



Full wwPDB EM Validation Report ⓘ

Aug 27, 2026 – 12:00 PM EDT

PDB ID : 10LM / pdb_000010lm
EMDB ID : EMD-75270
Title : Native flagellar filament from *Leptospira biflexa*
Authors : Brady, M.R.; San Martin, F.; Sindelar, C.V.; Buschiazzi, A.
Deposited on : 2026-01-26
Resolution : 3.50 Å (reported)
Based on initial model : .

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:

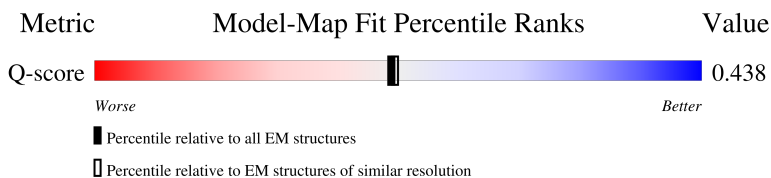
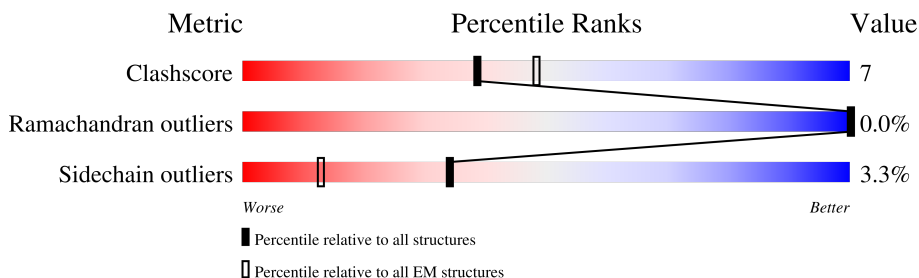
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 3.50 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.



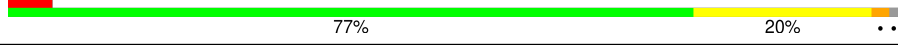
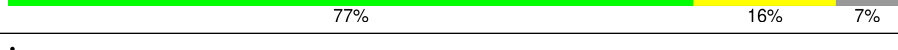
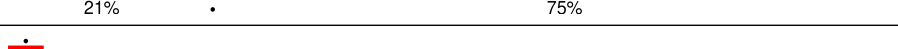
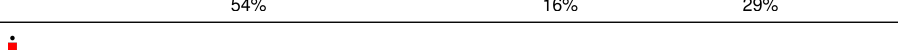
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	A3	282	
1	A4	282	
1	A5	282	
1	A6	282	

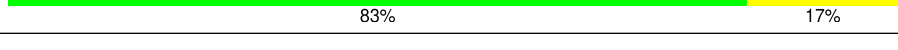
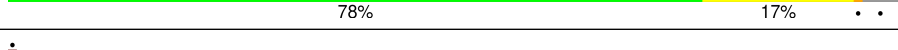
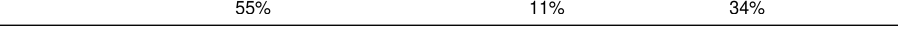
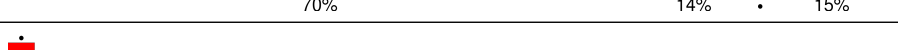
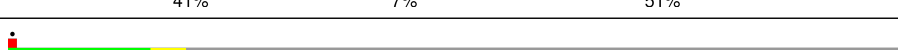
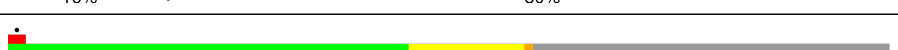
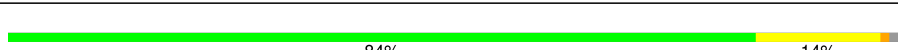
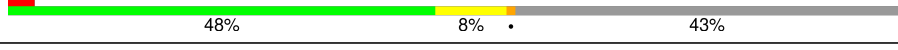
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Mol	Chain	Length	Quality of chain
1	A7	282	
1	A8	282	
1	B3	282	
1	B4	282	
1	B5	282	
1	B6	282	
1	B7	282	
1	B8	282	
1	C2	282	
1	C3	282	
1	C4	282	
1	C5	282	
1	C6	282	
1	C7	282	
1	C8	282	
1	D2	282	
1	D3	282	
1	D4	282	
1	D5	282	
1	D6	282	
1	D7	282	
1	E1	282	
1	E2	282	
1	E3	282	
1	E4	282	

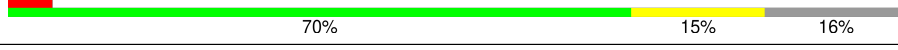
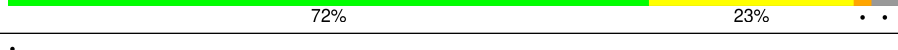
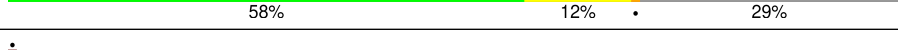
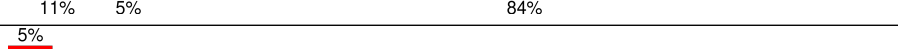
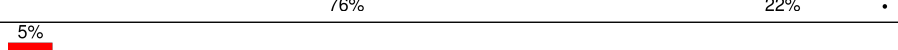
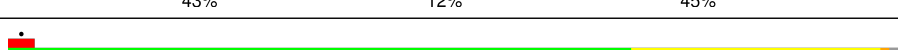
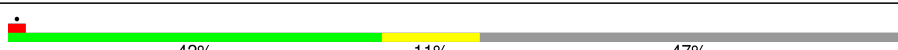
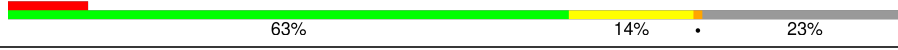
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Mol	Chain	Length	Quality of chain
1	E5	282	
1	E6	282	
1	E7	282	
1	F1	282	
1	F2	282	
1	F3	282	
1	F4	282	
1	F5	282	
1	F6	282	
1	G1	282	
1	G2	282	
1	G5	282	
1	G6	282	
1	G7	282	
1	G8	282	
1	G9	282	
1	H5	282	
1	H6	282	
1	H7	282	
1	H8	282	
1	H9	282	
1	I4	282	
1	I5	282	
1	I6	282	
1	I7	282	

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Mol	Chain	Length	Quality of chain
1	I8	282	
1	I9	282	
1	J4	282	
1	J5	282	
1	J6	282	
1	J7	282	
1	J8	282	
1	J9	282	
1	K3	282	
1	K4	282	
1	K5	282	
1	K6	282	
1	K7	282	
1	K8	282	
1	h0	282	
1	i0	282	
2	L1	300	
2	L2	300	
2	L3	300	
2	L4	300	
2	L5	300	
2	M1	300	
2	M2	300	
2	M3	300	
2	M4	300	

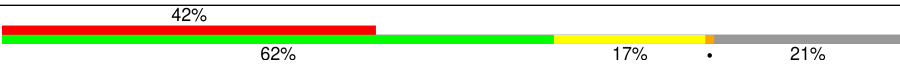
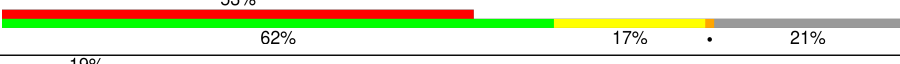
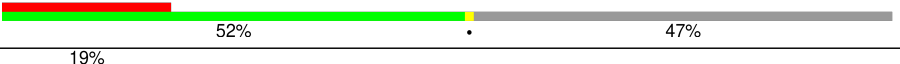
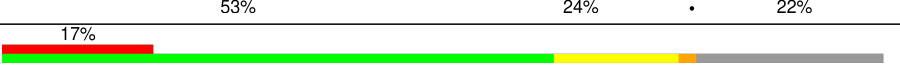
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Mol	Chain	Length	Quality of chain
2	M5	300	
2	N1	300	
2	N2	300	
2	N3	300	
2	N4	300	
2	N5	300	
2	N6	300	
2	O1	300	
2	O2	300	
2	O3	300	
2	O4	300	
2	O5	300	
2	P1	300	
2	P2	300	
2	P3	300	
2	P4	300	
2	P5	300	
2	P6	300	
3	Q1	277	
3	Q2	277	
3	Q3	277	
3	Q4	277	
3	R1	277	
3	R2	277	
3	R3	277	

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Mol	Chain	Length	Quality of chain
3	R4	277	
3	R5	277	
3	S2	277	
3	S3	277	
3	S4	277	
3	S5	277	
3	S6	277	
4	U3	321	
4	U4	321	
4	U5	321	
4	U6	321	
5	V0	241	
5	V1	241	
5	V2	241	
5	V3	241	
5	V4	241	
5	X0	241	
5	X1	241	
5	X2	241	
5	X3	241	
5	X4	241	
6	Y1	284	
6	Y2	284	
6	Y3	284	
6	Y4	284	

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Mol	Chain	Length	Quality of chain
7	Z0	367	
7	Z1	367	
7	Z2	367	
7	Za	367	
8	a1	239	
8	a2	239	
8	a3	239	
8	a4	239	
8	a5	239	
9	b2	269	
9	b3	269	
9	b4	269	
10	c1	175	
10	c2	175	
10	c3	175	

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 248112 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 Flagellin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A3	92	Total	C	N	O	S	0	1
			702	428	130	137	7		
1	A4	229	Total	C	N	O	S	0	1
			1781	1090	332	344	15		
1	A5	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	A6	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	A7	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	A8	222	Total	C	N	O	S	0	0
			1713	1049	313	339	12		
1	B3	127	Total	C	N	O	S	0	0
			964	581	181	193	9		
1	B4	280	Total	C	N	O	S	0	0
			2177	1335	401	425	16		
1	B5	281	Total	C	N	O	S	0	0
			2185	1340	402	427	16		
1	B6	281	Total	C	N	O	S	0	0
			2185	1340	402	427	16		
1	B7	263	Total	C	N	O	S	0	0
			2037	1249	374	401	13		
1	B8	176	Total	C	N	O	S	0	0
			1372	849	252	263	8		
1	C2	70	Total	C	N	O	S	0	0
			547	338	100	104	5		
1	C3	199	Total	C	N	O	S	0	0
			1542	945	284	298	15		
1	C4	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	C5	281	Total	C	N	O	S	0	0
			2185	1340	402	427	16		
1	C6	281	Total	C	N	O	S	0	0
			2185	1340	402	427	16		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	C7	228	Total	C	N	O	S	0	0
			1772	1085	324	351	12		
1	C8	124	Total	C	N	O	S	0	0
			956	597	168	188	3		
1	D2	114	Total	C	N	O	S	0	0
			881	533	166	174	8		
1	D3	266	Total	C	N	O	S	0	0
			2068	1275	380	397	16		
1	D4	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	D5	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	D6	266	Total	C	N	O	S	0	0
			2063	1264	379	406	14		
1	D7	181	Total	C	N	O	S	0	0
			1410	871	258	273	8		
1	E1	62	Total	C	N	O	S	0	0
			478	297	88	89	4		
1	E2	184	Total	C	N	O	S	0	0
			1430	877	267	272	14		
1	E3	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	E4	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	E5	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	E6	235	Total	C	N	O	S	0	0
			1831	1123	335	361	12		
1	E7	129	Total	C	N	O	S	0	0
			983	613	174	194	2		
1	F1	108	Total	C	N	O	S	0	1
			818	494	152	164	8		
1	F2	251	Total	C	N	O	S	0	1
			1953	1198	361	378	16		
1	F3	281	Total	C	N	O	S	0	0
			2185	1340	402	427	16		
1	F4	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	F5	270	Total	C	N	O	S	0	0
			2092	1280	386	412	14		
1	F6	185	Total	C	N	O	S	0	0
			1440	889	263	279	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	G1	240	Total	C	N	O	S	0	0
			1869	1145	341	371	12		
1	G2	137	Total	C	N	O	S	0	0
			1061	662	188	207	4		
1	G5	56	Total	C	N	O	S	0	0
			431	268	81	78	4		
1	G6	168	Total	C	N	O	S	0	0
			1318	810	244	250	14		
1	G7	281	Total	C	N	O	S	0	0
			2185	1340	402	427	16		
1	G8	281	Total	C	N	O	S	0	0
			2185	1340	402	427	16		
1	G9	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	H5	102	Total	C	N	O	S	0	0
			785	474	146	157	8		
1	H6	242	Total	C	N	O	S	0	0
			1896	1163	350	367	16		
1	H7	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	H8	281	Total	C	N	O	S	0	0
			2185	1340	402	427	16		
1	H9	276	Total	C	N	O	S	0	0
			2140	1312	393	419	16		
1	I4	53	Total	C	N	O	S	0	1
			405	250	77	74	4		
1	I5	161	Total	C	N	O	S	0	0
			1259	767	236	242	14		
1	I6	282	Total	C	N	O	S	0	0
			2192	1344	403	429	16		
1	I7	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	I8	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	I9	246	Total	C	N	O	S	0	0
			1914	1173	350	379	12		
1	J4	101	Total	C	N	O	S	0	0
			772	467	143	154	8		
1	J5	238	Total	C	N	O	S	0	0
			1854	1139	341	359	15		
1	J6	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	J7	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	J8	273	Total	C	N	O	S	0	0
			2121	1299	390	417	15		
1	J9	199	Total	C	N	O	S	0	0
			1556	955	287	304	10		
1	K3	46	Total	C	N	O	S	0	0
			351	217	66	64	4		
1	K4	281	Total	C	N	O	S	0	0
			2185	1340	402	427	16		
1	K5	155	Total	C	N	O	S	0	0
			1210	733	230	233	14		
1	K6	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	K7	280	Total	C	N	O	S	0	0
			2178	1335	401	426	16		
1	K8	253	Total	C	N	O	S	0	0
			1966	1202	362	389	13		
1	h0	190	Total	C	N	O	S	0	0
			1490	918	276	287	9		
1	i0	150	Total	C	N	O	S	0	0
			1168	727	208	227	6		

- Molecule 2 is a protein called Flagellar Coiling Protein FcpA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L1	133	Total	C	N	O	S	0	0
			1079	681	184	210	4		
2	L2	234	Total	C	N	O	S	0	0
			1959	1248	341	364	6		
2	L3	234	Total	C	N	O	S	0	0
			1959	1248	341	364	6		
2	L4	234	Total	C	N	O	S	0	0
			1959	1248	341	364	6		
2	L5	234	Total	C	N	O	S	0	0
			1959	1248	341	364	6		
2	M1	231	Total	C	N	O	S	0	0
			1924	1222	336	360	6		
2	M2	234	Total	C	N	O	S	0	0
			1959	1248	341	364	6		
2	M3	234	Total	C	N	O	S	0	0
			1959	1248	341	364	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	M4	234	Total	C	N	O	S	0	0
			1959	1248	341	364	6		
2	M5	194	Total	C	N	O	S	0	0
			1638	1046	288	299	5		
2	N1	107	Total	C	N	O	S	0	1
			855	539	147	168	1		
2	N2	234	Total	C	N	O	S	0	0
			1959	1248	341	364	6		
2	N3	234	Total	C	N	O	S	0	0
			1959	1248	341	364	6		
2	N4	234	Total	C	N	O	S	0	0
			1959	1248	341	364	6		
2	N5	234	Total	C	N	O	S	0	0
			1959	1248	341	364	6		
2	N6	145	Total	C	N	O	S	0	0
			1204	771	212	216	5		
2	O1	226	Total	C	N	O	S	0	0
			1860	1180	323	351	6		
2	O2	234	Total	C	N	O	S	0	0
			1950	1242	338	364	6		
2	O3	234	Total	C	N	O	S	0	0
			1955	1245	340	364	6		
2	O4	234	Total	C	N	O	S	0	0
			1955	1245	340	364	6		
2	O5	194	Total	C	N	O	S	0	0
			1638	1046	288	299	5		
2	P1	89	Total	C	N	O	S	0	0
			728	460	127	140	1		
2	P2	234	Total	C	N	O	S	0	0
			1959	1248	341	364	6		
2	P3	234	Total	C	N	O	S	0	0
			1960	1248	342	364	6		
2	P4	237	Total	C	N	O	S	0	0
			1983	1264	345	368	6		
2	P5	237	Total	C	N	O	S	0	0
			1983	1264	345	368	6		
2	P6	163	Total	C	N	O	S	0	0
			1365	872	238	250	5		

- Molecule 3 is a protein called Flagellar Coiling Protein FcpB.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Q1	236	Total	C	N	O	S	0	0
			1926	1218	331	372	5		
3	Q2	236	Total	C	N	O	S	0	0
			1926	1218	331	372	5		
3	Q3	236	Total	C	N	O	S	0	0
			1926	1218	331	372	5		
3	Q4	236	Total	C	N	O	S	0	0
			1926	1218	331	372	5		
3	R1	204	Total	C	N	O	S	0	0
			1654	1053	276	321	4		
3	R2	236	Total	C	N	O	S	0	0
			1926	1218	331	372	5		
3	R3	236	Total	C	N	O	S	0	0
			1926	1218	331	372	5		
3	R4	236	Total	C	N	O	S	0	0
			1926	1218	331	372	5		
3	R5	236	Total	C	N	O	S	0	0
			1926	1218	331	372	5		
3	S2	233	Total	C	N	O	S	0	0
			1899	1200	326	368	5		
3	S3	236	Total	C	N	O	S	0	0
			1922	1215	330	372	5		
3	S4	236	Total	C	N	O	S	0	0
			1926	1218	331	372	5		
3	S5	236	Total	C	N	O	S	0	0
			1926	1218	331	372	5		
3	S6	175	Total	C	N	O	S	0	0
			1426	907	247	268	4		

- Molecule 4 is a protein called LEPBI_I1029 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	U3	255	Total	C	N	O	S	0	0
			2101	1327	368	403	3		
4	U4	255	Total	C	N	O	S	0	0
			2101	1327	368	403	3		
4	U5	255	Total	C	N	O	S	0	0
			2101	1327	368	403	3		
4	U6	255	Total	C	N	O	S	0	0
			2101	1327	368	403	3		

- Molecule 5 is a protein called Flagellar filament outer layer protein (Sheath protein) putative signal peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	V0	128	Total	C	N	O	0	0
			645	385	128	132		
5	V1	190	Total	C	N	O	0	0
			1574	1019	275	280		
5	V2	190	Total	C	N	O	0	0
			1574	1019	275	280		
5	V3	189	Total	C	N	O	0	0
			1559	1008	273	278		
5	V4	190	Total	C	N	O	0	0
			1568	1016	272	280		
5	X0	156	Total	C	N	O	0	0
			786	471	156	159		
5	X1	189	Total	C	N	O	0	0
			1559	1008	273	278		
5	X2	189	Total	C	N	O	0	0
			1559	1008	273	278		
5	X3	190	Total	C	N	O	0	0
			1574	1019	275	280		
5	X4	190	Total	C	N	O	0	0
			1574	1019	275	280		

- Molecule 6 is a protein called FlaA2 associated protein B0STF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Y1	217	Total	C	N	O	S	0	0
			1808	1171	301	331	5		
6	Y2	227	Total	C	N	O	S	0	0
			1905	1231	320	349	5		
6	Y3	237	Total	C	N	O	S	0	0
			1979	1274	335	365	5		
6	Y4	231	Total	C	N	O	S	0	0
			1937	1248	329	355	5		

- Molecule 7 is a protein called FlaA2-associated protein FlaAP.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Z0	270	Total	C	N	O	S	0	0
			2271	1440	398	422	11		
7	Z1	303	Total	C	N	O	S	0	0
			2545	1616	444	472	13		
7	Z2	277	Total	C	N	O	S	0	0
			2329	1473	414	430	12		
7	Za	254	Total	C	N	O	S	0	0
			2121	1345	376	389	11		

- Molecule 8 is a protein called LEPBI_I3081 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	a1	166	Total	C	N	O	S	0	0
			1367	870	245	249	3		
8	a2	198	Total	C	N	O	S	0	0
			1596	1004	283	304	5		
8	a3	191	Total	C	N	O	S	0	0
			1546	978	274	289	5		
8	a4	195	Total	C	N	O	S	0	0
			1577	994	280	298	5		
8	a5	199	Total	C	N	O	S	0	0
			1605	1009	284	307	5		

- Molecule 9 is a protein called LEPBI_I0662 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	b2	238	Total	C	N	O		0	0
			1204	728	238	238			
9	b3	238	Total	C	N	O	S	0	0
			1944	1229	335	374	6		
9	b4	238	Total	C	N	O	S	0	0
			1944	1229	335	374	6		

- Molecule 10 is a protein called LEPBI_II0033 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	c1	119	Total	C	N	O		0	0
			600	362	119	119			
10	c2	119	Total	C	N	O	S	0	0
			1020	655	168	191	6		
10	c3	120	Total	C	N	O	S	0	0
			1025	656	170	193	6		

- Molecule 11 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
11	V0	1	Total	Ca	0
			1	1	
11	V1	1	Total	Ca	0
			1	1	
11	V2	1	Total	Ca	0
			1	1	

Continued on next page...

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Mol	Chain	Residues	Atoms		AltConf
11	V3	1	Total 1	Ca 1	0
11	V4	1	Total 1	Ca 1	0
11	X0	1	Total 1	Ca 1	0
11	X1	1	Total 1	Ca 1	0
11	X2	1	Total 1	Ca 1	0
11	X3	1	Total 1	Ca 1	0
11	X4	1	Total 1	Ca 1	0

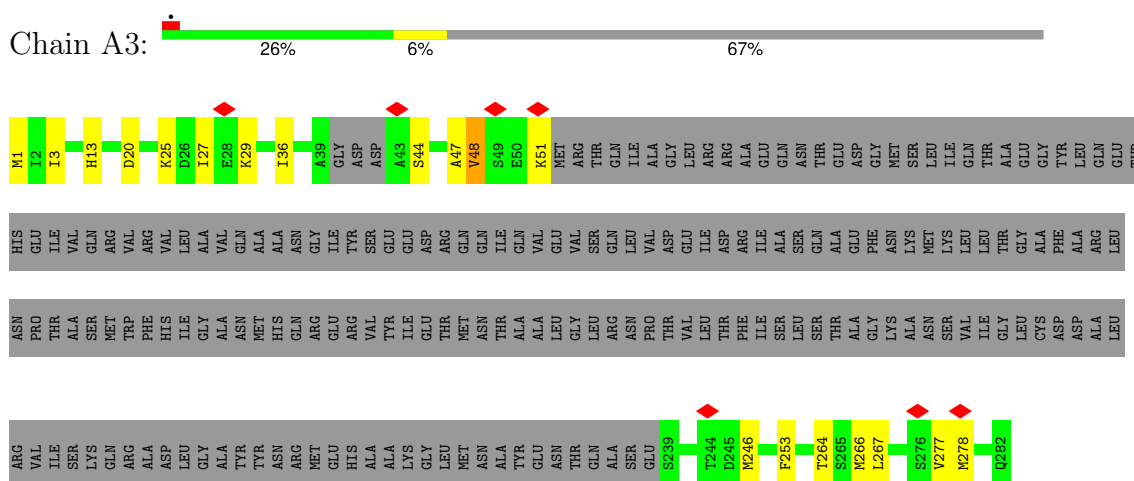
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		AltConf
12	V0	2	Total 2	O 2	0
12	V1	2	Total 2	O 2	0
12	V2	2	Total 2	O 2	0
12	V3	2	Total 2	O 2	0
12	V4	2	Total 2	O 2	0
12	X0	2	Total 2	O 2	0
12	X1	2	Total 2	O 2	0
12	X2	2	Total 2	O 2	0
12	X3	2	Total 2	O 2	0
12	X4	2	Total 2	O 2	0

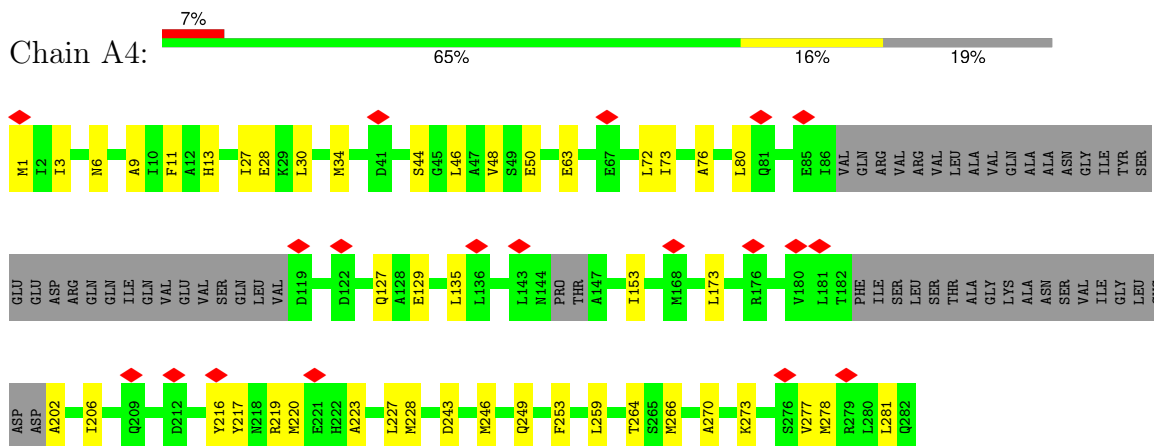
3 Residue-property plots [i](#)

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

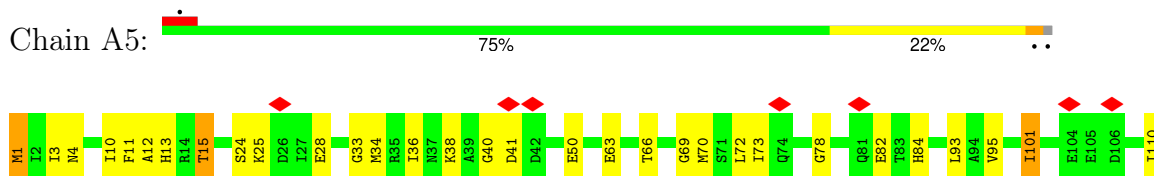
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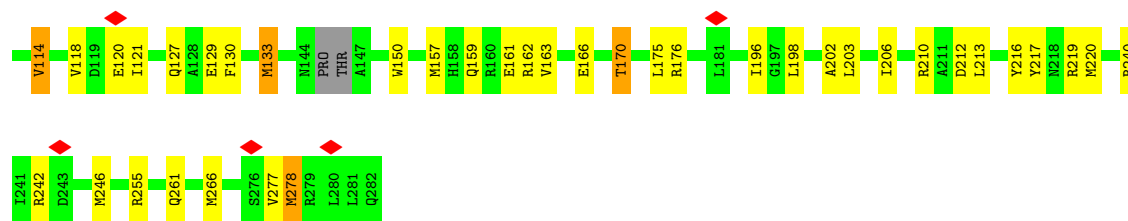


• Molecule 1: Flagellin

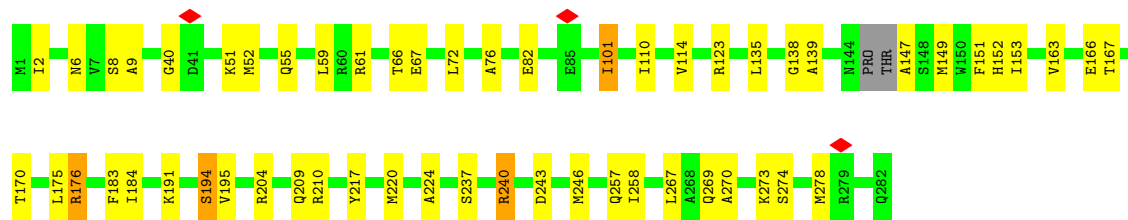
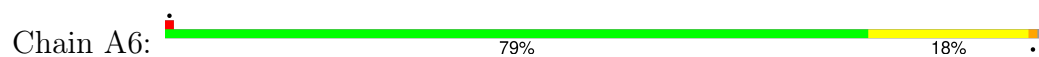


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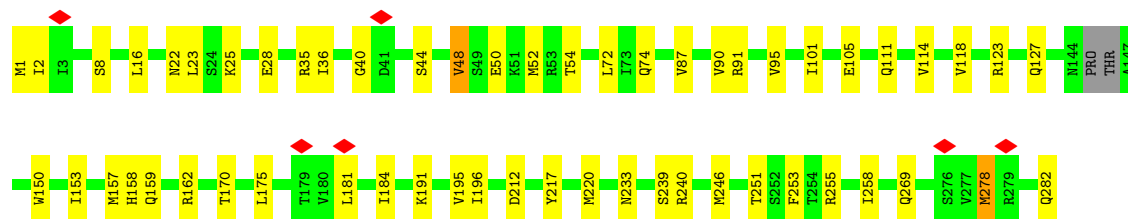
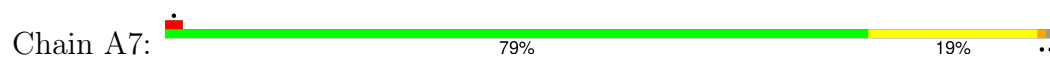




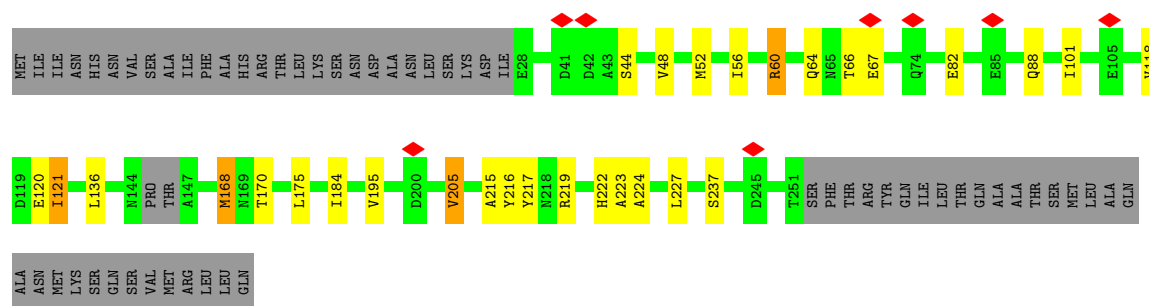
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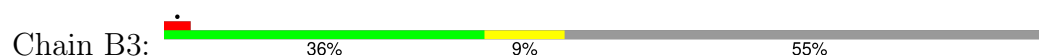
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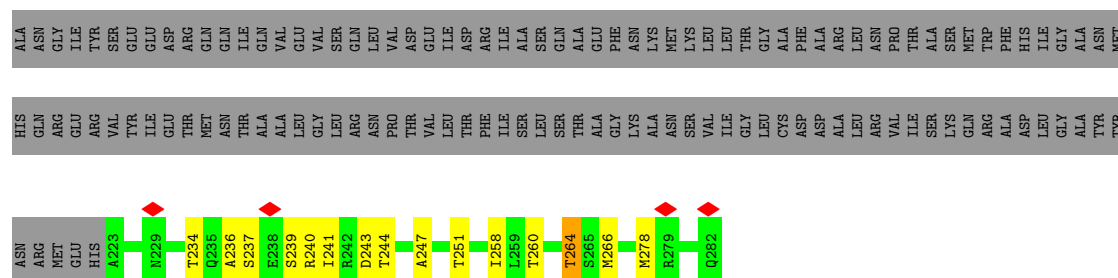


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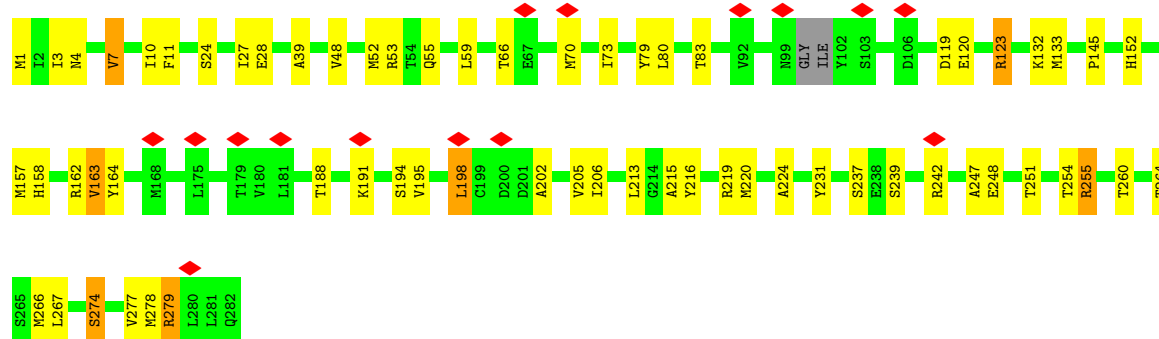
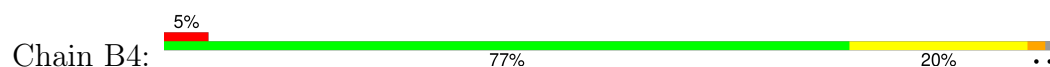


• Molecule 1: Flagellin

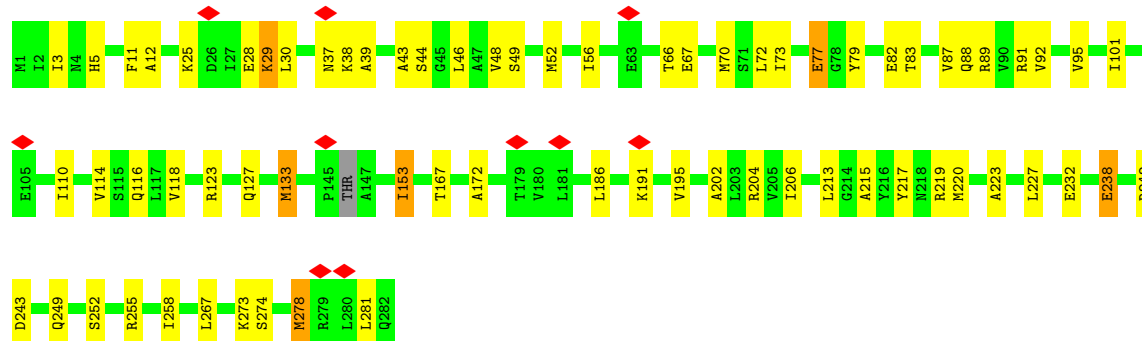
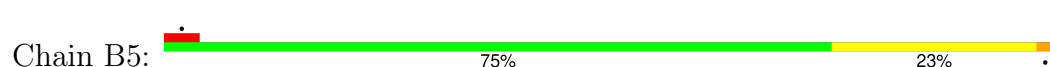




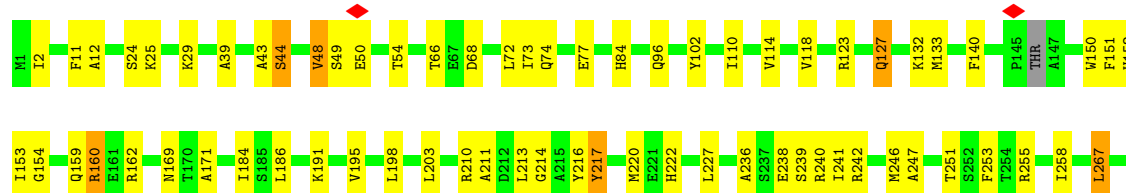
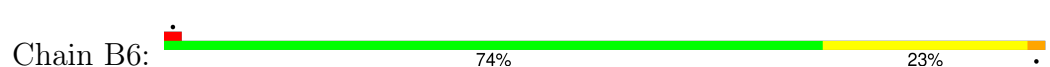
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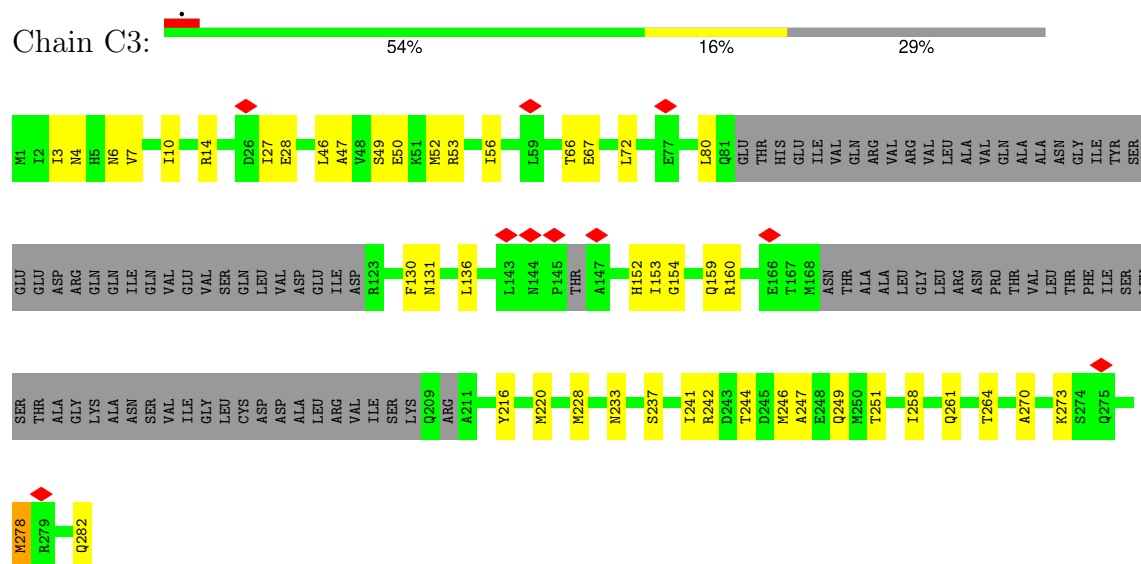


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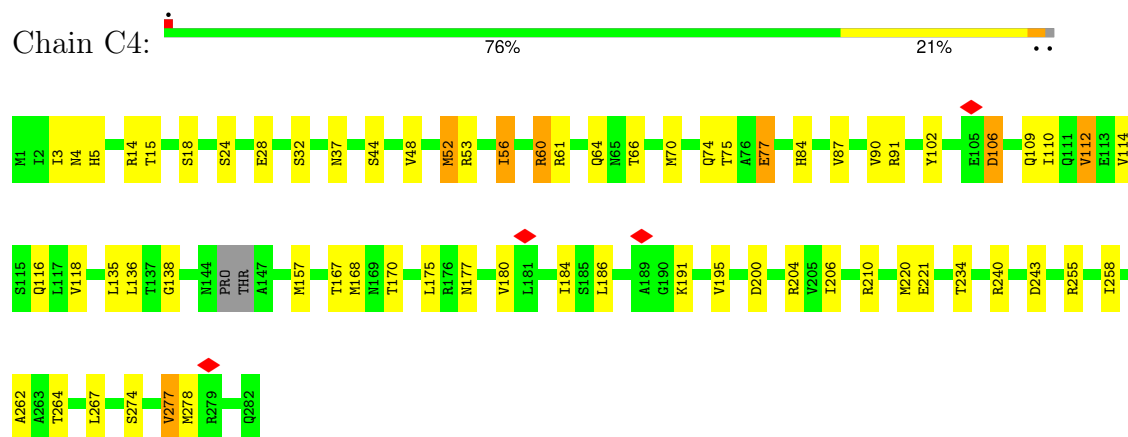


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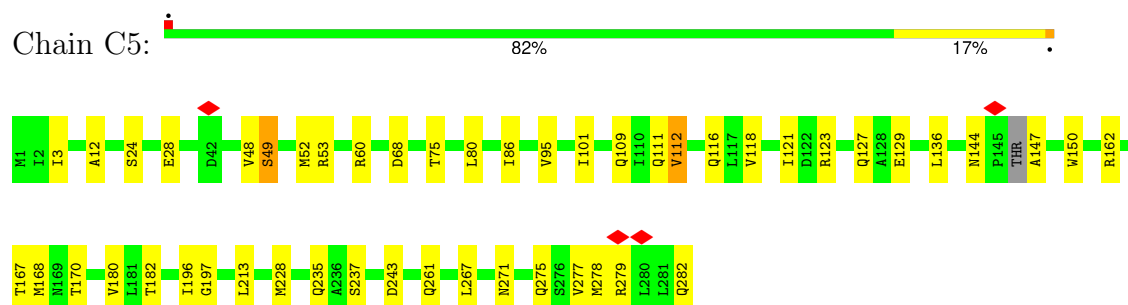




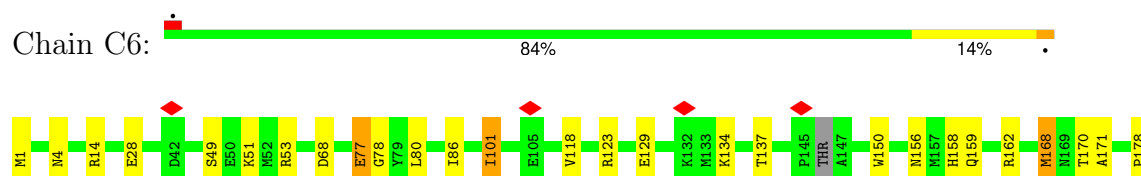
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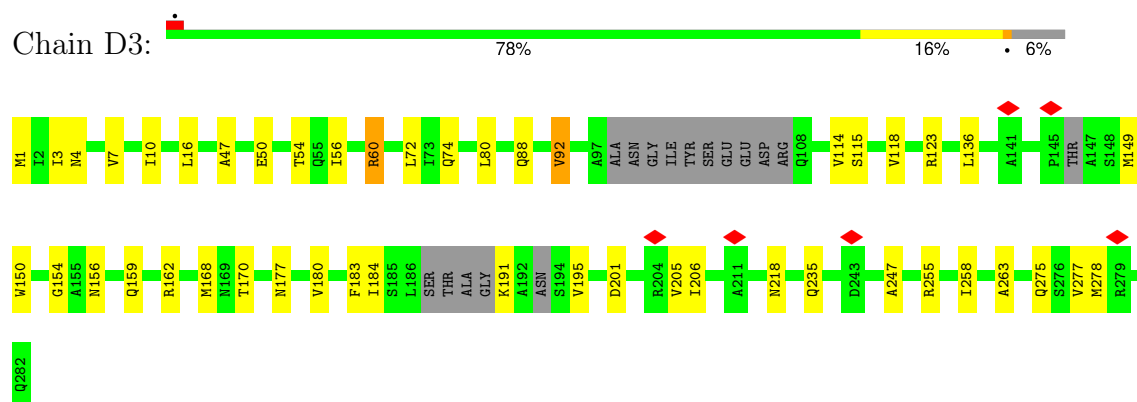
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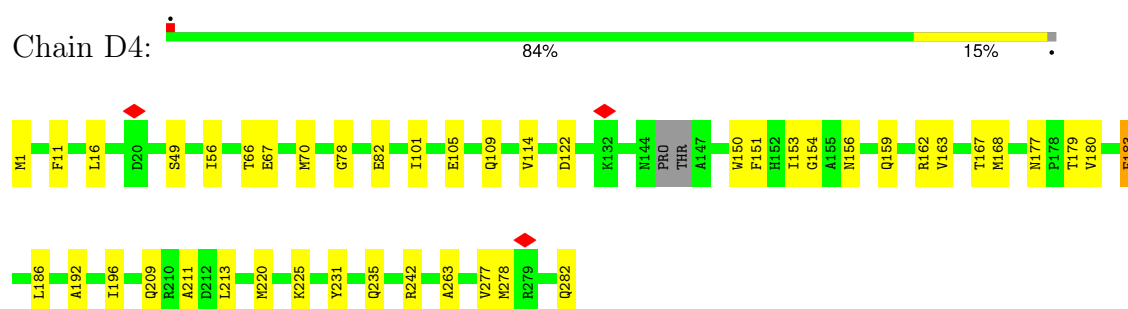
• Molecule 1: Flagellin



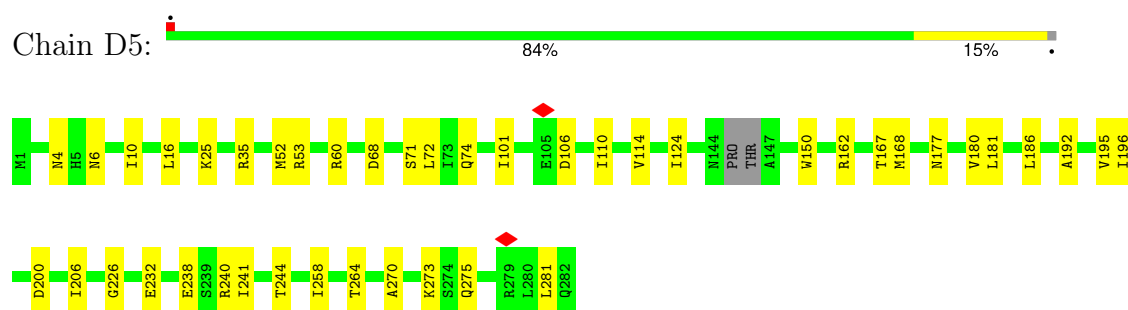
- Molecule 1: Flagellin



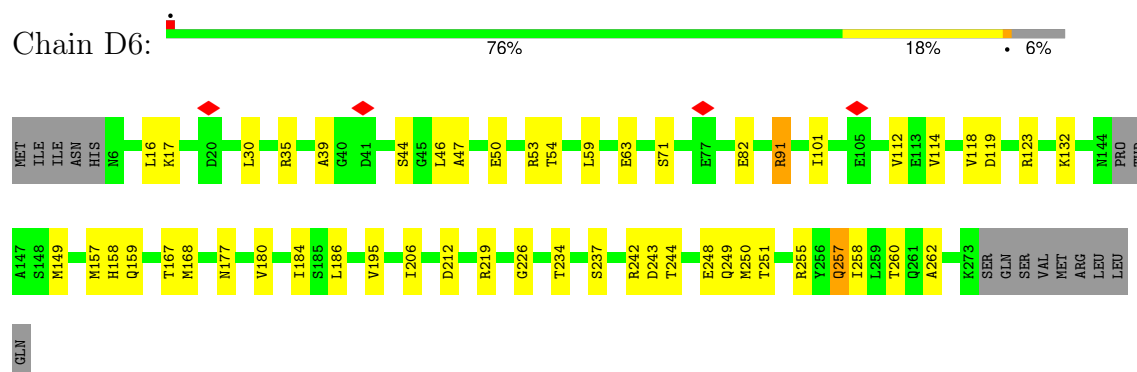
- Molecule 1: Flagellin



- Molecule 1: Flagellin

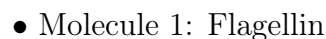


- Molecule 1: Flagellin

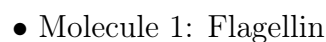


- Molecule 1: Flagellin

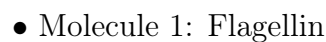
Response	Percentage
Used	54%
Not used	10%
Don't know	36%



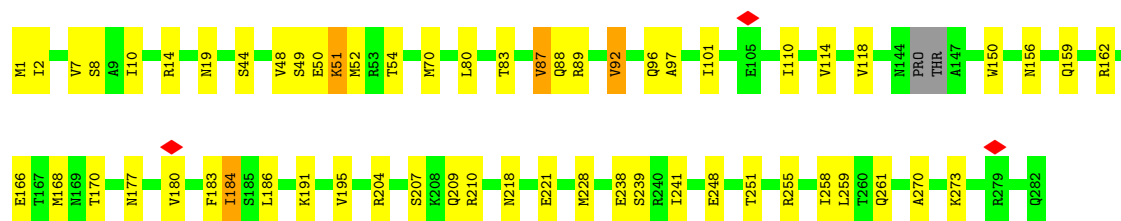
Response	Percentage
Yes	19%
No	78%



Response	Percentage
Good country	51%
Not a good country	13%
Don't know	35%

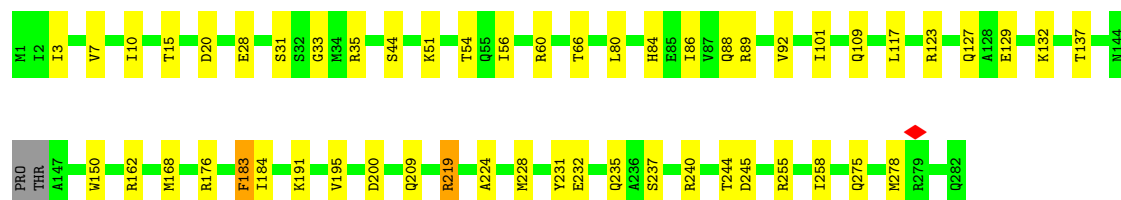


Response	Percentage
Yes	78%
No	20%



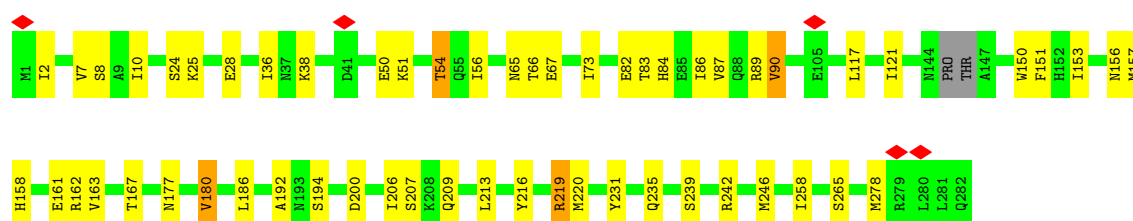
• Molecule 1: Flagellin

Chain E4: 80% 18% ..



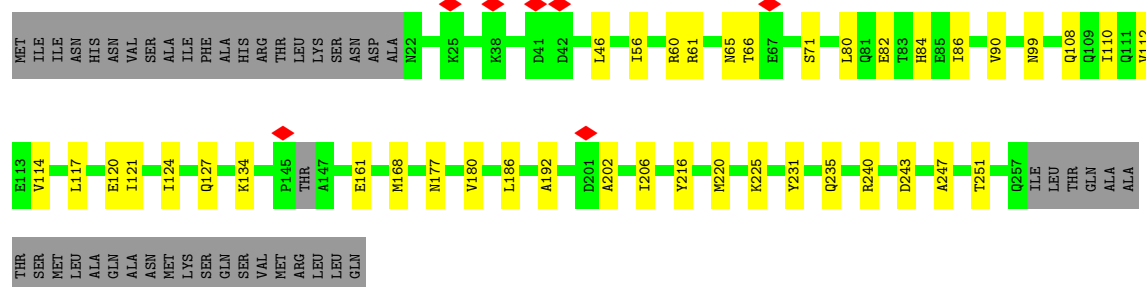
• Molecule 1: Flagellin

Chain E5: 79% 19% ..



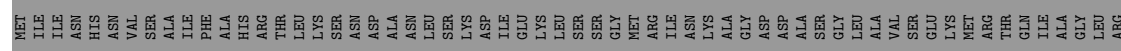
• Molecule 1: Flagellin

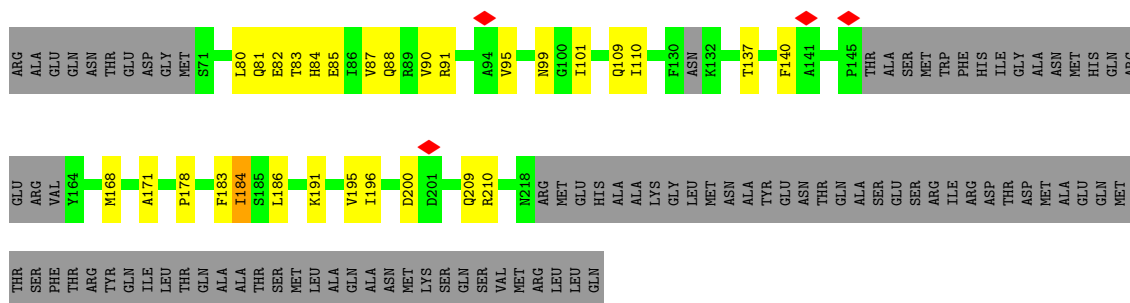
Chain E6: 69% 14% 17%



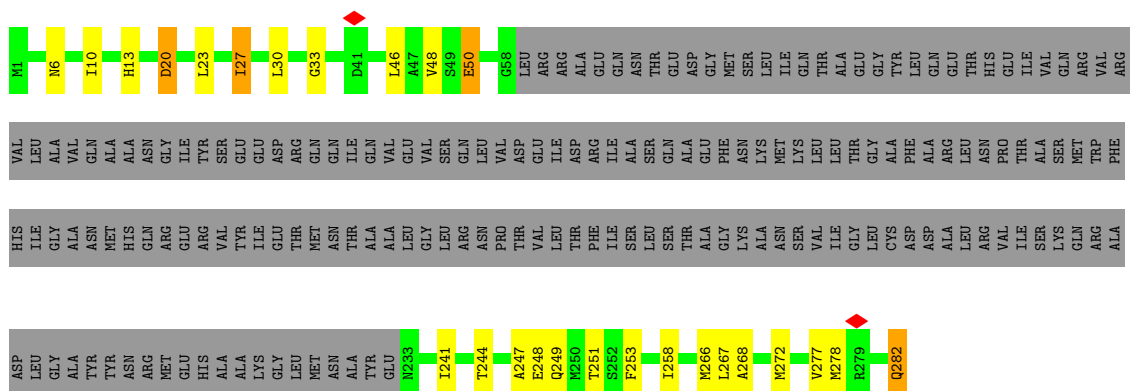
• Molecule 1: Flagellin

Chain E7: 35% 10% 54%

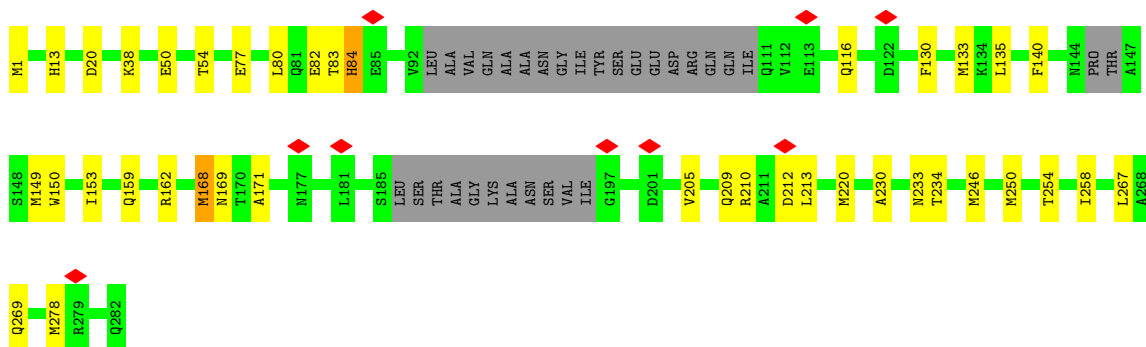
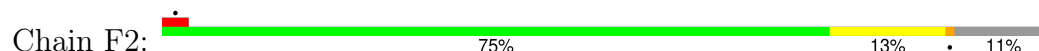




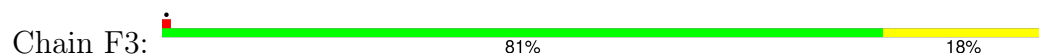
• Molecule 1: Flagellin



• Molecule 1: Flagellin

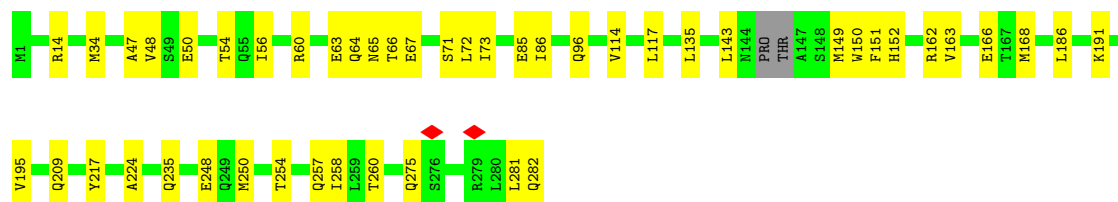
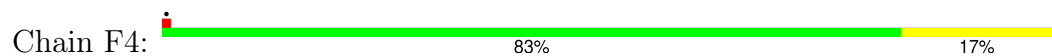


• Molecule 1: Flagellin

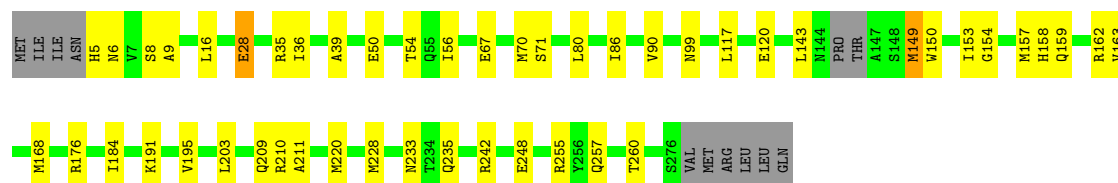
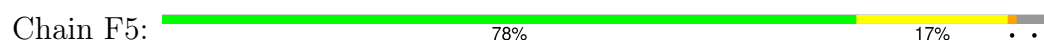




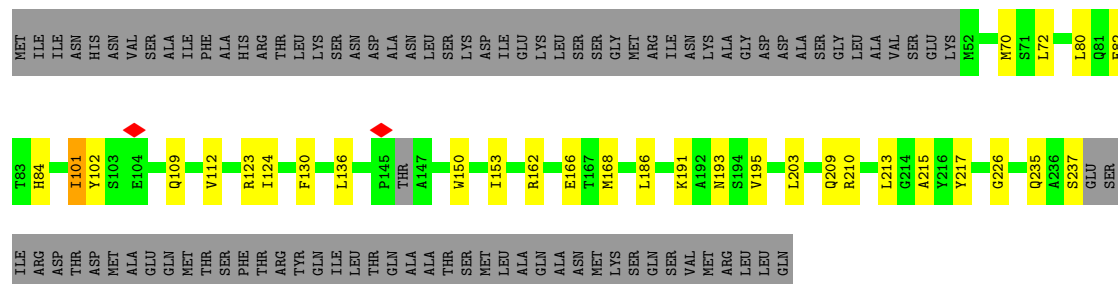
• Molecule 1: Flagellin



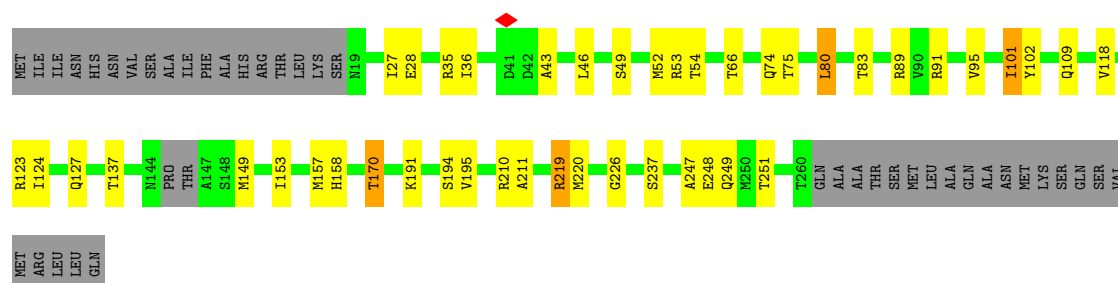
• Molecule 1: Flagellin



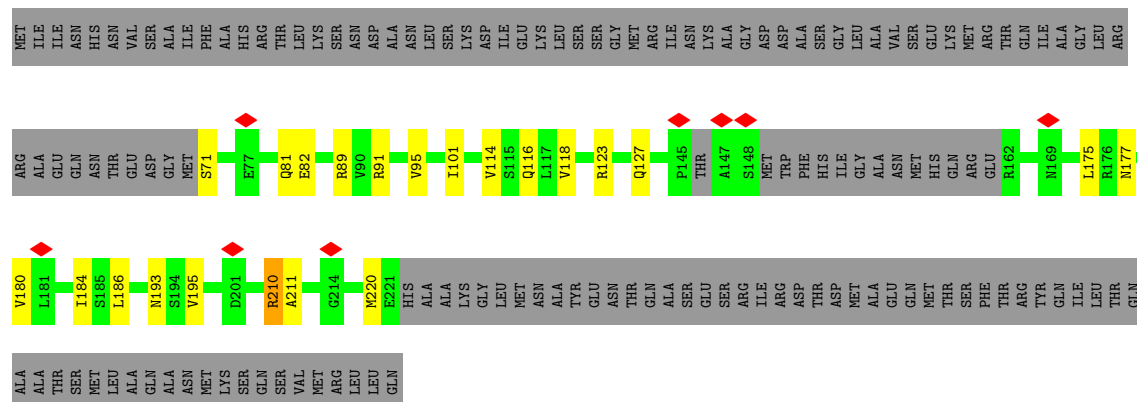
• Molecule 1: Flagellin



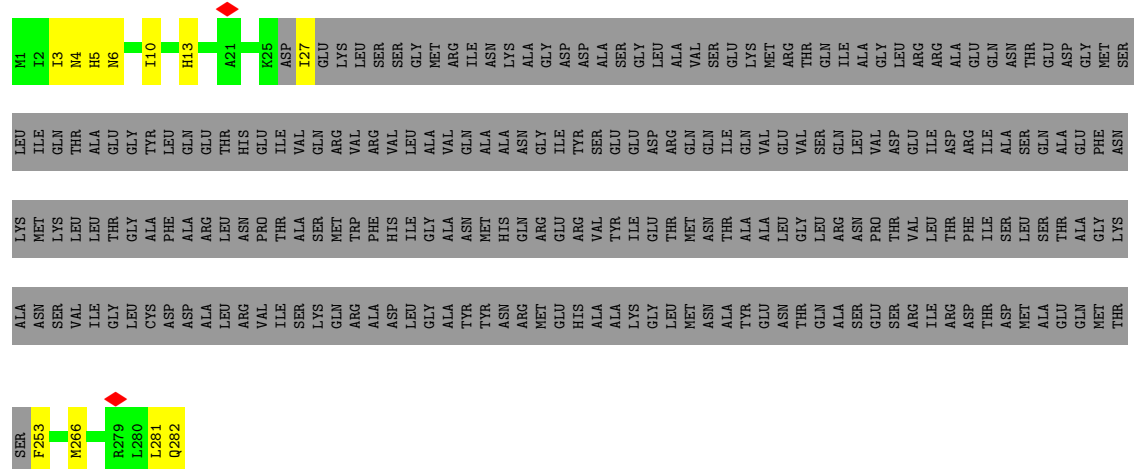
• Molecule 1: Flagellin



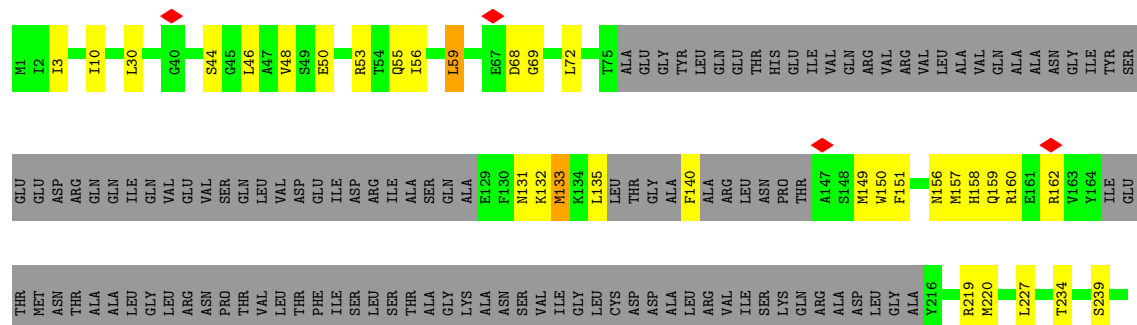
Chain G2:



Chain G5:

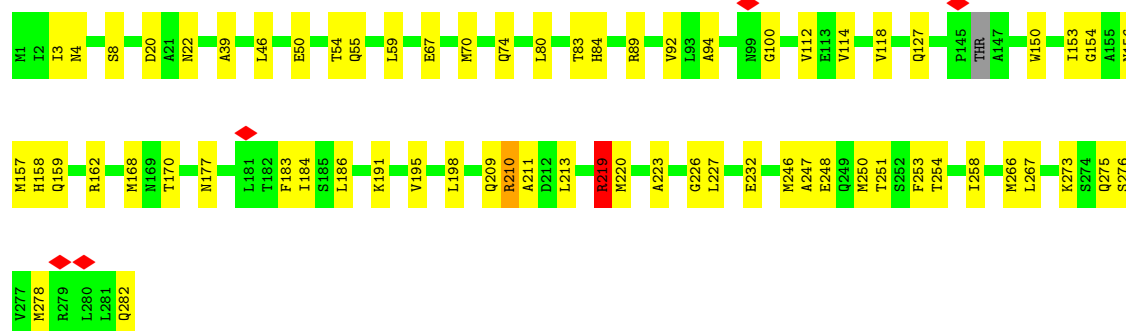
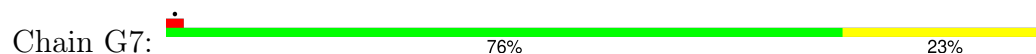


Chain G6:

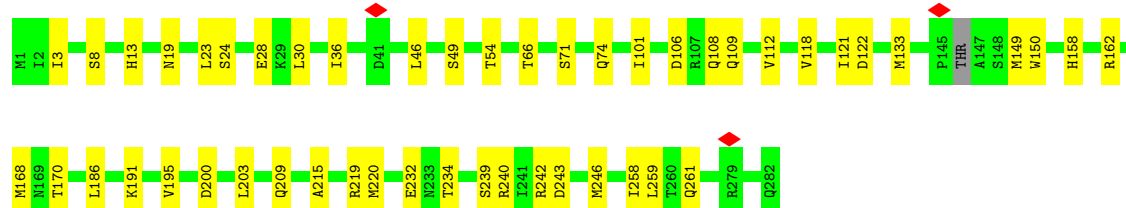
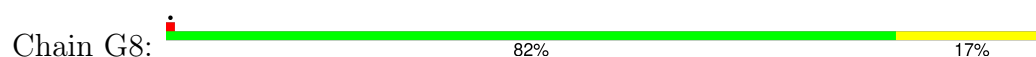




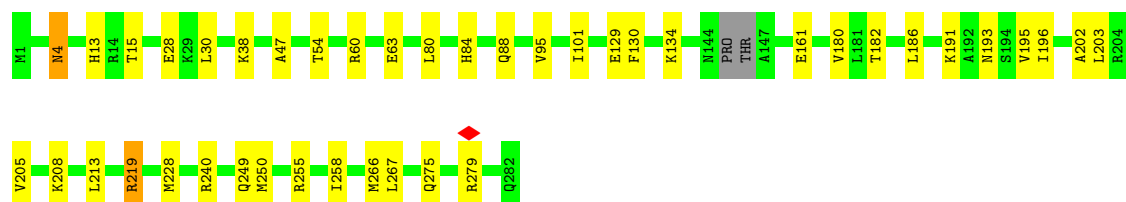
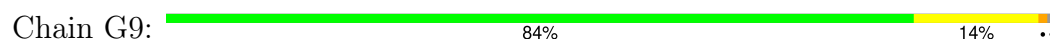
• Molecule 1: Flagellin



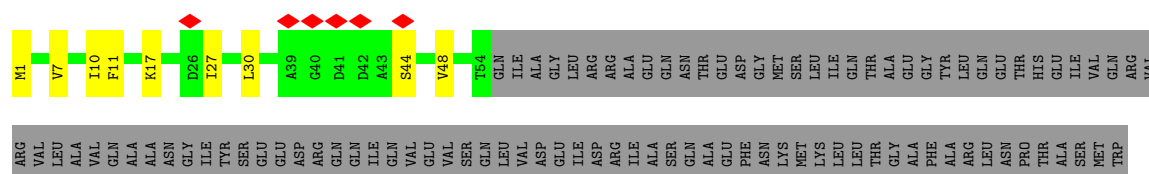
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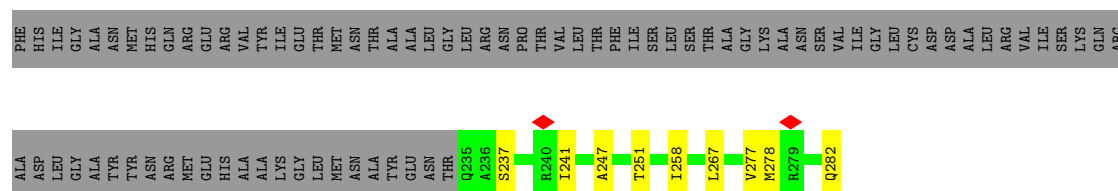


• Molecule 1: Flagellin



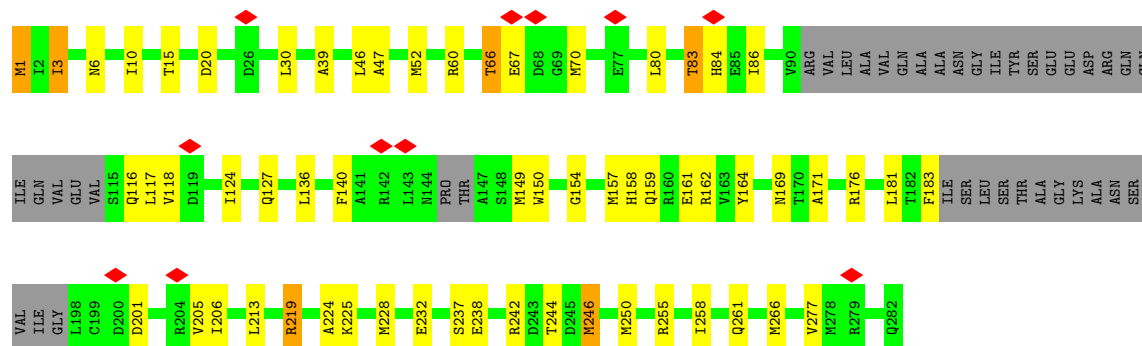
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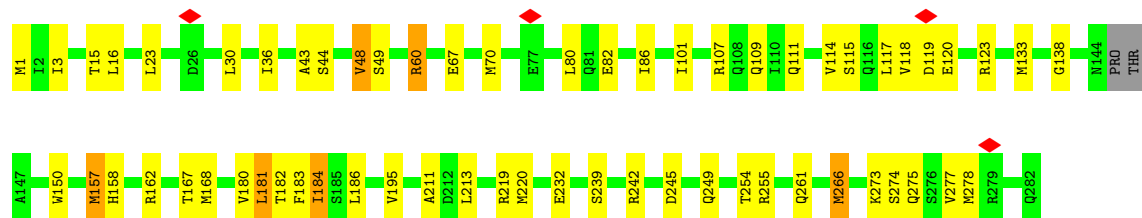
• Molecule 1: Flagellin

Chain H6: 65% 19% 14%



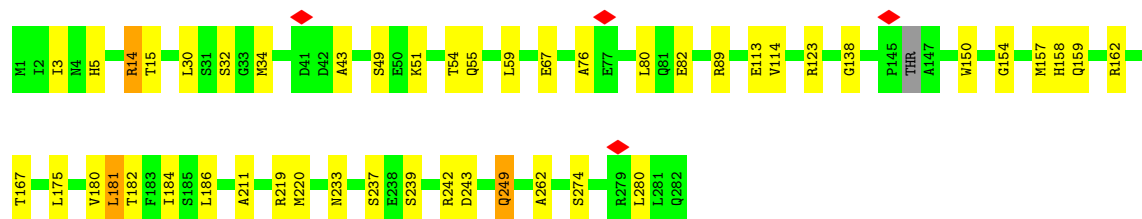
• Molecule 1: Flagellin

Chain H7: 78% 20%



• Molecule 1: Flagellin

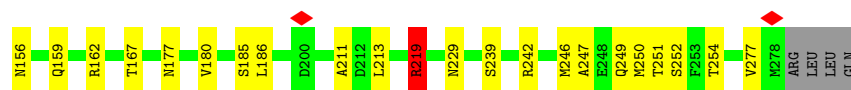
Chain H8: 83% 16%



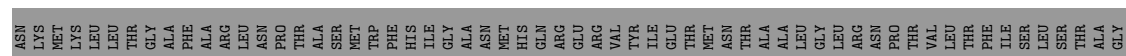
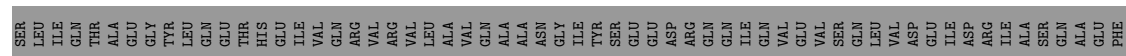
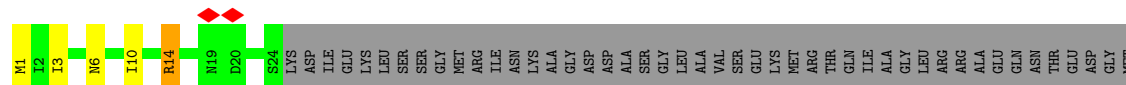
• Molecule 1: Flagellin

Chain H9: 80% 17%

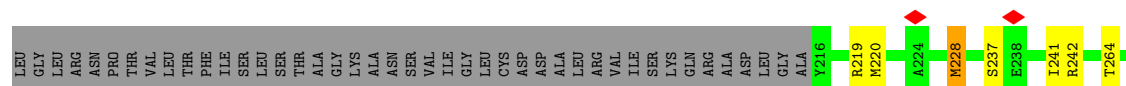




• Molecule 1: Flagellin

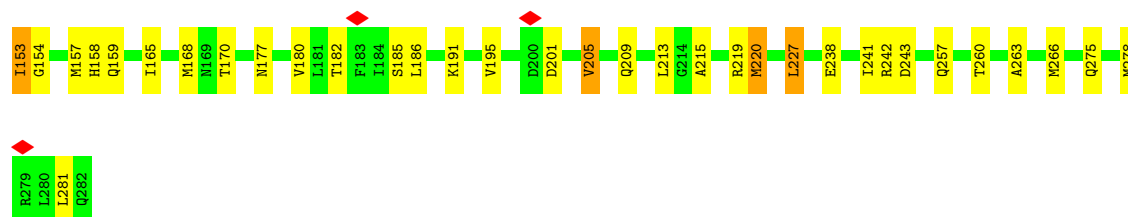


• Molecule 1: Flagellin



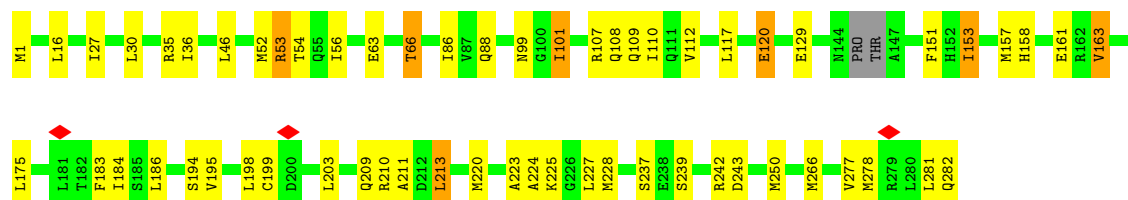
• Molecule 1: Flagellin





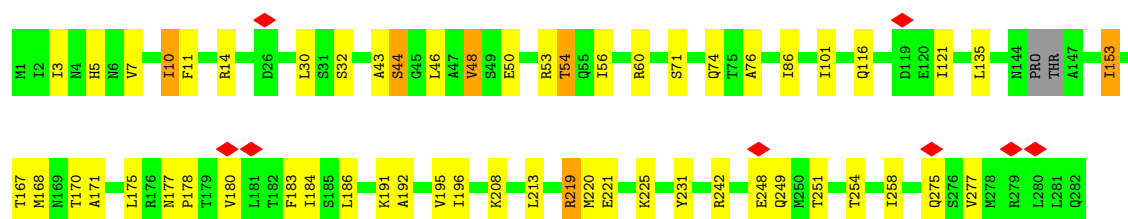
- Molecule 1: Flagellin

Chain I7: 78% 19% ..



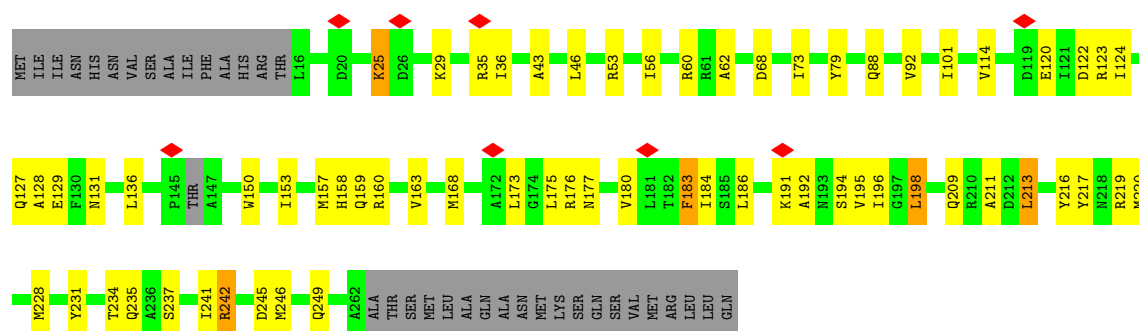
- Molecule 1: Flagellin

Chain I8: 79% 18% ..



