



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 11:34 AM UTC

PDB ID : 7R5K / pdb_00007r5k
EMDB ID : EMD-14322
Title : Human nuclear pore complex (constricted)
Authors : Mosalaganti, S.; Obarska-Kosinska, A.; Siggel, M.; Taniguchi, R.; Turonova, B.; Zimmerli, C.E.; Buczak, K.; Schmidt, F.H.; Margiotta, E.; Mackmull, M.T.; Hagen, W.J.H.; Hummer, G.; Kosinski, J.; Beck, M.
Deposited on : 2022-02-10
Resolution : 12.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

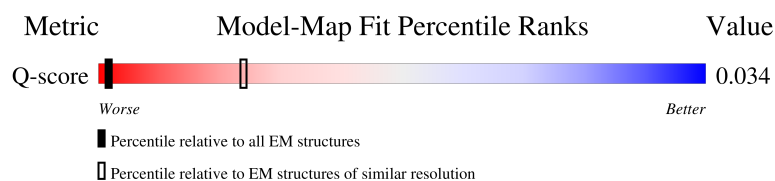
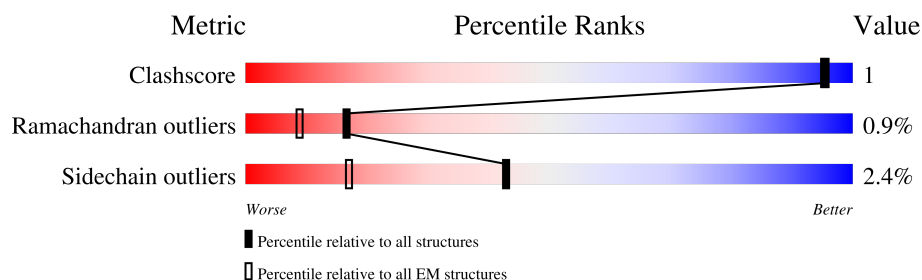
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 12.00 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	93 (11.50 - 12.50)

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	00	3224	
1	01	3224	
1	02	3224	
1	03	3224	

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Mol	Chain	Length	Quality of chain
1	04	3224	
2	10	1887	
2	11	1887	
2	12	1887	
2	13	1887	
2	14	1887	
2	15	1887	
2	16	1887	
2	17	1887	
3	40	546	
3	41	546	
4	A0	819	
4	A1	819	
4	A2	819	
4	A3	819	
4	A4	819	
4	A5	819	
4	A6	819	
5	B0	1749	
5	B1	1749	
6	C0	2012	
6	C1	2012	
6	C2	2012	
6	C3	2012	
6	C4	2012	

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Mol	Chain	Length	Quality of chain
7	D0	1391	
7	D1	1391	
7	D2	1391	
7	D3	1391	
7	D4	1391	
7	D5	1391	
8	E0	674	
8	E1	674	
9	F0	326	
9	F1	326	
9	F2	326	
9	F3	326	
10	H0	507	
10	H1	507	
10	H2	507	
10	H3	507	
11	I0	599	
11	I1	599	
11	I2	599	
11	I3	599	
12	J0	522	
12	J1	522	
12	J2	522	
12	J3	522	
12	J4	522	

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Mol	Chain	Length	Quality of chain
13	K0	1156	
13	K1	1156	
13	K2	1156	
13	K3	1156	
14	L0	925	
14	L1	925	
14	L2	925	
14	L3	925	
15	M0	937	
15	M1	937	
15	M2	937	
15	M3	937	
16	N0	322	
16	N1	322	
16	N2	322	
16	N3	322	
17	O0	360	
17	O1	360	
17	O2	360	
17	O3	360	
18	P0	656	
18	P1	656	
18	P2	656	
18	P3	656	
19	Q0	380	

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Mol	Chain	Length	Quality of chain
19	Q1	380	
19	Q2	380	
19	Q3	380	
20	R0	1436	
20	R1	1436	
20	R2	1436	
20	R3	1436	
21	S0	326	
21	S1	326	
21	S2	326	
21	S3	326	
22	T0	2266	
22	T1	2266	
23	U0	880	
23	U1	880	
23	U2	880	
23	U3	880	
23	U4	880	
23	U5	880	
23	U6	880	
24	V0	2090	
25	W0	741	

2 Entry composition [i](#)

There are 25 unique types of molecules in this entry. The entry contains 617133 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 E3 SUMO-protein ligase RanBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	00	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		
1	01	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		
1	02	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		
1	03	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		
1	04	756	Total	C	N	O	S	0	0
			6085	3866	1045	1147	27		

- Molecule 2 is a protein called Nuclear pore membrane glycoprotein 210.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	10	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	11	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	12	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	13	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	14	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	15	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	16	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		
2	17	1831	Total	C	N	O	S	0	0
			14046	8947	2406	2644	49		

- Molecule 3 is a protein called Aladin.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	40	383	Total	C	N	O	S	0	0
			2922	1864	509	533	16		
3	41	383	Total	C	N	O	S	0	0
			2922	1864	509	533	16		

- Molecule 4 is a protein called Nuclear pore complex protein Nup93.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A0	818	Total	C	N	O	S	0	0
			6568	4136	1145	1259	28		
4	A1	818	Total	C	N	O	S	0	0
			6568	4136	1145	1259	28		
4	A2	818	Total	C	N	O	S	0	0
			6568	4136	1145	1259	28		
4	A3	818	Total	C	N	O	S	0	0
			6568	4136	1145	1259	28		
4	A4	726	Total	C	N	O	S	0	0
			5860	3705	1018	1109	28		
4	A5	726	Total	C	N	O	S	0	0
			5860	3705	1018	1109	28		
4	A6	726	Total	C	N	O	S	0	0
			5860	3705	1018	1109	28		

- Molecule 5 is a protein called Nucleoporin NUP188 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B0	1748	Total	C	N	O	S	0	0
			13746	8743	2353	2559	91		
5	B1	1748	Total	C	N	O	S	0	0
			13746	8743	2353	2559	91		

- Molecule 6 is a protein called Nuclear pore complex protein Nup205.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C0	2011	Total	C	N	O	S	0	0
			16013	10208	2753	2965	87		
6	C1	2011	Total	C	N	O	S	0	0
			16013	10208	2753	2965	87		
6	C2	2011	Total	C	N	O	S	0	0
			16013	10208	2753	2965	87		
6	C3	2011	Total	C	N	O	S	0	0
			16013	10208	2753	2965	87		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	C4	2011	Total	C	N	O	S	0	0
			16013	10208	2753	2965	87		

- Molecule 7 is a protein called Nuclear pore complex protein Nup155.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D0	1312	Total	C	N	O	S	0	0
			10363	6569	1786	1949	59		
7	D1	1312	Total	C	N	O	S	0	0
			10363	6569	1786	1949	59		
7	D2	1312	Total	C	N	O	S	0	0
			10363	6569	1786	1949	59		
7	D3	1312	Total	C	N	O	S	0	0
			10363	6569	1786	1949	59		
7	D4	1312	Total	C	N	O	S	0	0
			10363	6569	1786	1949	59		
7	D5	1312	Total	C	N	O	S	0	0
			10363	6569	1786	1949	59		

- Molecule 8 is a protein called Nucleoporin NDC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E0	548	Total	C	N	O	S	0	0
			4432	2923	729	758	22		
8	E1	548	Total	C	N	O	S	0	0
			4432	2923	729	758	22		

- Molecule 9 is a protein called Nucleoporin NUP35.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F0	241	Total	C	N	O	S	0	0
			1837	1154	313	359	11		
9	F1	241	Total	C	N	O	S	0	0
			1837	1154	313	359	11		
9	F2	241	Total	C	N	O	S	0	0
			1837	1154	313	359	11		
9	F3	241	Total	C	N	O	S	0	0
			1837	1154	313	359	11		

