:436:LEU:HD21	1:Z:481:THR:HG23	2.00	0.43
1:Z:767:ILE:CD1	1:Z:768:VAL:HG23	2.49	0.43
3:D:353:GLN:CD	3:D:374:LYS:HB2	2.43	0.43
3:D:568:GLN:NE2	3:D:570:VAL:O	2.52	0.43
3:D:608:ILE:CD1	3:D:641:VAL:HG13	2.48	0.43
3:D:781:LEU:HD11	3:D:903:ILE:HG21	2.00	0.43
3:D:799:THR:HG23	3:D:803:PHE:O	2.18	0.43
4:E:216:TYR:CD1	4:E:220:PHE:HB2	2.51	0.43
5:F:547:PHE:HE2	5:F:619:VAL:HG11	1.82	0.43
5:F:659:ASN:OD1	5:F:659:ASN:N	2.51	0.43
5:F:726:SER:HA	5:F:730:VAL:HG22	2.01	0.43
5:F:742:GLN:HG3	5:F:747:VAL:HA	2.01	0.43
5:F:920:ILE:CG2	5:F:926:LEU:HG	2.48	0.43
6:J:372:PHE:O	6:J:372:PHE:CG	2.70	0.43
6:J:406:PHE:O	6:J:406:PHE:CD1	2.70	0.43
1:Z:56:LEU:HD22	1:Z:60:ASN:ND2	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:GLN:NE2	1:A:606:GLU:O	2.50	0.43
1:A:619:PHE:O	1:A:623:ILE:HG22	2.18	0.43
1:A:703:SER:OG	1:A:711:LYS:NZ	2.39	0.43
1:A:771:ILE:HD13	1:A:774:LEU:HD12	2.00	0.43
2:C:79:HIS:CE1	2:C:704:VAL:HG11	2.54	0.43
3:D:235:SER:CB	3:D:240:LEU:HD13	2.45	0.43
3:D:909:PHE:O	3:D:913:LEU:HG	2.18	0.43
3:D:1377:ASN:HD21	1:Z:758:GLN:HE21	1.59	0.43
4:E:36:GLN:HE22	4:E:943:VAL:HA	1.83	0.43
4:E:919:LEU:HA	4:E:919:LEU:HD12	1.86	0.43
4:E:1408:LEU:HD21	4:E:1456:ILE:HD11	2.00	0.43
5:F:1000:LEU:HD13	5:F:1000:LEU:HA	1.82	0.43
5:F:1257:LEU:HD23	5:F:1257:LEU:HA	1.84	0.43
5:F:1519:LYS:HA	5:F:1522:VAL:HG12	2.00	0.43
6:G:350:PHE:HE2	7:H:418:GLN:HE22	1.63	0.43
7:H:303:THR:HG23	7:H:353:TYR:CZ	2.53	0.43
6:J:300:ASP:HA	6:J:303:GLU:CD	2.43	0.43
8:L:664:SER:O	8:L:668:VAL:HG23	2.18	0.43
1:A:198:SER:HB3	1:A:543:LYS:HE2	2.01	0.43
1:A:591:GLY:HA3	1:A:600:ILE:O	2.18	0.43
1:A:735:THR:O	1:A:739:MET:HG2	2.18	0.43
3:D:394:GLU:O	3:D:398:ILE:HG13	2.17	0.43
3:D:1467:SER:CA	1:Z:621:HIS:CE1	3.02	0.43
4:E:598:VAL:HG11	4:E:638:ILE:HD11	2.00	0.43
4:E:950:ARG:HG3	4:E:1012:VAL:HA	2.01	0.43
4:E:1444:LEU:O	4:E:1448:SER:N	2.49	0.43
5:F:213:ILE:HB	5:F:240:LEU:HD13	2.00	0.43
6:G:297:ASP:HA	6:G:300:ASP:HB2	1.99	0.43
7:H:386:LEU:HD21	8:I:687:GLU:HA	2.00	0.43
7:H:412:ILE:O	7:H:415:LEU:HB2	2.17	0.43
8:I:798:ASN:O	8:I:801:PHE:CB	2.66	0.43
8:L:667:GLN:O	8:L:670:VAL:HG22	2.18	0.43
1:Z:505:HIS:HA	1:Z:508:ILE:HD12	2.00	0.43
1:Z:810:ALA:O	1:Z:836:ASP:CB	2.62	0.43
3:D:118:THR:HB	3:D:623:GLY:CA	2.35	0.43
3:D:491:ARG:HB2	3:D:521:LYS:H	1.84	0.43
3:D:508:LYS:CG	3:D:516:LEU:HA	2.49	0.43
3:D:993:GLY:C	3:D:995:PHE:N	2.76	0.43
3:D:1391:PHE:CD1	3:D:1426:MET:HE1	2.54	0.43
4:E:530:ILE:HA	4:E:552:LEU:O	2.19	0.43
4:E:1274:GLU:HA	4:E:1277:ILE:HD12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:227:ASP:CA	5:F:361:LEU:CB	2.97	0.43
5:F:676:ASP:HA	5:F:679:ILE:HB	1.99	0.43
5:F:905:SER:CB	8:I:749:GLN:O	2.66	0.43
5:F:1283:LYS:HA	5:F:1283:LYS:NZ	2.33	0.43
7:K:395:ALA:O	7:K:399:LEU:HD23	2.19	0.43
8:L:695:GLN:NE2	8:L:696:SER:OG	2.51	0.43
8:L:809:ASP:HA	8:L:812:THR:HB	2.00	0.43
1:Z:786:ILE:HD11	1:Z:838:SER:HA	2.01	0.43
1:A:649:GLU:OE1	1:A:652:ILE:HD12	2.19	0.43
3:D:214:VAL:HA	3:D:233:LEU:O	2.18	0.43
3:D:451:SER:HB2	3:D:458:GLU:HB2	2.01	0.43
3:D:509:PHE:CD1	3:D:515:VAL:HG23	2.54	0.43
4:E:291:ASP:OD1	4:E:291:ASP:N	2.52	0.43
5:F:563:SER:O	5:F:567:LYS:NZ	2.50	0.43
5:F:783:ILE:HG13	5:F:784:ILE:H	1.83	0.43
5:F:1088:ARG:HH11	5:F:1088:ARG:CG	2.23	0.43
5:F:1489:ILE:HA	5:F:1492:LEU:HD12	2.01	0.43
6:J:379:LEU:HG	6:J:379:LEU:O	2.19	0.43
8:L:637:LEU:CD2	8:L:640:LEU:HB2	2.48	0.43
1:Z:444:LYS:HA	1:Z:444:LYS:HD3	1.89	0.43
1:A:131:GLY:HA2	1:A:134:LYS:HD3	2.01	0.43
1:A:436:LEU:HD21	1:A:481:THR:HG23	2.00	0.43
3:D:484:GLN:NE2	3:D:566:LYS:H	2.16	0.43
3:D:713:ILE:HD12	3:D:769:ARG:CD	2.48	0.43
4:E:40:ILE:HD12	4:E:40:ILE:HA	1.90	0.43
4:E:605:LYS:O	4:E:605:LYS:NZ	2.37	0.43
4:E:787:PRO:HG2	4:E:1143:GLN:HE21	1.84	0.43
5:F:131:TYR:O	5:F:135:ILE:HG12	2.19	0.43
5:F:899:PHE:O	5:F:904:TYR:OH	2.24	0.43
5:F:900:LEU:HD13	5:F:904:TYR:CD1	2.53	0.43
5:F:1618:SER:CB	1:Z:634:ASP:O	2.67	0.43
8:I:805:ARG:CB	1:Z:88:LYS:HE2	2.47	0.43
6:J:305:ILE:HG21	8:L:665:TRP:NE1	2.34	0.43
6:J:435:GLY:O	6:J:440:VAL:CB	2.67	0.43
1:Z:78:LEU:HB3	1:Z:83:VAL:CG2	2.48	0.43
1:A:531:ASP:OD2	1:A:536:ASN:ND2	2.41	0.43
3:D:387:LEU:HA	3:D:391:MET:HE1	2.00	0.43
3:D:447:TYR:O	3:D:463:GLU:N	2.52	0.43
4:E:185:LEU:HD23	4:E:185:LEU:HA	1.89	0.43
4:E:305:ASP:O	4:E:309:ASN:CB	2.67	0.43
4:E:988:ILE:C	4:E:990:LYS:N	2.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:1387:LEU:O	4:E:1391:LEU:N	2.51	0.43
4:E:1561:LEU:HD13	4:E:1585:LEU:HD11	2.01	0.43
5:F:135:ILE:HG23	5:F:206:ILE:HA	2.01	0.43
5:F:229:PHE:O	5:F:233:TYR:N	2.52	0.43
5:F:354:ARG:C	5:F:356:ILE:H	2.26	0.43
5:F:522:MET:SD	5:F:523:ARG:N	2.92	0.43
5:F:680:PHE:HA	5:F:745:ARG:HH12	1.83	0.43
5:F:909:LEU:O	7:H:403:SER:CB	2.66	0.43
5:F:927:GLY:C	5:F:978:ILE:HD11	2.44	0.43
5:F:1362:ASP:CB	1:Z:125:ILE:CG2	2.97	0.43
5:F:1550:LEU:HD11	5:F:1604:ILE:HG21	2.00	0.43
8:I:792:GLN:HG2	1:Z:42:ILE:HD12	1.49	0.43
6:J:365:SER:N	7:K:424:ASN:HD21	2.04	0.43
1:Z:474:PHE:HB3	1:Z:477:TYR:HB3	2.00	0.43
3:D:401:ILE:CG2	3:D:462:LEU:HB3	2.30	0.43
3:D:491:ARG:HG3	3:D:521:LYS:N	2.34	0.43
3:D:582:ASP:O	3:D:585:ILE:HG22	2.19	0.43
3:D:766:LEU:HD22	3:D:889:GLU:HA	2.01	0.43
5:F:300:MET:HG3	5:F:303:LYS:HE2	2.00	0.43
5:F:841:PHE:CZ	5:F:922:LEU:HB2	2.54	0.43
5:F:925:HIS:HA	5:F:928:LEU:HD11	2.00	0.43
5:F:1545:ARG:HA	5:F:1548:ALA:HB3	2.01	0.43
6:J:334:SER:HA	6:J:337:LYS:HB2	2.01	0.43
6:J:431:GLN:O	8:L:782:ILE:HA	2.19	0.43
7:K:437:TRP:HB3	8:L:744:ALA:HB3	2.00	0.43
8:L:664:SER:O	8:L:667:GLN:HG3	2.19	0.43
1:Z:136:PHE:CD1	1:Z:136:PHE:O	2.71	0.43
1:Z:251:ALA:C	1:Z:253:LEU:H	2.23	0.43
1:Z:709:LYS:NZ	1:Z:764:ASP:HB3	2.34	0.43
1:A:681:SER:HA	1:A:687:LEU:HB3	2.01	0.42
3:D:793:PHE:CZ	3:D:934:SER:HB2	2.54	0.42
4:E:370:SER:O	4:E:372:ASP:N	2.48	0.42
4:E:916:TYR:CZ	4:E:963:LYS:HB2	2.54	0.42
4:E:1276:LYS:HA	4:E:1276:LYS:HD2	1.71	0.42
5:F:26:LYS:HZ3	5:F:26:LYS:HG2	1.68	0.42
5:F:606:VAL:HA	5:F:609:LEU:HG	2.01	0.42
5:F:731:PHE:CD2	5:F:790:SER:HA	2.54	0.42
6:G:296:ALA:CB	6:J:363:LYS:HD2	2.45	0.42
6:G:449:LEU:HA	1:Z:84:ASP:OD1	2.19	0.42
7:K:446:ARG:C	7:K:446:ARG:CD	2.92	0.42
8:L:733:ALA:HA	8:L:737:ASN:HD21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:510:LEU:HB3	1:Z:516:PHE:HB2	2.00	0.42
1:A:210:GLU:O	1:A:211:LYS:C	2.62	0.42
1:A:225:SER:O	1:A:229:ASN:N	2.51	0.42
3:D:822:ILE:HG22	3:D:824:GLN:H	1.84	0.42
3:D:884:VAL:HB	3:D:887:GLN:OE1	2.19	0.42
5:F:200:LEU:HA	5:F:200:LEU:HD13	1.79	0.42
5:F:825:ILE:O	5:F:825:ILE:HG23	2.19	0.42
5:F:935:GLN:CB	5:F:998:LEU:CD2	2.97	0.42
6:J:371:LYS:C	6:J:371:LYS:HD2	2.44	0.42
7:K:311:PHE:HD1	7:K:351:GLN:HG3	1.85	0.42
1:Z:116:LYS:NZ	1:Z:116:LYS:C	2.77	0.42
1:A:681:SER:OG	1:A:691:ARG:NH1	2.52	0.42
1:A:709:LYS:O	1:A:713:ILE:HG12	2.18	0.42
1:A:754:ARG:HA	1:A:819:MET:HE1	2.01	0.42
3:D:372:SER:OG	3:D:376:THR:OG1	2.22	0.42
3:D:375:SER:O	3:D:420:ILE:HD12	2.18	0.42
3:D:648:GLU:HG3	3:D:650:TYR:HE1	1.83	0.42
3:D:988:LEU:HA	3:D:992:CYS:CB	2.49	0.42
4:E:982:ILE:HD12	4:E:982:ILE:H	1.85	0.42
4:E:1356:LEU:CB	1:Z:453:VAL:HG21	2.49	0.42
5:F:158:ILE:HA	5:F:183:ARG:CZ	2.49	0.42
5:F:437:ASP:HA	5:F:440:GLN:HG3	2.01	0.42
6:G:440:VAL:HA	6:G:443:VAL:HB	2.01	0.42
7:H:420:ALA:CB	8:I:745:TYR:CD1	2.96	0.42
7:H:444:LEU:HA	7:H:447:SER:HB3	2.02	0.42
7:H:532:ALA:HA	8:I:821:ILE:HG13	2.01	0.42
8:I:795:LYS:HZ3	8:I:795:LYS:HA	1.83	0.42
7:K:525:GLU:O	7:K:529:LYS:CB	2.56	0.42
8:L:640:LEU:CD1	8:L:643:LYS:HG2	2.49	0.42
1:Z:551:ARG:NH2	1:Z:606:GLU:OE2	2.46	0.42
1:Z:687:LEU:HD23	1:Z:690:ARG:HD2	2.01	0.42
3:D:168:GLN:N	3:D:187:ASP:OD2	2.38	0.42
3:D:381:VAL:O	3:D:385:LYS:HA	2.19	0.42
3:D:491:ARG:HB2	3:D:520:THR:HB	2.01	0.42
3:D:605:VAL:HG11	3:D:608:ILE:HD11	2.01	0.42
3:D:611:LEU:HG	3:D:640:ALA:HB2	2.01	0.42
3:D:1367:LEU:HD23	3:D:1398:PHE:CE1	2.54	0.42
4:E:319:PRO:HG2	4:E:361:LYS:HD3	2.00	0.42
5:F:390:TRP:CB	5:F:393:SER:HB3	2.50	0.42
5:F:426:GLN:HA	5:F:429:GLU:HG3	2.00	0.42
5:F:1508:ILE:HG22	5:F:1511:LEU:HD23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:415:LEU:HD12	7:H:415:LEU:HA	1.79	0.42
8:I:815:GLU:HB3	8:I:816:LYS:HE3	2.02	0.42
6:J:283:TYR:CD2	6:J:286:LYS:HE2	2.55	0.42
6:J:311:ASP:OD2	7:K:376:LEU:HD11	2.20	0.42
1:Z:117:LYS:HB3	1:Z:117:LYS:HZ2	1.79	0.42
1:Z:432:ILE:HD12	1:Z:432:ILE:HA	1.90	0.42
1:Z:779:LEU:CB	1:Z:835:ILE:CA	2.97	0.42
1:A:140:ILE:HG23	4:E:1393:LYS:HD3	1.84	0.42
1:A:532:ILE:HG22	1:A:532:ILE:O	2.19	0.42
2:C:888:LEU:HA	2:C:892:PHE:HD2	1.85	0.42
3:D:467:PHE:CD1	3:D:473:THR:HG23	2.54	0.42
3:D:919:VAL:HG12	3:D:920:GLU:N	2.34	0.42
3:D:1241:GLY:O	1:Z:826:ARG:CB	2.67	0.42
4:E:343:ASP:O	4:E:347:THR:OG1	2.36	0.42
4:E:976:PHE:HZ	7:K:457:ASN:HB3	1.83	0.42
5:F:917:PHE:O	5:F:919:ASN:N	2.52	0.42
6:G:343:ASP:O	6:G:347:THR:OG1	2.30	0.42
6:J:298:THR:HA	8:L:658:TYR:CE1	2.54	0.42
7:K:365:GLN:O	7:K:369:VAL:HG23	2.20	0.42
1:A:370:TYR:CD2	1:A:390:LEU:HD13	2.54	0.42
1:A:516:PHE:CE2	1:A:534:PHE:HB2	2.54	0.42
3:D:367:ILE:HA	3:D:380:TYR:O	2.20	0.42
3:D:667:LEU:HD12	3:D:669:PHE:HB2	2.00	0.42
3:D:684:PHE:O	3:D:688:LYS:HB2	2.19	0.42
4:E:569:LEU:HD22	4:E:634:ILE:HD11	2.01	0.42
4:E:683:ASP:OD1	4:E:689:GLY:N	2.36	0.42
5:F:1090:PRO:CD	5:F:1093:SER:HB3	2.50	0.42
5:F:1545:ARG:HA	5:F:1545:ARG:HD2	1.91	0.42
6:G:465:LYS:CE	1:Z:20:LYS:HE2	2.49	0.42
7:H:365:GLN:HA	7:H:368:ASN:HD22	1.84	0.42
7:K:358:LEU:HD22	8:L:662:ILE:CD1	2.41	0.42
1:Z:122:LEU:HD23	1:Z:122:LEU:HA	1.73	0.42
1:Z:254:LEU:HG	1:Z:258:LYS:HE2	2.02	0.42
1:Z:599:ARG:HH22	1:Z:620:LEU:HD21	1.84	0.42
1:Z:826:ARG:O	1:Z:827:GLU:C	2.61	0.42
1:A:679:ASP:OD2	1:A:684:ASN:ND2	2.50	0.42
1:A:776:ILE:CD1	1:A:828:THR:HG23	2.49	0.42
2:C:899:ALA:HB3	2:C:941:ASN:HD22	1.83	0.42
3:D:514:SER:O	3:D:515:VAL:HG13	2.20	0.42
3:D:681:THR:O	3:D:685:VAL:HG23	2.20	0.42
4:E:443:ILE:HD12	4:E:590:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:599:THR:HG23	4:E:660:PHE:HA	2.02	0.42
4:E:1539:ASN:ND2	4:E:1611:TYR:OH	2.48	0.42
5:F:787:GLY:C	5:F:790:SER:H	2.27	0.42
5:F:1110:MET:HE2	5:F:1157:TRP:HZ2	1.80	0.42
7:K:483:VAL:CB	7:K:494:MET:HA	2.49	0.42
1:A:478:TYR:O	1:A:482:LEU:HG	2.20	0.42
4:E:36:GLN:NE2	4:E:36:GLN:O	2.53	0.42
4:E:120:PRO:HB3	4:E:127:TYR:CG	2.54	0.42
4:E:421:PHE:O	4:E:425:LEU:CB	2.68	0.42
5:F:296:ARG:H	5:F:296:ARG:HG3	1.71	0.42
5:F:1305:SER:O	5:F:1307:VAL:N	2.49	0.42
6:G:295:LYS:HB3	6:J:363:LYS:NZ	2.33	0.42
6:G:377:ILE:HD12	6:G:377:ILE:HA	1.96	0.42
7:H:462:ARG:HA	7:H:465:ILE:HB	2.02	0.42
7:K:455:LYS:HD3	7:K:455:LYS:H	1.75	0.42
8:L:671:LYS:O	8:L:675:GLN:NE2	2.47	0.42
1:Z:654:ILE:HG22	1:Z:710:ASN:HB2	2.01	0.42
1:A:137:ASP:HB2	4:E:1386:LEU:CA	2.43	0.42
1:A:215:TYR:CD2	1:A:238:PHE:HE1	2.37	0.42
3:D:381:VAL:HB	3:D:457:ILE:CG2	2.50	0.42
4:E:222:GLU:O	4:E:226:ASN:HB2	2.20	0.42
4:E:1043:LEU:HB3	4:E:1078:ILE:HD11	2.00	0.42
5:F:864:LEU:HD12	5:F:864:LEU:HA	1.81	0.42
5:F:920:ILE:CB	5:F:924:ALA:C	2.91	0.42
5:F:1144:VAL:HG11	5:F:1291:SER:OG	2.20	0.42
5:F:1550:LEU:HD12	5:F:1604:ILE:HG21	2.01	0.42
5:F:1634:LYS:HA	5:F:1637:VAL:HG22	2.00	0.42