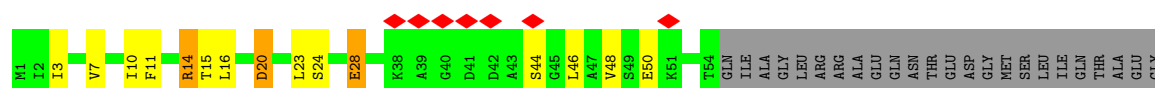
- Molecule 1: Flagellin

Chain I9: 64% 21% 13%

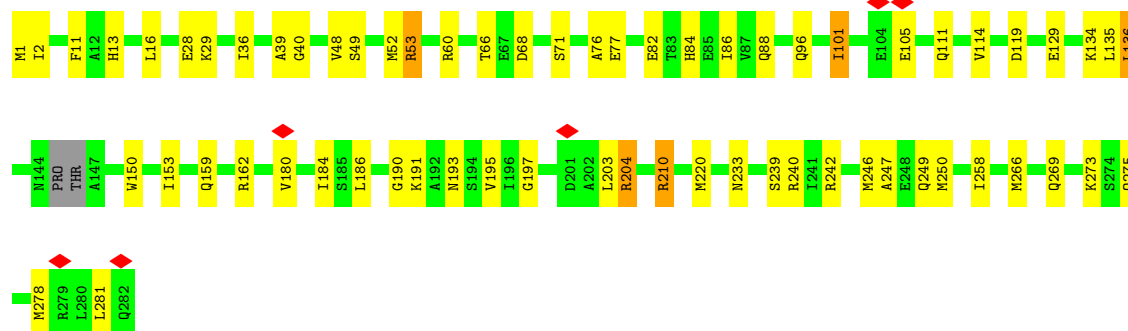


- Molecule 1: Flagellin

Chain J4: 28% 7% 64%

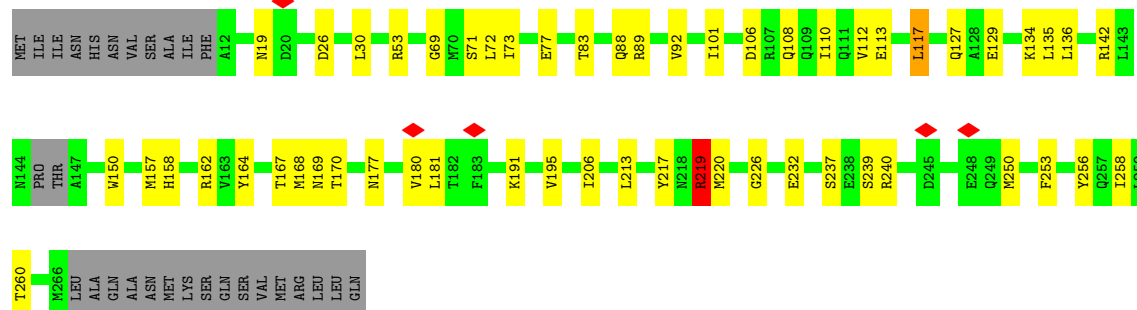


Chain K7: 



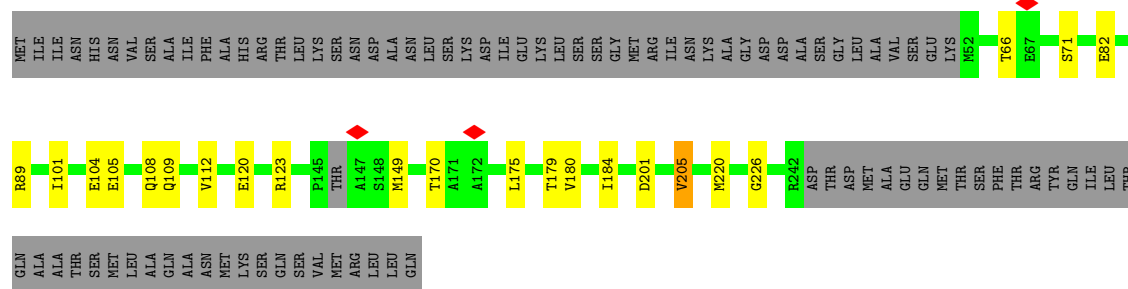
• Molecule 1: Flagellin

Chain K8: 

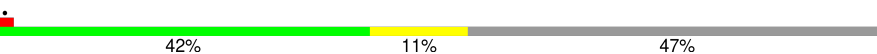


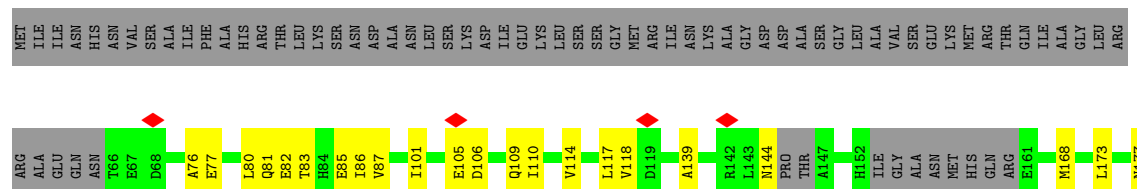
• Molecule 1: Flagellin

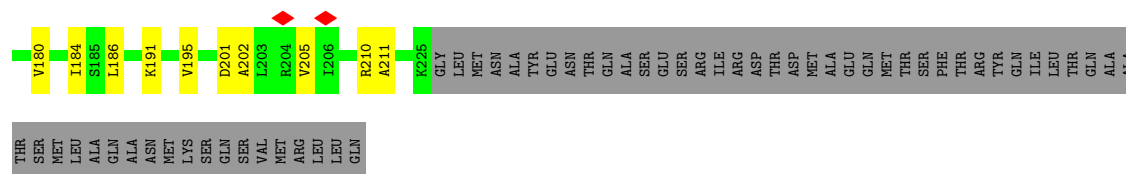
Chain h0: 



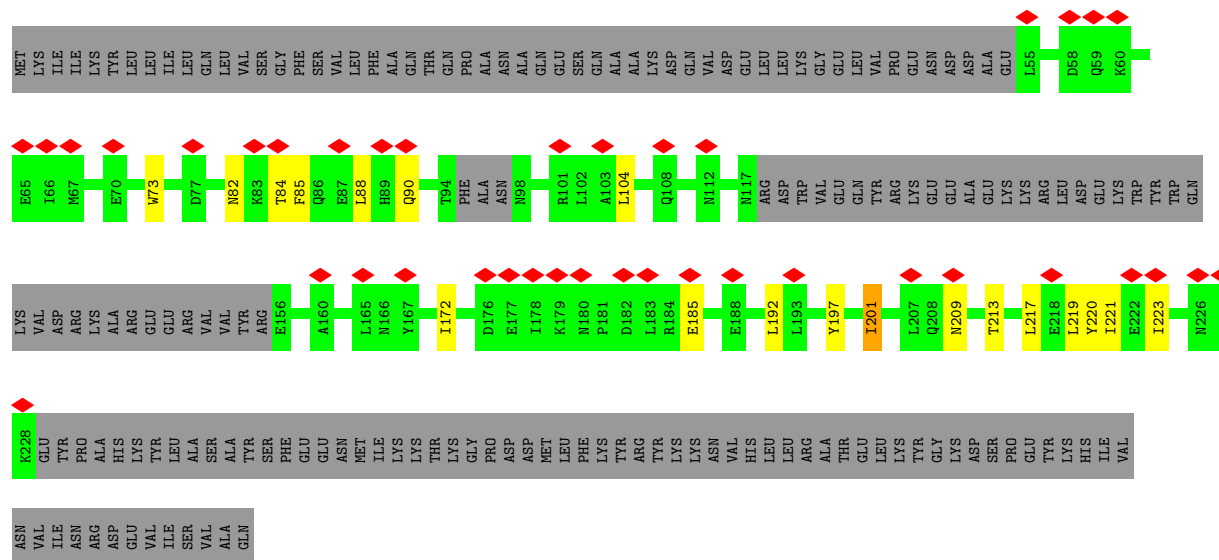
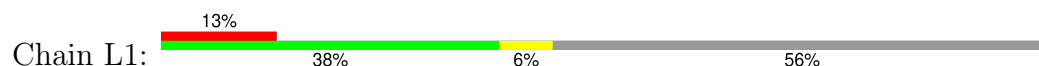
• Molecule 1: Flagellin

Chain i0: 

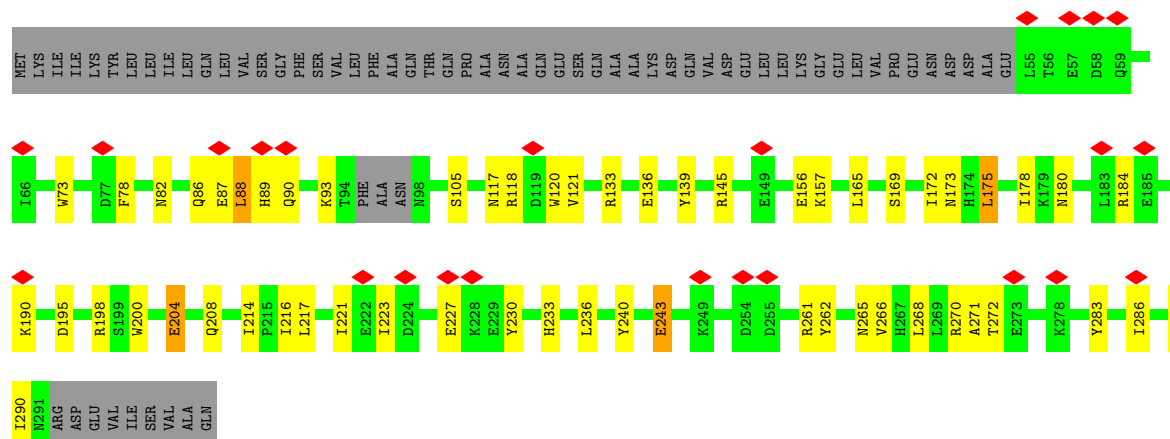




• Molecule 2: Flagellar Coiling Protein FcpA

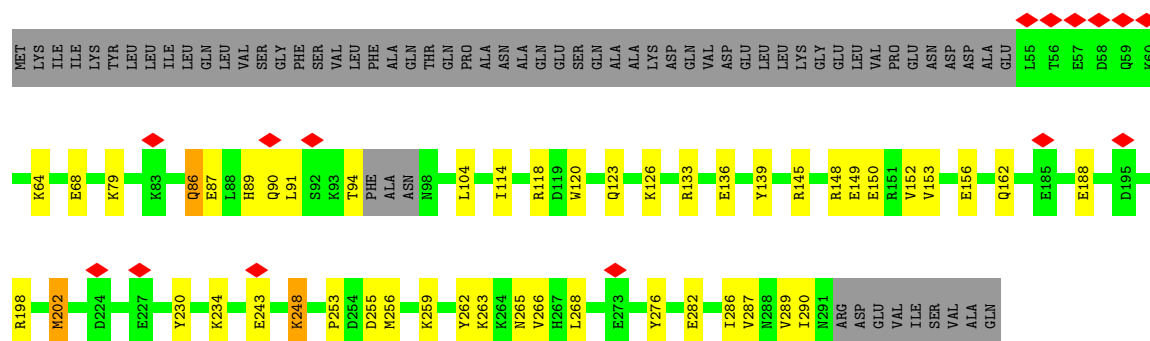


• Molecule 2: Flagellar Coiling Protein FcpA

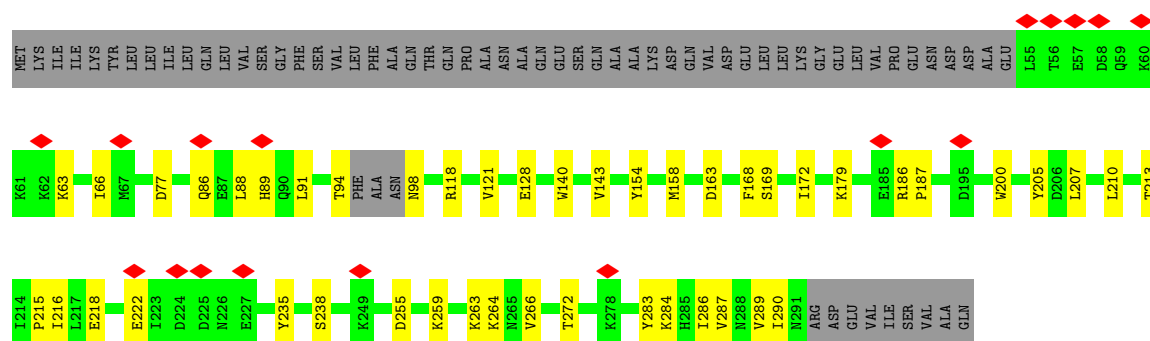


• Molecule 2: Flagellar Coiling Protein FcpA

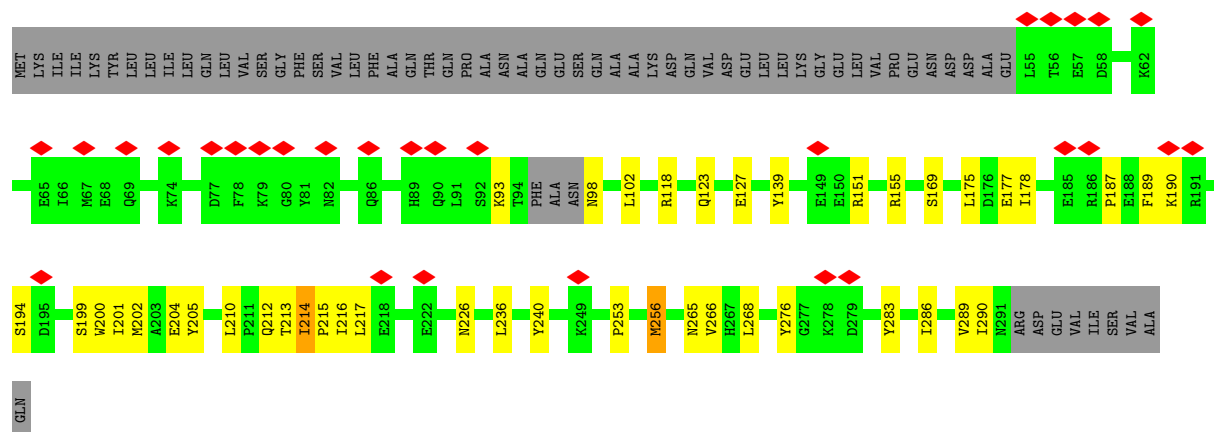




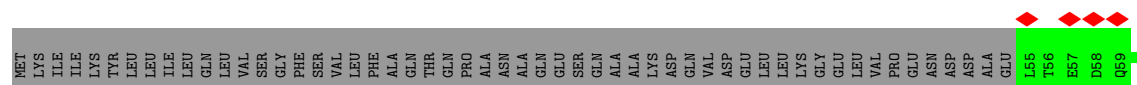
• Molecule 2: Flagellar Coiling Protein FcpA

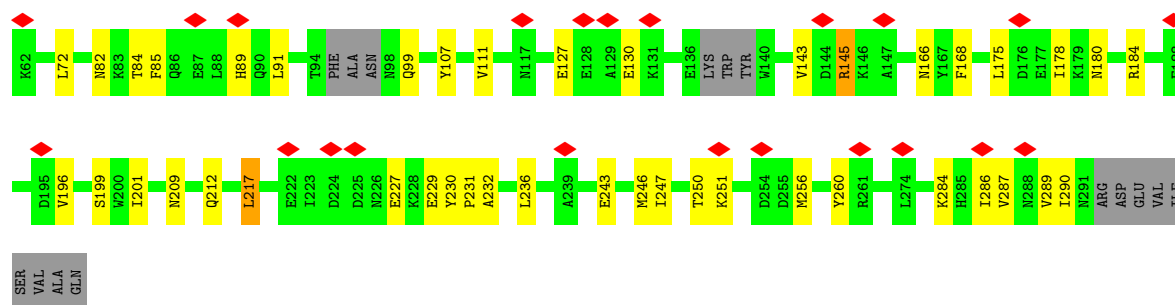


• Molecule 2: Flagellar Coiling Protein FcpA



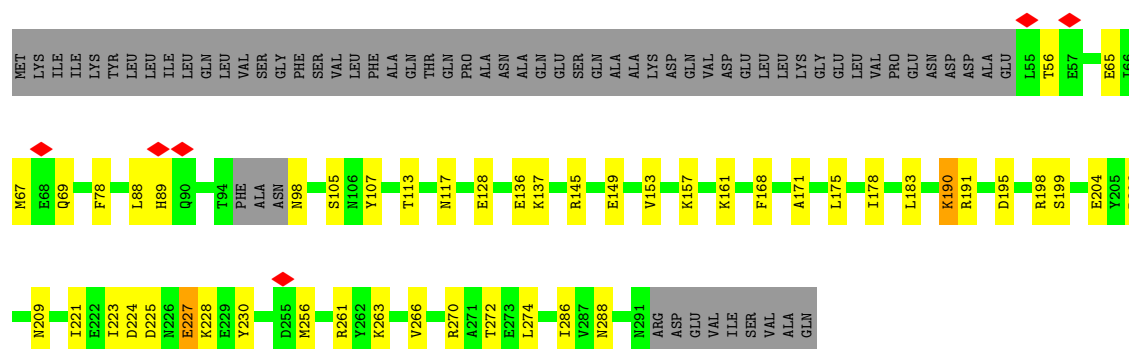
• Molecule 2: Flagellar Coiling Protein FcpA





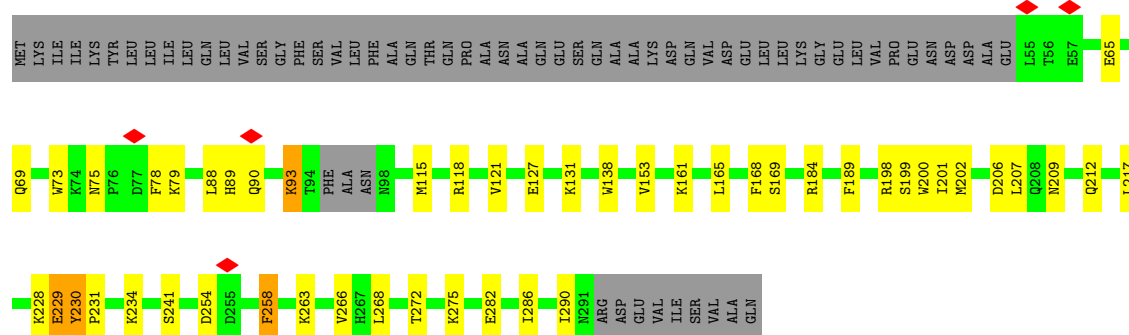
• Molecule 2: Flagellar Coiling Protein FcpA

Chain M2: 62% 16% 22%



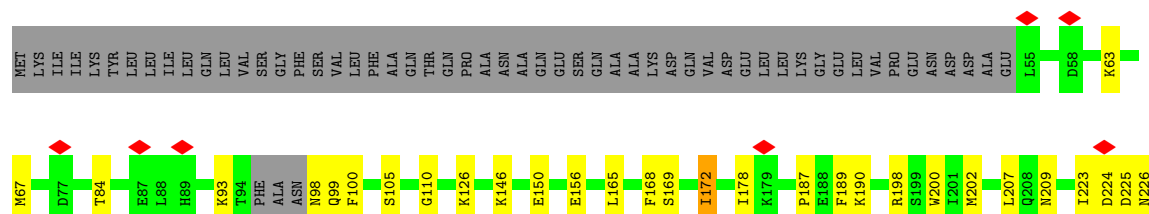
• Molecule 2: Flagellar Coiling Protein FcpA

Chain M3: 62% 15% 22%



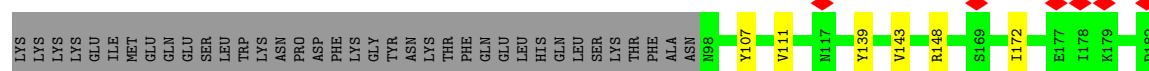
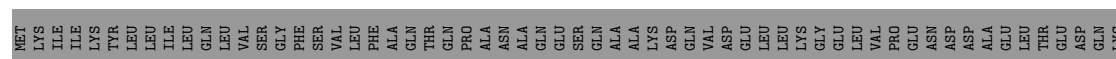
• Molecule 2: Flagellar Coiling Protein FcpA

Chain M4: 63% 15% 22%

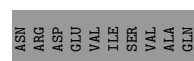
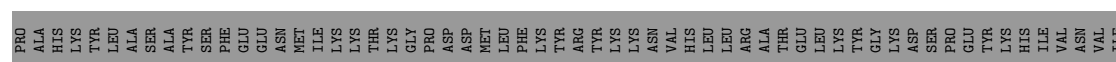
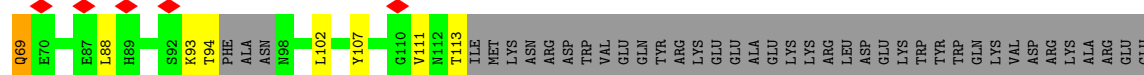
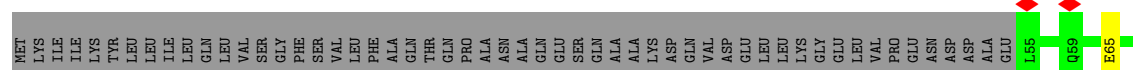




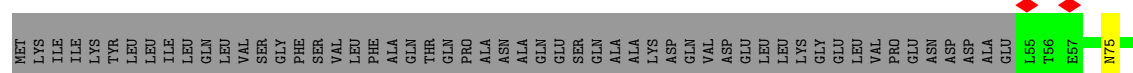
• Molecule 2: Flagellar Coiling Protein FcpA

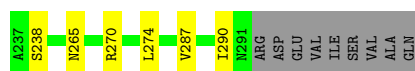


• Molecule 2: Flagellar Coiling Protein FcpA

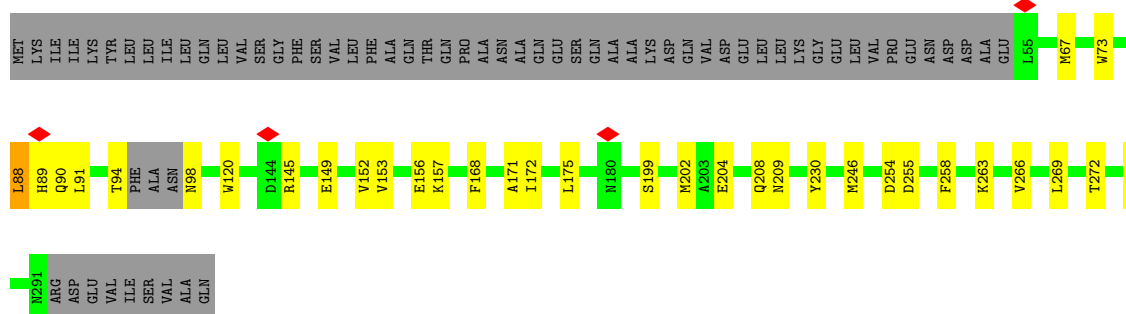


• Molecule 2: Flagellar Coiling Protein FcpA

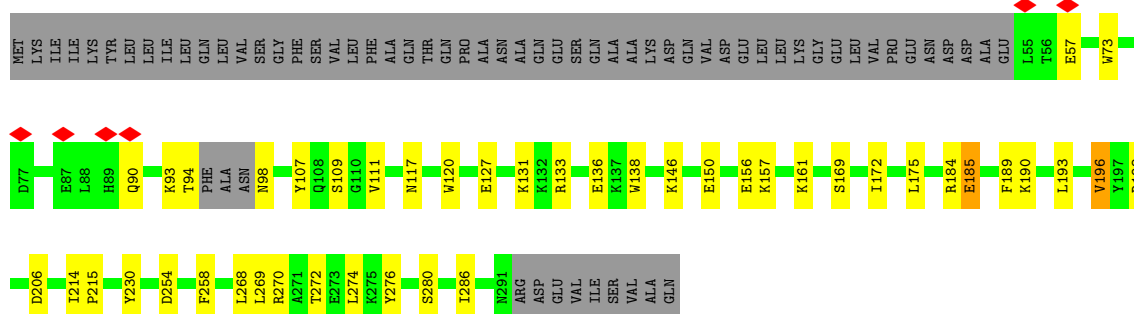




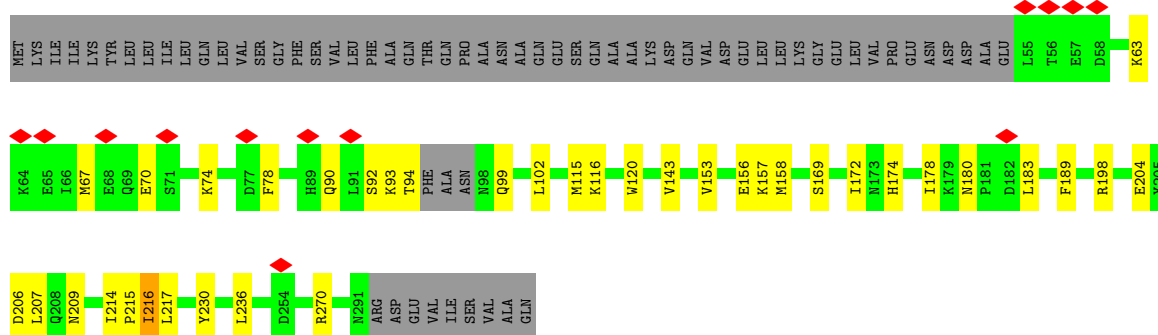
• Molecule 2: Flagellar Coiling Protein FcpA



• Molecule 2: Flagellar Coiling Protein FcpA

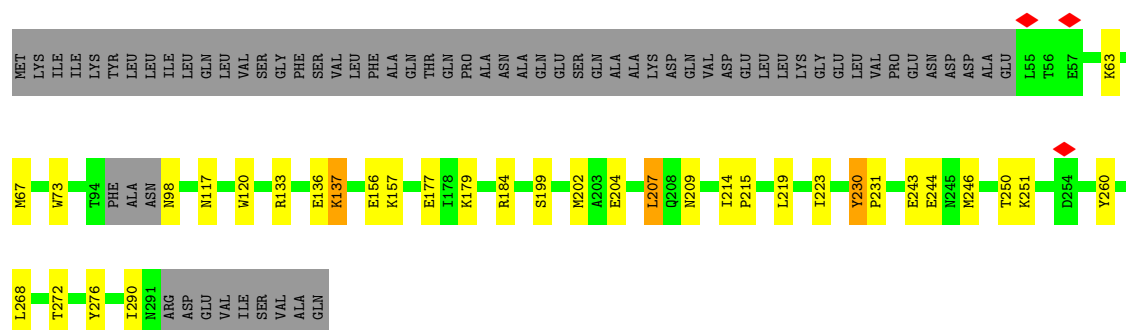


• Molecule 2: Flagellar Coiling Protein FcpA

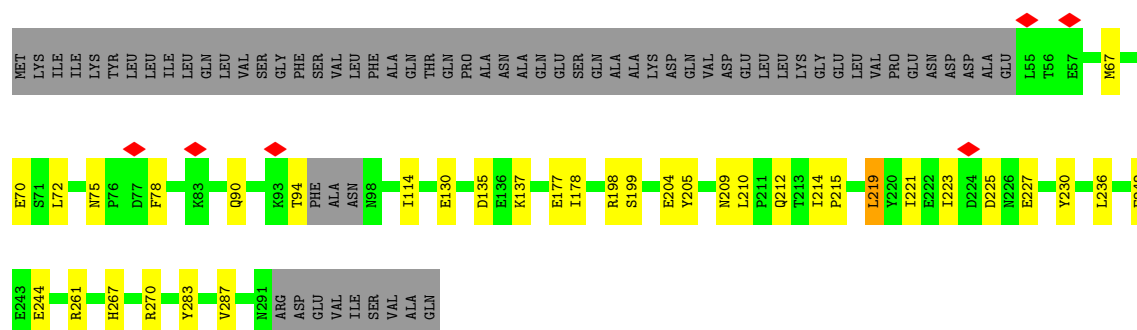


• Molecule 2: Flagellar Coiling Protein FcpA

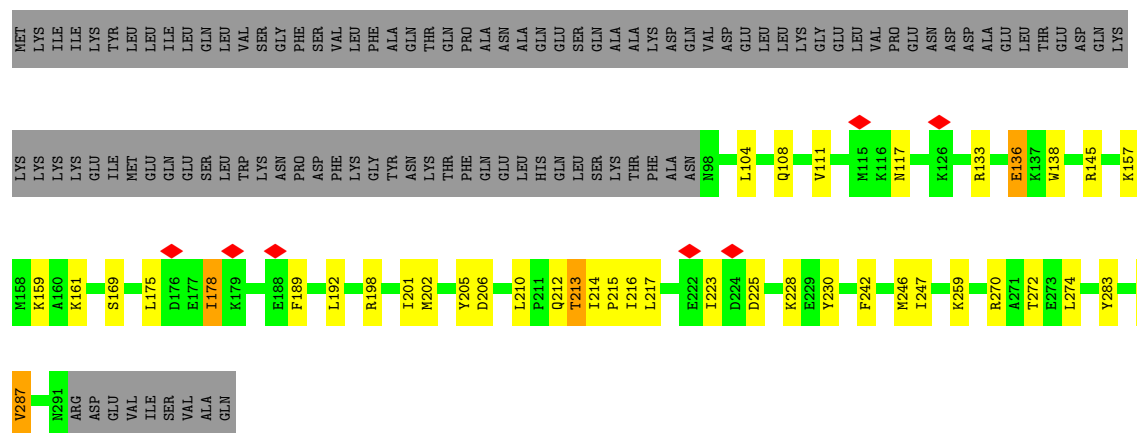




• Molecule 2: Flagellar Coiling Protein FcpA

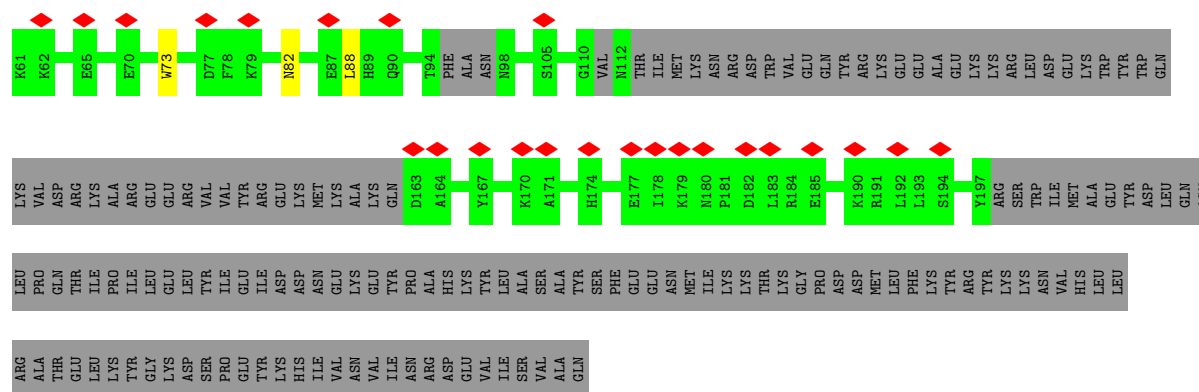


• Molecule 2: Flagellar Coiling Protein FcpA

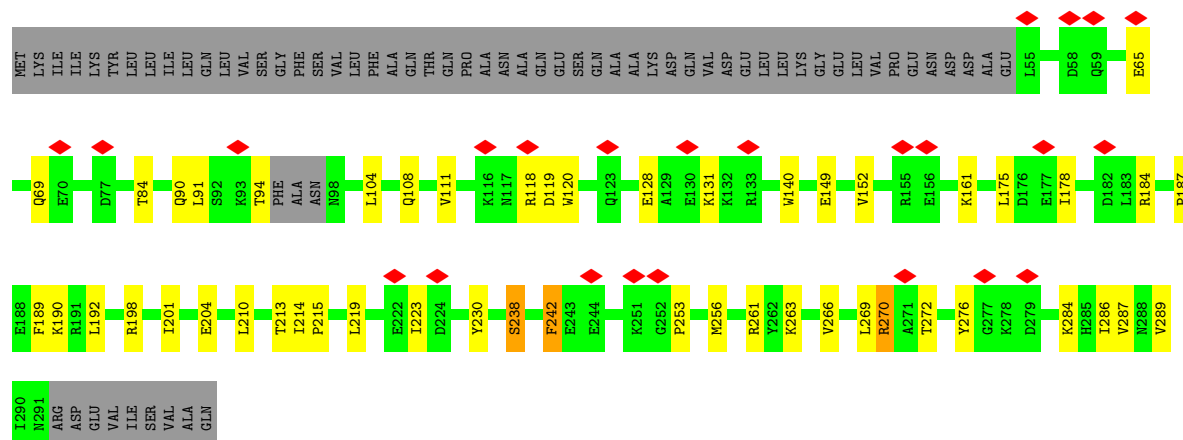


• Molecule 2: Flagellar Coiling Protein FcpA

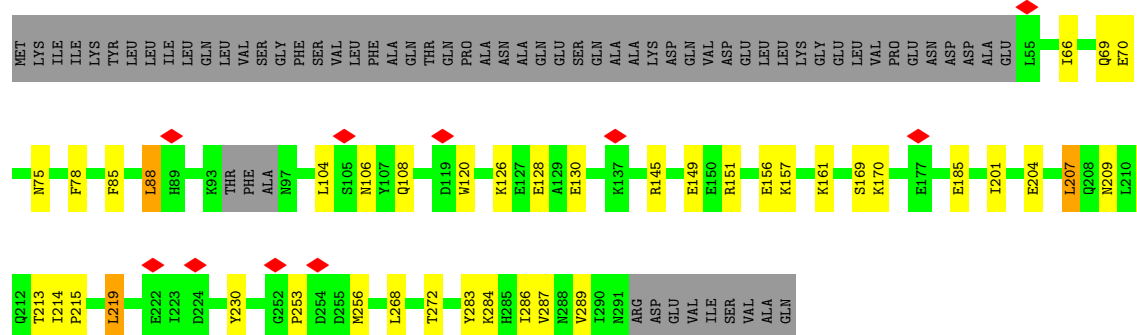




- Molecule 2: Flagellar Coiling Protein FcpA

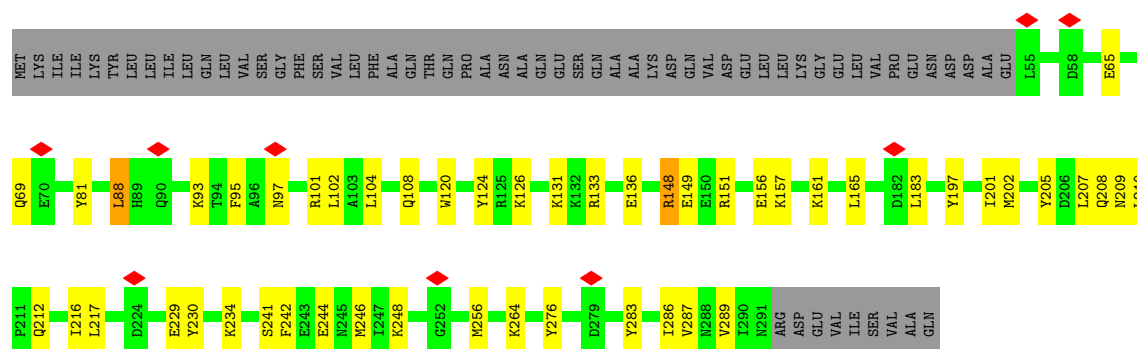


- Molecule 2: Flagellar Coiling Protein FcpA

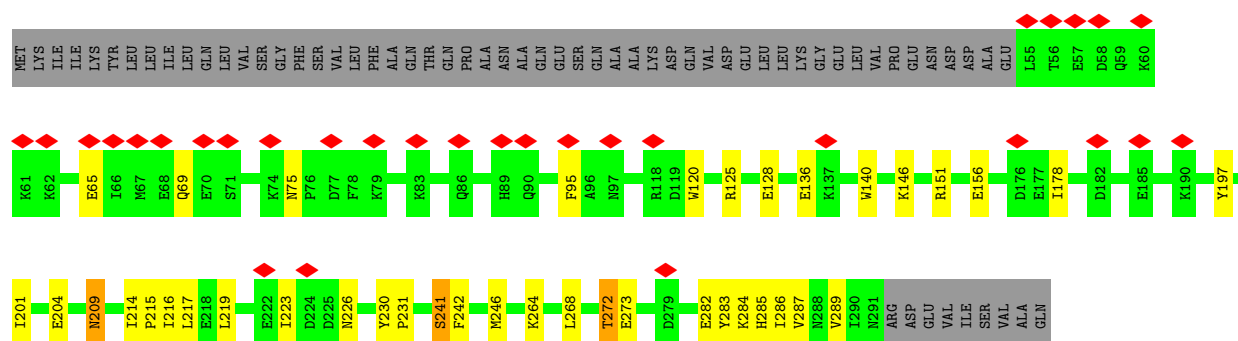


- Molecule 2: Flagellar Coiling Protein FcpA

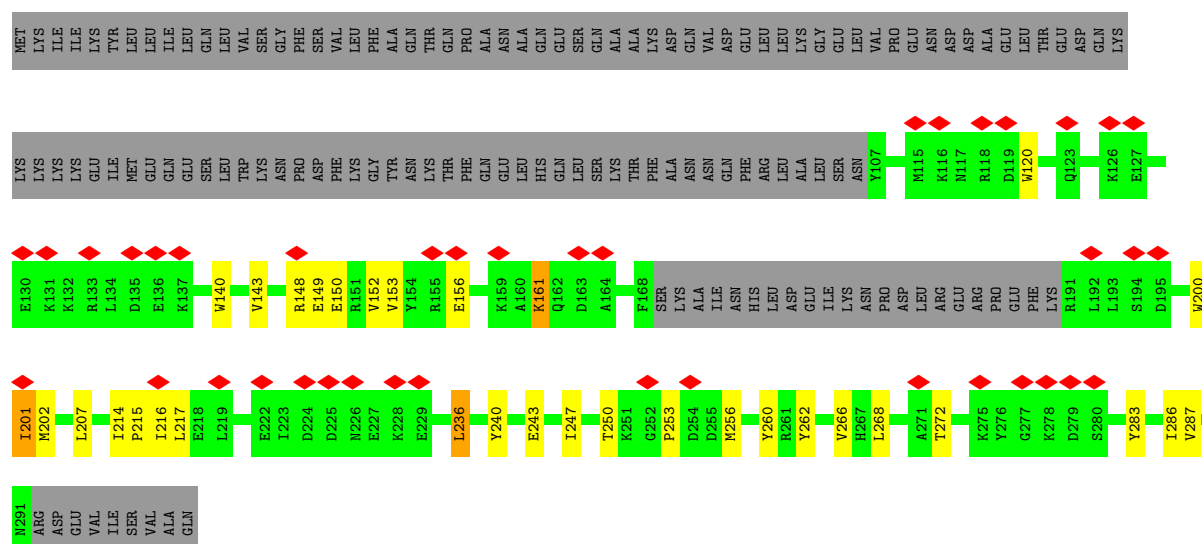
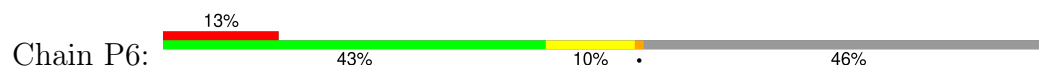




• Molecule 2: Flagellar Coiling Protein FcpA



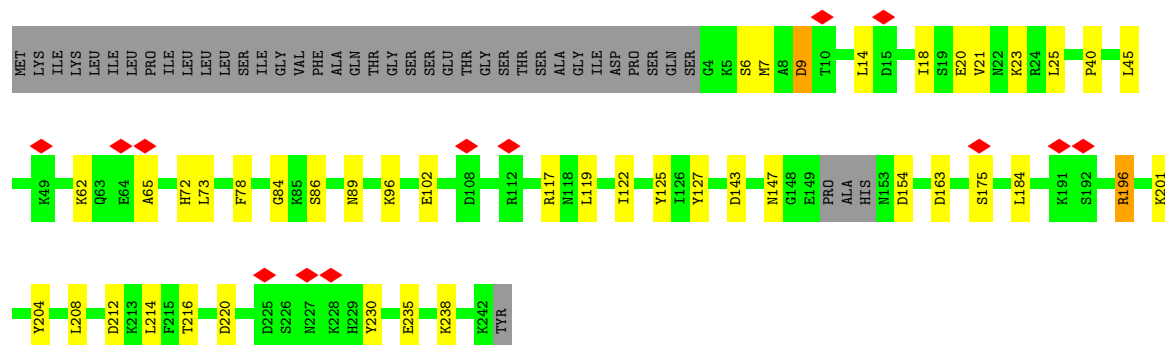
• Molecule 2: Flagellar Coiling Protein FcpA



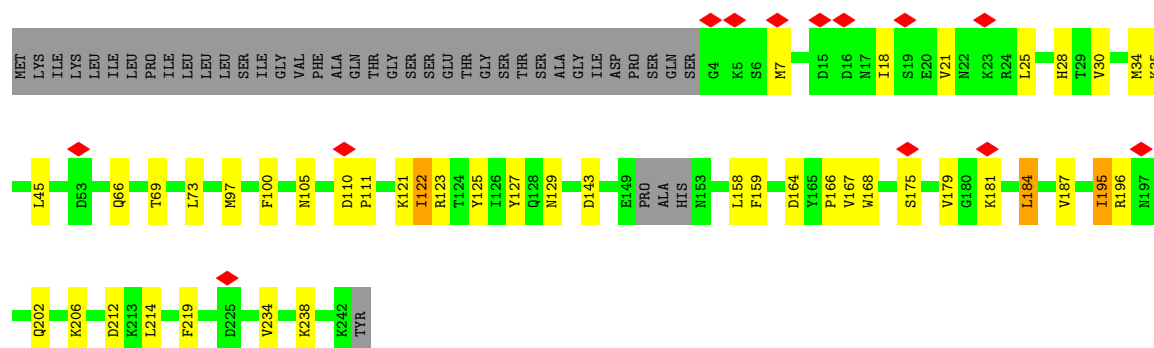
• Molecule 3: Flagellar Coiling Protein FcpB



- Molecule 3: Flagellar Coiling Protein FcpB

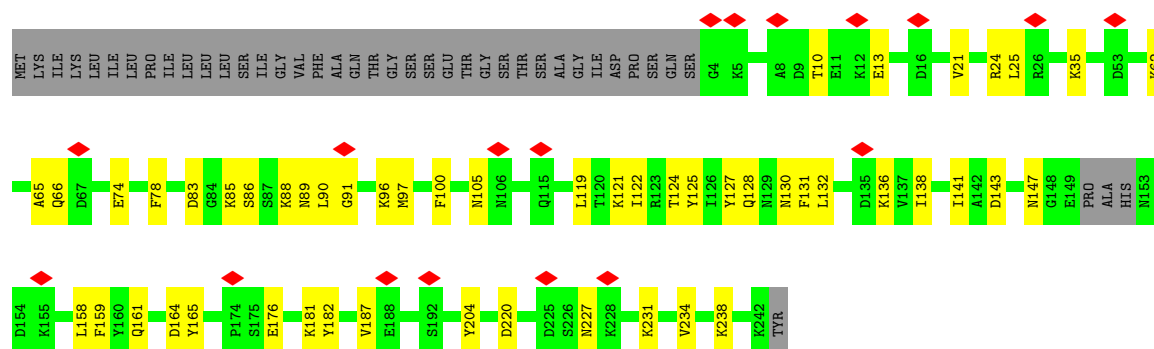


- Molecule 3: Flagellar Coiling Protein FcpB

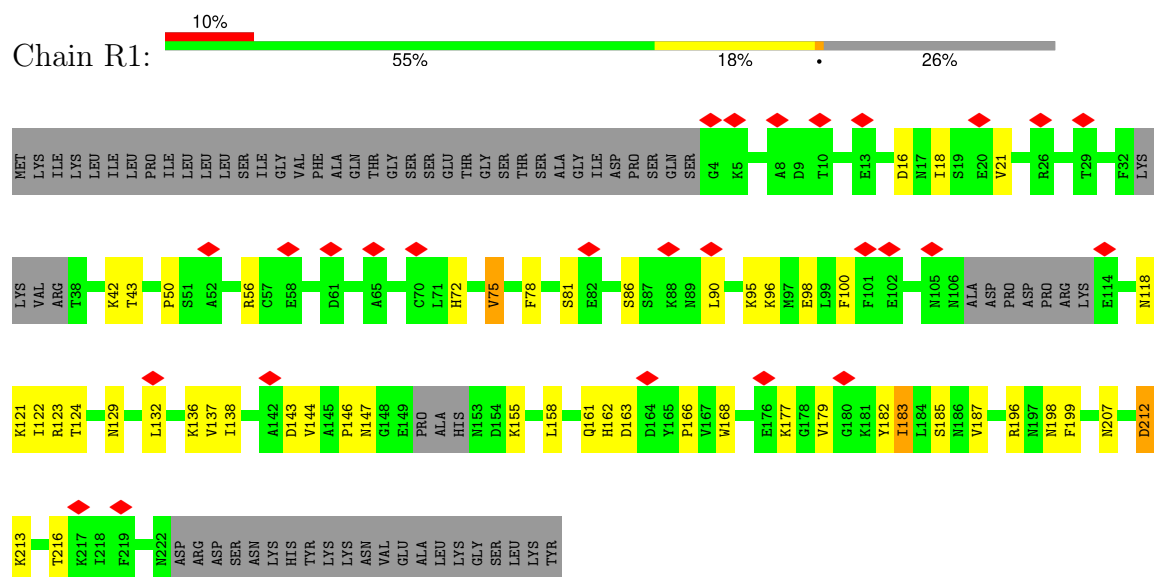


- Molecule 3: Flagellar Coiling Protein FcpB

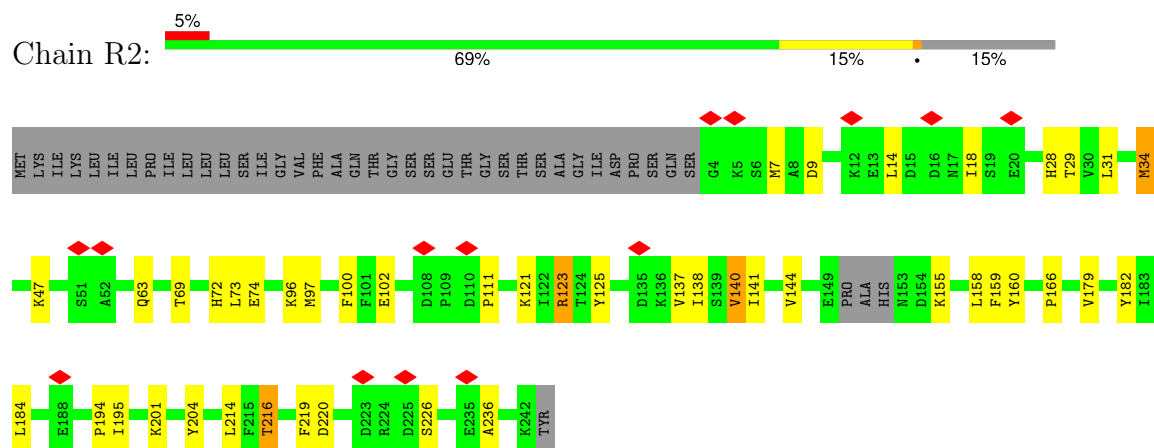




• Molecule 3: Flagellar Coiling Protein FcpB

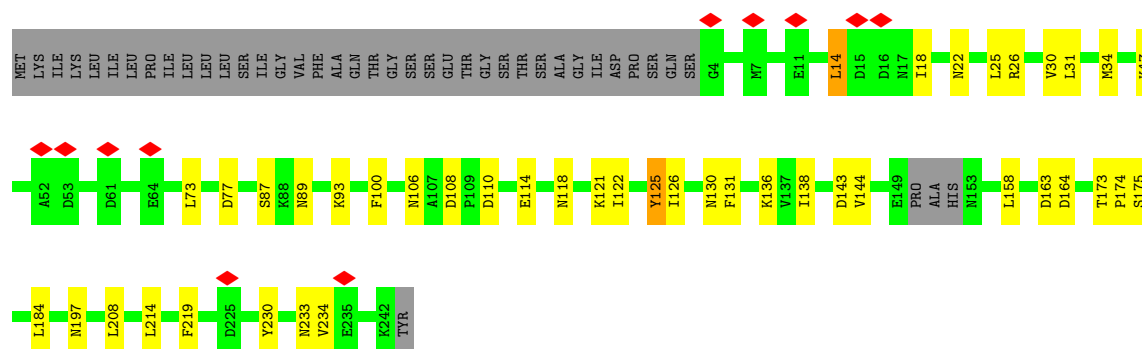


• Molecule 3: Flagellar Coiling Protein FcpB



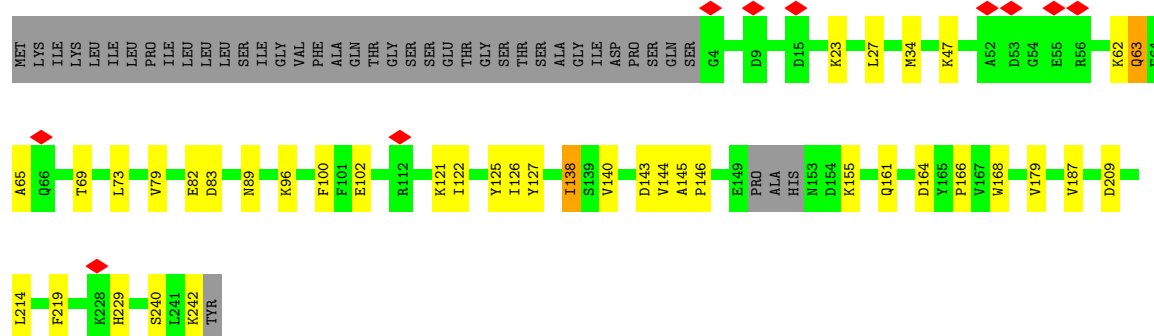
• Molecule 3: Flagellar Coiling Protein FcpB





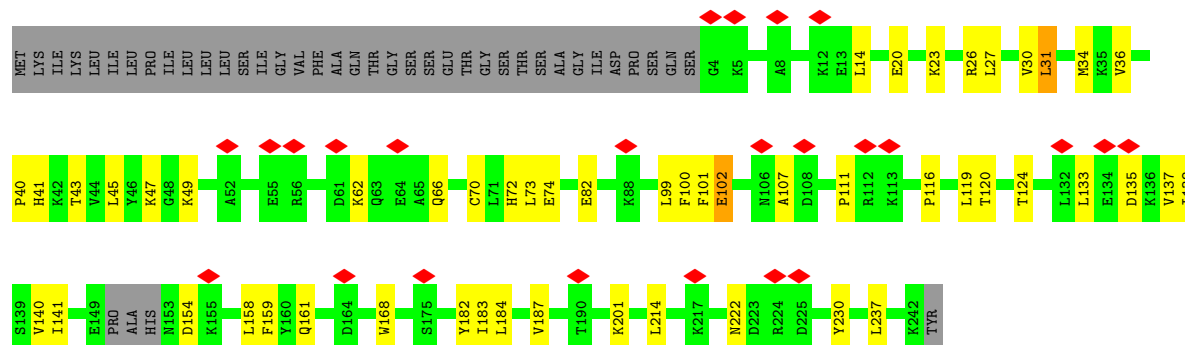
• Molecule 3: Flagellar Coiling Protein FcpB

Chain R4: 71% 14% 15%



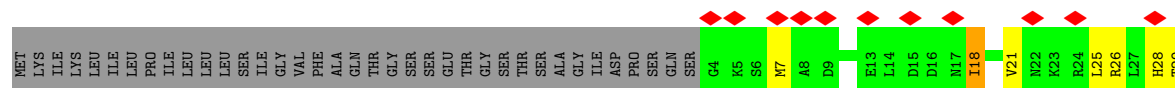
• Molecule 3: Flagellar Coiling Protein FcpB

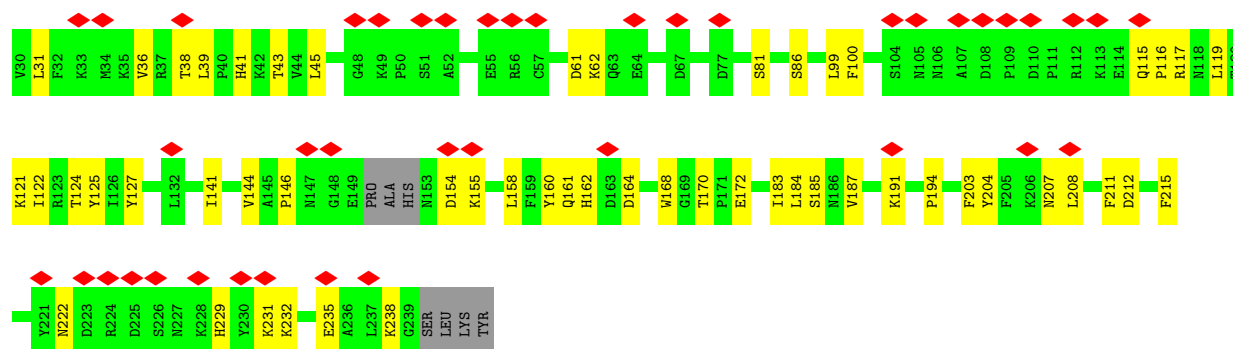
Chain R5: 9% 66% 18% 15%



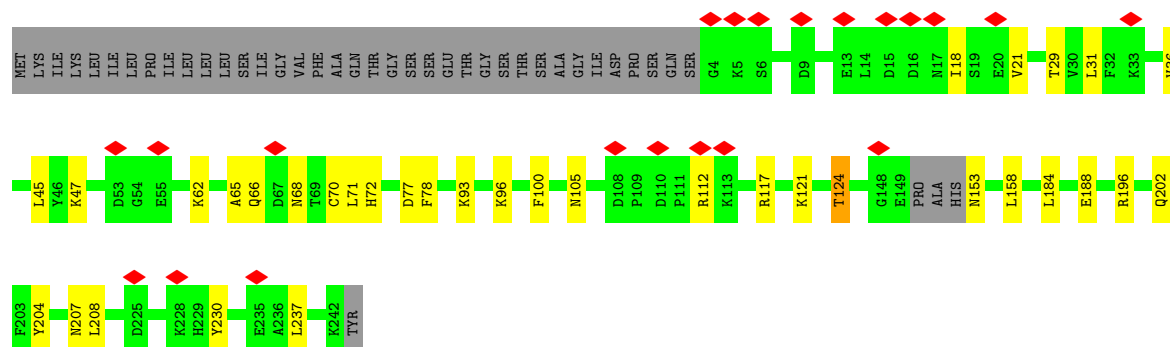
• Molecule 3: Flagellar Coiling Protein FcpB

Chain S2: 19% 62% 22% 16%

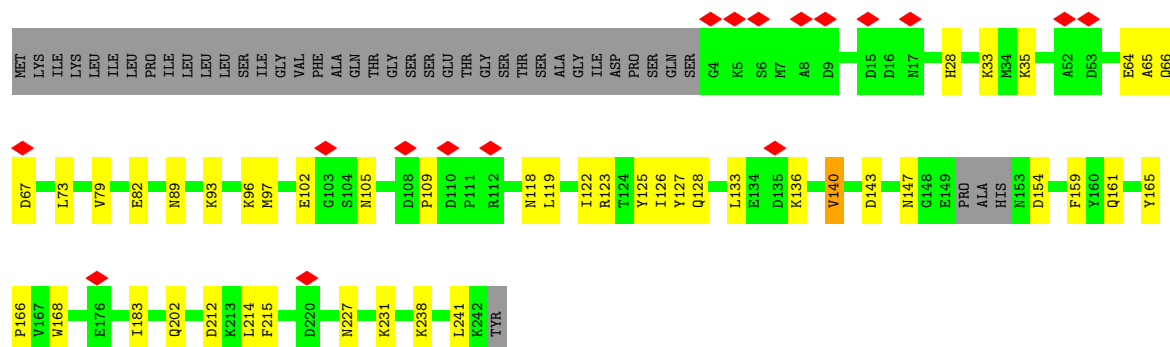




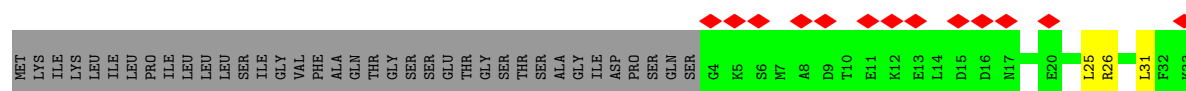
• Molecule 3: Flagellar Coiling Protein FcpB



• Molecule 3: Flagellar Coiling Protein FcpB

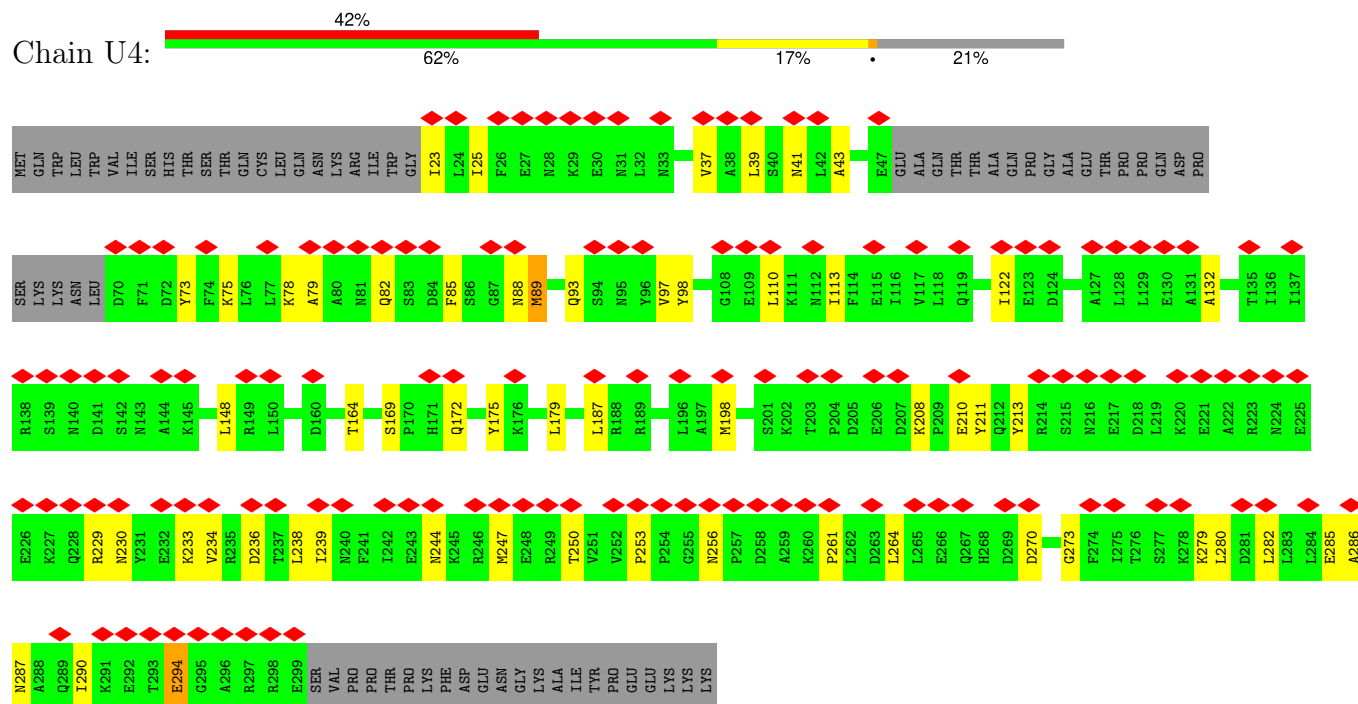


• Molecule 3: Flagellar Coiling Protein FcpB

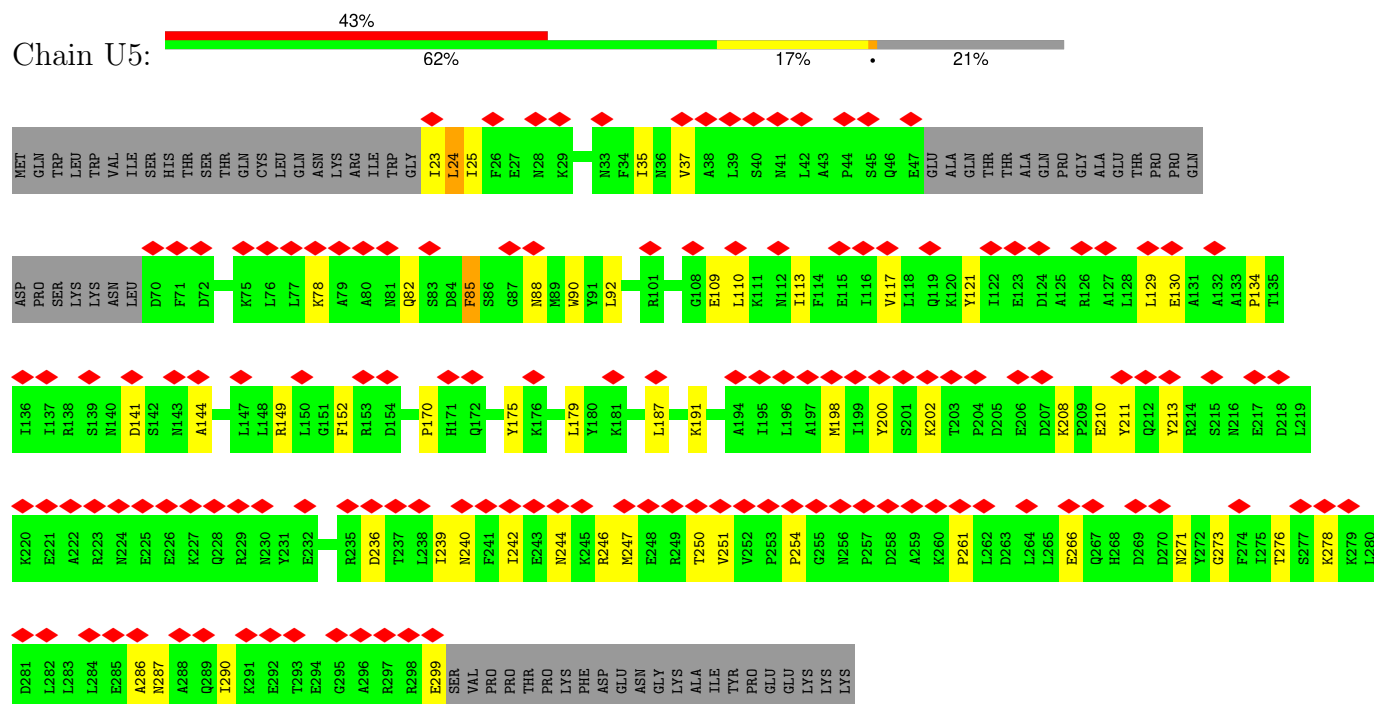


LYS

- Molecule 4: LEPBI_I1029 protein

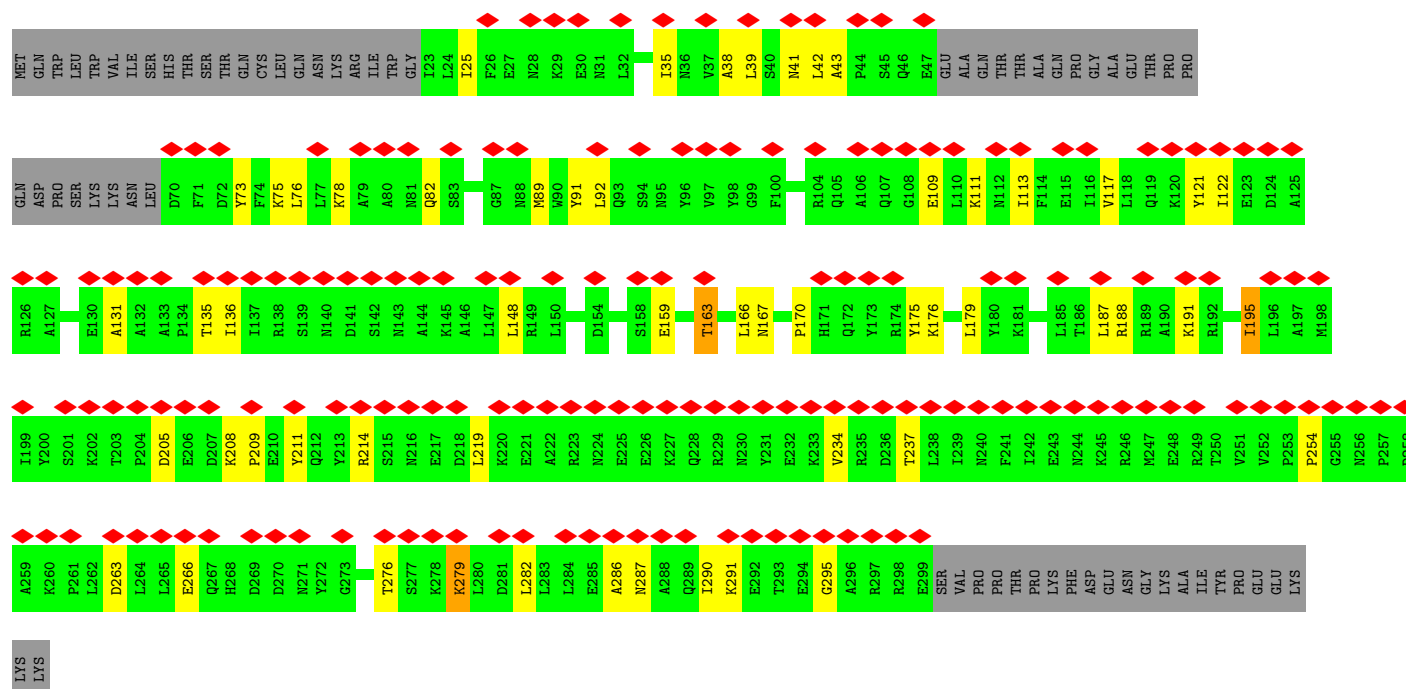


- Molecule 4: LEPBI_I1029 protein

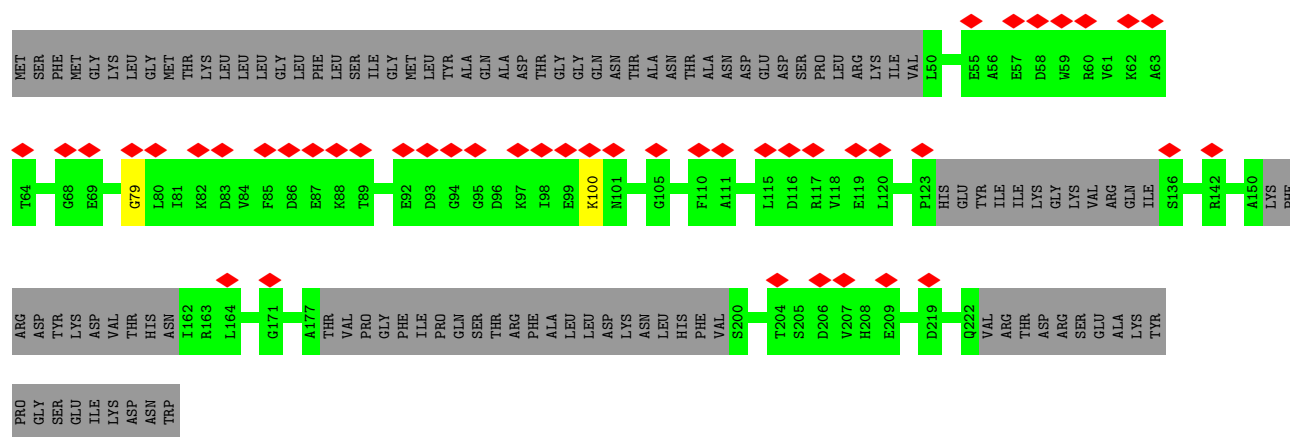


- Molecule 4: LEPBI_I1029 protein

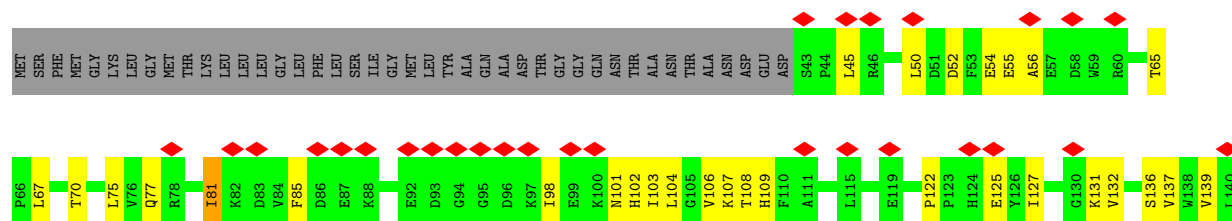




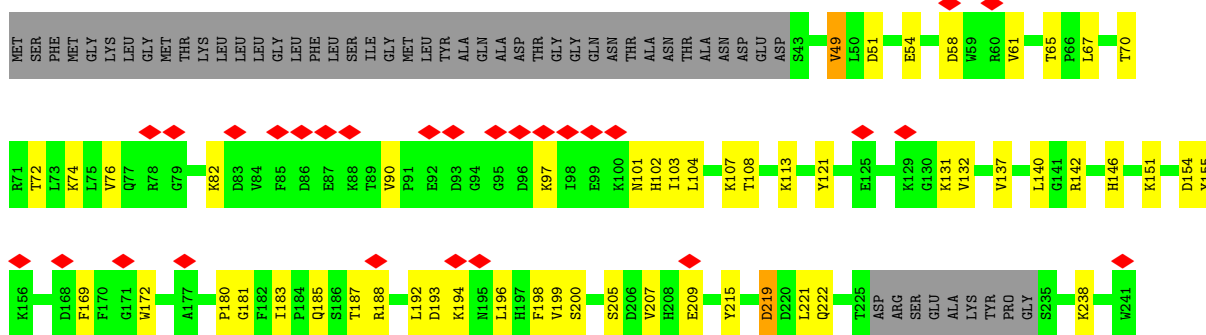
- Molecule 5: Flagellar filament outer layer protein (Sheath protein) putative signal peptide



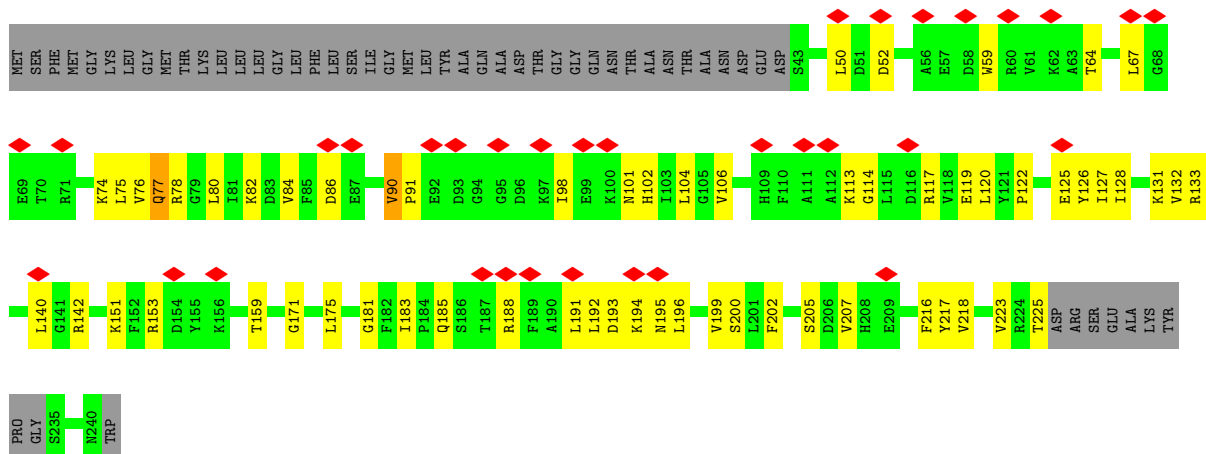
- Molecule 5: Flagellar filament outer layer protein (Sheath protein) putative signal peptide



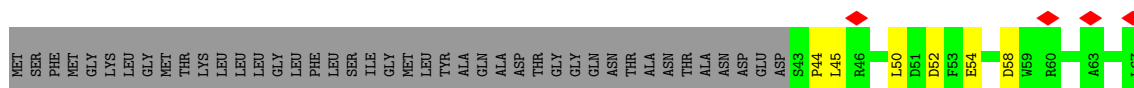
- Molecule 5: Flagellar filament outer layer protein (Sheath protein) putative signal peptide

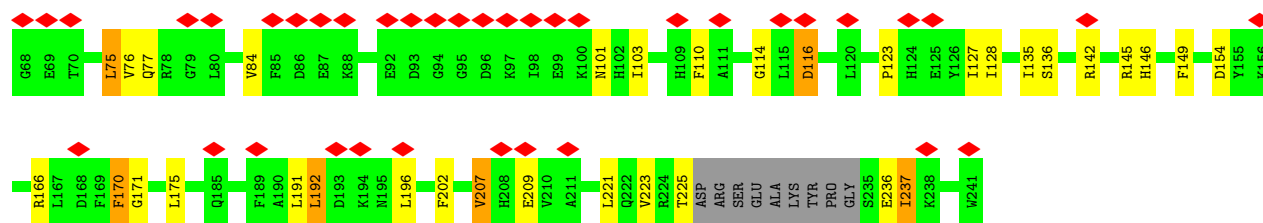


- Molecule 5: Flagellar filament outer layer protein (Sheath protein) putative signal peptide

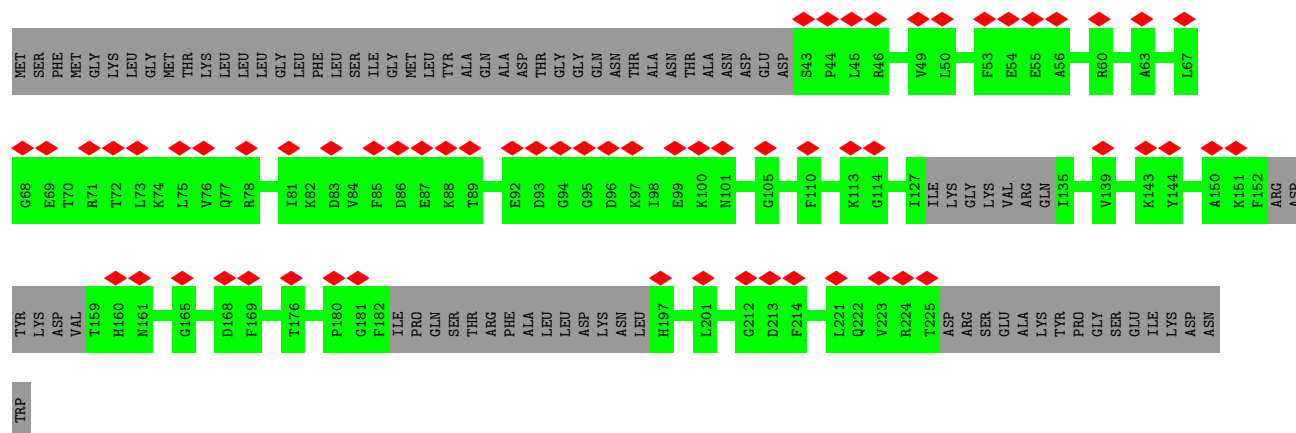


- Molecule 5: Flagellar filament outer layer protein (Sheath protein) putative signal peptide

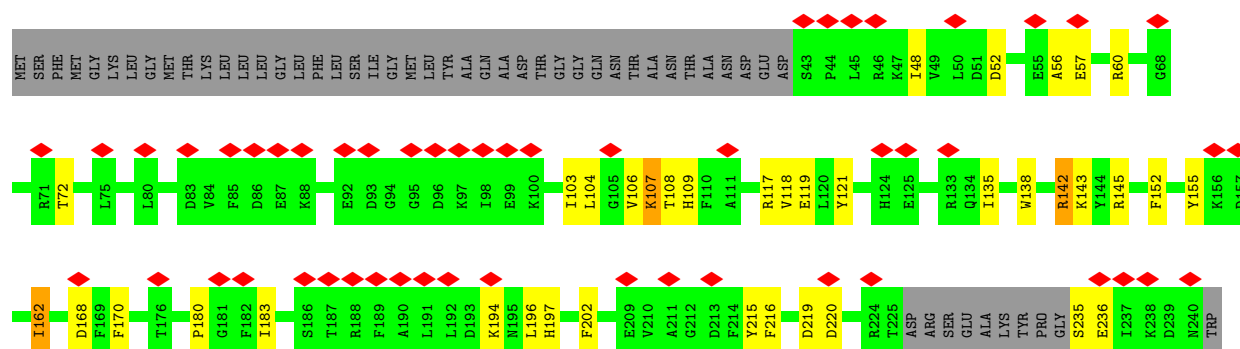




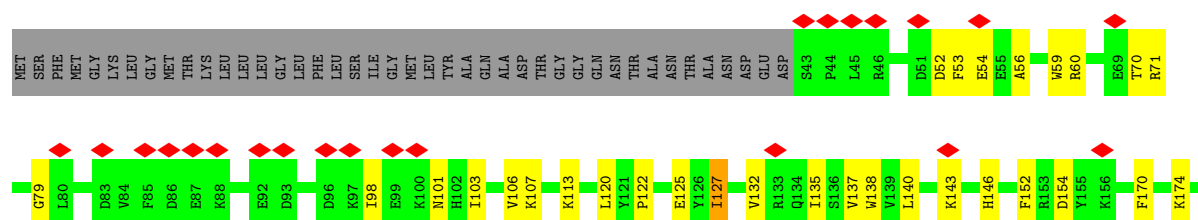
- Molecule 5: Flagellar filament outer layer protein (Sheath protein) putative signal peptide

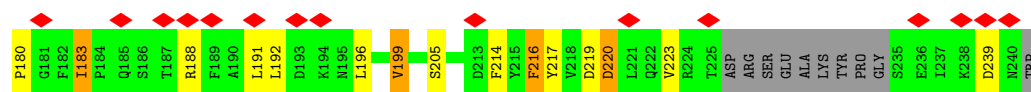


- Molecule 5: Flagellar filament outer layer protein (Sheath protein) putative signal peptide

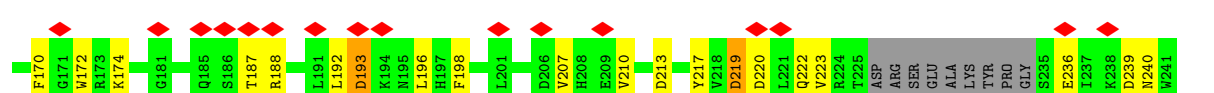
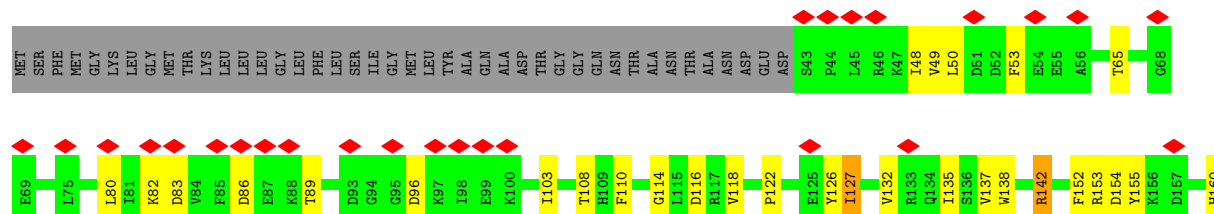


- Molecule 5: Flagellar filament outer layer protein (Sheath protein) putative signal peptide

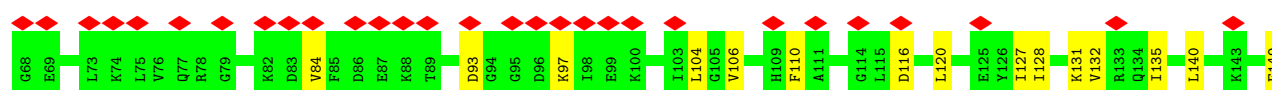
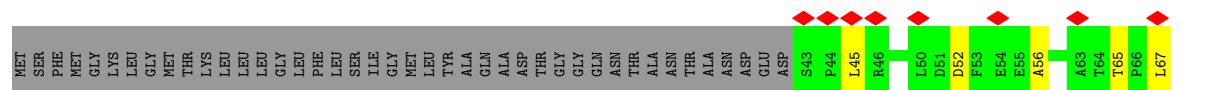




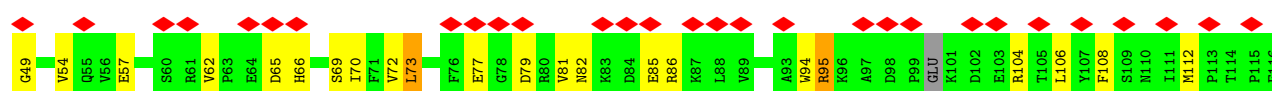
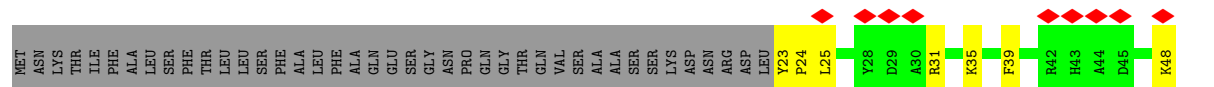
- Molecule 5: Flagellar filament outer layer protein (Sheath protein) putative signal peptide