- Molecule 10 is a protein called Nucleoporin p54.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H0	383	Total	C	N	O	S	0	0
			3066	1921	544	592	9		
10	H1	383	Total	C	N	O	S	0	0
			3066	1921	544	592	9		
10	H2	383	Total	C	N	O	S	0	0
			3066	1921	544	592	9		
10	H3	383	Total	C	N	O	S	0	0
			3066	1921	544	592	9		

- Molecule 11 is a protein called Nucleoporin p58/p45.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I0	173	Total	C	N	O	S	0	0
			1398	881	245	267	5		
11	I1	173	Total	C	N	O	S	0	0
			1398	881	245	267	5		
11	I2	173	Total	C	N	O	S	0	0
			1398	881	245	267	5		
11	I3	173	Total	C	N	O	S	0	0
			1398	881	245	267	5		

- Molecule 12 is a protein called Nuclear pore glycoprotein p62.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J0	171	Total	C	N	O	S	0	0
			1403	872	243	285	3		
12	J1	171	Total	C	N	O	S	0	0
			1403	872	243	285	3		
12	J2	171	Total	C	N	O	S	0	0
			1403	872	243	285	3		
12	J3	171	Total	C	N	O	S	0	0
			1403	872	243	285	3		
12	J4	171	Total	C	N	O	S	0	0
			1403	872	243	285	3		

- Molecule 13 is a protein called Nuclear pore complex protein Nup133.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K0	1086	Total	C	N	O	S	0	0
			8574	5420	1425	1692	37		
13	K1	1086	Total	C	N	O	S	0	0
			8574	5420	1425	1692	37		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	K2	1086	Total	C	N	O	S	0	0
			8574	5420	1425	1692	37		
13	K3	1086	Total	C	N	O	S	0	0
			8574	5420	1425	1692	37		

- Molecule 14 is a protein called Nuclear pore complex protein Nup107.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L0	782	Total	C	N	O	S	0	0
			6383	4064	1079	1208	32		
14	L1	782	Total	C	N	O	S	0	0
			6383	4064	1079	1208	32		
14	L2	782	Total	C	N	O	S	0	0
			6383	4064	1079	1208	32		
14	L3	782	Total	C	N	O	S	0	0
			6383	4064	1079	1208	32		

- Molecule 15 is a protein called Nuclear pore complex protein Nup96.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M0	673	Total	C	N	O	S	0	0
			5461	3467	964	1004	26		
15	M1	673	Total	C	N	O	S	0	0
			5461	3467	964	1004	26		
15	M2	673	Total	C	N	O	S	0	0
			5461	3467	964	1004	26		
15	M3	673	Total	C	N	O	S	0	0
			5461	3467	964	1004	26		

- Molecule 16 is a protein called Protein SEC13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N0	301	Total	C	N	O	S	0	0
			2352	1479	409	452	12		
16	N1	301	Total	C	N	O	S	0	0
			2352	1479	409	452	12		
16	N2	301	Total	C	N	O	S	0	0
			2352	1479	409	452	12		
16	N3	301	Total	C	N	O	S	0	0
			2352	1479	409	452	12		

- Molecule 17 is a protein called Nucleoporin SEH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O0	323	Total	C	N	O	S	0	0
			2528	1584	452	475	17		
17	O1	323	Total	C	N	O	S	0	0
			2528	1584	452	475	17		
17	O2	323	Total	C	N	O	S	0	0
			2528	1584	452	475	17		
17	O3	323	Total	C	N	O	S	0	0
			2528	1584	452	475	17		

- Molecule 18 is a protein called Nuclear pore complex protein Nup85.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P0	655	Total	C	N	O	S	0	0
			5257	3341	898	982	36		
18	P1	655	Total	C	N	O	S	0	0
			5257	3341	898	982	36		
18	P2	655	Total	C	N	O	S	0	0
			5257	3341	898	982	36		
18	P3	655	Total	C	N	O	S	0	0
			5257	3341	898	982	36		

- Molecule 19 is a protein called Nucleoporin Nup43.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q0	345	Total	C	N	O	S	0	0
			2703	1690	474	527	12		
19	Q1	345	Total	C	N	O	S	0	0
			2703	1690	474	527	12		
19	Q2	345	Total	C	N	O	S	0	0
			2703	1690	474	527	12		
19	Q3	345	Total	C	N	O	S	0	0
			2703	1690	474	527	12		

- Molecule 20 is a protein called Nuclear pore complex protein Nup160.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R0	1399	Total	C	N	O	S	0	0
			11132	7093	1878	2088	73		
20	R1	1399	Total	C	N	O	S	0	0
			11132	7093	1878	2088	73		
20	R2	1399	Total	C	N	O	S	0	0
			11132	7093	1878	2088	73		

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Mol	Chain	Residues	Atoms					AltConf	Trace
20	R3	1399	Total	C	N	O	S	0	0
			11132	7093	1878	2088	73		

- Molecule 21 is a protein called Nucleoporin Nup37.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S0	322	Total	C	N	O	S	0	0
			2552	1626	436	475	15		
21	S1	322	Total	C	N	O	S	0	0
			2552	1626	436	475	15		
21	S2	322	Total	C	N	O	S	0	0
			2552	1626	436	475	15		
21	S3	322	Total	C	N	O	S	0	0
			2552	1626	436	475	15		

- Molecule 22 is a protein called Protein ELYS.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T0	1004	Total	C	N	O	S	0	0
			7960	5069	1359	1490	42		
22	T1	1004	Total	C	N	O	S	0	0
			7960	5069	1359	1490	42		

- Molecule 23 is a protein called Nuclear pore complex protein Nup98.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U0	150	Total	C	N	O	S	0	0
			1193	756	205	229	3		
23	U1	19	Total	C	N	O		0	0
			151	98	27	26			
23	U2	19	Total	C	N	O		0	0
			151	98	27	26			
23	U3	19	Total	C	N	O		0	0
			151	98	27	26			
23	U4	19	Total	C	N	O		0	0
			151	98	27	26			
23	U5	19	Total	C	N	O		0	0
			151	98	27	26			
23	U6	19	Total	C	N	O		0	0
			151	98	27	26			

- Molecule 24 is a protein called Nuclear pore complex protein Nup214.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V0	273	Total	C	N	O	S	0	0
			2203	1376	398	423	6		

- Molecule 25 is a protein called Nuclear pore complex protein Nup88.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W0	735	Total	C	N	O	S	0	0
			5836	3714	988	1103	31		



- Molecule 1: E3 SUMO-protein ligase RanBP2





LEU	ASP	PHE	LYS	HIS	VAL	VAL	PHE	GLY	PHE	VAL	LYS	ASP	GLY	MET	ASP	THR	VAL	LYS	LYS	ILE	GLU	SER	PHE	GLY	SER	PRO	LYS	GLY	SER	VAL	CYS	ARG	ARG	ILE	THR	THR	ILE	THR	GLU	CYS	GLY	GLN	ILE
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Chain 02: 6% 22% 77%

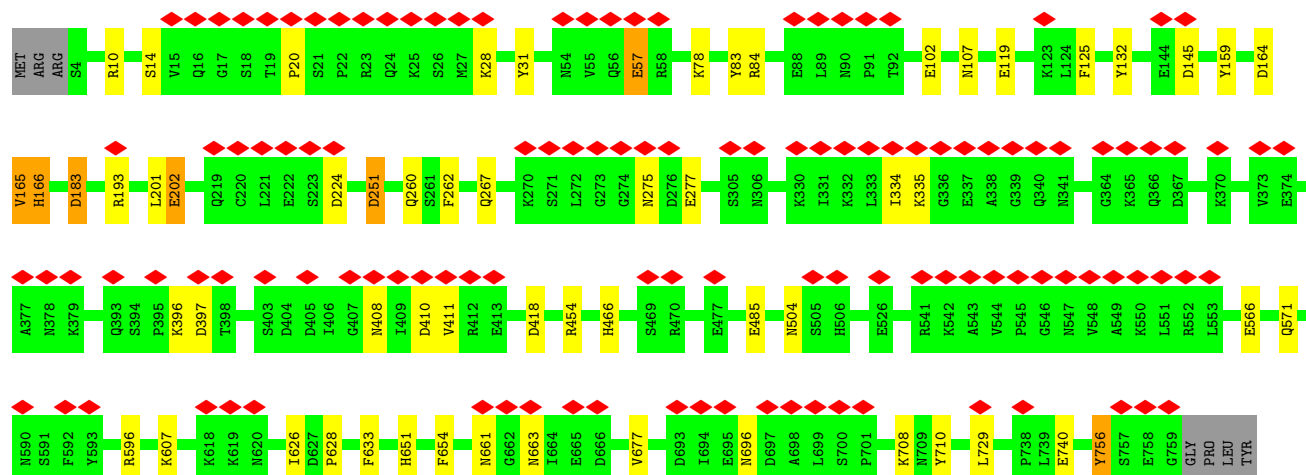




[illegible]