8:I:672:GLY:HA2	8:I:675:GLN:HG2	2.00	0.42
8:I:822:LYS:NZ	8:I:822:LYS:CB	2.82	0.42
6:J:371:LYS:O	6:J:371:LYS:CD	2.68	0.42
7:K:462:ARG:O	7:K:466:LEU:HD12	2.20	0.42
7:K:504:ASP:C	7:K:506:ILE:N	2.75	0.42
8:L:749:GLN:NE2	8:L:752:ASP:OD2	2.51	0.42
1:Z:121:ILE:HD12	1:Z:121:ILE:HA	1.64	0.42
1:Z:367:PHE:O	1:Z:370:TYR:HB2	2.20	0.42
1:A:775:LEU:CD1	1:A:832:LEU:CD1	2.95	0.42
2:C:1388:HIS:O	4:E:1331:LEU:HD13	2.19	0.42
3:D:292:ASN:OD1	3:D:293:ILE:N	2.53	0.42
3:D:680:SER:OG	3:D:772:GLY:HA2	2.20	0.42
3:D:873:SER:HB3	3:D:877:VAL:HB	2.01	0.42
3:D:976:THR:CB	3:D:981:ILE:CA	2.97	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:988:LEU:CB	3:D:1001:ILE:CB	2.98	0.42
4:E:429:LYS:HA	4:E:429:LYS:HD2	1.80	0.42
4:E:672:VAL:HG12	4:E:676:LEU:HD12	2.02	0.42
5:F:968:ILE:HA	7:H:392:LEU:HD11	2.02	0.42
6:J:304:LEU:O	6:J:308:ILE:HG12	2.19	0.42
6:J:334:SER:C	6:J:336:PHE:N	2.75	0.42
7:K:352:ILE:HG21	7:K:358:LEU:HD21	2.01	0.42
8:L:794:ILE:HA	8:L:797:LEU:HB3	2.02	0.42
1:A:21:LYS:HA	1:A:24:GLU:CD	2.45	0.41
1:A:785:MET:SD	1:A:806:LEU:HD11	2.60	0.41
2:C:693:LEU:HB3	2:C:694:PHE:CD1	2.54	0.41
3:D:131:VAL:HG21	3:D:467:PHE:H	1.84	0.41
3:D:508:LYS:HE3	3:D:518:GLU:HG2	2.01	0.41
3:D:662:LEU:HD23	3:D:662:LEU:HA	1.88	0.41
4:E:199:ILE:O	4:E:202:THR:OG1	2.38	0.41
4:E:1266:LYS:HD3	4:E:1266:LYS:HA	1.74	0.41
5:F:285:PHE:O	5:F:289:CYS:N	2.49	0.41
5:F:1196:SER:HB2	5:F:1198:LEU:H	1.84	0.41
5:F:1198:LEU:HD22	5:F:1201:LEU:HD13	2.02	0.41
6:G:398:VAL:HA	6:G:401:ILE:HG12	2.01	0.41
6:J:290:ILE:HD12	7:K:356:GLU:OE2	2.20	0.41
1:Z:21:LYS:HA	1:Z:24:GLU:CD	2.45	0.41
1:Z:641:ILE:HD12	1:Z:641:ILE:HA	1.88	0.41
1:A:432:ILE:HD12	1:A:435:TRP:HB3	2.02	0.41
3:D:135:PHE:CZ	3:D:485:GLN:HB2	2.55	0.41
5:F:672:TRP:O	5:F:675:LEU:HB3	2.19	0.41
5:F:718:SER:O	5:F:718:SER:OG	2.38	0.41
5:F:1068:ILE:HD12	5:F:1150:PHE:HD2	1.52	0.41
8:L:659:THR:HA	8:L:662:ILE:HG22	2.02	0.41
2:C:1389:GLY:HA2	4:E:1331:LEU:HD11	2.02	0.41
3:D:402:ILE:CG2	3:D:406:THR:H	2.29	0.41
3:D:846:ILE:HG13	3:D:907:LEU:CD1	2.51	0.41
4:E:1483:ILE:HG21	4:E:1492:HIS:CE1	2.56	0.41
5:F:405:ARG:HH12	5:F:407:ASN:CG	2.27	0.41
5:F:765:ASP:OD1	5:F:765:ASP:N	2.51	0.41
5:F:1251:ARG:HH22	5:F:1276:ASP:HB3	1.73	0.41
6:J:327:LYS:HG3	6:J:328:GLN:NE2	2.34	0.41
6:J:381:GLU:HA	6:J:381:GLU:OE2	2.19	0.41
6:J:389:ARG:NH1	6:J:389:ARG:HA	2.35	0.41
7:K:311:PHE:CD1	7:K:351:GLN:HG3	2.55	0.41
7:K:352:ILE:CG2	7:K:358:LEU:HG	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:503:ASN:HB2	7:K:506:ILE:CD1	2.50	0.41
1:Z:436:LEU:HA	1:Z:439:HIS:HB2	2.02	0.41
1:Z:807:LYS:CB	1:Z:837:VAL:HA	2.50	0.41
1:A:682:GLU:HG2	1:A:691:ARG:NH2	2.30	0.41
1:A:780:SER:O	1:A:784:ASN:ND2	2.53	0.41
3:D:178:GLU:HB3	3:D:230:HIS:NE2	2.35	0.41
4:E:268:THR:O	4:E:272:ILE:HG13	2.21	0.41
4:E:464:ALA:HB1	4:E:552:LEU:HD21	2.01	0.41
5:F:42:LEU:HD12	5:F:42:LEU:HA	1.95	0.41
5:F:189:GLU:HA	5:F:192:ILE:HG12	2.02	0.41
5:F:321:GLN:O	5:F:325:PHE:CB	2.68	0.41
5:F:589:ASP:OD1	5:F:589:ASP:N	2.52	0.41
5:F:866:GLN:OE1	5:F:940:ASN:HB2	2.20	0.41
5:F:1027:GLN:CG	5:F:1027:GLN:O	2.69	0.41
6:J:411:ASN:OD1	6:J:411:ASN:N	2.41	0.41
7:K:454:GLY:O	7:K:456:THR:N	2.52	0.41
1:Z:558:VAL:HG21	1:Z:607:ARG:HE	1.85	0.41
3:D:182:CYS:HB2	3:D:193:TRP:CE2	2.56	0.41
4:E:1066:VAL:HA	4:E:1069:ILE:HD12	2.02	0.41
4:E:1389:LEU:HA	4:E:1392:PHE:HD2	1.85	0.41
5:F:348:LEU:HD22	5:F:483:LEU:HD22	2.03	0.41
5:F:386:GLY:HA3	5:F:392:PRO:O	2.20	0.41
5:F:885:GLU:O	5:F:885:GLU:CG	2.68	0.41
8:I:816:LYS:N	8:I:816:LYS:CE	2.83	0.41
6:J:306:ASP:O	6:J:309:PRO:HD2	2.20	0.41
1:Z:90:LEU:HD23	1:Z:90:LEU:HA	1.69	0.41
3:D:903:ILE:HG12	3:D:953:PHE:CD1	2.56	0.41
5:F:159:LYS:HA	5:F:159:LYS:HD3	1.82	0.41
5:F:164:LYS:HA	5:F:167:ILE:HG12	2.02	0.41
5:F:220:VAL:HA	5:F:223:LEU:HG	2.01	0.41
5:F:450:LEU:HA	5:F:453:ILE:HG12	2.02	0.41
5:F:719:ILE:HG12	5:F:731:PHE:CD2	2.56	0.41
5:F:1158:THR:HG22	5:F:1197:PHE:CD2	2.55	0.41
5:F:1193:ARG:HA	5:F:1193:ARG:HD3	1.85	0.41
5:F:1282:ALA:O	5:F:1286:PHE:N	2.47	0.41
7:H:313:TYR:O	7:H:361:ARG:NH2	2.53	0.41
8:I:795:LYS:HZ3	8:I:795:LYS:HB2	1.85	0.41
8:L:676:ILE:HD13	8:L:679:LEU:HD22	2.01	0.41
1:A:512:SER:O	1:A:514:LYS:NZ	2.50	0.41
3:D:274:VAL:HG23	3:D:283:PHE:HB2	2.02	0.41
4:E:192:LEU:HD23	4:E:195:LEU:HD23	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:369:LEU:HD23	4:E:375:TYR:CD2	2.56	0.41
5:F:108:LEU:O	5:F:111:GLN:HB3	2.20	0.41
7:K:305:LYS:O	7:K:307:LYS:HE2	2.20	0.41
1:Z:91:GLN:O	1:Z:92:THR:C	2.64	0.41
1:Z:822:TYR:HB3	1:Z:824:MET:SD	2.60	0.41
1:A:650:TYR:CG	1:A:702:ILE:HG23	2.55	0.41
3:D:135:PHE:HD1	3:D:596:ALA:HB3	1.86	0.41
3:D:421:VAL:HG22	3:D:491:ARG:N	2.35	0.41
3:D:617:ALA:HA	3:D:630:THR:CG2	2.47	0.41
3:D:788:HIS:ND1	3:D:946:LYS:HA	2.35	0.41
4:E:331:TYR:HD1	4:E:331:TYR:HA	1.72	0.41
4:E:989:ASP:O	4:E:990:LYS:C	2.62	0.41
4:E:1133:LYS:HD2	4:E:1133:LYS:HA	1.90	0.41
5:F:245:ARG:NH2	5:F:284:TYR:O	2.45	0.41
5:F:260:MET:HE1	5:F:282:PHE:HA	2.03	0.41
5:F:321:GLN:O	5:F:325:PHE:HB3	2.21	0.41
8:I:694:ASP:O	8:I:698:GLN:NE2	2.54	0.41
8:I:822:LYS:HE3	8:I:822:LYS:CA	2.44	0.41
6:J:389:ARG:O	6:J:389:ARG:CZ	2.69	0.41
7:K:315:LYS:HG3	7:K:347:THR:HG22	2.02	0.41
7:K:506:ILE:HG13	7:K:507:ASN:H	1.85	0.41
1:Z:206:ASN:OD1	1:Z:206:ASN:N	2.53	0.41
1:A:232:PHE:CZ	1:A:237:GLU:HG3	2.56	0.41
1:A:479:LEU:HD12	1:A:491:ALA:HB1	2.02	0.41
3:D:585:ILE:HG23	3:D:586:LEU:HD12	2.03	0.41
4:E:699:GLU:C	4:E:701:SER:H	2.29	0.41
4:E:744:LEU:HD12	4:E:744:LEU:HA	1.90	0.41
5:F:37:LEU:HD22	5:F:146:SER:HB2	2.02	0.41
5:F:68:GLN:HA	5:F:71:ILE:HD13	2.03	0.41
5:F:144:ILE:HD13	5:F:197:LEU:HD23	2.01	0.41
5:F:633:LYS:HA	5:F:633:LYS:HD2	1.82	0.41
5:F:835:LYS:HD2	5:F:835:LYS:HA	1.75	0.41
5:F:920:ILE:CB	5:F:924:ALA:O	2.69	0.41
5:F:1550:LEU:HD23	5:F:1550:LEU:HA	1.88	0.41
7:H:394:THR:O	7:H:398:ILE:HB	2.21	0.41
8:I:795:LYS:NZ	8:I:799:SER:HB3	2.35	0.41
6:J:371:LYS:O	6:J:371:LYS:CE	2.68	0.41
7:K:509:ILE:HA	7:K:512:ILE:HB	2.01	0.41
1:Z:571:LEU:HA	1:Z:574:GLU:HG3	2.03	0.41
1:A:123:MET:CB	6:J:413:ASN:CG	2.94	0.41
1:A:531:ASP:CG	1:A:536:ASN:HD22	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:772:PRO:C	1:A:828:THR:CG2	2.94	0.41
1:A:776:ILE:HD11	1:A:828:THR:HG23	2.03	0.41
3:D:716:VAL:HG13	3:D:767:SER:HB3	2.02	0.41
3:D:778:THR:O	3:D:782:ARG:HB2	2.20	0.41
4:E:904:LEU:HD23	4:E:907:LEU:HD23	2.02	0.41
4:E:1529:ILE:HG21	4:E:1589:LEU:HD21	2.03	0.41
5:F:25:PHE:HB3	5:F:26:LYS:NZ	2.36	0.41
5:F:486:TYR:HD1	5:F:532:SER:HB3	1.86	0.41
5:F:1097:TYR:OH	5:F:1164:PHE:CD1	2.49	0.41
5:F:1300:LEU:HD23	5:F:1301:SER:N	2.36	0.41
6:J:381:GLU:OE2	6:J:381:GLU:CA	2.69	0.41
6:J:420:ASP:HB2	6:J:436:LEU:HD22	2.04	0.41
7:K:389:LYS:CB	7:K:393:ASP:CG	2.94	0.41
7:K:433:GLU:HB2	8:L:741:ARG:HE	1.85	0.41
7:K:503:ASN:HB2	7:K:506:ILE:HD13	2.03	0.41
1:A:451:ASP:OD1	1:A:455:GLU:HB2	2.22	0.40
1:A:533:ARG:HE	1:A:534:PHE:N	2.19	0.40
1:A:586:PHE:CD2	1:A:642:LEU:HD11	2.56	0.40
1:A:603:VAL:O	1:A:606:GLU:HG2	2.21	0.40
1:A:772:PRO:C	1:A:828:THR:HG21	2.43	0.40
3:D:212:GLN:N	3:D:235:SER:O	2.47	0.40
3:D:328:LEU:CD1	3:D:334:VAL:HG22	2.50	0.40
3:D:1431:LYS:HE2	3:D:1435:GLU:OE1	2.20	0.40
4:E:923:LEU:CD1	4:E:931:PHE:HE2	2.26	0.40
4:E:1319:LEU:CD2	4:E:1398:VAL:HG22	2.46	0.40
5:F:90:GLU:HA	5:F:93:LEU:HB2	2.03	0.40
5:F:460:SER:HB2	5:F:475:LYS:HB3	2.02	0.40
5:F:863:GLU:HA	5:F:866:GLN:HE21	1.87	0.40
5:F:964:LYS:O	5:F:964:LYS:CG	2.69	0.40
5:F:971:SER:HB3	7:H:392:LEU:CD2	2.50	0.40
5:F:1082:ILE:HA	5:F:1082:ILE:HD13	1.87	0.40
5:F:1360:LEU:C	5:F:1362:ASP:N	2.77	0.40
5:F:1626:VAL:HA	5:F:1629:LEU:HB3	2.03	0.40
8:I:815:GLU:HB3	8:I:816:LYS:CE	2.51	0.40
8:I:818:ILE:HD12	8:I:818:ILE:HA	1.80	0.40
6:J:356:GLN:HB3	7:K:423:LYS:NZ	2.36	0.40
6:J:402:ASP:HB2	7:K:466:LEU:CD2	2.51	0.40
7:K:425:ARG:HA	7:K:433:GLU:CD	2.47	0.40
7:K:446:ARG:O	7:K:446:ARG:CD	2.69	0.40
8:L:653:SER:O	8:L:657:GLN:HG2	2.21	0.40
8:L:679:LEU:O	8:L:682:ASP:HB2	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L:800:HIS:O	8:L:804:LEU:CB	2.65	0.40
3:D:371:LEU:HD21	3:D:420:ILE:HG22	2.04	0.40
3:D:586:LEU:HD11	3:D:593:VAL:H	1.86	0.40
3:D:673:TYR:O	3:D:677:GLU:HB2	2.22	0.40
4:E:79:LEU:HD11	4:E:99:VAL:HG22	2.04	0.40
4:E:1305:ASN:HA	4:E:1308:TYR:CZ	2.56	0.40
4:E:1329:ILE:O	4:E:1333:SER:HB3	2.21	0.40
5:F:651:GLY:HA3	5:F:705:ASP:HA	2.03	0.40
5:F:662:PRO:HG3	5:F:715:ASN:ND2	2.36	0.40
5:F:974:GLU:OE1	5:F:977:ARG:NH2	2.51	0.40
5:F:1431:ARG:HD2	5:F:1474:PHE:N	2.36	0.40
8:I:795:LYS:NZ	8:I:795:LYS:CB	2.84	0.40
7:K:315:LYS:HD2	7:K:347:THR:HG22	2.03	0.40
7:K:408:ILE:O	7:K:412:ILE:HG13	2.22	0.40
7:K:529:LYS:HB3	7:K:529:LYS:HE3	1.98	0.40
7:K:538:LYS:CB	8:L:818:ILE:CA	2.98	0.40
8:L:703:GLN:OE1	8:L:704:GLN:N	2.54	0.40
1:A:441:MET:HE3	1:A:441:MET:O	2.21	0.40
1:A:697:PHE:CD1	1:A:697:PHE:N	2.88	0.40
3:D:422:LYS:HE2	3:D:524:THR:OG1	2.21	0.40
3:D:574:HIS:HD1	3:D:576:LEU:HD12	1.87	0.40
3:D:924:ASN:O	3:D:925:GLN:HB2	2.21	0.40
4:E:1168:LYS:O	4:E:1174:ASN:ND2	2.45	0.40
5:F:245:ARG:HH22	5:F:288:TRP:N	2.18	0.40
5:F:409:MET:CB	5:F:410:PRO:HD2	2.51	0.40
5:F:661:VAL:CG1	5:F:712:LEU:HD12	2.50	0.40
5:F:1080:LEU:O	5:F:1156:TYR:CE2	2.74	0.40
5:F:1280:ILE:HD12	5:F:1280:ILE:C	2.47	0.40
6:G:319:GLU:HA	6:G:322:THR:HG22	2.03	0.40
6:J:309:PRO:HA	6:J:312:VAL:CB	2.50	0.40
6:J:357:LEU:HD22	7:K:423:LYS:HE3	2.03	0.40
1:Z:239:ILE:HG23	1:Z:258:LYS:HZ2	1.86	0.40
1:A:687:LEU:O	1:A:691:ARG:HG3	2.22	0.40
1:A:696:TYR:CD1	1:A:702:ILE:HG21	2.57	0.40
3:D:122:ASP:CG	3:D:466:LYS:HZ1	2.30	0.40
3:D:157:PRO:HD2	3:D:160:ILE:HD12	2.03	0.40
4:E:939:LEU:HB3	4:E:997:VAL:HG11	2.04	0.40
4:E:1451:CYS:HA	4:E:1457:ALA:HB2	2.04	0.40
5:F:283:ALA:HA	5:F:441:THR:HG21	2.04	0.40
5:F:1157:TRP:CD1	5:F:1161:LEU:HD13	2.56	0.40
5:F:1360:LEU:N	5:F:1360:LEU:HD12	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:1364:TYR:HB2	5:F:1374:LYS:CB	2.51	0.40
5:F:1370:LEU:C	5:F:1371:ILE:CG1	2.89	0.40
5:F:1442:TRP:NE1	5:F:1484:ARG:HB3	2.36	0.40
5:F:1660:ASN:O	5:F:1664:ASN:ND2	2.54	0.40
6:G:275:GLN:NE2	6:G:278:GLU:OE1	2.40	0.40
6:G:450:PHE:O	6:G:454:ALA:HB2	2.21	0.40
8:I:775:THR:OG1	8:I:776:PHE:N	2.55	0.40
8:I:778:LYS:HZ2	8:I:778:LYS:CA	2.34	0.40
7:K:339:MET:HG3	7:K:339:MET:O	2.22	0.40
8:L:658:TYR:HE1	8:L:665:TRP:HZ3	1.70	0.40
8:L:674:GLU:OE1	8:L:675:GLN:NE2	2.55	0.40
8:L:816:LYS:HD2	8:L:816:LYS:HA	1.83	0.40
1:Z:709:LYS:HZ1	1:Z:764:ASP:HB3	1.86	0.40
1:A:495:THR:HG22	1:A:503:ALA:HB2	2.03	0.40
3:D:168:GLN:H	3:D:187:ASP:CG	2.27	0.40
3:D:484:GLN:HE22	3:D:566:LYS:H	1.70	0.40
3:D:491:ARG:CA	3:D:520:THR:HB	2.51	0.40
5:F:918:PHE:HA	5:F:922:LEU:HD11	2.04	0.40
6:G:305:ILE:HD12	6:G:305:ILE:HA	1.91	0.40
6:G:391:LEU:HA	6:G:394:ILE:HG12	2.03	0.40
8:I:795:LYS:CA	8:I:795:LYS:HZ3	2.35	0.40
8:I:795:LYS:NZ	8:I:795:LYS:HA	2.36	0.40
7:K:427:LEU:N	7:K:427:LEU:HD22	2.36	0.40
1:Z:305:ILE:HD12	1:Z:339:TYR:HB3	2.02	0.40
1:Z:565:GLY:O	1:Z:569:VAL:N	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	722/839 (86%)	700 (97%)	20 (3%)	2 (0%)	36 65