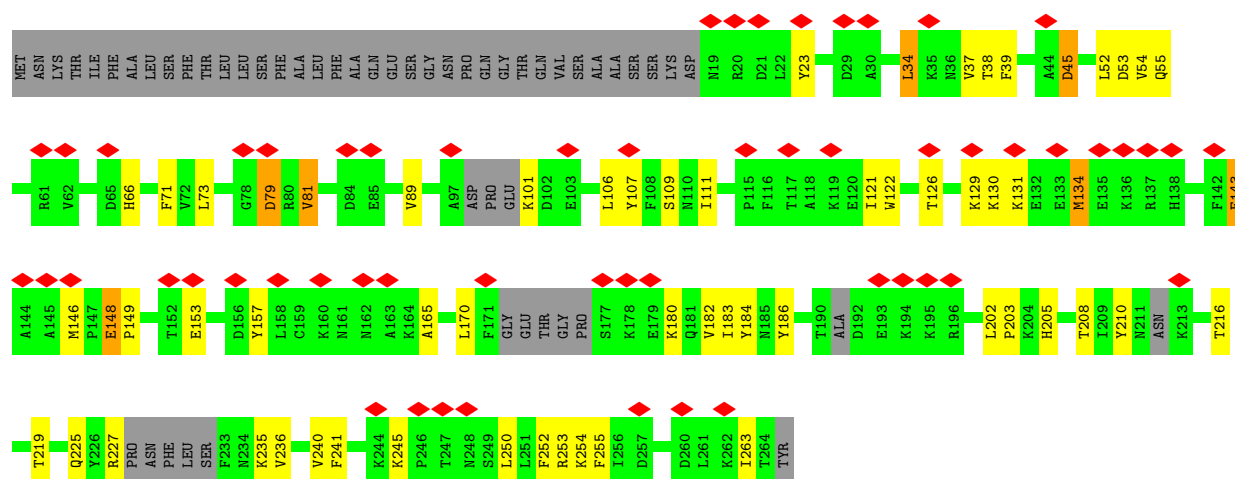


- Molecule 5: Flagellar filament outer layer protein (Sheath protein) putative signal peptide

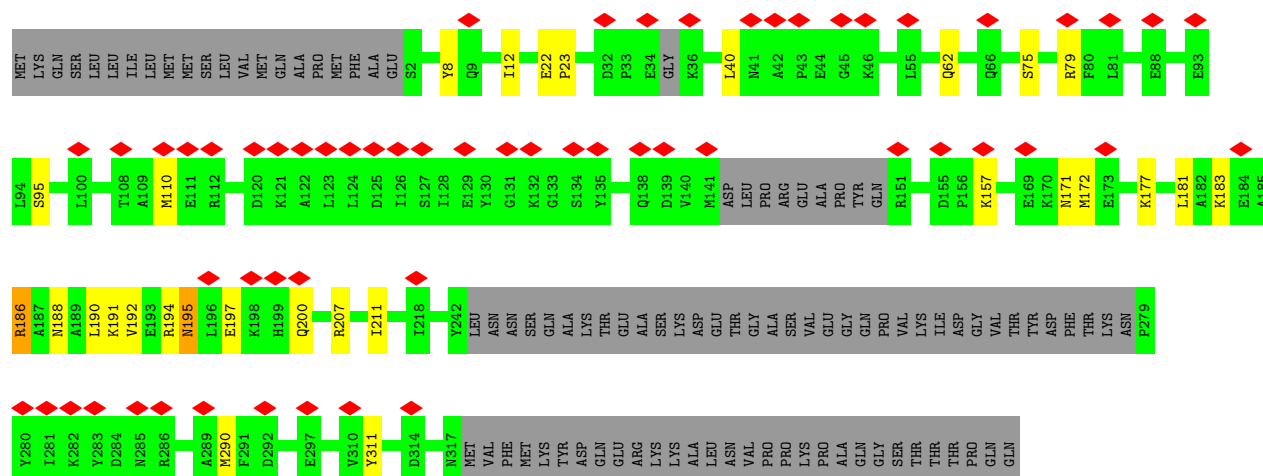


- Molecule 6: FlaA2 associated protein B0STF2

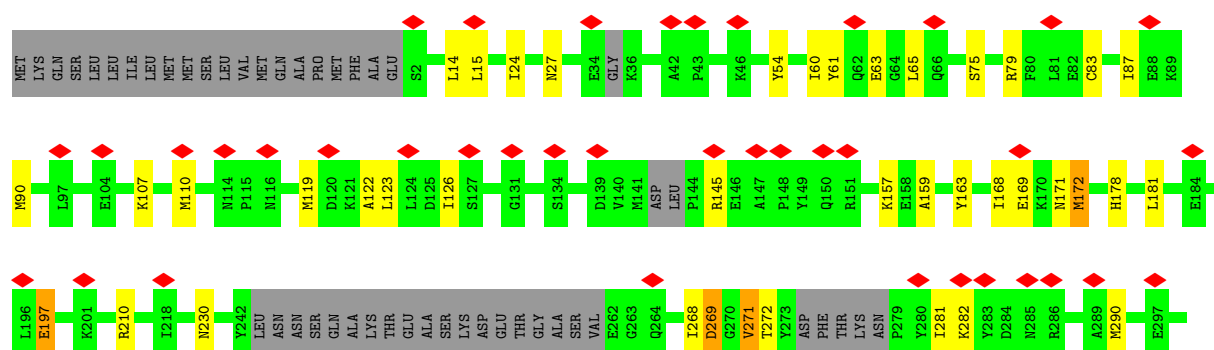


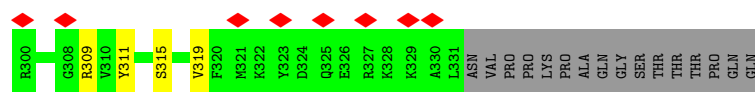


• Molecule 7: FlaA2-associated protein FlaAP



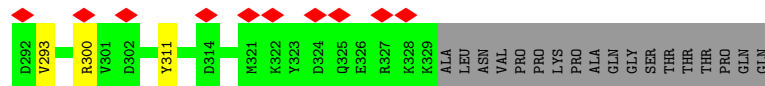
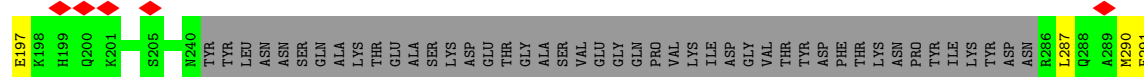
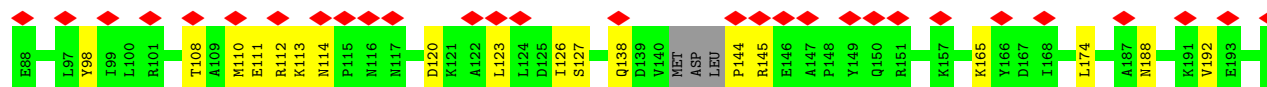
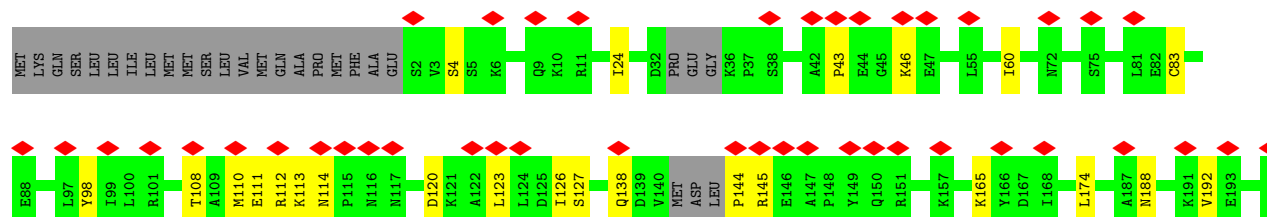
• Molecule 7: FlaA2-associated protein FlaAP





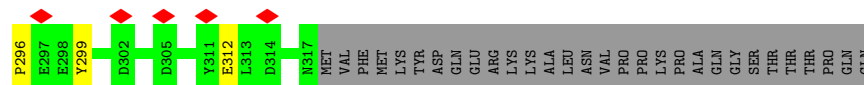
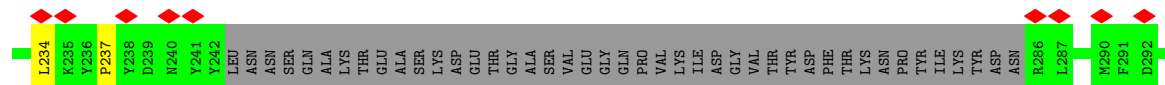
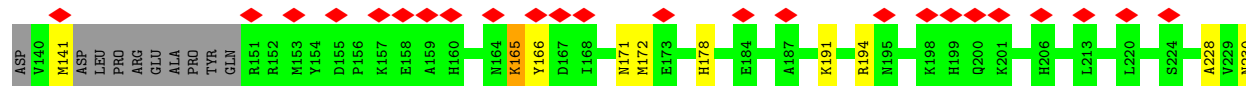
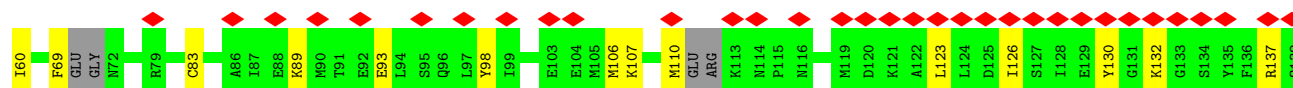
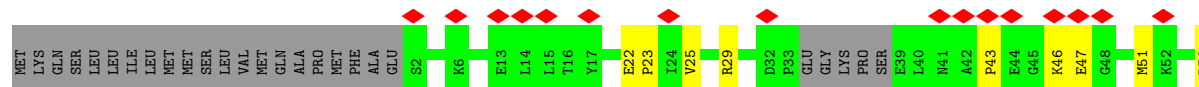
• Molecule 7: FlaA2-associated protein FlaAP

Chain Z2: 16% 67% 8% 25%



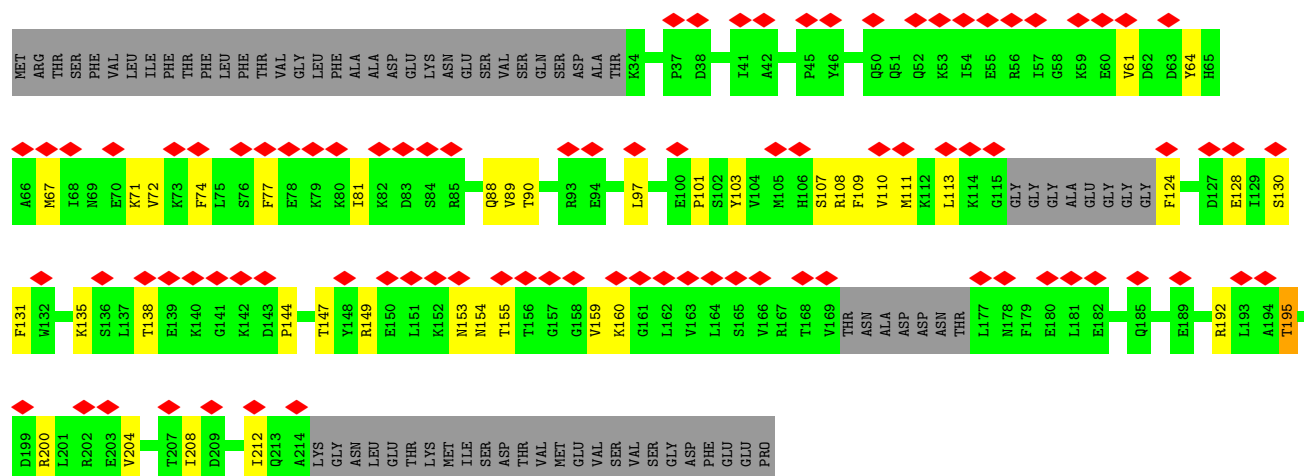
• Molecule 7: FlaA2-associated protein FlaAP

Chain Za: 24% 59% 10% 31%

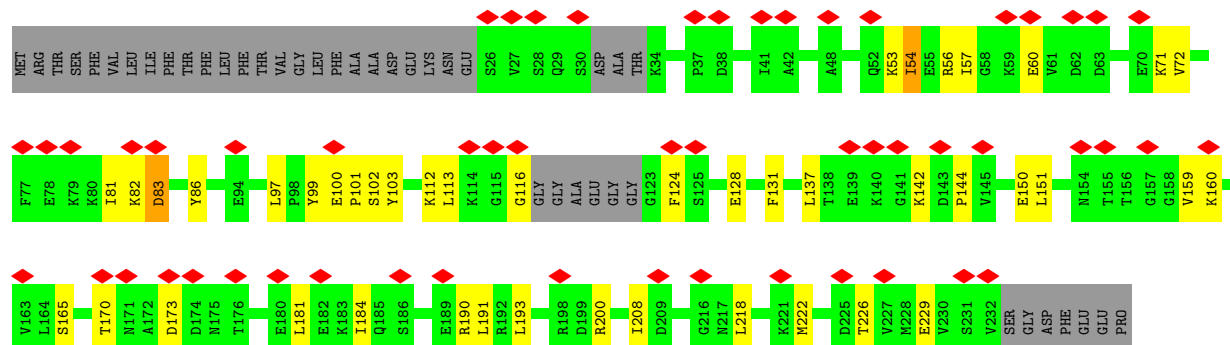


• Molecule 8: LEPBI_I3081 protein

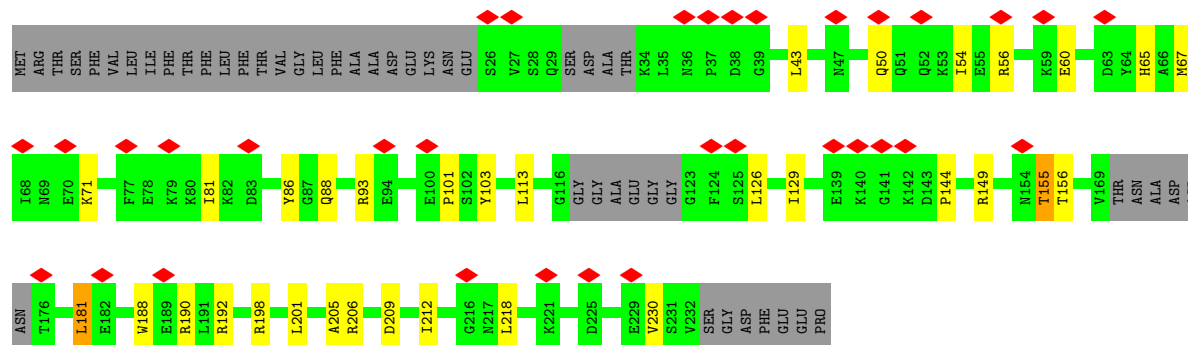
Chain a1: 37% 53% 16% 31%



• Molecule 8: LEPBI_I3081 protein

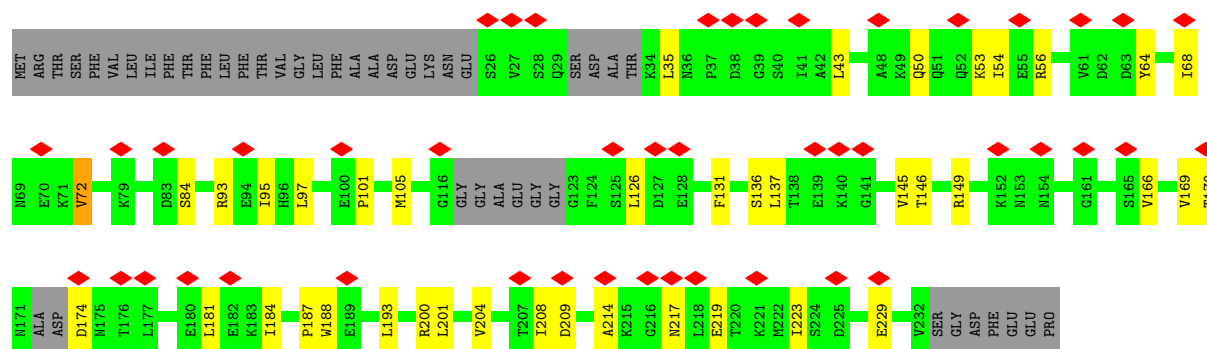


• Molecule 8: LEPBI_I3081 protein

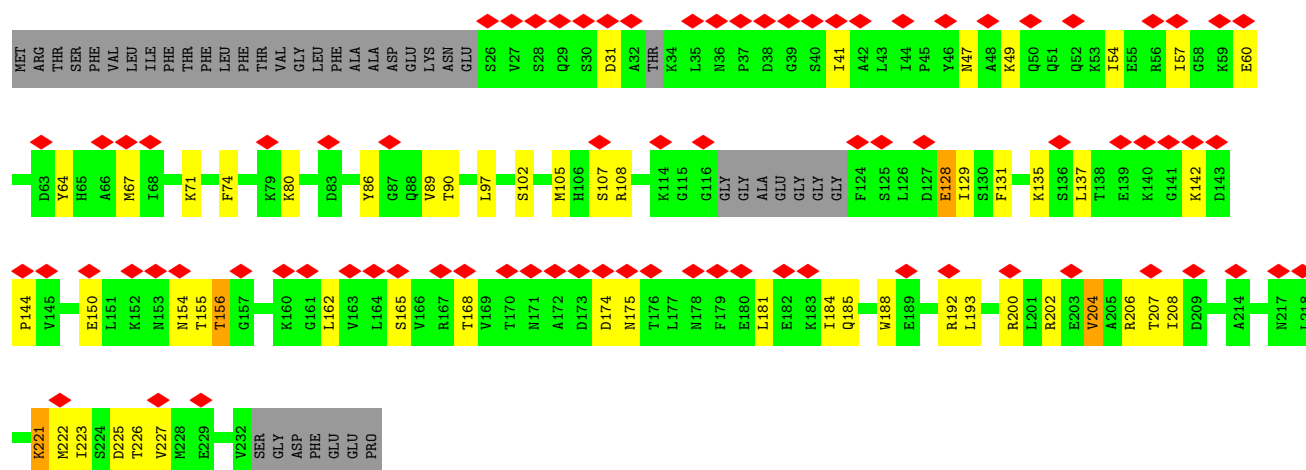


• Molecule 8: LEPBI_I3081 protein

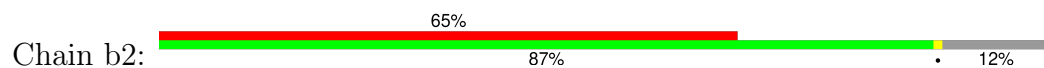




• Molecule 8: LEPBI_I3081 protein

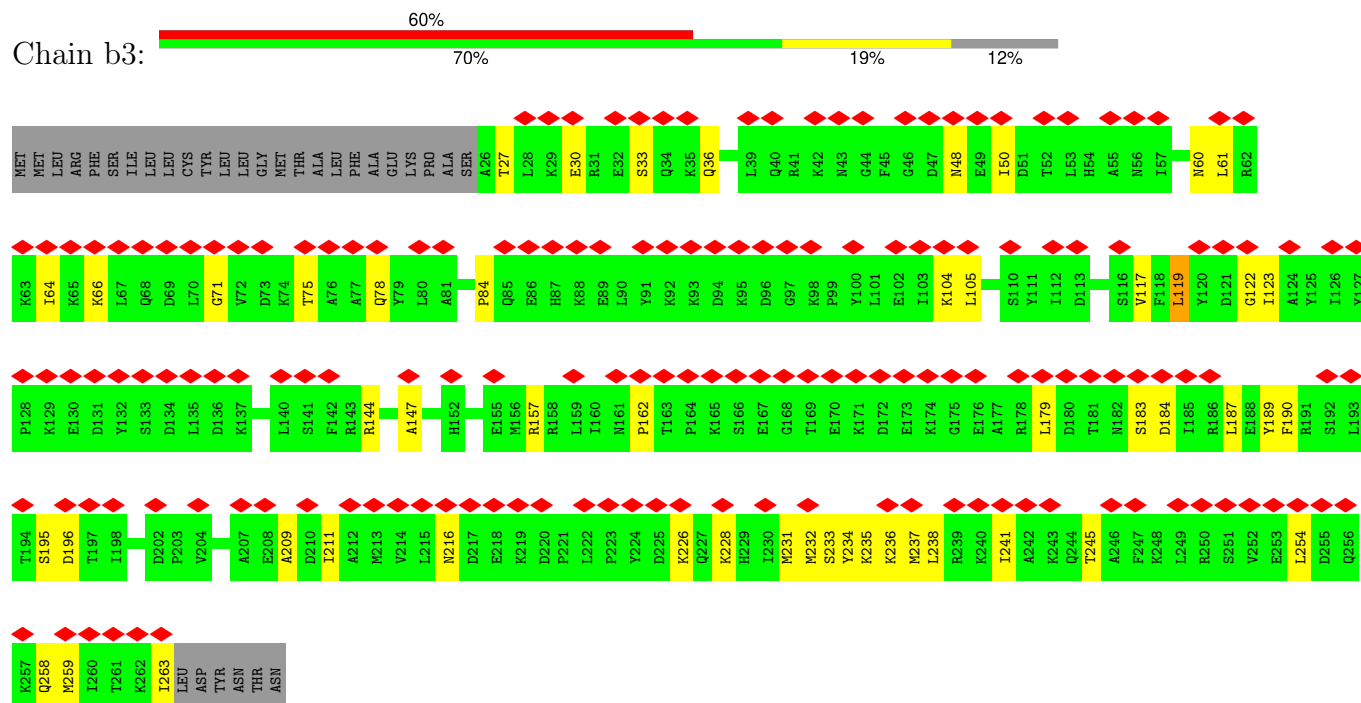


• Molecule 9: LEPBI_I0662 protein



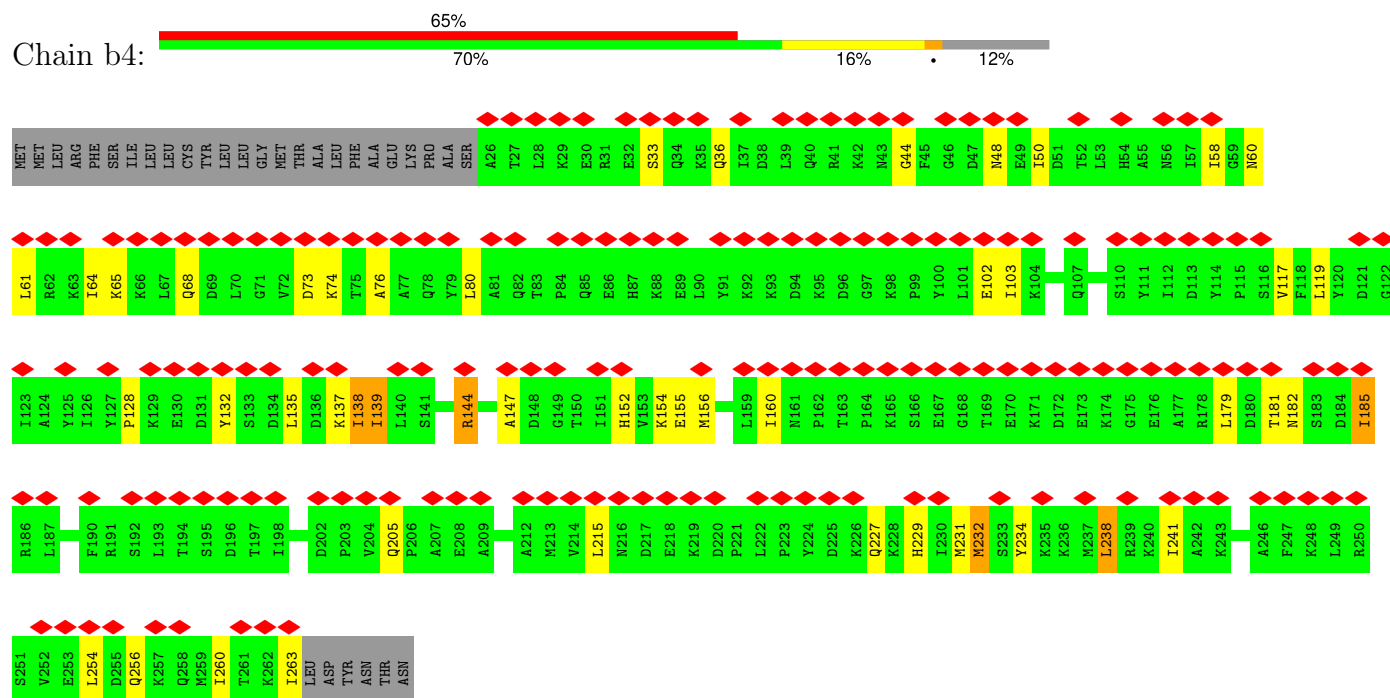
- Molecule 9: LEPBI_I0662 protein

Chain b3:



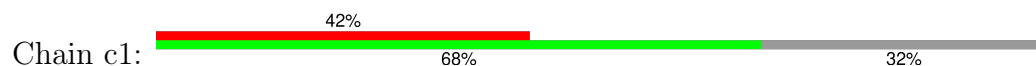
- Molecule 9: LEPBI_I0662 protein

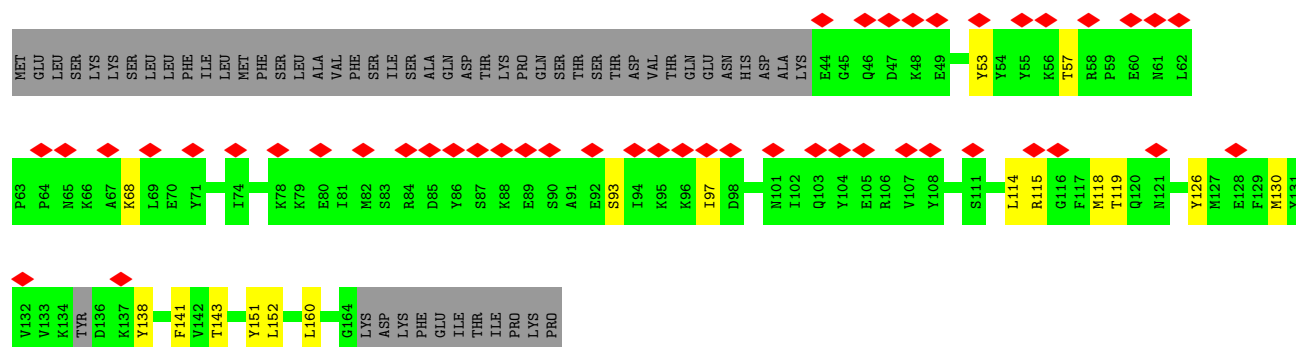
Chain b4:



- Molecule 10: LEPBI_II0033 protein

Chain c1:





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	176558	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25.7	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.994	Depositor
Minimum map value	-0.506	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	273.408, 273.408, 273.408	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

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

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	A3	0.21	0/704	0.50	0/937
1	A4	0.19	0/1797	0.45	0/2404
1	A5	0.21	0/2198	0.48	0/2953
1	A6	0.22	0/2198	0.47	0/2953
1	A7	0.22	0/2198	0.46	0/2953
1	A8	0.20	0/1728	0.44	0/2323
1	B3	0.20	0/968	0.45	0/1291
1	B4	0.24	0/2198	0.50	0/2954
1	B5	0.23	0/2206	0.52	0/2965
1	B6	0.23	0/2206	0.46	0/2965
1	B7	0.23	0/2057	0.49	0/2768
1	B8	0.19	0/1387	0.46	0/1868
1	C2	0.20	0/549	0.41	0/730
1	C3	0.21	0/1556	0.49	0/2077
1	C4	0.22	0/2198	0.47	0/2953
1	C5	0.22	0/2206	0.48	0/2965
1	C6	0.22	0/2206	0.44	0/2965
1	C7	0.19	0/1788	0.43	0/2402
1	C8	0.16	0/963	0.41	0/1302
1	D2	0.19	0/885	0.39	0/1181
1	D3	0.22	0/2085	0.48	0/2795
1	D4	0.22	0/2198	0.44	0/2953
1	D5	0.23	0/2198	0.47	0/2953
1	D6	0.22	0/2082	0.47	0/2799
1	D7	0.19	0/1425	0.43	0/1920
1	E1	0.22	0/480	0.46	0/637
1	E2	0.20	0/1443	0.44	0/1924
1	E3	0.23	0/2198	0.47	0/2953
1	E4	0.25	0/2198	0.49	0/2953
1	E5	0.24	0/2198	0.48	0/2953
1	E6	0.22	0/1849	0.45	0/2485
1	E7	0.20	0/988	0.51	0/1335

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	F1	0.24	0/821	0.48	0/1096
1	F2	0.22	0/1970	0.50	0/2640
1	F3	0.25	0/2206	0.47	0/2965
1	F4	0.25	0/2198	0.49	0/2953
1	F5	0.25	0/2112	0.48	0/2839
1	F6	0.22	0/1456	0.49	0/1963
1	G1	0.24	0/1886	0.49	0/2535
1	G2	0.19	0/1069	0.43	0/1441
1	G5	0.21	0/431	0.51	0/571
1	G6	0.22	0/1330	0.53	0/1769
1	G7	0.24	0/2206	0.51	0/2965
1	G8	0.25	0/2206	0.49	0/2965
1	G9	0.24	0/2198	0.46	0/2953
1	H5	0.19	0/788	0.41	0/1050
1	H6	0.21	0/1913	0.43	0/2564
1	H7	0.22	0/2198	0.48	0/2953
1	H8	0.23	0/2206	0.49	0/2965
1	H9	0.22	0/2160	0.47	0/2904
1	I4	0.17	0/407	0.38	0/542
1	I5	0.19	0/1270	0.45	0/1691
1	I6	0.22	0/2214	0.50	0/2978
1	I7	0.23	0/2198	0.47	0/2953
1	I8	0.23	0/2198	0.50	0/2953
1	I9	0.21	0/1932	0.51	0/2598
1	J4	0.24	0/775	0.53	0/1032
1	J5	0.20	0/1871	0.48	0/2505
1	J6	0.22	0/2198	0.48	0/2953
1	J7	0.23	0/2198	0.49	0/2953
1	J8	0.21	0/2140	0.49	0/2874
1	J9	0.18	0/1571	0.46	0/2114
1	K3	0.20	0/352	0.42	0/470
1	K4	0.23	0/2206	0.49	0/2965
1	K5	0.20	0/1218	0.46	0/1618
1	K6	0.24	0/2198	0.50	0/2953
1	K7	0.23	0/2198	0.51	0/2953
1	K8	0.21	0/1984	0.47	0/2667
1	h0	0.19	0/1506	0.41	0/2027
1	i0	0.19	0/1178	0.46	0/1587
2	L1	0.16	0/1097	0.44	0/1476
2	L2	0.19	0/2003	0.47	0/2698
2	L3	0.20	0/2003	0.46	0/2698
2	L4	0.20	0/2003	0.49	0/2698
2	L5	0.20	0/2003	0.48	0/2698

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	M1	0.19	0/1964	0.49	0/2643
2	M2	0.22	0/2003	0.47	0/2698
2	M3	0.23	0/2003	0.48	0/2698
2	M4	0.22	0/2003	0.44	0/2698
2	M5	0.18	0/1676	0.44	1/2259 (0.0%)
2	N1	0.15	0/868	0.39	0/1163
2	N2	0.21	0/2003	0.47	0/2698
2	N3	0.23	0/2003	0.48	0/2698
2	N4	0.23	0/2003	0.48	0/2698
2	N5	0.20	0/2003	0.46	0/2698
2	N6	0.16	0/1228	0.39	0/1646
2	O1	0.20	0/1893	0.47	0/2541
2	O2	0.21	0/1993	0.45	0/2686
2	O3	0.23	0/1999	0.49	0/2694
2	O4	0.22	0/1999	0.47	0/2694
2	O5	0.21	0/1676	0.50	0/2259
2	P1	0.13	0/740	0.36	0/990
2	P2	0.20	0/2003	0.49	0/2698
2	P3	0.21	0/2004	0.47	0/2699
2	P4	0.22	0/2029	0.48	0/2735
2	P5	0.19	0/2029	0.43	0/2735
2	P6	0.16	0/1395	0.42	0/1877
3	Q1	0.17	0/1965	0.50	0/2639
3	Q2	0.19	0/1965	0.53	0/2639
3	Q3	0.21	0/1965	0.54	1/2639 (0.0%)
3	Q4	0.20	0/1965	0.55	0/2639
3	R1	0.20	0/1687	0.52	0/2265
3	R2	0.21	0/1965	0.50	0/2639
3	R3	0.22	0/1965	0.53	0/2639
3	R4	0.21	0/1965	0.53	0/2639
3	R5	0.19	0/1965	0.53	0/2639
3	S2	0.18	0/1938	0.51	0/2605
3	S3	0.19	0/1961	0.51	0/2635
3	S4	0.19	0/1965	0.51	0/2639
3	S5	0.21	0/1965	0.61	0/2639
3	S6	0.17	0/1449	0.50	0/1934
4	U3	0.15	0/2137	0.40	0/2878
4	U4	0.17	0/2137	0.44	0/2878
4	U5	0.17	0/2137	0.44	0/2878
4	U6	0.17	0/2137	0.43	0/2878
5	V0	0.10	0/645	0.43	0/893
5	V1	0.19	0/1613	0.65	0/2178
5	V2	0.20	0/1613	0.64	0/2178

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	V3	0.18	0/1596	0.63	0/2155
5	V4	0.18	0/1607	0.57	0/2171
5	X0	0.12	0/788	0.49	0/1093
5	X1	0.16	0/1596	0.53	0/2155
5	X2	0.19	0/1596	0.58	0/2155
5	X3	0.18	0/1613	0.58	0/2178
5	X4	0.17	0/1613	0.54	0/2178
6	Y1	0.17	0/1853	0.54	0/2500
6	Y2	0.17	0/1950	0.51	0/2625
6	Y3	0.18	0/2027	0.53	0/2732
6	Y4	0.18	0/1982	0.53	0/2668
7	Z0	0.17	0/2317	0.44	0/3101
7	Z1	0.17	0/2597	0.46	0/3475
7	Z2	0.24	0/2374	0.49	0/3172
7	Za	0.15	0/2158	0.41	0/2882
8	a1	0.18	0/1390	0.52	0/1864
8	a2	0.18	0/1620	0.49	0/2175
8	a3	0.18	0/1569	0.49	0/2103
8	a4	0.19	0/1600	0.53	0/2146
8	a5	0.20	0/1629	0.53	0/2188
9	b2	0.13	0/1215	0.51	0/1703
9	b3	0.16	0/1978	0.49	0/2660
9	b4	0.18	0/1978	0.54	0/2660
10	c1	0.12	0/602	0.39	0/841
10	c2	0.17	0/1044	0.47	0/1402
10	c3	0.18	0/1048	0.52	0/1406
All	All	0.21	0/251774	0.49	2/338497 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A5	0	2
1	A6	0	3
1	A7	0	1
1	A8	0	1
1	B4	0	3
1	B5	0	1
1	B6	0	1
1	B7	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	C3	0	1
1	C4	0	1
1	C5	0	1
1	C6	0	3
1	C7	0	2
1	D2	0	1
1	D5	0	1
1	D6	0	1
1	E2	0	2
1	E4	0	1
1	E5	0	1
1	E6	0	1
1	F2	0	1
1	F3	0	2
1	F5	0	2
1	G1	0	1
1	G2	0	2
1	G6	0	1
1	G7	0	2
1	G9	0	1
1	H6	0	1
1	H7	0	2
1	H8	0	1
1	H9	0	1
1	I4	0	1
1	I5	0	2
1	I6	0	1
1	I7	0	2
1	I8	0	1
1	I9	0	3
1	J4	0	1
1	J5	0	1
1	J6	0	1
1	J7	0	2
1	J8	0	1
1	J9	0	2
1	K4	0	3
1	K5	0	1
1	K7	0	3
1	K8	0	2
1	h0	0	1
2	L2	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	M2	0	1
2	N2	0	1
2	O2	0	1
2	O3	0	1
2	P3	0	1
2	P5	0	1
3	Q4	0	1
3	R1	0	1
3	S2	0	1
3	S5	0	1
4	U6	0	1
5	X3	0	1
6	Y1	0	3
6	Y3	0	1
7	Z0	0	1
7	Z1	0	1
7	Z2	0	1
8	a5	0	1
9	b4	0	1
10	c2	0	1
All	All	0	100

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M5	224	ASP	CB-CA-C	-5.24	110.51	116.54
3	Q3	184	LEU	N-CA-C	5.22	117.71	111.71

There are no chirality outliers.

All (100) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A5	240	ARG	Sidechain
1	A5	255	ARG	Sidechain
1	A6	176	ARG	Sidechain
1	A6	204	ARG	Sidechain
1	A6	240	ARG	Sidechain
1	A7	240	ARG	Sidechain
1	A8	60	ARG	Sidechain
1	B4	123	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	B4	255	ARG	Sidechain
1	B4	279	ARG	Sidechain
1	B5	204	ARG	Sidechain
1	B6	255	ARG	Sidechain
1	B7	123	ARG	Sidechain
1	B7	219	ARG	Sidechain
1	B7	240	ARG	Sidechain
1	C3	14	ARG	Sidechain
1	C4	91	ARG	Sidechain
1	C5	60	ARG	Sidechain
1	C6	219	ARG	Sidechain
1	C6	255	ARG	Sidechain
1	C6	53	ARG	Sidechain
1	C7	53	ARG	Sidechain
1	C7	91	ARG	Sidechain
1	D2	53	ARG	Sidechain
1	D5	60	ARG	Sidechain
1	D6	91	ARG	Sidechain
1	E2	14	ARG	Sidechain
1	E2	61	ARG	Sidechain
1	E4	219	ARG	Sidechain
1	E5	219	ARG	Sidechain
1	E6	240	ARG	Sidechain
1	F2	210	ARG	Sidechain
1	F3	242	ARG	Sidechain
1	F3	255	ARG	Sidechain
1	F5	176	ARG	Sidechain
1	F5	242	ARG	Sidechain
1	G1	89	ARG	Sidechain
1	G2	210	ARG	Sidechain
1	G2	89	ARG	Sidechain
1	G6	53	ARG	Sidechain
1	G7	210	ARG	Sidechain
1	G7	219	ARG	Sidechain
1	G9	219	ARG	Sidechain
1	H6	219	ARG	Sidechain
1	H7	107	ARG	Sidechain
1	H7	60	ARG	Sidechain
1	H8	14	ARG	Sidechain
1	H9	219	ARG	Sidechain
1	I4	14	ARG	Sidechain
1	I5	162	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	I5	60	ARG	Sidechain
1	I6	142	ARG	Sidechain
1	I7	210	ARG	Sidechain
1	I7	53	ARG	Sidechain
1	I8	219	ARG	Sidechain
1	I9	176	ARG	Sidechain
1	I9	219	ARG	Sidechain
1	I9	242	ARG	Sidechain
1	J4	14	ARG	Sidechain
1	J5	14	ARG	Sidechain
1	J6	176	ARG	Sidechain
1	J7	14	ARG	Sidechain
1	J7	219	ARG	Sidechain
1	J8	219	ARG	Sidechain
1	J9	210	ARG	Sidechain
1	J9	91	ARG	Sidechain
1	K4	219	ARG	Sidechain
1	K4	53	ARG	Sidechain
1	K4	61	ARG	Sidechain
1	K5	61	ARG	Sidechain
1	K7	204	ARG	Sidechain
1	K7	210	ARG	Sidechain
1	K7	53	ARG	Sidechain
1	K8	219	ARG	Sidechain
1	K8	53	ARG	Sidechain
2	L2	261	ARG	Sidechain
2	L2	270	ARG	Sidechain
2	M2	191	ARG	Sidechain
2	N2	270	ARG	Sidechain
2	O2	145	ARG	Sidechain
2	O3	184	ARG	Sidechain
2	P3	151	ARG	Sidechain
2	P5	151	ARG	Sidechain
3	Q4	24	ARG	Sidechain
3	R1	56	ARG	Sidechain
3	S2	26	ARG	Sidechain
3	S5	117	ARG	Sidechain
4	U6	188	ARG	Sidechain
5	X3	188	ARG	Sidechain
6	Y1	104	ARG	Sidechain
6	Y1	86	ARG	Sidechain
6	Y1	95	ARG	Sidechain

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Mol	Chain	Res	Type	Group
6	Y3	253	ARG	Sidechain
7	Z0	186	ARG	Sidechain
7	Z1	309	ARG	Sidechain
7	Z2	112	ARG	Sidechain
8	a5	202	ARG	Sidechain
9	b4	144	ARG	Sidechain
10	c2	115	ARG	Sidechain
1	h0	89	ARG	Sidechain

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	A3	702	0	718	17	0
1	A4	1781	0	1770	39	0
1	A5	2178	0	2182	53	0
1	A6	2178	0	2182	44	0
1	A7	2178	0	2182	48	0
1	A8	1713	0	1691	25	0
1	B3	964	0	961	22	0
1	B4	2177	0	2178	54	0
1	B5	2185	0	2189	52	0
1	B6	2185	0	2189	55	0
1	B7	2037	0	2023	37	0
1	B8	1372	0	1359	28	0
1	C2	547	0	564	10	0
1	C3	1542	0	1519	38	0
1	C4	2178	0	2182	40	0
1	C5	2185	0	2189	28	0
1	C6	2185	0	2189	34	0
1	C7	1772	0	1758	29	0
1	C8	956	0	965	12	0
1	D2	881	0	895	6	0
1	D3	2068	0	2086	34	0
1	D4	2178	0	2182	30	0
1	D5	2178	0	2182	28	0
1	D6	2063	0	2056	36	0
1	D7	1410	0	1396	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E1	478	0	495	7	0
1	E2	1430	0	1418	30	0
1	E3	2178	0	2182	42	0
1	E4	2178	0	2182	39	0
1	E5	2178	0	2182	38	0
1	E6	1831	0	1815	31	0
1	E7	983	0	977	19	0
1	F1	818	0	830	26	0
1	F2	1953	0	1949	32	0
1	F3	2185	0	2189	37	0
1	F4	2178	0	2182	35	0
1	F5	2092	0	2080	36	0
1	F6	1440	0	1424	23	0
1	G1	1869	0	1852	35	0
1	G2	1061	0	1069	13	0
1	G5	431	0	448	12	0
1	G6	1318	0	1297	34	0
1	G7	2185	0	2189	57	0
1	G8	2185	0	2189	39	0
1	G9	2178	0	2182	31	0
1	H5	785	0	798	14	0
1	H6	1896	0	1894	46	0
1	H7	2178	0	2182	40	0
1	H8	2185	0	2189	28	0
1	H9	2140	0	2139	37	0
1	I4	405	0	422	6	0
1	I5	1259	0	1242	21	0
1	I6	2192	0	2197	50	0
1	I7	2178	0	2182	48	0
1	I8	2178	0	2182	42	0
1	I9	1914	0	1903	44	0
1	J4	772	0	785	16	0
1	J5	1854	0	1843	35	0
1	J6	2178	0	2182	60	0
1	J7	2178	0	2182	66	0
1	J8	2121	0	2120	58	0
1	J9	1556	0	1544	21	0
1	K3	351	0	370	18	0
1	K4	2185	0	2189	47	0
1	K5	1210	0	1203	28	0
1	K6	2178	0	2182	62	0
1	K7	2178	0	2182	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	K8	1966	0	1954	34	0
1	h0	1490	0	1482	15	0
1	i0	1168	0	1159	23	0
2	L1	1079	0	1027	17	0
2	L2	1959	0	1885	40	0
2	L3	1959	0	1885	34	0
2	L4	1959	0	1885	24	0
2	L5	1959	0	1885	25	0
2	M1	1924	0	1852	29	0
2	M2	1959	0	1885	35	0
2	M3	1959	0	1885	36	0
2	M4	1959	0	1885	33	0
2	M5	1638	0	1597	17	0
2	N1	855	0	785	12	0
2	N2	1959	0	1885	19	0
2	N3	1959	0	1885	21	0
2	N4	1959	0	1885	28	0
2	N5	1959	0	1885	20	0
2	N6	1204	0	1164	12	0
2	O1	1860	0	1786	35	0
2	O2	1950	0	1869	17	0
2	O3	1955	0	1874	24	0
2	O4	1955	0	1874	23	0
2	O5	1638	0	1597	30	0
2	P1	728	0	682	4	0
2	P2	1959	0	1885	31	0
2	P3	1960	0	1884	31	0
2	P4	1983	0	1906	41	0
2	P5	1983	0	1906	26	0
2	P6	1365	0	1310	22	0
3	Q1	1926	0	1895	41	0
3	Q2	1926	0	1895	28	0
3	Q3	1926	0	1895	26	0
3	Q4	1926	0	1895	32	0
3	R1	1654	0	1604	33	0
3	R2	1926	0	1893	32	0
3	R3	1926	0	1895	30	0
3	R4	1926	0	1895	25	0
3	R5	1926	0	1895	34	0
3	S2	1899	0	1855	40	0
3	S3	1922	0	1884	22	0
3	S4	1926	0	1895	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	S5	1926	0	1893	33	0
3	S6	1426	0	1410	21	0
4	U3	2101	0	2087	18	0
4	U4	2101	0	2087	37	0
4	U5	2101	0	2087	39	0
4	U6	2101	0	2087	40	0
5	V0	645	0	309	2	0
5	V1	1574	0	1578	49	0
5	V2	1574	0	1578	36	0
5	V3	1559	0	1568	42	0
5	V4	1568	0	1567	25	0
5	X0	786	0	375	0	0
5	X1	1559	0	1568	26	0
5	X2	1559	0	1568	30	0
5	X3	1574	0	1578	31	0
5	X4	1574	0	1578	23	0
6	Y1	1808	0	1783	36	0
6	Y2	1905	0	1886	35	0
6	Y3	1979	0	1953	37	0
6	Y4	1937	0	1919	42	0
7	Z0	2271	0	2238	18	0
7	Z1	2545	0	2513	31	0
7	Z2	2329	0	2309	17	0
7	Za	2121	0	2100	22	0
8	a1	1367	0	1399	25	0
8	a2	1596	0	1621	25	0
8	a3	1546	0	1583	20	0
8	a4	1577	0	1606	32	0
8	a5	1605	0	1627	37	0
9	b2	1204	0	584	2	0
9	b3	1944	0	1974	34	0
9	b4	1944	0	1974	38	0
10	c1	600	0	268	0	0
10	c2	1020	0	992	10	0
10	c3	1025	0	1000	9	0
11	V0	1	0	0	0	0
11	V1	1	0	0	0	0
11	V2	1	0	0	0	0
11	V3	1	0	0	0	0
11	V4	1	0	0	0	0
11	X0	1	0	0	0	0
11	X1	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	X2	1	0	0	0	0
11	X3	1	0	0	0	0
11	X4	1	0	0	0	0
12	V0	2	0	0	1	0
12	V1	2	0	0	0	0
12	V2	2	0	0	0	0
12	V3	2	0	0	1	0
12	V4	2	0	0	0	0
12	X0	2	0	0	0	0
12	X1	2	0	0	1	0
12	X2	2	0	0	0	0
12	X3	2	0	0	0	0
12	X4	2	0	0	3	0
All	All	248112	0	244001	3588	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 7.