- Molecule 1: E3 SUMO-protein ligase RanBP2

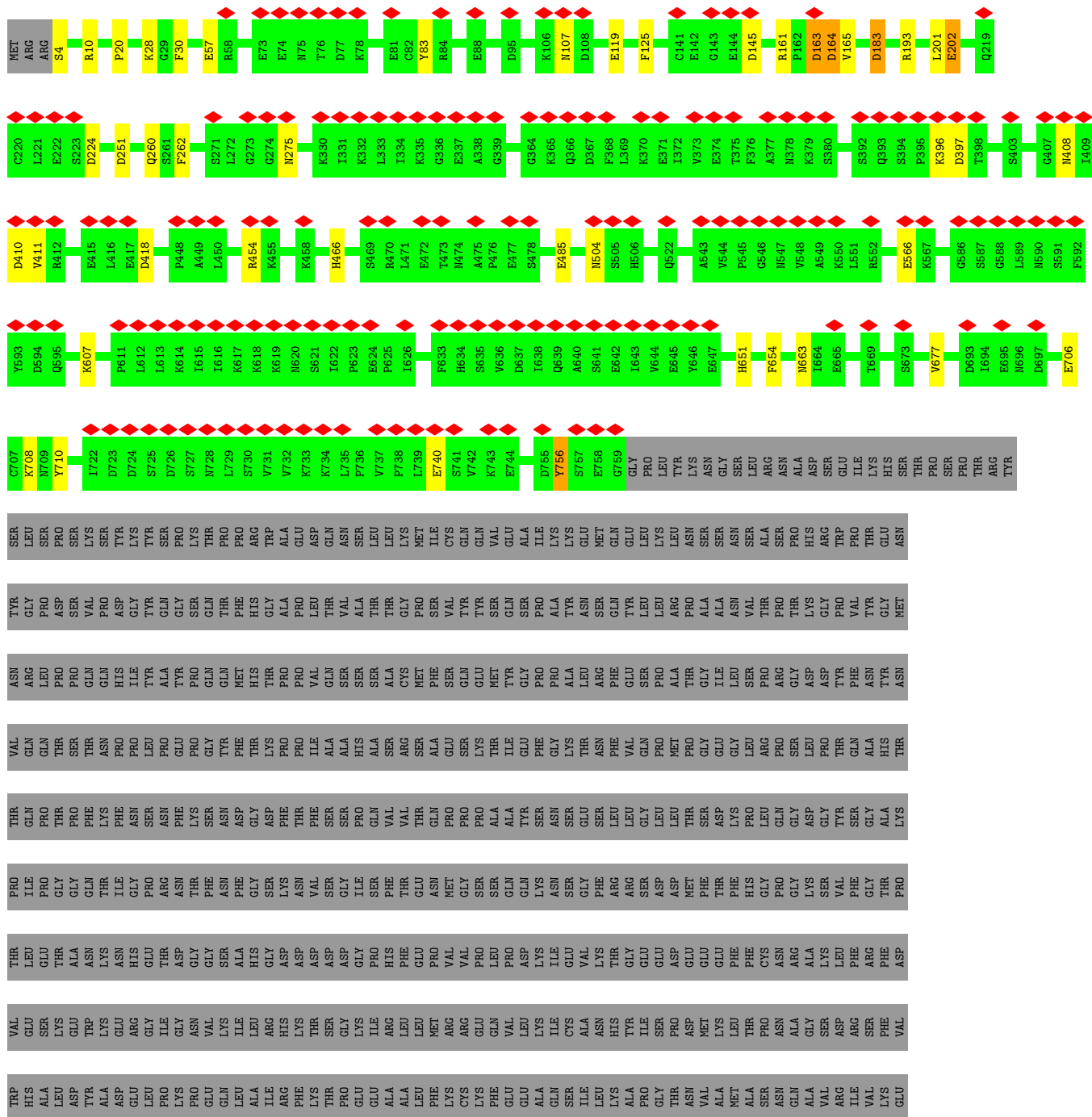
Chain 03: 22% 77%







- Molecule 1: E3 SUMO-protein ligase RanBP2







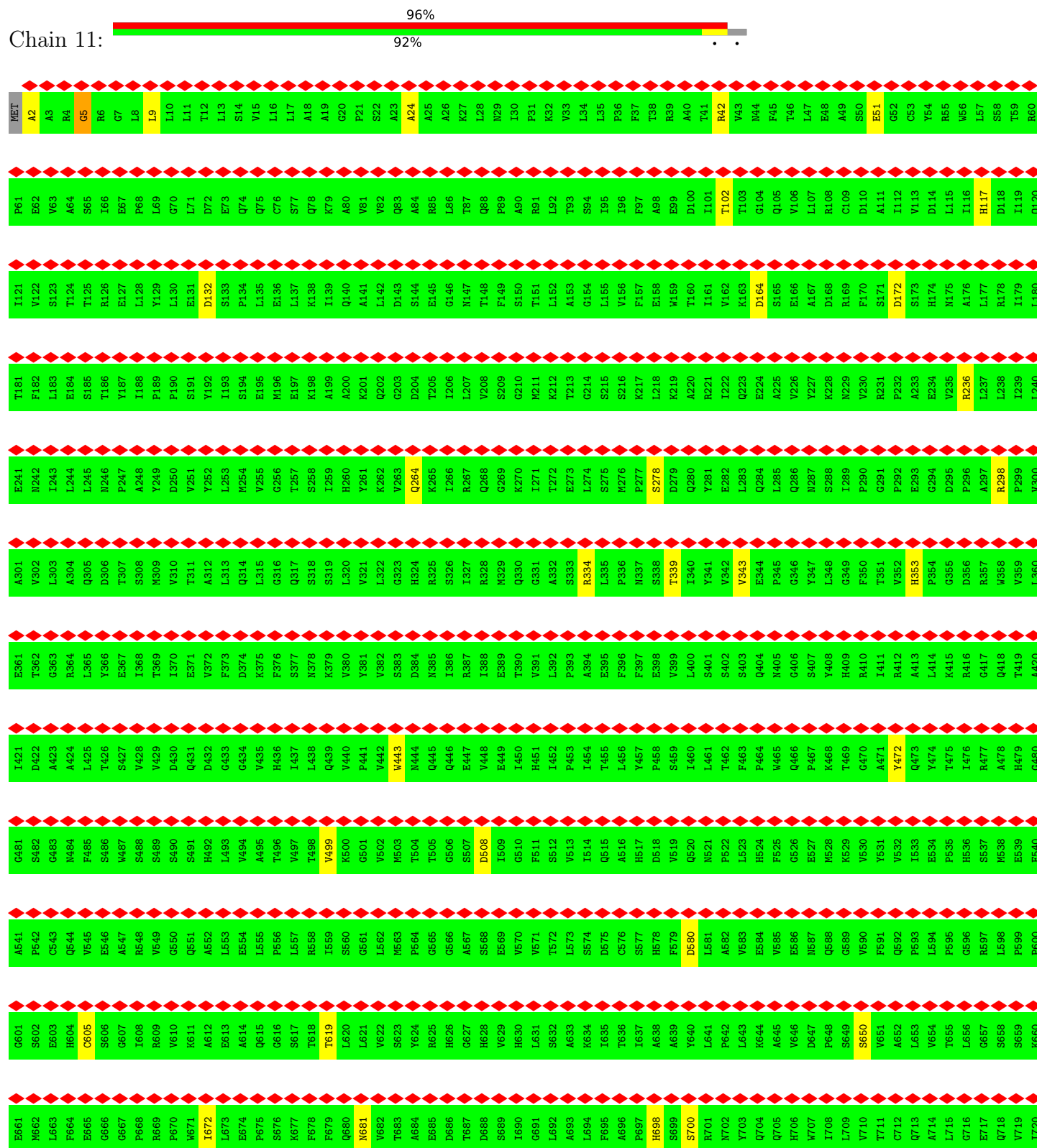
L1021	L961	E901	G841	S781	A721	E661	G601	A541	G481	I421	E361	A301
R1022	C962	V902	L842	H782	L722	M662	S602	P542	S482	D422	T362	V302
A1023	L963	T903	Q843	R783	S723	L663	E603	C543	G483	A423	G363	L303
A1024	V964	I904	A844	N784	V724	F664	H604	Q544	M484	A424	R364	A304
S1025	F965	Y905	T845	P785	G725	E665	C605	V545	F485	L425	L365	Q305
P1026	P966	N906	L846	R786	N726	G666	S606	E546	S486	T426	Y366	D306
I1027	A967	H907	V847	L787	K727	G667	G607	A547	W487	S427	E367	T307
T1028	P968	P908	H848	D788	P728	P668	I608	R548	S488	V428	I368	S308
T1029	A969	G909	E849	L789	S729	R669	R609	V549	S489	V429	T369	M309
L1030	K970	I910	A850	A790	L730	P670	V610	G550	S490	D430	I370	V310
V1031	A971	Q911	S851	A791	T731	M671	K611	Q551	S491	Q431	E371	T311
A1032	V972	A912	G852	Y792	N732	L672	A612	A552	H492	D432	V372	A312
L1033	V973	E913	T853	D793	P733	L673	E613	L553	L493	G433	F373	L313
D1034	V974	L914	T854	Q794	F734	E674	A614	E554	V494	G434	D374	Q314
E1035	V975	R915	A855	E795	P735	P675	Q615	L555	A495	V435	K375	L315
A1036	S976	I916	T856	G796	A736	S676	G616	P556	T496	H436	F376	G316
L1037	D977	R917	T857	R797	E737	K677	S617	L557	V497	I437	S377	Q317
D1038	I978	E918	A858	R798	E738	P678	T618	R558	T498	L438	N378	S318
M1039	Q979	G919	T859	F799	P739	F679	T619	I559	V499	Q439	K379	S319
Y1040	E980	S920	A860	D800	A740	Q680	L620	S560	K500	V440	V380	L320
T1041	L981	G921	T861	N801	V741	M681	L621	G561	G501	P441	Y381	V321
I1042	V982	Y922	G862	F802	T742	L682	V622	L562	V502	V442	V382	L322
T1043	F983	F923	Y863	S803	K743	T683	S623	M563	M503	W443	S383	G323
F1044	R984	F924	Q864	S804	F744	A684	Y624	P564	T504	N444	D384	H324
L1045	V985	L925	E865	L805	V745	E685	R625	G565	T505	Q445	N385	R325
I1046	V986	N926	S866	S806	G746	D686	H626	G566	G506	Q446	I386	S326
A1047	D987	T927	H867	L807	A747	T687	G627	A567	S507	E447	R387	I327
G1048	K988	S928	L868	Q808	P748	M688	H628	S568	D508	V448	I388	R328
V1049	V989	T929	S869	M809	P749	S689	V629	E569	I509	E449	S389	M329