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Z	736/839 (88%)	675 (92%)	39 (5%)	22 (3%)	3	26
2	C	1323/1391 (95%)	1269 (96%)	41 (3%)	13 (1%)	12	43
3	D	1396/1502 (93%)	1275 (91%)	113 (8%)	8 (1%)	21	52
4	E	1538/1655 (93%)	1376 (90%)	149 (10%)	13 (1%)	16	47
5	F	1616/1683 (96%)	1203 (74%)	317 (20%)	96 (6%)	1	15
6	G	198/472 (42%)	188 (95%)	9 (4%)	1 (0%)	24	56
6	J	191/472 (40%)	175 (92%)	13 (7%)	3 (2%)	7	35
7	H	242/541 (45%)	202 (84%)	36 (15%)	4 (2%)	7	34
7	K	252/541 (47%)	209 (83%)	32 (13%)	11 (4%)	2	19
8	I	185/823 (22%)	158 (85%)	16 (9%)	11 (6%)	1	15
8	L	185/823 (22%)	164 (89%)	15 (8%)	6 (3%)	3	25
All	All	8584/11581 (74%)	7594 (88%)	800 (9%)	190 (2%)	7	30

All (190) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	VAL
2	C	319	PRO
2	C	468	PHE
2	C	476	ASN
2	C	694	PHE
2	C	1255	SER
3	D	528	PRO
3	D	665	ASN
3	D	1000	ASP
3	D	1128	GLN
3	D	1134	SER
4	E	923	LEU
4	E	986	SER
4	E	989	ASP
4	E	990	LYS
5	F	353	PRO
5	F	357	PRO
5	F	380	ALA
5	F	391	ASN
5	F	394	TYR
5	F	395	PRO
5	F	410	PRO