All (3588) 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)
5:V0:100:LYS:O	12:V0:401:HOH:O	1.58	1.18
5:V4:50:LEU:HD11	5:V4:223:VAL:HG13	1.48	0.94
4:U5:149:ARG:HA	4:U6:92:LEU:HD21	1.51	0.93
3:Q1:189:ASN:HB2	3:Q1:196:ARG:HD3	1.51	0.91
9:b3:189:TYR:HB3	9:b3:211:ILE:HG12	1.52	0.91
5:X4:220:ASP:OD1	12:X4:401:HOH:O	1.90	0.90
1:C4:53:ARG:HA	1:C4:56:ILE:HD12	1.54	0.89
3:Q1:62:LYS:HG3	3:Q1:65:ALA:HB2	1.56	0.87
1:C3:154:GLY:HA3	1:C3:159:GLN:HG2	1.57	0.86
1:J6:3:ILE:HD12	1:J7:246:MET:HG3	1.56	0.85
2:M4:272:THR:HG21	2:M4:286:ILE:HG13	1.55	0.85
3:Q1:141:ILE:HD12	3:Q1:158:LEU:HD22	1.56	0.84
6:Y2:130:LYS:HZ1	6:Y2:147:PRO:HG2	1.40	0.84
3:Q4:74:GLU:HG3	3:Q4:96:LYS:HB3	1.60	0.84
3:R1:138:ILE:HG23	3:R1:161:GLN:HB3	1.60	0.84
3:S3:124:THR:HG21	3:S3:207:ASN:HD21	1.43	0.83
2:N2:265:ASN:HB3	2:N2:290:ILE:HD11	1.59	0.83
3:R2:160:TYR:HB2	3:R3:233:ASN:HD21	1.44	0.82
1:E4:184:ILE:HD11	1:E4:195:VAL:HG13	1.57	0.82
3:R2:47:LYS:H	3:R2:63:GLN:HE22	1.28	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:V1:170:PHE:HE1	6:Y2:47:GLY:HA2	1.45	0.81
1:h0:226:GLY:HA2	1:i0:82:GLU:HG3	1.59	0.81
1:K7:48:VAL:HG22	1:K7:52:MET:HE2	1.63	0.81
1:K7:66:THR:HG23	1:K7:220:MET:HE3	1.60	0.81
1:A4:3:ILE:HD12	1:A5:246:MET:HE3	1.62	0.80
1:G7:153:ILE:HG21	1:G7:220:MET:HE1	1.62	0.80
2:M3:272:THR:HG21	2:M3:286:ILE:HG13	1.62	0.80
1:A5:170:THR:HG22	1:A5:175:LEU:HB2	1.64	0.79
3:R2:140:VAL:HG22	3:R2:159:PHE:HB3	1.62	0.79
1:A6:138:GLY:HA3	1:A6:167:THR:HG22	1.64	0.79
2:O5:272:THR:HG21	2:O5:286:ILE:HG13	1.66	0.78
1:G7:276:SER:HB2	1:H7:261:GLN:HE22	1.49	0.77
1:J7:204:ARG:HH21	1:K7:105:GLU:HG2	1.50	0.77
4:U5:130:GLU:HG2	4:U6:89:MET:HE1	1.65	0.77
1:A5:157:MET:HE1	1:A6:194:SER:HA	1.66	0.77
1:A4:3:ILE:HD11	1:A4:278:MET:HG3	1.66	0.77
1:I6:281:LEU:HD12	1:I7:250:MET:HG2	1.66	0.77
1:G5:266:MET:HE3	1:H5:30:LEU:HB3	1.66	0.77
8:a1:155:THR:HG21	8:a1:160:LYS:HB3	1.66	0.76
1:I6:2:ILE:HD12	1:I7:243:ASP:HB3	1.66	0.76
2:M2:272:THR:HG21	2:M2:286:ILE:HG13	1.67	0.75
9:b4:139:ILE:HD12	9:b4:160:ILE:HG12	1.68	0.75
1:A7:251:THR:HG22	1:B6:271:ASN:HD21	1.51	0.75
1:B4:39:ALA:HB2	1:B5:77:GLU:HG2	1.68	0.75
1:K4:153:ILE:HG21	1:K4:220:MET:HE1	1.66	0.74
1:G8:219:ARG:HH22	1:H8:123:ARG:HD3	1.52	0.74
5:V1:139:VAL:HG22	5:V1:218:VAL:HG12	1.68	0.74
1:A5:93:LEU:HD12	1:A5:110:ILE:HG23	1.69	0.74
1:J5:53:ARG:HA	1:J5:56:ILE:HD12	1.70	0.74
1:A6:66:THR:HG23	1:A6:220:MET:HG3	1.68	0.74
5:X2:132:VAL:HG13	5:X2:223:VAL:HG23	1.69	0.73
3:S5:136:LYS:HE2	3:S5:138:ILE:HD11	1.70	0.73
2:O2:133:ARG:HG2	2:O2:133:ARG:HH11	1.54	0.73
1:G8:258:ILE:HD11	1:H7:275:GLN:HG2	1.70	0.73
5:V1:151:LYS:HB3	5:V1:200:SER:HB2	1.70	0.73
1:G6:69:GLY:HA3	1:G6:220:MET:HE1	1.71	0.72
1:H8:180:VAL:HG12	1:H8:182:THR:HG23	1.70	0.72
2:N2:75:ASN:HB2	2:N3:202:MET:HE3	1.70	0.72
6:Y2:46:THR:HG23	6:Y2:199:HIS:HB3	1.70	0.72
1:B4:52:MET:HE1	1:B4:237:SER:HB3	1.69	0.72
9:b3:235:LYS:HA	9:b3:238:LEU:HD12	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E5:83:THR:HG23	1:E5:121:ILE:HD12	1.71	0.72
8:a5:105:MET:HE2	8:a5:135:LYS:HD2	1.71	0.72
1:C4:114:VAL:HG21	1:C4:186:LEU:HD22	1.72	0.72
1:C5:180:VAL:HG12	1:C5:182:THR:HG23	1.72	0.71
3:R1:124:THR:HG21	3:R1:207:ASN:HD21	1.55	0.71
1:F3:260:THR:O	1:F3:264:THR:HG23	1.90	0.71
1:J9:111:GLN:HE22	1:J9:185:SER:HA	1.54	0.71
2:L3:86:GLN:HA	2:L3:89:HIS:CE1	2.25	0.71
3:S3:100:PHE:HB2	3:S3:121:LYS:HB3	1.72	0.71
1:A5:63:GLU:O	1:A5:66:THR:HG22	1.91	0.71
2:P4:148:ARG:HG2	2:P4:151:ARG:HH22	1.56	0.71
3:Q2:20:GLU:HA	3:Q2:23:LYS:HE2	1.71	0.71
4:U5:110:LEU:HD23	4:U5:113:ILE:HD11	1.73	0.70
1:K6:52:MET:HE1	1:K6:241:ILE:HD12	1.73	0.70
9:b3:61:LEU:HD23	9:b3:64:ILE:HD11	1.73	0.70
5:V3:98:ILE:HG22	5:V3:101:ASN:HD22	1.56	0.70
6:Y4:148:GLU:HG3	6:Y4:149:PRO:HD2	1.73	0.70
1:J8:210:ARG:HG2	1:J8:210:ARG:HH11	1.55	0.70
2:P1:88:LEU:HD22	2:P2:286:ILE:HD11	1.72	0.70
5:V1:56:ALA:HB1	5:V1:104:LEU:HD13	1.73	0.70
1:B6:258:ILE:HG23	1:C5:278:MET:HG2	1.73	0.70
1:J6:52:MET:O	1:J6:56:ILE:HG13	1.92	0.70
2:M2:256:MET:HE2	8:a2:97:LEU:HD22	1.73	0.70
3:S6:100:PHE:HB2	3:S6:121:LYS:HB3	1.73	0.70
1:G8:240:ARG:HD3	1:H8:67:GLU:HB3	1.74	0.70
1:B4:202:ALA:O	1:B4:206:ILE:HG13	1.92	0.70
9:b4:50:ILE:HD12	9:b4:231:MET:HE3	1.74	0.70
1:F2:153:ILE:HG21	1:F2:220:MET:HE1	1.73	0.70
1:J8:156:ASN:HB2	1:J8:159:GLN:HE21	1.56	0.69
1:J5:1:MET:HE3	1:K4:16:LEU:HG	1.75	0.69
6:Y1:240:VAL:HB	6:Y1:252:PHE:HB2	1.74	0.69
8:a1:61:VAL:HG11	8:a1:159:VAL:HG13	1.73	0.69
1:B5:38:LYS:HB2	1:B6:74:GLN:HE22	1.58	0.69
3:R1:118:ASN:HD22	3:R1:147:ASN:HB2	1.57	0.69
1:E5:66:THR:HG23	1:E5:220:MET:HE3	1.74	0.69
1:D5:52:MET:HE1	1:D5:241:ILE:HD12	1.75	0.69
1:F3:60:ARG:HH11	1:F3:60:ARG:HG3	1.57	0.69
1:C7:157:MET:HG2	1:C7:158:HIS:CD2	2.28	0.69
2:P3:126:LYS:HD3	9:b3:258:GLN:HE22	1.58	0.69
8:a4:149:ARG:HG2	8:a4:166:VAL:HG23	1.73	0.69
2:M4:223:ILE:HB	2:M4:226:ASN:HD22	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D6:47:ALA:HB2	1:E7:109:GLN:HE22	1.58	0.68
1:J7:114:VAL:O	1:J7:118:VAL:HG23	1.92	0.68
6:Y2:131:LYS:HA	6:Y2:134:MET:HE2	1.75	0.68
1:H5:11:PHE:CE2	1:I5:28:GLU:HG3	2.28	0.68
1:A7:44:SER:O	1:A7:48:VAL:HG23	1.94	0.68
1:K8:69:GLY:HA3	1:K8:220:MET:HE1	1.75	0.68
5:V3:142:ARG:HH21	5:V4:191:LEU:HD13	1.56	0.68
1:A5:69:GLY:O	1:A5:73:ILE:HG13	1.93	0.68
1:B5:3:ILE:HD12	1:B5:278:MET:HG3	1.76	0.68
1:K7:191:LYS:O	1:K7:195:VAL:HG23	1.94	0.68
1:i0:186:LEU:HD23	1:i0:195:VAL:HG21	1.76	0.68
1:A7:123:ARG:HD2	1:K7:153:ILE:HD11	1.74	0.68
3:S5:124:THR:HG21	3:S5:207:ASN:HD21	1.59	0.68
4:U5:244:ASN:HA	9:b4:48:ASN:ND2	2.08	0.68
2:M2:178:ILE:HD11	2:M2:183:LEU:HB3	1.74	0.68
3:R3:22:ASN:HA	3:R3:25:LEU:HD12	1.75	0.68
1:A8:120:GLU:HG2	1:K8:219:ARG:HB2	1.76	0.68
1:B4:260:THR:O	1:B4:264:THR:HG23	1.94	0.68
1:E5:2:ILE:HD12	1:E6:243:ASP:HB2	1.75	0.68
8:a5:222:MET:O	8:a5:226:THR:HG23	1.94	0.68
1:C3:80:LEU:HD21	1:C3:136:LEU:HD21	1.75	0.68
1:J5:38:LYS:HD2	1:J6:74:GLN:HE22	1.59	0.68
1:J9:219:ARG:HH11	1:J9:219:ARG:HG3	1.58	0.68
1:C3:153:ILE:HG21	1:C3:220:MET:HE1	1.77	0.67
1:I9:36:ILE:HD11	1:I9:46:LEU:HB2	1.74	0.67
1:B6:44:SER:O	1:B6:48:VAL:HG23	1.94	0.67
3:S2:184:LEU:O	3:S2:187:VAL:HG22	1.94	0.67
1:B4:66:THR:HG21	1:B4:224:ALA:HB2	1.76	0.67
1:C4:14:ARG:HG3	1:C5:228:MET:HG3	1.77	0.67
1:I7:46:LEU:HD12	1:I7:242:ARG:HH12	1.59	0.67
6:Y1:118:ALA:HA	6:Y1:121:ILE:HG22	1.77	0.67
2:P3:75:ASN:HB2	2:P4:202:MET:HE3	1.75	0.67
2:O3:98:ASN:HD22	3:S4:89:ASN:ND2	1.93	0.67
1:G1:158:HIS:H	1:G2:193:ASN:HD21	1.43	0.67
3:R2:141:ILE:HG12	3:R2:158:LEU:HD22	1.77	0.67
2:O5:104:LEU:O	2:O5:108:GLN:HG3	1.93	0.67
1:J6:244:THR:HG23	1:J6:249:GLN:HG3	1.77	0.67
1:K5:250:MET:O	1:K5:254:THR:HG23	1.94	0.67
6:Y4:121:ILE:HD11	6:Y4:149:PRO:HG3	1.77	0.67
1:J7:84:HIS:CE1	1:J7:203:LEU:HD22	2.30	0.67
2:L3:286:ILE:HA	2:L3:289:VAL:HG22	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R1:43:THR:HG22	3:R1:75:VAL:HG12	1.77	0.67
5:X1:72:THR:HG22	5:X1:106:VAL:HG22	1.76	0.67
1:G7:258:ILE:HG21	1:H6:3:ILE:HD12	1.76	0.66
8:a1:89:VAL:HG12	8:a1:108:ARG:HB3	1.77	0.66
1:A7:278:MET:HG2	1:K8:258:ILE:HG12	1.77	0.66
1:I6:51:LYS:O	1:I6:54:THR:HG22	1.94	0.66
5:X2:191:LEU:HG	5:X2:192:LEU:HD22	1.75	0.66
1:J8:250:MET:O	1:J8:254:THR:HG23	1.96	0.66
3:Q2:40:PRO:HG3	3:Q2:214:LEU:HD11	1.76	0.66
8:a2:71:LYS:HB3	8:a2:208:ILE:HG21	1.77	0.66
2:L2:88:LEU:HD13	2:L3:286:ILE:HD11	1.75	0.66
1:B6:154:GLY:HA3	1:B6:159:GLN:HE21	1.59	0.66
1:D5:72:LEU:HB2	1:D6:101:ILE:HD11	1.78	0.66
1:J6:114:VAL:O	1:J6:118:VAL:HG13	1.95	0.66
1:K6:66:THR:O	1:K6:70:MET:HG3	1.95	0.66
1:C4:138:GLY:HA3	1:C4:167:THR:HG22	1.76	0.66
5:V2:142:ARG:HD2	5:V3:191:LEU:HD22	1.77	0.66
2:M1:229:GLU:HG2	2:M1:231:PRO:HD2	1.76	0.66
2:O1:268:LEU:HD23	2:O1:290:ILE:HD11	1.78	0.66
3:Q1:31:LEU:HD23	3:Q1:34:MET:HE3	1.77	0.66
3:Q1:36:VAL:HG11	3:Q1:45:LEU:HD22	1.76	0.66
1:J4:258:ILE:HD11	1:K3:278:MET:HB3	1.76	0.66
3:R4:138:ILE:HG12	3:R4:161:GLN:HB3	1.77	0.66
10:c2:93:SER:O	10:c2:97:ILE:HG13	1.96	0.66
4:U5:286:ALA:O	4:U5:290:ILE:HG13	1.96	0.65
5:V3:140:LEU:HD22	5:V4:237:ILE:HD12	1.77	0.65
10:c3:53:TYR:O	10:c3:57:THR:HG23	1.95	0.65
1:C3:152:HIS:HD2	1:C3:160:ARG:HD2	1.61	0.65
1:A3:25:LYS:O	1:A3:29:LYS:HG3	1.97	0.65
1:B4:191:LYS:O	1:B4:195:VAL:HG23	1.97	0.65
2:P2:253:PRO:HD2	2:P2:256:MET:HE2	1.79	0.65
1:E3:168:MET:HE1	1:E3:209:GLN:HG3	1.79	0.65
1:G6:157:MET:HE2	1:G6:158:HIS:CE1	2.31	0.65
2:L2:172:ILE:HD11	6:Y2:94:TRP:HZ3	1.60	0.65
7:Z2:108:THR:HA	7:Z2:111:GLU:HB2	1.79	0.65
3:Q1:100:PHE:HB2	3:Q1:121:LYS:HB3	1.77	0.65
6:Y4:235:LYS:HE2	6:Y4:255:PHE:HB3	1.78	0.65
9:b4:119:LEU:O	9:b4:144:ARG:HA	1.96	0.65
1:B7:175:LEU:HD22	1:B7:184:ILE:HD13	1.79	0.65
1:D6:44:SER:HB3	1:E7:110:ILE:HG13	1.79	0.65
1:H6:30:LEU:HD12	1:H6:246:MET:HE2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L3:265:ASN:HB3	2:L3:290:ILE:HD11	1.78	0.65
2:P3:88:LEU:HD21	2:P4:276:TYR:CE2	2.32	0.65
6:Y1:121:ILE:HG21	6:Y1:149:PRO:HG2	1.78	0.65
1:I8:44:SER:O	1:I8:48:VAL:HG12	1.97	0.65
1:K5:66:THR:HG22	1:K5:153:ILE:HG22	1.79	0.65
1:E2:40:GLY:HA2	1:E3:218:ASN:HD21	1.60	0.64
1:F2:250:MET:O	1:F2:254:THR:HG23	1.97	0.64
1:K8:256:TYR:O	1:K8:260:THR:HG23	1.96	0.64
3:Q2:73:LEU:HD21	3:Q2:214:LEU:HD23	1.77	0.64
3:Q4:159:PHE:HB2	3:Q4:181:LYS:HD3	1.80	0.64
5:V3:122:PRO:HD2	5:V3:199:VAL:HG13	1.79	0.64
6:Y1:177:SER:HB3	6:Y1:180:LYS:HB2	1.78	0.64
1:H7:44:SER:O	1:H7:48:VAL:HG23	1.96	0.64
2:M4:98:ASN:HD22	3:Q4:131:PHE:HE2	1.43	0.64
6:Y1:175:GLY:H	6:Y1:213:LYS:HE3	1.62	0.64
8:a4:184:ILE:HG23	8:a5:223:ILE:HD13	1.78	0.64
1:B8:86:ILE:HG23	1:B8:117:LEU:HD12	1.80	0.64
1:E3:51:LYS:O	1:E3:54:THR:HG22	1.98	0.64
5:V1:107:LYS:HE3	5:V1:213:ASP:HB2	1.79	0.64
5:X3:108:THR:HG21	5:X3:118:VAL:HG21	1.79	0.64
1:K7:36:ILE:HG12	1:K7:242:ARG:HG3	1.79	0.64
3:R5:138:ILE:HG13	3:R5:161:GLN:HB3	1.79	0.64
4:U4:286:ALA:O	4:U4:290:ILE:HG23	1.98	0.64
7:Z0:197:GLU:HB3	7:Z0:200:GLN:HB2	1.78	0.64
8:a4:93:ARG:HD2	8:a4:105:MET:HE2	1.78	0.64
1:K4:118:VAL:HG13	1:K4:170:THR:HG21	1.80	0.64
2:P5:201:ILE:HD11	2:P5:216:ILE:HB	1.80	0.64
1:A3:1:MET:HE3	1:A3:277:VAL:HG11	1.80	0.64
6:Y3:53:ASP:HA	6:Y3:220:SER:O	1.98	0.64
6:Y3:176:PRO:HB2	6:Y3:181:GLN:HG2	1.80	0.64
1:B7:46:LEU:O	1:B7:50:GLU:HG2	1.98	0.63
1:E3:248:GLU:HB2	1:F2:13:HIS:CE1	2.33	0.63
1:G1:101:ILE:HD13	1:G9:130:PHE:HE2	1.63	0.63
1:H5:7:VAL:HA	1:H5:10:ILE:HD12	1.79	0.63
2:L4:255:ASP:O	2:L4:259:LYS:HG3	1.99	0.63
5:V2:154:ASP:HA	5:V2:196:LEU:HD12	1.80	0.63
1:F3:266:MET:SD	1:G8:30:LEU:HD23	2.37	0.63
1:K6:26:ASP:HA	1:K6:249:GLN:NE2	2.14	0.63
1:K7:135:LEU:HD22	1:K7:136:LEU:HD12	1.79	0.63
8:a5:162:LEU:HD13	8:a5:181:LEU:HD13	1.79	0.63
1:D4:154:GLY:HA3	1:D4:159:GLN:HE21	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J7:176:ARG:HH21	1:J7:183:PHE:HE1	1.44	0.63
3:R5:23:LYS:O	3:R5:26:ARG:HG2	1.98	0.63
3:S4:33:LYS:HZ3	3:S4:109:PRO:HA	1.64	0.63
1:A5:278:MET:HG2	1:K6:258:ILE:HG12	1.79	0.63
1:C4:186:LEU:HD11	1:C4:195:VAL:HG11	1.81	0.63
1:E2:258:ILE:HG23	1:F1:278:MET:HG2	1.80	0.63
1:E3:52:MET:HE1	1:E3:241:ILE:HD12	1.79	0.63
1:G6:282:GLN:HE22	1:G7:246:MET:HE3	1.63	0.63
1:G8:106:ASP:HA	1:G8:109:GLN:HE21	1.63	0.63
1:A7:278:MET:HE2	1:A7:282:GLN:HG3	1.81	0.63
1:B5:67:GLU:HA	1:B5:70:MET:HE2	1.81	0.63
1:B7:251:THR:HG22	1:C6:271:ASN:HD21	1.63	0.63
1:I7:66:THR:HG21	1:I7:224:ALA:HB2	1.79	0.63
1:B3:236:ALA:O	1:B3:240:ARG:HG3	1.98	0.63
1:B6:25:LYS:O	1:B6:29:LYS:HG3	1.99	0.63
1:J7:52:MET:O	1:J7:56:ILE:HG13	1.99	0.63
1:J8:88:GLN:O	1:J8:92:VAL:HG23	1.99	0.63
5:V4:50:LEU:HD21	5:V4:128:ILE:HD11	1.80	0.63
1:E3:83:THR:O	1:E3:87:VAL:HG23	1.98	0.63
1:F1:27:ILE:HG12	1:F1:253:PHE:HE2	1.63	0.63
1:F4:250:MET:O	1:F4:254:THR:HG23	1.98	0.63
3:S4:66:GLN:HG3	3:S4:105:ASN:HD21	1.63	0.63
1:B5:43:ALA:HB2	1:B6:214:GLY:HA3	1.81	0.63
1:I6:157:MET:HE3	1:I6:158:HIS:CE1	2.34	0.63
2:M2:149:GLU:O	2:M2:153:VAL:HG23	1.99	0.63
4:U6:287:ASN:HD22	4:U6:290:ILE:HD11	1.64	0.63
5:V2:132:VAL:HG22	5:V2:185:GLN:HB2	1.80	0.63
1:J7:157:MET:HE3	1:J8:194:SER:HA	1.80	0.63
2:L2:172:ILE:HD11	6:Y2:94:TRP:CZ3	2.34	0.63
3:S5:140:VAL:HG22	3:S5:159:PHE:HB3	1.79	0.63
3:S5:142:ALA:HB3	3:S5:157:GLU:HG3	1.80	0.63
1:i0:191:LYS:O	1:i0:195:VAL:HG23	1.99	0.62
1:E3:80:LEU:HD11	1:E3:168:MET:HE3	1.81	0.62
1:H9:44:SER:O	1:H9:48:VAL:HG23	1.98	0.62
1:A6:258:ILE:HG22	1:B5:3:ILE:HD11	1.81	0.62
1:B5:79:TYR:O	1:B5:83:THR:HG23	1.99	0.62
1:D3:1:MET:HB3	1:D3:277:VAL:HG11	1.81	0.62
1:E7:191:LYS:O	1:E7:195:VAL:HG23	1.99	0.62
1:G7:154:GLY:HA3	1:G7:159:GLN:HE21	1.64	0.62
1:J7:39:ALA:HB1	1:J8:214:GLY:HA2	1.80	0.62
1:E2:281:LEU:HD11	1:F2:267:LEU:HD22	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K4:88:GLN:O	1:K4:92:VAL:HG23	1.98	0.62
8:a5:188:TRP:O	8:a5:192:ARG:HG2	1.99	0.62
1:B6:191:LYS:O	1:B6:195:VAL:HG23	1.99	0.62
1:E2:1:MET:HB2	1:E2:277:VAL:HG11	1.80	0.62
1:H8:154:GLY:HA3	1:H8:159:GLN:HE21	1.62	0.62
1:I6:53:ARG:HA	1:I6:56:ILE:HD12	1.80	0.62
8:a5:168:THR:HB	8:a5:175:ASN:OD1	2.00	0.62
1:D7:120:GLU:O	1:D7:124:ILE:HG13	2.00	0.62
1:F5:54:THR:HG21	1:F6:203:LEU:HD13	1.81	0.62
2:L5:268:LEU:HD21	2:L5:286:ILE:HD11	1.80	0.62
1:I5:153:ILE:HD13	1:I5:220:MET:HE1	1.82	0.62
2:O1:213:THR:HG23	2:O1:217:LEU:HD23	1.81	0.62
2:O5:283:TYR:O	2:O5:287:VAL:HG23	1.99	0.62
8:a2:100:GLU:HG3	8:a2:101:PRO:HD2	1.80	0.62
1:H8:30:LEU:HD21	1:H8:249:GLN:HB3	1.82	0.62
2:M2:69:GLN:HG2	2:M3:229:GLU:HG3	1.81	0.62
6:Y3:39:PHE:CE2	6:Y3:236:VAL:HG11	2.34	0.62
1:F2:168:MET:SD	1:F2:209:GLN:HG3	2.39	0.62
2:L2:133:ARG:HE	2:L2:145:ARG:HD2	1.65	0.62
5:V2:49:VAL:HB	5:V2:222:GLN:HG2	1.82	0.62
1:B4:152:HIS:HD2	1:B5:95:VAL:HG13	1.65	0.62
1:G7:50:GLU:O	1:G7:54:THR:HG23	2.00	0.62
1:H9:50:GLU:O	1:H9:54:THR:HG23	2.00	0.62
1:J8:169:ASN:HD21	1:J8:171:ALA:HB3	1.64	0.62
2:O5:201:ILE:HD11	2:O5:216:ILE:HB	1.81	0.62
2:P3:88:LEU:HD21	2:P4:276:TYR:HE2	1.63	0.62
9:b3:71:GLY:O	9:b3:75:THR:HG22	2.00	0.62
1:h0:66:THR:HG23	1:h0:220:MET:HE3	1.81	0.62
1:H6:67:GLU:HA	1:H6:70:MET:HE2	1.80	0.61
1:J5:80:LEU:HD21	1:J5:168:MET:HE3	1.81	0.61
2:M2:136:GLU:OE2	2:M2:145:ARG:HD3	2.00	0.61
3:Q3:125:TYR:HE1	3:Q3:127:TYR:HB2	1.65	0.61
3:R2:31:LEU:HD23	3:R2:34:MET:HE2	1.81	0.61
1:B5:258:ILE:HG21	1:C4:3:ILE:HG12	1.82	0.61
1:H6:1:MET:HE3	1:I6:16:LEU:HG	1.81	0.61
2:L4:86:GLN:HA	2:L4:89:HIS:CE1	2.34	0.61
2:P2:270:ARG:HG2	2:P2:270:ARG:HH11	1.65	0.61
3:Q1:36:VAL:HA	3:Q1:222:ASN:ND2	2.14	0.61
1:H7:80:LEU:HD22	1:H7:168:MET:HE2	1.82	0.61
2:M1:209:ASN:HB3	2:M1:212:GLN:CD	2.25	0.61
1:A6:257:GLN:HE22	1:K6:269:GLN:HE21	1.46	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C6:260:THR:O	1:C6:264:THR:HG23	2.00	0.61
1:F5:191:LYS:O	1:F5:195:VAL:HG23	2.01	0.61
1:I6:220:MET:HA	1:I6:220:MET:HE3	1.82	0.61
2:M4:84:THR:HG21	2:M5:268:LEU:HD21	1.81	0.61
1:A3:27:ILE:HA	1:K3:266:MET:HE2	1.81	0.61
1:A4:219:ARG:HH21	1:B4:119:ASP:HB3	1.65	0.61
1:B5:91:ARG:O	1:B5:95:VAL:HG23	2.01	0.61
1:E2:61:ARG:HD3	1:E3:96:GLN:HB2	1.82	0.61
1:G1:191:LYS:O	1:G1:195:VAL:HG23	2.00	0.61
1:H8:138:GLY:HA3	1:H8:167:THR:HG22	1.81	0.61
8:a4:35:LEU:HD22	8:a5:74:PHE:HB2	1.81	0.61
1:A8:219:ARG:HH22	1:B8:119:ASP:HB3	1.66	0.61
3:Q4:122:ILE:HG12	3:Q4:143:ASP:HB3	1.80	0.61
1:A6:191:LYS:O	1:A6:195:VAL:HG23	2.01	0.61
1:F4:257:GLN:O	1:F4:260:THR:HG22	2.01	0.61
1:I6:118:VAL:HG23	1:I6:170:THR:HG21	1.80	0.61
1:I7:35:ARG:HG3	1:I7:36:ILE:HG13	1.83	0.61
1:J9:84:HIS:O	1:J9:88:GLN:HG2	2.01	0.61
1:K5:254:THR:O	1:K5:258:ILE:HG22	2.01	0.61
2:L5:169:SER:HG	2:L5:200:TRP:HZ3	1.47	0.61
2:N3:255:ASP:HB2	3:Q2:84:GLY:HA2	1.83	0.61
8:a4:181:LEU:HD13	8:a4:193:LEU:HD22	1.82	0.61
1:B3:23:LEU:O	1:B3:27:ILE:HG13	2.01	0.61
1:B8:114:VAL:O	1:B8:118:VAL:HG23	2.01	0.61
1:D3:47:ALA:HB2	1:E4:109:GLN:HE22	1.64	0.61
1:I8:7:VAL:HA	1:I8:10:ILE:HG22	1.83	0.61
2:L4:91:LEU:HD11	2:L4:179:LYS:HB2	1.81	0.61
2:O1:63:LYS:O	2:O1:67:MET:HG2	2.01	0.61
1:I7:223:ALA:O	1:I7:227:LEU:HD23	2.01	0.61
2:N4:270:ARG:O	2:N4:274:LEU:HD23	2.01	0.61
3:Q1:187:VAL:HG22	3:Q1:195:ILE:HD11	1.83	0.61
1:A5:73:ILE:HG23	1:A5:213:LEU:HD22	1.83	0.61
1:B6:236:ALA:O	1:B6:240:ARG:HG3	1.99	0.61
1:I9:68:ASP:HB3	1:i0:101:ILE:HD13	1.83	0.61
2:L2:88:LEU:HD11	2:L3:276:TYR:CE2	2.36	0.61
2:M2:224:ASP:CG	2:M2:225:ASP:H	2.07	0.61
4:U4:41:ASN:HD22	4:U4:270:ASP:HB2	1.65	0.61
8:a4:101:PRO:HB2	8:a4:137:LEU:HD11	1.83	0.61
1:A7:91:ARG:O	1:A7:95:VAL:HG23	2.01	0.60
1:C3:278:MET:HE1	1:C3:282:GLN:HE21	1.66	0.60
1:F2:168:MET:HA	1:F2:168:MET:HE3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O1:210:LEU:HB2	2:O1:242:PHE:HD2	1.66	0.60
2:P5:282:GLU:O	2:P5:286:ILE:HD12	2.01	0.60
4:U4:208:LYS:HE2	4:U4:210:GLU:HB2	1.83	0.60
4:U6:159:GLU:O	4:U6:163:THR:HG23	2.01	0.60
1:B7:63:GLU:O	1:B7:66:THR:HG22	2.00	0.60
1:C4:70:MET:HE2	1:C4:221:GLU:HA	1.83	0.60
1:E4:3:ILE:HD12	1:E5:246:MET:HG3	1.83	0.60
1:G6:30:LEU:HD13	1:G6:249:GLN:HB3	1.82	0.60
2:N5:78:PHE:CE2	2:N6:332:LYS:HE3	2.36	0.60
4:U3:24:LEU:HD21	4:U3:174:ARG:HH21	1.66	0.60
1:H9:138:GLY:HA3	1:H9:167:THR:HG22	1.84	0.60
1:K6:72:LEU:HD11	1:K6:135:LEU:HD11	1.82	0.60
1:G2:114:VAL:O	1:G2:118:VAL:HG23	2.00	0.60
1:H6:201:ASP:O	1:H6:205:VAL:HG23	2.02	0.60
1:A7:191:LYS:O	1:A7:195:VAL:HG23	2.00	0.60
1:D5:68:ASP:OD1	1:D6:101:ILE:HD13	2.01	0.60
2:O4:283:TYR:O	2:O4:287:VAL:HG23	2.02	0.60
6:Y4:38:THR:HB	6:Y4:55:GLN:HB2	1.84	0.60
1:H8:43:ALA:HB1	1:H9:211:ALA:HA	1.84	0.60
1:K6:82:GLU:O	1:K6:86:ILE:HG13	2.01	0.60
5:V1:98:ILE:HG22	5:V1:101:ASN:HD22	1.67	0.60
6:Y1:130:LYS:O	6:Y1:134:MET:HG2	2.01	0.60
1:F4:72:LEU:HD13	1:F4:149:MET:HE2	1.84	0.60
1:J8:248:GLU:HB2	1:K7:13:HIS:CE1	2.36	0.60
2:M4:259:LYS:HB2	8:a4:93:ARG:NH2	2.17	0.60
3:Q4:141:ILE:HG12	3:Q4:158:LEU:HD22	1.82	0.60
3:R1:98:GLU:HG3	3:R1:123:ARG:HB3	1.83	0.60
3:Q2:122:ILE:HG12	3:Q2:143:ASP:HB3	1.83	0.60
9:b4:117:VAL:HB	9:b4:147:ALA:HB3	1.83	0.60
10:c3:138:TYR:HB3	10:c3:160:LEU:HD11	1.83	0.60
1:B5:223:ALA:O	1:B5:227:LEU:HD23	2.01	0.60
1:C6:202:ALA:O	1:C6:206:ILE:HG22	2.01	0.60
1:D7:74:GLN:HG3	1:D7:217:TYR:HE2	1.67	0.60
1:G8:54:THR:HG21	1:G9:203:LEU:HD13	1.84	0.59
1:F5:56:ILE:HD11	1:F5:235:GLN:N	2.17	0.59
3:Q2:45:LEU:HD12	3:Q2:73:LEU:HD13	1.83	0.59
1:C6:171:ALA:HB1	1:C6:178:PRO:HB3	1.84	0.59
1:F3:254:THR:O	1:F3:258:ILE:HG22	2.02	0.59
1:J5:166:GLU:H	1:J5:209:GLN:HE22	1.50	0.59
1:J9:88:GLN:O	1:J9:92:VAL:HG23	2.01	0.59
2:L4:63:LYS:O	2:L4:66:ILE:HG22	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:b3:259:MET:HE3	9:b3:263:ILE:HD11	1.84	0.59
1:A3:20:ASP:OD2	1:K3:1:MET:HG3	2.03	0.59
1:B4:48:VAL:O	1:B4:52:MET:HG3	2.02	0.59
1:B5:219:ARG:HD2	1:C5:116:GLN:HG3	1.85	0.59
1:C2:1:MET:HE1	1:C2:273:LYS:HG2	1.85	0.59
1:C6:223:ALA:O	1:C6:227:LEU:HD23	2.03	0.59
1:J7:2:ILE:HD11	1:J8:239:SER:HB2	1.83	0.59
2:N2:287:VAL:O	2:N2:290:ILE:HG22	2.02	0.59
5:X4:191:LEU:HG	5:X4:192:LEU:HD12	1.84	0.59
1:C3:237:SER:O	1:C3:241:ILE:HG12	2.02	0.59
1:C7:82:GLU:O	1:C7:86:ILE:HG12	2.02	0.59
1:H7:67:GLU:O	1:H7:70:MET:HG2	2.02	0.59
1:J8:48:VAL:O	1:J8:52:MET:HG3	2.03	0.59
2:O1:246:MET:O	2:O1:250:THR:HG23	2.01	0.59
5:V2:137:VAL:HG22	5:V2:221:LEU:HA	1.84	0.59
10:c3:93:SER:O	10:c3:97:ILE:HG13	2.03	0.59
1:B5:202:ALA:O	1:B5:206:ILE:HG13	2.02	0.59
1:E3:70:MET:HE2	1:E3:221:GLU:HA	1.84	0.59
1:F1:27:ILE:HG12	1:F1:253:PHE:CE2	2.37	0.59
1:K3:260:THR:O	1:K3:264:THR:HG23	2.01	0.59
1:K8:72:LEU:HD11	1:K8:135:LEU:HD11	1.84	0.59
2:P6:262:TYR:O	2:P6:266:VAL:HG13	2.03	0.59
3:R2:195:ILE:CD1	3:R3:230:TYR:HB3	2.33	0.59
3:R4:34:MET:HE1	3:R4:219:PHE:CD2	2.37	0.59
3:S6:30:VAL:HG22	3:S6:114:GLU:HB3	1.84	0.59
6:Y2:108:PHE:HA	6:Y2:148:GLU:HG3	1.84	0.59
8:a1:77:PHE:CE2	8:a1:77:PHE:CE1	2.89	0.59
8:a1:128:GLU:HB3	8:a1:154:ASN:HB2	1.84	0.59
8:a5:90:THR:HG22	8:a5:107:SER:O	2.03	0.59
1:D3:201:ASP:O	1:D3:205:VAL:HG23	2.03	0.59
1:J7:72:LEU:HD13	1:J8:101:ILE:HG22	1.84	0.59
1:J7:255:ARG:O	1:J7:259:LEU:HD23	2.02	0.59
1:K4:117:LEU:O	1:K4:121:ILE:HG13	2.02	0.59
2:N2:201:ILE:HD11	2:N2:216:ILE:HB	1.85	0.59
6:Y1:31:ARG:HH11	6:Y1:66:HIS:CE1	2.21	0.59
1:E4:168:MET:HE1	1:E4:209:GLN:HG3	1.83	0.59
5:V2:82:LYS:HG2	5:V2:90:VAL:HG12	1.84	0.59
5:X3:103:ILE:HA	5:X3:219:ASP:HB2	1.85	0.59
8:a2:54:ILE:HG13	8:a2:159:VAL:HG21	1.85	0.59
1:A7:153:ILE:HD13	1:B7:123:ARG:HE	1.67	0.59
1:F5:257:GLN:O	1:F5:260:THR:HG22	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J7:87:VAL:HA	1:J7:90:VAL:HG12	1.85	0.59
1:A5:118:VAL:HA	1:A5:121:ILE:HD12	1.85	0.59
1:F5:158:HIS:HA	1:F6:193:ASN:HD21	1.68	0.59
1:G1:49:SER:O	1:G1:53:ARG:HD2	2.03	0.59
2:M3:118:ARG:O	2:M3:121:VAL:HG12	2.02	0.59
2:O1:157:LYS:O	2:O1:161:LYS:HG2	2.03	0.59
2:P6:201:ILE:HD11	2:P6:216:ILE:HB	1.84	0.59
5:V3:181:GLY:HA3	6:Y3:40:VAL:HB	1.84	0.59
5:V3:188:ARG:HG3	6:Y3:43:HIS:HE1	1.67	0.59
6:Y2:130:LYS:NZ	6:Y2:147:PRO:HG2	2.15	0.59
7:Z2:290:MET:HE1	7:Z2:311:TYR:CD1	2.38	0.59
1:I9:120:GLU:O	1:I9:124:ILE:HG13	2.02	0.58
2:M1:82:ASN:OD1	2:M1:84:THR:HG22	2.02	0.58
1:B4:3:ILE:HD11	1:B4:278:MET:SD	2.43	0.58
1:B5:215:ALA:O	1:B5:219:ARG:HG3	2.03	0.58
1:D4:159:GLN:HG2	1:E4:127:GLN:NE2	2.18	0.58
1:F5:50:GLU:HG3	1:F6:84:HIS:CE1	2.37	0.58
1:H8:157:MET:HG2	1:H8:158:HIS:CD2	2.38	0.58
1:J9:83:THR:O	1:J9:87:VAL:HG23	2.03	0.58
4:U6:287:ASN:HA	4:U6:290:ILE:HG12	1.85	0.58
7:Z0:22:GLU:HB3	7:Z0:23:PRO:HD3	1.85	0.58
1:A4:223:ALA:O	1:A4:227:LEU:HG	2.03	0.58
1:I6:257:GLN:O	1:I6:260:THR:HG22	2.03	0.58
1:J5:3:ILE:HD12	1:J6:246:MET:HG3	1.83	0.58
6:Y3:46:THR:HG23	6:Y3:48:LYS:H	1.68	0.58
6:Y4:180:LYS:HA	6:Y4:183:ILE:HD11	1.84	0.58
1:C5:49:SER:O	1:C5:53:ARG:HG3	2.03	0.58
1:E5:65:ASN:HB3	1:E6:99:ASN:HD22	1.68	0.58
1:G1:101:ILE:HD12	1:G1:101:ILE:O	2.03	0.58
1:K7:49:SER:HA	1:K7:52:MET:HE3	1.85	0.58
1:E2:1:MET:HE1	1:E2:273:LYS:HG2	1.84	0.58
1:E3:166:GLU:H	1:E3:209:GLN:NE2	2.02	0.58
1:G8:168:MET:HE3	1:G8:209:GLN:HB2	1.86	0.58
1:I7:199:CYS:O	1:I7:203:LEU:HD23	2.03	0.58
5:V2:74:LYS:HZ3	5:V2:102:HIS:CD2	2.21	0.58
1:A7:72:LEU:HD13	1:A8:101:ILE:HG22	1.85	0.58
1:B8:69:GLY:O	1:B8:73:ILE:HG12	2.03	0.58
1:D3:168:MET:HE1	1:D3:206:ILE:HA	1.85	0.58
1:E3:177:ASN:HD21	2:M1:166:ASN:HD21	1.52	0.58
1:G7:273:LYS:HE3	1:H7:23:LEU:HD23	1.85	0.58
1:I6:153:ILE:HG21	1:I6:220:MET:HE2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L2:118:ARG:O	2:L2:121:VAL:HG12	2.04	0.58
2:N5:204:GLU:HG2	2:N5:209:ASN:HB2	1.85	0.58
6:Y4:131:LYS:HA	6:Y4:134:MET:SD	2.44	0.58
1:I8:175:LEU:HD22	1:I8:184:ILE:HD13	1.86	0.58
1:K7:76:ALA:HB2	1:K7:135:LEU:HD11	1.85	0.58
2:M4:259:LYS:HB2	8:a4:93:ARG:HH21	1.68	0.58
2:P5:95:PHE:CD1	2:P5:178:ILE:HG12	2.38	0.58
4:U6:170:PRO:HD3	7:Z2:197:GLU:HG2	1.86	0.58
5:V4:50:LEU:HD13	5:V4:221:LEU:HG	1.84	0.58
1:G8:191:LYS:O	1:G8:195:VAL:HG23	2.03	0.58
1:I5:52:MET:O	1:I5:56:ILE:HG13	2.04	0.58
2:M4:168:PHE:O	2:M4:172:ILE:HG13	2.03	0.58
2:O3:243:GLU:HG2	2:O3:260:TYR:CE1	2.39	0.58
3:S3:124:THR:HG21	3:S3:207:ASN:ND2	2.18	0.58
5:V3:183:ILE:HG23	5:V3:185:GLN:HG3	1.84	0.58
1:A7:118:VAL:HG13	1:A7:170:THR:HG21	1.85	0.58
1:J8:237:SER:OG	1:K8:71:SER:HB3	2.04	0.58
2:L2:82:ASN:HD21	2:L3:268:LEU:HD21	1.68	0.58
3:Q1:224:ARG:HA	3:Q1:227:ASN:ND2	2.19	0.58
3:Q3:175:SER:HB2	3:Q4:35:LYS:HD2	1.86	0.58
3:R5:34:MET:HE2	3:R5:222:ASN:HB2	1.85	0.58
1:D7:201:ASP:O	1:D7:205:VAL:HG23	2.03	0.58
1:H6:154:GLY:HA3	1:H6:159:GLN:HE21	1.69	0.58
3:Q4:100:PHE:HB2	3:Q4:121:LYS:HB3	1.85	0.58
5:X1:60:ARG:HG2	5:X1:121:TYR:HB2	1.86	0.58
1:A6:76:ALA:HB2	1:A6:135:LEU:HD23	1.86	0.57
1:G1:46:LEU:HD21	1:G2:210:ARG:NH2	2.19	0.57
1:G1:80:LEU:HA	1:G1:83:THR:HG22	1.86	0.57
2:M3:263:LYS:HA	2:M3:266:VAL:HG12	1.86	0.57
3:R3:34:MET:HE1	3:R3:219:PHE:CD1	2.39	0.57
3:S2:161:GLN:HE21	3:S2:164:ASP:HA	1.68	0.57
5:X4:131:LYS:HG3	5:X4:185:GLN:HE21	1.68	0.57
8:a2:56:ARG:O	8:a2:60:GLU:HG3	2.04	0.57
1:A8:66:THR:HG21	1:A8:224:ALA:HB2	1.86	0.57
1:B5:191:LYS:O	1:B5:195:VAL:HG23	2.03	0.57
1:F1:247:ALA:HB3	1:G5:13:HIS:HD2	1.68	0.57
5:V3:80:LEU:HD23	5:V3:82:LYS:HE3	1.86	0.57
8:a3:188:TRP:O	8:a3:192:ARG:HG3	2.04	0.57
1:G7:4:ASN:HB3	1:G8:243:ASP:OD2	2.05	0.57
1:J8:191:LYS:O	1:J8:195:VAL:HG23	2.04	0.57
1:J9:173:LEU:HD22	1:J9:202:ALA:HB1	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O1:272:THR:HG21	2:O1:286:ILE:HG13	1.84	0.57
3:Q3:166:PRO:HD3	3:Q3:179:VAL:HG13	1.86	0.57
1:A8:223:ALA:O	1:A8:227:LEU:HD23	2.04	0.57
1:E1:3:ILE:HD12	1:E2:246:MET:HG3	1.86	0.57
1:F5:154:GLY:HA3	1:F5:159:GLN:HE21	1.68	0.57
1:G7:223:ALA:O	1:G7:227:LEU:HD23	2.04	0.57
1:I4:1:MET:HG2	1:I4:277:VAL:HG11	1.87	0.57
3:Q1:72:HIS:NE2	3:Q1:96:LYS:HG3	2.20	0.57
1:B3:52:MET:O	1:B3:56:ILE:HG13	2.04	0.57
1:I7:186:LEU:HD21	1:I7:195:VAL:HG11	1.85	0.57
1:I9:153:ILE:HD11	1:I9:220:MET:SD	2.45	0.57
1:K8:191:LYS:O	1:K8:195:VAL:HG23	2.05	0.57
2:O1:236:LEU:HD13	2:O1:267:HIS:CE1	2.39	0.57
2:O2:155:ARG:HH11	2:O2:155:ARG:HG3	1.69	0.57
4:U3:37:VAL:HG11	4:U3:273:GLY:HA2	1.86	0.57
9:b3:119:LEU:O	9:b3:144:ARG:HA	2.04	0.57
1:E7:140:PHE:CD1	1:E7:140:PHE:CZ	2.92	0.57
1:J9:120:GLU:O	1:J9:124:ILE:HG13	2.04	0.57
2:L4:118:ARG:O	2:L4:121:VAL:HG12	2.05	0.57
2:M2:98:ASN:HD22	3:Q2:89:ASN:ND2	2.01	0.57
3:S4:161:GLN:HA	3:S4:166:PRO:HG2	1.86	0.57
5:V3:50:LEU:HD11	5:V3:126:TYR:HB3	1.86	0.57
1:A5:212:ASP:HA	1:B5:116:GLN:HE22	1.67	0.57
1:I7:281:LEU:HD21	1:J7:267:LEU:HD22	1.85	0.57
1:J5:159:GLN:HG2	1:K4:127:GLN:NE2	2.19	0.57
1:K3:1:MET:HE2	1:K3:277:VAL:HG22	1.85	0.57
2:O5:198:ARG:O	2:O5:202:MET:HG3	2.05	0.57
2:P4:286:ILE:HA	2:P4:289:VAL:HG22	1.87	0.57
1:G9:60:ARG:HG3	1:G9:60:ARG:HH11	1.70	0.57
1:K7:150:TRP:CZ3	1:K7:162:ARG:HB2	2.39	0.57
2:L2:86:GLN:HA	2:L2:89:HIS:CE1	2.40	0.57
2:O4:209:ASN:HB3	2:O4:212:GLN:OE1	2.05	0.57
2:P4:201:ILE:HD11	2:P4:216:ILE:HB	1.85	0.57
5:V1:142:ARG:HH12	5:V1:217:TYR:HE1	1.51	0.57
1:C3:233:ASN:ND2	1:D3:74:GLN:HE21	2.02	0.57
1:H5:1:MET:HG2	1:H5:277:VAL:HG11	1.87	0.57
2:L3:150:GLU:HG3	8:a2:99:TYR:HB3	1.85	0.57
2:M1:286:ILE:HA	2:M1:289:VAL:HG12	1.87	0.57
2:N4:98:ASN:HD22	3:R4:89:ASN:ND2	2.03	0.57
3:Q3:30:VAL:HG23	3:Q3:111:PRO:O	2.05	0.57
3:Q4:97:MET:HE1	3:Q4:124:THR:OG1	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X4:106:VAL:HG11	5:X4:120:LEU:HD11	1.87	0.57
1:B3:35:ARG:HB2	1:B3:244:THR:HB	1.87	0.57
1:E2:140:PHE:CE1	1:E2:149:MET:HG2	2.40	0.57
1:J8:169:ASN:HD22	1:J8:171:ALA:H	1.51	0.57
2:L2:286:ILE:HA	2:L2:289:VAL:HG22	1.86	0.57
2:L5:286:ILE:HA	2:L5:289:VAL:HG22	1.85	0.57
2:N2:201:ILE:HD12	2:N2:217:LEU:HG	1.87	0.57
3:S2:100:PHE:HB2	3:S2:121:LYS:HB3	1.87	0.57
5:V2:180:PRO:HD2	5:V2:183:ILE:HD12	1.87	0.57
8:a3:60:GLU:HG2	8:a3:198:ARG:HD2	1.86	0.57
1:B5:252:SER:O	1:B5:255:ARG:HG2	2.05	0.56
1:J6:24:SER:O	1:J6:28:GLU:HG3	2.05	0.56
2:O1:184:ARG:HD3	2:O1:189:PHE:CE1	2.40	0.56
3:S6:14:LEU:HD13	3:S6:201:LYS:HB2	1.87	0.56
5:X4:45:LEU:HD11	5:X4:224:ARG:HB3	1.87	0.56
1:C3:6:ASN:O	1:C3:10:ILE:HG13	2.04	0.56
1:E2:66:THR:HG21	1:E2:224:ALA:HB2	1.87	0.56
1:F3:191:LYS:O	1:F3:195:VAL:HG23	2.06	0.56
1:I6:266:MET:HE3	1:J6:30:LEU:HD13	1.87	0.56
1:J8:10:ILE:H	1:J8:10:ILE:HD12	1.69	0.56
1:J8:44:SER:O	1:J8:48:VAL:HG12	2.05	0.56
2:M3:258:PHE:C	2:M3:258:PHE:CD1	2.83	0.56
2:N5:169:SER:O	2:N5:172:ILE:HG22	2.05	0.56
3:S4:93:LYS:HG3	3:S4:128:GLN:HG2	1.87	0.56
9:b4:256:GLN:O	9:b4:260:ILE:HG12	2.05	0.56
1:B3:52:MET:HE2	1:B3:234:THR:HG23	1.85	0.56
1:B6:50:GLU:O	1:B6:54:THR:HG23	2.05	0.56
1:C7:84:HIS:CD2	1:C7:88:GLN:HE21	2.23	0.56
1:D3:184:ILE:HD11	1:D3:195:VAL:HG22	1.87	0.56
1:H6:150:TRP:CZ3	1:H6:162:ARG:HB2	2.41	0.56
1:J6:201:ASP:O	1:J6:205:VAL:HG23	2.05	0.56
1:J8:258:ILE:HD11	1:K7:275:GLN:HA	1.86	0.56
1:K3:1:MET:HB2	1:K3:277:VAL:HG11	1.87	0.56
1:K5:62:ALA:O	1:K5:66:THR:HG23	2.04	0.56
2:L2:90:GLN:HB3	2:L2:93:LYS:HG2	1.87	0.56
2:L5:151:ARG:O	2:L5:155:ARG:HG3	2.05	0.56
5:V1:137:VAL:HG23	5:V1:220:ASP:O	2.05	0.56
6:Y1:25:LEU:HA	6:Y1:253:ARG:HH12	1.69	0.56
6:Y3:149:PRO:HB2	6:Y3:154:VAL:HG13	1.88	0.56
8:a2:137:LEU:HD21	8:a2:142:LYS:HB3	1.87	0.56
1:C7:83:THR:O	1:C7:87:VAL:HG23	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F4:50:GLU:O	1:F4:54:THR:HG23	2.05	0.56
1:G7:55:GLN:O	1:G7:59:LEU:HD23	2.05	0.56
1:H5:17:LYS:HD3	1:H6:228:MET:HE3	1.88	0.56
1:I8:60:ARG:HD3	1:I8:231:TYR:CE1	2.41	0.56
2:M5:107:TYR:O	2:M5:111:VAL:HG23	2.04	0.56
2:O4:214:ILE:HB	2:O4:215:PRO:HD3	1.87	0.56
5:X2:191:LEU:HD23	5:X2:191:LEU:H	1.70	0.56
6:Y4:130:LYS:O	6:Y4:134:MET:HG3	2.06	0.56
9:b4:234:TYR:O	9:b4:238:LEU:HD23	2.05	0.56
1:A4:30:LEU:HD23	1:A4:246:MET:HG2	1.87	0.56
1:J4:46:LEU:O	1:J4:50:GLU:HG3	2.05	0.56
2:O5:161:LYS:HD3	2:O5:206:ASP:HB2	1.87	0.56
4:U4:250:THR:HB	4:U4:261:PRO:HB2	1.87	0.56
5:V3:199:VAL:O	5:V3:200:SER:HB2	2.04	0.56
5:X1:143:LYS:HA	5:X1:168:ASP:HA	1.86	0.56
9:b4:61:LEU:HD13	9:b4:128:PRO:HG3	1.88	0.56
1:F2:169:ASN:HD21	1:F2:171:ALA:HB3	1.71	0.56
1:I6:201:ASP:O	1:I6:205:VAL:HG23	2.05	0.56
1:K6:91:ARG:O	1:K6:95:VAL:HG23	2.05	0.56
7:Za:132:LYS:HA	7:Za:137:ARG:HD3	1.87	0.56
1:B5:44:SER:O	1:B5:48:VAL:HG22	2.04	0.56
1:B6:43:ALA:HB1	1:B7:211:ALA:HA	1.88	0.56
1:C4:60:ARG:HH11	1:C4:60:ARG:HG2	1.71	0.56
1:E2:219:ARG:HD3	1:F2:116:GLN:HB3	1.87	0.56
1:E6:110:ILE:O	1:E6:114:VAL:HG23	2.06	0.56
2:O4:67:MET:HA	2:O4:70:GLU:HG2	1.87	0.56
3:Q1:45:LEU:HD12	3:Q1:73:LEU:HD13	1.87	0.56
1:A6:72:LEU:HD13	1:A7:101:ILE:HG22	1.87	0.56
1:B7:258:ILE:HD11	1:C6:275:GLN:HG3	1.88	0.56
1:G8:133:MET:HE1	1:G8:149:MET:HE1	1.87	0.56
1:H7:157:MET:HG2	1:H7:158:HIS:HD2	1.70	0.56
1:H9:123:ARG:NH1	1:H9:127:GLN:HE22	2.04	0.56
1:K6:87:VAL:HA	1:K6:90:VAL:HG12	1.87	0.56
2:O2:219:LEU:O	2:O2:223:ILE:HG12	2.05	0.56
6:Y4:208:THR:HG22	6:Y4:219:THR:HB	1.86	0.56
1:F2:230:ALA:O	1:F2:234:THR:HG23	2.06	0.56
1:J7:14:ARG:HG2	1:J8:228:MET:HE2	1.87	0.56
1:K4:217:TYR:CD1	1:K5:40:GLY:HA3	2.41	0.56
1:K6:157:MET:HE2	1:K7:197:GLY:HA3	1.87	0.56
2:L1:172:ILE:HD11	6:Y1:94:TRP:CZ3	2.40	0.56
3:R3:26:ARG:HD2	3:R3:118:ASN:HA	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:V3:151:LYS:HB3	5:V3:200:SER:HB3	1.87	0.56
6:Y1:39:PHE:CE2	6:Y1:236:VAL:HG11	2.40	0.56
9:b3:234:TYR:CE2	9:b3:238:LEU:HD11	2.41	0.56
9:b4:48:ASN:HB2	9:b4:179:LEU:HD11	1.87	0.56
1:A3:278:MET:HE2	1:A4:246:MET:HE2	1.88	0.56
1:A5:11:PHE:HZ	1:B5:37:ASN:ND2	2.04	0.56
1:C5:68:ASP:HB3	1:C6:101:ILE:HD13	1.87	0.56
1:H6:1:MET:HE2	1:H6:1:MET:N	2.20	0.56
1:K6:281:LEU:HD12	1:K7:250:MET:HG2	1.88	0.56
2:L2:272:THR:HG21	2:L2:286:ILE:HG12	1.88	0.56
2:M2:204:GLU:HG3	2:M2:209:ASN:HB2	1.88	0.56
2:M3:201:ILE:HG12	2:M3:217:LEU:HD22	1.87	0.56
2:O5:242:PHE:CZ	2:O5:246:MET:HE3	2.41	0.56
3:Q4:91:GLY:HA2	3:Q4:131:PHE:CD2	2.41	0.56
3:R3:173:THR:HG22	3:R3:175:SER:H	1.71	0.56
3:S5:163:ASP:HB3	3:S5:165:TYR:HE1	1.71	0.56
6:Y4:37:VAL:HG21	6:Y4:254:LYS:HD2	1.88	0.56
1:B4:194:SER:O	1:B4:198:LEU:HD23	2.06	0.55
1:B6:39:ALA:HB2	1:B7:77:GLU:HG2	1.88	0.55
1:H5:247:ALA:O	1:H5:251:THR:HG23	2.06	0.55
1:I7:52:MET:O	1:I7:56:ILE:HG13	2.05	0.55
1:I8:258:ILE:HD11	1:J7:275:GLN:HG2	1.88	0.55
1:K4:101:ILE:HD13	1:K5:68:ASP:HB3	1.88	0.55
2:M4:63:LYS:O	2:M4:67:MET:HG2	2.06	0.55
2:O1:263:LYS:HE3	2:O1:267:HIS:CE1	2.41	0.55
3:S4:119:LEU:H	3:S4:147:ASN:ND2	2.05	0.55
5:V1:103:ILE:HG22	5:V1:219:ASP:OD2	2.05	0.55
7:Z2:287:LEU:HD11	7:Z2:291:PHE:HB2	1.88	0.55
8:a5:222:MET:HA	8:a5:225:ASP:OD2	2.07	0.55
1:C7:52:MET:HE1	1:C7:241:ILE:HG13	1.88	0.55
1:I6:52:MET:O	1:I6:56:ILE:HG13	2.06	0.55
1:J8:162:ARG:HD3	1:J8:164:TYR:CZ	2.40	0.55
1:K4:91:ARG:O	1:K4:95:VAL:HG23	2.06	0.55
2:L2:265:ASN:ND2	2:L2:290:ILE:HG23	2.21	0.55
5:V3:128:ILE:HD11	5:V3:223:VAL:HG21	1.88	0.55
1:E3:88:GLN:O	1:E3:92:VAL:HG23	2.07	0.55
1:G9:30:LEU:HD21	1:G9:249:GLN:HB3	1.87	0.55
1:H9:111:GLN:HE22	1:H9:185:SER:HA	1.71	0.55
1:I9:157:MET:HE2	1:I9:158:HIS:CE1	2.40	0.55
2:N5:70:GLU:O	2:N5:74:LYS:HB2	2.07	0.55
3:Q1:36:VAL:HA	3:Q1:222:ASN:HD21	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R2:28:HIS:HE1	3:R2:216:THR:HG23	1.71	0.55
4:U4:244:ASN:HA	9:b3:48:ASN:HB3	1.88	0.55
5:X3:49:VAL:HG22	5:X3:222:GLN:HG3	1.89	0.55
1:B6:66:THR:HG23	1:B6:220:MET:HG3	1.88	0.55
1:D2:237:SER:O	1:D2:241:ILE:HG13	2.06	0.55
1:E3:177:ASN:HB3	1:E3:180:VAL:O	2.06	0.55
1:G2:91:ARG:O	1:G2:95:VAL:HG23	2.06	0.55
1:J5:52:MET:O	1:J5:56:ILE:HG13	2.06	0.55
1:J6:72:LEU:HD13	1:J7:101:ILE:HG22	1.88	0.55
2:M2:221:ILE:HG23	2:M2:227:GLU:HB2	1.88	0.55
2:N2:118:ARG:O	2:N2:121:VAL:HG12	2.07	0.55
2:P5:204:GLU:HG3	2:P5:209:ASN:HB2	1.89	0.55
3:R2:144:VAL:HG22	3:R2:155:LYS:HB3	1.88	0.55
9:b3:117:VAL:HB	9:b3:147:ALA:HB3	1.87	0.55
1:A4:202:ALA:O	1:A4:206:ILE:HG13	2.07	0.55
1:A5:114:VAL:O	1:A5:118:VAL:HG13	2.06	0.55
1:A8:170:THR:HG23	1:A8:175:LEU:HB2	1.87	0.55
1:G1:123:ARG:HD2	1:G1:127:GLN:HG3	1.88	0.55
1:I8:168:MET:O	1:I8:168:MET:HG3	2.07	0.55
1:I9:88:GLN:O	1:I9:92:VAL:HG23	2.06	0.55
2:L3:149:GLU:O	2:L3:153:VAL:HG22	2.07	0.55
3:Q2:235:GLU:HA	3:Q2:238:LYS:HE2	1.88	0.55
3:S2:28:HIS:CD2	3:S2:215:PHE:HB3	2.42	0.55
1:A3:44:SER:O	1:A3:48:VAL:HG23	2.06	0.55
1:D5:258:ILE:HD11	1:E4:275:GLN:HG2	1.89	0.55
1:G7:191:LYS:O	1:G7:195:VAL:HG23	2.07	0.55
1:J6:68:ASP:HB3	1:J7:101:ILE:HD13	1.89	0.55
2:M1:145:ARG:HG2	2:M1:145:ARG:HH11	1.72	0.55
2:P4:283:TYR:O	2:P4:287:VAL:HG22	2.06	0.55
7:Z0:207:ARG:O	7:Z0:211:ILE:HG12	2.05	0.55
9:b3:60:ASN:O	9:b3:64:ILE:HG12	2.05	0.55
1:B5:88:GLN:O	1:B5:92:VAL:HG13	2.06	0.55
1:E5:258:ILE:HD11	1:F4:275:GLN:HG2	1.88	0.55
1:F1:258:ILE:HG22	1:G5:3:ILE:HD11	1.87	0.55
1:G7:54:THR:HG21	1:G8:203:LEU:HD13	1.88	0.55
2:N4:161:LYS:HG3	2:N4:206:ASP:OD2	2.07	0.55
2:N6:315:LEU:HD23	2:N6:334:LEU:HG	1.87	0.55
5:X4:56:ALA:HB1	5:X4:104:LEU:HD22	1.88	0.55
1:A3:264:THR:HG23	1:K3:280:LEU:HD22	1.89	0.55
1:C5:48:VAL:HG12	1:C5:52:MET:HE3	1.89	0.55
1:C5:127:GLN:O	1:C5:129:GLU:HG2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E5:56:ILE:HD11	1:E5:235:GLN:N	2.22	0.55
1:G6:159:GLN:HG2	1:H6:127:GLN:CD	2.32	0.55
1:J6:261:GLN:HG3	1:K4:278:MET:HE2	1.88	0.55
7:Z1:290:MET:HG3	7:Z1:311:TYR:CE1	2.41	0.55
1:B5:11:PHE:CE1	1:C5:28:GLU:HG3	2.42	0.55
1:F6:191:LYS:O	1:F6:195:VAL:HG23	2.06	0.55
1:K8:73:ILE:HG21	1:K8:217:TYR:HB2	1.89	0.55
2:M5:256:MET:HE2	8:a5:97:LEU:HD22	1.89	0.55
2:O1:214:ILE:HD12	2:O1:240:TYR:CE1	2.41	0.55
2:O2:88:LEU:HD11	2:O3:276:TYR:CE2	2.42	0.55
2:O2:214:ILE:HB	2:O2:215:PRO:HD3	1.89	0.55
1:h0:201:ASP:O	1:h0:205:VAL:HG23	2.07	0.55
1:B5:25:LYS:O	1:B5:29:LYS:HG2	2.07	0.55
1:B5:25:LYS:O	1:B5:28:GLU:HG2	2.05	0.55
1:B8:111:GLN:NE2	1:B8:185:SER:HA	2.22	0.55
1:C5:118:VAL:HG13	1:C5:170:THR:HG21	1.89	0.55
1:I6:209:GLN:O	1:I6:213:LEU:HD23	2.07	0.55
2:L2:120:TRP:CH2	2:L2:156:GLU:HG3	2.42	0.55
2:O1:110:GLY:O	2:O1:113:THR:HG22	2.07	0.55
4:U5:198:MET:SD	4:U5:202:LYS:HE3	2.46	0.55
8:a3:43:LEU:H	8:a3:43:LEU:HD23	1.72	0.55
8:a4:64:TYR:O	8:a4:68:ILE:HG12	2.06	0.55
1:G5:27:ILE:HD11	1:G5:253:PHE:HE1	1.72	0.54
1:I7:1:MET:HE2	1:I7:1:MET:H1	1.72	0.54
1:K3:5:HIS:CE1	1:K5:53:ARG:HH22	2.25	0.54
2:L5:210:LEU:O	2:L5:213:THR:HG22	2.07	0.54
3:S4:140:VAL:HG22	3:S4:159:PHE:HB3	1.89	0.54
9:b4:60:ASN:O	9:b4:64:ILE:HG12	2.06	0.54
1:A4:219:ARG:HG2	1:B4:120:GLU:CG	2.37	0.54
1:C7:191:LYS:O	1:C7:195:VAL:HG23	2.07	0.54
1:D3:10:ILE:HD11	1:D4:231:TYR:CE2	2.42	0.54
1:E6:247:ALA:O	1:E6:251:THR:HG23	2.07	0.54
1:K4:192:ALA:O	1:K4:196:ILE:HG13	2.07	0.54
2:O1:181:PRO:O	2:O1:185:GLU:HG2	2.07	0.54
3:Q1:72:HIS:CD2	3:Q1:96:LYS:HG3	2.42	0.54
5:V1:220:ASP:O	5:V1:221:LEU:HD12	2.08	0.54
6:Y4:79:ASP:HB2	6:Y4:81:VAL:HG12	1.87	0.54
6:Y4:250:LEU:HD21	6:Y4:253:ARG:HG3	1.88	0.54
1:A7:35:ARG:HG3	1:A7:36:ILE:HG13	1.89	0.54
1:B4:152:HIS:CD2	1:B5:95:VAL:HG13	2.42	0.54
1:H9:219:ARG:HG2	1:H9:219:ARG:HH11	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I7:108:GLN:O	1:I7:112:VAL:HG13	2.07	0.54
2:P6:243:GLU:O	2:P6:247:ILE:HG12	2.06	0.54
5:X3:137:VAL:HG23	5:X3:220:ASP:O	2.07	0.54
9:b2:119:LEU:O	9:b2:144:ARG:HA	2.07	0.54
1:A3:253:PHE:CE2	1:K3:266:MET:HE1	2.42	0.54
1:B4:73:ILE:HD12	1:B4:213:LEU:HD22	1.90	0.54
1:C6:118:VAL:HG13	1:C6:170:THR:HG21	1.90	0.54
1:F4:14:ARG:HG3	1:F5:228:MET:HB3	1.89	0.54
1:H7:138:GLY:HA3	1:H7:167:THR:HG22	1.90	0.54
1:I8:170:THR:OG1	1:I8:175:LEU:HB2	2.08	0.54
2:O5:145:ARG:HH11	2:O5:145:ARG:HG3	1.72	0.54
5:V2:198:PHE:CE2	5:V2:221:LEU:HD21	2.43	0.54
1:D4:1:MET:HG2	1:D4:277:VAL:HG11	1.89	0.54
1:I5:65:ASN:ND2	1:I6:99:ASN:HD22	2.05	0.54
1:J4:254:THR:O	1:J4:258:ILE:HG22	2.07	0.54
1:J8:257:GLN:O	1:J8:261:GLN:HG2	2.07	0.54
2:O5:214:ILE:HB	2:O5:215:PRO:HD3	1.88	0.54
9:b4:58:ILE:HD11	9:b4:135:LEU:HG	1.90	0.54
1:I7:175:LEU:HD22	1:I7:184:ILE:HD13	1.88	0.54
1:J7:67:GLU:HA	1:J7:70:MET:HE3	1.90	0.54
1:J8:67:GLU:HA	1:J8:70:MET:HE3	1.89	0.54
2:L2:262:TYR:O	2:L2:266:VAL:HG12	2.06	0.54
2:P3:214:ILE:HB	2:P3:215:PRO:HD3	1.88	0.54
3:S5:26:ARG:HD2	3:S5:118:ASN:HA	1.88	0.54
7:Z2:126:ILE:HG22	7:Z2:165:LYS:HD3	1.89	0.54
10:c2:118:MET:HG3	10:c2:126:TYR:CZ	2.43	0.54
1:B3:247:ALA:O	1:B3:251:THR:HG23	2.07	0.54
1:C6:4:ASN:HB3	1:C7:243:ASP:OD2	2.08	0.54
1:F4:254:THR:O	1:F4:258:ILE:HG22	2.08	0.54
1:G1:118:VAL:HG13	1:G1:170:THR:HG21	1.88	0.54
1:G8:49:SER:OG	1:G8:242:ARG:HD2	2.08	0.54
1:J5:150:TRP:CZ3	1:J5:162:ARG:HB2	2.43	0.54
1:K8:181:LEU:HB2	7:Z2:174:LEU:HD21	1.89	0.54
2:M3:75:ASN:HB2	2:M4:202:MET:HE3	1.88	0.54
2:O3:246:MET:O	2:O3:250:THR:HG23	2.08	0.54
3:R2:100:PHE:HB2	3:R2:121:LYS:HB3	1.89	0.54
3:R5:66:GLN:HE22	3:R5:107:ALA:HA	1.72	0.54
7:Z2:113:LYS:N	7:Z2:120:ASP:OD2	2.40	0.54
8:a5:71:LYS:HB3	8:a5:208:ILE:HG21	1.89	0.54
1:G6:156:ASN:HB2	1:G6:159:GLN:NE2	2.23	0.54
1:H6:161:GLU:HG3	1:H6:219:ARG:HH22	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I6:114:VAL:O	1:I6:118:VAL:HG12	2.08	0.54
1:J6:65:ASN:HD21	1:J7:99:ASN:HB2	1.72	0.54
2:N4:127:GLU:HG2	2:N4:131:LYS:HZ2	1.72	0.54
3:R2:47:LYS:HE2	3:R2:63:GLN:HE21	1.72	0.54
3:R3:125:TYR:CE1	3:R3:138:ILE:HG23	2.42	0.54
3:R4:187:VAL:HA	3:R5:230:TYR:HE2	1.72	0.54
1:F5:39:ALA:HB2	1:F6:210:ARG:HG3	1.90	0.54
1:F5:168:MET:HE3	1:F5:209:GLN:HG2	1.90	0.54
1:G6:239:SER:O	1:G6:243:ASP:HB2	2.08	0.54
1:G8:158:HIS:H	1:G9:193:ASN:HD21	1.56	0.54
1:H7:67:GLU:HA	1:H7:70:MET:HE3	1.89	0.54
1:I6:50:GLU:CD	1:I6:242:ARG:HH12	2.16	0.54
1:I7:153:ILE:HD11	1:I7:161:GLU:HG2	1.90	0.54
1:I9:159:GLN:HE22	1:J9:129:GLU:CD	2.16	0.54
1:K7:53:ARG:NE	1:K7:242:ARG:HH11	2.06	0.54
3:R1:122:ILE:HG23	3:R1:146:PRO:HG3	1.90	0.54
8:a1:81:ILE:HD13	8:a1:113:LEU:HD13	1.89	0.54
9:b4:103:ILE:HD12	9:b4:241:ILE:HG23	1.89	0.54
1:A5:66:THR:OG1	1:A5:220:MET:HG3	2.07	0.54
1:B5:30:LEU:HD21	1:B5:249:GLN:HB3	1.90	0.54
1:C3:47:ALA:HB2	1:D4:109:GLN:HE22	1.71	0.54
1:E1:25:LYS:HG2	1:E1:38:LYS:HE2	1.90	0.54
1:G9:161:GLU:HG3	1:G9:219:ARG:NH2	2.23	0.54
1:H6:238:GLU:OE2	1:H6:242:ARG:HD2	2.08	0.54
1:J6:48:VAL:O	1:J6:52:MET:HG3	2.07	0.54
1:K4:173:LEU:HD22	1:K4:202:ALA:HB1	1.90	0.54
2:N5:217:LEU:HB3	2:N5:236:LEU:HD11	1.90	0.54
2:P2:286:ILE:HA	2:P2:289:VAL:HG22	1.89	0.54
2:P3:104:LEU:O	2:P3:108:GLN:HG2	2.08	0.54
3:R4:100:PHE:CD1	3:R4:121:LYS:HE3	2.42	0.54
4:U4:230:ASN:O	4:U4:234:VAL:HG12	2.08	0.54
9:b3:78:GLN:HA	9:b3:84:PRO:HA	1.90	0.54
1:D4:49:SER:OG	1:D4:242:ARG:HD2	2.08	0.53
1:F2:169:ASN:HD22	1:F2:171:ALA:H	1.55	0.53
1:J4:11:PHE:CE2	1:K5:28:GLU:HG3	2.43	0.53
1:J9:150:TRP:CZ2	1:J9:162:ARG:HD2	2.44	0.53
1:K5:221:GLU:O	1:K5:225:LYS:HG3	2.08	0.53
2:L2:217:LEU:HD22	2:L2:236:LEU:HD22	1.89	0.53
2:P2:104:LEU:O	2:P2:108:GLN:HG2	2.08	0.53
3:Q2:102:GLU:O	3:Q2:117:ARG:HD2	2.08	0.53
3:Q4:125:TYR:HE1	3:Q4:127:TYR:HB2	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U6:35:ILE:HD11	4:U6:117:VAL:HG21	1.89	0.53
6:Y2:110:ASN:HD21	6:Y2:222:HIS:HA	1.73	0.53
1:A5:13:HIS:HD2	1:K6:247:ALA:HB3	1.72	0.53
1:F1:50:GLU:HG2	1:F2:84:HIS:NE2	2.23	0.53
1:I6:1:MET:HE1	1:J6:16:LEU:HD11	1.90	0.53
1:J6:240:ARG:HE	1:K6:67:GLU:HB3	1.73	0.53
1:J7:1:MET:HE1	1:K7:16:LEU:HD11	1.89	0.53
1:J8:156:ASN:HB2	1:J8:159:GLN:NE2	2.24	0.53
1:J8:166:GLU:H	1:J8:209:GLN:NE2	2.06	0.53
2:M1:175:LEU:HD12	2:M1:196:VAL:HG11	1.89	0.53
2:M2:228:LYS:HE2	2:M2:274:LEU:HD11	1.89	0.53
2:N1:65:GLU:O	2:N1:69:GLN:HG2	2.08	0.53
2:N4:268:LEU:HD11	2:N4:286:ILE:HD12	1.90	0.53
2:P3:215:PRO:O	2:P3:219:LEU:HD12	2.07	0.53
2:P5:285:HIS:O	2:P5:289:VAL:HG13	2.08	0.53
3:Q4:10:THR:O	3:Q4:13:GLU:HG2	2.08	0.53
4:U5:134:PRO:HB2	4:U6:291:LYS:HG2	1.90	0.53
1:A5:261:GLN:HG3	1:B4:279:ARG:HH21	1.72	0.53
1:E1:1:MET:HG3	1:F1:20:ASP:OD2	2.08	0.53
1:E3:10:ILE:HG23	1:E4:232:GLU:HG3	1.89	0.53
1:H6:157:MET:HG2	1:H6:158:HIS:CD2	2.43	0.53
2:P4:126:LYS:HB3	9:b4:254:LEU:HD21	1.89	0.53
4:U4:43:ALA:HB2	4:U4:282:LEU:HD11	1.89	0.53
1:C6:1:MET:HE1	1:D6:16:LEU:HD11	1.90	0.53
1:E1:21:ALA:O	1:E1:25:LYS:HG3	2.07	0.53
1:F4:281:LEU:HD11	1:G9:267:LEU:HD22	1.91	0.53
1:F5:149:MET:HE2	1:F5:149:MET:HA	1.89	0.53
1:G1:91:ARG:O	1:G1:95:VAL:HG23	2.08	0.53
2:L1:197:TYR:O	2:L1:201:ILE:HG13	2.08	0.53
2:O4:204:GLU:HG3	2:O4:209:ASN:HB2	1.90	0.53
2:P3:126:LYS:CD	9:b3:258:GLN:HE22	2.21	0.53
5:V1:45:LEU:HD12	6:Y1:182:VAL:HG11	1.91	0.53
5:X4:154:ASP:HA	5:X4:196:LEU:HD12	1.90	0.53
6:Y1:161:ASN:HD21	6:Y1:164:LYS:HE2	1.73	0.53
8:a4:93:ARG:HB3	8:a4:105:MET:HG2	1.91	0.53
1:B7:123:ARG:HD2	1:B7:123:ARG:C	2.33	0.53
1:F2:150:TRP:CZ3	1:F2:162:ARG:HB2	2.43	0.53
1:G7:150:TRP:CZ3	1:G7:162:ARG:HB2	2.43	0.53
1:J6:151:PHE:HA	1:J7:99:ASN:ND2	2.24	0.53
2:N6:246:ARG:O	2:N6:250:VAL:HG12	2.09	0.53
2:O3:214:ILE:HB	2:O3:215:PRO:HD3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P5:284:LYS:O	2:P5:287:VAL:HG22	2.09	0.53
3:Q4:227:ASN:O	3:Q4:231:LYS:HG3	2.09	0.53
5:V2:181:GLY:HA3	6:Y2:40:VAL:HG22	1.91	0.53
1:C5:86:ILE:HG21	1:C5:121:ILE:HG13	1.90	0.53
1:F4:86:ILE:HG23	1:F4:117:LEU:HD22	1.91	0.53
1:G6:59:LEU:HD12	1:G6:227:LEU:HD22	1.91	0.53
1:I9:186:LEU:HD11	1:I9:195:VAL:HG11	1.89	0.53
1:J4:255:ARG:HD2	1:K3:4:ASN:O	2.08	0.53
1:K4:177:ASN:HB3	1:K4:180:VAL:O	2.08	0.53
4:U4:25:ILE:HD11	4:U4:88:ASN:CG	2.34	0.53
5:V2:187:THR:HG22	5:V2:188:ARG:O	2.09	0.53
5:V4:146:HIS:NE2	5:V4:209:GLU:HG2	2.24	0.53
1:A6:267:LEU:HD11	1:K7:247:ALA:HB1	1.90	0.53
1:C4:112:VAL:O	1:C4:116:GLN:HG2	2.07	0.53
1:D4:177:ASN:HB3	1:D4:180:VAL:O	2.08	0.53
1:H8:219:ARG:HD2	1:I8:116:GLN:HB3	1.91	0.53
1:I6:86:ILE:HG23	1:I6:117:LEU:HD12	1.90	0.53
1:K8:168:MET:HE1	1:K8:206:ILE:HG12	1.91	0.53
2:P5:214:ILE:HB	2:P5:215:PRO:HD3	1.89	0.53
3:R1:75:VAL:HG22	3:R1:95:LYS:HG2	1.90	0.53
5:V1:127:ILE:HG12	5:V1:197:HIS:CE1	2.44	0.53
5:V4:154:ASP:HA	5:V4:196:LEU:HD12	1.90	0.53
1:A5:40:GLY:HA3	1:A6:217:TYR:CD1	2.43	0.53
1:F2:168:MET:HE1	1:F2:205:VAL:HG12	1.90	0.53
1:I6:113:GLU:O	1:I6:117:LEU:HD23	2.08	0.53
1:K8:113:GLU:O	1:K8:117:LEU:HD23	2.09	0.53
2:O4:221:ILE:HD12	2:O4:227:GLU:HA	1.90	0.53
2:P3:145:ARG:O	2:P3:149:GLU:HG2	2.09	0.53
5:X2:137:VAL:HG23	5:X2:220:ASP:O	2.08	0.53
8:a4:169:VAL:HG13	8:a4:169:VAL:O	2.09	0.53
1:C2:17:LYS:HD2	1:C3:228:MET:HE3	1.89	0.53
1:C6:49:SER:OG	1:C6:242:ARG:HD2	2.08	0.53
1:G1:123:ARG:HE	1:G1:124:ILE:HD13	1.74	0.53
1:I8:11:PHE:CE2	1:J8:28:GLU:HG3	2.44	0.53
2:P5:268:LEU:O	2:P5:272:THR:HG22	2.09	0.53
3:Q1:189:ASN:ND2	3:Q1:196:ARG:HB2	2.24	0.53
3:S6:29:THR:HG21	3:S6:117:ARG:HG2	1.91	0.53
5:V3:119:GLU:HG3	5:V3:202:PHE:HB3	1.91	0.53
6:Y1:134:MET:HE3	6:Y1:147:PRO:HG3	1.90	0.53
7:Z0:8:TYR:CZ	7:Z0:12:ILE:HD11	2.44	0.53
1:B5:46:LEU:HD21	1:B6:210:ARG:HH21	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E3:184:ILE:HD13	1:E3:195:VAL:HG13	1.91	0.53
1:F4:258:ILE:HG12	1:G8:3:ILE:HD11	1.90	0.53
1:F5:67:GLU:HA	1:F5:70:MET:HE3	1.90	0.53
1:H5:237:SER:O	1:H5:241:ILE:HD12	2.09	0.53
1:I8:11:PHE:CZ	1:J8:28:GLU:HG3	2.44	0.53
1:J7:182:THR:HG22	4:U4:164:THR:HG23	1.91	0.53
2:N4:270:ARG:CZ	2:N4:274:LEU:HD21	2.39	0.53
3:R1:123:ARG:HH22	3:R1:168:TRP:HZ2	1.56	0.53
5:V1:85:PHE:HE1	6:Y2:48:LYS:HA	1.74	0.53
5:V2:146:HIS:CE1	5:V2:209:GLU:HG2	2.44	0.53
5:X1:103:ILE:HG22	5:X1:219:ASP:HB2	1.91	0.53
5:X4:132:VAL:HA	5:X4:225:THR:HG22	1.91	0.53
9:b3:105:LEU:HB2	9:b3:122:GLY:HA3	1.91	0.53
1:B3:56:ILE:HG12	1:B3:234:THR:HG22	1.91	0.52
1:B4:248:GLU:CD	1:C4:60:ARG:HH22	2.18	0.52
1:E4:51:LYS:O	1:E4:54:THR:HG22	2.09	0.52
1:G5:4:ASN:HB3	1:G6:243:ASP:OD2	2.08	0.52
1:I7:86:ILE:HG23	1:I7:117:LEU:HD12	1.92	0.52
1:J7:73:ILE:HG23	1:J7:213:LEU:HD12	1.91	0.52
1:K5:266:MET:HA	1:K5:266:MET:HE3	1.90	0.52
2:O4:215:PRO:O	2:O4:219:LEU:HD23	2.10	0.52
2:P4:241:SER:HB3	2:P4:264:LYS:HD2	1.91	0.52
3:R2:47:LYS:H	3:R2:63:GLN:NE2	2.02	0.52
3:R5:73:LEU:HD21	3:R5:214:LEU:HD23	1.90	0.52
3:S2:115:GLN:OE1	3:S2:116:PRO:HD2	2.09	0.52
3:S3:202:GLN:NE2	3:S4:238:LYS:HG3	2.24	0.52
7:Z2:138:GLN:O	7:Z2:144:PRO:HG2	2.09	0.52
1:A8:52:MET:O	1:A8:56:ILE:HG13	2.09	0.52
1:D5:16:LEU:HD11	1:D5:264:THR:HG22	1.92	0.52
1:E4:7:VAL:HA	1:E4:10:ILE:HG22	1.90	0.52
1:G2:175:LEU:HD22	1:G2:184:ILE:HD13	1.92	0.52
1:I4:273:LYS:HD3	1:J4:23:LEU:HD23	1.91	0.52
1:J7:219:ARG:HH22	1:K7:119:ASP:HB3	1.73	0.52
2:L4:210:LEU:O	2:L4:213:THR:HG22	2.10	0.52
2:P3:66:ILE:O	2:P3:70:GLU:HG2	2.10	0.52
3:Q2:78:PHE:HB2	3:Q2:86:SER:HB2	1.91	0.52
3:S2:154:ASP:HA	3:S2:183:ILE:HD11	1.90	0.52
6:Y2:121:ILE:HD13	6:Y2:157:TYR:CD2	2.45	0.52
6:Y3:134:MET:HG2	6:Y3:146:MET:HE2	1.91	0.52
6:Y4:148:GLU:HG3	6:Y4:149:PRO:CD	2.38	0.52
1:B7:123:ARG:HD2	1:B7:123:ARG:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C4:74:GLN:O	1:C4:77:GLU:HG3	2.08	0.52
1:E5:157:MET:HG3	1:E5:158:HIS:CD2	2.44	0.52
1:I8:219:ARG:HH22	1:J8:119:ASP:HB3	1.74	0.52
1:J6:87:VAL:HA	1:J6:90:VAL:HG12	1.90	0.52
2:L1:90:GLN:HG3	8:a1:144:PRO:HG3	1.92	0.52
2:P2:210:LEU:O	2:P2:213:THR:HG22	2.09	0.52
3:R1:144:VAL:HG22	3:R1:155:LYS:HB3	1.91	0.52
5:V4:45:LEU:HD11	6:Y4:210:TYR:CZ	2.43	0.52
1:A3:3:ILE:HD11	1:A3:278:MET:HG3	1.92	0.52
1:A5:12:ALA:O	1:A5:15:THR:HG22	2.10	0.52
1:A5:150:TRP:CZ3	1:A5:162:ARG:HB2	2.44	0.52
1:A6:110:ILE:O	1:A6:114:VAL:HG23	2.10	0.52
1:B6:114:VAL:O	1:B6:118:VAL:HG12	2.09	0.52
1:E2:140:PHE:CZ	1:E2:149:MET:HG2	2.45	0.52
1:K4:108:GLN:O	1:K4:112:VAL:HG23	2.10	0.52
2:L1:172:ILE:HD11	6:Y1:94:TRP:HZ3	1.74	0.52
2:M3:88:LEU:HD11	2:M4:282:GLU:HA	1.91	0.52
3:Q1:184:LEU:O	3:Q1:187:VAL:HG12	2.08	0.52
5:V1:170:PHE:CE1	6:Y2:47:GLY:HA2	2.35	0.52
6:Y1:73:LEU:O	6:Y1:236:VAL:HA	2.10	0.52
1:A7:153:ILE:CD1	1:B7:123:ARG:HE	2.22	0.52
1:B4:66:THR:HG23	1:B4:220:MET:HG3	1.91	0.52
1:B6:49:SER:HB2	1:B6:242:ARG:HD2	1.91	0.52
1:C3:247:ALA:O	1:C3:251:THR:HG23	2.09	0.52
1:F4:56:ILE:HD11	1:F4:235:GLN:N	2.24	0.52
1:H6:154:GLY:HA3	1:H6:159:GLN:NE2	2.25	0.52
1:I4:3:ILE:HG13	1:I4:278:MET:SD	2.49	0.52
1:K4:181:LEU:HD11	7:Za:178:HIS:CE1	2.45	0.52
1:K8:150:TRP:CZ3	1:K8:162:ARG:HB2	2.45	0.52
2:L4:286:ILE:HA	2:L4:289:VAL:HG22	1.91	0.52
2:M4:268:LEU:O	2:M4:272:THR:HG23	2.10	0.52
2:O5:117:ASN:HD21	2:O5:157:LYS:HG2	1.73	0.52
2:P5:283:TYR:O	2:P5:287:VAL:HG13	2.09	0.52
5:V2:181:GLY:H	6:Y2:38:THR:HG21	1.74	0.52
7:Z0:188:ASN:HA	7:Z0:191:LYS:HG2	1.91	0.52
7:Z1:210:ARG:HH22	10:c3:151:TYR:HE1	1.56	0.52
8:a2:82:LYS:HG3	8:a2:83:ASP:OD1	2.10	0.52
9:b4:185:ILE:HG13	9:b4:185:ILE:O	2.09	0.52
1:E3:248:GLU:O	1:E3:251:THR:HG22	2.08	0.52
1:E4:89:ARG:HH21	1:E4:92:VAL:HB	1.74	0.52
1:F1:266:MET:HE3	1:G6:30:LEU:HD23	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G7:250:MET:O	1:G7:254:THR:HG23	2.10	0.52
1:J6:244:THR:CG2	1:J6:249:GLN:HG3	2.40	0.52
1:K6:61:ARG:HD3	1:K7:96:GLN:HB2	1.91	0.52
2:L1:82:ASN:HD21	2:L1:84:THR:CG2	2.23	0.52
2:L5:178:ILE:HD12	2:L5:189:PHE:HE2	1.75	0.52
2:N6:237:TYR:O	2:N6:241:VAL:HG12	2.10	0.52
5:V1:45:LEU:HD11	6:Y1:210:TYR:CE1	2.44	0.52
9:b4:44:GLY:HA3	9:b4:181:THR:HB	1.92	0.52
1:B4:202:ALA:O	1:B4:205:VAL:HG12	2.09	0.52
1:J4:11:PHE:HE2	1:K5:28:GLU:HG3	1.75	0.52
1:J4:271:ASN:O	1:J4:275:GLN:HG3	2.09	0.52
1:J6:127:GLN:O	1:J6:129:GLU:HG3	2.10	0.52
1:J8:199:CYS:O	1:J8:203:LEU:HD12	2.10	0.52
9:b3:187:LEU:HD13	9:b4:263:ILE:HG21	1.91	0.52
1:A7:159:GLN:HG2	1:B7:127:GLN:NE2	2.25	0.52
1:A8:219:ARG:NH2	1:B8:119:ASP:HB3	2.24	0.52
1:B5:114:VAL:O	1:B5:118:VAL:HG22	2.10	0.52
1:E4:176:ARG:HG2	1:E4:183:PHE:HA	1.90	0.52
1:F2:1:MET:HG2	1:G7:20:ASP:OD2	2.10	0.52
1:H5:44:SER:O	1:H5:48:VAL:HG23	2.09	0.52
1:I9:53:ARG:HA	1:I9:56:ILE:HG22	1.91	0.52
1:J6:133:MET:HA	1:J6:133:MET:HE3	1.92	0.52
2:N3:88:LEU:HD21	2:N4:276:TYR:CE2	2.45	0.52
2:O4:223:ILE:HG22	2:O4:225:ASP:OD1	2.09	0.52
2:P3:130:GLU:HG3	9:b3:254:LEU:HD11	1.92	0.52
4:U6:39:LEU:HD22	4:U6:73:TYR:HB3	1.91	0.52
5:V3:78:ARG:HB3	5:V4:236:GLU:OE2	2.10	0.52
5:X3:135:ILE:HD12	5:X3:152:PHE:HZ	1.74	0.52
5:X4:127:ILE:HG12	5:X4:197:HIS:CD2	2.44	0.52
5:X4:220:ASP:CG	12:X4:401:HOH:O	2.49	0.52
8:a3:67:MET:HE2	8:a3:205:ALA:HB1	1.91	0.52
8:a3:181:LEU:O	8:a3:190:ARG:HD3	2.10	0.52
8:a4:169:VAL:HG23	8:a4:174:ASP:N	2.25	0.52
1:B6:110:ILE:O	1:B6:114:VAL:HG23	2.09	0.52
1:B7:191:LYS:O	1:B7:195:VAL:HG23	2.10	0.52
1:D6:186:LEU:HD11	1:D6:195:VAL:HG11	1.92	0.52
1:E4:150:TRP:CZ3	1:E4:162:ARG:HB2	2.45	0.52
1:F4:47:ALA:HB2	1:G1:109:GLN:HE22	1.75	0.52
1:J7:65:ASN:CG	1:J8:99:ASN:HD22	2.18	0.52
2:L3:64:LYS:O	2:L3:68:GLU:HG3	2.10	0.52
2:P3:286:ILE:HA	2:P3:289:VAL:HG22	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P5:201:ILE:HD12	2:P5:217:LEU:HG	1.91	0.52
2:P5:223:ILE:HB	2:P5:226:ASN:HB2	1.91	0.52
3:R2:160:TYR:HB2	3:R3:233:ASN:ND2	2.21	0.52
5:V4:45:LEU:HA	5:V4:225:THR:O	2.10	0.52
6:Y3:106:LEU:O	6:Y3:148:GLU:HB2	2.10	0.52
6:Y3:151:PHE:CZ	6:Y3:237:ALA:HB2	2.45	0.52
1:E6:86:ILE:HG23	1:E6:117:LEU:HD22	1.91	0.52
1:H5:258:ILE:HG21	1:I4:3:ILE:HD12	1.90	0.52
1:H8:76:ALA:O	1:H8:80:LEU:HD23	2.10	0.52
1:J6:257:GLN:O	1:J6:261:GLN:HG2	2.10	0.52
2:M4:259:LYS:HD3	8:a4:93:ARG:HH22	1.74	0.52
2:P3:268:LEU:O	2:P3:272:THR:HG22	2.10	0.52
2:P5:209:ASN:HD22	2:P5:209:ASN:N	2.08	0.52
6:Y3:50:GLU:HG3	6:Y3:226:TYR:HE1	1.75	0.52
1:A4:73:ILE:HG21	1:A4:217:TYR:HB2	1.91	0.51
1:E3:150:TRP:CZ3	1:E3:162:ARG:HB2	2.45	0.51
1:F2:38:LYS:HE2	1:F3:74:GLN:HE21	1.74	0.51
1:H6:261:GLN:HB3	1:I5:278:MET:HE3	1.92	0.51
2:P4:205:TYR:CE2	2:P4:210:LEU:HD21	2.45	0.51
3:R3:173:THR:HG23	3:R3:174:PRO:HD2	1.92	0.51
3:S2:99:LEU:HD22	3:S2:119:LEU:HD12	1.93	0.51
5:V1:50:LEU:HD12	5:V1:50:LEU:O	2.10	0.51
6:Y3:91:TYR:OH	6:Y3:95:ARG:HD3	2.10	0.51
6:Y3:134:MET:HE2	6:Y3:138:HIS:CE1	2.44	0.51
8:a4:146:THR:HG22	8:a4:170:THR:HG23	1.92	0.51
8:a4:214:ALA:HA	8:a4:217:ASN:ND2	2.24	0.51
9:b4:61:LEU:HD23	9:b4:64:ILE:HD11	1.92	0.51
1:i0:114:VAL:O	1:i0:118:VAL:HG13	2.09	0.51
1:B7:257:GLN:OE1	1:B7:258:ILE:HD13	2.10	0.51
1:D5:226:GLY:HA2	1:E5:82:GLU:HG3	1.91	0.51
1:E5:24:SER:O	1:E5:28:GLU:HG3	2.10	0.51
1:G6:247:ALA:O	1:G6:251:THR:HG23	2.10	0.51
1:H6:15:THR:HG21	1:I6:32:SER:HA	1.92	0.51
1:J8:68:ASP:OD1	1:J9:101:ILE:HD13	2.11	0.51
3:Q1:34:MET:SD	3:Q1:222:ASN:HB3	2.50	0.51
4:U6:263:ASP:HB3	4:U6:266:GLU:OE1	2.09	0.51
6:Y2:32:ILE:HG23	6:Y2:252:PHE:HE2	1.74	0.51
8:a2:53:LYS:HE2	8:a2:191:LEU:HD21	1.93	0.51
1:A6:278:MET:HB2	1:K7:258:ILE:HG23	1.92	0.51
1:D5:281:LEU:HB3	1:D6:250:MET:SD	2.50	0.51
1:D6:248:GLU:O	1:D6:251:THR:HG22	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E5:177:ASN:HB3	1:E5:180:VAL:O	2.10	0.51
1:E6:56:ILE:HD11	1:E6:235:GLN:HA	1.92	0.51
1:J8:114:VAL:O	1:J8:118:VAL:HG13	2.10	0.51
2:L4:283:TYR:O	2:L4:287:VAL:HG13	2.09	0.51
3:R5:31:LEU:O	3:R5:47:LYS:HE2	2.09	0.51
3:S4:28:HIS:HE1	3:S4:212:ASP:OD1	1.92	0.51
4:U6:191:LYS:O	4:U6:195:ILE:HG13	2.10	0.51
8:a5:41:ILE:HG22	8:a5:185:GLN:NE2	2.25	0.51
1:A6:2:ILE:HD12	1:A7:239:SER:HB3	1.91	0.51
1:C4:204:ARG:HH12	1:D4:105:GLU:CD	2.17	0.51
1:G6:135:LEU:HA	1:G6:140:PHE:HE2	1.76	0.51
1:I7:1:MET:HE3	1:J7:16:LEU:HG	1.91	0.51
2:N4:138:TRP:CZ3	2:O3:246:MET:HE2	2.46	0.51
2:O3:137:LYS:HE2	2:P3:209:ASN:HA	1.93	0.51
4:U6:287:ASN:HA	4:U6:290:ILE:CG1	2.41	0.51
5:X1:108:THR:HG22	5:X1:109:HIS:N	2.25	0.51
5:X3:110:PHE:HE1	5:X3:118:VAL:HG23	1.75	0.51
6:Y3:227:ARG:HG2	6:Y3:227:ARG:HH11	1.76	0.51
7:Z1:159:ALA:HB1	7:Z1:163:TYR:CZ	2.46	0.51
7:Za:296:PRO:HG2	7:Za:299:TYR:HD2	1.75	0.51
9:b3:50:ILE:HD12	9:b3:231:MET:HE3	1.92	0.51
1:D5:6:ASN:O	1:D5:10:ILE:HG13	2.10	0.51
1:E3:204:ARG:HD3	1:F3:105:GLU:HG3	1.93	0.51
1:F4:191:LYS:O	1:F4:195:VAL:HG23	2.11	0.51
1:J6:152:HIS:H	1:J7:99:ASN:HD22	1.56	0.51
2:L3:282:GLU:O	2:L3:286:ILE:HD13	2.10	0.51
2:L5:187:PRO:HA	2:L5:190:LYS:HE2	1.91	0.51
2:O1:270:ARG:NH2	3:R1:213:LYS:HE2	2.25	0.51
2:P1:88:LEU:HD21	2:P2:276:TYR:HE2	1.75	0.51
2:P4:104:LEU:O	2:P4:108:GLN:HG3	2.10	0.51
3:R3:73:LEU:HD21	3:R3:214:LEU:HD23	1.92	0.51
3:R4:122:ILE:HG12	3:R4:143:ASP:HB3	1.92	0.51
3:R5:140:VAL:HG12	3:R5:159:PHE:HB3	1.92	0.51
4:U5:276:THR:HG22	4:U5:278:LYS:H	1.76	0.51
8:a2:81:ILE:HG12	8:a2:86:TYR:HB2	1.92	0.51
8:a5:105:MET:HG2	8:a5:135:LYS:HG2	1.92	0.51
9:b3:211:ILE:HD11	9:b4:263:ILE:HG13	1.93	0.51
1:A7:74:GLN:HG3	1:K7:233:ASN:HD21	1.75	0.51
1:B5:133:MET:HE2	1:B5:133:MET:HA	1.92	0.51
1:B6:186:LEU:HD23	1:B6:195:VAL:HG21	1.92	0.51
1:C4:118:VAL:HG13	1:C4:170:THR:HG21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G9:219:ARG:HH21	1:H9:123:ARG:HD3	1.76	0.51
1:H6:176:ARG:HD3	1:H6:181:LEU:HD22	1.91	0.51
1:H6:219:ARG:CD	1:I6:120:GLU:HB2	2.41	0.51
1:I6:80:LEU:HD21	1:I6:168:MET:SD	2.50	0.51
1:I9:73:ILE:HG21	1:I9:217:TYR:HB2	1.93	0.51
1:J6:269:GLN:HE21	1:K6:257:GLN:HE22	1.59	0.51
1:J7:156:ASN:HB2	1:J7:159:GLN:NE2	2.26	0.51
1:K6:39:ALA:HB2	1:K7:77:GLU:CD	2.36	0.51
1:K7:153:ILE:CG2	1:K7:220:MET:HE1	2.41	0.51
4:U6:43:ALA:HB2	4:U6:282:LEU:HD11	1.92	0.51
5:V1:142:ARG:O	5:V1:143:LYS:HG2	2.11	0.51
5:X2:103:ILE:HG22	5:X2:219:ASP:HB2	1.93	0.51
5:X3:110:PHE:CE1	5:X3:118:VAL:HG23	2.45	0.51
1:G9:208:LYS:HE3	1:H9:112:VAL:HG21	1.91	0.51
1:I5:150:TRP:CZ2	1:I5:162:ARG:HD2	2.45	0.51
1:J6:105:GLU:O	1:J6:109:GLN:HG2	2.11	0.51
1:J7:133:MET:HE1	1:J8:100:GLY:O	2.10	0.51
1:J8:266:MET:HE1	1:K8:253:PHE:CE2	2.46	0.51
2:M2:263:LYS:HA	2:M2:266:VAL:HG12	1.92	0.51
2:P6:214:ILE:HB	2:P6:215:PRO:HD3	1.91	0.51
3:R2:125:TYR:CE1	3:R2:138:ILE:HG23	2.46	0.51
3:S2:115:GLN:CD	3:S2:116:PRO:HD2	2.35	0.51
3:S5:163:ASP:HB3	3:S5:165:TYR:CE1	2.46	0.51
3:S5:184:LEU:HD11	3:S5:200:LYS:HE3	1.91	0.51
1:A4:63:GLU:OE2	1:A4:228:MET:HG2	2.10	0.51
1:A4:216:TYR:O	1:A4:219:ARG:HB2	2.09	0.51
1:A4:278:MET:HE2	1:A5:246:MET:HB3	1.93	0.51
1:A6:170:THR:OG1	1:A6:175:LEU:HB2	2.11	0.51
1:C3:154:GLY:CA	1:C3:159:GLN:HG2	2.35	0.51
1:E1:7:VAL:HA	1:E1:10:ILE:HG22	1.92	0.51
1:E2:220:MET:HA	1:E2:220:MET:HE3	1.92	0.51
1:E4:86:ILE:HG23	1:E4:117:LEU:HD22	1.92	0.51
1:E5:153:ILE:HG22	1:E5:153:ILE:O	2.11	0.51
1:F3:258:ILE:HG12	1:G7:3:ILE:HD11	1.92	0.51
1:H8:15:THR:HG21	1:I8:32:SER:HA	1.93	0.51
1:K5:153:ILE:HD11	1:K5:161:GLU:OE1	2.10	0.51
2:N4:157:LYS:O	2:N4:161:LYS:HG2	2.10	0.51
2:N5:204:GLU:CG	2:N5:209:ASN:HB2	2.41	0.51
3:R2:125:TYR:HE1	3:R2:138:ILE:HG23	1.76	0.51
3:S2:7:MET:HE1	3:S2:191:LYS:HA	1.92	0.51
4:U5:200:TYR:OH	4:U5:208:LYS:HE3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X3:138:TRP:CE2	5:X3:174:LYS:HB2	2.46	0.51
1:B6:11:PHE:CZ	1:C6:28:GLU:HG3	2.46	0.51
1:D7:74:GLN:HG3	1:D7:217:TYR:CE2	2.44	0.51
1:E4:88:GLN:O	1:E4:92:VAL:HG23	2.11	0.51
1:F2:50:GLU:HG3	1:F3:84:HIS:CE1	2.46	0.51
1:H7:211:ALA:HB2	1:I7:109:GLN:HE21	1.75	0.51
1:I8:248:GLU:O	1:I8:251:THR:HG22	2.11	0.51
1:K5:149:MET:HG3	1:K5:163:VAL:HB	1.92	0.51
3:S2:187:VAL:HA	3:S3:230:TYR:CE2	2.45	0.51
4:U4:41:ASN:HA	4:U4:279:LYS:HD2	1.93	0.51
5:V1:131:LYS:O	5:V1:225:THR:HA	2.11	0.51
5:X1:152:PHE:CE1	5:X1:162:ILE:HD11	2.45	0.51
5:X1:152:PHE:HD2	5:X1:196:LEU:HD11	1.76	0.51
1:B7:133:MET:HE2	1:B8:100:GLY:O	2.11	0.51
1:E2:14:ARG:HB2	1:E3:228:MET:HE2	1.93	0.51
1:G6:46:LEU:HD21	1:G7:210:ARG:HH21	1.76	0.51
1:G7:282:GLN:HE21	1:G8:30:LEU:HD21	1.76	0.51
2:P3:78:PHE:HE2	2:P4:234:LYS:HE3	1.75	0.51
3:R4:73:LEU:HD21	3:R4:214:LEU:HD23	1.91	0.51
4:U4:280:LEU:HD21	4:U4:285:GLU:HG3	1.93	0.51
6:Y3:175:GLY:HA2	6:Y3:213:LYS:HD2	1.92	0.51
6:Y4:182:VAL:HG22	6:Y4:184:TYR:HD2	1.76	0.51
9:b3:228:LYS:HE3	9:b3:232:MET:HE3	1.93	0.51
1:A4:50:GLU:HG2	1:A5:210:ARG:HH12	1.76	0.50
1:F6:136:LEU:HD12	1:F6:168:MET:HB3	1.92	0.50
1:K4:87:VAL:HA	1:K4:90:VAL:HG12	1.92	0.50
3:Q3:195:ILE:HG13	3:Q3:196:ARG:N	2.25	0.50
3:Q3:234:VAL:O	3:Q3:238:LYS:HG3	2.11	0.50
4:U5:129:LEU:HB3	4:U5:152:PHE:CZ	2.47	0.50
1:i0:201:ASP:O	1:i0:205:VAL:HG23	2.10	0.50
1:A5:120:GLU:HB2	1:K4:219:ARG:CD	2.41	0.50
1:B4:4:ASN:HB3	1:B5:243:ASP:CG	2.36	0.50
1:E5:86:ILE:HG23	1:E5:117:LEU:HD22	1.93	0.50
1:H6:66:THR:HG21	1:H6:224:ALA:HB2	1.92	0.50
1:I5:16:LEU:HD11	1:I5:264:THR:HG22	1.93	0.50
1:I9:25:LYS:HE2	1:I9:25:LYS:HA	1.93	0.50
2:N6:296:ARG:HA	2:N6:299:ILE:HD12	1.92	0.50
4:U6:208:LYS:HE3	4:U6:211:TYR:HB2	1.92	0.50
5:V1:109:HIS:HA	5:V1:213:ASP:HA	1.93	0.50
7:Z1:123:LEU:HD12	7:Z1:168:ILE:HG22	1.93	0.50
8:a2:181:LEU:HA	8:a2:184:ILE:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A4:223:ALA:HB2	1:B4:123:ARG:HH22	1.76	0.50
1:B4:24:SER:O	1:B4:28:GLU:HG3	2.10	0.50
1:B7:52:MET:HE1	1:B7:237:SER:HB3	1.91	0.50
1:C6:80:LEU:O	1:C6:206:ILE:HD11	2.11	0.50
1:D3:150:TRP:CZ3	1:D3:162:ARG:HB2	2.47	0.50
1:E4:191:LYS:O	1:E4:195:VAL:HG23	2.11	0.50
1:J6:84:HIS:CE1	1:J6:203:LEU:HD22	2.46	0.50
1:K6:29:LYS:HB2	1:K6:249:GLN:NE2	2.26	0.50
2:L4:263:LYS:HA	2:L4:266:VAL:HG12	1.94	0.50
3:Q1:187:VAL:CG2	3:Q1:195:ILE:HD11	2.42	0.50
3:S2:7:MET:HE2	3:S2:194:PRO:HB3	1.92	0.50
3:S5:100:PHE:HB2	3:S5:121:LYS:HB3	1.93	0.50
4:U5:202:LYS:HZ2	4:U5:247:MET:HA	1.76	0.50
1:h0:179:THR:HG23	1:h0:180:VAL:HG23	1.94	0.50
1:A4:266:MET:HG3	1:B4:27:ILE:HG23	1.92	0.50
1:A5:33:GLY:HA2	1:A5:246:MET:HE1	1.92	0.50
1:A8:216:TYR:HA	1:A8:219:ARG:HG3	1.92	0.50
1:B3:260:THR:O	1:B3:264:THR:HG22	2.12	0.50
1:B4:7:VAL:HA	1:B4:10:ILE:HD12	1.93	0.50
1:C8:95:VAL:HA	1:C8:196:ILE:HD11	1.94	0.50
1:D6:39:ALA:HA	1:D6:46:LEU:HD22	1.93	0.50
1:I7:153:ILE:HG21	1:I7:220:MET:HE1	1.94	0.50
1:I8:254:THR:O	1:I8:258:ILE:HD13	2.11	0.50
1:J6:176:ARG:NH2	1:J6:181:LEU:HB3	2.26	0.50
1:K5:25:LYS:O	1:K5:29:LYS:HG2	2.12	0.50
1:K6:215:ALA:O	1:K6:219:ARG:HG3	2.12	0.50
1:K7:281:LEU:HB3	1:K8:250:MET:HG3	1.93	0.50
2:L5:194:SER:HB2	2:L5:226:ASN:HD21	1.76	0.50
3:S2:144:VAL:HG22	3:S2:155:LYS:O	2.12	0.50
5:V4:77:GLN:HB2	5:V4:101:ASN:O	2.12	0.50
9:b4:234:TYR:CE1	9:b4:238:LEU:HD21	2.46	0.50
1:A6:240:ARG:NH2	1:B6:68:ASP:HA	2.27	0.50
1:C3:49:SER:O	1:C3:53:ARG:HG3	2.10	0.50
1:H9:30:LEU:HD21	1:H9:249:GLN:HB3	1.94	0.50
1:J5:1:MET:H2	1:J6:246:MET:N	2.08	0.50
3:R4:122:ILE:HG23	3:R4:146:PRO:HG3	1.93	0.50
3:S6:120:THR:HA	3:S6:146:PRO:HD2	1.93	0.50
4:U4:39:LEU:HD22	4:U4:73:TYR:HB3	1.94	0.50
5:V2:107:LYS:HE3	5:V2:215:TYR:CZ	2.46	0.50
5:X3:142:ARG:HB3	5:X3:170:PHE:CE1	2.46	0.50
9:b3:233:SER:O	9:b3:236:LYS:HG2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A6:152:HIS:CE1	1:A7:196:ILE:HD13	2.47	0.50
1:A7:23:LEU:HD23	1:K7:273:LYS:HZ3	1.77	0.50
1:B7:80:LEU:HA	1:B7:83:THR:HG22	1.94	0.50
1:F2:258:ILE:HG22	1:G6:3:ILE:HD12	1.92	0.50
1:F3:50:GLU:O	1:F3:54:THR:HG23	2.12	0.50
1:G6:46:LEU:HD21	1:G7:210:ARG:NH2	2.26	0.50
1:G7:80:LEU:HA	1:G7:83:THR:HG22	1.94	0.50
2:L4:215:PRO:HA	2:L4:218:GLU:HG2	1.94	0.50
2:N1:107:TYR:O	2:N1:111:VAL:HG23	2.11	0.50
3:Q1:90:LEU:HD22	3:Q1:132:LEU:HD22	1.93	0.50
3:Q1:122:ILE:CG2	3:Q1:143:ASP:HB3	2.42	0.50
3:Q3:7:MET:HE2	3:Q3:7:MET:H	1.75	0.50
3:S4:102:GLU:HG2	3:S4:118:ASN:HB2	1.92	0.50
1:A3:253:PHE:CZ	1:K3:266:MET:HE1	2.47	0.50
1:E2:153:ILE:HG21	1:E2:220:MET:HE1	1.94	0.50
1:G7:211:ALA:HB2	1:H7:109:GLN:HE21	1.76	0.50
1:I7:209:GLN:HE21	1:I7:213:LEU:HD22	1.75	0.50
1:I9:237:SER:O	1:I9:241:ILE:HD12	2.11	0.50
1:K4:106:ASP:O	1:K4:110:ILE:HG13	2.11	0.50
2:L2:93:LYS:HE2	8:a2:144:PRO:HB3	1.92	0.50
2:N6:334:LEU:HD13	2:N6:365:HIS:CE1	2.47	0.50
6:Y1:77:GLU:H	6:Y1:234:ASN:ND2	2.09	0.50
8:a1:204:VAL:O	8:a1:208:ILE:HD13	2.10	0.50
1:A6:82:GLU:OE2	1:K6:225:LYS:HG2	2.11	0.50
1:B4:255:ARG:HG2	1:B4:255:ARG:HH11	1.77	0.50
1:D3:7:VAL:HA	1:D3:10:ILE:HG22	1.93	0.50
1:D4:278:MET:HG2	1:D4:282:GLN:HG3	1.94	0.50
2:L2:82:ASN:ND2	2:L3:268:LEU:HD21	2.27	0.50
2:P2:270:ARG:HG2	2:P2:270:ARG:NH1	2.25	0.50
2:P5:75:ASN:HB2	2:P6:202:MET:HE3	1.93	0.50
3:Q2:125:TYR:HE1	3:Q2:127:TYR:HB2	1.77	0.50
3:R5:140:VAL:CG1	3:R5:159:PHE:HB3	2.41	0.50
3:S5:85:LYS:HE3	3:S5:90:LEU:HD11	1.92	0.50
4:U4:247:MET:HE2	4:U4:264:LEU:HD11	1.93	0.50
5:V3:98:ILE:CG2	5:V3:101:ASN:HD22	2.25	0.50
5:X2:154:ASP:HA	5:X2:196:LEU:HD12	1.93	0.50
7:Z0:75:SER:O	7:Z0:79:ARG:HG2	2.12	0.50
7:Z1:54:TYR:HB2	7:Z1:90:MET:HE1	1.94	0.50
7:Z1:122:ALA:O	7:Z1:126:ILE:HG13	2.11	0.50
1:B5:5:HIS:HB2	1:B6:239:SER:OG	2.12	0.50
1:I9:194:SER:O	1:I9:198:LEU:HD23	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J6:177:ASN:HB3	1:J6:180:VAL:O	2.12	0.50
2:N2:217:LEU:HB3	2:N2:236:LEU:HD21	1.93	0.50
2:O2:262:TYR:O	2:O2:266:VAL:HG13	2.12	0.50
2:P4:97:ASN:O	2:P4:101:ARG:HB2	2.11	0.50
3:Q3:122:ILE:HG12	3:Q3:143:ASP:HB3	1.93	0.50
3:Q4:85:LYS:HE2	3:Q4:88:LYS:HD2	1.94	0.50
6:Y3:23:TYR:C	6:Y3:25:LEU:H	2.20	0.50
6:Y3:155:VAL:HG13	6:Y3:239:LEU:HD21	1.93	0.50
7:Za:107:LYS:O	7:Za:110:MET:HG3	2.12	0.50
8:a2:170:THR:HG23	8:a2:173:ASP:H	1.76	0.50
1:D3:72:LEU:HD11	1:D3:149:MET:HE3	1.94	0.49
1:H7:43:ALA:HB1	1:H8:211:ALA:HA	1.93	0.49
1:J8:151:PHE:HD2	1:J8:220:MET:HE3	1.76	0.49
1:J9:140:PHE:CE2	1:J9:149:MET:HE3	2.47	0.49
4:U4:122:ILE:HA	4:U4:187:LEU:HD11	1.93	0.49
5:V1:107:LYS:HD3	5:V1:215:TYR:CE2	2.47	0.49
5:X3:53:PHE:CD2	5:X3:219:ASP:HA	2.47	0.49
6:Y2:187:VAL:HG23	6:Y2:201:THR:HB	1.93	0.49
7:Z2:60:ILE:HG22	7:Z2:83:CYS:HB2	1.93	0.49
1:D4:78:GLY:O	1:D4:82:GLU:HG2	2.12	0.49
1:I5:278:MET:HG2	1:I5:282:GLN:HE21	1.76	0.49
1:K7:39:ALA:HB2	1:K8:77:GLU:HG3	1.94	0.49
2:L4:154:TYR:CE1	2:L4:158:MET:HE3	2.47	0.49
2:M2:117:ASN:HD21	2:M2:157:LYS:HG2	1.77	0.49
2:O2:120:TRP:CH2	2:O2:156:GLU:HG3	2.47	0.49
3:S3:36:VAL:HG11	3:S3:45:LEU:HD22	1.94	0.49
4:U5:90:TRP:HE1	4:U5:299:GLU:HA	1.76	0.49
6:Y2:122:TRP:CE2	6:Y2:149:PRO:HG3	2.48	0.49
1:B8:110:ILE:O	1:B8:114:VAL:HG23	2.12	0.49
1:E5:150:TRP:CZ3	1:E5:162:ARG:HB2	2.47	0.49
1:E6:202:ALA:O	1:E6:206:ILE:HG12	2.12	0.49
1:G1:66:THR:HG23	1:G1:220:MET:HG3	1.94	0.49
1:G7:168:MET:HE3	1:G7:209:GLN:HG2	1.93	0.49
1:G7:248:GLU:CD	1:H7:60:ARG:HH21	2.20	0.49
1:H9:156:ASN:HB2	1:H9:159:GLN:NE2	2.26	0.49
1:K3:3:ILE:HD11	1:K5:246:MET:HE3	1.94	0.49
1:K4:36:ILE:HG23	1:K4:41:ASP:HB2	1.94	0.49
2:L1:104:LEU:HD23	2:L1:192:LEU:HD13	1.95	0.49
2:N3:254:ASP:O	2:N3:258:PHE:HD1	1.95	0.49
2:N4:117:ASN:HD21	2:N4:157:LYS:HA	1.75	0.49
2:O3:117:ASN:HD21	2:O3:157:LYS:HG2	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P6:268:LEU:O	2:P6:272:THR:HG22	2.11	0.49
3:R3:122:ILE:HG12	3:R3:143:ASP:HB3	1.94	0.49
3:R5:40:PRO:HG2	3:R5:43:THR:HG21	1.92	0.49
3:R5:133:LEU:HD22	3:R5:135:ASP:CG	2.36	0.49
3:S2:158:LEU:HD11	3:S2:184:LEU:HD13	1.94	0.49
4:U3:71:PHE:CE1	4:U3:74:PHE:HB2	2.47	0.49
1:A5:120:GLU:HB2	1:K4:219:ARG:HD3	1.95	0.49
1:C7:184:ILE:HG12	1:C7:195:VAL:HG22	1.93	0.49
1:D5:270:ALA:O	1:D5:273:LYS:HG2	2.12	0.49
1:E4:35:ARG:HG3	1:E4:244:THR:HA	1.94	0.49
1:E5:87:VAL:O	1:E5:90:VAL:HG12	2.11	0.49
1:H8:114:VAL:HG21	1:H8:186:LEU:HD22	1.94	0.49
1:K4:176:ARG:HD3	1:K4:181:LEU:HB2	1.95	0.49
2:L1:82:ASN:ND2	2:L1:85:PHE:H	2.11	0.49
2:L2:165:LEU:HD11	2:L2:204:GLU:HG3	1.94	0.49
2:L5:283:TYR:O	2:L5:286:ILE:HG22	2.11	0.49
2:N2:161:LYS:HG2	2:N2:206:ASP:OD2	2.12	0.49
3:R1:119:LEU:HG	3:R1:146:PRO:HG2	1.93	0.49
3:R2:195:ILE:HD13	3:R3:230:TYR:HB3	1.95	0.49
3:S2:161:GLN:NE2	3:S2:164:ASP:HA	2.27	0.49
3:S4:227:ASN:O	3:S4:231:LYS:HG3	2.11	0.49
3:S6:43:THR:HG22	3:S6:75:VAL:HG22	1.94	0.49
1:A6:55:GLN:O	1:A6:59:LEU:HD23	2.12	0.49
1:B8:104:GLU:HA	1:B8:107:ARG:HG2	1.94	0.49
1:C4:102:TYR:HB3	1:C4:106:ASP:HB2	1.93	0.49
1:C4:258:ILE:HD11	1:D3:275:GLN:HG2	1.94	0.49
1:I8:208:LYS:HA	1:J8:109:GLN:HE22	1.77	0.49
1:J9:130:PHE:O	1:J9:133:MET:HG2	2.12	0.49
1:K7:184:ILE:HD13	1:K7:195:VAL:HG13	1.94	0.49
2:M1:99:GLN:NE2	3:Q1:89:ASN:HD22	2.10	0.49
3:R1:212:ASP:O	3:R1:216:THR:HG23	2.13	0.49
5:V3:90:VAL:HG12	5:V3:91:PRO:HD2	1.95	0.49
10:c2:142:VAL:HG23	10:c2:155:SER:HB3	1.95	0.49
1:A5:202:ALA:O	1:A5:206:ILE:HG13	2.12	0.49
1:A7:127:GLN:NE2	1:K7:159:GLN:HA	2.26	0.49
1:B6:169:ASN:HD21	1:B6:171:ALA:HB3	1.77	0.49
1:C6:80:LEU:HD22	1:C6:206:ILE:HG13	1.95	0.49
1:D3:80:LEU:HD22	1:D3:168:MET:HE3	1.93	0.49
1:E4:255:ARG:O	1:E4:258:ILE:HG22	2.13	0.49
1:G8:239:SER:O	1:G8:243:ASP:HB2	2.11	0.49
1:G9:15:THR:HG21	1:H9:32:SER:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I9:43:ALA:HB1	1:I0:211:ALA:HA	1.93	0.49
1:J5:72:LEU:HD13	1:J6:101:ILE:HG22	1.94	0.49
1:J7:39:ALA:HB2	1:J8:77:GLU:CD	2.38	0.49
1:J8:209:GLN:O	1:J8:213:LEU:HD23	2.13	0.49
1:K7:153:ILE:HG21	1:K7:220:MET:HE1	1.94	0.49
2:N1:69:GLN:OE1	2:N2:229:GLU:HG2	2.13	0.49
3:R5:141:ILE:HG22	3:R5:158:LEU:HD22	1.94	0.49
4:U5:88:ASN:O	4:U5:92:LEU:HD13	2.12	0.49
5:V4:149:PHE:HB2	5:V4:202:PHE:CE1	2.48	0.49
5:X2:180:PRO:HG2	5:X2:183:ILE:HG23	1.94	0.49
6:Y2:134:MET:HE1	6:Y2:146:MET:SD	2.53	0.49
8:a3:113:LEU:HD23	8:a3:126:LEU:HA	1.95	0.49
1:A4:270:ALA:O	1:A4:273:LYS:HG2	2.12	0.49
1:C4:87:VAL:O	1:C4:90:VAL:HG12	2.13	0.49
1:D5:114:VAL:HG21	1:D5:186:LEU:HD22	1.95	0.49
1:E2:248:GLU:HB2	1:F1:13:HIS:CE1	2.48	0.49
1:F2:159:GLN:CD	1:G7:127:GLN:HE22	2.20	0.49
1:I6:180:VAL:HG22	1:I6:182:THR:HG23	1.95	0.49
1:J7:68:ASP:OD1	1:J8:101:ILE:HD13	2.13	0.49
1:K6:70:MET:HB3	1:K6:217:TYR:CE2	2.48	0.49
1:K7:68:ASP:HB3	1:K8:101:ILE:HD13	1.94	0.49
2:N1:113:THR:HG21	2:N1:163:ASP:HB2	1.95	0.49
2:N5:214:ILE:HB	2:N5:215:PRO:HD3	1.94	0.49
2:P4:97:ASN:HA	2:P4:101:ARG:HH21	1.78	0.49
3:R3:30:VAL:HA	3:R3:114:GLU:HB3	1.94	0.49
8:a2:101:PRO:HG2	8:a2:103:TYR:CE2	2.48	0.49
1:B3:258:ILE:HG12	1:C2:278:MET:SD	2.53	0.49
1:F4:150:TRP:CZ3	1:F4:162:ARG:HB2	2.47	0.49
1:J5:237:SER:HA	1:J5:240:ARG:HD3	1.95	0.49
1:J5:268:ALA:O	1:J5:272:MET:HG3	2.13	0.49
1:K8:19:ASN:HB3	1:K8:260:THR:HG22	1.95	0.49
1:K8:26:ASP:O	1:K8:30:LEU:HD23	2.12	0.49
2:M1:217:LEU:HG	2:M1:236:LEU:HG	1.95	0.49
2:O3:219:LEU:O	2:O3:223:ILE:HG12	2.12	0.49
2:O5:270:ARG:O	2:O5:274:LEU:HD23	2.13	0.49
2:P2:215:PRO:O	2:P2:219:LEU:HD23	2.13	0.49
2:P3:204:GLU:CD	2:P3:209:ASN:HB2	2.38	0.49
3:S2:61:ASP:C	3:S2:62:LYS:HE2	2.37	0.49
3:S5:127:TYR:HE1	3:S5:136:LYS:HE3	1.78	0.49
4:U5:208:LYS:HD3	4:U5:211:TYR:CE1	2.48	0.49
5:V1:125:GLU:HG2	5:V1:199:VAL:HG21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Z1:123:LEU:HD13	7:Z1:172:MET:HG3	1.94	0.49
1:A7:159:GLN:HA	1:B7:127:GLN:HE21	1.78	0.49
1:B8:83:THR:O	1:B8:87:VAL:HG23	2.13	0.49
1:E5:186:LEU:HD22	1:E5:192:ALA:HA	1.95	0.49
1:E6:66:THR:HG23	1:E6:220:MET:HE3	1.94	0.49
1:G8:261:GLN:HB3	1:H7:278:MET:HE1	1.95	0.49
1:H7:186:LEU:HD11	1:H7:195:VAL:HG11	1.93	0.49
2:O4:72:LEU:HD21	2:O5:198:ARG:NE	2.28	0.49
3:Q1:122:ILE:HG22	3:Q1:143:ASP:HB3	1.94	0.49
4:U4:290:ILE:O	4:U4:294:GLU:HB2	2.13	0.49
4:U5:170:PRO:HD3	7:Z1:197:GLU:HG2	1.95	0.49
4:U5:287:ASN:HA	4:U5:290:ILE:HD12	1.95	0.49
6:Y4:241:PHE:CE2	6:Y4:250:LEU:HD12	2.48	0.49
7:Z1:27:ASN:HD21	7:Z1:311:TYR:H	1.60	0.49
1:A4:6:ASN:HD22	1:A4:9:ALA:HB2	1.77	0.49
1:C4:44:SER:HB3	1:D5:110:ILE:HG13	1.93	0.49
1:E7:168:MET:SD	1:E7:209:GLN:HG3	2.53	0.49
1:F2:140:PHE:CE2	1:F2:149:MET:HE2	2.48	0.49
1:F3:262:ALA:HB2	1:G7:278:MET:HE2	1.95	0.49
1:G9:95:VAL:HA	1:G9:196:ILE:HD11	1.95	0.49
1:H6:6:ASN:O	1:H6:10:ILE:HG12	2.13	0.49
1:K6:50:GLU:HG3	1:K7:210:ARG:NH2	2.28	0.49
2:L5:201:ILE:HG12	2:L5:217:LEU:HD22	1.94	0.49
2:N4:120:TRP:CH2	2:N4:156:GLU:HG3	2.48	0.49
2:N5:94:THR:HG22	2:N5:99:GLN:HB2	1.94	0.49
3:R1:138:ILE:CG2	3:R1:161:GLN:HB3	2.38	0.49
5:V3:84:VAL:HB	5:V3:171:GLY:HA3	1.95	0.49
8:a1:64:TYR:HA	8:a1:67:MET:HE3	1.95	0.49
8:a4:43:LEU:HD23	8:a4:43:LEU:H	1.78	0.49
1:i0:80:LEU:HD13	1:i0:168:MET:CE	2.43	0.49
1:C6:191:LYS:O	1:C6:195:VAL:HG23	2.13	0.48
1:F6:166:GLU:HG2	1:F6:209:GLN:HE22	1.78	0.48
1:F6:168:MET:HG3	1:F6:168:MET:O	2.13	0.48
1:H8:239:SER:HA	1:H8:243:ASP:OD2	2.12	0.48
1:I8:43:ALA:HB1	1:I9:211:ALA:HA	1.93	0.48
1:J7:80:LEU:HA	1:J7:83:THR:HG22	1.95	0.48
1:K4:105:GLU:H	1:K4:105:GLU:CD	2.20	0.48
2:L5:98:ASN:O	2:L5:102:LEU:HD12	2.12	0.48
2:M1:230:TYR:CG	2:M1:231:PRO:HD3	2.48	0.48
2:N1:168:PHE:CE2	2:N1:199:SER:HB3	2.48	0.48
2:P3:69:GLN:HE22	2:P4:229:GLU:HA	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P4:126:LYS:CB	9:b4:254:LEU:HD21	2.43	0.48
2:P5:95:PHE:HD1	2:P5:178:ILE:HG12	1.78	0.48
3:R4:125:TYR:HE1	3:R4:127:TYR:HB2	1.78	0.48
4:U5:23:ILE:HG22	4:U5:24:LEU:H	1.78	0.48
8:a3:101:PRO:HG2	8:a3:103:TYR:CE2	2.47	0.48
8:a5:89:VAL:HG12	8:a5:108:ARG:HB3	1.95	0.48
1:C4:277:VAL:HG12	1:C4:278:MET:SD	2.52	0.48
1:D6:114:VAL:HG21	1:D6:186:LEU:HD22	1.96	0.48
1:F5:159:GLN:HG2	1:G1:127:GLN:NE2	2.27	0.48
1:G7:80:LEU:HD12	1:G7:213:LEU:HD12	1.95	0.48
1:I7:88:GLN:HG2	1:I7:203:LEU:HD11	1.95	0.48
1:J7:84:HIS:HB2	1:J7:206:ILE:HG21	1.95	0.48
2:M1:230:TYR:CD2	2:M1:231:PRO:HD3	2.48	0.48
2:M5:217:LEU:O	2:M5:221:ILE:HG12	2.14	0.48
2:N3:153:VAL:HG12	2:N3:157:LYS:HE2	1.93	0.48
2:P2:178:ILE:HD12	2:P2:189:PHE:HE2	1.78	0.48
3:Q4:85:LYS:HG2	3:Q4:90:LEU:HD11	1.94	0.48
4:U5:250:THR:HB	4:U5:261:PRO:HB2	1.96	0.48
5:X2:138:TRP:CZ2	5:X2:174:LYS:HB2	2.48	0.48
1:i0:184:ILE:HG12	1:i0:195:VAL:HG22	1.94	0.48
1:B3:52:MET:HE1	1:C3:131:ASN:HB2	1.96	0.48
1:B8:111:GLN:HE22	1:B8:185:SER:HA	1.79	0.48
1:C6:158:HIS:CD2	1:C7:193:ASN:HD21	2.31	0.48
1:D6:177:ASN:HB3	1:D6:180:VAL:O	2.12	0.48
1:I8:53:ARG:HA	1:I8:56:ILE:HG22	1.94	0.48
1:I8:153:ILE:HD11	1:I8:220:MET:SD	2.53	0.48
1:J5:38:LYS:HD2	1:J6:74:GLN:NE2	2.26	0.48
1:K7:1:MET:H1	1:K7:1:MET:HE2	1.77	0.48
2:L1:209:ASN:O	2:L1:213:THR:HG23	2.13	0.48
2:M5:139:TYR:O	2:M5:143:VAL:HG22	2.14	0.48
3:Q2:184:LEU:HG	3:Q2:196:ARG:HD2	1.95	0.48
8:a3:50:GLN:O	8:a3:54:ILE:HG22	2.12	0.48
1:A7:181:LEU:HD12	5:X3:160:HIS:ND1	2.29	0.48
1:D4:211:ALA:HB2	1:E4:109:GLN:HE21	1.78	0.48
1:H7:266:MET:HE2	1:I7:27:ILE:HD13	1.94	0.48
1:H9:55:GLN:HG3	1:H9:59:LEU:HD23	1.96	0.48
1:K6:3:ILE:HD12	1:K7:246:MET:HG3	1.94	0.48
1:K6:133:MET:HE1	1:K7:101:ILE:HA	1.95	0.48
2:P2:242:PHE:C	2:P2:242:PHE:CD1	2.91	0.48
3:Q2:204:TYR:O	3:Q2:208:LEU:HD23	2.13	0.48
3:Q4:25:LEU:HB3	3:Q4:119:LEU:HD11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Y1:54:VAL:O	6:Y1:219:THR:HA	2.13	0.48
7:Z1:123:LEU:HD11	7:Z1:169:GLU:HA	1.95	0.48
1:B8:223:ALA:HB2	1:C8:123:ARG:HH22	1.78	0.48
1:E4:245:ASP:OD2	1:F3:13:HIS:CE1	2.66	0.48
1:F4:248:GLU:HB2	1:G8:13:HIS:NE2	2.29	0.48
1:J8:16:LEU:HD13	1:J8:263:ALA:HB3	1.95	0.48
2:M2:168:PHE:CE2	2:M2:199:SER:HB2	2.48	0.48
2:P2:65:GLU:O	2:P2:69:GLN:HG3	2.12	0.48
2:P2:128:GLU:HA	2:P2:131:LYS:HZ1	1.79	0.48
2:P3:204:GLU:OE1	2:P3:207:LEU:HD11	2.14	0.48
3:R2:7:MET:HE1	3:R2:194:PRO:HB3	1.96	0.48
6:Y4:89:VAL:HG23	6:Y4:89:VAL:O	2.13	0.48
6:Y4:170:LEU:HD13	6:Y4:216:THR:HG22	1.95	0.48
8:a1:64:TYR:O	8:a1:67:MET:HG2	2.13	0.48
1:i0:105:GLU:O	1:i0:109:GLN:HG3	2.12	0.48
1:A4:281:LEU:HD11	1:B4:267:LEU:HD23	1.95	0.48
1:A5:72:LEU:HD13	1:A6:101:ILE:HG22	1.95	0.48
1:A5:161:GLU:HG3	1:A5:219:ARG:NH2	2.29	0.48
1:A7:16:LEU:HG	1:K7:1:MET:HE3	1.94	0.48
1:A7:23:LEU:HD23	1:K7:273:LYS:NZ	2.29	0.48
1:A8:60:ARG:O	1:A8:64:GLN:HG3	2.13	0.48
1:C3:4:ASN:HB3	1:C4:243:ASP:CG	2.38	0.48
1:D3:88:GLN:O	1:D3:92:VAL:HG23	2.13	0.48
1:D4:150:TRP:CZ3	1:D4:162:ARG:HB2	2.49	0.48
1:G7:177:ASN:HD21	2:O1:166:ASN:HD21	1.61	0.48
1:J7:61:ARG:HA	1:J7:61:ARG:HD2	1.71	0.48
3:Q4:78:PHE:HB2	3:Q4:86:SER:HB2	1.95	0.48
3:R1:137:VAL:HG11	3:R2:236:ALA:HB1	1.96	0.48
5:X3:127:ILE:HG23	7:Z2:145:ARG:HH21	1.78	0.48
6:Y1:23:TYR:HA	6:Y1:24:PRO:HD3	1.76	0.48
7:Za:123:LEU:HA	7:Za:126:ILE:HD12	1.95	0.48
8:a2:112:LYS:HB3	8:a2:128:GLU:HB3	1.96	0.48
8:a4:145:VAL:HA	8:a4:170:THR:HG21	1.96	0.48
1:A5:127:GLN:HB3	1:K4:159:GLN:HE21	1.79	0.48
1:A6:40:GLY:HA3	1:A7:217:TYR:CD1	2.49	0.48
1:C4:5:HIS:CE1	1:C5:235:GLN:HE21	2.32	0.48
1:C4:157:MET:CE	1:C5:197:GLY:HA3	2.43	0.48
1:D7:175:LEU:HD22	1:D7:184:ILE:HD13	1.96	0.48
1:F1:23:LEU:O	1:F1:27:ILE:HG13	2.13	0.48
1:F4:60:ARG:CZ	1:F4:64:GLN:HE21	2.27	0.48
1:I5:220:MET:HA	1:I5:220:MET:HE3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K3:273:LYS:O	1:K3:277:VAL:HG23	2.14	0.48
2:N6:315:LEU:HD21	2:N6:333:TYR:HB3	1.95	0.48
2:O5:178:ILE:HD12	2:O5:189:PHE:HE2	1.78	0.48
3:Q1:73:LEU:HD21	3:Q1:214:LEU:HD23	1.96	0.48
5:V2:146:HIS:CD2	5:V2:205:SER:HA	2.47	0.48
1:B5:12:ALA:HB3	1:B5:267:LEU:HD13	1.96	0.48
1:D5:177:ASN:HB3	1:D5:180:VAL:O	2.14	0.48
1:E2:66:THR:HG23	1:E2:220:MET:HE2	1.94	0.48
1:G7:114:VAL:HG21	1:G7:186:LEU:HD11	1.96	0.48
1:J5:237:SER:OG	1:K4:71:SER:HB3	2.13	0.48
1:J7:237:SER:OG	1:K7:71:SER:HB3	2.13	0.48
2:M1:107:TYR:O	2:M1:111:VAL:HG22	2.13	0.48
2:M4:256:MET:HE2	8:a4:97:LEU:HD22	1.95	0.48
2:O4:135:ASP:C	2:P4:212:GLN:HE22	2.22	0.48
3:Q4:62:LYS:HB2	3:Q4:65:ALA:HB2	1.96	0.48
4:U5:239:ILE:O	4:U5:242:ILE:HG13	2.14	0.48
5:V2:107:LYS:HE3	5:V2:215:TYR:OH	2.13	0.48
5:V3:133:ARG:HH12	6:Y3:40:VAL:HG11	1.78	0.48
6:Y3:241:PHE:CE2	6:Y3:250:LEU:HD12	2.49	0.48
1:A7:28:GLU:HG3	1:K7:11:PHE:CE1	2.49	0.48
1:B3:278:MET:HA	1:B3:278:MET:HE2	1.96	0.48
1:B7:266:MET:SD	1:C7:27:ILE:HG13	2.54	0.48
1:C3:66:THR:HG23	1:C3:220:MET:HE3	1.93	0.48
1:D4:114:VAL:HG21	1:D4:186:LEU:HD22	1.94	0.48
1:E1:282:GLN:HG2	1:E2:250:MET:HE2	1.96	0.48
1:E2:61:ARG:HD3	1:E3:96:GLN:CB	2.43	0.48
1:E6:60:ARG:HH11	1:E6:60:ARG:HG3	1.79	0.48
1:F3:118:VAL:O	1:F3:121:ILE:HG22	2.14	0.48
1:I6:68:ASP:HB3	1:I7:101:ILE:HD13	1.96	0.48
1:J7:83:THR:O	1:J7:86:ILE:HG22	2.14	0.48
1:K4:32:SER:CB	1:K4:37:ASN:HD21	2.27	0.48
2:L2:283:TYR:O	2:L2:286:ILE:HG22	2.13	0.48
2:M2:270:ARG:O	2:M2:274:LEU:HD23	2.14	0.48
2:M5:291:ASN:HD21	8:a5:206:ARG:HH11	1.62	0.48
2:P3:69:GLN:NE2	2:P4:229:GLU:HG2	2.28	0.48
2:P3:284:LYS:O	2:P3:287:VAL:HG22	2.14	0.48
3:R1:129:ASN:ND2	3:R1:136:LYS:HE2	2.29	0.48
3:S6:120:THR:HG23	3:S6:120:THR:O	2.13	0.48
5:V2:49:VAL:HG23	5:V2:221:LEU:O	2.14	0.48
5:V3:104:LEU:HD21	5:V3:120:LEU:HD11	1.95	0.48
5:X3:142:ARG:HH12	5:X3:217:TYR:HE1	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Y4:186:TYR:HD1	6:Y4:205:HIS:HB2	1.78	0.48
1:A5:130:PHE:O	1:A5:133:MET:HG2	2.14	0.48
1:A5:159:GLN:HB3	1:B5:127:GLN:OE1	2.14	0.48
1:A6:151:PHE:HE2	1:A6:163:VAL:HG21	1.79	0.48
1:C3:72:LEU:HD23	1:C3:130:PHE:CD2	2.49	0.48
1:C4:4:ASN:HB3	1:C5:243:ASP:CG	2.39	0.48
1:D4:153:ILE:HG13	1:D4:153:ILE:O	2.14	0.48
1:E3:114:VAL:HG21	1:E3:186:LEU:HD12	1.96	0.48
1:E7:81:GLN:O	1:E7:84:HIS:HB3	2.14	0.48
1:F3:273:LYS:HE3	1:G8:23:LEU:HD23	1.95	0.48
1:G1:157:MET:HE3	1:G1:158:HIS:NE2	2.29	0.48
1:G1:248:GLU:HB2	1:H9:13:HIS:NE2	2.28	0.48
1:K4:150:TRP:CE3	1:K4:160:ARG:HG3	2.49	0.48
2:N4:175:LEU:HD12	2:N4:196:VAL:HG11	1.96	0.48
2:O1:65:GLU:O	2:O1:69:GLN:HG3	2.13	0.48
2:O1:210:LEU:HB2	2:O1:242:PHE:CD2	2.48	0.48
2:O3:207:LEU:HD12	2:O3:209:ASN:OD1	2.14	0.48
2:P4:120:TRP:CH2	2:P4:156:GLU:HG3	2.48	0.48
2:P6:253:PRO:HG2	2:P6:256:MET:HG3	1.94	0.48
3:R3:100:PHE:HB2	3:R3:121:LYS:HB3	1.95	0.48
5:X4:135:ILE:HD12	5:X4:152:PHE:HZ	1.79	0.48
6:Y3:235:LYS:HE2	6:Y3:255:PHE:HB3	1.95	0.48
1:i0:83:THR:O	1:i0:87:VAL:HG23	2.14	0.48
1:A4:50:GLU:HG3	1:A5:84:HIS:NE2	2.29	0.47
1:A4:76:ALA:O	1:A4:80:LEU:HG	2.14	0.47
1:A5:95:VAL:HG22	1:A5:196:ILE:HD13	1.96	0.47
1:A7:111:GLN:HA	1:A7:114:VAL:HG12	1.94	0.47
1:A7:253:PHE:HZ	1:K7:269:GLN:HE21	1.62	0.47
1:B5:52:MET:O	1:B5:56:ILE:HD12	2.14	0.47
1:C3:53:ARG:HA	1:C3:56:ILE:HD12	1.96	0.47
1:C6:80:LEU:HD21	1:C6:168:MET:SD	2.54	0.47
1:D3:156:ASN:HB2	1:D3:159:GLN:OE1	2.14	0.47
1:E3:10:ILE:CG2	1:E4:232:GLU:HG3	2.44	0.47
1:E3:52:MET:HE3	1:E3:238:GLU:HA	1.96	0.47
1:F3:80:LEU:HD21	1:F3:168:MET:HG3	1.95	0.47
1:F5:35:ARG:NH2	1:F5:36:ILE:HD11	2.29	0.47
1:F5:150:TRP:CZ3	1:F5:162:ARG:HB2	2.49	0.47
1:J5:255:ARG:O	1:J5:258:ILE:HG22	2.14	0.47
1:J7:39:ALA:HB2	1:J8:77:GLU:OE1	2.14	0.47
2:L5:93:LYS:HE3	8:a5:144:PRO:HB2	1.95	0.47
2:M3:258:PHE:CZ	8:a3:93:ARG:HD2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N4:133:ARG:HD3	2:N4:136:GLU:OE1	2.14	0.47
2:O1:213:THR:HG23	2:O1:217:LEU:CD2	2.44	0.47
2:P3:283:TYR:O	2:P3:287:VAL:HG13	2.14	0.47
2:P5:215:PRO:O	2:P5:219:LEU:HD23	2.14	0.47
3:S2:172:GLU:O	3:S2:172:GLU:HG2	2.13	0.47
4:U5:109:GLU:O	4:U5:113:ILE:HG12	2.14	0.47
5:V1:141:GLY:O	5:V1:170:PHE:HA	2.14	0.47
5:V3:75:LEU:HD12	5:V3:217:TYR:HE2	1.79	0.47
5:V4:75:LEU:HD23	5:V4:103:ILE:HD11	1.96	0.47
5:X1:138:TRP:H	5:X1:220:ASP:HB3	1.78	0.47
6:Y1:35:LYS:HD3	6:Y1:57:GLU:CD	2.38	0.47
1:i0:168:MET:O	1:i0:168:MET:HG2	2.13	0.47
1:A7:54:THR:HG22	1:A8:88:GLN:HG2	1.96	0.47
1:C6:237:SER:OG	1:D6:71:SER:HB3	2.14	0.47
1:F1:258:ILE:CG2	1:G5:3:ILE:HD11	2.44	0.47
1:F3:17:LYS:HE3	1:F4:63:GLU:OE2	2.14	0.47
1:G9:186:LEU:HD21	1:G9:195:VAL:HG11	1.95	0.47
1:G9:275:GLN:HE22	1:G9:279:ARG:HD2	1.78	0.47
1:H8:237:SER:OG	1:I8:71:SER:HB2	2.14	0.47
1:J7:39:ALA:HB1	1:J8:214:GLY:CA	2.44	0.47
2:N3:120:TRP:CH2	2:N3:156:GLU:HG3	2.49	0.47
2:N4:214:ILE:HB	2:N4:215:PRO:HD3	1.95	0.47
2:O2:133:ARG:HG2	2:O2:133:ARG:NH1	2.28	0.47
2:O3:120:TRP:CH2	2:O3:156:GLU:HG3	2.50	0.47
5:V2:103:ILE:HG22	5:V2:219:ASP:OD2	2.13	0.47
5:V3:52:ASP:HB2	12:V3:402:HOH:O	2.14	0.47
6:Y2:32:ILE:HG21	6:Y2:251:LEU:HD13	1.96	0.47
6:Y4:73:LEU:HD11	6:Y4:109:SER:HB2	1.96	0.47
1:A6:166:GLU:N	1:A6:209:GLN:HE22	2.12	0.47
1:B6:96:GLN:HG2	1:B6:102:TYR:HE2	1.80	0.47
1:C2:260:THR:O	1:C2:264:THR:HG23	2.15	0.47
1:D6:114:VAL:O	1:D6:118:VAL:HG13	2.14	0.47
1:E4:123:ARG:O	1:E4:127:GLN:HG2	2.14	0.47
1:F1:248:GLU:HA	1:F1:251:THR:HG22	1.95	0.47
1:F2:212:ASP:OD1	1:G7:112:VAL:HG21	2.14	0.47
1:F3:11:PHE:CZ	1:G8:28:GLU:HG3	2.49	0.47
1:F3:262:ALA:CB	1:G7:278:MET:HE2	2.44	0.47
1:H8:154:GLY:HA3	1:H8:159:GLN:NE2	2.29	0.47
1:I6:133:MET:HE1	1:I7:101:ILE:HA	1.95	0.47
2:L2:73:TRP:CZ2	2:L3:198:ARG:HG3	2.50	0.47
2:M1:168:PHE:CZ	2:M1:199:SER:HB2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M4:165:LEU:HD22	2:M4:207:LEU:HD12	1.96	0.47
2:N3:152:VAL:O	2:N3:156:GLU:HG2	2.14	0.47
2:P6:256:MET:HE3	3:S6:82:GLU:HA	1.97	0.47
3:S2:122:ILE:HD11	3:S2:146:PRO:HB3	1.96	0.47
5:V4:142:ARG:HA	5:V4:170:PHE:HA	1.95	0.47
1:E5:161:GLU:HB3	1:E5:219:ARG:HH22	1.79	0.47
1:E5:209:GLN:HA	1:E5:209:GLN:HE21	1.79	0.47
1:G7:4:ASN:HB3	1:G8:243:ASP:CG	2.38	0.47
1:J4:24:SER:O	1:J4:28:GLU:HG2	2.14	0.47
1:J7:177:ASN:HB3	1:J7:180:VAL:O	2.14	0.47
1:K6:160:ARG:HD3	1:K7:193:ASN:HD22	1.79	0.47
2:L4:140:TRP:HA	2:L4:143:VAL:HG22	1.96	0.47
2:M3:228:LYS:HE3	8:a3:56:ARG:CZ	2.44	0.47
2:P2:184:ARG:HD2	2:P2:189:PHE:CE1	2.50	0.47
2:P5:65:GLU:O	2:P5:69:GLN:HG3	2.14	0.47
2:P5:241:SER:HB3	2:P5:264:LYS:HD3	1.95	0.47
3:Q1:224:ARG:HA	3:Q1:227:ASN:HD21	1.78	0.47
3:Q3:28:HIS:HE1	3:Q3:212:ASP:HA	1.79	0.47
3:Q4:122:ILE:HD11	3:Q4:204:TYR:OH	2.14	0.47
5:V4:192:LEU:H	5:V4:192:LEU:HD12	1.79	0.47
5:X2:106:VAL:HB	5:X2:216:PHE:CE1	2.49	0.47
6:Y2:208:THR:HG22	6:Y2:219:THR:HB	1.97	0.47
6:Y4:54:VAL:O	6:Y4:219:THR:HA	2.13	0.47
7:Z1:281:ILE:HG22	7:Z1:282:LYS:H	1.79	0.47
8:a4:181:LEU:HD12	8:a4:184:ILE:HD12	1.94	0.47
9:b4:182:ASN:O	9:b4:185:ILE:HG23	2.15	0.47
1:A6:51:LYS:HE2	1:B6:132:LYS:HG3	1.96	0.47
1:A7:251:THR:HG22	1:B6:271:ASN:ND2	2.27	0.47
1:C5:150:TRP:CZ3	1:C5:162:ARG:HB2	2.49	0.47
1:C6:14:ARG:HG3	1:C7:228:MET:HG3	1.95	0.47
1:D3:136:LEU:HB3	1:D3:168:MET:HB2	1.95	0.47
1:F1:30:LEU:HG	1:F1:249:GLN:CG	2.44	0.47
1:F5:248:GLU:HB2	1:G9:13:HIS:NE2	2.29	0.47
1:G9:202:ALA:O	1:G9:205:VAL:HG12	2.15	0.47
1:H6:86:ILE:HG23	1:H6:117:LEU:HD22	1.95	0.47
1:I5:219:ARG:HD2	1:J5:120:GLU:HB2	1.96	0.47
1:I9:29:LYS:HD2	1:I9:249:GLN:CD	2.39	0.47
1:I9:36:ILE:HG23	1:I9:242:ARG:HG3	1.97	0.47
1:J7:176:ARG:HD3	1:J7:181:LEU:HD22	1.97	0.47
1:J8:84:HIS:HB2	1:J8:206:ILE:HG21	1.97	0.47
1:K4:61:ARG:HE	1:K6:96:GLN:HB2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K6:35:ARG:HG3	1:K6:244:THR:HA	1.96	0.47
1:K6:257:GLN:O	1:K6:260:THR:HG22	2.14	0.47
2:M3:169:SER:HB3	2:M3:200:TRP:CZ3	2.49	0.47
2:O1:263:LYS:HE3	2:O1:267:HIS:NE2	2.29	0.47
2:P4:133:ARG:HB3	2:P4:136:GLU:HG2	1.96	0.47
3:R1:119:LEU:HD23	3:R1:119:LEU:H	1.78	0.47
5:V0:79:GLY:HA3	5:V1:236:GLU:OE1	2.15	0.47
6:Y1:130:LYS:HD2	6:Y1:147:PRO:HG2	1.97	0.47
9:b3:241:ILE:O	9:b3:245:THR:HG22	2.14	0.47
1:i0:173:LEU:HD23	1:i0:202:ALA:HB1	1.95	0.47
1:A4:264:THR:HG21	1:K5:277:VAL:HA	1.96	0.47
1:A6:257:GLN:HE22	1:K6:269:GLN:NE2	2.10	0.47
1:B4:215:ALA:O	1:B4:219:ARG:HG3	2.15	0.47
1:B5:153:ILE:HD13	1:C5:123:ARG:NH1	2.30	0.47
1:D6:168:MET:SD	1:D6:206:ILE:HD13	2.55	0.47
1:E7:84:HIS:CE1	1:E7:210:ARG:HH11	2.33	0.47
1:F1:48:VAL:HG23	1:F1:241:ILE:HG21	1.95	0.47
1:F3:133:MET:HE1	1:F3:149:MET:HE1	1.95	0.47
1:F5:8:SER:HB3	1:G1:27:ILE:HG21	1.97	0.47
1:J5:168:MET:HE1	1:J5:209:GLN:HE21	1.79	0.47
2:L4:168:PHE:O	2:L4:172:ILE:HG12	2.14	0.47
2:M1:201:ILE:HD13	2:M1:217:LEU:HD13	1.95	0.47
2:N5:216:ILE:HD13	2:N5:216:ILE:HA	1.78	0.47
3:Q2:72:HIS:CE1	3:Q2:96:LYS:HD2	2.49	0.47
4:U5:23:ILE:HG22	4:U5:24:LEU:N	2.29	0.47
5:V2:155:TYR:HB2	5:V2:194:LYS:HD2	1.95	0.47
8:a4:204:VAL:O	8:a4:208:ILE:HG12	2.14	0.47
1:B4:11:PHE:CE1	1:C4:28:GLU:HG3	2.50	0.47
1:B5:167:THR:HG23	1:B5:172:ALA:HB2	1.96	0.47
1:B7:15:THR:HG21	1:C7:32:SER:HA	1.97	0.47
1:B7:223:ALA:O	1:B7:227:LEU:HD23	2.14	0.47
1:C2:15:THR:HG21	1:D2:32:SER:HA	1.96	0.47
1:C3:270:ALA:O	1:C3:273:LYS:HG2	2.14	0.47
1:D3:56:ILE:HD11	1:D3:235:GLN:HA	1.97	0.47
1:D6:226:GLY:CA	1:E6:82:GLU:HG3	2.45	0.47
1:D6:257:GLN:O	1:D6:260:THR:HG22	2.15	0.47
1:E4:168:MET:HE1	1:E4:209:GLN:CG	2.45	0.47
1:E5:86:ILE:HB	1:E5:121:ILE:HD11	1.95	0.47
1:F4:166:GLU:HG2	1:F4:209:GLN:OE1	2.14	0.47
1:G1:153:ILE:HD11	1:h0:123:ARG:HD2	1.95	0.47
1:G6:3:ILE:HD13	1:G7:246:MET:HE2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G9:255:ARG:HH12	1:H8:5:HIS:CE1	2.33	0.47
1:H9:177:ASN:HB3	1:H9:180:VAL:O	2.15	0.47
1:I6:43:ALA:HB1	1:I7:211:ALA:HA	1.97	0.47
1:I9:53:ARG:O	1:I9:56:ILE:HG22	2.15	0.47
1:J7:111:GLN:HA	1:J7:114:VAL:HG22	1.97	0.47
1:J8:169:ASN:ND2	1:J8:171:ALA:H	2.13	0.47
1:J8:175:LEU:HD22	1:J8:184:ILE:HD11	1.97	0.47
1:J8:261:GLN:HB2	1:K7:278:MET:HE2	1.96	0.47
1:K4:70:MET:HA	1:K4:73:ILE:HG22	1.97	0.47
1:K6:83:THR:O	1:K6:87:VAL:HG22	2.15	0.47
2:N1:102:LEU:HD22	3:R1:78:PHE:CE1	2.49	0.47
2:O1:120:TRP:HE1	2:O1:156:GLU:HG3	1.80	0.47
3:Q1:34:MET:HE1	3:Q1:219:PHE:CD1	2.50	0.47
3:R2:34:MET:HG2	3:R2:111:PRO:HB3	1.97	0.47
3:R4:62:LYS:HB2	3:R4:65:ALA:HB2	1.97	0.47
3:S2:229:HIS:O	3:S2:232:LYS:HG3	2.14	0.47
3:S4:165:TYR:HB3	3:S4:166:PRO:HD3	1.97	0.47
3:S6:122:ILE:HG22	3:S6:143:ASP:HB3	1.97	0.47
4:U4:110:LEU:HA	4:U4:113:ILE:HG22	1.97	0.47
4:U5:239:ILE:HG13	4:U5:240:ASN:N	2.30	0.47
5:X4:128:ILE:HD11	5:X4:198:PHE:HB2	1.97	0.47
6:Y1:82:ASN:HB2	6:Y1:85:GLU:CD	2.39	0.47
1:h0:105:GLU:O	1:h0:109:GLN:HG3	2.15	0.47
1:i0:76:ALA:O	1:i0:80:LEU:HD23	2.14	0.47
1:A7:1:MET:HE2	1:A7:1:MET:N	2.29	0.47
1:C7:71:SER:HA	1:C7:74:GLN:CD	2.39	0.47
1:C8:191:LYS:O	1:C8:195:VAL:HG23	2.14	0.47
1:D5:4:ASN:HB3	1:D6:243:ASP:CG	2.39	0.47
1:F3:30:LEU:HD21	1:F3:249:GLN:HB3	1.97	0.47
1:F3:150:TRP:CZ3	1:F3:162:ARG:HB2	2.49	0.47
1:F5:233:ASN:HD22	1:G1:75:THR:HA	1.80	0.47
1:G1:43:ALA:HB1	1:G2:211:ALA:HA	1.96	0.47
1:G9:129:GLU:HB3	1:G9:134:LYS:NZ	2.30	0.47
1:J6:40:GLY:HA3	1:J7:217:TYR:CD1	2.50	0.47
1:J8:237:SER:O	1:J8:241:ILE:HG13	2.15	0.47
2:M3:290:ILE:HD13	8:a3:206:ARG:HH11	1.79	0.47
2:O1:243:GLU:O	2:O1:247:ILE:HD13	2.15	0.47
3:S2:38:THR:H	3:S2:222:ASN:HD21	1.62	0.47
7:Z0:177:LYS:O	7:Z0:181:LEU:HG	2.14	0.47
8:a4:219:GLU:O	8:a4:223:ILE:HG12	2.14	0.47
9:b3:104:LYS:HA	9:b3:123:ILE:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A4:253:PHE:CE1	1:K5:266:MET:HE1	2.50	0.47
1:A7:50:GLU:O	1:A7:54:THR:HG23	2.14	0.47
1:D3:154:GLY:HA3	1:D3:159:GLN:NE2	2.30	0.47
1:G6:44:SER:O	1:G6:48:VAL:HG23	2.15	0.47
1:H9:50:GLU:OE1	1:H9:50:GLU:HA	2.15	0.47
1:I6:4:ASN:HB3	1:I7:243:ASP:OD2	2.15	0.47
1:J5:153:ILE:O	1:J5:153:ILE:HG13	2.14	0.47
1:J6:151:PHE:HA	1:J7:99:ASN:HD21	1.80	0.47
1:J7:91:ARG:NH1	1:J7:91:ARG:HB3	2.30	0.47
2:L2:180:ASN:O	2:L2:184:ARG:HG3	2.14	0.47
2:L3:259:LYS:HD3	6:Y3:88:LEU:HD11	1.97	0.47
2:L4:186:ARG:HG3	2:L4:187:PRO:HD2	1.97	0.47
2:M1:72:LEU:HD11	2:M2:198:ARG:CZ	2.45	0.47
2:M2:224:ASP:CG	2:M2:225:ASP:N	2.73	0.47
2:M4:146:LYS:O	2:M4:150:GLU:HG2	2.14	0.47
2:P2:187:PRO:O	2:P2:190:LYS:HG3	2.14	0.47
2:P4:201:ILE:HD12	2:P4:217:LEU:HG	1.97	0.47
2:P6:201:ILE:HD12	2:P6:217:LEU:HG	1.97	0.47
3:S4:28:HIS:CD2	3:S4:215:PHE:HB3	2.50	0.47
6:Y1:70:ILE:HG23	6:Y1:112:MET:HE1	1.97	0.47
6:Y2:112:MET:HE2	6:Y2:112:MET:HB3	1.83	0.47
7:Z2:188:ASN:O	7:Z2:192:VAL:HG23	2.15	0.47
8:a4:50:GLN:O	8:a4:54:ILE:HG22	2.14	0.47
9:b4:229:HIS:HA	9:b4:232:MET:HG3	1.97	0.47
1:i0:177:ASN:HB3	1:i0:180:VAL:O	2.15	0.47
1:D6:59:LEU:HD12	1:D6:234:THR:HG21	1.98	0.47
1:E2:151:PHE:CE2	1:E2:163:VAL:HG21	2.50	0.47
1:J7:80:LEU:HD12	1:J7:206:ILE:HG23	1.97	0.47
1:J9:143:LEU:HD11	7:Z2:4:SER:HB3	1.97	0.47
2:L5:201:ILE:HD13	2:L5:217:LEU:HD13	1.97	0.47
2:M1:217:LEU:HD11	2:M1:232:ALA:HB1	1.96	0.47
2:M3:73:TRP:CZ2	2:M4:198:ARG:HG3	2.50	0.47
2:N5:102:LEU:HG	2:N5:174:HIS:CE1	2.50	0.47
3:Q1:22:ASN:HA	3:Q1:25:LEU:HD12	1.97	0.47
3:R1:122:ILE:HG13	3:R1:143:ASP:HB3	1.96	0.47
3:S2:141:ILE:O	3:S2:141:ILE:HG13	2.14	0.47
4:U4:132:ALA:HB2	4:U4:198:MET:HE3	1.96	0.47
4:U6:122:ILE:HG13	4:U6:187:LEU:HD11	1.97	0.47
5:V1:142:ARG:NH1	5:V1:217:TYR:HE1	2.13	0.47
5:X4:153:ARG:HG2	5:X4:197:HIS:HB2	1.97	0.47
8:a5:204:VAL:O	8:a5:207:THR:HG22	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A4:34:MET:HA	1:A4:243:ASP:HA	1.97	0.46
1:A6:270:ALA:O	1:A6:273:LYS:HB3	2.15	0.46
1:B5:278:MET:SD	1:B6:246:MET:HG2	2.55	0.46
1:B6:238:GLU:HA	1:B6:241:ILE:HG22	1.97	0.46
1:C7:150:TRP:CZ3	1:C7:162:ARG:HB2	2.49	0.46
1:D5:168:MET:HE1	1:D5:206:ILE:HA	1.97	0.46
1:E3:168:MET:HE2	1:E3:168:MET:HB2	1.71	0.46
1:I6:238:GLU:HA	1:I6:241:ILE:HG22	1.97	0.46
1:J7:156:ASN:HB2	1:J7:159:GLN:HE21	1.79	0.46
1:K4:203:LEU:HD13	1:K5:54:THR:HG21	1.96	0.46
2:M3:121:VAL:HG21	2:M3:153:VAL:HG13	1.97	0.46
2:M3:168:PHE:CE2	2:M3:199:SER:HB3	2.50	0.46
2:O3:215:PRO:O	2:O3:219:LEU:HD13	2.16	0.46
2:O5:259:LYS:HE3	3:R5:82:GLU:HB3	1.96	0.46
2:P5:120:TRP:CH2	2:P5:156:GLU:HG3	2.50	0.46
3:Q2:21:VAL:O	3:Q2:25:LEU:HD13	2.15	0.46
3:Q2:212:ASP:O	3:Q2:216:THR:HG23	2.15	0.46
3:S2:29:THR:HG21	3:S2:117:ARG:HB2	1.97	0.46
6:Y2:73:LEU:HD13	6:Y2:111:ILE:HD11	1.97	0.46
9:b4:33:SER:O	9:b4:36:GLN:HG2	2.15	0.46
1:A4:46:LEU:HD21	1:A5:210:ARG:HH21	1.81	0.46
1:A5:13:HIS:CD2	1:K6:248:GLU:HG2	2.51	0.46
1:B3:266:MET:CE	1:C3:27:ILE:HG12	2.45	0.46
1:C4:255:ARG:HD2	1:D3:4:ASN:O	2.15	0.46
1:G7:226:GLY:HA2	1:H7:82:GLU:HG3	1.97	0.46
1:J6:111:GLN:HA	1:J6:114:VAL:HG22	1.97	0.46
1:J6:212:ASP:OD1	1:K6:112:VAL:HG11	2.15	0.46
1:J7:150:TRP:CZ3	1:J7:162:ARG:HB2	2.50	0.46
2:M3:198:ARG:O	2:M3:202:MET:HG3	2.14	0.46
3:S4:73:LEU:HD21	3:S4:214:LEU:HD23	1.98	0.46
3:S5:205:PHE:CD1	3:S5:205:PHE:C	2.92	0.46
5:V1:122:PRO:HD2	5:V1:199:VAL:HG13	1.97	0.46
5:V4:44:PRO:HG3	6:Y4:186:TYR:CG	2.50	0.46
5:X3:240:ASN:OD1	7:Z1:281:ILE:HA	2.15	0.46
7:Z0:191:LYS:HB2	7:Z0:194:ARG:NH2	2.30	0.46
7:Z0:290:MET:HG3	7:Z0:311:TYR:CE1	2.50	0.46
1:A8:44:SER:O	1:A8:48:VAL:HG23	2.16	0.46
1:B3:47:ALA:HB1	1:C4:109:GLN:HE21	1.80	0.46
1:C3:7:VAL:HA	1:C3:10:ILE:HD12	1.98	0.46
1:C3:152:HIS:HA	1:C3:160:ARG:HB3	1.98	0.46
1:C6:134:LYS:HE2	1:C6:134:LYS:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C8:170:THR:HG22	1:C8:175:LEU:HD12	1.97	0.46
1:D6:46:LEU:HG	1:D6:50:GLU:OE2	2.15	0.46
1:E3:19:ASN:ND2	1:E3:259:LEU:HB3	2.30	0.46