A1050	E990	A930	S870	E810	S750	L690	H630	V570	G510	I450	T390	Q330
I1051	I991	D931	A871	S811	R751	G691	L631	V571	F511	H451	V391	G331
Q1052	G992	V932	R872	T812	L752	L692	S632	T572	S512	I452	L392	A332
Q1053	K993	V933	T873	R813	T753	A693	A633	L573	V513	I453	P393	S333
T1054	K994	K934	K874	P814	L754	L694	K634	S574	I514	I454	A394	R334
V1055	V995	V935	Q875	V815	A755	F695	I635	D575	Q515	T455	E395	L335
L1056	K996	A936	P876	L816	P756	A696	T636	C576	A516	I456	F396	P336
T1057	A997	Y937	H877	A817	P757	P697	I637	S577	H517	I457	F397	N337
A1058	D998	Q938	D878	S818	V758	H698	A638	H578	D518	P458	E398	S338
S1059	V999	E939	P879	L819	T759	S699	A639	F579	V519	S459	V399	T339
V1060	R1000	A940	L880	E820	S760	S700	Y640	D580	Q520	I460	L400	I340
T1061	V1001	R941	V881	P821	P761	R701	L641	L581	N521	L461	S401	Y341
T1062	L1002	G942	P882	E822	Q762	N702	P642	P522	P522	T462	S402	V342
K1063	D1003	V943	L883	L823	L763	Y703	L643	V583	L523	F463	S403	V343
A1064	L1004	A944	S884	P824	D764	Q704	K644	E584	H524	P464	Q404	E344
K1065	H1005	H945	A885	M825	V765	Q705	A645	V585	F525	W465	N405	P345
Q1066	K1006	V946	S886	Q826	S766	H706	V646	E586	G526	Q466	G406	G346
R1067	X1007	H947	T887	L827	C767	W707	D647	N587	E527	P467	S407	Y347
I1068	P1008	P948	E888	V828	P768	I708	P648	Q588	M528	K468	Y408	L348
M1069	F1009	L949	L889	S829	L769	L709	S649	G589	K529	T469	H409	G349
S1070	I1010	L950	T890	Q830	L770	V710	S650	V590	V530	R470	R410	F350
A1071	A1011	P951	L891	D831	Q771	T711	V651	F591	Y531	A471	I411	T351
P1072	K1012	G952	V892	D832	T772	G712	A652	Q592	V532	Y472	R412	V352
Q1073	Y1013	S953	E893	E833	N773	Q713	L653	P593	I533	Q473	A413	H353
Q1074	F1014	S954	D894	S834	K774	A714	V654	L594	E534	I474	L414	P354
I1075	P1015	T955	V895	G835	Q775	L715	T655	P595	F535	T475	K415	G355
E1076	F1016	V956	R896	Q836	V776	G716	L656	G596	H536	I476	R416	D356
V1077	M1017	H957	H897	K837	V777	E717	G657	R597	S537	R477	G417	R357
T1078	K958	T958	K838	L838	P778	Q718	S658	L598	M538	A478	Q418	V358
P1079	L1019	H959	P899	L839	V779	V719	S659	P599	E539	H479	T419	V359
P1080	K1020	D960	E900	H840	S780	I720	K660	P600	F540	G480	A420	L360