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Mol	Chain	Res	Type
5	F	823	PRO
5	F	825	ILE
5	F	885	GLU
5	F	888	PRO
5	F	919	ASN
5	F	921	PRO
5	F	934	ASP
5	F	935	GLN
5	F	1031	VAL
5	F	1036	PRO
5	F	1090	PRO
5	F	1183	TYR
5	F	1187	ASN
5	F	1188	THR
5	F	1195	PHE
5	F	1295	ALA
5	F	1314	VAL
5	F	1371	ILE
5	F	1381	LEU
5	F	1387	THR
5	F	1392	ILE
5	F	1395	PRO
5	F	1680	GLN
6	G	425	GLU
7	H	506	ILE
7	H	507	ASN
8	I	732	ALA
8	I	740	LYS
8	I	793	LEU
8	I	799	SER
6	J	338	SER
6	J	339	LEU
6	J	438	ALA
7	K	321	ALA
7	K	449	ASP
7	K	450	PRO
7	K	457	ASN
8	L	780	THR
8	L	781	ASN
1	Z	44	VAL
1	Z	92	THR
1	Z	248	THR

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Mol	Chain	Res	Type
1	Z	249	ARG
1	Z	250	ASN
1	Z	252	GLN
1	Z	751	LEU
1	Z	752	SER
1	Z	765	ASP
1	Z	767	ILE
1	Z	824	MET
2	C	526	ASN
4	E	259	SER
4	E	701	SER
4	E	1248	THR
5	F	361	LEU
5	F	396	GLY
5	F	412	ASN
5	F	922	LEU
5	F	926	LEU
5	F	936	ILE
5	F	958	SER
5	F	964	LYS
5	F	974	GLU
5	F	1039	ALA
5	F	1041	PHE
5	F	1059	SER
5	F	1062	SER
5	F	1124	GLY
5	F	1134	LYS
5	F	1135	CYS
5	F	1189	MET
5	F	1204	GLY
5	F	1210	LYS
5	F	1374	LYS
5	F	1389	ILE
5	F	1421	VAL
7	H	319	THR
7	H	424	ASN
8	I	728	THR
7	K	405	ASN
7	K	501	GLU
7	K	504	ASP
7	K	505	ARG
8	L	779	THR