1:E5:36:ILE:HD12	1:E5:242:ARG:HA	1.96	0.46
1:H7:219:ARG:HG3	1:I7:120:GLU:CG	2.45	0.46
1:I5:237:SER:O	1:I5:241:ILE:HG22	2.15	0.46
1:J6:77:GLU:OE2	1:J6:210:ARG:HD2	2.16	0.46
1:K8:127:GLN:O	1:K8:129:GLU:HG3	2.14	0.46
2:L5:200:TRP:NE1	2:L5:216:ILE:HG13	2.29	0.46
2:M3:268:LEU:O	2:M3:272:THR:HG23	2.15	0.46
3:Q2:62:LYS:HG3	3:Q2:65:ALA:HB2	1.96	0.46
3:R5:45:LEU:HD12	3:R5:73:LEU:HD12	1.96	0.46
5:V1:77:GLN:NE2	5:V1:81:ILE:HG23	2.31	0.46
5:V2:54:GLU:O	5:V2:74:LYS:HE2	2.16	0.46
5:V3:133:ARG:HH22	6:Y3:42:ARG:HD3	1.80	0.46
6:Y4:146:MET:HE2	6:Y4:146:MET:HB2	1.78	0.46
6:Y4:240:VAL:HB	6:Y4:252:PHE:HB2	1.97	0.46
6:Y4:250:LEU:HD13	6:Y4:253:ARG:HE	1.80	0.46
8:a1:192:ARG:O	8:a1:195:THR:HG22	2.16	0.46
1:D4:183:PHE:N	1:D4:183:PHE:HD1	2.14	0.46
1:F1:50:GLU:HG2	1:F2:84:HIS:CE1	2.51	0.46
1:F3:258:ILE:HD12	1:G7:275:GLN:HA	1.96	0.46
1:H8:49:SER:OG	1:H8:242:ARG:HD2	2.16	0.46
1:K6:44:SER:O	1:K6:48:VAL:HG12	2.16	0.46
2:L1:220:TYR:O	2:L1:223:ILE:HG22	2.16	0.46
2:N3:171:ALA:O	2:N3:175:LEU:HD12	2.15	0.46
3:S2:18:ILE:HA	3:S2:21:VAL:HG22	1.97	0.46
3:S3:72:HIS:NE2	3:S3:96:LYS:HD3	2.31	0.46
3:S5:213:LYS:O	3:S5:216:THR:HG22	2.15	0.46
5:V1:149:PHE:HB2	5:V1:202:PHE:CE2	2.50	0.46
5:V2:131:LYS:HD2	5:V2:185:GLN:HE21	1.81	0.46
5:V3:82:LYS:HG2	5:V3:90:VAL:HG13	1.97	0.46
5:X1:56:ALA:HB1	5:X1:104:LEU:HD11	1.97	0.46
6:Y2:82:ASN:HB2	6:Y2:85:GLU:HB2	1.98	0.46
6:Y2:236:VAL:HG23	6:Y2:256:ILE:HB	1.98	0.46
1:A5:50:GLU:HG3	1:A6:210:ARG:NH1	2.30	0.46
1:B4:277:VAL:HG12	1:B4:278:MET:SD	2.55	0.46
1:C3:216:TYR:O	1:C3:220:MET:HG2	2.15	0.46
1:E5:50:GLU:HG3	1:E6:84:HIS:HE1	1.80	0.46
1:E6:65:ASN:CG	1:E7:99:ASN:HD22	2.23	0.46
1:H9:254:THR:HG23	1:I8:275:GLN:HE21	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J7:219:ARG:NH2	1:K7:119:ASP:HB3	2.30	0.46
2:M1:243:GLU:O	2:M1:247:ILE:HD12	2.16	0.46
2:P6:272:THR:HG21	2:P6:286:ILE:HG21	1.98	0.46
3:Q1:83:ASP:O	3:Q1:85:LYS:HD3	2.15	0.46
4:U4:229:ARG:O	4:U4:233:LYS:HG3	2.14	0.46
7:Za:47:GLU:HG3	7:Za:51:MET:HB3	1.98	0.46
8:a5:57:ILE:HD13	8:a5:60:GLU:OE2	2.15	0.46
1:A4:127:GLN:O	1:A4:129:GLU:HG2	2.15	0.46
1:A6:66:THR:CG2	1:A6:220:MET:HG3	2.40	0.46
1:A7:150:TRP:CE2	1:A7:162:ARG:HD3	2.50	0.46
1:C8:118:VAL:HG23	1:C8:170:THR:HG21	1.97	0.46
1:I5:153:ILE:HG21	1:I5:220:MET:CE	2.46	0.46
1:J5:86:ILE:HD13	1:J5:120:GLU:HG3	1.97	0.46
1:J6:36:ILE:HD12	1:J6:42:ASP:HB3	1.98	0.46
1:J6:258:ILE:HD12	1:K4:275:GLN:HA	1.96	0.46
1:K6:56:ILE:HD11	1:K6:235:GLN:N	2.30	0.46
1:K7:180:VAL:HG11	7:Z1:171:ASN:ND2	2.30	0.46
2:M3:165:LEU:HD22	2:M3:207:LEU:HD12	1.97	0.46
2:M4:93:LYS:HD3	3:Q4:131:PHE:CZ	2.50	0.46
2:N4:107:TYR:O	2:N4:111:VAL:HG22	2.16	0.46
2:P6:240:TYR:CD1	2:P6:260:TYR:HD1	2.34	0.46
3:R2:14:LEU:HD21	3:R2:201:LYS:HD3	1.97	0.46
3:S3:204:TYR:CZ	3:S3:208:LEU:HD11	2.51	0.46
4:U5:266:GLU:HG2	4:U5:276:THR:HG21	1.96	0.46
6:Y3:258:ILE:HB	6:Y3:261:LEU:HD12	1.96	0.46
7:Za:126:ILE:HA	7:Za:130:TYR:HD2	1.80	0.46
1:A8:216:TYR:CD1	1:A8:219:ARG:HD2	2.51	0.46
1:B4:157:MET:HG2	1:B4:158:HIS:ND1	2.30	0.46
1:C5:109:GLN:O	1:C5:112:VAL:HG12	2.14	0.46
1:G1:101:ILE:HD13	1:G9:130:PHE:CE2	2.48	0.46
1:J5:245:ASP:OD2	1:K5:13:HIS:HE1	1.99	0.46
2:M2:89:HIS:NE2	2:M3:275:LYS:HE2	2.31	0.46
2:M2:128:GLU:HG2	2:M2:149:GLU:HG2	1.96	0.46
2:P6:161:LYS:C	2:P6:161:LYS:HE3	2.41	0.46
3:R1:183:ILE:HD11	3:R1:185:SER:HB2	1.97	0.46
3:S6:43:THR:HG22	3:S6:75:VAL:HG13	1.98	0.46
4:U6:38:ALA:O	4:U6:42:LEU:HD23	2.16	0.46
6:Y1:54:VAL:HG11	6:Y1:72:VAL:HG11	1.97	0.46
7:Za:43:PRO:HD2	7:Za:46:LYS:HE2	1.97	0.46
7:Za:89:LYS:O	7:Za:93:GLU:HG3	2.16	0.46
1:A3:267:LEU:HD11	1:K5:247:ALA:HB1	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A7:258:ILE:HG23	1:B6:278:MET:HG3	1.97	0.46
1:A8:215:ALA:O	1:A8:219:ARG:HG3	2.16	0.46
1:B7:198:LEU:HD13	5:V3:67:LEU:HD23	1.97	0.46
1:C3:244:THR:HG23	1:C3:249:GLN:HG3	1.98	0.46
1:E5:65:ASN:HB3	1:E6:99:ASN:ND2	2.31	0.46
1:G1:153:ILE:CD1	1:h0:123:ARG:HD2	2.46	0.46
1:G9:266:MET:HE3	1:H9:30:LEU:HB3	1.98	0.46
1:I8:50:GLU:O	1:I8:54:THR:HG22	2.16	0.46
1:J7:192:ALA:O	1:J7:196:ILE:HG13	2.16	0.46
3:Q1:153:ASN:HD21	3:Q1:196:ARG:NH2	2.13	0.46
3:R5:101:PHE:CE2	3:R5:119:LEU:HD13	2.51	0.46
3:S2:160:TYR:CZ	3:S2:162:HIS:HB2	2.51	0.46
3:S4:119:LEU:H	3:S4:147:ASN:HD21	1.64	0.46
3:S5:143:ASP:HA	3:S5:156:ILE:HD12	1.98	0.46
5:X2:59:TRP:CE3	5:X2:120:LEU:HG	2.51	0.46
5:X4:192:LEU:HB2	5:X4:194:LYS:HE2	1.98	0.46
6:Y4:122:TRP:CZ3	6:Y4:130:LYS:HG3	2.51	0.46
9:b4:138:ILE:C	9:b4:139:ILE:HD13	2.41	0.46
1:C7:151:PHE:CE2	1:C7:163:VAL:HG21	2.51	0.46
1:E4:33:GLY:C	1:E4:244:THR:HG22	2.41	0.46
1:E4:56:ILE:HG23	1:E4:231:TYR:HE1	1.81	0.46
1:G5:4:ASN:HB3	1:G6:243:ASP:CG	2.41	0.46
1:G7:211:ALA:HB2	1:H7:109:GLN:NE2	2.30	0.46
1:G8:258:ILE:HG22	1:H7:3:ILE:HD11	1.97	0.46
1:I5:65:ASN:HD22	1:I6:99:ASN:HD22	1.63	0.46
1:I9:186:LEU:HD12	1:I9:195:VAL:HG21	1.97	0.46
1:K6:247:ALA:O	1:K6:251:THR:HG23	2.16	0.46
1:K7:184:ILE:CD1	1:K7:195:VAL:HG13	2.45	0.46
2:L2:200:TRP:CD1	2:L2:216:ILE:HG13	2.51	0.46
2:M3:89:HIS:CG	2:M3:90:GLN:H	2.34	0.46
2:O3:98:ASN:HD22	3:S4:89:ASN:HD22	1.62	0.46
3:R1:162:HIS:HD2	3:R1:163:ASP:CG	2.24	0.46
3:S4:126:ILE:HG13	3:S5:237:LEU:HD12	1.97	0.46
3:S6:62:LYS:HB3	3:S6:65:ALA:HB2	1.98	0.46
5:X4:93:ASP:O	5:X4:97:LYS:HG3	2.15	0.46
1:A4:72:LEU:HD13	1:A5:101:ILE:HG22	1.97	0.46
1:A8:168:MET:HE1	1:A8:205:VAL:HG13	1.98	0.46
1:C5:95:VAL:HA	1:C5:196:ILE:HD11	1.96	0.46
1:D6:255:ARG:O	1:D6:258:ILE:HG22	2.15	0.46
1:E2:161:GLU:HB3	1:E2:219:ARG:HH22	1.81	0.46
1:F5:233:ASN:ND2	1:G1:74:GLN:HG2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H6:118:VAL:HG11	1:H6:183:PHE:CZ	2.51	0.46
1:K4:3:ILE:HD12	1:K6:246:MET:HG3	1.96	0.46
1:K5:60:ARG:HD3	1:K5:231:TYR:CE2	2.50	0.46
2:M1:72:LEU:HD11	2:M2:198:ARG:NH2	2.31	0.46
2:N1:190:LYS:NZ	2:N1:224:ASP:HA	2.31	0.46
3:Q4:21:VAL:O	3:Q4:25:LEU:HD13	2.15	0.46
6:Y3:41:ARG:HD2	6:Y3:263:ILE:HB	1.98	0.46
1:h0:108:GLN:O	1:h0:112:VAL:HG23	2.16	0.46
1:A5:70:MET:HE3	1:A5:217:TYR:CZ	2.51	0.45
1:A6:61:ARG:HH11	1:A6:61:ARG:HG3	1.81	0.45
1:C4:3:ILE:HD11	1:C4:274:SER:HB3	1.98	0.45
1:C7:81:GLN:NE2	1:C7:210:ARG:HH22	2.14	0.45
1:D4:183:PHE:N	1:D4:183:PHE:CD1	2.83	0.45
1:E3:156:ASN:HB2	1:E3:159:GLN:OE1	2.16	0.45
1:E4:258:ILE:HG13	1:F3:278:MET:HE2	1.98	0.45
1:F3:120:GLU:O	1:F3:124:ILE:HG22	2.16	0.45
1:G8:118:VAL:HG13	1:G8:170:THR:HG21	1.98	0.45
1:H5:278:MET:HG2	1:H5:282:GLN:OE1	2.16	0.45
1:I4:6:ASN:O	1:I4:10:ILE:HG13	2.16	0.45
1:I8:5:HIS:CE1	1:I9:235:GLN:HE22	2.34	0.45
1:I9:114:VAL:HG21	1:I9:186:LEU:HD22	1.98	0.45
1:I9:175:LEU:HD22	1:I9:184:ILE:HD13	1.98	0.45
1:J5:61:ARG:HH21	1:J6:96:GLN:HG3	1.81	0.45
1:K6:86:ILE:HG23	1:K6:117:LEU:HD22	1.97	0.45
2:L2:88:LEU:HD13	2:L3:286:ILE:CD1	2.45	0.45
2:L3:136:GLU:HG3	2:L3:136:GLU:O	2.16	0.45
2:M2:137:LYS:HB2	2:N2:212:GLN:HE22	1.81	0.45
2:O3:137:LYS:HD3	2:P3:211:PRO:HD2	1.98	0.45
2:O3:268:LEU:O	2:O3:272:THR:HG22	2.16	0.45
2:O4:75:ASN:HD21	2:O4:78:PHE:HB2	1.81	0.45
3:S2:125:TYR:HE1	3:S2:127:TYR:HB2	1.81	0.45
4:U6:121:TYR:HB3	4:U6:187:LEU:HD13	1.98	0.45
5:V1:136:SER:HA	5:V1:175:LEU:O	2.16	0.45
5:V3:113:LYS:HB3	5:V3:207:VAL:HA	1.98	0.45
6:Y4:34:LEU:O	6:Y4:34:LEU:HD13	2.15	0.45
7:Z1:281:ILE:HG22	7:Z1:282:LYS:N	2.31	0.45
9:b4:64:ILE:O	9:b4:68:GLN:HG3	2.16	0.45
1:h0:170:THR:CG2	1:h0:175:LEU:HB2	2.46	0.45
1:i0:114:VAL:HG21	1:i0:186:LEU:HD11	1.98	0.45
1:A6:123:ARG:HD2	1:K6:153:ILE:HD11	1.97	0.45
1:B7:43:ALA:HB1	1:B8:211:ALA:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C6:226:GLY:HA2	1:D6:82:GLU:HG3	1.97	0.45
1:D6:17:LYS:HD3	1:D7:228:MET:HE1	1.97	0.45
1:D7:157:MET:HG2	1:D7:158:HIS:ND1	2.31	0.45
1:E3:191:LYS:O	1:E3:195:VAL:HG23	2.17	0.45
1:F2:80:LEU:HD12	1:F2:213:LEU:HD12	1.97	0.45
1:F4:149:MET:HE3	1:F4:151:PHE:HE1	1.82	0.45
1:I6:191:LYS:O	1:I6:195:VAL:HG23	2.16	0.45
1:I7:107:ARG:O	1:I7:110:ILE:HG22	2.16	0.45
1:I7:209:GLN:HE21	1:I7:213:LEU:CD2	2.29	0.45
1:I9:192:ALA:O	1:I9:196:ILE:HG13	2.16	0.45
1:K6:158:HIS:HA	1:K7:193:ASN:HD21	1.80	0.45
1:K6:175:LEU:O	1:K6:184:ILE:HG12	2.16	0.45
1:K7:180:VAL:HG11	7:Z1:171:ASN:HD21	1.81	0.45
2:L1:73:TRP:CZ2	2:L2:198:ARG:HG3	2.51	0.45
2:M2:168:PHE:CZ	2:M2:199:SER:HB2	2.51	0.45
2:N2:148:ARG:HD3	2:N2:151:ARG:HH21	1.81	0.45
2:N3:73:TRP:CZ2	2:N4:198:ARG:HG3	2.52	0.45
2:O2:75:ASN:HB2	2:O3:202:MET:SD	2.57	0.45
3:R1:18:ILE:O	3:R1:21:VAL:HG12	2.16	0.45
3:R5:99:LEU:HB3	3:R5:119:LEU:HD11	1.97	0.45
3:R5:100:PHE:O	3:R5:119:LEU:HD12	2.15	0.45
4:U5:25:ILE:HD11	4:U5:88:ASN:CG	2.41	0.45
5:V3:192:LEU:HD11	5:V3:194:LYS:HE2	1.98	0.45
6:Y4:71:PHE:CE2	6:Y4:165:ALA:HB2	2.51	0.45
7:Z1:178:HIS:HA	7:Z1:181:LEU:HD12	1.98	0.45
8:a1:149:ARG:NE	8:a2:226:THR:HG22	2.31	0.45
9:b3:50:ILE:HD11	9:b3:235:LYS:HB2	1.98	0.45
10:c3:68:LYS:HE3	10:c3:152:LEU:HG	1.98	0.45
1:B3:44:SER:O	1:B3:48:VAL:HG13	2.16	0.45
1:D4:209:GLN:HE21	1:D4:213:LEU:CD2	2.29	0.45
1:E4:3:ILE:HD11	1:E4:278:MET:HB3	1.98	0.45
1:F1:278:MET:HE1	1:F2:246:MET:HE2	1.98	0.45
1:F6:226:GLY:HA2	1:G2:82:GLU:HG3	1.97	0.45
1:H7:157:MET:HE3	1:H7:157:MET:HB3	1.78	0.45
1:H8:3:ILE:HG21	1:H9:246:MET:HE2	1.97	0.45
1:I9:183:PHE:N	1:I9:183:PHE:CD1	2.84	0.45
2:M1:85:PHE:CE2	2:M1:89:HIS:HE1	2.35	0.45
2:P3:78:PHE:HE1	2:P4:205:TYR:CZ	2.35	0.45
3:S5:164:ASP:C	3:S5:166:PRO:HD2	2.41	0.45
4:U5:121:TYR:HB3	4:U5:187:LEU:HD13	1.98	0.45
5:V3:106:VAL:HB	5:V3:216:PHE:CE1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:V3:131:LYS:O	5:V3:225:THR:HG23	2.16	0.45
5:X1:142:ARG:HB2	5:X2:191:LEU:HD13	1.98	0.45
5:X4:52:ASP:HB2	12:X4:401:HOH:O	2.14	0.45
5:X4:110:PHE:HB2	5:X4:211:ALA:HB1	1.98	0.45
8:a4:131:PHE:CE2	8:a4:200:ARG:HB3	2.51	0.45
8:a5:80:LYS:HD3	8:a5:86:TYR:CE1	2.52	0.45
1:A7:153:ILE:HG21	1:A7:220:MET:SD	2.56	0.45
1:B4:66:THR:O	1:B4:70:MET:HG3	2.16	0.45
1:B4:251:THR:O	1:B4:254:THR:HG22	2.16	0.45
1:D3:247:ALA:HB1	1:E2:267:LEU:HD11	1.98	0.45
1:E6:61:ARG:HD2	1:E6:61:ARG:HA	1.73	0.45
1:F6:82:GLU:HG3	1:F6:124:ILE:HD13	1.98	0.45
1:G6:150:TRP:CE3	1:G6:160:ARG:HG3	2.51	0.45
1:G7:22:ASN:HD22	1:G7:22:ASN:N	2.14	0.45
1:I6:177:ASN:HB3	1:I6:180:VAL:O	2.15	0.45
1:J5:40:GLY:HA3	1:J6:217:TYR:CD1	2.52	0.45
1:J5:66:THR:HG23	1:J5:220:MET:SD	2.56	0.45
1:K7:129:GLU:OE2	1:K7:134:LYS:HE2	2.16	0.45
2:L1:85:PHE:CZ	2:L2:230:TYR:HE1	2.34	0.45
2:N1:169:SER:HA	2:N1:172:ILE:HG22	1.98	0.45
2:P3:106:ASN:OD1	2:P3:170:LYS:HE3	2.16	0.45
3:Q2:14:LEU:HD21	3:Q2:201:LYS:HD3	1.99	0.45
3:R2:73:LEU:HD21	3:R2:214:LEU:HD23	1.99	0.45
3:R2:166:PRO:HD3	3:R2:179:VAL:HG13	1.98	0.45
3:S6:34:MET:HE3	3:S6:34:MET:HB3	1.75	0.45
4:U4:175:TYR:CE1	4:U4:179:LEU:HD11	2.52	0.45
5:V3:77:GLN:HG3	5:V3:101:ASN:O	2.17	0.45
5:X2:71:ARG:HE	5:X2:71:ARG:HB2	1.62	0.45
5:X2:127:ILE:HG21	7:Z1:145:ARG:HA	1.97	0.45
6:Y2:145:ALA:O	6:Y2:147:PRO:HD3	2.16	0.45
7:Z0:62:GLN:HG3	7:Z1:110:MET:HE2	1.98	0.45
7:Z1:14:LEU:HD22	7:Z1:87:ILE:HD12	1.98	0.45
8:a5:47:ASN:HD22	8:a5:49:LYS:H	1.63	0.45
1:A5:3:ILE:HD12	1:A6:246:MET:HG3	1.98	0.45
1:B7:238:GLU:HA	1:B7:241:ILE:HG22	1.97	0.45
1:D5:150:TRP:CZ3	1:D5:162:ARG:HB2	2.52	0.45
1:D6:262:ALA:HB2	1:E5:278:MET:HE2	1.97	0.45
1:F1:50:GLU:HG2	1:F2:84:HIS:HE2	1.82	0.45
1:G9:47:ALA:HB2	1:h0:109:GLN:HE22	1.80	0.45
1:J6:133:MET:HE3	1:J6:134:LYS:H	1.82	0.45
2:L3:287:VAL:O	2:L3:290:ILE:HG22	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M4:225:ASP:HA	8:a4:53:LYS:HZ1	1.81	0.45
2:N1:93:LYS:HD3	2:N1:94:THR:HG23	1.99	0.45
2:N2:127:GLU:HA	2:N2:130:GLU:HG2	1.99	0.45
2:N3:98:ASN:HD22	3:R3:89:ASN:ND2	2.14	0.45
2:P3:120:TRP:CH2	2:P3:156:GLU:HG3	2.52	0.45
3:R4:242:LYS:HA	3:R4:242:LYS:HD2	1.75	0.45
3:R5:40:PRO:HG3	3:R5:214:LEU:HD11	1.98	0.45
4:U4:287:ASN:HA	4:U4:290:ILE:HG12	1.98	0.45
4:U5:208:LYS:HD3	4:U5:211:TYR:HE1	1.80	0.45
6:Y1:202:LEU:HB3	6:Y1:203:PRO:HD3	1.99	0.45
7:Z1:27:ASN:ND2	7:Z1:311:TYR:H	2.14	0.45
8:a1:110:VAL:HG23	8:a1:130:SER:HB2	1.99	0.45
9:b3:190:PHE:CE2	9:b3:209:ALA:HA	2.52	0.45
1:A4:44:SER:O	1:A4:48:VAL:HG12	2.17	0.45
1:A5:4:ASN:HB3	1:A6:243:ASP:CG	2.42	0.45
1:A5:36:ILE:HG23	1:A5:41:ASP:HB2	1.98	0.45
1:A6:166:GLU:H	1:A6:209:GLN:HE22	1.65	0.45
1:B4:66:THR:HG22	1:B4:70:MET:HE3	1.97	0.45
1:B5:70:MET:HB3	1:B5:217:TYR:CE2	2.52	0.45
1:B6:127:GLN:OE1	1:B6:127:GLN:HA	2.16	0.45
1:B6:169:ASN:ND2	1:B6:171:ALA:HB3	2.30	0.45
1:C3:46:LEU:HD21	1:C4:210:ARG:HE	1.81	0.45
1:D3:114:VAL:O	1:D3:118:VAL:HG12	2.17	0.45
1:F6:186:LEU:HD11	1:F6:195:VAL:HG11	1.99	0.45
1:G5:282:GLN:HE22	1:G6:246:MET:HE3	1.81	0.45
1:H8:150:TRP:CZ3	1:H8:162:ARG:HB2	2.51	0.45
1:I6:5:HIS:HD2	1:I7:243:ASP:OD2	2.00	0.45
1:I6:97:ALA:HB2	1:I6:110:ILE:HG21	1.99	0.45
1:I8:3:ILE:HD12	1:I9:246:MET:HG3	1.97	0.45
1:I9:183:PHE:N	1:I9:183:PHE:HD1	2.14	0.45
1:J6:225:LYS:HB2	1:J6:225:LYS:HE2	1.79	0.45
1:K8:134:LYS:HD3	1:K8:134:LYS:N	2.32	0.45
2:L2:208:GLN:NE2	2:L2:208:GLN:HA	2.32	0.45
2:L4:169:SER:HG	2:L4:200:TRP:HZ3	1.63	0.45
2:N3:88:LEU:HD21	2:N4:276:TYR:HE2	1.81	0.45
2:N4:146:LYS:O	2:N4:150:GLU:HG2	2.17	0.45
2:N6:384:ILE:O	2:N6:388:ILE:HG12	2.17	0.45
3:Q1:187:VAL:HG23	3:Q2:230:TYR:CE2	2.51	0.45
5:V1:54:GLU:HA	5:V1:102:HIS:HB2	1.97	0.45
5:V3:86:ASP:HB2	6:Y3:213:LYS:NZ	2.32	0.45
5:V3:125:GLU:HA	5:V3:199:VAL:CG2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X4:84:VAL:HG21	5:X4:171:GLY:HA3	1.98	0.45
1:B6:2:ILE:HG21	1:B7:239:SER:OG	2.17	0.45
1:C4:177:ASN:HB3	1:C4:180:VAL:O	2.16	0.45
1:C6:68:ASP:HB3	1:C7:101:ILE:HD13	1.97	0.45
1:D5:192:ALA:O	1:D5:196:ILE:HG13	2.15	0.45
1:E2:150:TRP:CZ2	1:E2:162:ARG:HD2	2.52	0.45
1:E5:56:ILE:HG23	1:E5:231:TYR:CE1	2.52	0.45
1:E7:171:ALA:HB1	1:E7:178:PRO:HB3	1.98	0.45
1:F1:33:GLY:C	1:F1:244:THR:HG22	2.42	0.45
1:F5:153:ILE:HD11	1:F5:220:MET:HE1	1.98	0.45
1:F5:153:ILE:O	1:F5:153:ILE:HG22	2.16	0.45
1:K8:177:ASN:HB3	1:K8:180:VAL:O	2.17	0.45
2:L3:114:ILE:O	2:L3:118:ARG:HG3	2.17	0.45
2:L3:120:TRP:CH2	2:L3:156:GLU:HG3	2.52	0.45
2:L3:188:GLU:CD	2:L3:188:GLU:H	2.25	0.45
2:L3:262:TYR:O	2:L3:266:VAL:HG12	2.16	0.45
2:L4:86:GLN:HA	2:L4:89:HIS:NE2	2.31	0.45
2:P4:131:LYS:HE2	2:P4:131:LYS:HB2	1.65	0.45
3:S4:202:GLN:HB3	3:S5:238:LYS:HE2	1.99	0.45
4:U3:75:LYS:O	4:U3:78:LYS:HG2	2.16	0.45
4:U6:266:GLU:HG3	4:U6:276:THR:HG21	1.98	0.45
5:X1:145:ARG:NH2	5:X2:188:ARG:HH22	2.15	0.45
5:X2:79:GLY:HA3	5:X3:236:GLU:OE2	2.16	0.45
9:b3:144:ARG:NE	9:b3:157:ARG:HH21	2.14	0.45
9:b4:58:ILE:CD1	9:b4:135:LEU:HG	2.47	0.45
10:c2:144:PHE:CD2	10:c2:148:PRO:HG3	2.52	0.45
1:B3:266:MET:HE2	1:C3:27:ILE:HA	1.98	0.45
1:B6:153:ILE:HD11	1:C6:123:ARG:HD2	1.99	0.45
1:C4:191:LYS:O	1:C4:195:VAL:HG23	2.17	0.45
1:E3:270:ALA:O	1:E3:273:LYS:HG2	2.17	0.45
1:F2:130:PHE:CB	1:F2:135:LEU:HD21	2.46	0.45
1:G1:149:MET:HE2	1:G1:149:MET:HA	1.99	0.45
1:H7:111:GLN:HA	1:H7:114:VAL:HG12	1.99	0.45
1:H8:175:LEU:O	1:H8:184:ILE:HG23	2.17	0.45
1:I8:219:ARG:NH2	1:J8:119:ASP:HB3	2.32	0.45
1:I9:191:LYS:O	1:I9:195:VAL:HG23	2.16	0.45
1:J6:176:ARG:HH21	1:J6:181:LEU:HB3	1.82	0.45
1:K4:40:GLY:HA3	1:K6:217:TYR:CD1	2.52	0.45
2:L5:175:LEU:HD12	2:L5:175:LEU:HA	1.75	0.45
2:N1:175:LEU:HD12	2:N1:196:VAL:HG21	1.99	0.45
2:N4:269:LEU:O	2:N4:272:THR:HG22	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O1:223:ILE:HB	2:O1:226:ASN:ND2	2.32	0.45
2:P5:230:TYR:CD2	2:P5:231:PRO:HD3	2.52	0.45
3:R3:34:MET:HE1	3:R3:219:PHE:HD1	1.78	0.45
4:U3:91:TYR:HD1	4:U3:91:TYR:O	1.99	0.45
5:V1:139:VAL:HG11	5:V1:167:LEU:HD22	1.98	0.45
5:V3:188:ARG:HG3	6:Y3:43:HIS:CE1	2.49	0.45
8:a3:149:ARG:HE	8:a4:229:GLU:CD	2.25	0.45
1:A6:269:GLN:HG2	1:B6:253:PHE:HZ	1.80	0.45
1:B5:66:THR:HA	1:B5:220:MET:CE	2.46	0.45
1:B8:177:ASN:HB3	1:B8:180:VAL:O	2.17	0.45
1:D5:52:MET:HE3	1:D5:238:GLU:HA	1.98	0.45
1:F5:154:GLY:HA3	1:F5:159:GLN:NE2	2.32	0.45
1:K8:108:GLN:O	1:K8:112:VAL:HG23	2.17	0.45
2:L3:139:TYR:HE1	2:M2:256:MET:HE3	1.81	0.45
2:N2:88:LEU:HD21	2:N3:276:TYR:CE2	2.51	0.45
2:P2:214:ILE:HB	2:P2:215:PRO:HD3	1.98	0.45
2:P6:120:TRP:CH2	2:P6:156:GLU:HG3	2.52	0.45
3:S2:41:HIS:O	3:S2:43:THR:HG23	2.16	0.45
3:S3:188:GLU:OE1	3:S3:188:GLU:HA	2.17	0.45
5:X1:108:THR:HG21	5:X1:118:VAL:HG22	1.99	0.45
6:Y1:49:GLY:HA3	6:Y1:223:TYR:CE1	2.52	0.45
7:Za:22:GLU:HB3	7:Za:23:PRO:HD3	1.99	0.45
8:a1:101:PRO:HG2	8:a1:103:TYR:CE2	2.52	0.45
1:C2:3:ILE:HD11	1:C3:246:MET:HE2	1.98	0.45
1:D3:118:VAL:HG23	1:D3:170:THR:HG21	1.98	0.45
1:E3:19:ASN:HD22	1:E3:259:LEU:HB3	1.82	0.45
1:E3:118:VAL:HG22	1:E3:170:THR:HG21	1.99	0.45
1:F3:56:ILE:HG12	1:F3:234:THR:HG23	1.99	0.45
1:G6:55:GLN:O	1:G6:59:LEU:HD22	2.17	0.45
1:J6:53:ARG:HA	1:J6:56:ILE:HD12	1.99	0.45
2:M2:78:PHE:CE2	2:M3:234:LYS:HD3	2.52	0.45
2:P2:149:GLU:O	2:P2:152:VAL:HG12	2.17	0.45
2:P4:102:LEU:HD21	9:b4:147:ALA:HB1	1.99	0.45
3:Q1:43:THR:HG22	3:Q1:75:VAL:HG22	1.99	0.45
4:U6:209:PRO:HB2	4:U6:214:ARG:HH21	1.82	0.45
5:V1:143:LYS:HA	5:V1:168:ASP:O	2.16	0.45
5:V3:114:GLY:HA2	5:V3:205:SER:O	2.17	0.45
6:Y2:238:ILE:O	6:Y2:253:ARG:HA	2.17	0.45
1:A6:52:MET:HE1	1:A6:237:SER:OG	2.18	0.44
1:A8:219:ARG:HD3	1:B8:120:GLU:OE2	2.17	0.44
1:B6:133:MET:HE2	1:B6:140:PHE:CZ	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C6:150:TRP:CZ3	1:C6:162:ARG:HB2	2.53	0.44
1:C7:168:MET:HE2	1:C7:168:MET:HB2	1.79	0.44
1:E3:7:VAL:O	1:E3:10:ILE:HG22	2.17	0.44
1:E3:261:GLN:NE2	1:F2:278:MET:HG3	2.32	0.44
1:G8:66:THR:HG23	1:G8:220:MET:HG3	1.99	0.44
1:H9:111:GLN:NE2	1:H9:185:SER:HA	2.31	0.44
1:I8:171:ALA:HB1	1:I8:178:PRO:HG3	1.98	0.44
2:L5:139:TYR:HE1	2:M4:256:MET:HE3	1.81	0.44
3:Q4:138:ILE:HD12	3:Q4:161:GLN:OE1	2.17	0.44
3:R3:158:LEU:HD11	3:R3:184:LEU:HB2	1.99	0.44
3:R5:124:THR:HB	3:R5:141:ILE:HG13	1.98	0.44
4:U5:141:ASP:HB3	4:U5:144:ALA:HB3	1.99	0.44
4:U6:82:GLN:HB3	4:U6:290:ILE:HG22	1.99	0.44
4:U6:287:ASN:O	4:U6:291:LYS:HG3	2.17	0.44
5:V1:146:HIS:ND1	5:V1:205:SER:HA	2.32	0.44
6:Y2:69:SER:HB2	6:Y2:165:ALA:HB3	1.99	0.44
7:Za:191:LYS:HG2	7:Za:194:ARG:NH2	2.32	0.44
8:a5:64:TYR:HD1	8:a5:67:MET:HE2	1.80	0.44
1:B6:198:LEU:HD13	5:V2:67:LEU:HD23	1.99	0.44
1:C6:77:GLU:HG3	1:C6:78:GLY:N	2.32	0.44
1:D3:47:ALA:HB2	1:E4:109:GLN:NE2	2.32	0.44
1:D5:53:ARG:HE	1:D5:238:GLU:CD	2.25	0.44
1:E2:46:LEU:HD21	1:E3:210:ARG:CZ	2.48	0.44
1:E4:66:THR:HG21	1:E4:224:ALA:HB2	1.99	0.44
1:H6:47:ALA:HB2	1:I7:109:GLN:NE2	2.32	0.44
1:I7:266:MET:HE3	1:J7:30:LEU:HD13	1.99	0.44
1:J5:257:GLN:O	1:J5:260:THR:HG22	2.17	0.44
2:M3:201:ILE:HD13	2:M3:217:LEU:HD13	1.98	0.44
2:M4:93:LYS:HD3	3:Q4:131:PHE:HZ	1.81	0.44
2:P2:263:LYS:O	2:P2:266:VAL:HG12	2.17	0.44
3:R1:177:LYS:O	3:R1:177:LYS:HG3	2.16	0.44
4:U4:37:VAL:HG11	4:U4:273:GLY:HA2	1.98	0.44
4:U4:97:VAL:HG23	4:U4:98:TYR:HD1	1.82	0.44
4:U6:287:ASN:O	4:U6:290:ILE:HG13	2.17	0.44
5:V1:75:LEU:O	5:V1:102:HIS:HA	2.17	0.44
6:Y1:77:GLU:H	6:Y1:234:ASN:HD21	1.64	0.44
7:Z0:110:MET:SD	7:Z0:172:MET:HE2	2.57	0.44
8:a5:181:LEU:HD12	8:a5:184:ILE:HD12	2.00	0.44
9:b4:234:TYR:CZ	9:b4:238:LEU:HD21	2.52	0.44
1:B5:73:ILE:HD13	1:B5:213:LEU:HD22	1.99	0.44
1:C3:233:ASN:HD22	1:D3:74:GLN:HE21	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C6:129:GLU:HB3	1:C6:134:LYS:NZ	2.32	0.44
1:D6:53:ARG:HH21	1:D6:242:ARG:CZ	2.30	0.44
1:E2:278:MET:HE3	1:E2:278:MET:HB3	1.91	0.44
1:F3:30:LEU:CD2	1:F3:249:GLN:HB3	2.48	0.44
1:H6:169:ASN:ND2	1:H6:171:ALA:HB3	2.32	0.44
1:I8:14:ARG:CD	1:I9:228:MET:HB3	2.47	0.44
1:I9:62:ALA:HB1	1:I9:153:ILE:O	2.18	0.44
1:J4:258:ILE:HG13	1:K3:3:ILE:HD12	1.99	0.44
1:J6:209:GLN:HE21	1:J6:213:LEU:CD2	2.30	0.44
2:L1:219:LEU:HD23	2:L1:219:LEU:HA	1.81	0.44
2:O5:117:ASN:HD21	2:O5:157:LYS:HA	1.82	0.44
3:Q2:122:ILE:HD11	3:Q2:204:TYR:OH	2.17	0.44
3:Q3:97:MET:HA	3:Q3:123:ARG:O	2.17	0.44
3:Q3:202:GLN:O	3:Q3:206:LYS:HE2	2.17	0.44
3:R1:177:LYS:HE3	3:R2:226:SER:HB3	2.00	0.44
3:S2:29:THR:OG1	3:S2:116:PRO:HA	2.16	0.44
3:S5:72:HIS:NE2	3:S5:96:LYS:HD2	2.33	0.44
4:U4:172:GLN:HB3	4:U4:175:TYR:HB3	1.99	0.44
4:U5:175:TYR:CZ	4:U5:179:LEU:HD11	2.52	0.44
6:Y4:121:ILE:HD11	6:Y4:149:PRO:CG	2.44	0.44
9:b4:182:ASN:HD22	9:b4:182:ASN:N	2.15	0.44
1:A7:48:VAL:HG11	1:B8:102:TYR:CE1	2.53	0.44
1:A8:48:VAL:O	1:A8:52:MET:HG3	2.17	0.44
1:A8:67:GLU:HB3	1:K8:240:ARG:CZ	2.48	0.44
1:E2:247:ALA:HB1	1:F1:267:LEU:HD11	1.99	0.44
1:E4:240:ARG:HG2	1:F4:67:GLU:HB3	1.98	0.44
1:E7:91:ARG:HG2	1:E7:91:ARG:HH11	1.83	0.44
1:H6:1:MET:HB3	1:H6:277:VAL:HG11	2.00	0.44
1:I6:111:GLN:HE22	1:I6:185:SER:HA	1.82	0.44
1:J4:11:PHE:O	1:J4:15:THR:HG22	2.16	0.44
1:J7:153:ILE:HG13	1:J7:153:ILE:O	2.16	0.44
1:J7:248:GLU:CD	1:K7:60:ARG:HH12	2.26	0.44
1:J9:108:GLN:O	1:J9:112:VAL:HG23	2.17	0.44
1:K8:157:MET:HG2	1:K8:158:HIS:CD2	2.52	0.44
2:L5:205:TYR:CE2	2:L5:210:LEU:HD11	2.52	0.44
2:N5:153:VAL:HG12	2:N5:157:LYS:HE2	1.98	0.44
3:S2:28:HIS:HE1	3:S2:212:ASP:OD1	1.99	0.44
4:U3:136:ILE:HG12	4:U3:144:ALA:HB1	2.00	0.44
4:U6:75:LYS:O	4:U6:78:LYS:HG2	2.18	0.44
6:Y3:19:ASN:O	6:Y3:20:ARG:HD3	2.17	0.44
7:Z0:195:ASN:CG	7:Z0:195:ASN:O	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i0:139:ALA:HA	1:i0:144:ASN:ND2	2.33	0.44
1:G6:10:ILE:HG22	1:G7:232:GLU:HG3	2.00	0.44
1:G6:149:MET:HE1	1:G7:100:GLY:C	2.43	0.44
1:G8:122:ASP:OD1	1:G8:170:THR:HG23	2.18	0.44
1:G9:191:LYS:O	1:G9:195:VAL:HG23	2.18	0.44
1:H6:1:MET:HE2	1:H6:1:MET:H2	1.81	0.44
1:J5:60:ARG:HD3	1:J5:231:TYR:CE1	2.52	0.44
1:J6:269:GLN:HE21	1:K6:257:GLN:NE2	2.15	0.44
1:K4:180:VAL:HG21	7:Za:230:ASN:ND2	2.32	0.44
2:L2:233:HIS:HB3	2:L2:271:ALA:HB2	2.00	0.44
2:L4:88:LEU:HD11	2:L5:276:TYR:HE2	1.83	0.44
2:O5:228:LYS:HB3	2:O5:228:LYS:HE2	1.68	0.44
2:P4:208:GLN:HG2	2:P4:208:GLN:O	2.18	0.44
3:R5:20:GLU:HA	3:R5:23:LYS:HE3	1.99	0.44
3:S2:31:LEU:O	3:S2:31:LEU:HD23	2.18	0.44
3:S3:62:LYS:HB2	3:S3:65:ALA:HB2	1.99	0.44
3:S3:66:GLN:NE2	3:S3:105:ASN:HB2	2.33	0.44
4:U6:131:ALA:HB2	4:U6:254:PRO:HD3	1.99	0.44
5:V1:65:THR:HG22	5:V1:67:LEU:H	1.83	0.44
6:Y2:176:PRO:HG2	6:Y2:181:GLN:HG2	2.00	0.44
6:Y2:180:LYS:HG3	6:Y2:183:ILE:HD11	1.98	0.44
1:A7:22:ASN:HA	1:A7:25:LYS:HE3	2.00	0.44
1:E7:186:LEU:HD12	1:E7:195:VAL:HG21	2.00	0.44
1:F1:268:ALA:O	1:F1:272:MET:HG3	2.18	0.44
1:G7:266:MET:HE3	1:H7:30:LEU:HD13	1.98	0.44
1:H7:30:LEU:HD21	1:H7:249:GLN:HB3	1.99	0.44
1:H8:14:ARG:HH12	1:H9:229:ASN:CG	2.25	0.44
1:J5:1:MET:H2	1:J6:246:MET:H	1.64	0.44
1:J5:61:ARG:HE	1:J6:96:GLN:HB2	1.83	0.44
1:K4:266:MET:HE2	1:K4:266:MET:HA	1.99	0.44
2:L2:243:GLU:OE1	2:L2:243:GLU:HA	2.16	0.44
2:M1:168:PHE:CE2	2:M1:199:SER:HB2	2.52	0.44
2:O1:178:ILE:HD12	2:O1:189:PHE:HE2	1.82	0.44
2:O2:263:LYS:O	2:O2:266:VAL:HG22	2.17	0.44
2:P4:95:PHE:CD2	2:P4:183:LEU:HD13	2.53	0.44
2:P4:165:LEU:HD22	2:P4:207:LEU:HD21	2.00	0.44
3:Q1:96:LYS:HG2	3:Q1:97:MET:N	2.33	0.44
3:R4:83:ASP:O	3:R4:83:ASP:OD1	2.34	0.44
3:R5:26:ARG:HE	3:R5:116:PRO:HB2	1.82	0.44
3:S2:18:ILE:HG13	3:S2:204:TYR:CE2	2.53	0.44
3:S6:97:MET:HG2	3:S6:122:ILE:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U6:286:ALA:O	4:U6:290:ILE:HG12	2.18	0.44
5:V2:107:LYS:HG3	5:V2:215:TYR:CE2	2.53	0.44
5:X3:80:LEU:HD22	5:X3:96:ASP:OD1	2.18	0.44
6:Y2:47:GLY:C	6:Y2:48:LYS:HG2	2.43	0.44
8:a2:160:LYS:HE3	8:a2:160:LYS:HB3	1.67	0.44
1:A4:153:ILE:HD13	1:A4:220:MET:HE1	2.00	0.44
1:C5:278:MET:SD	1:C5:282:GLN:HG3	2.57	0.44
1:H6:171:ALA:HA	1:H6:176:ARG:O	2.17	0.44
1:H7:120:GLU:OE1	1:H7:123:ARG:HD3	2.17	0.44
1:I8:168:MET:HE2	1:I8:168:MET:HB2	1.83	0.44
1:J9:111:GLN:NE2	1:J9:185:SER:HA	2.29	0.44
1:K7:40:GLY:HA3	1:K8:217:TYR:CD1	2.53	0.44
2:L5:118:ARG:HG3	2:L5:118:ARG:HH11	1.83	0.44
2:M2:157:LYS:HB3	2:M2:157:LYS:HE3	1.88	0.44
2:M4:84:THR:CG2	2:M5:268:LEU:HD21	2.48	0.44
2:M5:230:TYR:CD1	2:M5:275:LYS:HB2	2.52	0.44
2:N4:57:GLU:H	2:N4:57:GLU:CD	2.26	0.44
2:N4:193:LEU:O	2:N4:196:VAL:HG12	2.18	0.44
2:N5:270:ARG:HA	2:N5:270:ARG:HD2	1.81	0.44
2:P2:90:GLN:O	2:P2:94:THR:HG23	2.18	0.44
2:P3:253:PRO:HG2	2:P3:256:MET:HG3	2.00	0.44
3:R5:14:LEU:HD21	3:R5:201:LYS:HD3	2.00	0.44
3:S6:207:ASN:C	3:S6:207:ASN:HD22	2.25	0.44
4:U4:187:LEU:HA	4:U4:187:LEU:HD23	1.72	0.44
5:V1:107:LYS:HD2	5:V1:108:THR:N	2.33	0.44
5:V4:84:VAL:HG21	5:V4:171:GLY:HA3	1.99	0.44
7:Z1:271:VAL:HG13	7:Z1:272:THR:N	2.33	0.44
8:a3:201:LEU:HD23	8:a3:201:LEU:HA	1.86	0.44
1:B3:11:PHE:CZ	1:C3:28:GLU:HG3	2.53	0.44
1:B3:237:SER:O	1:B3:241:ILE:HG13	2.17	0.44
1:B5:123:ARG:HD3	1:B5:127:GLN:NE2	2.32	0.44
1:B8:223:ALA:HB2	1:C8:123:ARG:NH2	2.33	0.44
1:D5:72:LEU:HB2	1:D6:101:ILE:CD1	2.46	0.44
1:F4:54:THR:HG21	1:F5:203:LEU:HD13	1.99	0.44
1:F5:86:ILE:HG23	1:F5:117:LEU:HD22	2.00	0.44
1:G8:36:ILE:HG21	1:G8:46:LEU:HB2	2.00	0.44
1:G8:150:TRP:CZ3	1:G8:162:ARG:HB2	2.53	0.44
1:H6:261:GLN:HB3	1:I5:278:MET:CE	2.47	0.44
1:H7:150:TRP:CZ3	1:H7:162:ARG:HB2	2.53	0.44
1:H8:262:ALA:HB2	1:I7:278:MET:SD	2.57	0.44
1:I8:183:PHE:N	1:I8:183:PHE:CD1	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I9:79:TYR:CD2	1:I9:128:ALA:HB1	2.53	0.44
1:J5:61:ARG:HH21	1:J6:96:GLN:CD	2.26	0.44
1:J6:150:TRP:CZ3	1:J6:162:ARG:HB2	2.53	0.44
2:L2:195:ASP:HA	2:L2:198:ARG:NH1	2.33	0.44
2:M1:286:ILE:O	2:M1:290:ILE:HG12	2.17	0.44
2:M4:263:LYS:O	2:M4:266:VAL:HG12	2.18	0.44
2:O1:168:PHE:CE2	2:O1:199:SER:HB3	2.53	0.44
2:P5:286:ILE:HA	2:P5:289:VAL:HG22	1.99	0.44
3:S5:66:GLN:HE22	3:S5:105:ASN:HB2	1.82	0.44
4:U5:24:LEU:HD23	4:U5:24:LEU:HA	1.84	0.44
5:V3:153:ARG:O	5:V3:196:LEU:HD12	2.17	0.44
8:a3:81:ILE:HG12	8:a3:86:TYR:HB2	2.00	0.44
8:a3:209:ASP:HA	8:a3:212:ILE:HG22	2.00	0.44
1:A3:266:MET:HB3	1:B3:27:ILE:HG23	1.99	0.44
1:A4:13:HIS:CG	1:K4:248:GLU:OE2	2.71	0.44
1:B4:66:THR:CG2	1:B4:220:MET:HG3	2.47	0.44
1:C5:275:GLN:NE2	1:C5:279:ARG:HG3	2.33	0.44
1:F2:233:ASN:OD1	1:G7:74:GLN:HG2	2.18	0.44
1:F3:225:LYS:HE2	1:F3:225:LYS:HB3	1.75	0.44
1:H6:237:SER:OG	1:I6:71:SER:HB3	2.18	0.44
1:H7:1:MET:HE1	1:I7:16:LEU:HD21	1.99	0.44
1:K6:130:PHE:HB3	1:K6:135:LEU:HD21	2.00	0.44
2:N3:269:LEU:O	2:N3:272:THR:HG22	2.18	0.44
2:O1:270:ARG:CZ	3:R1:213:LYS:HE2	2.48	0.44
3:R1:90:LEU:HD22	3:R1:132:LEU:HD12	1.98	0.44
4:U5:152:PHE:HB2	4:U6:92:LEU:HD22	2.00	0.44
4:U6:279:LYS:N	4:U6:279:LYS:HD2	2.33	0.44
5:V2:70:THR:HG22	5:V2:108:THR:HA	1.99	0.44
6:Y2:87:LYS:HB2	6:Y2:87:LYS:HE3	1.70	0.44
6:Y3:242:ASP:HB2	6:Y3:251:LEU:HD11	2.00	0.44
1:B4:53:ARG:HH21	1:B4:242:ARG:HG2	1.83	0.43
1:B6:73:ILE:HD12	1:B6:213:LEU:HD22	2.00	0.43
1:B6:222:HIS:CG	1:C6:86:ILE:HD11	2.53	0.43
1:C5:237:SER:OG	1:D5:71:SER:HB3	2.18	0.43
1:D6:159:GLN:HG2	1:E6:127:GLN:HG2	1.99	0.43
1:E5:265:SER:OG	1:F4:282:GLN:HG2	2.18	0.43
1:E7:80:LEU:O	1:E7:83:THR:HG22	2.18	0.43
1:F5:28:GLU:OE1	1:F5:28:GLU:HA	2.17	0.43
1:H7:266:MET:SD	1:I7:30:LEU:HB2	2.58	0.43
1:I7:151:PHE:CE2	1:I7:163:VAL:HG11	2.53	0.43
1:J7:3:ILE:HG13	1:J7:4:ASN:N	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M2:67:MET:HE1	3:Q2:163:ASP:O	2.17	0.43
2:M4:169:SER:HB3	2:M4:200:TRP:CH2	2.53	0.43
2:O1:88:LEU:HD11	2:O2:286:ILE:HD11	1.99	0.43
2:O1:110:GLY:HA3	2:O1:168:PHE:CE1	2.53	0.43
2:O1:125:ARG:HH21	2:O1:153:VAL:HG21	1.83	0.43
2:O3:73:TRP:CZ2	2:O4:198:ARG:HG3	2.52	0.43
2:P1:82:ASN:HB2	2:P2:238:SER:HA	1.99	0.43
2:P2:204:GLU:OE1	2:P2:204:GLU:HA	2.18	0.43
2:P6:217:LEU:HB3	2:P6:236:LEU:CD2	2.48	0.43
3:R2:18:ILE:HD12	3:R2:204:TYR:CD2	2.53	0.43
3:R2:72:HIS:NE2	3:R2:96:LYS:HD3	2.33	0.43
3:R3:163:ASP:O	3:R3:164:ASP:OD1	2.36	0.43
4:U4:78:LYS:NZ	4:U4:82:GLN:HB3	2.33	0.43
4:U6:234:VAL:HA	4:U6:237:THR:HG22	2.00	0.43
5:V2:51:ASP:HB3	5:V2:221:LEU:HD23	2.00	0.43
5:X2:140:LEU:HD23	5:X2:217:TYR:CD1	2.52	0.43
6:Y4:34:LEU:HD12	6:Y4:252:PHE:CZ	2.53	0.43
1:A4:277:VAL:HG23	1:A4:278:MET:SD	2.58	0.43
1:A5:24:SER:O	1:A5:28:GLU:HG3	2.18	0.43
1:A5:212:ASP:CA	1:B5:116:GLN:HE22	2.30	0.43
1:A6:66:THR:HG21	1:A6:224:ALA:HB2	2.01	0.43
1:C6:51:LYS:HE3	1:C6:51:LYS:HB2	1.93	0.43
1:C7:223:ALA:O	1:C7:227:LEU:HD23	2.18	0.43
1:D3:50:GLU:HA	1:D3:50:GLU:OE1	2.18	0.43
1:D4:16:LEU:HD13	1:D4:263:ALA:HB3	2.00	0.43
1:E4:237:SER:OG	1:F4:71:SER:HB3	2.17	0.43
1:E6:90:VAL:HG13	1:E6:114:VAL:HG13	2.00	0.43
1:K8:88:GLN:O	1:K8:92:VAL:HG22	2.17	0.43
2:L2:208:GLN:HA	2:L2:208:GLN:HE21	1.83	0.43
2:L4:284:LYS:O	2:L4:287:VAL:HG22	2.18	0.43
2:M3:138:TRP:CZ3	2:N3:246:MET:HE2	2.53	0.43
2:N2:175:LEU:HD21	2:N2:192:LEU:HD12	2.00	0.43
2:O3:268:LEU:HD23	2:O3:290:ILE:HD11	1.99	0.43
2:P2:161:LYS:HE2	2:P2:161:LYS:HB2	1.90	0.43
2:P2:175:LEU:HD21	2:P2:192:LEU:HD22	1.99	0.43
3:R2:34:MET:HE1	3:R2:219:PHE:HA	1.99	0.43
3:R2:195:ILE:HG13	3:R3:234:VAL:HG21	1.99	0.43
3:S3:66:GLN:HE22	3:S3:105:ASN:HB2	1.83	0.43
3:S5:40:PRO:HG2	3:S5:43:THR:HG21	1.99	0.43
4:U4:175:TYR:HE1	4:U4:179:LEU:HD11	1.83	0.43
5:V2:113:LYS:HB3	5:V2:207:VAL:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:V3:76:VAL:HG13	5:V3:101:ASN:ND2	2.33	0.43
5:X3:65:THR:HB	5:X3:116:ASP:OD1	2.19	0.43
1:A5:1:MET:SD	1:A5:277:VAL:HG21	2.59	0.43
1:B8:66:THR:HG23	1:B8:220:MET:HE2	2.00	0.43
1:C2:25:LYS:HE3	1:C2:25:LYS:HB2	1.75	0.43
1:C3:46:LEU:O	1:C3:50:GLU:HG2	2.18	0.43
1:H9:247:ALA:O	1:H9:251:THR:HG23	2.18	0.43
1:I7:66:THR:OG1	1:I7:153:ILE:HG22	2.16	0.43
1:J5:255:ARG:O	1:J5:259:LEU:HD23	2.19	0.43
1:K6:186:LEU:HD22	1:K6:192:ALA:HA	1.99	0.43
2:L1:217:LEU:O	2:L1:221:ILE:HG23	2.17	0.43
2:M4:209:ASN:N	2:M4:209:ASN:HD22	2.17	0.43
2:N5:120:TRP:CH2	2:N5:156:GLU:HG3	2.54	0.43
2:N6:231:ARG:CZ	2:N6:243:ARG:HD3	2.49	0.43
2:O5:175:LEU:HD21	2:O5:192:LEU:HD23	2.00	0.43
3:Q1:14:LEU:HD13	3:Q1:200:LYS:HB2	2.00	0.43
3:S2:29:THR:HG21	3:S2:117:ARG:H	1.83	0.43
3:S3:202:GLN:HE22	3:S4:238:LYS:HG3	1.82	0.43
5:V1:151:LYS:HB2	5:V1:202:PHE:HE1	1.84	0.43
7:Z0:188:ASN:O	7:Z0:192:VAL:HG23	2.18	0.43
7:Z2:110:MET:SD	7:Z2:123:LEU:HB2	2.58	0.43
7:Z2:113:LYS:O	7:Z2:114:ASN:C	2.61	0.43
7:Za:59:ARG:HD2	10:c2:86:TYR:CE2	2.53	0.43
8:a1:149:ARG:HD2	8:a2:229:GLU:OE2	2.17	0.43
1:i0:106:ASP:O	1:i0:110:ILE:HG13	2.17	0.43
1:A4:135:LEU:HD23	1:A4:135:LEU:HA	1.82	0.43
1:A5:78:GLY:O	1:A5:82:GLU:HG2	2.18	0.43
1:A6:269:GLN:HG2	1:B6:253:PHE:CZ	2.53	0.43
1:B4:79:TYR:O	1:B4:83:THR:HG22	2.19	0.43
1:B8:84:HIS:CE1	1:B8:203:LEU:HD22	2.53	0.43
1:B8:103:SER:O	1:B8:107:ARG:HG2	2.18	0.43
1:C3:159:GLN:HE21	1:D3:123:ARG:NH1	2.16	0.43
1:C5:167:THR:O	1:C5:168:MET:HE2	2.18	0.43
1:D3:255:ARG:O	1:D3:258:ILE:HG22	2.18	0.43
1:D7:191:LYS:O	1:D7:195:VAL:HG23	2.18	0.43
1:F3:237:SER:OG	1:G8:71:SER:HB3	2.18	0.43
1:F6:215:ALA:HB1	1:G2:116:GLN:HG3	2.00	0.43
1:G6:131:ASN:C	1:G6:133:MET:H	2.27	0.43
1:G8:118:VAL:HA	1:G8:121:ILE:HG22	1.98	0.43
1:J6:198:LEU:O	1:J6:201:ASP:OD1	2.36	0.43
1:J8:72:LEU:HD13	1:J8:130:PHE:CD2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J8:109:GLN:O	1:J8:112:VAL:HG12	2.18	0.43
2:M2:65:GLU:HG2	2:M2:69:GLN:NE2	2.33	0.43
2:M3:93:LYS:HE3	3:Q3:129:ASN:ND2	2.33	0.43
2:M5:220:TYR:CE1	2:M5:226:ASN:HB3	2.52	0.43
2:N6:222:TYR:OH	2:N6:250:VAL:HG11	2.19	0.43
2:O3:133:ARG:HD2	2:O3:136:GLU:OE2	2.18	0.43
2:P6:148:ARG:O	2:P6:152:VAL:HG23	2.19	0.43
3:R3:31:LEU:O	3:R3:47:LYS:HE2	2.18	0.43
3:R4:187:VAL:HA	3:R5:230:TYR:CE2	2.53	0.43
3:S2:203:PHE:CZ	3:S3:237:LEU:HD22	2.52	0.43
3:S5:45:LEU:HD12	3:S5:73:LEU:HD13	2.01	0.43
3:S5:205:PHE:O	3:S5:205:PHE:HD1	2.01	0.43
4:U6:111:LYS:CD	4:U6:176:LYS:HD2	2.48	0.43
4:U6:136:ILE:HG21	4:U6:148:LEU:HD22	1.99	0.43
5:V1:55:GLU:O	5:V1:55:GLU:HG2	2.18	0.43
5:V2:151:LYS:HB3	5:V2:200:SER:HB2	1.99	0.43
1:A4:173:LEU:HB3	1:A4:202:ALA:HB1	1.99	0.43
1:A4:219:ARG:HG2	1:B4:120:GLU:HG3	1.99	0.43
1:A4:259:LEU:HD11	1:B3:4:ASN:HD22	1.82	0.43
1:A5:120:GLU:OE1	1:K4:219:ARG:HD2	2.18	0.43
1:B6:251:THR:HG22	1:C5:271:ASN:OD1	2.18	0.43
1:C2:14:ARG:HG2	1:C2:14:ARG:HH11	1.83	0.43
1:C3:52:MET:HE1	1:C3:241:ILE:HG13	2.00	0.43
1:C4:52:MET:HE2	1:C4:234:THR:HG23	2.00	0.43
1:C4:240:ARG:HG2	1:D4:67:GLU:HB3	2.00	0.43
1:D6:30:LEU:HD21	1:D6:249:GLN:HB3	2.00	0.43
1:D6:157:MET:HE2	1:D6:158:HIS:NE2	2.33	0.43
1:F1:278:MET:HE1	1:F1:282:GLN:HE22	1.84	0.43
1:H6:140:PHE:CD1	1:H6:149:MET:HG2	2.54	0.43
1:H6:162:ARG:HD3	1:H6:164:TYR:CZ	2.53	0.43
1:H8:55:GLN:HG3	1:H8:59:LEU:CD2	2.49	0.43
1:I6:59:LEU:HG	1:I6:227:LEU:CD1	2.48	0.43
1:I8:177:ASN:HB3	1:I8:180:VAL:O	2.18	0.43
1:J6:237:SER:OG	1:K6:71:SER:HB3	2.19	0.43
1:K4:35:ARG:NH2	1:K4:36:ILE:HD11	2.33	0.43
1:K7:186:LEU:HD23	1:K7:195:VAL:HG21	2.01	0.43
2:L5:265:ASN:ND2	2:L5:290:ILE:HG23	2.32	0.43
2:M2:190:LYS:HG2	2:M2:223:ILE:HG23	2.00	0.43
2:M4:100:PHE:HE2	2:M4:189:PHE:HA	1.83	0.43
2:M5:263:LYS:HA	2:M5:266:VAL:HG12	1.99	0.43
2:N5:90:GLN:HA	2:N5:93:LYS:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N5:178:ILE:HD12	2:N5:189:PHE:HE2	1.83	0.43
2:O3:63:LYS:O	2:O3:67:MET:HG2	2.18	0.43
2:O4:137:LYS:NZ	2:P4:209:ASN:HA	2.34	0.43
2:P4:242:PHE:C	2:P4:242:PHE:CD1	2.97	0.43
5:V1:106:VAL:HB	5:V1:216:PHE:CE1	2.53	0.43
6:Y4:143:GLU:H	6:Y4:143:GLU:CD	2.26	0.43
8:a1:88:GLN:HB3	8:a1:109:PHE:CE1	2.53	0.43
10:c3:118:MET:HG2	10:c3:126:TYR:CZ	2.53	0.43
1:B3:247:ALA:HB1	1:C2:267:LEU:HD21	1.99	0.43
1:B4:66:THR:HG23	1:B4:220:MET:SD	2.58	0.43
1:B5:89:ARG:O	1:B5:92:VAL:HG22	2.18	0.43
1:B8:215:ALA:HB2	1:C8:113:GLU:HG2	2.00	0.43
1:D3:177:ASN:HB3	1:D3:180:VAL:O	2.18	0.43
1:D4:225:LYS:HB2	1:D4:225:LYS:HE2	1.80	0.43
1:F1:247:ALA:HB3	1:G5:13:HIS:CD2	2.52	0.43
1:F5:70:MET:HG3	1:F5:220:MET:CB	2.49	0.43
1:I6:114:VAL:HG21	1:I6:186:LEU:HD22	2.01	0.43
1:I9:60:ARG:HD3	1:I9:231:TYR:CZ	2.54	0.43
1:I9:245:ASP:OD2	1:J8:13:HIS:HE1	2.01	0.43
1:K6:3:ILE:CD1	1:K7:246:MET:HG3	2.48	0.43
1:K6:180:VAL:HG11	7:Z0:171:ASN:OD1	2.19	0.43
1:K7:180:VAL:HG21	7:Z1:230:ASN:CG	2.44	0.43
1:K8:169:ASN:OD1	1:K8:170:THR:N	2.51	0.43
2:O1:225:ASP:OD1	2:O1:225:ASP:C	2.61	0.43
2:O1:236:LEU:HB3	2:O1:267:HIS:ND1	2.32	0.43
3:S4:65:ALA:HB1	3:S4:67:ASP:OD1	2.19	0.43
3:S4:241:LEU:HD23	3:S4:241:LEU:HA	1.87	0.43
4:U3:137:ILE:HD12	4:U4:85:PHE:CE1	2.54	0.43
4:U5:37:VAL:HG11	4:U5:273:GLY:HA2	2.00	0.43
5:V1:52:ASP:CG	5:V1:54:GLU:HG2	2.43	0.43
5:V3:74:LYS:HE2	5:V3:102:HIS:CD2	2.53	0.43
5:X3:132:VAL:HG13	5:X3:223:VAL:CG2	2.49	0.43
5:X4:219:ASP:OD1	5:X4:220:ASP:OD1	2.36	0.43
6:Y4:182:VAL:HG22	6:Y4:184:TYR:CD2	2.52	0.43
7:Z1:107:LYS:HE2	7:Z1:107:LYS:HB2	1.89	0.43
8:a4:53:LYS:NZ	8:a4:56:ARG:HH12	2.17	0.43
1:A6:139:ALA:O	1:A6:147:ALA:HB3	2.18	0.43
1:A7:40:GLY:HA3	1:A8:217:TYR:CD1	2.54	0.43
1:A7:253:PHE:CE2	1:K7:266:MET:HE1	2.54	0.43
1:A8:82:GLU:OE2	1:K8:226:GLY:HA3	2.18	0.43
1:D7:72:LEU:HD21	1:D7:149:MET:HE2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G1:35:ARG:HG3	1:G1:36:ILE:HG13	1.99	0.43
1:G1:219:ARG:HE	1:h0:120:GLU:HB2	1.83	0.43
1:G8:54:THR:HG22	1:G9:88:GLN:OE1	2.18	0.43
1:G9:240:ARG:HD2	1:H9:67:GLU:HG2	2.00	0.43
1:H7:1:MET:SD	1:H7:277:VAL:HG11	2.58	0.43
1:H7:180:VAL:O	1:H7:182:THR:N	2.52	0.43
1:I4:14:ARG:HD2	1:I5:228:MET:HG3	2.00	0.43
1:I7:194:SER:O	1:I7:198:LEU:HD23	2.18	0.43
1:I9:29:LYS:CG	1:I9:35:ARG:HA	2.48	0.43
1:J5:166:GLU:N	1:J5:209:GLN:HE22	2.13	0.43
1:K3:266:MET:HA	1:K3:266:MET:HE3	2.01	0.43
1:K8:89:ARG:HA	1:K8:89:ARG:HD2	1.93	0.43
2:L4:200:TRP:NE1	2:L4:216:ILE:HG13	2.34	0.43
2:N6:299:ILE:HG21	2:N6:315:LEU:HD11	2.01	0.43
2:O4:90:GLN:HE22	3:S5:89:ASN:HD21	1.66	0.43
2:O5:133:ARG:NH2	2:O5:145:ARG:HD3	2.34	0.43
2:O5:223:ILE:HG22	2:O5:225:ASP:OD1	2.19	0.43
2:P4:197:TYR:CD1	2:P4:216:ILE:HG23	2.53	0.43
2:P6:217:LEU:HB3	2:P6:236:LEU:HD22	2.00	0.43
3:Q1:49:LYS:HE2	3:Q1:67:ASP:HB3	2.01	0.43
3:Q3:158:LEU:HD11	3:Q3:184:LEU:HB2	2.01	0.43
3:S2:124:THR:OG1	3:S2:141:ILE:HG12	2.18	0.43
4:U3:145:LYS:HE2	4:U3:145:LYS:HB2	1.67	0.43
4:U3:208:LYS:HG2	4:U3:210:GLU:H	1.83	0.43
5:X1:52:ASP:HB3	12:X1:402:HOH:O	2.19	0.43
5:X2:135:ILE:HG21	5:X2:152:PHE:CZ	2.54	0.43
5:X3:126:TYR:HB2	5:X3:198:PHE:HB3	1.99	0.43
6:Y1:213:LYS:HD3	6:Y1:214:TYR:H	1.83	0.43
6:Y3:39:PHE:HZ	6:Y3:256:ILE:HD12	1.84	0.43
6:Y3:71:PHE:CE2	6:Y3:165:ALA:HB2	2.54	0.43
8:a2:81:ILE:HD13	8:a2:113:LEU:HD22	2.01	0.43
10:c3:130:MET:HG2	10:c3:143:THR:HG22	2.00	0.43
1:A4:11:PHE:CD2	1:B4:28:GLU:HG2	2.54	0.43
1:A7:233:ASN:ND2	1:B7:74:GLN:HB3	2.33	0.43
1:B6:247:ALA:O	1:B6:251:THR:HG23	2.19	0.43
1:B7:52:MET:HE1	1:B7:237:SER:CB	2.49	0.43
1:C6:219:ARG:HH12	1:D6:123:ARG:HD3	1.83	0.43
1:D7:84:HIS:HA	1:D7:206:ILE:HD12	1.99	0.43
1:F5:211:ALA:HB2	1:G1:109:GLN:HE21	1.84	0.43
1:H7:186:LEU:HD12	1:H7:195:VAL:HG21	2.01	0.43
1:H8:89:ARG:HH11	1:H8:89:ARG:HG3	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I7:53:ARG:HA	1:I7:56:ILE:HD12	2.00	0.43
1:J6:208:LYS:HE2	1:J6:208:LYS:HB2	1.85	0.43
1:J7:76:ALA:HB2	1:J7:135:LEU:HD13	2.00	0.43
1:K4:181:LEU:HD11	7:Za:178:HIS:HE1	1.84	0.43
1:K6:26:ASP:HA	1:K6:249:GLN:HE22	1.82	0.43
2:L3:90:GLN:HG3	8:a3:144:PRO:HG3	2.01	0.43
2:L3:148:ARG:O	2:L3:152:VAL:HG12	2.19	0.43
2:M4:255:ASP:OD2	8:a4:95:ILE:HG23	2.19	0.43
2:P6:201:ILE:HD13	2:P6:201:ILE:HA	1.82	0.43
2:P6:247:ILE:HA	2:P6:250:THR:HG22	2.01	0.43
3:Q1:91:GLY:HA2	3:Q1:131:PHE:CE2	2.53	0.43
3:R5:62:LYS:HA	3:R5:62:LYS:HD3	1.87	0.43
3:S4:122:ILE:CG1	3:S4:143:ASP:HB3	2.49	0.43
5:V2:76:VAL:HG22	5:V2:102:HIS:NE2	2.33	0.43
5:V2:199:VAL:HG22	5:V2:199:VAL:O	2.19	0.43
5:X2:146:HIS:HD2	5:X2:214:PHE:CD1	2.36	0.43
6:Y4:121:ILE:HG22	6:Y4:157:TYR:CE1	2.53	0.43
1:i0:80:LEU:HD13	1:i0:168:MET:HE1	2.00	0.43
1:A7:87:VAL:O	1:A7:90:VAL:HG22	2.18	0.43
1:B3:239:SER:O	1:B3:243:ASP:HB2	2.19	0.43
1:B4:163:VAL:HG22	1:B4:216:TYR:CD2	2.53	0.43
1:B5:73:ILE:HG21	1:B5:217:TYR:HB2	2.01	0.43
1:C6:258:ILE:HD11	1:D5:275:GLN:HG2	2.01	0.43
1:D3:218:ASN:ND2	1:E3:89:ARG:HH22	2.17	0.43
1:D6:219:ARG:HD2	1:E6:120:GLU:HB2	2.01	0.43
1:D7:202:ALA:O	1:D7:206:ILE:HG23	2.19	0.43
1:F3:3:ILE:HD13	1:F3:3:ILE:HA	1.87	0.43
1:F4:114:VAL:HG21	1:F4:186:LEU:HD12	2.00	0.43
1:H6:60:ARG:HH22	1:H6:228:MET:CE	2.32	0.43
1:H6:80:LEU:HD12	1:H6:213:LEU:HD12	2.00	0.43
1:H7:49:SER:OG	1:H7:242:ARG:HB2	2.19	0.43
1:I6:149:MET:HE1	1:I6:165:ILE:HD11	2.01	0.43
1:I7:153:ILE:CG2	1:I7:220:MET:HE1	2.48	0.43
1:I9:123:ARG:HG3	1:I9:127:GLN:OE1	2.19	0.43
1:J4:11:PHE:HE1	1:J4:14:ARG:NH2	2.15	0.43
1:J8:161:GLU:HG3	1:J8:219:ARG:NH2	2.34	0.43
2:L2:139:TYR:CE1	2:M1:256:MET:HE3	2.53	0.43
2:N4:98:ASN:HD22	3:R4:89:ASN:HD22	1.65	0.43
2:P3:272:THR:HG21	2:P3:286:ILE:HG21	2.00	0.43
3:Q3:34:MET:HE3	3:Q3:34:MET:HB2	1.77	0.43
3:R2:97:MET:HA	3:R2:123:ARG:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U4:23:ILE:HG22	4:U4:25:ILE:H	1.84	0.43
5:V1:151:LYS:HB2	5:V1:202:PHE:CE1	2.54	0.43
5:V2:74:LYS:HZ3	5:V2:102:HIS:CG	2.37	0.43
5:X1:145:ARG:HH22	5:X2:188:ARG:HH22	1.65	0.43
7:Za:25:VAL:O	7:Za:51:MET:HE1	2.19	0.43
8:a1:88:GLN:HB3	8:a1:109:PHE:CZ	2.54	0.43
8:a5:150:GLU:HB2	8:a5:165:SER:OG	2.18	0.43
10:c2:77:LEU:HD22	10:c2:97:ILE:HD13	2.01	0.43
1:A3:253:PHE:HZ	1:K3:269:GLN:HG2	1.83	0.43
1:B5:52:MET:HB3	1:B5:238:GLU:HB2	2.01	0.43
1:B6:216:TYR:O	1:B6:220:MET:HE2	2.19	0.43
1:C4:262:ALA:HB2	1:D3:278:MET:HE1	2.01	0.43
1:C8:86:ILE:HG21	1:C8:121:ILE:HG13	2.01	0.43
1:D3:16:LEU:HD13	1:D3:263:ALA:HB3	2.01	0.43
1:E3:14:ARG:HG3	1:E4:228:MET:HB3	2.01	0.43
1:F6:70:MET:HE3	1:F6:217:TYR:CZ	2.54	0.43
1:G6:72:LEU:HD13	1:G6:151:PHE:CZ	2.53	0.43
1:I6:65:ASN:ND2	1:I7:99:ASN:OD1	2.51	0.43
1:J9:180:VAL:HG11	4:U6:167:ASN:CB	2.49	0.43
1:K4:61:ARG:HA	1:K4:61:ARG:HD2	1.85	0.43
1:K6:163:VAL:HG13	1:K6:216:TYR:CE2	2.54	0.43
2:L5:214:ILE:HB	2:L5:215:PRO:HD3	2.00	0.43
2:N3:204:GLU:CG	2:N3:209:ASN:HB2	2.49	0.43
2:O4:270:ARG:HA	2:O4:270:ARG:HD2	1.78	0.43
2:P1:73:TRP:CH2	2:P2:198:ARG:HG3	2.54	0.43
3:R1:72:HIS:NE2	3:R1:96:LYS:HD2	2.32	0.43
5:V3:64:THR:HG23	5:V3:117:ARG:O	2.19	0.43
6:Y2:32:ILE:HG23	6:Y2:252:PHE:CE2	2.52	0.43
6:Y2:151:PHE:CZ	6:Y2:237:ALA:HB2	2.54	0.43
7:Z1:119:MET:HE3	7:Z1:157:LYS:HD2	2.01	0.43
8:a1:138:THR:HG22	8:a1:138:THR:O	2.19	0.43
8:a4:72:VAL:HG21	8:a4:126:LEU:HB2	2.00	0.43
1:i0:81:GLN:HG2	1:i0:210:ARG:NH2	2.33	0.43
1:A6:184:ILE:HD11	1:A6:195:VAL:HG22	2.00	0.42
1:B4:1:MET:HA	1:B4:1:MET:HE3	2.01	0.42
1:B5:83:THR:O	1:B5:87:VAL:HG23	2.18	0.42
1:B6:72:LEU:HD22	1:B6:151:PHE:HZ	1.83	0.42
1:B6:184:ILE:HG13	1:B6:195:VAL:HG22	2.00	0.42
1:B6:217:TYR:CD1	1:B6:217:TYR:C	2.97	0.42
1:B7:266:MET:HE2	1:C7:30:LEU:HD22	2.01	0.42
1:C7:48:VAL:HG12	1:C7:52:MET:HE2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C7:96:GLN:HG2	1:C7:102:TYR:HE2	1.84	0.42
1:C8:108:GLN:O	1:C8:112:VAL:HG13	2.19	0.42
1:D7:150:TRP:CZ2	1:D7:162:ARG:HD2	2.54	0.42
1:F1:30:LEU:HG	1:F1:249:GLN:HG3	2.01	0.42
1:F3:26:ASP:O	1:F3:30:LEU:HD23	2.19	0.42
1:G7:89:ARG:O	1:G7:92:VAL:HG22	2.19	0.42
1:H7:86:ILE:HG23	1:H7:117:LEU:HD22	2.00	0.42
1:J8:88:GLN:HG2	1:J8:203:LEU:HD21	2.01	0.42
1:K7:29:LYS:HE2	1:K7:249:GLN:NE2	2.34	0.42
2:L2:175:LEU:HD12	2:L2:175:LEU:HA	1.83	0.42
2:M3:263:LYS:HA	2:M3:266:VAL:CG1	2.48	0.42
2:O2:159:LYS:HB2	2:O2:159:LYS:HE2	1.88	0.42
2:P4:81:TYR:HE2	2:P5:242:PHE:HA	1.84	0.42
3:Q2:62:LYS:HE2	3:Q2:65:ALA:HA	2.01	0.42
3:R4:82:GLU:H	3:R4:82:GLU:CD	2.27	0.42
3:R5:49:LYS:HE2	3:R5:49:LYS:HB3	1.76	0.42
4:U6:76:LEU:HG	4:U6:113:ILE:HG12	2.01	0.42
5:V1:170:PHE:O	5:V1:170:PHE:HD1	2.02	0.42
5:V3:113:LYS:H	5:V3:113:LYS:HD2	1.82	0.42
5:V4:77:GLN:HB2	5:V4:101:ASN:HB2	2.01	0.42
5:X2:70:THR:HA	5:X2:107:LYS:O	2.19	0.42
5:X3:122:PRO:HG3	5:X3:126:TYR:CE1	2.53	0.42
7:Z2:293:VAL:HG13	7:Z2:300:ARG:NH2	2.34	0.42
8:a5:64:TYR:HA	8:a5:67:MET:HG2	2.01	0.42
8:a5:80:LYS:HD3	8:a5:86:TYR:HE1	1.82	0.42
1:A6:6:ASN:HB3	1:A6:9:ALA:HB3	2.01	0.42
1:A6:176:ARG:NH2	1:A6:183:PHE:HE1	2.16	0.42
1:B4:247:ALA:O	1:B4:251:THR:HG23	2.19	0.42
1:B5:38:LYS:HD2	1:B6:74:GLN:OE1	2.20	0.42
1:C3:220:MET:HE3	1:C3:220:MET:HA	2.01	0.42
1:C3:261:GLN:O	1:C3:264:THR:HG22	2.20	0.42
1:C4:32:SER:CB	1:C4:37:ASN:HD21	2.32	0.42
1:E5:151:PHE:CE2	1:E5:163:VAL:HG21	2.53	0.42
1:E6:80:LEU:HD21	1:E6:168:MET:HG2	2.01	0.42
1:E7:87:VAL:HA	1:E7:90:VAL:HG12	2.01	0.42
1:G1:80:LEU:HD23	1:G1:210:ARG:HG3	2.01	0.42
1:G9:80:LEU:HD12	1:G9:213:LEU:HD12	2.01	0.42
1:H7:219:ARG:HG3	1:I7:120:GLU:HG3	2.00	0.42
1:H9:114:VAL:HG21	1:H9:186:LEU:HD22	2.01	0.42
1:I8:153:ILE:O	1:I8:153:ILE:CG2	2.67	0.42
1:J4:273:LYS:HD3	1:K5:23:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J9:177:ASN:HA	1:J9:178:PRO:HD3	1.88	0.42
1:K3:278:MET:HE2	1:K3:278:MET:HB2	1.93	0.42
1:K8:142:ARG:HG2	1:K8:164:TYR:CD1	2.55	0.42
2:L5:123:GLN:O	2:L5:127:GLU:HG3	2.18	0.42
2:M5:172:ILE:HD13	2:M5:197:TYR:CE1	2.53	0.42
2:O1:79:LYS:HA	2:O1:79:LYS:HD3	1.81	0.42
2:P3:157:LYS:O	2:P3:161:LYS:HG2	2.19	0.42
5:X1:142:ARG:HB3	5:X1:170:PHE:CE1	2.54	0.42
5:X3:154:ASP:HA	5:X3:196:LEU:HD12	2.01	0.42
1:i0:77:GLU:OE1	1:i0:210:ARG:HG3	2.19	0.42
1:A7:157:MET:HE3	1:A7:158:HIS:CE1	2.53	0.42
1:B8:114:VAL:HG21	1:B8:186:LEU:HD12	2.01	0.42
1:C5:261:GLN:OE1	1:D4:278:MET:HE1	2.19	0.42
1:C6:180:VAL:HG12	1:C6:182:THR:HG23	2.01	0.42
1:C6:219:ARG:HH21	1:D6:119:ASP:HB3	1.83	0.42
1:D4:11:PHE:HB2	1:D5:232:GLU:OE2	2.19	0.42
1:D6:47:ALA:HB2	1:E7:109:GLN:NE2	2.30	0.42
1:E2:66:THR:HG23	1:E2:220:MET:CE	2.49	0.42
1:E4:10:ILE:HD11	1:E5:231:TYR:CE2	2.55	0.42
1:E6:216:TYR:O	1:E6:220:MET:HG2	2.19	0.42
1:E7:95:VAL:HG22	1:E7:196:ILE:HD12	2.01	0.42
1:G7:39:ALA:HA	1:G7:46:LEU:HD22	2.02	0.42
1:G7:184:ILE:HD12	1:G7:184:ILE:HA	1.84	0.42
1:G9:63:GLU:OE2	1:G9:228:MET:HE2	2.19	0.42
1:G9:258:ILE:HG21	1:H8:3:ILE:HD11	2.01	0.42
1:K4:14:ARG:HB2	1:K6:228:MET:SD	2.59	0.42
1:K6:160:ARG:HH12	1:K7:190:GLY:HA2	1.85	0.42
2:L4:98:ASN:ND2	8:a4:136:SER:HB2	2.34	0.42
2:M1:256:MET:HG3	2:M1:260:TYR:CE2	2.55	0.42
2:M3:65:GLU:O	2:M3:69:GLN:HG3	2.18	0.42
2:M4:99:GLN:NE2	3:Q4:89:ASN:HD22	2.18	0.42
2:N4:73:TRP:CZ2	2:N5:198:ARG:HG3	2.53	0.42
2:O4:244:GLU:OE2	2:O4:261:ARG:HD3	2.20	0.42
2:O5:210:LEU:HD12	2:O5:242:PHE:CD2	2.54	0.42
2:P2:263:LYS:HA	2:P2:266:VAL:HG12	2.00	0.42
3:R4:47:LYS:H	3:R4:63:GLN:NE2	2.18	0.42
3:R4:96:LYS:HG2	3:R4:125:TYR:HB3	2.00	0.42
5:V2:238:LYS:HB2	5:V2:238:LYS:HE2	1.78	0.42
5:X1:180:PRO:HD2	5:X1:183:ILE:HD12	2.00	0.42
8:a1:131:PHE:CE2	8:a1:200:ARG:HD2	2.54	0.42
8:a4:200:ARG:O	8:a4:204:VAL:HG23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:a5:31:ASP:OD1	8:a5:31:ASP:N	2.52	0.42
1:B4:157:MET:HE3	1:B4:158:HIS:CE1	2.54	0.42
1:B4:188:THR:HG23	1:B4:191:LYS:H	1.85	0.42
1:B7:72:LEU:HD21	1:B7:149:MET:HE1	2.01	0.42
1:E2:56:ILE:HD11	1:E2:235:GLN:HA	2.02	0.42
1:E5:219:ARG:HD2	1:F5:120:GLU:HB2	2.00	0.42
1:F1:241:ILE:HD11	1:G6:68:ASP:OD1	2.19	0.42
1:F5:5:HIS:HB3	1:F6:235:GLN:HE21	1.84	0.42
1:G7:278:MET:HE1	1:G8:246:MET:HE3	2.00	0.42
1:G8:19:ASN:ND2	1:G8:259:LEU:HB3	2.35	0.42
1:G9:84:HIS:HE1	1:G9:203:LEU:HD22	1.85	0.42
1:H9:36:ILE:HB	1:H9:242:ARG:HD2	2.01	0.42
1:I5:16:LEU:HD11	1:I5:264:THR:CG2	2.49	0.42
1:I6:219:ARG:HG3	1:J6:120:GLU:OE1	2.20	0.42
1:I9:157:MET:HE2	1:I9:158:HIS:HE1	1.83	0.42
1:J7:25:LYS:HE3	1:J7:38:LYS:HE2	2.02	0.42
1:J7:245:ASP:OD2	1:K6:13:HIS:HE1	2.02	0.42
2:L2:221:ILE:HD11	2:L2:227:GLU:HG2	2.00	0.42
2:L3:263:LYS:HA	2:L3:266:VAL:HG12	2.01	0.42
2:N3:168:PHE:CZ	2:N3:199:SER:HB3	2.54	0.42
2:O3:73:TRP:CE2	2:O4:198:ARG:HG3	2.54	0.42
2:O5:138:TRP:CZ3	2:P5:246:MET:HE3	2.55	0.42
2:P4:148:ARG:HG2	2:P4:151:ARG:NH2	2.31	0.42
3:Q2:6:SER:HB3	3:Q2:9:ASP:OD2	2.19	0.42
3:Q2:62:LYS:CG	3:Q2:65:ALA:HB2	2.49	0.42
3:Q4:66:GLN:OE1	3:Q4:105:ASN:HB2	2.19	0.42
3:R3:122:ILE:CG1	3:R3:143:ASP:HB3	2.48	0.42
3:S3:47:LYS:HG2	3:S3:71:LEU:HD22	2.01	0.42
3:S5:119:LEU:H	3:S5:147:ASN:HD21	1.67	0.42
4:U3:35:ILE:HD11	4:U3:117:VAL:HG21	2.01	0.42
4:U4:234:VAL:O	4:U4:238:LEU:HD23	2.19	0.42
4:U4:287:ASN:O	4:U4:290:ILE:HG12	2.19	0.42
5:V1:132:VAL:HG12	5:V1:179:VAL:HG21	2.01	0.42
5:X2:52:ASP:CG	5:X2:54:GLU:HG2	2.45	0.42
5:X3:114:GLY:HA3	5:X3:207:VAL:HG22	2.00	0.42
5:X3:192:LEU:HG	5:X3:193:ASP:N	2.35	0.42
8:a1:128:GLU:HA	8:a1:153:ASN:O	2.19	0.42
1:A3:253:PHE:C	1:A3:253:PHE:CD1	2.98	0.42
1:A5:170:THR:HB	1:A5:176:ARG:HB2	2.01	0.42
1:A5:261:GLN:HE21	1:B4:279:ARG:NH2	2.18	0.42
1:B7:151:PHE:CE2	1:B7:163:VAL:HG21	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B8:170:THR:HG22	1:B8:175:LEU:HB2	2.01	0.42
1:D2:56:ILE:HG12	1:D2:234:THR:HG22	2.01	0.42
1:F4:48:VAL:HG21	1:G1:102:TYR:HE1	1.85	0.42
1:H9:142:ARG:NH2	2:P5:140:TRP:HE3	2.17	0.42
2:L2:214:ILE:HD12	2:L2:240:TYR:CZ	2.54	0.42
2:N4:185:GLU:HA	2:N4:190:LYS:HE3	2.01	0.42
2:N4:254:ASP:O	2:N4:258:PHE:HD2	2.03	0.42
2:O3:204:GLU:HG3	2:O3:209:ASN:HB2	2.00	0.42
3:Q1:189:ASN:CB	3:Q1:196:ARG:HH11	2.31	0.42
3:Q2:175:SER:HB2	3:Q3:35:LYS:HE3	2.02	0.42
3:R3:77:ASP:O	3:R3:93:LYS:HB3	2.19	0.42
3:R4:145:ALA:HB2	3:R4:155:LYS:HD2	2.02	0.42
3:S4:96:LYS:CG	3:S4:125:TYR:HB3	2.50	0.42
4:U3:198:MET:HB3	4:U3:198:MET:HE3	1.75	0.42
4:U5:208:LYS:HG2	4:U5:210:GLU:H	1.84	0.42
4:U5:236:ASP:HA	4:U5:239:ILE:HG12	2.01	0.42
4:U6:234:VAL:O	4:U6:237:THR:HG22	2.19	0.42
5:V1:98:ILE:HG22	5:V1:98:ILE:O	2.20	0.42
5:X3:103:ILE:HG22	5:X3:219:ASP:HB3	2.01	0.42
6:Y3:39:PHE:HD2	6:Y3:54:VAL:HG22	1.83	0.42
6:Y4:250:LEU:C	6:Y4:250:LEU:HD23	2.45	0.42
8:a5:221:LYS:HE2	8:a5:221:LYS:HB2	1.73	0.42
9:b3:27:THR:HG23	9:b3:30:GLU:H	1.85	0.42
9:b4:215:LEU:HD11	9:b4:227:GLN:HG3	2.02	0.42
1:A3:13:HIS:CD2	1:K5:248:GLU:HB2	2.55	0.42
1:A5:150:TRP:CE3	1:A5:162:ARG:HB2	2.54	0.42
1:B3:258:ILE:HG22	1:C2:3:ILE:HD12	2.00	0.42
1:B7:257:GLN:O	1:B7:260:THR:HG22	2.19	0.42
1:D5:35:ARG:HG3	1:D5:244:THR:HA	2.01	0.42
1:E2:1:MET:HG2	1:F2:20:ASP:OD2	2.18	0.42
1:E3:50:GLU:HG3	1:E4:84:HIS:NE2	2.34	0.42
1:E5:25:LYS:HG2	1:E5:38:LYS:NZ	2.34	0.42
1:E5:89:ARG:HG3	1:E5:117:LEU:HD11	2.00	0.42
1:E6:108:GLN:O	1:E6:112:VAL:HG23	2.19	0.42
1:F2:269:GLN:HG2	1:G7:253:PHE:CZ	2.55	0.42
1:G1:226:GLY:HA2	1:h0:82:GLU:HG3	2.02	0.42
1:G1:247:ALA:O	1:G1:251:THR:HG23	2.19	0.42
1:G2:114:VAL:HG21	1:G2:186:LEU:HD12	2.02	0.42
1:H6:80:LEU:HA	1:H6:83:THR:HG22	2.02	0.42
1:H6:84:HIS:HB2	1:H6:206:ILE:HG21	2.01	0.42
1:H6:169:ASN:HD21	1:H6:171:ALA:HB3	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K5:257:GLN:O	1:K5:260:THR:HG22	2.19	0.42
2:L3:133:ARG:CZ	2:L3:145:ARG:HD2	2.50	0.42
2:M5:246:MET:HG3	2:M5:249:LYS:NZ	2.35	0.42
2:N2:200:TRP:CH2	2:N2:204:GLU:HG3	2.54	0.42
2:P3:85:PHE:CE2	2:P4:234:LYS:HD3	2.55	0.42
2:P4:65:GLU:O	2:P4:69:GLN:HG3	2.19	0.42
2:P4:246:MET:HE3	2:P4:246:MET:HB3	1.95	0.42
3:Q1:189:ASN:HB2	3:Q1:196:ARG:HH11	1.85	0.42
3:Q4:128:GLN:HE21	3:Q4:130:ASN:HD21	1.66	0.42
3:R3:125:TYR:HD1	3:R3:126:ILE:N	2.18	0.42
3:S3:31:LEU:HD21	3:S3:45:LEU:HD11	2.02	0.42
3:S5:124:THR:HG21	3:S5:207:ASN:ND2	2.30	0.42
4:U5:191:LYS:HB3	4:U5:271:ASN:HD21	1.85	0.42
5:V3:128:ILE:HD13	5:V3:132:VAL:HB	2.01	0.42
8:a3:155:THR:HG22	8:a3:156:THR:H	1.84	0.42
9:b4:50:ILE:HD13	9:b4:234:TYR:HD2	1.85	0.42
1:A4:27:ILE:HA	1:K5:266:MET:HE2	2.02	0.42
1:A5:163:VAL:HG13	1:A5:216:TYR:CE2	2.54	0.42
1:B4:132:LYS:HE2	1:B4:132:LYS:HB3	1.80	0.42
1:C3:258:ILE:HG21	1:D2:3:ILE:HD12	2.01	0.42
1:D4:151:PHE:CE2	1:D4:163:VAL:HG21	2.55	0.42
1:D6:35:ARG:HG3	1:D6:244:THR:HA	2.01	0.42
1:E4:60:ARG:HD3	1:E4:231:TYR:CE2	2.54	0.42
1:E4:129:GLU:CD	1:E4:132:LYS:HA	2.45	0.42
1:E5:50:GLU:HG3	1:E6:84:HIS:CE1	2.54	0.42
1:F5:184:ILE:HD13	1:F5:195:VAL:HG13	2.00	0.42
1:G9:180:VAL:HG12	1:G9:182:THR:HG23	2.01	0.42
1:H6:266:MET:HG3	1:I6:27:ILE:HG23	2.01	0.42
1:I8:56:ILE:HD11	1:I8:231:TYR:CD1	2.54	0.42
1:I9:168:MET:SD	1:I9:173:LEU:HD21	2.59	0.42
2:M4:110:GLY:HA3	2:M4:168:PHE:CE1	2.55	0.42
2:O3:177:GLU:O	2:O3:179:LYS:HD2	2.19	0.42
2:O5:213:THR:HG23	2:O5:217:LEU:HD12	2.00	0.42
2:P2:284:LYS:HA	2:P2:287:VAL:HG22	2.01	0.42
3:Q1:28:HIS:CE1	3:Q1:212:ASP:HA	2.54	0.42
3:Q4:159:PHE:HB2	3:Q4:181:LYS:CD	2.49	0.42
3:R4:34:MET:HE2	3:R4:34:MET:HB2	1.79	0.42
3:R5:30:VAL:HG23	3:R5:111:PRO:O	2.18	0.42
3:S4:165:TYR:HB3	3:S4:166:PRO:CD	2.50	0.42
3:S6:31:LEU:HD23	3:S6:34:MET:HE1	2.02	0.42
3:S6:34:MET:SD	3:S6:222:ASN:HB2	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X2:59:TRP:HE3	5:X2:120:LEU:HG	1.84	0.42
6:Y1:213:LYS:HD3	6:Y1:214:TYR:N	2.34	0.42
6:Y4:122:TRP:CH2	6:Y4:149:PRO:HD3	2.55	0.42
7:Z0:183:LYS:HE3	10:c2:154:GLN:HE22	1.85	0.42
8:a5:102:SER:O	8:a5:137:LEU:HD12	2.19	0.42
8:a5:131:PHE:CZ	8:a5:200:ARG:HB3	2.54	0.42
8:a5:142:LYS:HD2	8:a5:142:LYS:HA	1.85	0.42
10:c3:115:ARG:O	10:c3:119:THR:HG23	2.19	0.42
1:A5:198:LEU:HD23	1:A5:198:LEU:HA	1.92	0.42
1:A6:149:MET:HE2	1:A6:151:PHE:CE1	2.53	0.42
1:A7:105:GLU:OE2	1:K7:204:ARG:HD3	2.20	0.42
1:A8:118:VAL:HA	1:A8:121:ILE:HG22	2.01	0.42
1:B5:39:ALA:HB2	1:B6:77:GLU:HG2	2.01	0.42
1:B5:186:LEU:HD23	1:B5:195:VAL:HG21	2.02	0.42
1:D4:167:THR:O	1:D4:168:MET:HE2	2.19	0.42
1:E2:142:ARG:HA	1:E2:164:TYR:CD1	2.54	0.42
1:G6:219:ARG:HD2	1:H6:116:GLN:HB3	2.01	0.42
1:G9:60:ARG:HG3	1:G9:60:ARG:NH1	2.35	0.42
1:H9:44:SER:HB3	1:i0:110:ILE:HG12	2.01	0.42
1:J5:61:ARG:HH21	1:J6:96:GLN:CG	2.32	0.42
1:K8:213:LEU:HD23	1:K8:213:LEU:HA	1.87	0.42
2:L2:117:ASN:HD21	2:L2:157:LYS:HA	1.85	0.42
2:L3:123:GLN:O	2:L3:126:LYS:HG2	2.20	0.42
2:L3:253:PRO:HD2	2:L3:256:MET:SD	2.60	0.42
2:M3:209:ASN:HB3	2:M3:212:GLN:OE1	2.20	0.42
2:M5:107:TYR:CZ	2:M5:195:ASP:HB3	2.55	0.42
2:P4:256:MET:HE1	3:S4:82:GLU:O	2.20	0.42
2:P5:197:TYR:CD1	2:P5:216:ILE:HG23	2.54	0.42
3:R1:166:PRO:HD3	3:R1:179:VAL:HG13	2.02	0.42
4:U4:39:LEU:HD21	4:U4:113:ILE:HD11	2.01	0.42
4:U5:254:PRO:HB2	4:U6:295:GLY:HA3	2.01	0.42
5:X2:113:LYS:N	5:X2:113:LYS:HD3	2.35	0.42
5:X3:155:TYR:CE2	5:X3:187:THR:HG22	2.55	0.42
5:X4:140:LEU:HD23	5:X4:217:TYR:CD1	2.55	0.42
6:Y4:250:LEU:HD11	6:Y4:253:ARG:HG2	2.01	0.42
7:Z1:15:LEU:HB2	7:Z1:61:TYR:OH	2.19	0.42
8:a4:193:LEU:HD12	8:a5:227:VAL:HG22	2.02	0.42
9:b4:65:LYS:HE3	9:b4:132:TYR:CE1	2.54	0.42
1:C3:152:HIS:CD2	1:C3:160:ARG:HD2	2.49	0.42
1:C8:176:ARG:NH2	1:C8:181:LEU:HB3	2.34	0.42
1:D7:203:LEU:HD23	1:D7:206:ILE:HD11	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F4:114:VAL:HG21	1:F4:186:LEU:CD1	2.50	0.42
1:F6:237:SER:OG	1:G2:71:SER:HB3	2.19	0.42
1:G2:186:LEU:HD21	1:G2:195:VAL:HG11	2.02	0.42
1:G7:219:ARG:HH11	1:G7:219:ARG:HG2	1.85	0.42
1:I5:1:MET:SD	1:I5:277:VAL:HG11	2.60	0.42
1:J4:44:SER:O	1:J4:48:VAL:HG23	2.20	0.42
2:L4:163:ASP:OD1	2:L4:163:ASP:C	2.62	0.42
2:M3:168:PHE:CZ	2:M3:199:SER:HB3	2.55	0.42
2:M4:247:ILE:HA	2:M4:250:THR:HG22	2.02	0.42
2:O5:159:LYS:HB2	2:O5:159:LYS:HE2	1.81	0.42
2:P3:69:GLN:NE2	2:P4:229:GLU:HA	2.34	0.42
3:Q4:83:ASP:OD1	3:Q4:83:ASP:O	2.37	0.42
3:R3:136:LYS:HB2	3:R3:136:LYS:HZ3	1.85	0.42
3:S2:122:ILE:HG13	3:S2:146:PRO:HG3	2.02	0.42
4:U5:35:ILE:HD11	4:U5:117:VAL:HG21	2.02	0.42
5:V1:237:ILE:HG13	5:V1:237:ILE:O	2.20	0.42
5:V4:135:ILE:CD1	5:V4:223:VAL:HG12	2.50	0.42
6:Y2:151:PHE:HZ	6:Y2:237:ALA:HB2	1.84	0.42
7:Z0:186:ARG:NH1	10:c2:153:GLN:HE21	2.17	0.42
7:Z2:43:PRO:HD2	7:Z2:46:LYS:HD3	2.02	0.42
8:a1:74:PHE:CZ	8:a1:212:ILE:HG23	2.55	0.42
1:A7:246:MET:HE2	1:A7:246:MET:HB3	1.82	0.42
1:B5:29:LYS:HE3	1:B5:249:GLN:CD	2.45	0.42
1:B6:150:TRP:CZ3	1:B6:162:ARG:HB2	2.54	0.42
1:E3:44:SER:O	1:E3:48:VAL:HG12	2.20	0.42
1:F1:6:ASN:O	1:F1:10:ILE:HG13	2.19	0.42
1:F4:34:MET:HE2	1:F4:34:MET:HB2	1.89	0.42
1:G2:123:ARG:HD3	1:G2:127:GLN:HG3	2.01	0.42
1:G7:183:PHE:N	1:G7:183:PHE:CD1	2.88	0.42
1:G7:219:ARG:HG2	1:G7:219:ARG:NH1	2.35	0.42
1:H6:161:GLU:HG3	1:H6:219:ARG:NH2	2.35	0.42
1:J9:219:ARG:HH11	1:J9:219:ARG:CG	2.30	0.42
1:K4:171:ALA:HA	1:K4:176:ARG:O	2.19	0.42
1:K7:11:PHE:HB2	1:K8:232:GLU:OE2	2.20	0.42
2:M3:290:ILE:HD13	8:a3:206:ARG:NH1	2.35	0.42
2:N2:88:LEU:HD23	2:N2:88:LEU:C	2.44	0.42
2:O4:94:THR:OG1	2:O4:178:ILE:HG12	2.20	0.42
3:R2:9:ASP:C	3:R2:9:ASP:OD1	2.63	0.42
3:R2:158:LEU:HD11	3:R2:184:LEU:HD13	2.02	0.42
3:R5:72:HIS:HE1	3:R5:74:GLU:HB2	1.84	0.42
3:R5:102:GLU:HG2	3:R5:120:THR:CG2	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S2:81:SER:HA	3:S2:86:SER:HB3	2.02	0.42
3:S2:231:LYS:O	3:S2:235:GLU:HG2	2.20	0.42
3:S3:153:ASN:HD22	3:S3:196:ARG:HD2	1.84	0.42
3:S4:97:MET:HA	3:S4:123:ARG:O	2.20	0.42
4:U3:148:LEU:HD21	4:U4:89:MET:HE1	2.01	0.42
4:U4:253:PRO:HB2	4:U4:256:ASN:OD1	2.19	0.42
5:V4:114:GLY:HA3	5:V4:207:VAL:HG23	2.02	0.42
5:X1:57:GLU:HG2	7:Z0:157:LYS:HG3	2.02	0.42
5:X1:119:GLU:HG3	5:X1:202:PHE:HB3	2.01	0.42
5:X2:98:ILE:HG23	5:X2:101:ASN:HB3	2.02	0.42
5:X2:122:PRO:HD2	5:X2:199:VAL:O	2.20	0.42
5:X3:127:ILE:O	5:X3:127:ILE:HD12	2.19	0.42
6:Y4:202:LEU:HB3	6:Y4:203:PRO:HD3	2.01	0.42
8:a3:65:HIS:CE1	8:a3:201:LEU:HD11	2.55	0.42
1:B4:274:SER:O	1:B4:278:MET:HE2	2.20	0.41
1:B5:49:SER:OG	1:B5:242:ARG:HD2	2.19	0.41
1:B7:118:VAL:HG22	1:B7:170:THR:HG21	2.00	0.41
1:C7:247:ALA:O	1:C7:251:THR:HG23	2.20	0.41
1:D4:154:GLY:HA3	1:D4:159:GLN:NE2	2.30	0.41
1:G6:149:MET:HE3	1:G6:150:TRP:H	1.84	0.41
1:H6:258:ILE:HD11	1:I5:275:GLN:HG3	2.02	0.41
1:H7:115:SER:O	1:H7:118:VAL:HG12	2.20	0.41
1:H8:233:ASN:OD1	1:I8:74:GLN:HG3	2.20	0.41
1:H9:80:LEU:HD12	1:H9:213:LEU:HD12	2.00	0.41
1:I5:12:ALA:HB3	1:I5:267:LEU:HD13	2.02	0.41
2:L1:82:ASN:HD21	2:L1:84:THR:HG22	1.85	0.41
2:L3:255:ASP:O	2:L3:259:LYS:HG3	2.19	0.41
2:M2:78:PHE:CZ	2:M3:234:LYS:HD3	2.55	0.41
2:M3:184:ARG:HA	2:M3:189:PHE:CD2	2.55	0.41
2:N4:184:ARG:HA	2:N4:189:PHE:CD2	2.55	0.41
2:O2:106:ASN:OD1	2:O2:170:LYS:HE2	2.20	0.41
2:P5:146:LYS:HD3	2:P5:146:LYS:HA	1.93	0.41
2:P6:283:TYR:O	2:P6:287:VAL:HG13	2.20	0.41
3:Q4:158:LEU:HB2	3:Q4:182:TYR:CZ	2.55	0.41
3:R3:106:ASN:HD21	3:R3:108:ASP:HB3	1.85	0.41
3:S3:158:LEU:HD11	3:S3:184:LEU:HB2	2.00	0.41
4:U4:79:ALA:O	4:U4:82:GLN:HG3	2.19	0.41
4:U6:41:ASN:HA	4:U6:279:LYS:HG3	2.01	0.41
5:X1:108:THR:HG22	5:X1:109:HIS:H	1.84	0.41
7:Z1:315:SER:O	7:Z1:319:VAL:HG22	2.20	0.41
7:Za:106:MET:SD	7:Za:228:ALA:HB2	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:b3:162:PRO:HG2	9:b3:184:ASP:OD2	2.19	0.41
1:A5:242:ARG:HA	1:A5:242:ARG:HD3	1.83	0.41
1:A8:118:VAL:HG13	1:A8:170:THR:HG21	2.02	0.41
1:B4:255:ARG:HH11	1:B4:255:ARG:CG	2.33	0.41
1:C3:50:GLU:HG3	1:C4:210:ARG:NH2	2.35	0.41
1:C4:61:ARG:NH2	1:C4:64:GLN:HB3	2.36	0.41
1:D2:52:MET:HE1	1:D2:241:ILE:HD12	2.02	0.41
1:D5:240:ARG:HG2	1:E5:67:GLU:HB3	2.02	0.41
1:E6:46:LEU:HD11	1:E7:210:ARG:NH2	2.35	0.41
1:E6:186:LEU:HD22	1:E6:192:ALA:HA	2.01	0.41
1:F4:65:ASN:HB3	1:F5:99:ASN:ND2	2.35	0.41
1:F6:153:ILE:HG13	1:F6:153:ILE:O	2.20	0.41
1:G2:177:ASN:HB3	1:G2:180:VAL:O	2.20	0.41
1:G6:56:ILE:CG1	1:G6:234:THR:HG23	2.50	0.41
1:G7:67:GLU:HA	1:G7:70:MET:HE2	2.02	0.41
1:G8:108:GLN:O	1:G8:112:VAL:HG23	2.20	0.41
1:H9:111:GLN:HA	1:H9:111:GLN:OE1	2.20	0.41
1:J7:157:MET:HE2	1:J7:158:HIS:CE1	2.55	0.41
1:K4:26:ASP:HA	1:K4:249:GLN:HE22	1.85	0.41
2:L3:248:LYS:HA	2:L3:248:LYS:HD2	1.88	0.41
2:L4:205:TYR:CG	2:L4:235:TYR:HE1	2.38	0.41
2:M1:127:GLU:HA	2:M1:130:GLU:HG2	2.02	0.41
2:M2:261:ARG:HD2	2:M2:261:ARG:C	2.45	0.41
2:M3:161:LYS:HE2	2:M3:206:ASP:OD2	2.19	0.41
2:M4:126:LYS:HD2	2:M4:126:LYS:C	2.45	0.41
2:M4:187:PRO:HA	2:M4:190:LYS:NZ	2.35	0.41
2:N1:214:ILE:N	2:N1:215:PRO:HD2	2.34	0.41
2:N2:200:TRP:CZ3	2:N2:204:GLU:HG3	2.55	0.41
2:N3:145:ARG:O	2:N3:149:GLU:HG3	2.20	0.41
2:N4:90:GLN:O	2:N4:94:THR:HG23	2.20	0.41
2:O1:214:ILE:HB	2:O1:215:PRO:HD3	2.02	0.41
2:P6:200:TRP:CD1	2:P6:200:TRP:C	2.98	0.41
3:R3:126:ILE:HG21	3:R4:240:SER:HB3	2.02	0.41
3:R4:166:PRO:HD3	3:R4:179:VAL:HG13	2.02	0.41
3:S2:25:LEU:HD11	3:S2:208:LEU:CD1	2.50	0.41
4:U4:25:ILE:HD11	4:U4:88:ASN:ND2	2.35	0.41
5:V3:59:TRP:CZ2	5:V3:122:PRO:HB3	2.55	0.41
5:V4:110:PHE:CD1	5:V4:116:ASP:HB3	2.55	0.41
5:V4:136:SER:HA	5:V4:175:LEU:O	2.20	0.41
5:X1:155:TYR:CG	5:X1:194:LYS:HB3	2.56	0.41
6:Y1:132:GLU:O	6:Y1:136:LYS:HD3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Y3:39:PHE:CD2	6:Y3:54:VAL:HG22	2.56	0.41
6:Y4:122:TRP:CZ2	6:Y4:149:PRO:HB3	2.54	0.41
7:Z2:127:SER:HA	7:Z2:165:LYS:HE2	2.02	0.41
8:a5:128:GLU:HG2	8:a5:154:ASN:HA	2.02	0.41
8:a5:174:ASP:OD1	8:a5:174:ASP:O	2.37	0.41
9:b2:188:GLU:HA	9:b2:211:ILE:O	2.20	0.41
1:A7:48:VAL:HG11	1:B8:102:TYR:HE1	1.85	0.41
1:B7:43:ALA:HB3	1:C8:113:GLU:CD	2.45	0.41
1:D2:3:ILE:HD13	1:D2:3:ILE:HA	1.87	0.41
1:D4:56:ILE:HD13	1:D4:235:GLN:OE1	2.21	0.41
1:D5:177:ASN:HD22	2:L3:162:GLN:NE2	2.19	0.41
1:E7:183:PHE:N	1:E7:183:PHE:CD1	2.88	0.41
1:F3:233:ASN:OD1	1:G8:74:GLN:HG2	2.19	0.41
1:H9:36:ILE:HD12	1:H9:242:ARG:HA	2.02	0.41
1:H9:219:ARG:HH11	1:H9:219:ARG:CG	2.32	0.41
1:I8:46:LEU:HD12	1:I8:242:ARG:NH2	2.35	0.41
1:I8:186:LEU:HD21	1:I8:195:VAL:HG11	2.02	0.41
1:J4:20:ASP:OD1	1:J4:20:ASP:C	2.62	0.41
1:K4:82:GLU:OE1	1:K4:82:GLU:HA	2.19	0.41
1:K6:68:ASP:OD2	1:K7:101:ILE:HD13	2.20	0.41
1:K6:191:LYS:O	1:K6:195:VAL:HG23	2.20	0.41
2:L2:169:SER:HB3	2:L2:200:TRP:CZ3	2.55	0.41
2:L5:253:PRO:HD2	2:L5:256:MET:SD	2.60	0.41
2:M5:291:ASN:ND2	8:a5:206:ARG:HH11	2.18	0.41
2:O2:227:GLU:OE2	2:O2:270:ARG:HD3	2.20	0.41
2:O2:263:LYS:HA	2:O2:266:VAL:HG22	2.02	0.41
2:O4:236:LEU:HD13	2:O4:267:HIS:CD2	2.55	0.41
2:O5:205:TYR:CD2	2:O5:210:LEU:HD22	2.55	0.41
3:Q1:42:LYS:HE2	3:Q1:42:LYS:HB2	1.79	0.41
3:Q1:79:VAL:HG21	3:Q1:130:ASN:OD1	2.20	0.41
3:Q3:73:LEU:HD21	3:Q3:214:LEU:HD23	2.03	0.41
3:R4:126:ILE:HD12	3:R5:237:LEU:HD23	2.00	0.41
3:R5:41:HIS:O	3:R5:43:THR:HG23	2.20	0.41
4:U3:32:LEU:HD21	4:U3:283:LEU:HD13	2.01	0.41
4:U5:85:PHE:CD1	4:U5:85:PHE:C	2.99	0.41
5:V4:58:ASP:HB3	5:V4:123:PRO:HB3	2.01	0.41
5:X1:107:LYS:HG2	5:X1:215:TYR:CD2	2.55	0.41
8:a2:151:LEU:HD11	8:a3:230:VAL:HG21	2.03	0.41
1:A7:1:MET:HE2	1:A7:1:MET:H1	1.84	0.41
1:A7:175:LEU:HG	1:A7:184:ILE:HD13	2.02	0.41
1:B4:277:VAL:HG22	1:C4:264:THR:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B6:84:HIS:CE1	1:B6:203:LEU:HD22	2.55	0.41
1:D4:66:THR:HG22	1:D4:70:MET:HE3	2.02	0.41
1:D7:150:TRP:CH2	1:D7:162:ARG:HD2	2.55	0.41
1:E1:281:LEU:HD11	1:F1:267:LEU:HD22	2.01	0.41
1:E3:97:ALA:HB2	1:E3:110:ILE:HG21	2.03	0.41
1:E5:7:VAL:O	1:E5:10:ILE:HG22	2.21	0.41
1:F5:6:ASN:HB3	1:F5:9:ALA:HB3	2.02	0.41
1:F6:150:TRP:CZ3	1:F6:162:ARG:HB2	2.56	0.41
1:G5:4:ASN:ND2	1:G5:5:HIS:CD2	2.88	0.41
1:G6:132:LYS:HB3	1:G6:132:LYS:HE3	1.77	0.41
1:H6:1:MET:HG3	1:H6:277:VAL:HG21	2.02	0.41
1:H7:80:LEU:HD12	1:H7:213:LEU:HD12	2.01	0.41
1:I6:153:ILE:HG21	1:I6:220:MET:CE	2.50	0.41
1:I7:239:SER:O	1:I7:243:ASP:HB2	2.20	0.41
2:M2:107:TYR:CZ	2:M2:195:ASP:HB3	2.55	0.41
2:O4:75:ASN:HB3	2:O5:202:MET:HE2	2.01	0.41
2:O4:205:TYR:CE2	2:O4:210:LEU:HD22	2.56	0.41
2:O5:178:ILE:HD12	2:O5:189:PHE:CE2	2.53	0.41
2:P2:118:ARG:HA	2:P2:118:ARG:HD3	1.82	0.41
2:P5:125:ARG:O	2:P5:128:GLU:HG3	2.20	0.41
2:P6:150:GLU:HA	2:P6:153:VAL:HG22	2.01	0.41
3:Q3:159:PHE:HD1	3:Q3:181:LYS:HB2	1.85	0.41
3:Q3:184:LEU:O	3:Q3:187:VAL:HG12	2.20	0.41
3:Q4:234:VAL:O	3:Q4:238:LYS:HG3	2.20	0.41
3:R5:138:ILE:CG1	3:R5:161:GLN:HB3	2.48	0.41
3:S2:18:ILE:HG13	3:S2:204:TYR:CD2	2.56	0.41
3:S4:35:LYS:HE3	3:S4:64:GLU:OE2	2.20	0.41
4:U3:91:TYR:CD1	4:U3:91:TYR:C	2.98	0.41
1:B7:43:ALA:HB2	1:B8:214:GLY:HA3	2.03	0.41
1:C7:52:MET:O	1:C7:56:ILE:HG13	2.21	0.41
1:E2:60:ARG:HG3	1:E2:231:TYR:CE1	2.55	0.41
1:E3:8:SER:HB3	1:F3:27:ILE:HG21	2.01	0.41
1:G6:261:GLN:OE1	1:H5:278:MET:HE1	2.20	0.41
1:G7:94:ALA:HA	1:G7:186:LEU:HD13	2.03	0.41
1:G8:186:LEU:HD23	1:G8:195:VAL:HG21	2.02	0.41
1:G8:215:ALA:HA	1:H8:113:GLU:HG3	2.02	0.41
1:H6:39:ALA:HA	1:H6:46:LEU:HD22	2.01	0.41
1:H9:121:ILE:O	1:H9:124:ILE:HG22	2.21	0.41
1:J8:73:ILE:HG21	1:J8:217:TYR:HB2	2.02	0.41
1:K7:2:ILE:HG21	1:K8:239:SER:OG	2.20	0.41
1:K7:84:HIS:CD2	1:K7:88:GLN:OE1	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M3:127:GLU:O	2:M3:131:LYS:HG3	2.20	0.41
2:M5:236:LEU:HD13	2:M5:267:HIS:CE1	2.55	0.41
2:O4:205:TYR:CD2	2:O4:210:LEU:HD22	2.56	0.41
2:O5:133:ARG:HG3	2:O5:136:GLU:OE2	2.21	0.41
2:P2:184:ARG:HD2	2:P2:189:PHE:CZ	2.55	0.41
2:P3:88:LEU:HD23	2:P3:88:LEU:C	2.45	0.41
3:Q2:119:LEU:H	3:Q2:147:ASN:ND2	2.19	0.41
3:Q3:66:GLN:OE1	3:Q3:105:ASN:HB2	2.20	0.41
3:R3:131:PHE:N	3:R3:131:PHE:CD1	2.86	0.41
3:S3:18:ILE:HA	3:S3:21:VAL:HG12	2.03	0.41
4:U5:244:ASN:OD1	4:U5:246:ARG:HG3	2.21	0.41
4:U6:109:GLU:O	4:U6:113:ILE:HG13	2.21	0.41
5:V2:97:LYS:O	5:V2:101:ASN:HB3	2.21	0.41
5:V3:151:LYS:HG3	5:V3:159:THR:HG23	2.03	0.41
5:X1:196:LEU:HD13	5:X1:197:HIS:N	2.35	0.41
5:X3:135:ILE:HD12	5:X3:152:PHE:CZ	2.55	0.41
7:Z1:60:ILE:HG22	7:Z1:83:CYS:HB2	2.02	0.41
8:a1:135:LYS:HG2	8:a1:147:THR:HB	2.02	0.41
8:a2:102:SER:O	8:a2:137:LEU:HD12	2.20	0.41
8:a5:155:THR:HG22	8:a5:156:THR:N	2.36	0.41
10:c2:58:ARG:HG3	10:c2:59:PRO:HD2	2.02	0.41
1:A6:6:ASN:ND2	1:A6:274:SER:HB3	2.36	0.41
1:C4:84:HIS:HB2	1:C4:206:ILE:HG21	2.03	0.41
1:D3:60:ARG:HD3	1:D3:60:ARG:HA	1.89	0.41
1:E4:56:ILE:HD11	1:E4:235:GLN:N	2.36	0.41
1:E6:134:LYS:HD3	1:E6:134:LYS:HA	1.93	0.41
1:E6:161:GLU:OE2	1:F6:123:ARG:HD3	2.20	0.41
1:F3:61:ARG:NH1	1:F4:96:GLN:HE21	2.19	0.41
1:F4:66:THR:HG21	1:F4:224:ALA:HB2	2.01	0.41
1:F4:73:ILE:HG21	1:F4:217:TYR:HB2	2.02	0.41
1:F5:143:LEU:HD21	2:N5:143:VAL:HG21	2.01	0.41
1:G7:118:VAL:HG13	1:G7:170:THR:HG21	2.02	0.41
1:G8:19:ASN:HD22	1:G8:259:LEU:HB3	1.86	0.41
1:H6:30:LEU:HD21	1:H6:250:MET:CE	2.51	0.41
1:H6:30:LEU:HD21	1:H6:250:MET:HE2	2.02	0.41
1:I8:86:ILE:HG21	1:I8:121:ILE:HG13	2.01	0.41
1:I9:124:ILE:HG13	1:I9:124:ILE:H	1.69	0.41
1:J7:7:VAL:O	1:J7:10:ILE:HG22	2.20	0.41
1:K6:177:ASN:HB3	1:K6:180:VAL:O	2.21	0.41
1:K8:106:ASP:O	1:K8:110:ILE:HG13	2.20	0.41
2:L3:198:ARG:O	2:L3:202:MET:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N2:168:PHE:CE2	2:N2:199:SER:HB3	2.56	0.41
3:Q1:36:VAL:O	3:Q1:36:VAL:HG13	2.21	0.41
3:R1:81:SER:HA	3:R1:86:SER:OG	2.21	0.41
3:R4:96:LYS:HE3	3:R4:125:TYR:CG	2.56	0.41
3:S2:207:ASN:HD21	3:S2:211:PHE:HE2	1.68	0.41
3:S6:38:THR:H	3:S6:222:ASN:HD21	1.69	0.41
4:U3:78:LYS:HG3	4:U3:79:ALA:N	2.34	0.41
4:U4:236:ASP:O	4:U4:239:ILE:HG22	2.20	0.41
5:V1:214:PHE:CZ	5:V1:216:PHE:HB3	2.56	0.41
5:X1:104:LEU:HD23	5:X1:104:LEU:HA	1.94	0.41
5:X3:83:ASP:HB3	5:X3:86:ASP:O	2.20	0.41
5:X4:149:PHE:HB2	5:X4:202:PHE:CZ	2.56	0.41
6:Y4:37:VAL:HG12	6:Y4:39:PHE:CE1	2.55	0.41
9:b4:137:LYS:HD3	9:b4:139:ILE:HD11	2.02	0.41
1:A4:219:ARG:NH2	1:B4:119:ASP:HB3	2.35	0.41
1:A5:84:HIS:CE1	1:A5:203:LEU:HD22	2.55	0.41
1:B6:39:ALA:HB2	1:B7:77:GLU:CG	2.50	0.41
1:B6:152:HIS:HA	1:B6:160:ARG:HG3	2.03	0.41
1:C3:50:GLU:CD	1:C3:242:ARG:HH12	2.29	0.41
1:C4:48:VAL:HG22	1:D5:106:ASP:OD2	2.21	0.41
1:C4:66:THR:HG23	1:C4:220:MET:HG3	2.01	0.41
1:C5:80:LEU:HD12	1:C5:213:LEU:HD12	2.01	0.41
1:D7:153:ILE:HD11	1:D7:161:GLU:HG2	2.02	0.41
1:F3:247:ALA:HB1	1:G7:267:LEU:HD11	2.02	0.41
1:F5:80:LEU:HD23	1:F5:210:ARG:HG3	2.02	0.41
1:G6:150:TRP:CD2	1:G6:162:ARG:HB2	2.56	0.41
1:H9:162:ARG:HA	1:H9:162:ARG:HD2	1.94	0.41
1:I6:278:MET:HE2	1:I6:278:MET:HB2	1.93	0.41
1:J8:40:GLY:HA3	1:J9:217:TYR:CD1	2.56	0.41
1:K4:180:VAL:HG11	7:Za:171:ASN:OD1	2.20	0.41
2:L1:82:ASN:HD21	2:L1:84:THR:HG23	1.85	0.41
2:L2:175:LEU:HD12	2:L2:178:ILE:HD12	2.03	0.41
2:P4:157:LYS:O	2:P4:161:LYS:HG2	2.21	0.41
3:Q3:18:ILE:HA	3:Q3:21:VAL:HG22	2.01	0.41
3:Q4:125:TYR:CE1	3:Q4:127:TYR:HB2	2.55	0.41
3:R4:161:GLN:NE2	3:R4:164:ASP:HA	2.36	0.41
3:S5:127:TYR:CE1	3:S5:136:LYS:HE3	2.54	0.41
3:S5:205:PHE:C	3:S5:205:PHE:HD1	2.29	0.41
4:U3:175:TYR:CE2	4:U3:179:LEU:HD11	2.56	0.41
5:V2:70:THR:HA	5:V2:107:LYS:O	2.20	0.41
5:X2:53:PHE:HA	5:X2:56:ALA:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Y2:130:LYS:O	6:Y2:134:MET:HG3	2.21	0.41
6:Y3:21:ASP:HB3	6:Y3:248:ASN:HD22	1.86	0.41
7:Za:165:LYS:HG3	7:Za:166:TYR:N	2.36	0.41
7:Za:172:MET:O	7:Za:172:MET:HE3	2.21	0.41
8:a1:72:VAL:HG22	8:a1:111:MET:HE2	2.01	0.41
9:b4:76:ALA:HB1	9:b4:80:LEU:HD23	2.01	0.41
9:b4:156:MET:HE1	9:b4:205:GLN:NE2	2.36	0.41
1:i0:86:ILE:HG23	1:i0:117:LEU:HD22	2.03	0.41
1:A5:25:LYS:HG2	1:A5:38:LYS:NZ	2.35	0.41
1:B7:51:LYS:O	1:B7:54:THR:HG22	2.21	0.41
1:C7:175:LEU:HD12	1:C7:184:ILE:HG21	2.03	0.41
1:D5:181:LEU:H	6:Y3:94:TRP:HB3	1.86	0.41
1:D5:186:LEU:HD11	1:D5:195:VAL:HG11	2.01	0.41
1:E5:51:LYS:O	1:E5:54:THR:HG22	2.20	0.41
1:F6:70:MET:HE3	1:F6:217:TYR:CE1	2.56	0.41
1:F6:101:ILE:HG12	1:F6:102:TYR:N	2.31	0.41
1:F6:109:GLN:O	1:F6:112:VAL:HG12	2.21	0.41
1:G7:247:ALA:O	1:G7:251:THR:HG23	2.20	0.41
1:H9:133:MET:HE2	1:H9:133:MET:HB2	1.77	0.41
1:I6:168:MET:HE2	1:I6:168:MET:HA	2.03	0.41
1:I8:30:LEU:HD21	1:I8:249:GLN:HB3	2.02	0.41
1:J4:16:LEU:HD11	1:J4:264:THR:HG23	2.02	0.41
1:J5:80:LEU:HD12	1:J5:213:LEU:HD12	2.02	0.41
1:J8:262:ALA:O	1:J8:266:MET:HG2	2.21	0.41
1:J9:86:ILE:HG23	1:J9:117:LEU:HD22	2.02	0.41
1:K4:149:MET:HG2	1:K4:163:VAL:HG22	2.03	0.41
1:K6:123:ARG:HH11	1:K6:127:GLN:NE2	2.18	0.41
1:K6:160:ARG:HD3	1:K7:193:ASN:ND2	2.36	0.41
2:M2:88:LEU:HD11	2:M3:282:GLU:HA	2.02	0.41
2:N3:90:GLN:HB3	2:N3:94:THR:HG21	2.03	0.41
2:O4:210:LEU:HD12	2:O4:242:PHE:CD2	2.56	0.41
3:R5:184:LEU:O	3:R5:187:VAL:HG22	2.20	0.41
3:S5:163:ASP:O	3:S5:166:PRO:HD2	2.21	0.41
4:U5:78:LYS:O	4:U5:82:GLN:HG2	2.21	0.41
5:X1:135:ILE:HD12	5:X1:152:PHE:HZ	1.86	0.41
5:X3:48:ILE:HB	5:X3:223:VAL:CG1	2.50	0.41
6:Y1:179:GLU:OE1	6:Y1:180:LYS:HG3	2.21	0.41
6:Y4:106:LEU:O	6:Y4:148:GLU:HB3	2.21	0.41
8:a2:131:PHE:CZ	8:a2:200:ARG:HB3	2.56	0.41
9:b3:50:ILE:CD1	9:b3:231:MET:HE3	2.50	0.41
1:A4:28:GLU:HG2	1:K5:11:PHE:CD1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A4:127:GLN:HG2	1:K5:159:GLN:HG2	2.02	0.41
1:A7:48:VAL:HG12	1:A7:52:MET:HE3	2.03	0.41
1:A7:181:LEU:HD23	1:A7:181:LEU:HA	1.94	0.41
1:A8:52:MET:HE1	1:A8:237:SER:HB3	2.03	0.41
1:B4:3:ILE:HG12	1:B4:278:MET:HG2	2.02	0.41
1:B4:55:GLN:O	1:B4:59:LEU:HD23	2.21	0.41
1:C5:80:LEU:HD23	1:C5:80:LEU:HA	1.93	0.41
1:C6:156:ASN:HB2	1:C6:159:GLN:NE2	2.35	0.41
1:D3:7:VAL:O	1:D3:10:ILE:HG22	2.21	0.41
1:D3:168:MET:HE1	1:D3:206:ILE:HG12	2.02	0.41
1:D3:191:LYS:O	1:D3:195:VAL:HG23	2.21	0.41
1:E3:150:TRP:CE3	1:E3:162:ARG:HB2	2.55	0.41
1:E6:225:LYS:HE3	1:E6:225:LYS:HB3	1.91	0.41
1:G1:237:SER:HB2	1:h0:71:SER:HB2	2.03	0.41
1:G7:156:ASN:HB2	1:G7:159:GLN:OE1	2.20	0.41
1:G8:258:ILE:HD13	1:H7:278:MET:HE3	2.01	0.41
1:I6:16:LEU:HD13	1:I6:263:ALA:HB3	2.03	0.41
1:I7:63:GLU:HG2	1:I7:228:MET:SD	2.61	0.41
1:I8:191:LYS:O	1:I8:195:VAL:HG23	2.21	0.41
1:I8:221:GLU:HG2	1:I8:225:LYS:NZ	2.36	0.41
1:J6:25:LYS:N	1:J6:25:LYS:HE2	2.36	0.41
1:J6:107:ARG:HA	1:J6:110:ILE:HD12	2.02	0.41
1:J6:281:LEU:CD2	1:K6:264:THR:HG23	2.51	0.41
1:J7:2:ILE:CD1	1:J8:239:SER:HB2	2.51	0.41
1:J7:4:ASN:HB3	1:J8:243:ASP:CG	2.45	0.41
1:K6:210:ARG:HE	1:K6:210:ARG:HB2	1.67	0.41
2:L1:88:LEU:HD22	2:L2:286:ILE:HD13	2.02	0.41
2:L2:86:GLN:NE2	2:L2:87:GLU:HG2	2.35	0.41
2:N3:263:LYS:HA	2:N3:266:VAL:HG12	2.03	0.41
2:N4:127:GLU:HG2	2:N4:131:LYS:NZ	2.36	0.41
2:N5:180:ASN:CG	2:N5:183:LEU:HD13	2.46	0.41
2:P2:119:ASP:OD1	2:P2:120:TRP:N	2.54	0.41
2:P4:88:LEU:HD23	2:P4:88:LEU:C	2.46	0.41
2:P6:140:TRP:HA	2:P6:143:VAL:HG22	2.02	0.41
3:Q3:21:VAL:O	3:Q3:25:LEU:HD23	2.21	0.41
3:R1:158:LEU:HD13	3:R1:182:TYR:CE2	2.55	0.41
3:R1:187:VAL:CG1	3:R1:196:ARG:HB2	2.50	0.41
3:R1:198:ASN:OD1	3:R1:199:PHE:N	2.54	0.41
3:R2:121:LYS:HB2	3:R2:121:LYS:HE2	1.75	0.41
3:R3:18:ILE:HD12	3:R3:208:LEU:HD12	2.02	0.41
3:R4:140:VAL:HG21	3:R4:168:TRP:CH2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S2:25:LEU:HA	3:S2:28:HIS:HD1	1.86	0.41
3:S5:71:LEU:O	3:S5:98:GLU:HA	2.20	0.41
3:S5:132:LEU:HD13	3:S5:132:LEU:HA	1.91	0.41
4:U6:25:ILE:HG13	4:U6:91:TYR:CD2	2.55	0.41
4:U6:176:LYS:HB3	4:U6:176:LYS:HE2	1.88	0.41
5:V1:70:THR:HA	5:V1:107:LYS:O	2.21	0.41
5:V2:140:LEU:HD13	5:V2:172:TRP:CD1	2.56	0.41
5:V4:145:ARG:CZ	5:V4:166:ARG:HH21	2.33	0.41
5:X2:60:ARG:HD3	7:Z1:163:TYR:CE1	2.56	0.41
5:X2:127:ILE:O	5:X2:127:ILE:HG13	2.21	0.41
5:X3:80:LEU:HD13	5:X3:82:LYS:HE3	2.02	0.41
6:Y1:95:ARG:HA	6:Y1:95:ARG:HD2	1.89	0.41
7:Z0:190:LEU:HD13	7:Z0:190:LEU:HA	1.89	0.41
7:Z1:60:ILE:HD13	7:Z1:63:GLU:OE2	2.21	0.41
7:Z1:75:SER:O	7:Z1:79:ARG:HG2	2.20	0.41
7:Z1:268:ILE:HG22	7:Z1:269:ASP:OD1	2.21	0.41
7:Za:234:LEU:O	7:Za:237:PRO:HD3	2.21	0.41
8:a2:116:GLY:HA3	8:a2:124:PHE:CE1	2.56	0.41
8:a5:200:ARG:O	8:a5:204:VAL:HG12	2.21	0.41
9:b3:33:SER:O	9:b3:36:GLN:HG2	2.21	0.41
9:b3:183:SER:HB3	9:b3:216:ASN:HB2	2.02	0.41
9:b3:226:LYS:HB3	9:b4:260:ILE:HG21	2.02	0.41
9:b4:102:GLU:H	9:b4:102:GLU:HG3	1.61	0.41
10:c2:82:MET:HE2	10:c2:82:MET:HB2	1.88	0.41
10:c3:130:MET:HB3	10:c3:141:PHE:CE1	2.55	0.41
1:A6:153:ILE:HD11	1:B6:123:ARG:HD2	2.03	0.41
1:A8:222:HIS:HE1	1:B8:85:GLU:HB2	1.86	0.41
1:B8:215:ALA:O	1:B8:219:ARG:HG3	2.21	0.41
1:E5:258:ILE:HD11	1:F4:275:GLN:CG	2.51	0.41
1:G5:281:LEU:HD21	1:H5:267:LEU:HD13	2.03	0.41
1:H5:11:PHE:CD2	1:I5:28:GLU:HG3	2.56	0.41
1:H9:48:VAL:HG13	1:I9:131:ASN:ND2	2.36	0.41
1:I8:76:ALA:HB2	1:I8:135:LEU:HD13	2.02	0.41
1:I9:163:VAL:HG13	1:I9:216:TYR:CE2	2.55	0.41
1:I9:209:GLN:O	1:I9:213:LEU:HD23	2.21	0.41
1:J8:171:ALA:HB1	1:J8:178:PRO:HB3	2.01	0.41
1:K7:36:ILE:O	1:K7:36:ILE:HG13	2.21	0.41
2:L1:172:ILE:HD12	6:Y1:95:ARG:NH1	2.35	0.41
2:L4:286:ILE:O	2:L4:290:ILE:HG12	2.21	0.41
2:M2:67:MET:HB3	2:M2:67:MET:HE3	1.77	0.41
2:M4:228:LYS:HE2	2:M4:274:LEU:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N5:158:MET:SD	2:N5:207:LEU:HD23	2.61	0.41
2:O1:175:LEU:HD12	2:O1:196:VAL:HG21	2.03	0.41
2:O2:102:LEU:HD12	3:S3:78:PHE:CE1	2.56	0.41
2:O2:190:LYS:HD3	2:O2:224:ASP:OD2	2.21	0.41
3:R2:72:HIS:HE1	3:R2:74:GLU:HB2	1.86	0.41
3:S3:29:THR:HG21	3:S3:117:ARG:H	1.86	0.41
4:U6:175:TYR:CE2	4:U6:179:LEU:HD11	2.56	0.41
4:U6:205:ASP:O	4:U6:208:LYS:HG2	2.21	0.41
5:X4:65:THR:HG22	5:X4:67:LEU:H	1.86	0.41
6:Y1:121:ILE:HG23	6:Y1:122:TRP:N	2.35	0.41
6:Y3:151:PHE:CE2	6:Y3:235:LYS:HD3	2.55	0.41
6:Y4:45:ASP:OD1	6:Y4:45:ASP:N	2.47	0.41
7:Za:29:ARG:HH21	7:Za:312:GLU:HB2	1.86	0.41
8:a4:187:PRO:HD2	8:a4:188:TRP:CE3	2.56	0.41
1:A5:63:GLU:CD	1:K4:240:ARG:HH22	2.29	0.40
1:A8:184:ILE:HG13	1:A8:195:VAL:HG22	2.04	0.40
1:C7:154:GLY:HA3	1:C7:159:GLN:NE2	2.36	0.40
1:C7:239:SER:O	1:C7:243:ASP:HB2	2.21	0.40
1:D6:212:ASP:OD1	1:E6:112:VAL:HG11	2.21	0.40
1:D7:75:THR:HG22	1:D7:79:TYR:CE2	2.56	0.40
1:E7:184:ILE:HD13	1:E7:195:VAL:HG13	2.02	0.40
1:F3:59:LEU:HD12	1:F3:234:THR:HG21	2.03	0.40
1:F4:152:HIS:H	1:F5:99:ASN:HD22	1.69	0.40
1:F6:72:LEU:HD12	1:F6:130:PHE:CD1	2.55	0.40
1:G1:66:THR:CG2	1:G1:220:MET:HG3	2.50	0.40
1:G6:56:ILE:HG13	1:G6:234:THR:HG23	2.02	0.40
1:G7:157:MET:HE2	1:G7:158:HIS:CE1	2.56	0.40
1:G9:84:HIS:CE1	1:G9:203:LEU:HD22	2.56	0.40
1:H9:55:GLN:O	1:H9:59:LEU:HD23	2.20	0.40
1:I5:2:ILE:HG12	1:I6:243:ASP:HB2	2.03	0.40
1:I7:1:MET:HG3	1:I7:277:VAL:HG21	2.03	0.40
1:I7:52:MET:HE1	1:I7:237:SER:CB	2.51	0.40
1:I8:183:PHE:N	1:I8:183:PHE:HD1	2.18	0.40
1:I9:150:TRP:CE3	1:I9:160:ARG:HG3	2.56	0.40
1:J7:99:ASN:OD1	1:J7:101:ILE:HG23	2.20	0.40
1:K6:93:LEU:HD11	1:K6:113:GLU:OE2	2.22	0.40
1:K7:82:GLU:O	1:K7:86:ILE:HG13	2.21	0.40
2:L5:214:ILE:HD13	2:L5:240:TYR:CE1	2.56	0.40
2:M1:180:ASN:O	2:M1:184:ARG:HG3	2.21	0.40
2:N2:157:LYS:HB2	2:N2:157:LYS:HE2	1.90	0.40
2:N6:232:LEU:O	2:O5:212:GLN:HG2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R5:70:CYS:HA	3:R5:99:LEU:O	2.21	0.40
3:S5:189:ASN:HB2	3:S5:196:ARG:HE	1.86	0.40
3:S6:14:LEU:O	3:S6:18:ILE:HG23	2.21	0.40
4:U4:75:LYS:HA	4:U4:75:LYS:HD2	1.81	0.40
5:X1:103:ILE:HG22	5:X1:219:ASP:CG	2.45	0.40
5:X2:239:ASP:C	5:X2:239:ASP:OD1	2.64	0.40
6:Y3:40:VAL:HG13	6:Y3:53:ASP:OD2	2.22	0.40
8:a1:67:MET:O	8:a1:71:LYS:HG2	2.21	0.40
1:A3:27:ILE:HG13	1:K3:266:MET:CE	2.52	0.40
1:B4:231:TYR:CD1	1:B4:231:TYR:C	2.99	0.40
1:B5:43:ALA:HB1	1:B6:211:ALA:HA	2.03	0.40
1:B6:217:TYR:C	1:B6:217:TYR:HD1	2.29	0.40
1:C5:12:ALA:HB3	1:C5:267:LEU:HD13	2.04	0.40
1:C5:144:ASN:HD21	1:C5:147:ALA:N	2.19	0.40
1:D4:156:ASN:HB2	1:D4:159:GLN:OE1	2.21	0.40
1:E5:73:ILE:HG23	1:E5:213:LEU:HD12	2.02	0.40
1:F4:48:VAL:HG21	1:G1:102:TYR:CE1	2.56	0.40
1:G1:211:ALA:HB2	1:h0:109:GLN:NE2	2.36	0.40
1:H7:184:ILE:CD1	1:H7:195:VAL:HG22	2.51	0.40
1:H9:154:GLY:HA3	1:H9:159:GLN:OE1	2.21	0.40
1:J7:73:ILE:HD11	1:J7:151:PHE:HE2	1.86	0.40
1:K6:54:THR:HG21	1:K7:203:LEU:HD13	2.03	0.40
2:L4:272:THR:HG21	2:L4:286:ILE:HG21	2.03	0.40
2:L5:204:GLU:OE1	2:L5:213:THR:HA	2.21	0.40
2:M1:175:LEU:HD23	2:M1:175:LEU:HA	1.89	0.40
2:M1:246:MET:HE2	2:M1:246:MET:HB2	1.87	0.40
2:M2:171:ALA:O	2:M2:175:LEU:HD22	2.22	0.40
2:M5:230:TYR:N	2:M5:231:PRO:HD2	2.36	0.40
2:O5:108:GLN:HA	2:O5:111:VAL:HG12	2.03	0.40
2:P4:124:TYR:HE2	2:P4:149:GLU:HG2	1.85	0.40
3:Q3:45:LEU:HD12	3:Q3:73:LEU:HD13	2.04	0.40
3:Q3:159:PHE:CD1	3:Q3:181:LYS:HB2	2.56	0.40
3:R1:50:PRO:HG3	3:R1:100:PHE:CD2	2.56	0.40
3:R2:158:LEU:HD12	3:R2:182:TYR:CE2	2.57	0.40
3:S2:36:VAL:HG21	3:S2:45:LEU:HD22	2.03	0.40
3:S3:47:LYS:HB2	3:S3:68:ASN:HD22	1.86	0.40
3:S4:127:TYR:CE2	3:S4:136:LYS:HE3	2.56	0.40
3:S5:100:PHE:CD2	3:S5:121:LYS:HD2	2.57	0.40
3:S5:130:ASN:HB2	3:S5:133:LEU:HB2	2.03	0.40
4:U3:91:TYR:HD1	4:U3:91:TYR:C	2.29	0.40
4:U3:276:THR:HG23	4:U3:279:LYS:HG2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X2:143:LYS:HD2	5:X2:170:PHE:CE2	2.56	0.40
6:Y4:126:THR:HA	6:Y4:129:LYS:HE2	2.04	0.40
9:b3:66:LYS:HB3	9:b3:66:LYS:HE3	1.90	0.40
9:b3:237:MET:HE3	9:b3:237:MET:HB3	1.80	0.40
9:b4:74:LYS:HE3	9:b4:74:LYS:HB3	1.88	0.40
1:h0:104:GLU:CD	1:h0:104:GLU:H	2.29	0.40
1:B6:280:LEU:HD13	1:C6:264:THR:OG1	2.22	0.40
1:D4:66:THR:HG23	1:D4:220:MET:HG3	2.02	0.40
1:D7:93:LEU:HD11	1:D7:113:GLU:HG2	2.03	0.40
1:E3:255:ARG:O	1:E3:258:ILE:HG22	2.20	0.40
1:E4:35:ARG:HG3	1:E4:244:THR:HB	2.03	0.40
1:E4:80:LEU:HD21	1:E4:168:MET:HE3	2.04	0.40
1:G5:6:ASN:O	1:G5:10:ILE:HG13	2.22	0.40
1:G6:50:GLU:HG3	1:G7:84:HIS:CE1	2.56	0.40
1:G8:261:GLN:HB3	1:H7:278:MET:CE	2.51	0.40
1:I6:154:GLY:HA3	1:I6:159:GLN:HE21	1.85	0.40
1:I9:183:PHE:HD1	1:I9:183:PHE:H	1.69	0.40
1:J7:56:ILE:HD13	1:J7:235:GLN:HA	2.04	0.40
1:J8:175:LEU:HB3	1:J8:184:ILE:HD11	2.04	0.40
2:L3:79:LYS:HE2	2:L3:79:LYS:HB3	1.91	0.40
2:L3:243:GLU:HA	2:L3:243:GLU:OE1	2.22	0.40
2:M2:161:LYS:HE2	2:M2:206:ASP:OD2	2.21	0.40
2:M3:230:TYR:CD2	2:M3:231:PRO:HD3	2.56	0.40
2:N3:204:GLU:HG3	2:N3:209:ASN:HB2	2.03	0.40
3:Q2:18:ILE:HD13	3:Q2:18:ILE:HA	1.91	0.40
3:Q3:100:PHE:CD1	3:Q3:121:LYS:HB3	2.56	0.40
3:Q3:167:VAL:HG22	3:Q3:168:TRP:H	1.85	0.40
3:S6:209:ASP:O	3:S6:213:LYS:HG2	2.22	0.40
5:V1:136:SER:HB3	5:V1:176:THR:HG22	2.02	0.40
5:X4:152:PHE:O	5:X4:159:THR:HA	2.20	0.40
6:Y1:241:PHE:CE2	6:Y1:250:LEU:HD13	2.55	0.40
6:Y3:48:LYS:HE2	6:Y3:48:LYS:HB3	1.87	0.40
8:a1:90:THR:HG22	8:a1:107:SER:H	1.85	0.40
8:a2:112:LYS:HE3	8:a2:112:LYS:HB2	1.93	0.40
1:B4:80:LEU:HD22	1:B4:206:ILE:HG23	2.03	0.40
1:C7:95:VAL:HA	1:C7:196:ILE:HD11	2.03	0.40
1:C7:157:MET:HE3	1:C7:158:HIS:NE2	2.36	0.40
1:C8:171:ALA:HB1	1:C8:178:PRO:HG3	2.03	0.40
1:D6:237:SER:OG	1:E6:71:SER:HB2	2.22	0.40
1:E5:84:HIS:HB2	1:E5:206:ILE:HG21	2.03	0.40
1:E5:216:TYR:O	1:E5:220:MET:HG2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E6:60:ARG:HD3	1:E6:231:TYR:CE2	2.56	0.40
1:E6:177:ASN:HB3	1:E6:180:VAL:O	2.22	0.40
1:F2:213:LEU:HD23	1:F2:213:LEU:HA	1.90	0.40
1:F3:138:GLY:HA3	1:F3:167:THR:HG22	2.02	0.40
1:F3:258:ILE:CG1	1:G7:3:ILE:HD11	2.52	0.40
1:H5:278:MET:HE3	1:H5:278:MET:HB3	1.98	0.40
1:H6:60:ARG:HH22	1:H6:228:MET:HE1	1.86	0.40
1:H6:225:LYS:HE3	1:H6:225:LYS:HB2	1.86	0.40
1:I7:46:LEU:CD1	1:I7:242:ARG:HH12	2.32	0.40
1:I7:157:MET:HE2	1:I7:158:HIS:NE2	2.36	0.40
1:I9:60:ARG:HD3	1:I9:231:TYR:CE2	2.55	0.40
1:I9:177:ASN:HB3	1:I9:180:VAL:O	2.22	0.40
1:J5:7:VAL:HA	1:J5:10:ILE:HG22	2.03	0.40
1:J5:258:ILE:HG13	1:K5:278:MET:HE2	2.03	0.40
1:J9:198:LEU:HD23	1:J9:198:LEU:HA	1.93	0.40
1:K7:111:GLN:HA	1:K7:114:VAL:HG22	2.04	0.40
2:M1:250:THR:O	2:M1:251:LYS:HG2	2.21	0.40
2:M1:284:LYS:HA	2:M1:287:VAL:HG22	2.03	0.40
2:M3:78:PHE:CZ	2:M4:234:LYS:HE3	2.56	0.40
2:M5:148:ARG:HB3	2:M5:148:ARG:NH1	2.37	0.40
2:N1:184:ARG:HA	2:N1:189:PHE:CD2	2.56	0.40
2:N3:67:MET:HE1	3:R3:164:ASP:HB2	2.03	0.40
2:O5:108:GLN:HB2	3:S6:41:HIS:CE1	2.56	0.40
2:P2:253:PRO:HD2	2:P2:256:MET:CE	2.50	0.40
2:P2:269:LEU:HA	2:P2:272:THR:HG22	2.03	0.40
3:Q1:94:PHE:CD1	3:Q1:94:PHE:C	3.00	0.40
3:Q1:97:MET:HE2	3:Q1:211:PHE:CD2	2.56	0.40
3:Q3:34:MET:HE1	3:Q3:219:PHE:CE1	2.56	0.40
3:Q4:136:LYS:HE2	3:Q4:138:ILE:HD11	2.04	0.40
5:V1:98:ILE:CG2	5:V1:101:ASN:HD22	2.32	0.40
5:V1:201:LEU:HD23	5:V1:201:LEU:HA	1.92	0.40
5:V2:72:THR:HB	5:V2:104:LEU:HD11	2.03	0.40
5:V2:103:ILE:HA	5:V2:219:ASP:OD2	2.20	0.40
5:X3:49:VAL:HG22	5:X3:222:GLN:CG	2.51	0.40
6:Y1:106:LEU:O	6:Y1:148:GLU:HB2	2.21	0.40
7:Za:60:ILE:HG22	7:Za:83:CYS:HB2	2.03	0.40
8:a2:150:GLU:HB3	8:a2:165:SER:HB2	2.03	0.40
8:a5:64:TYR:CD1	8:a5:67:MET:HE2	2.55	0.40
1:A3:47:ALA:O	1:A3:51:LYS:HG2	2.22	0.40
1:A6:67:GLU:OE1	1:K6:240:ARG:HD3	2.22	0.40
1:B4:162:ARG:HG2	1:B4:164:TYR:CE1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:82:GLU:OE1	1:B5:82:GLU:HA	2.20	0.40
1:B6:12:ALA:HB3	1:B6:267:LEU:HD23	2.03	0.40
1:B7:252:SER:O	1:B7:255:ARG:HB3	2.22	0.40
1:B8:134:LYS:HB3	1:B8:137:THR:HG22	2.02	0.40
1:C4:175:LEU:HD22	1:C4:184:ILE:HD13	2.03	0.40
1:D4:192:ALA:O	1:D4:196:ILE:HG13	2.22	0.40
1:D6:91:ARG:HH11	1:D6:91:ARG:HG2	1.87	0.40
1:D7:222:HIS:HB3	1:E7:82:GLU:OE2	2.22	0.40
1:E3:49:SER:HA	1:E3:52:MET:HE2	2.04	0.40
1:E4:35:ARG:HG3	1:E4:244:THR:CA	2.51	0.40
1:E6:121:ILE:HA	1:E6:124:ILE:HD12	2.03	0.40
1:F2:82:GLU:OE1	1:F2:82:GLU:C	2.64	0.40
1:F2:169:ASN:ND2	1:F2:171:ALA:HB3	2.37	0.40
1:F4:149:MET:HE3	1:F4:151:PHE:CE1	2.56	0.40
1:F5:255:ARG:HG3	1:G9:4:ASN:O	2.22	0.40
1:F6:80:LEU:HD22	1:F6:213:LEU:HD12	2.02	0.40
1:H7:254:THR:HG23	1:I6:275:GLN:HE21	1.87	0.40
1:I6:215:ALA:HB1	1:J6:116:GLN:HB2	2.02	0.40
1:I7:225:LYS:HB2	1:I7:225:LYS:HE3	1.83	0.40
1:I8:192:ALA:O	1:I8:196:ILE:HG13	2.20	0.40
1:I8:258:ILE:HD11	1:J7:275:GLN:CG	2.51	0.40
1:J6:10:ILE:CD1	1:J7:235:GLN:HG2	2.52	0.40
1:J7:270:ALA:O	1:J7:273:LYS:HG2	2.22	0.40
1:K4:17:LYS:HB3	1:K4:17:LYS:HE2	1.72	0.40
1:K6:66:THR:HG23	1:K6:220:MET:HB3	2.04	0.40
2:L2:78:PHE:CZ	2:L3:234:LYS:HE3	2.57	0.40
2:N5:63:LYS:O	2:N5:67:MET:HG2	2.20	0.40
2:O1:230:TYR:CD2	2:O1:231:PRO:HD3	2.57	0.40
2:O1:242:PHE:CD1	2:O1:242:PHE:C	3.00	0.40
2:O3:230:TYR:CD2	2:O3:231:PRO:HD3	2.57	0.40
2:P4:248:LYS:HB3	2:P4:248:LYS:HE3	1.87	0.40
3:Q2:18:ILE:HA	3:Q2:21:VAL:HG22	2.04	0.40
3:Q4:220:ASP:C	3:Q4:220:ASP:OD1	2.64	0.40
3:R1:121:LYS:HG3	3:R1:144:VAL:HA	2.03	0.40
3:R3:14:LEU:HD21	3:R3:197:ASN:OD1	2.21	0.40
3:R5:36:VAL:HG21	3:R5:45:LEU:HD22	2.03	0.40
3:S4:154:ASP:O	3:S4:183:ILE:HD11	2.21	0.40
3:S6:99:LEU:HD13	3:S6:122:ILE:HD13	2.02	0.40
5:V4:52:ASP:CG	5:V4:54:GLU:HG2	2.47	0.40
5:X1:106:VAL:HB	5:X1:216:PHE:CE1	2.56	0.40
6:Y4:245:LYS:HE3	6:Y4:245:LYS:HB3	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:b3:189:TYR:HB3	9:b3:211:ILE:CG1	2.36	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	A3	86/282 (30%)	83 (96%)	3 (4%)	0	100	100
1	A4	221/282 (78%)	216 (98%)	5 (2%)	0	100	100
1	A5	276/282 (98%)	270 (98%)	6 (2%)	0	100	100
1	A6	276/282 (98%)	271 (98%)	5 (2%)	0	100	100
1	A7	276/282 (98%)	269 (98%)	7 (2%)	0	100	100
1	A8	218/282 (77%)	215 (99%)	3 (1%)	0	100	100
1	B3	123/282 (44%)	121 (98%)	2 (2%)	0	100	100
1	B4	276/282 (98%)	266 (96%)	9 (3%)	1 (0%)	30	62
1	B5	277/282 (98%)	270 (98%)	7 (2%)	0	100	100
1	B6	277/282 (98%)	272 (98%)	5 (2%)	0	100	100
1	B7	259/282 (92%)	254 (98%)	5 (2%)	0	100	100
1	B8	172/282 (61%)	169 (98%)	3 (2%)	0	100	100
1	C2	64/282 (23%)	64 (100%)	0	0	100	100
1	C3	190/282 (67%)	185 (97%)	5 (3%)	0	100	100
1	C4	276/282 (98%)	270 (98%)	6 (2%)	0	100	100
1	C5	277/282 (98%)	271 (98%)	6 (2%)	0	100	100
1	C6	277/282 (98%)	272 (98%)	5 (2%)	0	100	100
1	C7	224/282 (79%)	221 (99%)	3 (1%)	0	100	100
1	C8	118/282 (42%)	116 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D2	110/282 (39%)	109 (99%)	1 (1%)	0	100	100
1	D3	256/282 (91%)	250 (98%)	6 (2%)	0	100	100
1	D4	276/282 (98%)	270 (98%)	6 (2%)	0	100	100
1	D5	276/282 (98%)	271 (98%)	5 (2%)	0	100	100
1	D6	262/282 (93%)	255 (97%)	7 (3%)	0	100	100
1	D7	177/282 (63%)	171 (97%)	6 (3%)	0	100	100
1	E1	56/282 (20%)	55 (98%)	1 (2%)	0	100	100
1	E2	176/282 (62%)	174 (99%)	2 (1%)	0	100	100
1	E3	276/282 (98%)	272 (99%)	4 (1%)	0	100	100
1	E4	276/282 (98%)	271 (98%)	5 (2%)	0	100	100
1	E5	276/282 (98%)	270 (98%)	6 (2%)	0	100	100
1	E6	231/282 (82%)	224 (97%)	7 (3%)	0	100	100
1	E7	123/282 (44%)	121 (98%)	2 (2%)	0	100	100
1	F1	104/282 (37%)	102 (98%)	2 (2%)	0	100	100
1	F2	243/282 (86%)	236 (97%)	7 (3%)	0	100	100
1	F3	277/282 (98%)	271 (98%)	6 (2%)	0	100	100
1	F4	276/282 (98%)	270 (98%)	6 (2%)	0	100	100
1	F5	266/282 (94%)	261 (98%)	5 (2%)	0	100	100
1	F6	181/282 (64%)	179 (99%)	2 (1%)	0	100	100
1	G1	236/282 (84%)	230 (98%)	6 (2%)	0	100	100
1	G2	131/282 (46%)	129 (98%)	2 (2%)	0	100	100
1	G5	51/282 (18%)	51 (100%)	0	0	100	100
1	G6	159/282 (56%)	154 (97%)	5 (3%)	0	100	100
1	G7	277/282 (98%)	270 (98%)	7 (2%)	0	100	100
1	G8	277/282 (98%)	271 (98%)	6 (2%)	0	100	100
1	G9	276/282 (98%)	271 (98%)	5 (2%)	0	100	100
1	H5	98/282 (35%)	98 (100%)	0	0	100	100
1	H6	234/282 (83%)	227 (97%)	7 (3%)	0	100	100
1	H7	276/282 (98%)	270 (98%)	5 (2%)	1 (0%)	30	62
1	H8	277/282 (98%)	272 (98%)	4 (1%)	1 (0%)	30	62
1	H9	272/282 (96%)	266 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I4	49/282 (17%)	49 (100%)	0	0	100	100
1	I5	153/282 (54%)	150 (98%)	3 (2%)	0	100	100
1	I6	280/282 (99%)	272 (97%)	8 (3%)	0	100	100
1	I7	276/282 (98%)	271 (98%)	5 (2%)	0	100	100
1	I8	276/282 (98%)	271 (98%)	5 (2%)	0	100	100
1	I9	242/282 (86%)	238 (98%)	4 (2%)	0	100	100
1	J4	97/282 (34%)	94 (97%)	3 (3%)	0	100	100
1	J5	230/282 (82%)	224 (97%)	6 (3%)	0	100	100
1	J6	276/282 (98%)	272 (99%)	4 (1%)	0	100	100
1	J7	276/282 (98%)	269 (98%)	7 (2%)	0	100	100
1	J8	269/282 (95%)	262 (97%)	6 (2%)	1 (0%)	30	62
1	J9	195/282 (69%)	192 (98%)	3 (2%)	0	100	100
1	K3	42/282 (15%)	41 (98%)	1 (2%)	0	100	100
1	K4	277/282 (98%)	271 (98%)	6 (2%)	0	100	100
1	K5	147/282 (52%)	143 (97%)	4 (3%)	0	100	100
1	K6	276/282 (98%)	271 (98%)	5 (2%)	0	100	100
1	K7	276/282 (98%)	270 (98%)	6 (2%)	0	100	100
1	K8	249/282 (88%)	245 (98%)	4 (2%)	0	100	100
1	h0	186/282 (66%)	183 (98%)	3 (2%)	0	100	100
1	i0	144/282 (51%)	143 (99%)	1 (1%)	0	100	100
2	L1	127/300 (42%)	124 (98%)	3 (2%)	0	100	100
2	L2	230/300 (77%)	228 (99%)	2 (1%)	0	100	100
2	L3	230/300 (77%)	229 (100%)	1 (0%)	0	100	100
2	L4	230/300 (77%)	226 (98%)	4 (2%)	0	100	100
2	L5	230/300 (77%)	228 (99%)	2 (1%)	0	100	100
2	M1	225/300 (75%)	223 (99%)	2 (1%)	0	100	100
2	M2	230/300 (77%)	224 (97%)	6 (3%)	0	100	100
2	M3	230/300 (77%)	224 (97%)	6 (3%)	0	100	100
2	M4	230/300 (77%)	227 (99%)	3 (1%)	0	100	100
2	M5	192/300 (64%)	189 (98%)	3 (2%)	0	100	100
2	N1	96/300 (32%)	92 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	N2	230/300 (77%)	226 (98%)	3 (1%)	1 (0%)	30	62
2	N3	230/300 (77%)	225 (98%)	5 (2%)	0	100	100
2	N4	230/300 (77%)	226 (98%)	4 (2%)	0	100	100
2	N5	230/300 (77%)	227 (99%)	3 (1%)	0	100	100
2	N6	138/300 (46%)	136 (99%)	1 (1%)	1 (1%)	18	51
2	O1	216/300 (72%)	211 (98%)	5 (2%)	0	100	100
2	O2	230/300 (77%)	225 (98%)	4 (2%)	1 (0%)	30	62
2	O3	230/300 (77%)	227 (99%)	3 (1%)	0	100	100
2	O4	230/300 (77%)	226 (98%)	4 (2%)	0	100	100
2	O5	192/300 (64%)	190 (99%)	2 (1%)	0	100	100
2	P1	82/300 (27%)	80 (98%)	2 (2%)	0	100	100
2	P2	230/300 (77%)	224 (97%)	6 (3%)	0	100	100
2	P3	230/300 (77%)	225 (98%)	5 (2%)	0	100	100
2	P4	235/300 (78%)	231 (98%)	4 (2%)	0	100	100
2	P5	235/300 (78%)	232 (99%)	3 (1%)	0	100	100
2	P6	159/300 (53%)	156 (98%)	3 (2%)	0	100	100
3	Q1	232/277 (84%)	227 (98%)	5 (2%)	0	100	100
3	Q2	232/277 (84%)	226 (97%)	6 (3%)	0	100	100
3	Q3	232/277 (84%)	224 (97%)	8 (3%)	0	100	100
3	Q4	232/277 (84%)	228 (98%)	4 (2%)	0	100	100
3	R1	196/277 (71%)	189 (96%)	7 (4%)	0	100	100
3	R2	232/277 (84%)	223 (96%)	9 (4%)	0	100	100
3	R3	232/277 (84%)	225 (97%)	7 (3%)	0	100	100
3	R4	232/277 (84%)	227 (98%)	5 (2%)	0	100	100
3	R5	232/277 (84%)	227 (98%)	5 (2%)	0	100	100
3	S2	229/277 (83%)	225 (98%)	4 (2%)	0	100	100
3	S3	232/277 (84%)	225 (97%)	7 (3%)	0	100	100
3	S4	232/277 (84%)	225 (97%)	7 (3%)	0	100	100
3	S5	232/277 (84%)	218 (94%)	13 (6%)	1 (0%)	30	62
3	S6	167/277 (60%)	162 (97%)	5 (3%)	0	100	100
4	U3	251/321 (78%)	251 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	U4	251/321 (78%)	251 (100%)	0	0	100	100
4	U5	251/321 (78%)	250 (100%)	1 (0%)	0	100	100
4	U6	251/321 (78%)	250 (100%)	1 (0%)	0	100	100
5	V0	120/241 (50%)	112 (93%)	8 (7%)	0	100	100
5	V1	186/241 (77%)	172 (92%)	13 (7%)	1 (0%)	24	57
5	V2	186/241 (77%)	171 (92%)	14 (8%)	1 (0%)	24	57
5	V3	185/241 (77%)	171 (92%)	13 (7%)	1 (0%)	24	57
5	V4	186/241 (77%)	178 (96%)	7 (4%)	1 (0%)	24	57
5	X0	148/241 (61%)	139 (94%)	9 (6%)	0	100	100
5	X1	185/241 (77%)	177 (96%)	8 (4%)	0	100	100
5	X2	185/241 (77%)	171 (92%)	14 (8%)	0	100	100
5	X3	186/241 (77%)	178 (96%)	7 (4%)	1 (0%)	24	57
5	X4	186/241 (77%)	173 (93%)	13 (7%)	0	100	100
6	Y1	203/284 (72%)	192 (95%)	11 (5%)	0	100	100
6	Y2	213/284 (75%)	203 (95%)	9 (4%)	1 (0%)	24	57
6	Y3	225/284 (79%)	220 (98%)	4 (2%)	1 (0%)	30	62
6	Y4	219/284 (77%)	206 (94%)	13 (6%)	0	100	100
7	Z0	262/367 (71%)	253 (97%)	9 (3%)	0	100	100
7	Z1	293/367 (80%)	280 (96%)	13 (4%)	0	100	100
7	Z2	269/367 (73%)	258 (96%)	11 (4%)	0	100	100
7	Za	240/367 (65%)	237 (99%)	3 (1%)	0	100	100
8	a1	160/239 (67%)	155 (97%)	5 (3%)	0	100	100
8	a2	192/239 (80%)	189 (98%)	3 (2%)	0	100	100
8	a3	183/239 (77%)	178 (97%)	5 (3%)	0	100	100
8	a4	187/239 (78%)	180 (96%)	7 (4%)	0	100	100
8	a5	193/239 (81%)	189 (98%)	4 (2%)	0	100	100
9	b2	236/269 (88%)	228 (97%)	8 (3%)	0	100	100
9	b3	236/269 (88%)	223 (94%)	13 (6%)	0	100	100
9	b4	236/269 (88%)	229 (97%)	7 (3%)	0	100	100
10	c1	115/175 (66%)	112 (97%)	3 (3%)	0	100	100
10	c2	115/175 (66%)	112 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	c3	116/175 (66%)	113 (97%)	3 (3%)	0	100	100
All	All	30432/40543 (75%)	29680 (98%)	737 (2%)	15 (0%)	100	100