M180	F181	L182	T183	F184	L185	T186	F187	L188	T189	F190	L191	T192	F193	L194	T195	F196	L197	T198	F199	L200
F1081	R1082	L1083	M1084	P1085	R1086	K1087	V1088	T1089	L1090	K1101	V1102	G1103	P1104	L1105	P1106	Q1107	S1108	M1109	I1110	L1111
L1141	V1142	Q1143	A1144	V1145	D1146	A1147	E1148	T1149	G1150	K1151	V1152	V1153	I1154	I1155	S1156	Q1157	D1158	L1159	V1160	Q1161
F1201	G1202	M1203	A1204	V1205	P1206	G1207	L1208	T1209	F1210	H1211	W1212	S1213	V1214	T1215	K1216	R1217	D1218	V1219	L1220	D1221
D1261	P1262	T1263	S1264	G1265	Q1266	L1267	V1268	G1269	L1270	A1271	R1272	E1273	L1274	S1275	D1276	E1277	I1278	Q1279	V1280	Q1281
R1321	V1322	L1323	D1324	G1325	P1326	E1327	K1328	V1329	P1330	V1331	V1332	H1333	V1334	D1335	E1336	K1337	G1338	F1339	L1340	A1341
M1381	S1382	P1383	V1384	V1385	H1386	L1387	Q1388	M1389	K1390	E1391	A1392	L1393	V1394	A1395	V1396	P1397	L1398	G1399	M1400	T1401
N1441	M1442	T1443	C1444	V1445	V1446	R1447	T1448	V1449	S1450	V1451	G1452	L1453	V1454	L1455	L1456	R1457	V1458	W1459	D1460	A1461
L1501	E1502	G1503	L1504	S1505	G1506	T1507	W1508	S1509	S1510	S1511	A1512	M1513	S1514	I1515	L1516	H1517	I1518	D1519	P1520	K1521
H1561	L1562	H1563	P1564	I1565	Q1566	T1567	S1568	F1569	Q1570	E1571	A1572	T1573	A1574	S1575	K1576	V1577	I1578	V1579	A1580	V1581
D1621	F1622	P1623	S1624	D1625	V1626	F1627	F1628	P1629	V1630	E1631	P1632	F1633	F1634	D1635	T1636	L1637	L1638	G1639	Q1640	Y1641
V1681	G1682	A1683	E1684	V1685	P1686	F1687	S1688	P1689	G1690	L1691	F1692	D1693	A1694	Q1695	A1696	E1697	T1698	L1699	L1700	S1701
W1741	P1742	S1743	F1744	L1745	T1746	Y1747	T1748	V1749	G1750	V1751	L1752	D1753	P1754	A1755	A1756	G1757	S1758	Q1759	G1760	Y1761
L1762	S1763	T1764	L1765	L1766	L1767	E1768	S1769	P1770	R1771	V1772	F1773	G1774	A1775	P1776	E1777	V1778	L1779	M1780	L1781	L1782
V1830	F1831	C1832	THR	PRO	ARG	ASP	LEU	ALA	VAL	PRO	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
T1830	F1831	C1832	THR	PRO	ARG	ASP	LEU	ALA	VAL	PRO	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
L1806	T1807	L1808	L1809	L1810	L1811	L1812	L1813	L1814	L1815	L1816	L1817	L1818	L1819	L1820	L1821	L1822	L1823	L1824	L1825	L1826
L1806	T1807	L1808	L1809	L1810	L1811	L1812	L1813	L1814	L1815	L1816	L1817	L1818	L1819	L1820	L1821	L1822	L1823	L1824	L1825	L1826

TRP
SER
PRO
ALA
TYR
ALA
SER
HIS

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Chain 11:



M1381	M1441	R1321	D1261	F1201	L1141	F1081	L1021	L961	E901	G841	A721
S1382	M1442	V1322	P1262	G1202	V1142	R1082	R1022	C962	V902	L842	L722
P1383	P1383	L1323	T1263	M1203	Q1143	L1083	A1023	L963	V903	Q843	S723
V1384	C1444	D1324	S1264	A1204	A1144	M1084	A1024	V964	I904	A844	V724
L1385	V1445	G1325	G1265	V1205	V1145	P1085	S1025	F965	Y905	P785	G725
H1386	V1446	P1326	Q1266	P1206	D1146	R1086	P1026	P966	N906	L846	N726
T1387	T1447	E1327	L1267	G1207	A1147	K1087	I1027	A967	H907	L787	K727
Q1388	R1448	K1328	Y1268	L1208	E1148	V1088	I1028	P968	P908	H848	P728
V1449	V1449	V1329	G1269	T1209	T1149	T1089	T1029	A969	G909	E849	S729
K1390	S1450	P1330	L1270	F1210	G1150	L1090	L1030	K970	I910	A850	L730
E1391	V1451	V1331	A1271	H1211	K1151	L1091	V1031	A971	Q911	S851	T731
A1392	G1452	V1332	R1272	W1212	V1152	I1092	A1032	V972	A912	G852	N732
L1393	L1453	H1333	E1273	S1213	V1153	G1093	L1033	V973	E913	T853	P733
V1394	T1454	V1334	L1274	V1214	I1154	A1094	D1034	Y974	L914	T854	F734
A1395	L1455	D1335	S1275	T1215	I1155	T1095	A1036	V975	R915	E795	A735
V1396	L1456	E1336	D1276	K1216	S1156	M1096	E1036	S976	I916	G796	P736
P1397	L1457	K1337	E1277	R1217	Q1157	Q1097	L1037	D977	R917	T857	V737
L1398	V1458	G1338	I1278	D1218	D1158	V1098	D1038	T978	E918	A858	E738
G1399	V1459	F1339	Q1279	V1219	L1159	T1099	M1039	Q979	G919	T859	P739
M1400	D1460	L1340	V1280	L1220	V1160	S1100	Y1040	E980	S920	A860	A740
T1401	A1461	A1341	Q1281	D1221	Q1161	E1101	T1041	L981	G921	T861	
V1402	E1462	S1342	V1282	L1222	V1162	G1102	I1042	Y982	Y922	G862	V742
T1403	P1463	F1343	E1283	R1223	E1163	G1103	T1043	I983	F923	S863	
P1464	P1464	S1344	G1284	G1224	V1164	P1104	F1044	R984	F924	Q864	K744
G1465	G1465	M1345	K1285	R1225	L1165	Q1105	L1045	V985	L925	E865	V745
V1406	L1466	I1346	L1286	H1226	L1166	P1106	I1046	V986	N926	S866	C746
H1407	S1467	G1347	Q1287	L1227	L1167	Q1107	R1047	D987	T927	H867	A747
F1408	D1468	T1348	L1288	E1228	R1168	S1108	G1048	K988	S928	L868	P748
H1409	F1469	S1349	L1289	A1229	A1169	M1109	V1049	V989	T929	W809	
D1410	M1470	T1350	N1290	S1230	V1170	I1110	A1050	E990	A930	S870	P749
N1411	P1471	I1351	P1291	I1231	R1171	L1111	I1051	T991	D931	E810	S750
G1412	G1413	E1352	E1292	R1232	I1172	F1112	G1052	G992	V932	T812	R751
D1414	V1474	V1353	L1293	L1233	R1173	S1113	Q1053	K993	V933	R813	L752
V1415	L1475	I1354	E1294	P1234	A1174	T1114	T1054	T994	K934	K874	L754
F1416	Q1476	A1355	A1295	S1235	P1175	S1115	S1055	V995	V935	Q875	A755
H1417	A1477	Q1356	E1296	Q1236	I1176	E1117	L1056	K996	A936	P876	P756
A1418	L1478	E1357	Q1297	Y1237	M1177	S1118	T1057	A997	Y937	H877	V757
H1419	S1479	P1358	I1298	M1238	R1178	S1118	A1058	V998	Q938	D878	V758
S1420	H1480	F1359	L1299	F1239	M1179	V1119	S1059	V999	E939	P879	T759
E1481	E1481	G1360	M1300	A1240	R1180	A1120	V1060	R1000	A940	L880	S760
S1421	V1422	A1361	S1301	M1241	T1181	L1121	T1061	V1001	R941	P881	P761
L1482	L1422	M1362	P1302	N1242	G1182	V1122	M1062	L1002	G942	P882	Q762
G1484	G1484	Q1363	N1303	V1243	T1183	S1123	K1063	D1003	L883	L823	L763
A1485	F1425	T1364	S1304	L1244	Q1184	A1124	A1064	L1004	A944	S884	D764
M1486	A1426	I1365	Y1305	G1245	M1185	A1125	G1065	H1005	M945	M825	M765
V1487	A1426	I1366	I1306	R1246	P1186	G1126	Q1066	K1006	V946	Q826	S766
T1427	T1427	V1367	K1307	V1247	L1187	L1127	R1067	K1007	H947	I887	C767
N1428	V1488	A1368	L1308	K1248	Y1188	V1128	I1068	P1008	P948	E888	P768
R1429	G1489	V1369	Q1309	G1249	V1189	Q1129	M1069	F1009	L849	S829	S729
D1430	D1490	K1370	T1310	R1250	T1190	G1130	S1070	L1010	L950	I890	L770
F1431	V1491	V1371	N1311	T1251	G1191	L1131	A1071	A1011	P951	L891	Q771
F1432	L1492	S1372	R1312	G1252	I1192	A1132	P1072	K1012	G952	V892	Q772
V1433	C1493	P1373	D1313	L1253	T1193	I1133	Q1073	Y1013	E953	E893	N773
Q1434	L1494	V1374	G1314	R1254	N1194	G1134	Q1074	F1014	S954	D894	K774
I1435	T1495	S1375	A1315	V1255	H1195	N1135	I1075	P1015	T955	V895	Q775
G1436	V1496	Y1376	A1316	V1256	Q1196	G1136	E1076	F1016	I956	R896	V776
V1497	L1498	L1377	S1317	V1257	N1197	T1137	V1077	M1017	M957	V897	P778
G1438		R1378	L1318	K1258	P1198	V1138	F1078	D1018	I958	S898	
T1439		V1379	S1319	L1259	F1199	S1139	P1079	L1019	H959	P899	
T1440		S1380	Y1320	V1260	S1200	G1140	P1080	K1020	D960	S780	