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Mol	Chain	Res	Type
1	Z	245	ALA
1	Z	821	GLN
1	A	134	LYS
2	C	75	ASP
2	C	334	ASP
2	C	479	ASP
4	E	980	LYS
5	F	335	ASP
5	F	350	ARG
5	F	358	LYS
5	F	367	PHE
5	F	381	THR
5	F	406	LEU
5	F	591	ASP
5	F	902	LYS
5	F	1030	ASN
5	F	1035	GLY
5	F	1038	LEU
5	F	1064	THR
5	F	1084	LEU
5	F	1123	ASN
5	F	1193	ARG
5	F	1200	PRO
5	F	1269	GLU
5	F	1370	LEU
5	F	1396	LEU
5	F	1675	THR
8	I	738	ASP
8	I	789	GLU
8	I	790	ASN
7	K	392	LEU
8	L	783	ASP
1	Z	134	LYS
1	Z	825	PRO
2	C	315	THR
2	C	1252	ASP
3	D	1441	ASN
5	F	363	ASP
5	F	444	THR
5	F	930	VAL
5	F	951	ARG
5	F	1067	ASN

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Mol	Chain	Res	Type
5	F	1129	ASN
5	F	1236	ILE
5	F	1361	PHE
5	F	1372	THR
5	F	1676	LEU
7	K	455	LYS
1	Z	91	GLN
1	Z	648	GLU
1	Z	762	ASN
1	Z	771	ILE
1	Z	777	ILE
3	D	998	ALA
4	E	702	THR
4	E	977	ALA
4	E	1027	TRP
5	F	1122	TRP
5	F	1194	LEU
5	F	1420	GLN
1	Z	244	SER
1	Z	828	THR
5	F	352	ILE
5	F	713	PHE
5	F	923	VAL
5	F	1296	LEU
5	F	1307	VAL
5	F	1365	ASN
5	F	1390	GLN
8	I	798	ASN
8	L	704	GLN
2	C	684	GLY
4	E	1489	PRO
8	L	794	ILE
8	I	782	ILE
7	K	427	LEU
3	D	993	GLY
4	E	974	GLY
5	F	1032	ILE
5	F	1063	ILE
5	F	422	VAL
5	F	1266	VAL
8	I	791	ILE
2	C	469	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	609/762 (80%)	586 (96%)	23 (4%)	29	53
1	Z	611/762 (80%)	559 (92%)	52 (8%)	10	34
2	C	1177/1250 (94%)	1149 (98%)	28 (2%)	43	62
3	D	1215/1353 (90%)	1201 (99%)	14 (1%)	63	72
4	E	1421/1557 (91%)	1389 (98%)	32 (2%)	44	62
5	F	1260/1538 (82%)	1166 (92%)	94 (8%)	12	39
6	G	167/377 (44%)	162 (97%)	5 (3%)	36	57
6	J	162/377 (43%)	146 (90%)	16 (10%)	7	30
7	H	171/439 (39%)	163 (95%)	8 (5%)	23	48
7	K	153/439 (35%)	130 (85%)	23 (15%)	3	16
8	I	152/674 (23%)	136 (90%)	16 (10%)	6	28
8	L	138/674 (20%)	136 (99%)	2 (1%)	59	70
All	All	7236/10202 (71%)	6923 (96%)	313 (4%)	27	50

All (313) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	21	LYS
1	A	22	LEU
1	A	27	GLU
1	A	30	ASP
1	A	45	SER
1	A	53	VAL
1	A	54	PHE
1	A	57	ARG
1	A	79	SER
1	A	82	ASP
1	A	115	THR
1	A	116	LYS
1	A	119	GLU

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Mol	Chain	Res	Type
1	A	122	LEU
1	A	130	ASN
1	A	134	LYS
1	A	137	ASP
1	A	138	ASN
1	A	139	PHE
1	A	827	GLU
1	A	830	SER
1	A	833	ILE
2	C	68	THR
2	C	85	LEU
2	C	294	LEU
2	C	315	THR
2	C	318	ILE
2	C	326	LEU
2	C	331	LEU
2	C	337	THR
2	C	462	LEU
2	C	476	ASN
2	C	520	LEU
2	C	530	LEU
2	C	577	PHE
2	C	691	GLN
2	C	695	ASP
2	C	826	LEU
2	C	828	THR
2	C	896	CYS
2	C	910	LEU
2	C	918	MET
2	C	1034	SER
2	C	1252	ASP
2	C	1253	VAL
2	C	1262	LEU
2	C	1298	ASP
2	C	1299	LYS
2	C	1301	SER
2	C	1387	HIS
3	D	528	PRO
3	D	980	SER
3	D	982	GLU
3	D	984	THR
3	D	990	GLU

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Mol	Chain	Res	Type
3	D	1000	ASP
3	D	1039	VAL
3	D	1115	VAL
3	D	1118	LEU
3	D	1129	ASN
3	D	1160	HIS
3	D	1413	VAL
3	D	1472	ILE
3	D	1495	LEU
4	E	55	LEU
4	E	138	VAL
4	E	194	ILE
4	E	254	SER
4	E	257	LEU
4	E	258	ILE
4	E	310	ILE
4	E	368	ILE
4	E	665	THR
4	E	698	VAL
4	E	719	ILE
4	E	771	LEU
4	E	773	LEU
4	E	808	THR
4	E	827	PRO
4	E	843	LEU
4	E	895	HIS
4	E	900	ILE
4	E	923	LEU
4	E	931	PHE
4	E	975	GLN
4	E	976	PHE
4	E	980	LYS
4	E	984	ASP
4	E	1026	THR
4	E	1079	VAL
4	E	1167	LEU
4	E	1259	PHE
4	E	1424	LEU
4	E	1447	ILE
4	E	1514	VAL
4	E	1557	LEU
5	F	278	ILE

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Mol	Chain	Res	Type
5	F	331	ILE
5	F	334	GLN
5	F	355	LEU
5	F	356	ILE
5	F	389	LEU
5	F	397	MET
5	F	399	SER
5	F	407	ASN
5	F	409	MET
5	F	444	THR
5	F	712	LEU
5	F	750	TRP
5	F	782	LYS
5	F	813	GLU
5	F	825	ILE
5	F	835	LYS
5	F	836	ILE
5	F	837	TYR
5	F	888	PRO
5	F	900	LEU
5	F	920	ILE
5	F	921	PRO
5	F	922	LEU
5	F	926	LEU
5	F	928	LEU
5	F	950	GLU
5	F	951	ARG
5	F	955	SER
5	F	958	SER
5	F	962	ARG
5	F	965	LEU
5	F	1027	GLN
5	F	1029	SER
5	F	1032	ILE
5	F	1060	LEU
5	F	1068	ILE
5	F	1083	ILE
5	F	1090	PRO
5	F	1092	THR
5	F	1118	ARG
5	F	1128	ASP
5	F	1129	ASN

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Mol	Chain	Res	Type
5	F	1144	VAL
5	F	1147	PHE
5	F	1149	SER
5	F	1150	PHE
5	F	1153	TYR
5	F	1155	ASN
5	F	1159	GLN
5	F	1165	ILE
5	F	1166	HIS
5	F	1167	LYS
5	F	1169	SER
5	F	1174	LYS
5	F	1181	VAL
5	F	1191	SER
5	F	1192	VAL
5	F	1210	LYS
5	F	1276	ASP
5	F	1277	VAL
5	F	1278	GLU
5	F	1280	ILE
5	F	1281	LYS
5	F	1283	LYS
5	F	1284	SER
5	F	1285	HIS
5	F	1289	ILE
5	F	1291	SER
5	F	1293	ASN
5	F	1296	LEU
5	F	1297	GLU
5	F	1300	LEU
5	F	1301	SER
5	F	1302	VAL
5	F	1303	LEU
5	F	1309	LEU
5	F	1313	ILE
5	F	1314	VAL
5	F	1315	THR
5	F	1349	PHE
5	F	1352	GLU
5	F	1356	LEU
5	F	1358	VAL
5	F	1363	ILE

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Mol	Chain	Res	Type
5	F	1364	TYR
5	F	1365	ASN
5	F	1372	THR
5	F	1373	ASP
5	F	1387	THR
5	F	1417	LEU
5	F	1550	LEU
5	F	1635	ARG
5	F	1680	GLN
6	G	303	GLU
6	G	333	ILE
6	G	374	GLN
6	G	411	ASN
6	G	460	LEU
7	H	325	THR
7	H	398	ILE
7	H	418	GLN
7	H	507	ASN
7	H	508	LYS
7	H	512	ILE
7	H	529	LYS
7	H	534	VAL
8	I	727	SER
8	I	736	ASN
8	I	740	LYS
8	I	778	LYS
8	I	792	GLN
8	I	795	LYS
8	I	797	LEU
8	I	808	ASP
8	I	810	ASN
8	I	812	THR
8	I	815	GLU
8	I	818	ILE
8	I	819	ASN
8	I	821	ILE
8	I	822	LYS
8	I	823	LYS
6	J	357	LEU
6	J	368	ASP
6	J	370	ASP
6	J	371	LYS

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Mol	Chain	Res	Type
6	J	375	LYS
6	J	376	LYS
6	J	385	GLU
6	J	389	ARG
6	J	390	ILE
6	J	391	LEU
6	J	395	GLU
6	J	398	VAL
6	J	399	ASN
6	J	401	ILE
6	J	411	ASN
6	J	444	ILE
7	K	325	THR
7	K	341	LYS
7	K	384	THR
7	K	385	GLN
7	K	387	GLN
7	K	391	GLU
7	K	393	ASP
7	K	394	THR
7	K	397	ARG
7	K	398	ILE
7	K	399	LEU
7	K	400	LYS
7	K	402	GLN
7	K	404	ARG
7	K	423	LYS
7	K	424	ASN
7	K	429	LEU
7	K	443	LEU
7	K	446	ARG
7	K	448	GLU
7	K	449	ASP
7	K	453	LEU
7	K	455	LYS
8	L	648	LEU
8	L	703	GLN
1	Z	19	ASN
1	Z	20	LYS
1	Z	21	LYS
1	Z	22	LEU
1	Z	27	GLU

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Mol	Chain	Res	Type
1	Z	30	ASP
1	Z	46	ILE
1	Z	49	LEU
1	Z	53	VAL
1	Z	56	LEU
1	Z	79	SER
1	Z	80	PHE
1	Z	81	GLU
1	Z	84	ASP
1	Z	87	ILE
1	Z	88	LYS
1	Z	89	ASP
1	Z	90	LEU
1	Z	92	THR
1	Z	115	THR
1	Z	116	LYS
1	Z	117	LYS
1	Z	119	GLU
1	Z	121	ILE
1	Z	122	LEU
1	Z	125	ILE
1	Z	127	GLN
1	Z	128	LEU
1	Z	129	LEU
1	Z	130	ASN
1	Z	133	THR
1	Z	134	LYS
1	Z	138	ASN
1	Z	139	PHE
1	Z	144	LEU
1	Z	146	LEU
1	Z	248	THR
1	Z	758	GLN
1	Z	765	ASP
1	Z	766	ASN
1	Z	767	ILE
1	Z	768	VAL
1	Z	772	PRO
1	Z	775	LEU
1	Z	776	ILE
1	Z	777	ILE
1	Z	805	SER