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H7	181	LEU
6	Y2	250	LEU
1	B4	145	PRO
3	S5	164	ASP
5	V1	193	ASP
5	V3	193	ASP
5	X3	193	ASP
2	N2	224	ASP
2	O2	224	ASP
5	V2	193	ASP
6	Y3	21	ASP
2	N6	262	ALA
1	H8	181	LEU
1	J8	181	LEU
5	V4	237	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	A3	77/234 (33%)	74 (96%)	3 (4%)	28	54
1	A4	185/234 (79%)	183 (99%)	2 (1%)	65	74
1	A5	232/234 (99%)	220 (95%)	12 (5%)	21	47
1	A6	232/234 (99%)	229 (99%)	3 (1%)	61	72
1	A7	232/234 (99%)	225 (97%)	7 (3%)	36	60
1	A8	178/234 (76%)	174 (98%)	4 (2%)	45	65
1	B3	103/234 (44%)	101 (98%)	2 (2%)	50	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B4	232/234 (99%)	225 (97%)	7 (3%)	36	60
1	B5	233/234 (100%)	220 (94%)	13 (6%)	19	46
1	B6	233/234 (100%)	225 (97%)	8 (3%)	32	57
1	B7	214/234 (92%)	210 (98%)	4 (2%)	50	68
1	B8	142/234 (61%)	139 (98%)	3 (2%)	47	66
1	C2	61/234 (26%)	61 (100%)	0	100	100
1	C3	159/234 (68%)	156 (98%)	3 (2%)	50	68
1	C4	232/234 (99%)	215 (93%)	17 (7%)	13	38
1	C5	233/234 (100%)	224 (96%)	9 (4%)	28	54
1	C6	233/234 (100%)	228 (98%)	5 (2%)	47	66
1	C7	187/234 (80%)	184 (98%)	3 (2%)	55	70
1	C8	102/234 (44%)	97 (95%)	5 (5%)	22	48
1	D2	96/234 (41%)	93 (97%)	3 (3%)	35	59
1	D3	220/234 (94%)	214 (97%)	6 (3%)	39	62
1	D4	232/234 (99%)	228 (98%)	4 (2%)	53	70
1	D5	232/234 (99%)	226 (97%)	6 (3%)	40	62
1	D6	218/234 (93%)	210 (96%)	8 (4%)	30	56
1	D7	146/234 (62%)	145 (99%)	1 (1%)	76	78
1	E1	52/234 (22%)	52 (100%)	0	100	100
1	E2	147/234 (63%)	140 (95%)	7 (5%)	23	49
1	E3	232/234 (99%)	222 (96%)	10 (4%)	26	51
1	E4	232/234 (99%)	222 (96%)	10 (4%)	26	51
1	E5	232/234 (99%)	222 (96%)	10 (4%)	26	51
1	E6	193/234 (82%)	193 (100%)	0	100	100
1	E7	104/234 (44%)	98 (94%)	6 (6%)	18	44
1	F1	90/234 (38%)	84 (93%)	6 (7%)	15	41
1	F2	207/234 (88%)	201 (97%)	6 (3%)	37	60
1	F3	233/234 (100%)	225 (97%)	8 (3%)	32	57
1	F4	232/234 (99%)	227 (98%)	5 (2%)	45	65
1	F5	222/234 (95%)	215 (97%)	7 (3%)	34	59
1	F6	149/234 (64%)	148 (99%)	1 (1%)	76	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G1	198/234 (85%)	188 (95%)	10 (5%)	21	48
1	G2	112/234 (48%)	109 (97%)	3 (3%)	39	62
1	G5	47/234 (20%)	47 (100%)	0	100	100
1	G6	139/234 (59%)	137 (99%)	2 (1%)	59	71
1	G7	233/234 (100%)	230 (99%)	3 (1%)	61	72
1	G8	233/234 (100%)	227 (97%)	6 (3%)	40	62
1	G9	232/234 (99%)	226 (97%)	6 (3%)	40	62
1	H5	87/234 (37%)	86 (99%)	1 (1%)	65	74
1	H6	202/234 (86%)	190 (94%)	12 (6%)	18	44
1	H7	232/234 (99%)	213 (92%)	19 (8%)	10	34
1	H8	233/234 (100%)	223 (96%)	10 (4%)	26	51
1	H9	228/234 (97%)	218 (96%)	10 (4%)	25	51
1	I4	45/234 (19%)	44 (98%)	1 (2%)	45	65
1	I5	133/234 (57%)	129 (97%)	4 (3%)	36	60
1	I6	234/234 (100%)	226 (97%)	8 (3%)	32	57
1	I7	232/234 (99%)	222 (96%)	10 (4%)	26	51
1	I8	232/234 (99%)	223 (96%)	9 (4%)	28	54
1	I9	203/234 (87%)	194 (96%)	9 (4%)	25	51
1	J4	86/234 (37%)	81 (94%)	5 (6%)	18	44
1	J5	194/234 (83%)	188 (97%)	6 (3%)	35	59
1	J6	232/234 (99%)	224 (97%)	8 (3%)	32	57
1	J7	232/234 (99%)	228 (98%)	4 (2%)	53	70
1	J8	225/234 (96%)	216 (96%)	9 (4%)	28	54
1	J9	163/234 (70%)	158 (97%)	5 (3%)	35	59
1	K3	39/234 (17%)	37 (95%)	2 (5%)	21	48
1	K4	233/234 (100%)	224 (96%)	9 (4%)	28	54
1	K5	129/234 (55%)	126 (98%)	3 (2%)	44	64
1	K6	232/234 (99%)	220 (95%)	12 (5%)	21	47
1	K7	232/234 (99%)	227 (98%)	5 (2%)	45	65
1	K8	208/234 (89%)	202 (97%)	6 (3%)	37	60
1	h0	156/234 (67%)	152 (97%)	4 (3%)	40	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	i0	123/234 (53%)	122 (99%)	1 (1%)	73	77
2	L1	115/275 (42%)	113 (98%)	2 (2%)	53	70
2	L2	204/275 (74%)	194 (95%)	10 (5%)	22	48
2	L3	204/275 (74%)	196 (96%)	8 (4%)	28	54
2	L4	204/275 (74%)	197 (97%)	7 (3%)	32	57
2	L5	204/275 (74%)	196 (96%)	8 (4%)	28	54
2	M1	201/275 (73%)	195 (97%)	6 (3%)	36	60
2	M2	204/275 (74%)	197 (97%)	7 (3%)	32	57
2	M3	204/275 (74%)	196 (96%)	8 (4%)	28	54
2	M4	204/275 (74%)	198 (97%)	6 (3%)	37	60
2	M5	171/275 (62%)	169 (99%)	2 (1%)	63	73
2	N1	91/275 (33%)	89 (98%)	2 (2%)	45	65
2	N2	204/275 (74%)	194 (95%)	10 (5%)	22	48
2	N3	204/275 (74%)	198 (97%)	6 (3%)	37	60
2	N4	204/275 (74%)	196 (96%)	8 (4%)	28	54
2	N5	204/275 (74%)	198 (97%)	6 (3%)	37	60
2	N6	121/275 (44%)	118 (98%)	3 (2%)	42	63
2	O1	192/275 (70%)	185 (96%)	7 (4%)	31	57
2	O2	202/275 (74%)	193 (96%)	9 (4%)	24	50
2	O3	203/275 (74%)	197 (97%)	6 (3%)	36	60
2	O4	203/275 (74%)	197 (97%)	6 (3%)	36	60
2	O5	171/275 (62%)	164 (96%)	7 (4%)	27	53
2	P1	77/275 (28%)	77 (100%)	0	100	100
2	P2	204/275 (74%)	193 (95%)	11 (5%)	20	46
2	P3	204/275 (74%)	195 (96%)	9 (4%)	25	51
2	P4	206/275 (75%)	201 (98%)	5 (2%)	43	64
2	P5	206/275 (75%)	201 (98%)	5 (2%)	43	64
2	P6	138/275 (50%)	133 (96%)	5 (4%)	31	57
3	Q1	214/248 (86%)	207 (97%)	7 (3%)	33	58
3	Q2	214/248 (86%)	209 (98%)	5 (2%)	44	64
3	Q3	214/248 (86%)	209 (98%)	5 (2%)	44	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Q4	214/248 (86%)	208 (97%)	6 (3%)	38	61
3	R1	184/248 (74%)	179 (97%)	5 (3%)	39	62
3	R2	214/248 (86%)	205 (96%)	9 (4%)	26	52
3	R3	214/248 (86%)	208 (97%)	6 (3%)	38	61
3	R4	214/248 (86%)	204 (95%)	10 (5%)	23	49
3	R5	214/248 (86%)	206 (96%)	8 (4%)	30	56
3	S2	210/248 (85%)	204 (97%)	6 (3%)	37	60
3	S3	213/248 (86%)	208 (98%)	5 (2%)	44	64
3	S4	214/248 (86%)	210 (98%)	4 (2%)	50	68
3	S5	214/248 (86%)	201 (94%)	13 (6%)	17	43
3	S6	155/248 (62%)	151 (97%)	4 (3%)	40	62
4	U3	226/285 (79%)	217 (96%)	9 (4%)	28	54
4	U4	226/285 (79%)	219 (97%)	7 (3%)	35	59
4	U5	226/285 (79%)	222 (98%)	4 (2%)	51	69
4	U6	226/285 (79%)	220 (97%)	6 (3%)	39	62
5	V0	6/209 (3%)	6 (100%)	0	100	100
5	V1	170/209 (81%)	166 (98%)	4 (2%)	43	64
5	V2	170/209 (81%)	162 (95%)	8 (5%)	23	49
5	V3	169/209 (81%)	163 (96%)	6 (4%)	31	57
5	V4	169/209 (81%)	162 (96%)	7 (4%)	27	53
5	X0	8/209 (4%)	8 (100%)	0	100	100
5	X1	169/209 (81%)	162 (96%)	7 (4%)	27	53
5	X2	169/209 (81%)	162 (96%)	7 (4%)	27	53
5	X3	170/209 (81%)	160 (94%)	10 (6%)	18	44
5	X4	170/209 (81%)	168 (99%)	2 (1%)	63	73
6	Y1	197/254 (78%)	184 (93%)	13 (7%)	15	41
6	Y2	208/254 (82%)	198 (95%)	10 (5%)	23	49
6	Y3	216/254 (85%)	208 (96%)	8 (4%)	30	56
6	Y4	211/254 (83%)	192 (91%)	19 (9%)	9	32
7	Z0	241/325 (74%)	238 (99%)	3 (1%)	63	73
7	Z1	270/325 (83%)	264 (98%)	6 (2%)	45	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	Z2	247/325 (76%)	245 (99%)	2 (1%)	73	77
7	Za	224/325 (69%)	220 (98%)	4 (2%)	51	69
8	a1	150/209 (72%)	147 (98%)	3 (2%)	48	67
8	a2	178/209 (85%)	170 (96%)	8 (4%)	24	50
8	a3	172/209 (82%)	166 (96%)	6 (4%)	32	57
8	a4	176/209 (84%)	172 (98%)	4 (2%)	44	64
8	a5	179/209 (86%)	172 (96%)	7 (4%)	28	54
9	b2	12/242 (5%)	12 (100%)	0	100	100
9	b3	215/242 (89%)	211 (98%)	4 (2%)	50	68
9	b4	215/242 (89%)	206 (96%)	9 (4%)	26	52
10	c1	4/166 (2%)	4 (100%)	0	100	100
10	c2	113/166 (68%)	111 (98%)	2 (2%)	51	69
10	c3	114/166 (69%)	113 (99%)	1 (1%)	70	76
All	All	26175/35092 (75%)	25311 (97%)	864 (3%)	34	58