L1501	H1561	D1621	V1681	W1741	F1811	LEU
E1502	L1562	F1622	G1682	P1742	F1812	TRP
G1503	H1563	P1623	A1683	S1743	T1813	SER
L1504	P1564	S1624	E1684	F1744	L1814	PRO
S1505	I1565	Q1625	V1685	T1745	F1815	ALA
G1506	Q1566	D1626	P1686	T1746	A1816	TYR
T1507	T1567	V1627	F1687	Y1747	L1817	ALA
W1508	S1568	F1628	S1688	T1748	L1818	SER
S1509	F1569	T1629	P1689	V1749	A1819	HIS
S1510	Q1570	V1630	G1690	G1750	G1820	
S1511	E1571	E1631	L1691	V1751	T1821	
A1512	A1572	P1632	F1692	L1752	A1822	
M1513	T1573	Q1633	A1693	D1753	C1832	THR
S1514	A1574	F1634	D1694	P1754	PRO	ARG
I1515	S1575	D1635	Q1695	A1755	ASP	LEU
L1516	K1576	T1636	A1696	A1756	ASP	ALA
H1517	V1577	A1637	E1697	E1757	LEU	VAL
I1518	I1578	L1638	I1698	S1758	ALA	ALA
D1519	V1579	G1639	L1699	Q1759	VAL	PRO
P1520	A1580	Q1640	L1700	G1760	PRO	ALA
L1521	V1581	Y1641	S1701	P1761	ALA	ALA
T1522	G1582	F1642	N1702	L1762	THR	THR
G1523	D1583	C1643	H1703	S1763	PRO	ARG
V1524	R1584	S1644	Y1704	T1764	ALA	ALA
A1525	S1585	I1645	T1705	T1765	SER	SER
V1526	S1586	T1646	S1706	L1766	PRO	GLY
A1527	N1587	M1647	S1707	T1767	GLY	GLY
R1528	L1588	H1648	E1708	F1768	HIS	HIS
A1529	R1589	I1649	I1709	S1769	SER	SER
V1530	G1590	L1650	R1710	S1770	PRO	PRO
G1531	E1591	T1651	V1711	P1771	TVR	TVR
S1532	C1592	D1652	F1712	V1772	PHE	PHE
V1533	V1593	K1653	G1713	T1773	ALA	ALA
T1534	P1594	Q1654	A1714	N1774	ALA	ALA
V1535	T1595	R1655	P1715	Q1775	SER	SER
Y1536	Q1596	K1656	E1716	A1776	PRO	PRO
Y1537	R1597	H1657	V1717	I1777	THR	THR
E1538	E1598	L1658	L1718	A1778	PRO	PRO
V1539	V1599	S1659	E1719	I1779	ASN	ASN
A1540	I1600	M1660	N1720	P1780	ALA	ALA
G1541	Q1601	K1661	L1721	V1781	LEU	LEU
H1542	A1602	K1662	E1722	T1782	PRO	PRO
L1543	L1603	T1663	V1723	V1783	ALA	ALA
R1544	H1604	A1664	K1724	A1784	ARG	ARG
T1545	P1605	L1665	S1725	F1785	LYS	LYS
Y1546	E1606	V1666	G1726	V1786	ALA	ALA
K1547	T1607	V1667	S1727	V1787	PRO	PRO
E1548	L1608	S1668	P1728	D1788	PRO	PRO
V1549	I1609	A1669	A1729	R1789	SER	SER
V1550	S1610	S1670	V1730	G1791	GLY	GLY
V1551	C1611	L1671	L1731	P1792		
S1552	Q1612	S1672	A1732	G1793		
V1553	S1613	S1673	F1733	P1794		
P1554	Q1614	S1674	A1734			
Q1555	F1615	H1675	K1735			
I1556	K1616	F1676	E1736			
I1557	P1617	S1677	K1737			
M1558	A1618	T1678	S1738			
A1559	V1619	E1679	F1739			
R1560	F1620	Q1680	G1740			

• Molecule 2: Nuclear pore membrane glycoprotein 210



MET	A2	A3	R4	O5	R6	G7	L8	L9	L10	L11	T12	L13	S14	V15	L16	L17	A18	A19	G20	P21	S22	A23	A24	A25	A26	K27	L28	N29	I30	P31	K32	V33	L34	L35	P36	F37	T38	R39	A40	T41	R42	V43	M44	F45	T46	L47	E48	A49	S50	E51	G52	C53	Y54	R55	W56	L57	D58	T59	R60
	P61	E62	V63		A64	S65	I66	E67	P68	L69	G70	L71	D72	E73	Q74	Q75	C76	S77	Q78	K79	A80	V81		V82	Q83	A84	R85	L86	T87	Q88	P89	A90	R91	L92	T93	S94	I95	I96	F97	A98		E99	D100	I101	T102	T103	G104	Q105	V106		L107	A108	R109	C110	D111	I112	S113	V114	D115