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Mol	Chain	Res	Type
1	Z	808	ASN
1	Z	824	MET
1	Z	827	GLU
1	Z	828	THR
1	Z	837	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (159) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	130	ASN
1	A	138	ASN
1	A	269	ASN
1	A	397	HIS
1	A	464	ASN
1	A	733	GLN
1	A	784	ASN
1	A	787	HIS
1	A	795	GLN
1	A	808	ASN
2	C	199	HIS
2	C	271	GLN
2	C	593	GLN
2	C	627	ASN
2	C	691	GLN
2	C	827	ASN
2	C	897	HIS
2	C	914	GLN
2	C	941	ASN
2	C	1049	ASN
2	C	1239	ASN
2	C	1258	GLN
2	C	1365	GLN
2	C	1387	HIS
3	D	112	GLN
3	D	431	ASN
3	D	449	ASN
3	D	484	GLN
3	D	568	GLN
3	D	850	ASN
3	D	1086	ASN
3	D	1129	ASN

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Mol	Chain	Res	Type
3	D	1224	ASN
3	D	1445	ASN
4	E	20	ASN
4	E	36	GLN
4	E	80	GLN
4	E	165	ASN
4	E	190	GLN
4	E	210	ASN
4	E	299	ASN
4	E	388	ASN
4	E	517	ASN
4	E	571	ASN
4	E	600	ASN
4	E	636	GLN
4	E	677	ASN
4	E	759	ASN
4	E	770	HIS
4	E	822	ASN
4	E	964	GLN
4	E	1001	ASN
4	E	1029	ASN
4	E	1102	GLN
4	E	1110	HIS
4	E	1143	GLN
4	E	1306	ASN
4	E	1383	GLN
4	E	1462	ASN
4	E	1509	GLN
4	E	1535	ASN
4	E	1539	ASN
4	E	1558	GLN
4	E	1565	ASN
4	E	1613	ASN
5	F	38	ASN
5	F	101	ASN
5	F	105	GLN
5	F	154	GLN
5	F	163	ASN
5	F	177	GLN
5	F	334	GLN
5	F	383	ASN
5	F	428	GLN

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Mol	Chain	Res	Type
5	F	542	ASN
5	F	602	ASN
5	F	725	ASN
5	F	758	ASN
5	F	1293	ASN
5	F	1299	ASN
5	F	1365	ASN
5	F	1664	ASN
6	G	301	HIS
6	G	328	GLN
6	G	355	GLN
6	G	428	ASN
7	H	329	HIS
7	H	362	ASN
7	H	363	GLN
7	H	368	ASN
7	H	377	ASN
7	H	418	GLN
7	H	445	GLN
7	H	524	ASN
8	I	647	GLN
8	I	657	GLN
8	I	690	GLN
8	I	691	ASN
8	I	695	GLN
8	I	703	GLN
8	I	749	GLN
8	I	754	ASN
8	I	781	ASN
8	I	786	ASN
8	I	800	HIS
8	I	819	ASN
6	J	275	GLN
6	J	324	GLN
6	J	328	GLN
6	J	355	GLN
6	J	367	ASN
6	J	374	GLN
6	J	378	HIS
6	J	399	ASN
7	K	329	HIS
7	K	337	GLN

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Mol	Chain	Res	Type
7	K	359	ASN
7	K	362	ASN
7	K	365	GLN
7	K	368	ASN
7	K	377	ASN
7	K	385	GLN
7	K	387	GLN
7	K	402	GLN
7	K	424	ASN
7	K	515	ASN
7	K	539	ASN
8	L	647	GLN
8	L	695	GLN
8	L	704	GLN
8	L	749	GLN
8	L	754	ASN
8	L	774	ASN
8	L	800	HIS
8	L	819	ASN
1	Z	19	ASN
1	Z	60	ASN
1	Z	127	GLN
1	Z	130	ASN
1	Z	138	ASN
1	Z	196	ASN
1	Z	203	ASN
1	Z	214	ASN
1	Z	229	ASN
1	Z	295	ASN
1	Z	301	ASN
1	Z	380	HIS
1	Z	397	HIS
1	Z	463	GLN
1	Z	464	ASN
1	Z	621	HIS
1	Z	658	ASN
1	Z	758	GLN
1	Z	770	ASN
1	Z	784	ASN
1	Z	790	ASN
1	Z	802	GLN
1	Z	834	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.

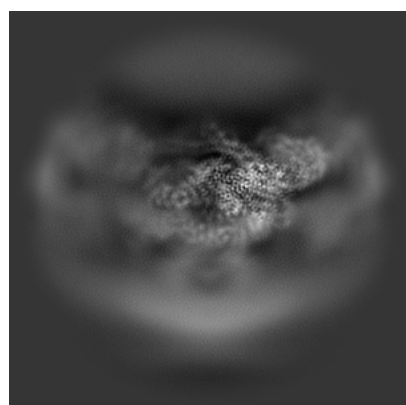
6 Map visualisation [i](#)

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

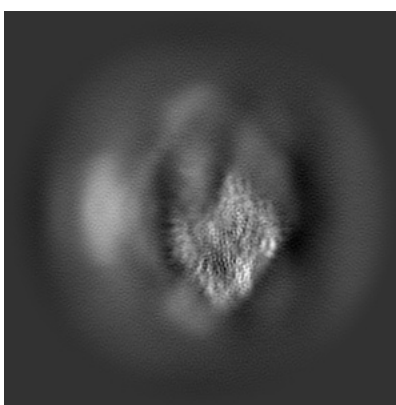
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

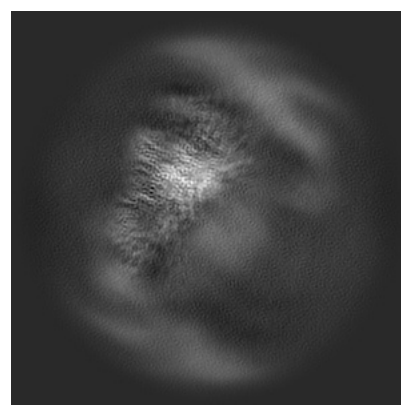
6.1.1 Primary map



X



Y

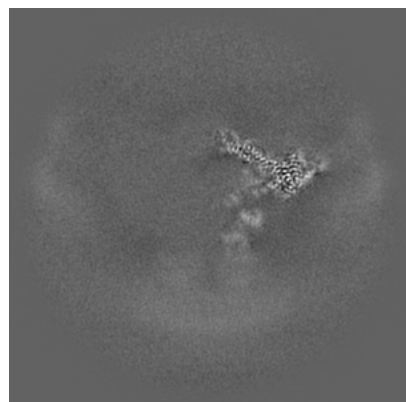


Z

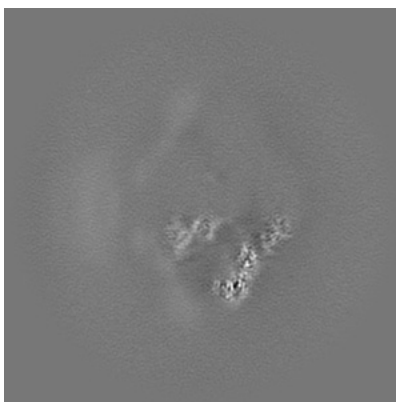
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

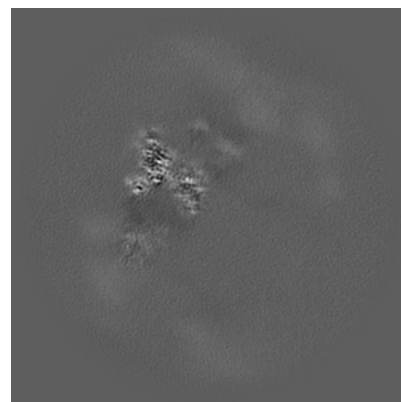
6.2.1 Primary map



X Index: 175



Y Index: 175

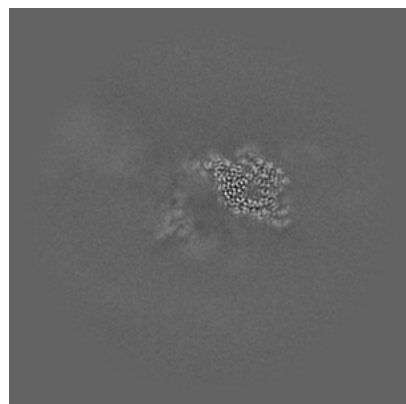


Z Index: 175

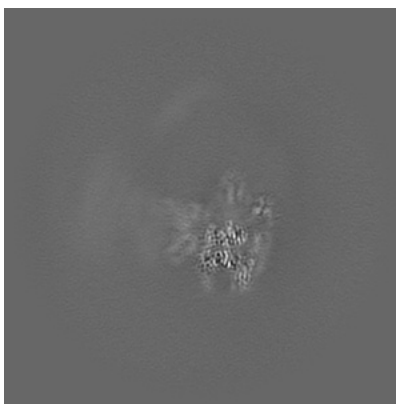
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

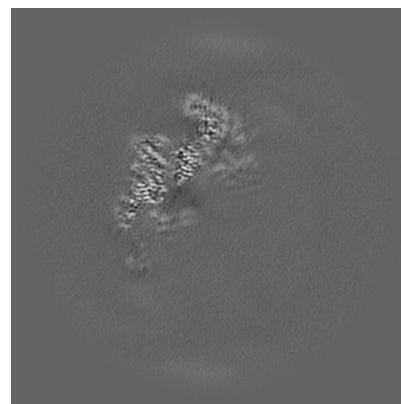
6.3.1 Primary map



X Index: 124



Y Index: 203

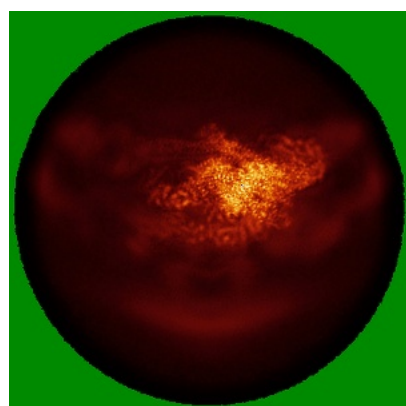


Z Index: 204

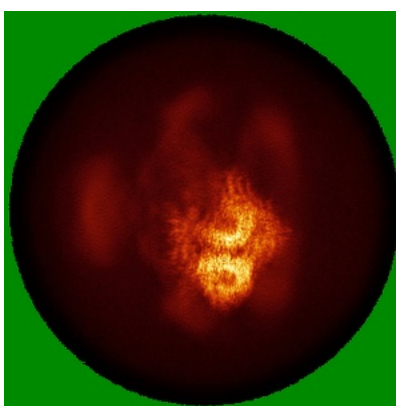
The images above show the largest variance slices of the map in three orthogonal directions.