All (864) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A3	36	ILE
1	A3	48	VAL
1	A3	246	MET
1	A4	1	MET
1	A4	249	GLN
1	A5	1	MET
1	A5	10	ILE
1	A5	15	THR
1	A5	34	MET
1	A5	101	ILE
1	A5	114	VAL
1	A5	129	GLU
1	A5	133	MET
1	A5	166	GLU
1	A5	170	THR
1	A5	266	MET
1	A5	278	MET
1	A6	8	SER
1	A6	101	ILE

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Mol	Chain	Res	Type
1	A6	194	SER
1	A7	2	ILE
1	A7	8	SER
1	A7	48	VAL
1	A7	212	ASP
1	A7	255	ARG
1	A7	269	GLN
1	A7	278	MET
1	A8	121	ILE
1	A8	136	LEU
1	A8	168	MET
1	A8	205	VAL
1	B3	55	GLN
1	B3	264	THR
1	B4	7	VAL
1	B4	133	MET
1	B4	163	VAL
1	B4	198	LEU
1	B4	239	SER
1	B4	266	MET
1	B4	274	SER
1	B5	29	LYS
1	B5	72	LEU
1	B5	77	GLU
1	B5	101	ILE
1	B5	110	ILE
1	B5	133	MET
1	B5	153	ILE
1	B5	232	GLU
1	B5	238	GLU
1	B5	273	LYS
1	B5	274	SER
1	B5	278	MET
1	B5	281	LEU
1	B6	24	SER
1	B6	44	SER
1	B6	48	VAL
1	B6	127	GLN
1	B6	160	ARG
1	B6	217	TYR
1	B6	227	LEU
1	B6	267	LEU

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Mol	Chain	Res	Type
1	B7	67	GLU
1	B7	112	VAL
1	B7	123	ARG
1	B7	183	PHE
1	B8	77	GLU
1	B8	170	THR
1	B8	220	MET
1	C3	3	ILE
1	C3	67	GLU
1	C3	278	MET
1	C4	15	THR
1	C4	18	SER
1	C4	24	SER
1	C4	52	MET
1	C4	56	ILE
1	C4	60	ARG
1	C4	75	THR
1	C4	77	GLU
1	C4	106	ASP
1	C4	110	ILE
1	C4	112	VAL
1	C4	135	LEU
1	C4	136	LEU
1	C4	168	MET
1	C4	200	ASP
1	C4	267	LEU
1	C4	277	VAL
1	C5	3	ILE
1	C5	24	SER
1	C5	49	SER
1	C5	75	THR
1	C5	101	ILE
1	C5	111	GLN
1	C5	112	VAL
1	C5	136	LEU
1	C5	277	VAL
1	C6	77	GLU
1	C6	101	ILE
1	C6	137	THR
1	C6	168	MET
1	C6	206	ILE
1	C7	71	SER

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Mol	Chain	Res	Type
1	C7	112	VAL
1	C7	206	ILE
1	C8	77	GLU
1	C8	93	LEU
1	C8	101	ILE
1	C8	113	GLU
1	C8	198	LEU
1	D2	3	ILE
1	D2	26	ASP
1	D2	250	MET
1	D3	3	ILE
1	D3	54	THR
1	D3	60	ARG
1	D3	92	VAL
1	D3	115	SER
1	D3	183	PHE
1	D4	101	ILE
1	D4	122	ASP
1	D4	179	THR
1	D4	183	PHE
1	D5	25	LYS
1	D5	74	GLN
1	D5	101	ILE
1	D5	124	ILE
1	D5	167	THR
1	D5	200	ASP
1	D6	54	THR
1	D6	63	GLU
1	D6	112	VAL
1	D6	132	LYS
1	D6	149	MET
1	D6	167	THR
1	D6	184	ILE
1	D6	257	GLN
1	D7	114	VAL
1	E2	2	ILE
1	E2	26	ASP
1	E2	133	MET
1	E2	239	SER
1	E2	258	ILE
1	E2	269	GLN
1	E2	282	GLN

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Mol	Chain	Res	Type
1	E3	1	MET
1	E3	2	ILE
1	E3	51	LYS
1	E3	87	VAL
1	E3	92	VAL
1	E3	101	ILE
1	E3	183	PHE
1	E3	184	ILE
1	E3	207	SER
1	E3	239	SER
1	E4	15	THR
1	E4	20	ASP
1	E4	28	GLU
1	E4	31	SER
1	E4	44	SER
1	E4	101	ILE
1	E4	137	THR
1	E4	183	PHE
1	E4	200	ASP
1	E4	219	ARG
1	E5	8	SER
1	E5	54	THR
1	E5	90	VAL
1	E5	156	ASN
1	E5	167	THR
1	E5	180	VAL
1	E5	194	SER
1	E5	200	ASP
1	E5	207	SER
1	E5	239	SER
1	E7	85	GLU
1	E7	88	GLN
1	E7	101	ILE
1	E7	137	THR
1	E7	184	ILE
1	E7	200	ASP
1	F1	20	ASP
1	F1	27	ILE
1	F1	46	LEU
1	F1	50	GLU
1	F1	277	VAL
1	F1	282	GLN

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Mol	Chain	Res	Type
1	F2	54	THR
1	F2	77	GLU
1	F2	83	THR
1	F2	84	HIS
1	F2	133	MET
1	F2	168	MET
1	F3	83	THR
1	F3	101	ILE
1	F3	110	ILE
1	F3	124	ILE
1	F3	126	SER
1	F3	184	ILE
1	F3	188	THR
1	F3	221	GLU
1	F4	85	GLU
1	F4	135	LEU
1	F4	143	LEU
1	F4	163	VAL
1	F4	168	MET
1	F5	16	LEU
1	F5	28	GLU
1	F5	71	SER
1	F5	90	VAL
1	F5	149	MET
1	F5	157	MET
1	F5	163	VAL
1	F6	101	ILE
1	G1	28	GLU
1	G1	52	MET
1	G1	54	THR
1	G1	80	LEU
1	G1	101	ILE
1	G1	137	THR
1	G1	170	THR
1	G1	194	SER
1	G1	219	ARG
1	G1	249	GLN
1	G2	81	GLN
1	G2	101	ILE
1	G2	220	MET
1	G6	59	LEU
1	G6	133	MET

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Mol	Chain	Res	Type
1	G7	8	SER
1	G7	198	LEU
1	G7	219	ARG
1	G8	8	SER
1	G8	24	SER
1	G8	101	ILE
1	G8	200	ASP
1	G8	232	GLU
1	G8	234	THR
1	G9	4	ASN
1	G9	28	GLU
1	G9	38	LYS
1	G9	54	THR
1	G9	101	ILE
1	G9	250	MET
1	H5	27	ILE
1	H6	1	MET
1	H6	3	ILE
1	H6	20	ASP
1	H6	52	MET
1	H6	66	THR
1	H6	83	THR
1	H6	124	ILE
1	H6	136	LEU
1	H6	232	GLU
1	H6	244	THR
1	H6	246	MET
1	H6	255	ARG
1	H7	15	THR
1	H7	16	LEU
1	H7	36	ILE
1	H7	48	VAL
1	H7	101	ILE
1	H7	119	ASP
1	H7	133	MET
1	H7	157	MET
1	H7	181	LEU
1	H7	183	PHE
1	H7	184	ILE
1	H7	220	MET
1	H7	232	GLU
1	H7	239	SER

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Mol	Chain	Res	Type
1	H7	245	ASP
1	H7	255	ARG
1	H7	266	MET
1	H7	273	LYS
1	H7	274	SER
1	H8	32	SER
1	H8	34	MET
1	H8	51	LYS
1	H8	54	THR
1	H8	82	GLU
1	H8	181	LEU
1	H8	220	MET
1	H8	249	GLN
1	H8	274	SER
1	H8	280	LEU
1	H9	28	GLU
1	H9	38	LYS
1	H9	70	MET
1	H9	71	SER
1	H9	115	SER
1	H9	219	ARG
1	H9	239	SER
1	H9	250	MET
1	H9	252	SER
1	H9	277	VAL
1	I4	273	LYS
1	I5	16	LEU
1	I5	54	THR
1	I5	228	MET
1	I5	242	ARG
1	I6	7	VAL
1	I6	80	LEU
1	I6	81	GLN
1	I6	117	LEU
1	I6	153	ILE
1	I6	205	VAL
1	I6	220	MET
1	I6	227	LEU
1	I7	54	THR
1	I7	66	THR
1	I7	101	ILE
1	I7	120	GLU

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Mol	Chain	Res	Type
1	I7	129	GLU
1	I7	153	ILE
1	I7	163	VAL
1	I7	183	PHE
1	I7	213	LEU
1	I7	282	GLN
1	I8	10	ILE
1	I8	44	SER
1	I8	48	VAL
1	I8	54	THR
1	I8	101	ILE
1	I8	153	ILE
1	I8	167	THR
1	I8	213	LEU
1	I8	277	VAL
1	I9	25	LYS
1	I9	101	ILE
1	I9	122	ASP
1	I9	129	GLU
1	I9	136	LEU
1	I9	183	PHE
1	I9	198	LEU
1	I9	213	LEU
1	I9	234	THR
1	J4	3	ILE
1	J4	7	VAL
1	J4	10	ILE
1	J4	20	ASP
1	J4	28	GLU
1	J5	15	THR
1	J5	28	GLU
1	J5	35	ARG
1	J5	38	LYS
1	J5	48	VAL
1	J5	228	MET
1	J6	1	MET
1	J6	24	SER
1	J6	25	LYS
1	J6	103	SER
1	J6	118	VAL
1	J6	133	MET
1	J6	206	ILE