F1081	L1021	E901	G841	S781	A721	E661	G601	A541	G481	I421	E361
R1082	R1022	V902	L842	H782	L722	M662	S602	P542	S482	D422	T362
L1083	L1023	T903	Q843	R783	S723	L663	E503	C543	G483	A423	G363
M1084	A1024	I904	A844	N784	V724	F664	H604	Q544	N484	A424	R364
P1085	S1025	Y905	L845	P785	G725	E665	C505	E545	F485	L425	L365
K1087	P1026	N906	L846	R786	N726	G666	S606	E546	S486	T426	Y366
V1088	A967	H907	H847	L787	K727	G667	G607	A547	W487	S427	E367
T1089	P968	P908	H848	D788	P728	P668	I608	R548	S488	V428	I368
L1090	A969	G909	E849	L789	S729	R669	R609	V549	S489	V429	T369
T1091	K970	I910	A850	A790	L730	P670	V610	P670	S490	D430	I370
L1092	A971	Q911	S851	A791	T731	W671	K611	Q551	S491	Q431	E371
G1093	V972	A912	G852	Y792	N732	I672	A612	A552	H492	D432	V372
A1094	L1033	E913	T853	D793	P733	L673	E513	L553	L493	G433	F373
T1095	Y974	L914	T854	Q794	F734	E674	A614	E554	V494	G434	D374
M1096	V975	R915	A855	E795	P735	P675	Q615	L555	A495	V435	K375
Q1097	S976	I916	T856	G796	A736	S676	G616	P556	T496	H436	F376
V1098	D977	R917	T857	R797	E737	K677	S617	L557	T497	I437	S377
T1099	I978	E918	A858	R798	E738	F678	T618	R558	T498	L438	N378
S1100	Q979	G919	T859	F799	P739	F679	T619	I559	V499	Q439	K379
E1101	E980	S920	A860	D800	A740	Q680	L620	S560	K500	V440	V380
G1102	T1041	G921	T861	N801	V741	N681	L621	G561	G501	P441	Y381
L1103	Y982	Y922	G862	F902	V742	V682	V622	L562	V502	V442	S382
P1104	I983	F923	Y863	S803	K743	T683	S623	M563	M503	W443	S383
Q1105	R984	F924	Q864	S804	F744	A684	Y624	P564	T504	N444	D384
L1106	V985	L925	E865	L805	V745	E685	R625	G565	T505	Q445	N385
Q1107	V986	N926	S866	S806	G746	D686	H626	G566	G506	Q446	I386
S1108	D987	T927	H867	L807	A747	T687	G627	A567	S507	E447	R387
I1109	K988	S928	L868	Q808	P748	D688	H628	S568	D508	V448	I388
I1110	V989	T929	S869	W809	P749	S689	V629	E569	I509	E449	E389
L1111	E990	A930	S870	E810	S750	I690	H630	V570	G510	I450	T390
F1112	I991	D931	A871	S811	R751	G691	L631	V571	F511	H451	V391
S1113	G992	V932	R872	T812	L752	L692	S632	T572	S512	I452	L392
I1114	K993	V933	T873	R813	T753	A693	A633	L573	V513	P453	P393
S1115	T994	K934	K874	P814	L754	L694	K634	S574	I514	I454	A394
N1116	V995	V935	Q875	V815	A755	F695	I635	D575	Q515	T455	E395
E1117	A997	A936	P876	L816	P756	A696	T636	C576	A516	L456	F396
S1118	Y998	Q938	H877	A817	V757	P697	I637	S577	H517	Y457	F397
V1119	E999	I939	D878	S818	V758	H698	A638	H578	D518	P458	E398
A1120	R1000	E940	P879	I819	T759	S699	A639	F579	V519	S459	V399
L1121	V1001	R941	L880	E820	S760	S700	Y640	D580	Q520	I460	L400
V1122	L1002	G942	V881	P821	P761	R701	L641	L581	N521	L461	S401
S1123	D1003	Q943	R882	E822	Q762	N702	P642	A582	P522	L462	S402
A1124	L1004	A944	L883	L823	L763	Y703	L643	V583	L523	F463	S403
G1125	A1064	A945	S884	P824	T764	Q704	K644	E584	H524	P464	Q404
A1126	H1005	H946	A885	M825	M765	Q705	A645	V585	F525	W465	N405
L1127	K1006	V946	S886	Q826	S766	H706	V646	E586	G526	Q466	N406
V1128	K1007	H947	L887	L827	C767	W707	D647	N587	E527	P467	S407
T1129	P1008	P948	E888	V828	P768	I708	P648	Q588	M528	K468	Y408
Q1130	F1009	L949	L889	S829	L769	L709	S649	G589	K529	T469	H409
L1131	L1010	I950	T890	Q830	L770	V710	Y650	V590	V530	Q470	R410
A1132	A1011	P951	L891	D831	Q771	T711	V651	F591	Y531	A471	I411
I1133	K1012	G952	V892	D832	Q772	G712	A652	Q592	V532	Y472	R412
G1134	Y1013	S953	E893	E833	N773	Q713	L653	P593	I533	Q473	A413
N1135	F1014	R954	D894	S834	K774	A714	V654	L594	E534	Y474	L414
T1136	P1015	T955	V895	G835	Q775	L715	T655	P595	P535	T475	K415
G1137	E1076	I956	R896	Q836	Q776	G716	L656	G596	H536	I476	R416
V1138	M1017	N957	H897	K837	V777	E717	G657	R597	S537	R477	Q417
S1139	F1078	I958	S898	K838	P778	Q718	S658	L598	M538	A478	Q418
G1140	P1079	H959	P899	L839	V779	V719	S659	P599	E539	H479	T419
	K1020	D960	E900	H840	S780	I720	K660	P600	F540	G480	A420



MET	A2	A3	R4	G5	R6	G7	L8	L9	L10	L11	T12	L13	S14	V15	L16	L17	A18	A19	G20	P21	S22	A23	A24	A25	A26	K27	L28	N29	I30	P31	K32	V33	L34	L35	P36	F37	T38	R39	A40	T41	R42	V43	N44	F45	T46	L47	E48	A49	S50	E51	G52	C53	Y54	R55	W56	L57	S58	T59	R60
P61	E62	V63	A64	S65	I66	E67	P68	L69	G70	L71	D72	E73	Q74	Q75	C76	S77	Q78	K79	A80	V81	S82	Q83	A84	R85	L86	T87	Q88	P89	A90	R91	L92	T93	S94	I95	I96	F97	A98	E99	D100	I101	T102	T103	G104	Q105	V106	L107	R108	C109	D110	A111	I112	V113	D114	L115	I116	H117	D118	I119	Q120
I121	V122	S123	T124	T125	R126	E127	L128	Y129	L130	E131	D132	S133	P134	L135	E136	L137	K138	I139	Q140	A141	L142	D143	S144	E145	G146	N147	T148	F149	S150	T151	L152	A153	G154	L155	V156	F157	E158	W159	T160	I161	V162	K163	D164	S165	E166	A167	D168	R169	F170	S171	D172	S173	H174	N175	A176	L177	R178	I179	L180
T181	F182	L183	E184	T185	T186	Y187	I188	P189	P190	S191	Y192	I193	S194	E195	M196	E197	K198	A199	A200	K201	L202	G203	D204	T205	L206	L207	V208	S209	G210	M211	K212	L213	G214	S215	S216	K217	L218	K219	A220	R221	L222	Q223	E224	A225	V226	Y227	K228	M229	V230	R231	P232	A233	E234	V235	L236	R237	L238	I239	L240
E241	N242	L243	L244	L245	N246	P247	A248	Y249	D250	V251	Y252	L253	D254	V255	G256	T257	S258	I259	H260	Y261	K262	V263	Q264	K265	L266	R267	Q268	G269	K270	I271	T272	E273	L274	S275	N276	P277	S278	D279	Q280	Y281	E282	L283	Q284	L285	Q286	N287	S288	I289	P290	G291	P292	E293	G294	D295	P296	A297	R298	P299	V300
A301	V302	L303	A304	Q305	Q306	T307	S308	K309	V310	T311	A312	L313	Q314	L315	Q316	Q317	S318	S319	L320	V321	L322	G323	H324	K325	S326	L327	R328	K329	Q330	G331	A332	S333	R334	L335	P336	N337	S338	T339	L340	Y341	V342	V343	E344	P345	G346	Y347	L348	G349	F350	T351	V352	H353	P354	G355	D356	R357	K358	V359	L360
E361	T362	G363	R364	L365	V366	E367	L368	T369	L370	E371	V372	F373	D374	K375	F376	S377	K378	K379	V380	Y381	V382	S383	D384	N385	L386	R387	L388	E389	T390	V391	L392	P393	A394	E395	F396	F397	E398	V399	L400	N401	T402	F403	Q404	N405	Q406	S407	Y408	H409	R410	A411	R412	A413	L414	K415	R416	G417	T418	Y419	A420
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G481	S482	G483	H484	F485	S486	W487	S488	S489	S490	S491	H492	L493	V494	A495	T496	V497	T498	V499	K500	G501	V502	M503	T504	T505	G506	S507	D508	I509	G510	F511	S512	V513	L514	Q515	A516	H517	D518	V519	Q520	N521	P522	L523	H524	F525	G526	E527	H528	K529	V530	Y531	V532	I533	E534	P535	H536	S537	L538	E539	F540
A541	P542	C543	Q544	V545	E546	A547	R548	V549	G550	Q551	A552	L553	E554	L555	P556	L557	R558	I559	S560	G561	L562	M563	P564	G565	G566	A567	S568	E569	V570	V571	T572	L573	S574	D575	C576	S577	H578	F579	D580	L581	A582	V583	E584	V585	E586	N587	Q588	G589	V590	F591	Q592	P593	L594	P595	G596	A597	L598	P599	P600
G601	S602	E603	H604	C605	S606	G607	T608	R609	V610	K611	A612	E613	A614	Q615	G616	S617	T618	T619	L620	L621	V622	S623	Y624	H625	H626	G627	H628	V629	H630	L631	S632	A633	K634	L635	T636	L637	A638	A639	V640	L641	P642	L643	K644	A645	V646	D647	P648	S649	V650	V651	A652	L653	V654	T655	L656	G657	L658	S659	K660
E661	M662	L663	F664	E665	G666	G667	P668	R669	P670	W671	L672	L673	E674	P675	S676	K677	F678	F679	G680	N681	V682	T683	A684	E685	D686	T687	D688	S689	I690	G691	L692	A693	L694	F695	P696	P697	H698	S699	S700	R701	M702	Y703	Q704	Q705	T706	W707	I708	L709	L710	T711	Q712	Q713	A714	L715	G716	E717	Q718	V719	I720
A721	L722	S723	V724	G725	N726	K727	P728	S729	L730	W731	N732	F733	F734	P735	A736	V737	E738	F739	A740	V741	V742	K743	F744	V745	C746	A747	F748	P749	S750	R751	L752	A753	L754	A755	P756	V757	V758	T759	S760	P761	Q762	L763	D764	M765	S766	C767	P768	L769	L770	Q771	Q772	N773	K774	Q775	V776	V777	P778	V779	S780