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

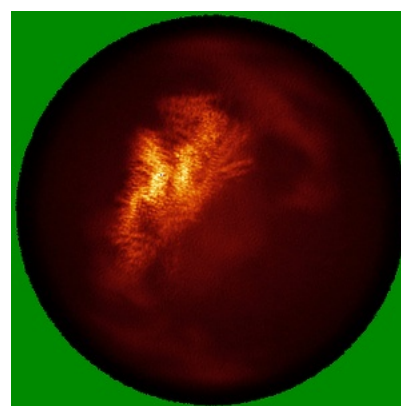
6.4.1 Primary map



X



Y

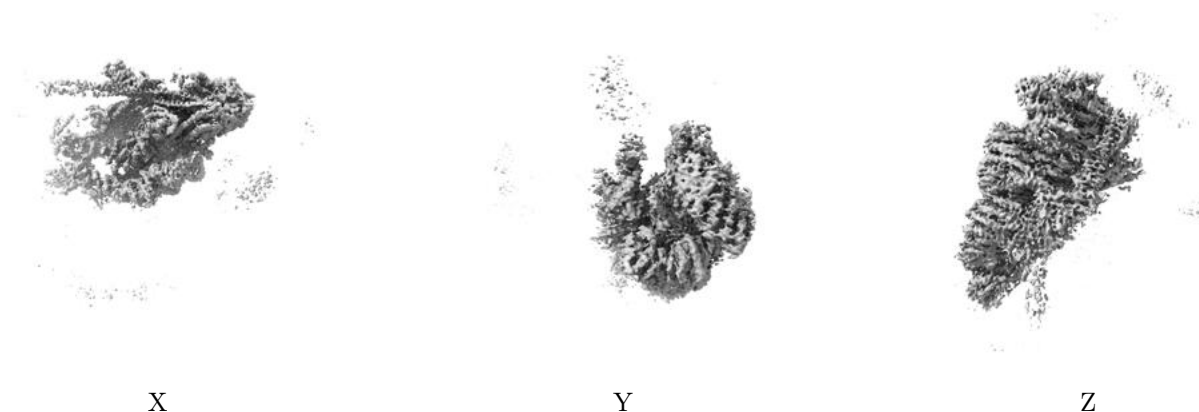


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

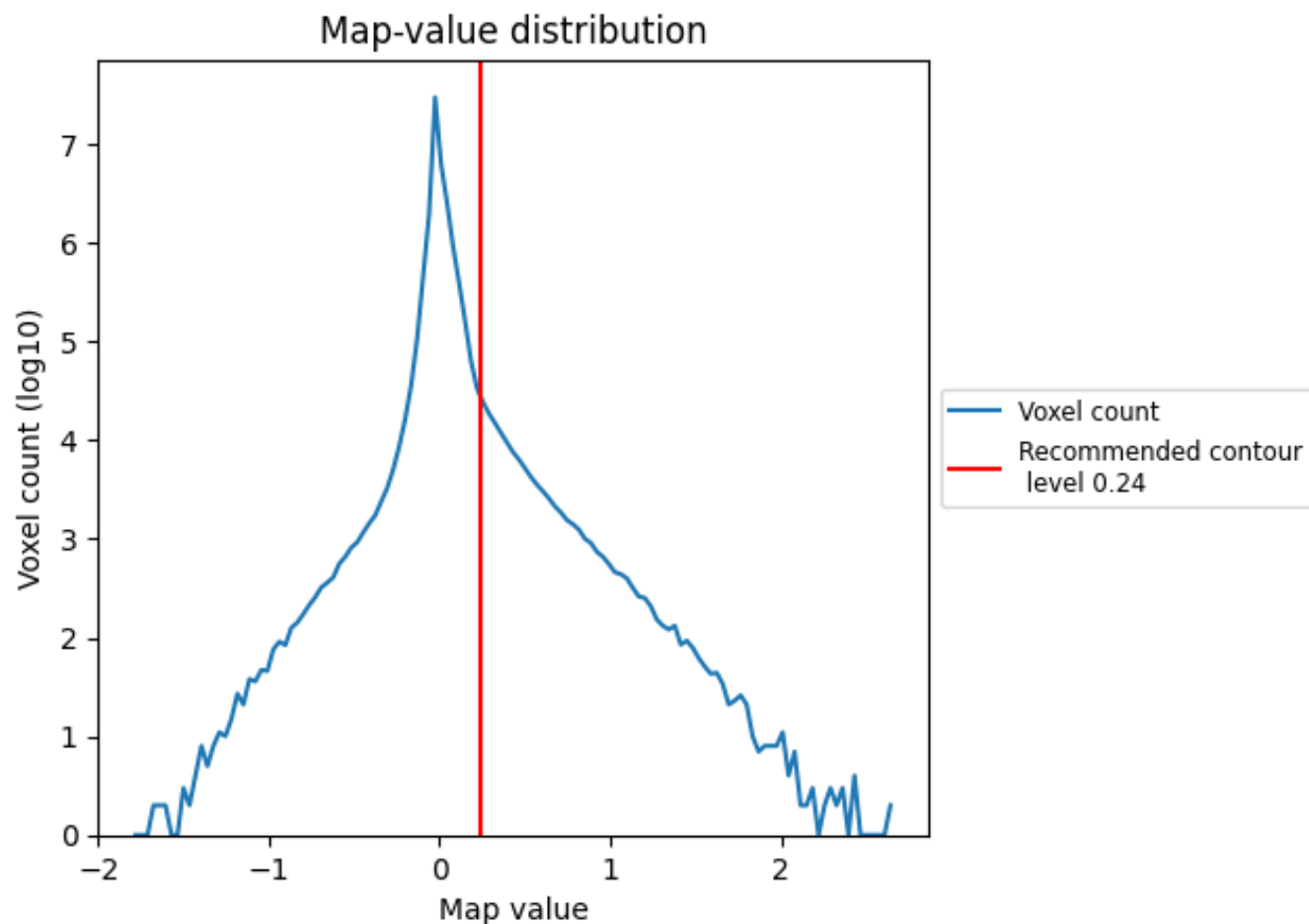
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

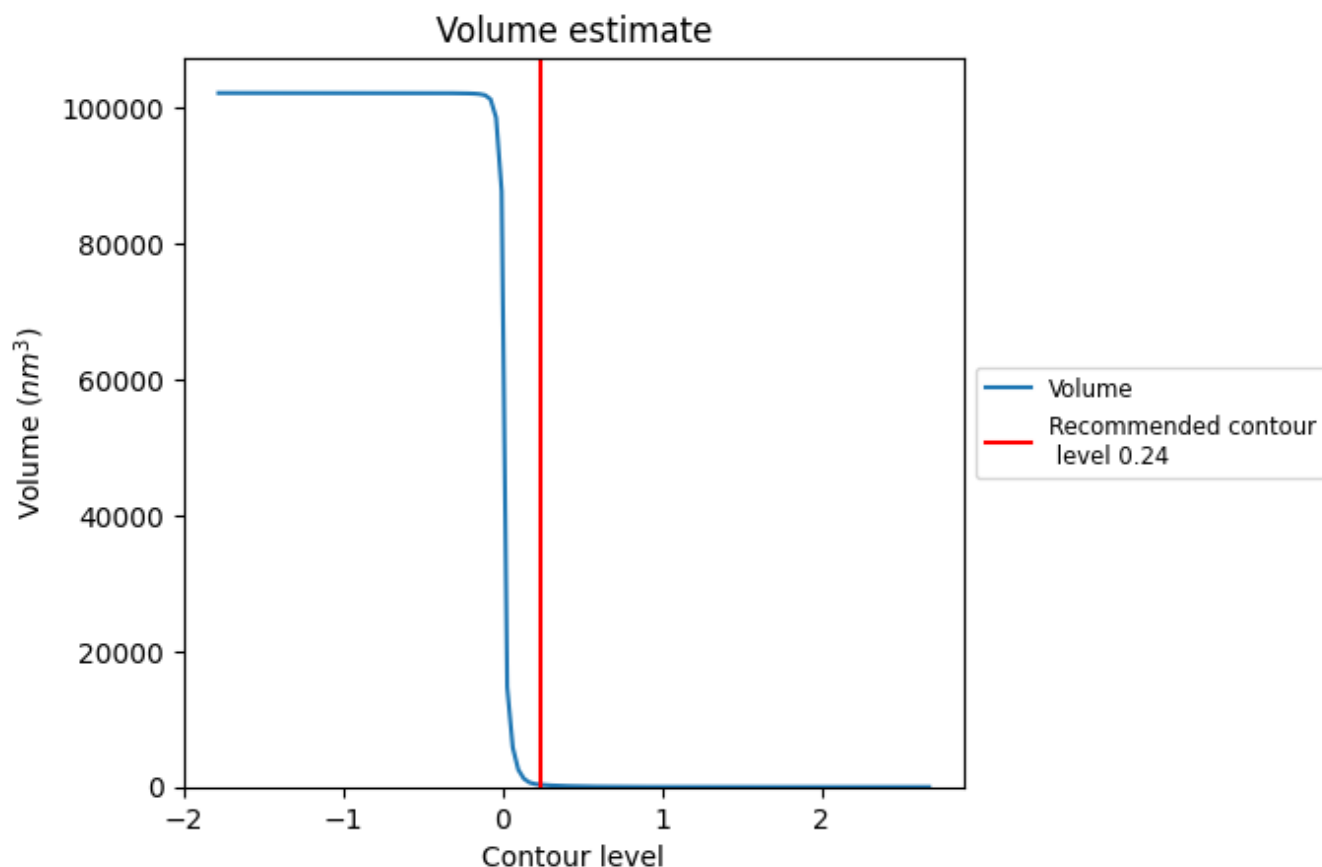
This section contains the results of statistical analysis of the map.

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.