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Mol	Chain	Res	Type
1	J6	225	LYS
1	J7	80	LEU
1	J7	118	VAL
1	J7	220	MET
1	J7	239	SER
1	J8	32	SER
1	J8	37	ASN
1	J8	48	VAL
1	J8	67	GLU
1	J8	80	LEU
1	J8	101	ILE
1	J8	106	ASP
1	J8	143	LEU
1	J8	220	MET
1	J9	90	VAL
1	J9	101	ILE
1	J9	124	ILE
1	J9	127	GLN
1	J9	158	HIS
1	K3	2	ILE
1	K3	274	SER
1	K4	63	GLU
1	K4	86	ILE
1	K4	92	VAL
1	K4	135	LEU
1	K4	184	ILE
1	K4	249	GLN
1	K4	252	SER
1	K4	277	VAL
1	K4	281	LEU
1	K5	8	SER
1	K5	161	GLU
1	K5	281	LEU
1	K6	1	MET
1	K6	8	SER
1	K6	31	SER
1	K6	101	ILE
1	K6	134	LYS
1	K6	135	LEU
1	K6	166	GLU
1	K6	203	LEU
1	K6	244	THR

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Mol	Chain	Res	Type
1	K6	250	MET
1	K6	252	SER
1	K6	277	VAL
1	K7	28	GLU
1	K7	101	ILE
1	K7	136	LEU
1	K7	239	SER
1	K7	240	ARG
1	K8	83	THR
1	K8	117	LEU
1	K8	136	LEU
1	K8	167	THR
1	K8	219	ARG
1	K8	237	SER
2	L1	185	GLU
2	L1	201	ILE
2	L2	88	LEU
2	L2	105	SER
2	L2	136	GLU
2	L2	173	ASN
2	L2	175	LEU
2	L2	190	LYS
2	L2	204	GLU
2	L2	223	ILE
2	L2	243	GLU
2	L2	268	LEU
2	L3	86	GLN
2	L3	87	GLU
2	L3	91	LEU
2	L3	94	THR
2	L3	104	LEU
2	L3	202	MET
2	L3	230	TYR
2	L3	248	LYS
2	L4	77	ASP
2	L4	94	THR
2	L4	128	GLU
2	L4	207	LEU
2	L4	222	GLU
2	L4	238	SER
2	L4	264	LYS
2	L5	177	GLU

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Mol	Chain	Res	Type
2	L5	199	SER
2	L5	202	MET
2	L5	212	GLN
2	L5	214	ILE
2	L5	236	LEU
2	L5	256	MET
2	L5	266	VAL
2	M1	91	LEU
2	M1	143	VAL
2	M1	145	ARG
2	M1	178	ILE
2	M1	217	LEU
2	M1	227	GLU
2	M2	56	THR
2	M2	105	SER
2	M2	113	THR
2	M2	190	LYS
2	M2	227	GLU
2	M2	230	TYR
2	M2	288	ASN
2	M3	79	LYS
2	M3	93	LYS
2	M3	115	MET
2	M3	229	GLU
2	M3	230	TYR
2	M3	241	SER
2	M3	254	ASP
2	M3	258	PHE
2	M4	105	SER
2	M4	156	GLU
2	M4	172	ILE
2	M4	178	ILE
2	M4	224	ASP
2	M4	230	TYR
2	M5	230	TYR
2	M5	289	VAL
2	N1	69	GLN
2	N1	88	LEU
2	N2	88	LEU
2	N2	91	LEU
2	N2	105	SER
2	N2	149	GLU

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Mol	Chain	Res	Type
2	N2	158	MET
2	N2	169	SER
2	N2	216	ILE
2	N2	230	TYR
2	N2	238	SER
2	N2	274	LEU
2	N3	88	LEU
2	N3	89	HIS
2	N3	91	LEU
2	N3	172	ILE
2	N3	208	GLN
2	N3	230	TYR
2	N4	93	LYS
2	N4	109	SER
2	N4	169	SER
2	N4	172	ILE
2	N4	185	GLU
2	N4	196	VAL
2	N4	230	TYR
2	N4	280	SER
2	N5	92	SER
2	N5	115	MET
2	N5	116	LYS
2	N5	206	ASP
2	N5	216	ILE
2	N5	230	TYR
2	N6	315	LEU
2	N6	328	TYR
2	N6	336	SER
2	O1	117	ASN
2	O1	145	ARG
2	O1	176	ASP
2	O1	213	THR
2	O1	230	TYR
2	O1	247	ILE
2	O1	274	LEU
2	O2	88	LEU
2	O2	91	LEU
2	O2	102	LEU
2	O2	126	LYS
2	O2	133	ARG
2	O2	145	ARG

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Mol	Chain	Res	Type
2	O2	169	SER
2	O2	230	TYR
2	O2	246	MET
2	O3	137	LYS
2	O3	199	SER
2	O3	207	LEU
2	O3	230	TYR
2	O3	244	GLU
2	O3	251	LYS
2	O4	114	ILE
2	O4	130	GLU
2	O4	177	GLU
2	O4	199	SER
2	O4	219	LEU
2	O4	230	TYR
2	O5	136	GLU
2	O5	169	SER
2	O5	178	ILE
2	O5	213	THR
2	O5	230	TYR
2	O5	247	ILE
2	O5	287	VAL
2	P2	84	THR
2	P2	91	LEU
2	P2	111	VAL
2	P2	140	TRP
2	P2	201	ILE
2	P2	223	ILE
2	P2	230	TYR
2	P2	238	SER
2	P2	242	PHE
2	P2	261	ARG
2	P2	270	ARG
2	P3	88	LEU
2	P3	128	GLU
2	P3	169	SER
2	P3	185	GLU
2	P3	201	ILE
2	P3	207	LEU
2	P3	213	THR
2	P3	219	LEU
2	P3	230	TYR

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Mol	Chain	Res	Type
2	P4	88	LEU
2	P4	93	LYS
2	P4	148	ARG
2	P4	230	TYR
2	P4	244	GLU
2	P5	136	GLU
2	P5	209	ASN
2	P5	241	SER
2	P5	272	THR
2	P5	273	GLU
2	P6	149	GLU
2	P6	161	LYS
2	P6	201	ILE
2	P6	207	LEU
2	P6	236	LEU
3	Q1	29	THR
3	Q1	62	LYS
3	Q1	117	ARG
3	Q1	131	PHE
3	Q1	185	SER
3	Q1	195	ILE
3	Q1	235	GLU
3	Q2	7	MET
3	Q2	9	ASP
3	Q2	154	ASP
3	Q2	196	ARG
3	Q2	220	ASP
3	Q3	69	THR
3	Q3	110	ASP
3	Q3	122	ILE
3	Q3	164	ASP
3	Q3	195	ILE
3	Q4	132	LEU
3	Q4	147	ASN
3	Q4	164	ASP
3	Q4	165	TYR
3	Q4	176	GLU
3	Q4	187	VAL
3	R1	16	ASP
3	R1	42	LYS
3	R1	75	VAL
3	R1	183	ILE

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Mol	Chain	Res	Type
3	R1	212	ASP
3	R2	29	THR
3	R2	34	MET
3	R2	69	THR
3	R2	102	GLU
3	R2	123	ARG
3	R2	137	VAL
3	R2	140	VAL
3	R2	216	THR
3	R2	220	ASP
3	R3	14	LEU
3	R3	87	SER
3	R3	110	ASP
3	R3	125	TYR
3	R3	130	ASN
3	R3	144	VAL
3	R4	23	LYS
3	R4	27	LEU
3	R4	63	GLN
3	R4	69	THR
3	R4	79	VAL
3	R4	102	GLU
3	R4	138	ILE
3	R4	144	VAL
3	R4	209	ASP
3	R4	229	HIS
3	R5	27	LEU
3	R5	31	LEU
3	R5	102	GLU
3	R5	137	VAL
3	R5	154	ASP
3	R5	168	TRP
3	R5	182	TYR
3	R5	183	ILE
3	S2	18	ILE
3	S2	39	LEU
3	S2	168	TRP
3	S2	170	THR
3	S2	185	SER
3	S2	238	LYS
3	S3	70	CYS
3	S3	77	ASP

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Mol	Chain	Res	Type
3	S3	93	LYS
3	S3	112	ARG
3	S3	124	THR
3	S4	79	VAL
3	S4	133	LEU
3	S4	140	VAL
3	S4	168	TRP
3	S5	25	LEU
3	S5	31	LEU
3	S5	38	THR
3	S5	46	TYR
3	S5	66	GLN
3	S5	124	THR
3	S5	126	ILE
3	S5	128	GLN
3	S5	132	LEU
3	S5	140	VAL
3	S5	153	ASN
3	S5	198	ASN
3	S5	241	LEU
3	S6	34	MET
3	S6	122	ILE
3	S6	124	THR
3	S6	241	LEU
4	U3	45	SER
4	U3	91	TYR
4	U3	98	TYR
4	U3	145	LYS
4	U3	155	LEU
4	U3	160	ASP
4	U3	195	ILE
4	U3	219	LEU
4	U3	276	THR
4	U4	89	MET
4	U4	93	GLN
4	U4	148	LEU
4	U4	169	SER
4	U4	211	TYR
4	U4	213	TYR
4	U4	294	GLU
4	U5	24	LEU
4	U5	85	PHE

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Mol	Chain	Res	Type
4	U5	213	TYR
4	U5	251	VAL
4	U6	135	THR
4	U6	163	THR
4	U6	166	LEU
4	U6	195	ILE
4	U6	219	LEU
4	U6	279	LYS
5	V1	81	ILE
5	V1	192	LEU
5	V1	202	PHE
5	V1	236	GLU
5	V2	49	VAL
5	V2	58	ASP
5	V2	61	VAL
5	V2	65	THR
5	V2	121	TYR
5	V2	169	PHE
5	V2	192	LEU
5	V2	219	ASP
5	V3	77	GLN
5	V3	90	VAL
5	V3	127	ILE
5	V3	175	LEU
5	V3	195	ASN
5	V3	218	VAL
5	V4	75	LEU
5	V4	76	VAL
5	V4	116	ASP
5	V4	127	ILE
5	V4	170	PHE
5	V4	192	LEU
5	V4	207	VAL
5	X1	48	ILE
5	X1	107	LYS
5	X1	117	ARG
5	X1	142	ARG
5	X1	162	ILE
5	X1	235	SER
5	X1	236	GLU
5	X2	125	GLU
5	X2	127	ILE

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Mol	Chain	Res	Type
5	X2	183	ILE
5	X2	199	VAL
5	X2	205	SER
5	X2	216	PHE
5	X2	220	ASP
5	X3	50	LEU
5	X3	89	THR
5	X3	127	ILE
5	X3	142	ARG
5	X3	153	ARG
5	X3	172	TRP
5	X3	210	VAL
5	X3	213	ASP
5	X3	219	ASP
5	X3	239	ASP
5	X4	116	ASP
5	X4	236	GLU
6	Y1	48	LYS
6	Y1	62	VAL
6	Y1	65	ASP
6	Y1	69	SER
6	Y1	73	LEU
6	Y1	79	ASP
6	Y1	81	VAL
6	Y1	108	PHE
6	Y1	154	VAL
6	Y1	213	LYS
6	Y1	224	THR
6	Y1	236	VAL
6	Y1	251	LEU
6	Y2	25	LEU
6	Y2	35	LYS
6	Y2	37	VAL
6	Y2	46	THR
6	Y2	50	GLU
6	Y2	52	LEU
6	Y2	80	ARG
6	Y2	202	LEU
6	Y2	243	THR
6	Y2	253	ARG
6	Y3	23	TYR
6	Y3	38	THR

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Mol	Chain	Res	Type
6	Y3	56	VAL
6	Y3	73	LEU
6	Y3	84	ASP
6	Y3	170	LEU
6	Y3	236	VAL
6	Y3	259	SER
6	Y4	23	TYR
6	Y4	34	LEU
6	Y4	45	ASP
6	Y4	52	LEU
6	Y4	53	ASP
6	Y4	66	HIS
6	Y4	79	ASP
6	Y4	81	VAL
6	Y4	101	LYS
6	Y4	107	TYR
6	Y4	111	ILE
6	Y4	134	MET
6	Y4	143	GLU
6	Y4	148	GLU
6	Y4	153	GLU
6	Y4	225	GLN
6	Y4	227	ARG
6	Y4	236	VAL
6	Y4	263	ILE
7	Z0	40	LEU
7	Z0	95	SER
7	Z0	195	ASN
7	Z1	24	ILE
7	Z1	65	LEU
7	Z1	172	MET
7	Z1	197	GLU
7	Z1	269	ASP
7	Z1	271	VAL
7	Z2	24	ILE
7	Z2	98	TYR
7	Za	69	PHE
7	Za	98	TYR
7	Za	141	MET
7	Za	165	LYS
8	a1	97	LEU
8	a1	124	PHE

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Mol	Chain	Res	Type
8	a1	195	THR
8	a2	54	ILE
8	a2	57	ILE
8	a2	72	VAL
8	a2	83	ASP
8	a2	190	ARG
8	a2	193	LEU
8	a2	218	LEU
8	a2	222	MET
8	a3	71	LYS
8	a3	88	GLN
8	a3	129	ILE
8	a3	155	THR
8	a3	181	LEU
8	a3	218	LEU
8	a4	72	VAL
8	a4	84	SER
8	a4	201	LEU
8	a4	209	ASP
8	a5	54	ILE
8	a5	128	GLU
8	a5	129	ILE
8	a5	156	THR
8	a5	193	LEU
8	a5	204	VAL
8	a5	221	LYS
9	b3	119	LEU
9	b3	179	LEU
9	b3	195	SER
9	b3	196	ASP
9	b4	73	ASP
9	b4	138	ILE
9	b4	139	ILE
9	b4	152	HIS
9	b4	154	LYS
9	b4	155	GLU
9	b4	185	ILE
9	b4	232	MET
9	b4	238	LEU
10	c2	55	TYR
10	c2	82	MET
10	c3	114	LEU

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Mol	Chain	Res	Type
1	h0	101	ILE
1	h0	149	MET
1	h0	184	ILE
1	h0	205	VAL
1	i0	85	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (675) such sidechains are listed below:

Mol	Chain	Res	Type
1	A4	6	ASN
1	A4	55	GLN
1	A4	152	HIS
1	A4	158	HIS
1	A4	235	GLN
1	A5	5	HIS
1	A5	37	ASN
1	A5	55	GLN
1	A5	74	GLN
1	A5	88	GLN
1	A5	156	ASN
1	A5	261	GLN
1	A6	22	ASN
1	A6	64	GLN
1	A6	74	GLN
1	A6	84	HIS
1	A6	88	GLN
1	A6	108	GLN
1	A6	218	ASN
1	A6	222	HIS
1	A6	269	GLN
1	A7	4	ASN
1	A7	5	HIS
1	A7	13	HIS
1	A7	37	ASN
1	A7	88	GLN
1	A7	96	GLN
1	A7	152	HIS
1	A7	158	HIS
1	A7	218	ASN
1	A7	233	ASN
1	A7	269	GLN
1	A8	108	GLN

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Mol	Chain	Res	Type
1	A8	222	HIS
1	A8	229	ASN
1	B3	13	HIS
1	B4	5	HIS
1	B4	13	HIS
1	B4	64	GLN
1	B4	84	HIS
1	B4	108	GLN
1	B4	109	GLN
1	B4	218	ASN
1	B4	282	GLN
1	B5	22	ASN
1	B5	37	ASN
1	B5	55	GLN
1	B5	84	HIS
1	B5	88	GLN
1	B5	96	GLN
1	B5	116	GLN
1	B5	156	ASN
1	B5	158	HIS
1	B5	209	GLN
1	B5	235	GLN
1	B6	5	HIS
1	B6	6	ASN
1	B6	74	GLN
1	B6	88	GLN
1	B6	116	GLN
1	B6	152	HIS
1	B6	156	ASN
1	B6	158	HIS
1	B6	159	GLN
1	B6	193	ASN
1	B6	233	ASN
1	B6	257	GLN
1	B6	271	ASN
1	B7	55	GLN
1	B7	84	HIS
1	B7	131	ASN
1	B7	261	GLN
1	B8	177	ASN
1	C2	282	GLN
1	C3	5	HIS

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Mol	Chain	Res	Type
1	C3	37	ASN
1	C3	55	GLN
1	C3	152	HIS
1	C3	159	GLN
1	C3	233	ASN
1	C3	282	GLN
1	C4	37	ASN
1	C4	84	HIS
1	C4	96	GLN
1	C4	109	GLN
1	C4	116	GLN
1	C4	131	ASN
1	C4	152	HIS
1	C4	235	GLN
1	C4	261	GLN
1	C5	111	GLN
1	C5	131	ASN
1	C5	235	GLN
1	C5	249	GLN
1	C5	269	GLN
1	C5	275	GLN
1	C6	74	GLN
1	C6	84	HIS
1	C6	108	GLN
1	C6	158	HIS
1	C6	233	ASN
1	C6	271	ASN
1	C7	65	ASN
1	C7	81	GLN
1	C7	88	GLN
1	C7	131	ASN
1	C7	249	GLN
1	D2	22	ASN
1	D2	37	ASN
1	D2	257	GLN
1	D2	282	GLN
1	D3	55	GLN
1	D3	84	HIS
1	D3	88	GLN
1	D3	96	GLN
1	D3	152	HIS
1	D3	156	ASN

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Mol	Chain	Res	Type
1	D3	261	GLN
1	D4	81	GLN
1	D4	96	GLN
1	D4	109	GLN
1	D4	116	GLN
1	D4	152	HIS
1	D4	159	GLN
1	D4	235	GLN
1	D5	5	HIS
1	D5	81	GLN
1	D5	96	GLN
1	D5	152	HIS
1	D5	156	ASN
1	D5	218	ASN
1	D6	152	HIS
1	D6	156	ASN
1	D7	209	GLN
1	E1	4	ASN
1	E1	5	HIS
1	E1	19	ASN
1	E2	5	HIS
1	E2	152	HIS
1	E2	158	HIS
1	E3	108	GLN
1	E3	152	HIS
1	E3	156	ASN
1	E3	159	GLN
1	E3	209	GLN
1	E3	218	ASN
1	E3	261	GLN
1	E4	5	HIS
1	E4	109	GLN
1	E4	116	GLN
1	E4	152	HIS
1	E4	209	GLN
1	E5	22	ASN
1	E5	37	ASN
1	E5	65	ASN
1	E5	84	HIS
1	E5	152	HIS
1	E5	158	HIS
1	E6	74	GLN

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Mol	Chain	Res	Type
1	E6	152	HIS
1	E7	74	GLN
1	E7	88	GLN
1	E7	99	ASN
1	E7	109	GLN
1	E7	144	ASN
1	E7	209	GLN
1	E7	218	ASN
1	F1	5	HIS
1	F1	19	ASN
1	F1	275	GLN
1	F1	282	GLN
1	F2	22	ASN
1	F2	169	ASN
1	F3	5	HIS
1	F3	13	HIS
1	F3	19	ASN
1	F3	22	ASN
1	F3	74	GLN
1	F3	96	GLN
1	F3	108	GLN
1	F3	116	GLN
1	F3	152	HIS
1	F3	269	GLN
1	F4	5	HIS
1	F4	19	ASN
1	F4	64	GLN
1	F4	74	GLN
1	F4	81	GLN
1	F4	96	GLN
1	F4	152	HIS
1	F4	257	GLN
1	F5	37	ASN
1	F5	81	GLN
1	F5	99	ASN
1	F5	152	HIS
1	F5	156	ASN
1	F5	158	HIS
1	F5	159	GLN
1	F5	177	ASN
1	F5	233	ASN
1	F5	235	GLN

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Mol	Chain	Res	Type
1	F6	65	ASN
1	F6	74	GLN
1	F6	84	HIS
1	F6	88	GLN
1	F6	209	GLN
1	F6	229	ASN
1	G1	55	GLN
1	G1	109	GLN
1	G1	152	HIS
1	G1	156	ASN
1	G2	193	ASN
1	G5	5	HIS
1	G5	275	GLN
1	G5	282	GLN
1	G6	37	ASN
1	G6	158	HIS
1	G6	282	GLN
1	G7	22	ASN
1	G7	84	HIS
1	G7	116	GLN
1	G7	152	HIS
1	G7	156	ASN
1	G7	158	HIS
1	G7	159	GLN
1	G7	177	ASN
1	G7	249	GLN
1	G7	282	GLN
1	G8	5	HIS
1	G8	88	GLN
1	G8	96	GLN
1	G8	108	GLN
1	G8	109	GLN
1	G8	116	GLN
1	G8	156	ASN
1	G8	235	GLN
1	G8	257	GLN
1	G9	5	HIS
1	G9	65	ASN
1	G9	96	GLN
1	G9	131	ASN
1	G9	152	HIS
1	G9	193	ASN

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Mol	Chain	Res	Type
1	H5	261	GLN
1	H6	5	HIS
1	H6	88	GLN
1	H6	152	HIS
1	H6	156	ASN
1	H6	158	HIS
1	H6	159	GLN
1	H6	249	GLN
1	H6	261	GLN
1	H7	4	ASN
1	H7	74	GLN
1	H7	84	HIS
1	H7	109	GLN
1	H7	158	HIS
1	H7	209	GLN
1	H7	235	GLN
1	H7	257	GLN
1	H7	261	GLN
1	H8	96	GLN
1	H8	116	GLN
1	H8	152	HIS
1	H8	158	HIS
1	H8	159	GLN
1	H8	209	GLN
1	H8	235	GLN
1	H8	249	GLN
1	H9	37	ASN
1	H9	99	ASN
1	H9	116	GLN
1	H9	127	GLN
1	H9	152	HIS
1	H9	209	GLN
1	H9	233	ASN
1	I4	6	ASN
1	I5	22	ASN
1	I5	65	ASN
1	I5	152	HIS
1	I5	249	GLN
1	I5	275	GLN
1	I6	6	ASN
1	I6	81	GLN
1	I6	96	GLN

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Mol	Chain	Res	Type
1	I6	111	GLN
1	I6	156	ASN
1	I6	158	HIS
1	I6	218	ASN
1	I6	233	ASN
1	I6	235	GLN
1	I6	249	GLN
1	I6	275	GLN
1	I6	282	GLN
1	I7	37	ASN
1	I7	109	GLN
1	I7	116	GLN
1	I7	127	GLN
1	I7	152	HIS
1	I7	156	ASN
1	I7	209	GLN
1	I7	218	ASN
1	I8	5	HIS
1	I8	19	ASN
1	I8	65	ASN
1	I8	152	HIS
1	I8	159	GLN
1	I8	275	GLN
1	I9	88	GLN
1	I9	131	ASN
1	I9	152	HIS
1	I9	159	GLN
1	I9	209	GLN
1	I9	218	ASN
1	I9	235	GLN
1	J4	6	ASN
1	J5	5	HIS
1	J5	13	HIS
1	J5	19	ASN
1	J5	65	ASN
1	J5	152	HIS
1	J5	158	HIS
1	J5	209	GLN
1	J5	218	ASN
1	J6	19	ASN
1	J6	152	HIS
1	J6	156	ASN

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Mol	Chain	Res	Type
1	J6	159	GLN
1	J6	269	GLN
1	J6	271	ASN
1	J6	275	GLN
1	J7	13	HIS
1	J7	55	GLN
1	J7	74	GLN
1	J7	88	GLN
1	J7	152	HIS
1	J7	233	ASN
1	J7	271	ASN
1	J7	282	GLN
1	J8	13	HIS
1	J8	74	GLN
1	J8	99	ASN
1	J8	108	GLN
1	J8	109	GLN
1	J8	111	GLN
1	J8	158	HIS
1	J8	159	GLN
1	J8	169	ASN
1	J8	193	ASN
1	J8	209	GLN
1	J8	229	ASN
1	J8	233	ASN
1	J9	55	GLN
1	J9	109	GLN
1	J9	111	GLN
1	J9	156	ASN
1	J9	158	HIS
1	K4	5	HIS
1	K4	37	ASN
1	K4	64	GLN
1	K4	88	GLN
1	K4	109	GLN
1	K4	116	GLN
1	K4	152	HIS
1	K4	233	ASN
1	K5	13	HIS
1	K5	37	ASN
1	K5	249	GLN
1	K6	5	HIS

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Mol	Chain	Res	Type
1	K6	13	HIS
1	K6	22	ASN
1	K6	88	GLN
1	K6	127	GLN
1	K6	152	HIS
1	K6	233	ASN
1	K6	269	GLN
1	K6	282	GLN
1	K7	37	ASN
1	K7	84	HIS
1	K7	233	ASN
1	K7	249	GLN
1	K7	269	GLN
1	K8	13	HIS
1	K8	37	ASN
1	K8	65	ASN
1	K8	96	GLN
1	K8	144	ASN
1	K8	222	HIS
2	L1	82	ASN
2	L1	117	ASN
2	L2	82	ASN
2	L2	86	GLN
2	L2	89	HIS
2	L2	90	GLN
2	L2	99	GLN
2	L2	166	ASN
2	L2	174	HIS
2	L2	208	GLN
2	L3	82	ASN
2	L3	89	HIS
2	L3	162	GLN
2	L4	89	HIS
2	L4	99	GLN
2	L4	106	ASN
2	L4	141	GLN
2	L4	208	GLN
2	L4	226	ASN
2	L5	99	GLN
2	L5	162	GLN
2	L5	174	HIS
2	L5	212	GLN

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Mol	Chain	Res	Type
2	L5	226	ASN
2	L5	265	ASN
2	M1	99	GLN
2	M1	106	ASN
2	M1	166	ASN
2	M1	173	ASN
2	M1	233	HIS
2	M2	82	ASN
2	M2	98	ASN
2	M2	99	GLN
2	M2	106	ASN
2	M2	117	ASN
2	M2	173	ASN
2	M2	226	ASN
2	M2	245	ASN
2	M2	267	HIS
2	M3	69	GLN
2	M3	99	GLN
2	M3	162	GLN
2	M4	98	ASN
2	M4	106	ASN
2	M4	162	GLN
2	M4	173	ASN
2	M4	174	HIS
2	M4	209	ASN
2	M4	226	ASN
2	M5	99	GLN
2	M5	173	ASN
2	M5	265	ASN
2	M5	291	ASN
2	N1	69	GLN
2	N1	82	ASN
2	N2	98	ASN
2	N2	106	ASN
2	N2	108	GLN
2	N2	208	GLN
2	N3	82	ASN
2	N3	98	ASN
2	N3	162	GLN
2	N3	209	ASN
2	N4	98	ASN
2	N4	106	ASN

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Mol	Chain	Res	Type
2	N4	117	ASN
2	N4	166	ASN
2	N4	209	ASN
2	N4	226	ASN
2	N4	245	ASN
2	N4	288	ASN
2	N5	75	ASN
2	N5	106	ASN
2	N5	112	ASN
2	N5	174	HIS
2	N5	209	ASN
2	N5	291	ASN
2	O1	112	ASN
2	O1	233	HIS
2	O1	267	HIS
2	O1	291	ASN
2	O2	82	ASN
2	O2	99	GLN
2	O2	174	HIS
2	O2	208	GLN
2	O2	285	HIS
2	O3	75	ASN
2	O3	98	ASN
2	O3	117	ASN
2	O3	174	HIS
2	O3	245	ASN
2	O4	75	ASN
2	O4	98	ASN
2	O4	106	ASN
2	O4	267	HIS
2	O5	117	ASN
2	O5	141	GLN
2	O5	291	ASN
2	P1	98	ASN
2	P2	108	GLN
2	P2	173	ASN
2	P3	69	GLN
2	P3	108	GLN
2	P3	162	GLN
2	P3	212	GLN
2	P3	265	ASN
2	P3	288	ASN

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Mol	Chain	Res	Type
2	P4	106	ASN
2	P4	123	GLN
2	P4	174	HIS
2	P4	212	GLN
2	P4	267	HIS
2	P5	89	HIS
2	P5	99	GLN
2	P5	174	HIS
2	P5	209	ASN
2	P5	226	ASN
2	P5	265	ASN
2	P5	285	HIS
2	P6	112	ASN
2	P6	117	ASN
2	P6	245	ASN
3	Q1	28	HIS
3	Q1	41	HIS
3	Q1	105	ASN
3	Q1	153	ASN
3	Q1	162	HIS
3	Q1	222	ASN
3	Q1	233	ASN
3	Q2	72	HIS
3	Q2	105	ASN
3	Q2	147	ASN
3	Q2	186	ASN
3	Q2	233	ASN
3	Q3	28	HIS
3	Q3	129	ASN
3	Q3	147	ASN
3	Q3	207	ASN
3	Q4	89	ASN
3	Q4	128	GLN
3	R1	28	HIS
3	R1	41	HIS
3	R1	118	ASN
3	R1	161	GLN
3	R1	186	ASN
3	R1	193	ASN
3	R1	207	ASN
3	R2	63	GLN
3	R2	68	ASN

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Mol	Chain	Res	Type
3	R2	186	ASN
3	R2	207	ASN
3	R3	22	ASN
3	R3	89	ASN
3	R3	106	ASN
3	R3	162	HIS
3	R3	193	ASN
3	R3	233	ASN
3	R4	63	GLN
3	R4	72	HIS
3	R4	89	ASN
3	R4	106	ASN
3	R4	118	ASN
3	R4	147	ASN
3	R4	161	GLN
3	R4	227	ASN
3	R5	22	ASN
3	R5	68	ASN
3	R5	89	ASN
3	R5	115	GLN
3	S2	28	HIS
3	S2	105	ASN
3	S2	118	ASN
3	S2	161	GLN
3	S2	162	HIS
3	S2	198	ASN
3	S2	207	ASN
3	S2	222	ASN
3	S3	153	ASN
3	S3	207	ASN
3	S4	28	HIS
3	S4	66	GLN
3	S4	89	ASN
3	S4	105	ASN
3	S4	147	ASN
3	S4	153	ASN
3	S4	161	GLN
3	S4	207	ASN
3	S4	233	ASN
3	S5	89	ASN
3	S5	106	ASN
3	S5	128	GLN

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Mol	Chain	Res	Type
3	S5	147	ASN
3	S5	197	ASN
3	S5	202	GLN
3	S5	227	ASN
3	S6	41	HIS
3	S6	68	ASN
3	S6	207	ASN
3	S6	222	ASN
3	S6	229	HIS
4	U3	31	ASN
4	U3	102	GLN
4	U3	268	HIS
4	U3	271	ASN
4	U4	81	ASN
4	U4	82	GLN
4	U4	88	ASN
4	U4	268	HIS
4	U4	271	ASN
4	U5	36	ASN
4	U5	81	ASN
4	U5	82	GLN
4	U5	88	ASN
4	U5	112	ASN
4	U5	268	HIS
4	U5	271	ASN
4	U5	287	ASN
4	U6	31	ASN
4	U6	216	ASN
4	U6	268	HIS
4	U6	287	ASN
5	V1	101	ASN
5	V1	102	HIS
5	V1	124	HIS
5	V1	160	HIS
5	V2	109	HIS
5	V2	124	HIS
5	V2	195	ASN
5	V3	101	ASN
5	V3	197	HIS
5	V4	124	HIS
5	V4	146	HIS
5	V4	160	HIS

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Mol	Chain	Res	Type
5	X1	109	HIS
5	X2	146	HIS
5	X3	195	ASN
5	X3	197	HIS
5	X4	124	HIS
5	X4	185	GLN
6	Y1	43	HIS
6	Y1	110	ASN
6	Y2	205	HIS
6	Y2	221	HIS
6	Y3	43	HIS
6	Y3	211	ASN
6	Y4	19	ASN
6	Y4	82	ASN
7	Z0	72	ASN
7	Z0	303	HIS
7	Z1	9	GLN
7	Z1	27	ASN
7	Z1	171	ASN
7	Z1	230	ASN
7	Z1	240	ASN
7	Z2	41	ASN
7	Z2	116	ASN
7	Z2	200	GLN
7	Z2	230	ASN
7	Z2	316	ASN
7	Za	160	HIS
7	Za	288	GLN
8	a1	185	GLN
8	a2	65	HIS
8	a3	51	GLN
8	a3	65	HIS
8	a3	217	ASN
8	a5	47	ASN
8	a5	96	HIS
9	b3	56	ASN
9	b3	227	GLN
9	b3	244	GLN
9	b3	258	GLN
9	b4	36	GLN
9	b4	60	ASN
9	b4	216	ASN

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Mol	Chain	Res	Type
10	c2	61	ASN
10	c2	123	HIS
10	c2	125	ASN
10	c2	153	GLN
10	c2	157	GLN
10	c2	159	HIS
10	c3	125	ASN
10	c3	153	GLN
1	h0	109	GLN
1	h0	209	GLN
1	i0	81	GLN
1	i0	96	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

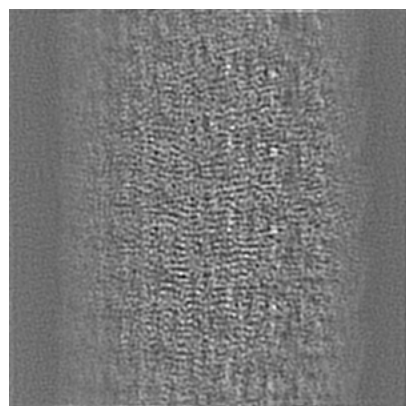
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75270. These allow visual inspection of the internal detail of the map and identification of artifacts.

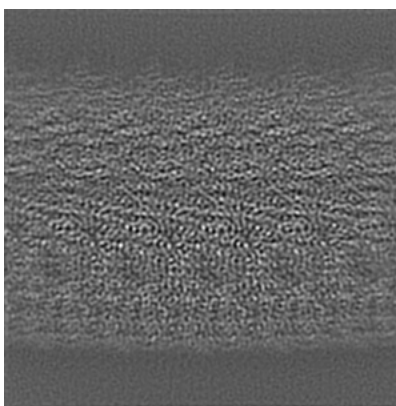
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

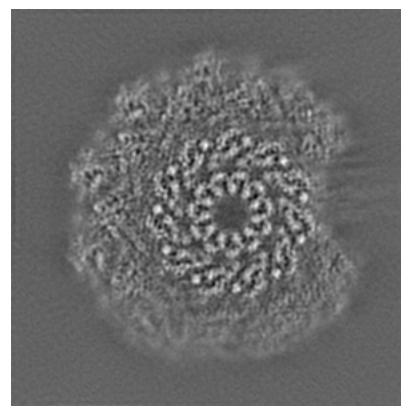
6.1.1 Primary map



X

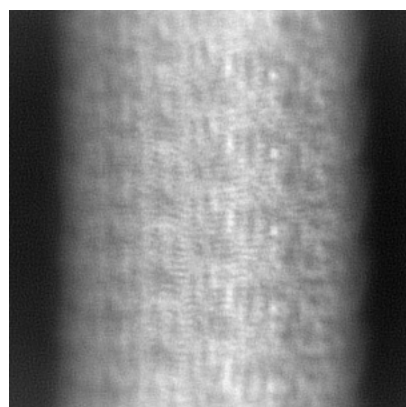


Y

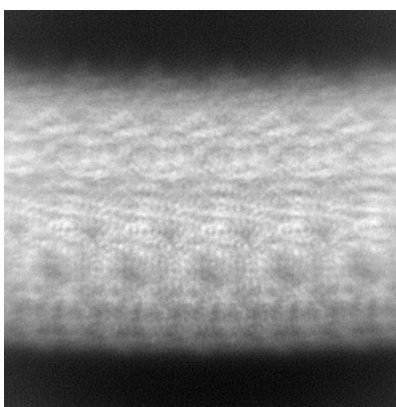


Z

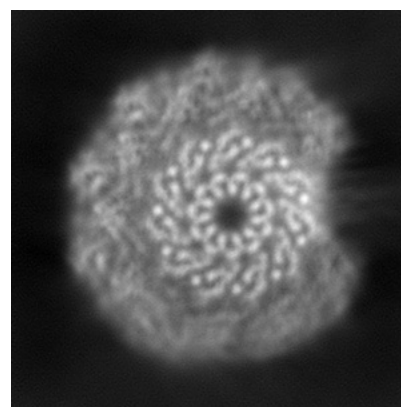
6.1.2 Raw map



X



Y

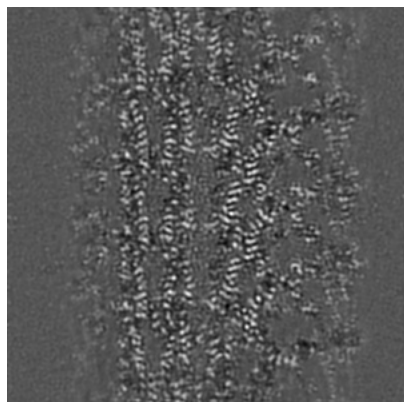


Z

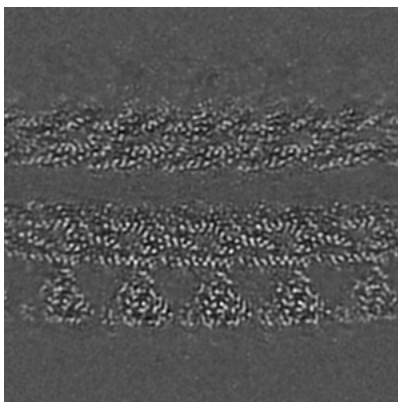
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

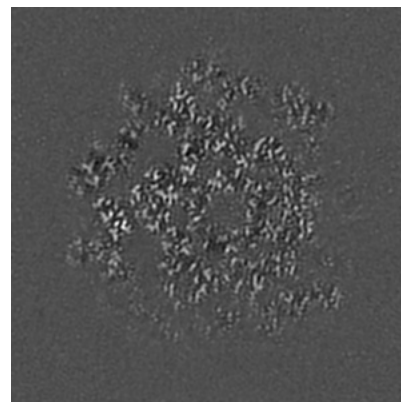
6.2.1 Primary map



X Index: 128

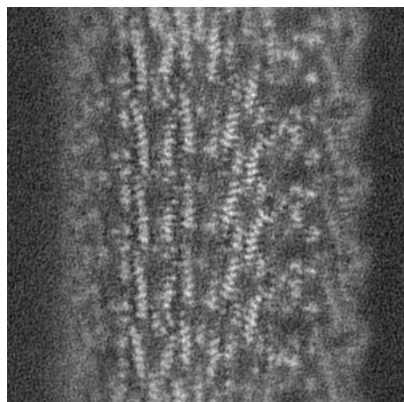


Y Index: 128

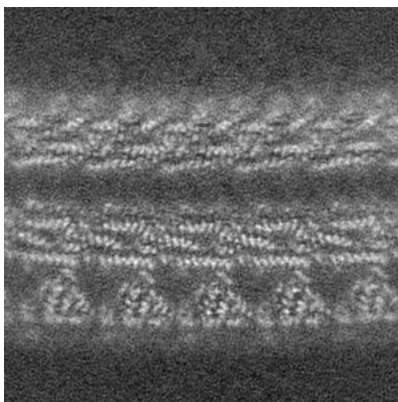


Z Index: 128

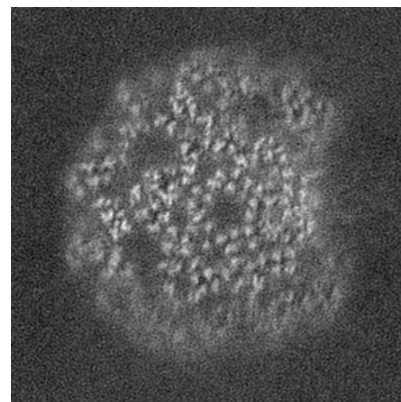
6.2.2 Raw map



X Index: 128



Y Index: 128

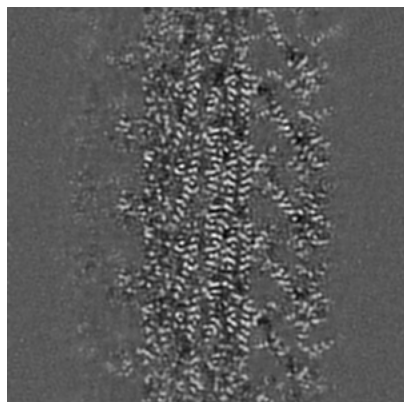


Z Index: 128

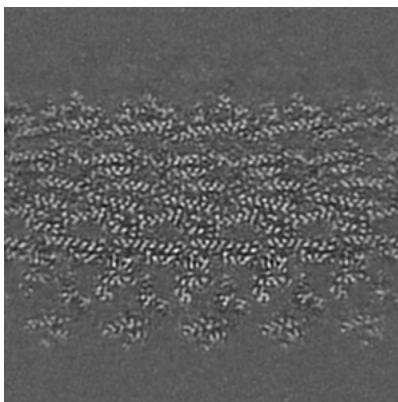
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

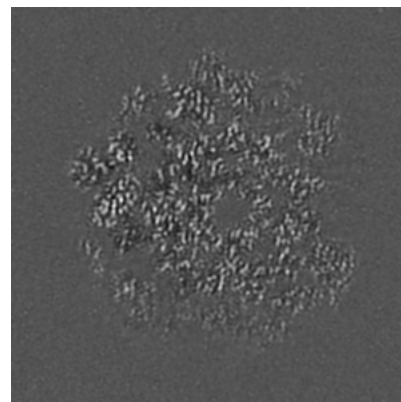
6.3.1 Primary map



X Index: 102

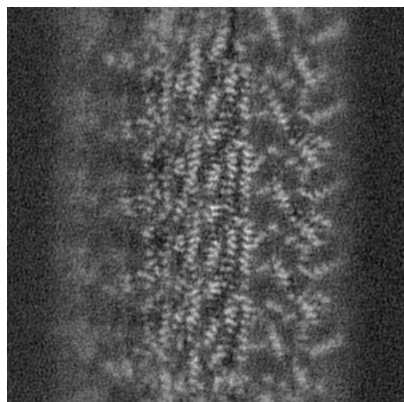


Y Index: 141

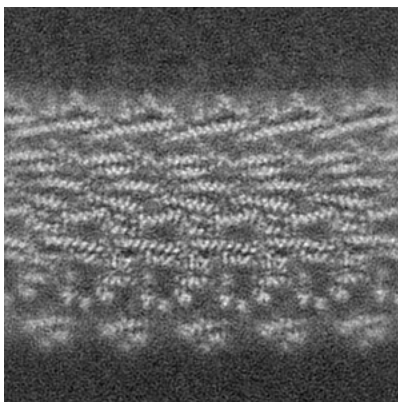


Z Index: 139

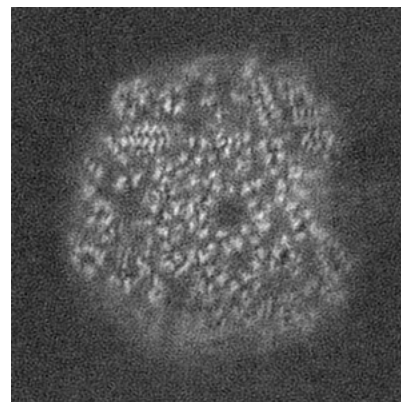
6.3.2 Raw map



X Index: 101



Y Index: 141

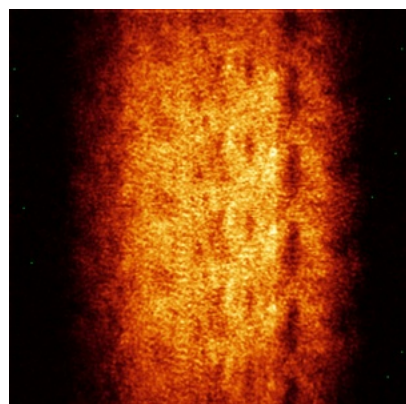


Z Index: 113

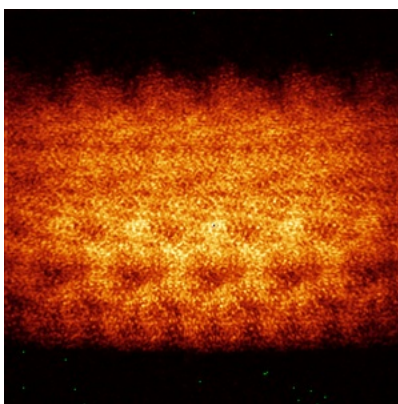
The images above show the largest variance slices of the map in three orthogonal directions.

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

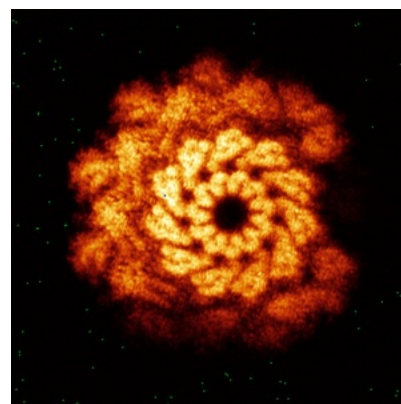
6.4.1 Primary map



X

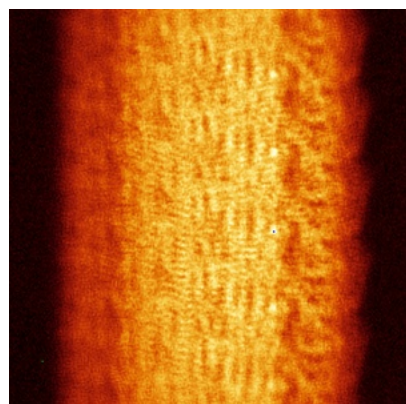


Y

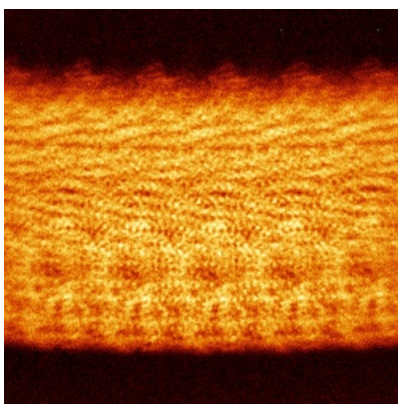


Z

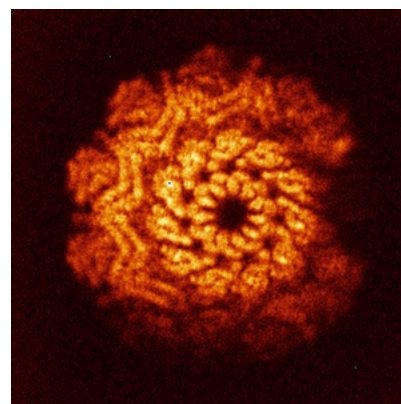
6.4.2 Raw map



X



Y

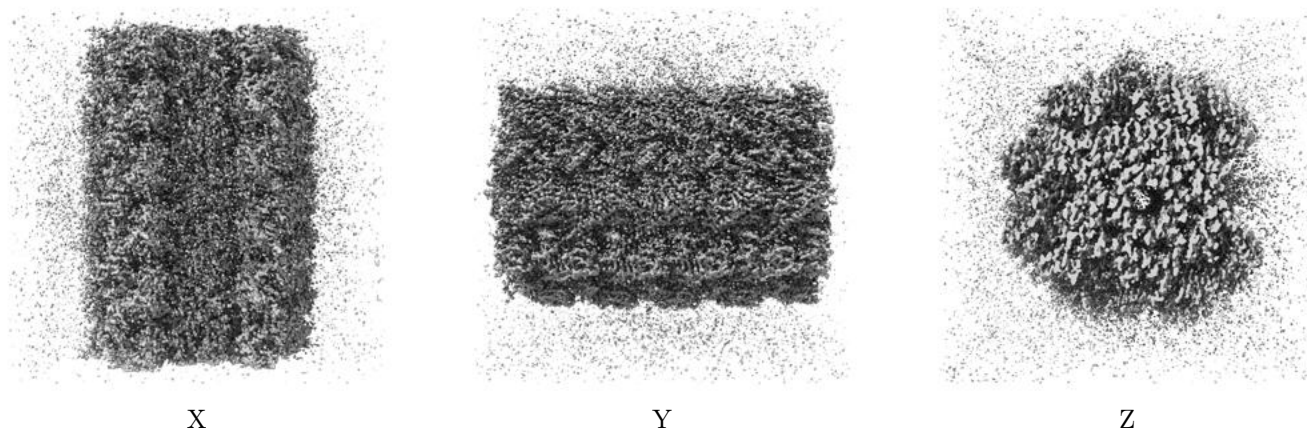


Z

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

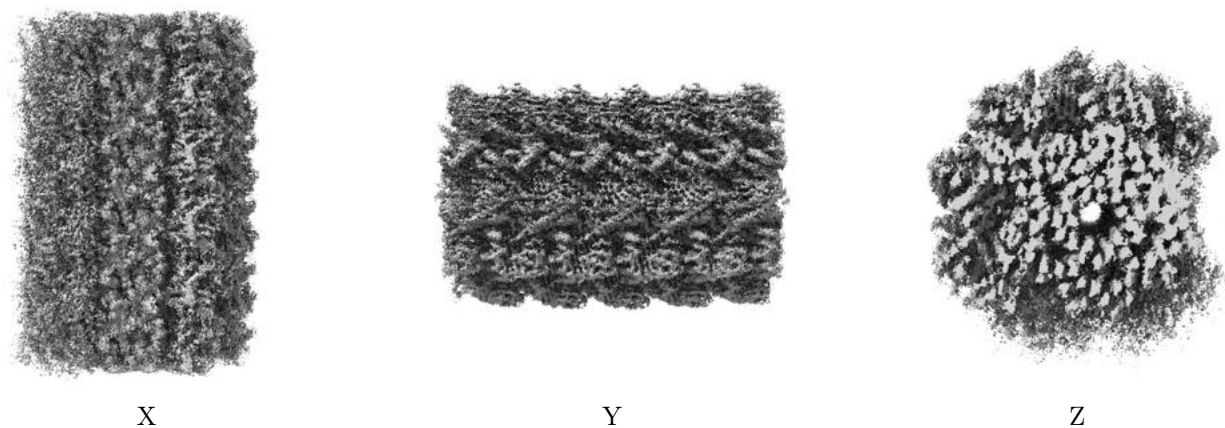
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

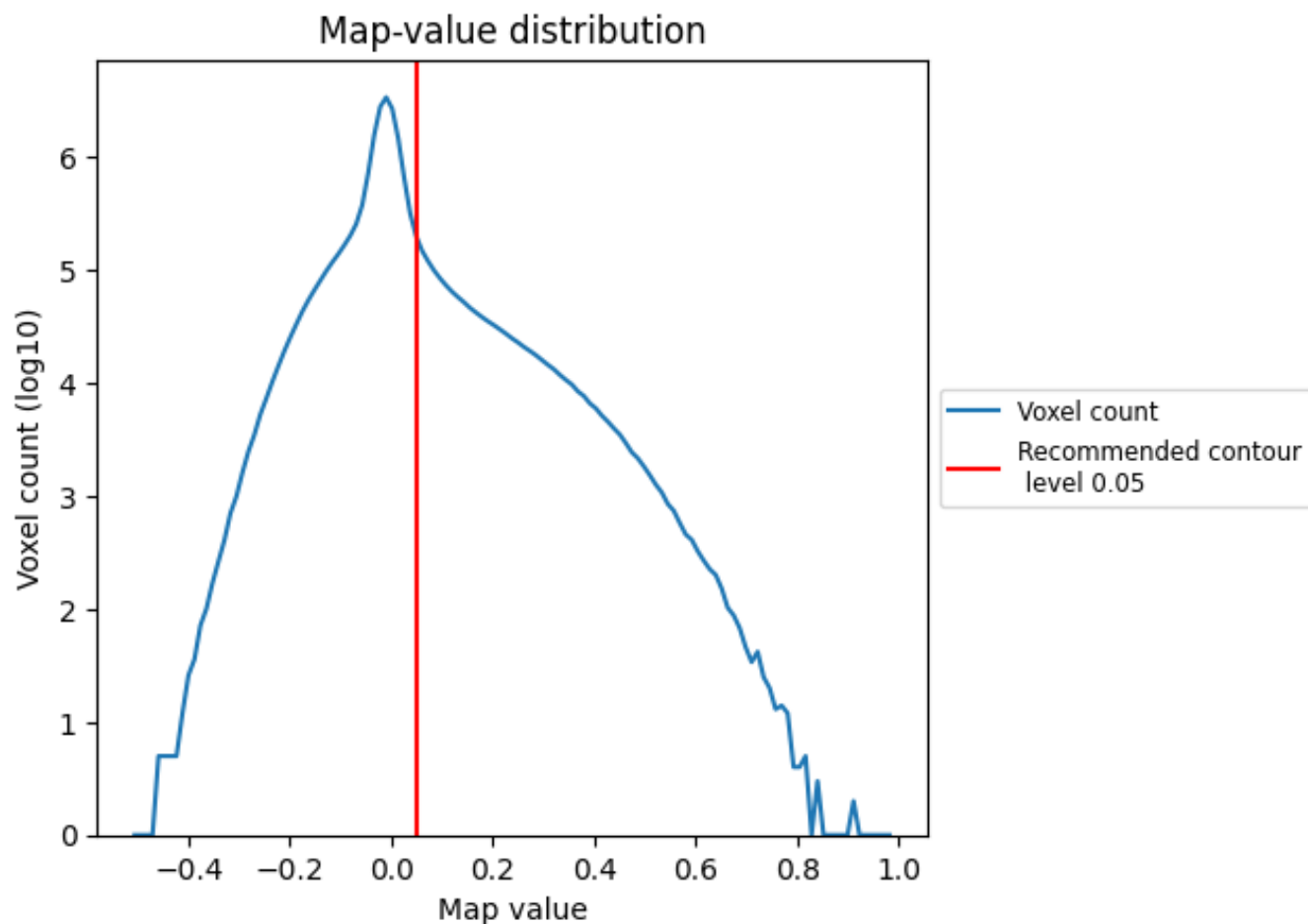
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

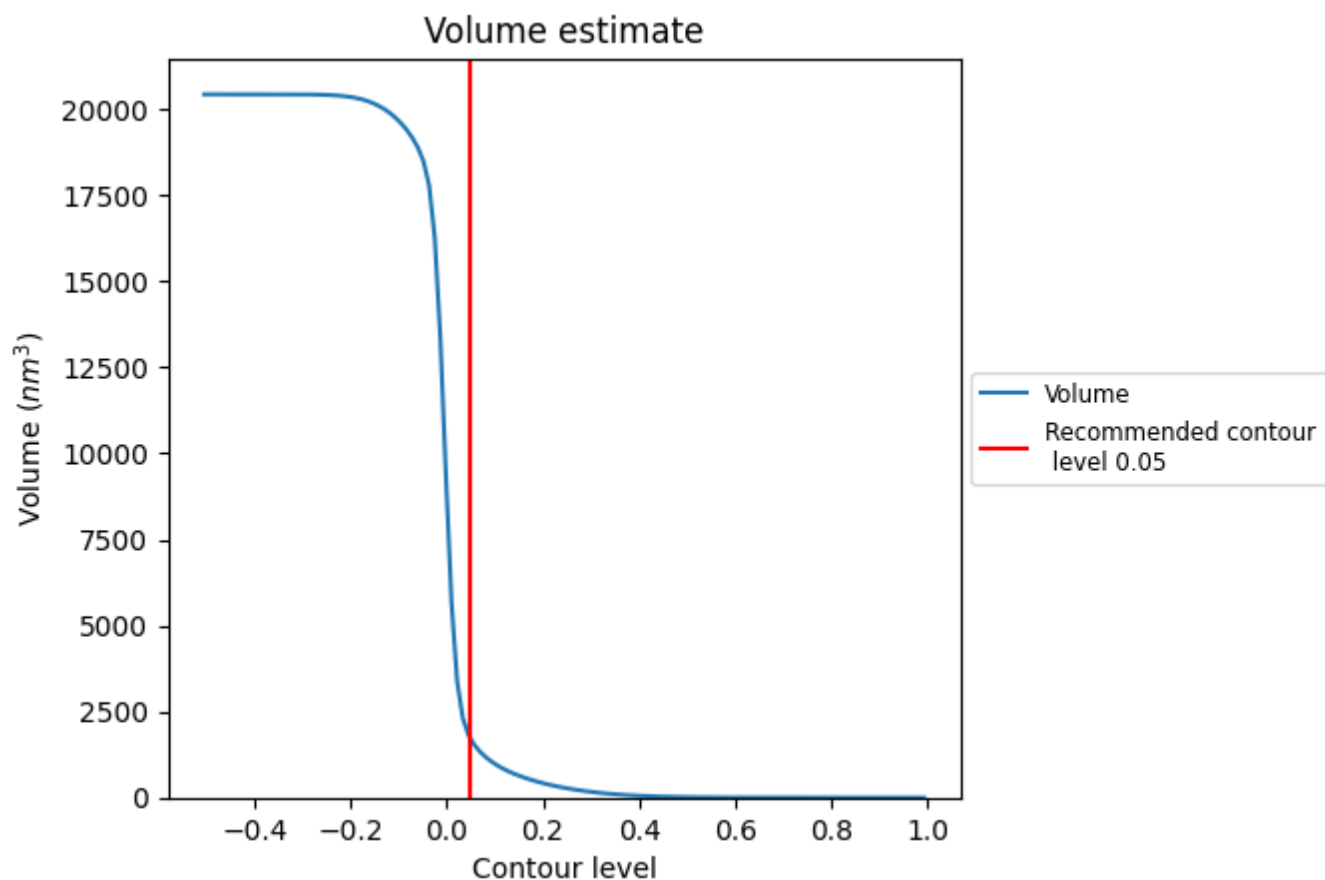
This section contains the results of statistical analysis of the map.

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.

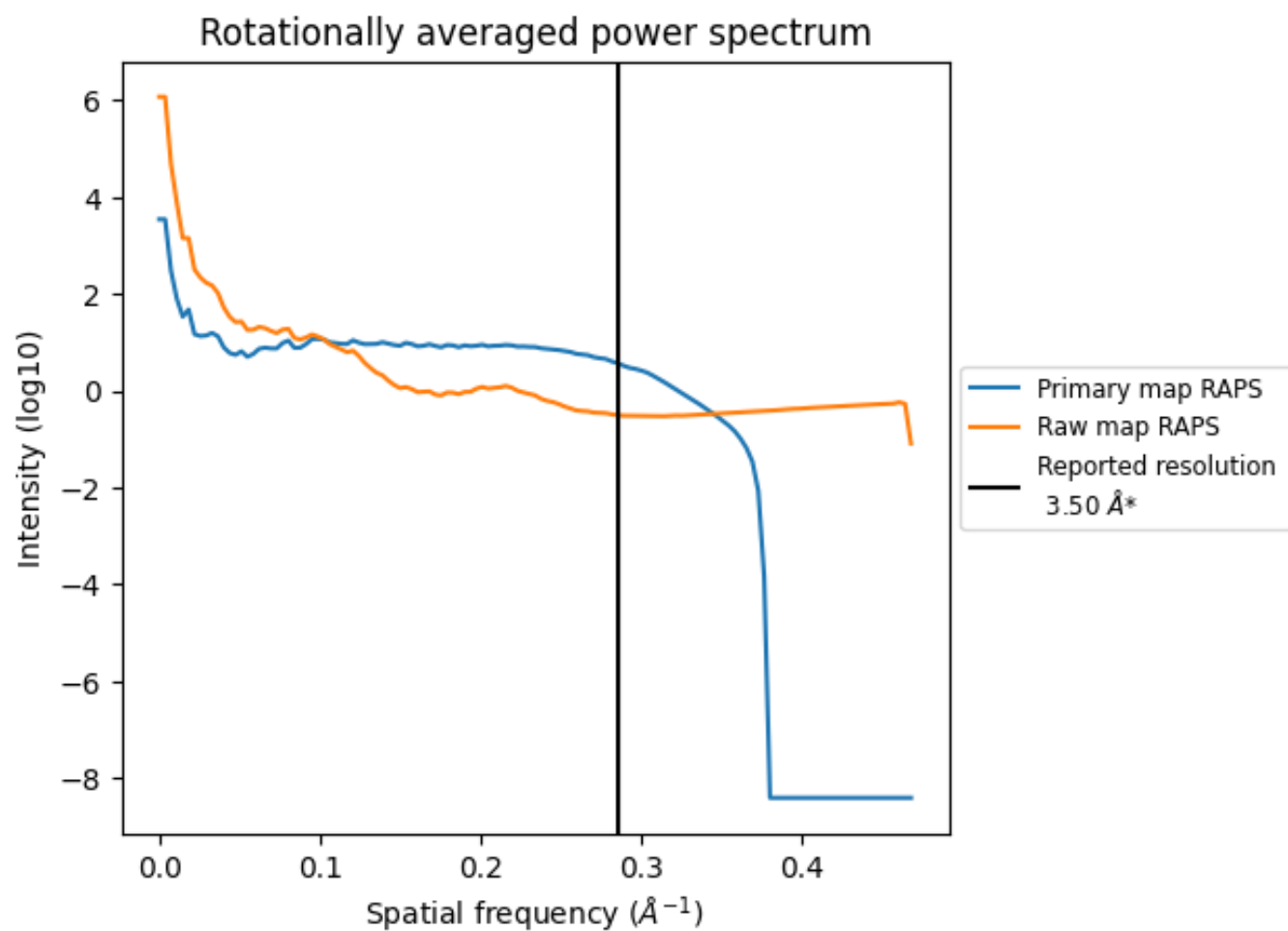
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1700 nm^3 ; this corresponds to an approximate mass of 1536 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 ⓘ

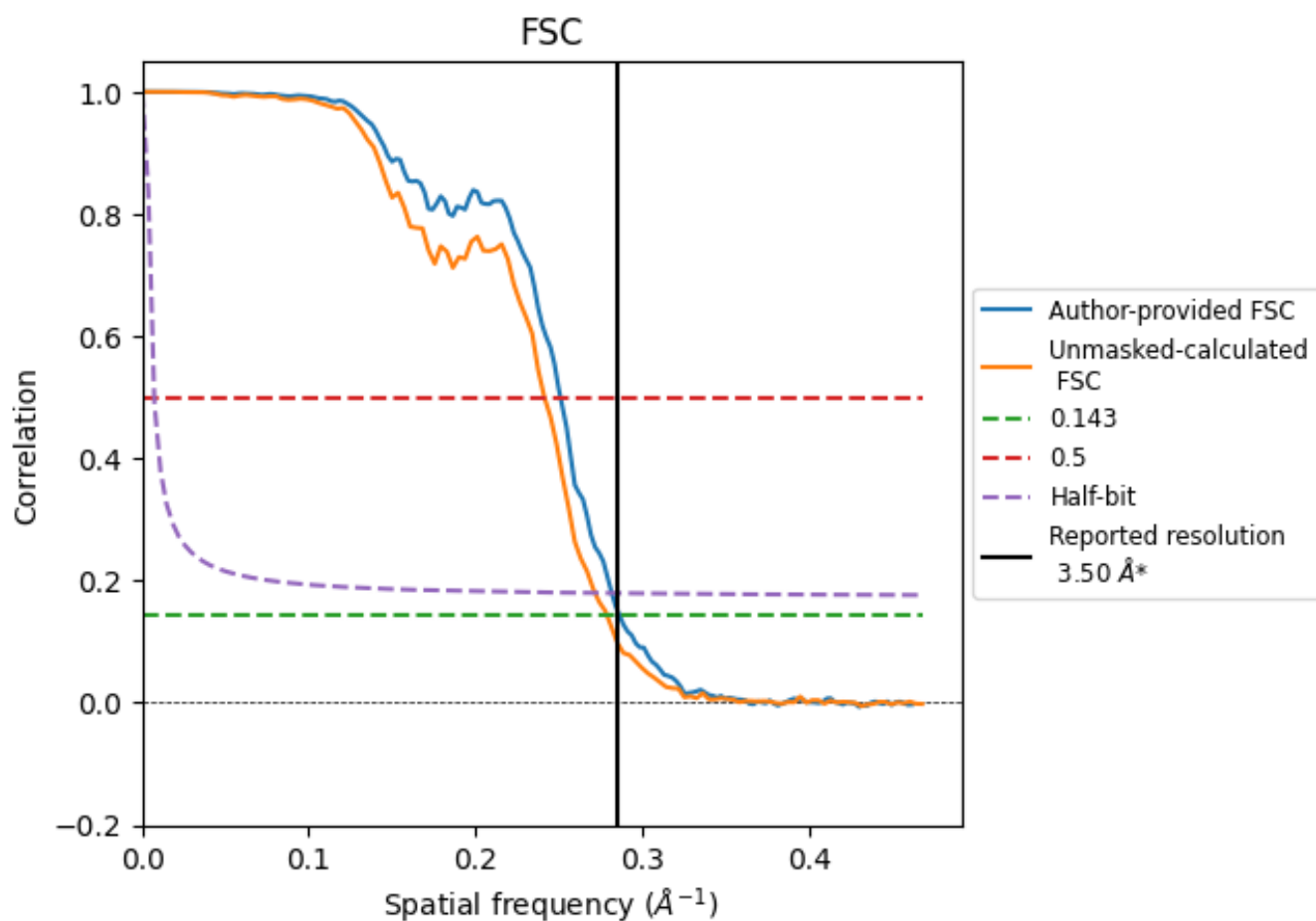


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

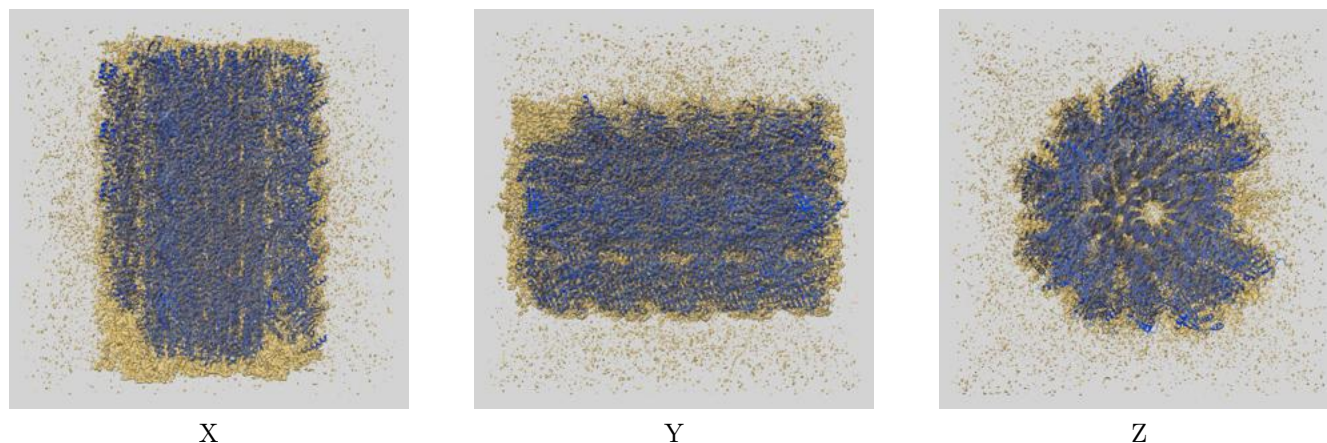
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.49	3.98	3.54
Unmasked-calculated*	3.58	4.14	3.68

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

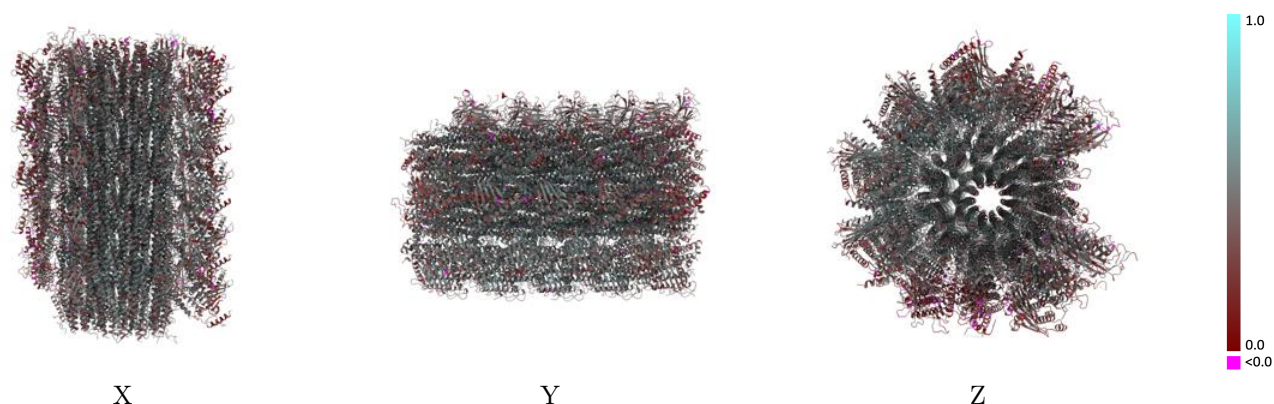
This section contains information regarding the fit between EMDB map EMD-75270 and PDB model 10LM. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



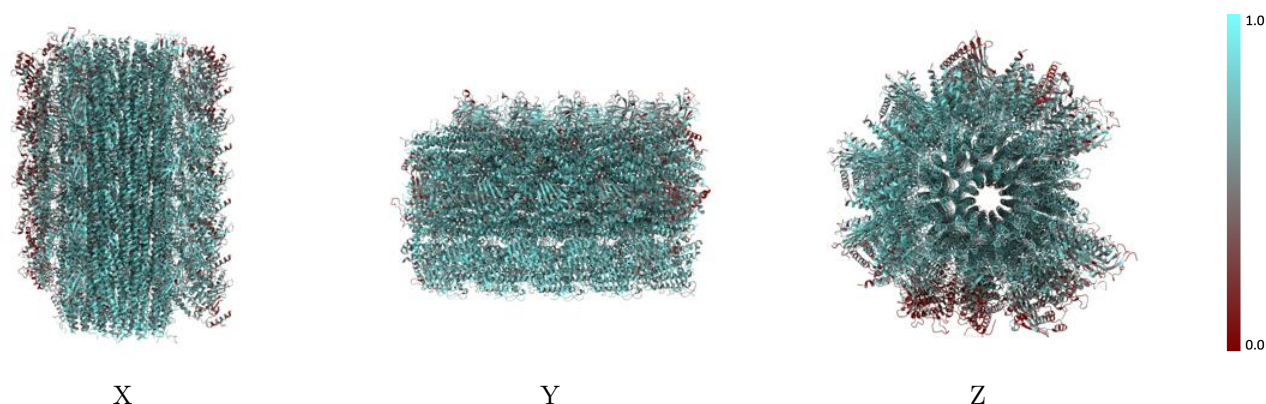
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



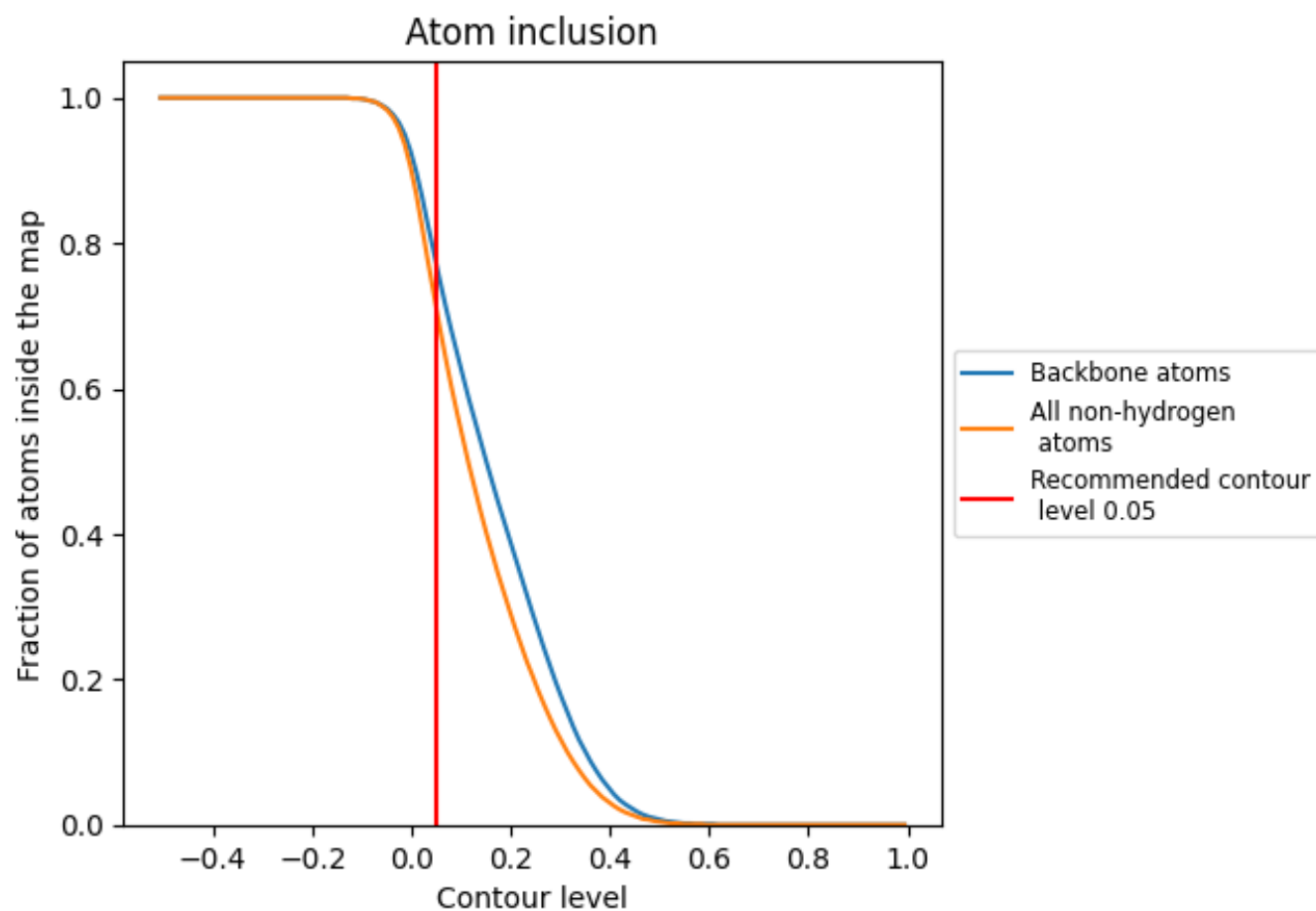
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 71% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7100	 0.4380
A3	 0.7200	 0.4270
A4	 0.7120	 0.4180
A5	 0.7730	 0.4600
A6	 0.7990	 0.4810
A7	 0.7970	 0.4870
A8	 0.7840	 0.4760
B3	 0.7360	 0.4220
B4	 0.7330	 0.4260
B5	 0.7840	 0.4760
B6	 0.8170	 0.4940
B7	 0.7990	 0.4770
B8	 0.7480	 0.4490
C2	 0.7800	 0.4640
C3	 0.7780	 0.4760
C4	 0.8120	 0.5040
C5	 0.8160	 0.5050
C6	 0.8040	 0.4900
C7	 0.7610	 0.4570
C8	 0.6890	 0.4120
D2	 0.7900	 0.4880
D3	 0.7800	 0.4760
D4	 0.8320	 0.5150
D5	 0.8400	 0.5210
D6	 0.8240	 0.5080
D7	 0.7790	 0.4630
E1	 0.7430	 0.4500
E2	 0.8030	 0.4950
E3	 0.8140	 0.5130
E4	 0.8360	 0.5260
E5	 0.8310	 0.5180
E6	 0.8250	 0.5120
E7	 0.7480	 0.4550
F1	 0.8110	 0.4950
F2	 0.7900	 0.4930



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Chain	Atom inclusion	Q-score
F3	 0.8360	 0.5230
F4	 0.8410	 0.5220
F5	 0.8360	 0.5150
F6	 0.8200	 0.5090
G1	 0.8280	 0.5090
G2	 0.7530	 0.4700
G5	 0.7780	 0.4690
G6	 0.8110	 0.4930
G7	 0.8040	 0.5060
G8	 0.8360	 0.5190
G9	 0.8400	 0.5130
H5	 0.7690	 0.4690
H6	 0.7620	 0.4530
H7	 0.8230	 0.5040
H8	 0.8150	 0.5090
H9	 0.8280	 0.5150
I4	 0.7640	 0.4500
I5	 0.7650	 0.4700
I6	 0.7690	 0.4660
I7	 0.8090	 0.4890
I8	 0.8080	 0.4860
I9	 0.7610	 0.4640
J4	 0.7420	 0.4500
J5	 0.7230	 0.4250
J6	 0.7880	 0.4760
J7	 0.7850	 0.4750
J8	 0.7780	 0.4650
J9	 0.7630	 0.4640
K3	 0.7320	 0.4310
K4	 0.7590	 0.4470
K5	 0.7470	 0.4500
K6	 0.7830	 0.4710
K7	 0.7870	 0.4710
K8	 0.7780	 0.4630
L1	 0.5590	 0.3250
L2	 0.7120	 0.4190
L3	 0.7730	 0.4510
L4	 0.7410	 0.4360
L5	 0.6820	 0.3950
M1	 0.7050	 0.3970
M2	 0.8070	 0.4950
M3	 0.8150	 0.5040

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Chain	Atom inclusion	Q-score
M4	 0.7860	 0.4860
M5	 0.7490	 0.4400
N1	 0.7020	 0.4120
N2	 0.7950	 0.4890
N3	 0.8210	 0.5100
N4	 0.8160	 0.5070
N5	 0.7800	 0.4850
N6	 0.7400	 0.4510
O1	 0.7120	 0.4370
O2	 0.8130	 0.4930
O3	 0.8320	 0.5100
O4	 0.8060	 0.4850
O5	 0.7610	 0.4620
P1	 0.5340	 0.3600
P2	 0.6870	 0.4130
P3	 0.7690	 0.4600
P4	 0.7620	 0.4560
P5	 0.6910	 0.4210
P6	 0.6260	 0.3850
Q1	 0.6240	 0.3710
Q2	 0.7350	 0.4350
Q3	 0.7480	 0.4410
Q4	 0.7130	 0.4300
R1	 0.6420	 0.3950
R2	 0.7520	 0.4540
R3	 0.7850	 0.4730
R4	 0.7730	 0.4660
R5	 0.6970	 0.4270
S2	 0.5930	 0.3760
S3	 0.6950	 0.4290
S4	 0.7280	 0.4430
S5	 0.6650	 0.4170
S6	 0.5450	 0.3600
U3	 0.2780	 0.2550
U4	 0.3890	 0.2700
U5	 0.3910	 0.2760
U6	 0.3300	 0.2600
V0	 0.5510	 0.3660
V1	 0.5930	 0.3580
V2	 0.6550	 0.3840
V3	 0.6440	 0.3740
V4	 0.5860	 0.3530

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Chain	Atom inclusion	Q-score
X0	 0.5220	 0.3750
X1	 0.5440	 0.3640
X2	 0.6010	 0.3770
X3	 0.6060	 0.3760
X4	 0.5390	 0.3590
Y1	 0.4500	 0.3050
Y2	 0.6120	 0.3580
Y3	 0.6170	 0.3640
Y4	 0.5720	 0.3480
Z0	 0.6110	 0.3950
Z1	 0.6260	 0.3920
Z2	 0.5980	 0.3780
Za	 0.5220	 0.3730
a1	 0.3980	 0.2940
a2	 0.5470	 0.3440
a3	 0.6560	 0.4100
a4	 0.6240	 0.3790
a5	 0.4630	 0.3110
b2	 0.2820	 0.2650
b3	 0.3190	 0.2380
b4	 0.2870	 0.2380
c1	 0.3650	 0.2930
c2	 0.3880	 0.3040
c3	 0.4600	 0.3200
h0	 0.7860	 0.4890
i0	 0.7060	 0.4310