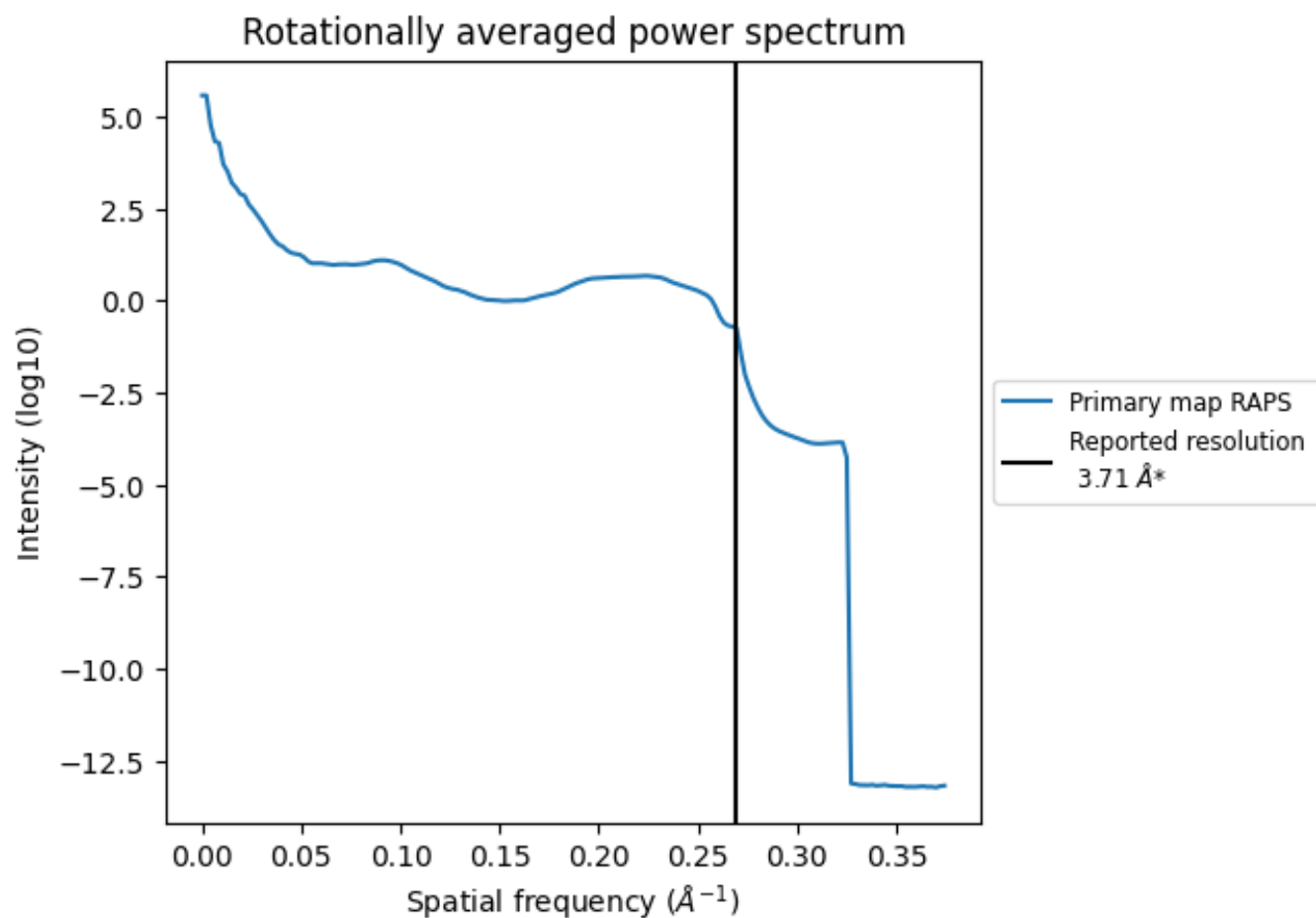
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 332 nm³; this corresponds to an approximate mass of 300 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

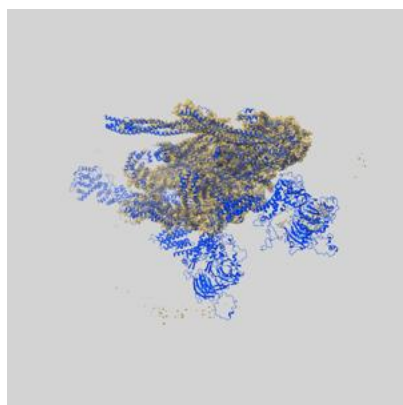
8 Fourier-Shell correlation

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

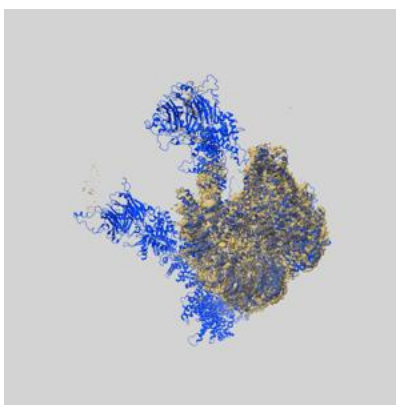
9 Map-model fit [i](#)

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

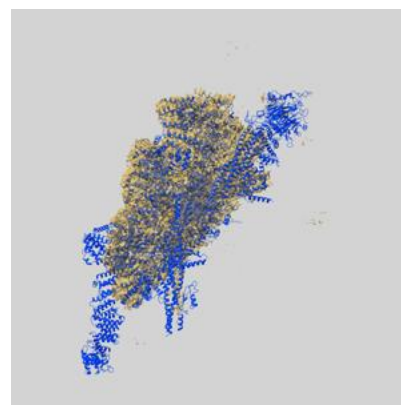
9.1 Map-model overlay [i](#)



X



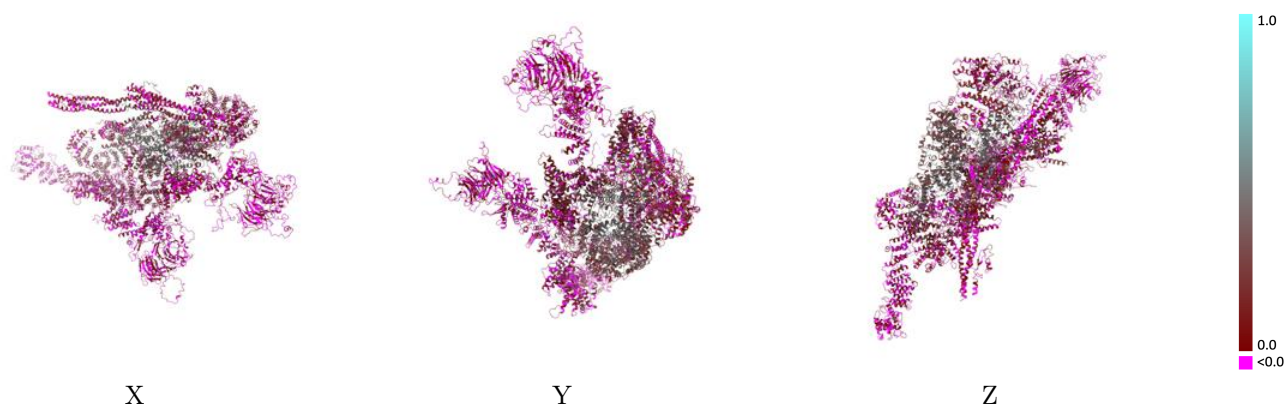
Y



Z

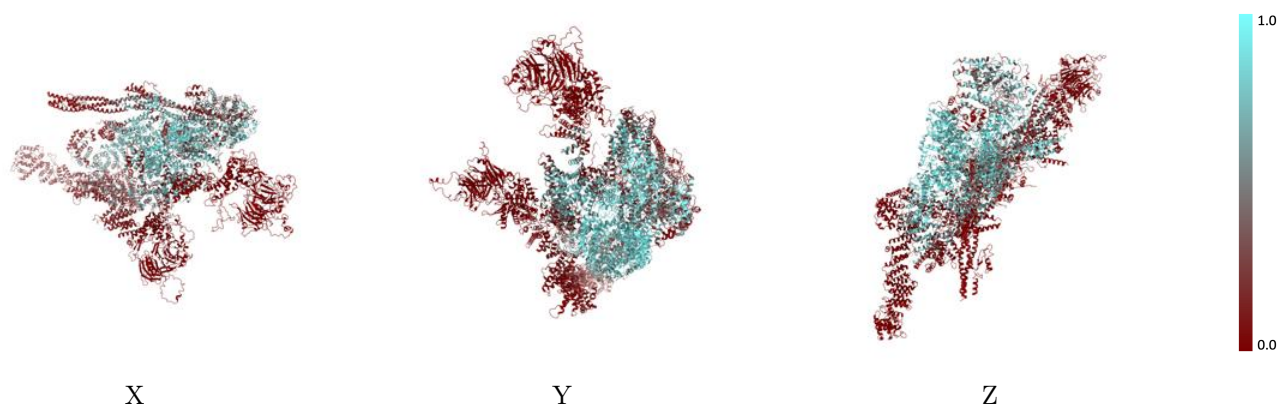
The images above show the 3D surface view of the map at the recommended contour level 0.24 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



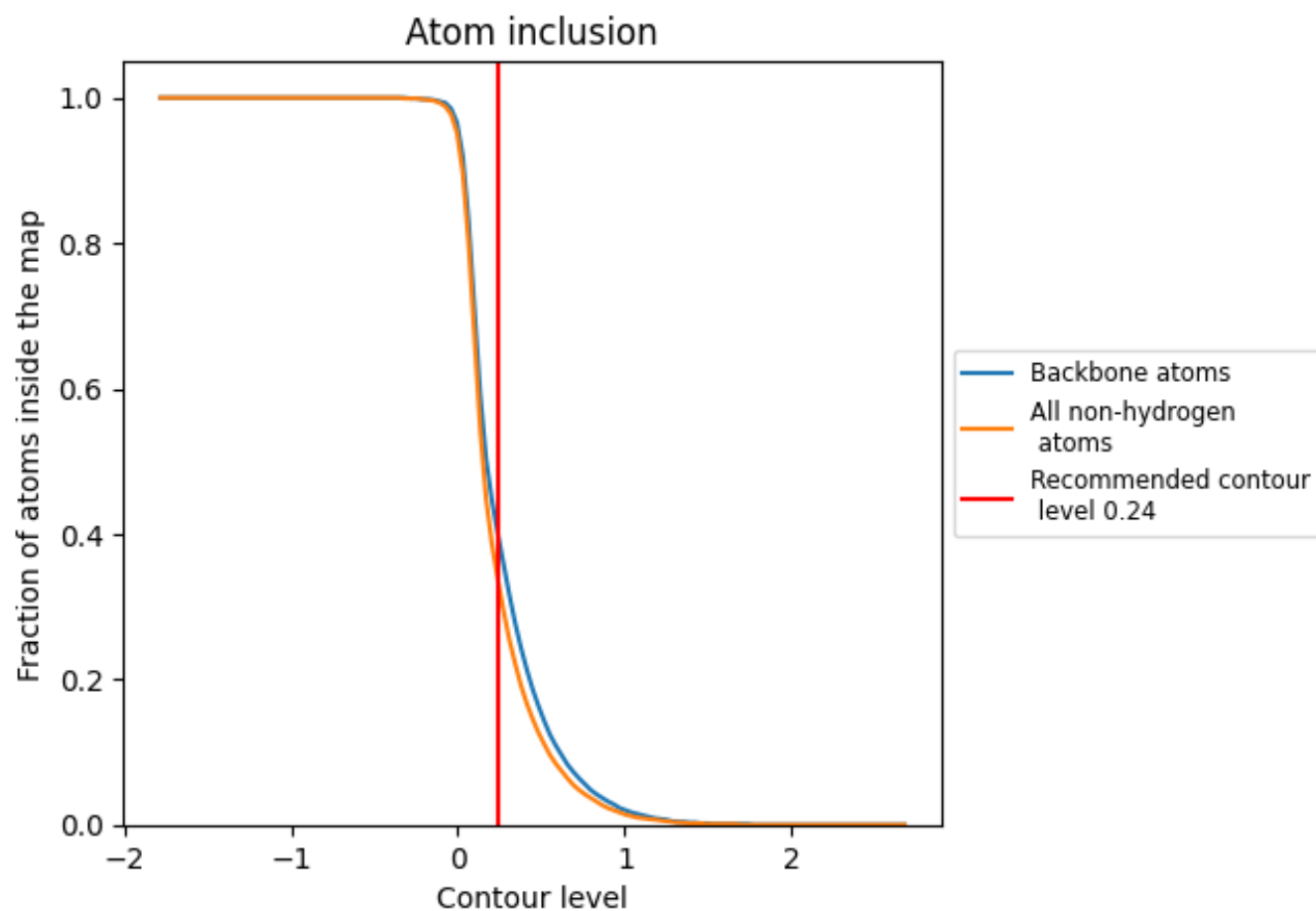
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.24).

9.4 Atom inclusion [i](#)



At the recommended contour level, 40% of all backbone atoms, 34% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.24) and Q-score for the entire model and for each chain.

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

1.0

0.0

<0.0