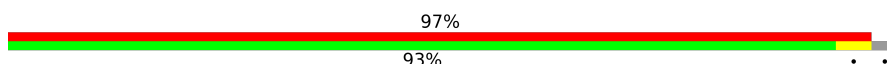
L1501	L1502	L1503	L1504	L1505	L1506	L1507	L1508	L1509	L1510	L1511	L1512	L1513	L1514	L1515	L1516	L1517	L1518	L1519	P1520	K1521	L1522	G1523	V1524	A1525	V1526	A1527	R1528	A1529	V1530	G1531	S1532	V1533	T1534	V1535	V1536	Y1537	V1538	V1539	A1540	G1541	H1542	L1543	R1544	T1545	V1546	K1547	E1548	V1549	V1550	V1551	S1552	V1553	P1554	Q1555	R1556	L1557	M1558	A1559	R1560
N1441	N1442	T1443	C1444	V1445	V1446	R1447	T1448	S1449	S1450	V1451	G1452	L1453	T1454	L1455	L1456	R1457	V1458	V1459	D1460	A1461	E1462	H1463	P1464	G1465	L1466	S1467	F1468	F1469	M1470	P1471	L1472	P1473	V1474	L1475	Q1476	A1477	T1478	S1479	P1480	E1481	L1482	S1483	G1484	A1485	M1486	V1487	V1488	G1489	V1490	V1491	L1492	C1493	Q1494	I1495	T1496	V1497	K1498	T1499	S1500
M1381	S1382	P1383	V1384	L1385	H1386	T1387	Q1388	L1389	K1390	E1391	A1392	L1393	V1394	A1395	V1396	P1397	L1398	G1399	M1400	T1401	V1402	T1403	F1404	T1405	V1406	H1407	F1408	H1409	D1410	N1411	S1412	G1413	D1414	V1415	F1416	H1417	A1418	H1419	S1420	S1421	V1422	L1423	M1424	F1425	A1426	T1427	M1428	R1429	D1430	D1431	F1432	V1433	Q1434	I1435	G1436	K1437	L1438	P1439	T1440
R1321	V1322	L1323	D1324	G1325	P1326	E1327	K1328	V1329	P1330	V1331	V1332	H1333	V1334	D1335	E1336	K1337	G1338	F1339	L1340	A1341	S1342	G1343	S1344	M1345	I1346	G1347	T1348	S1349	L1350	I1351	E1352	L1353	I1354	A1355	Q1356	E1357	P1358	F1359	G1360	A1361	N1362	Q1363	M1364	I1365	I1366	V1367	A1368	V1369	K1370	V1371	S1372	P1373	V1374	S1375	Y1376	L1377	R1378	V1379	S1380
D1261	P1262	T1263	S1264	G1265	Q1266	L1267	Y1268	G1269	L1270	A1271	R1272	E1273	L1274	S1275	D1276	E1277	L1278	Q1279	V1280	Q1281	V1282	F1283	E1284	L1285	L1286	Q1287	L1288	L1289	N1290	P1291	E1292	L1293	E1294	A1295	E1296	Q1297	L1298	L1299	M1300	S1301	P1302	M1303	S1304	Y1305	I1306	K1307	L1308	Q1309	T1310	M1311	R1312	G1313	G1314	A1315	S1316	S1317	L1318	S1319	Y1320
F1201	G1202	N1203	A1204	V1205	P1206	G1207	L1208	T1209	F1210	H1211	V1212	S1213	V1214	T1215	K1216	R1217	D1218	V1219	L1220	D1221	L1222	R1223	E1224	L1225	H1226	H1227	E1228	A1229	S1230	I1231	L1232	L1233	P1234	S1235	S1236	Y1237	N1238	F1239	A1240	M1241	G1242	V1243	L1244	G1245	R1246	V1247	K1248	G1249	R1250	T1251	G1252	L1253	R1254	V1255	V1256	V1257	A1259	V1260	
L1141	V1142	Q1143	A1144	V1145	D1146	A1147	E1148	T1149	G1150	K1151	V1152	V1153	T1154	L1155	S1156	L1157	D1158	L1159	V1160	Q1161	L1162	E1163	V1164	L1165	L1166	L1167	R1168	A1169	V1170	R1171	L1172	R1173	A1174	P1175	L1176	M1177	R1178	M1179	R1180	T1181	G1182	T1183	Q1184	M1185	P1186	L1187	V1188	V1189	T1190	G1191	L1192	T1193	L1194	H1195	Q1196	N1197	P1198	F1199	S1200
F1081	R1082	L1083	M1084	V1085	P1086	K1087	V1088	L1089	L1090	L1091	I1092	G1093	A1094	T1095	M1096	Q1097	V1098	T1099	S1100	E1101	I1042	G1103	P1104	L1105	Q1106	Q1107	S1108	N1109	I1110	L1111	F1112	S1113	I1114	S1115	M1116	E1117	S1118	V1119	A1120	L1121	L1122	S1123	A1124	G1125	L1126	L1127	V1128	Q1129	L1130	L1131	A1132	I1133	G1134	N1135	G1136	T1137	L1138	S1139	G1140
L1021	R1022	A1023	A1024	S1025	P1026	I1027	I1028	T1029	L1030	V1031	A1032	L1033	D1034	E1035	A1036	L1037	L1038	N1039	Y1040	T1041	I1042	T1043	F1044	L1045	I1046	R1047	G1048	V1049	A1050	I1051	Q1052	Q1053	T1054	S1055	L1056	T1057	A1058	S1059	V1060	T1061	N1062	K1063	A1064	G1065	Q1066	R1067	I1068	N1069	S1070	A1071	P1072	Q1073	Q1074	I1075	E1076	V1077	L1078	P1079	P1080
L961	C962	L963	V964	F965	P966	A967	P968	G969	I970	Q971	V972	G973	L974	R975	S976	D977	L978	Q979	E980	L981	V982	F983	R984	V985	V986	D987	K988	V989	E990	I991	G992	K993	T994	V995	K996	A997	V998	V999	R1000	V1001	L1002	D1003	L1004	H1005	K1006	K1007	P1008	F1009	L1010	A1011	K1012	S953	S954	T955	I956	M957	D1018	L1019	K1020
E901	V902	T903	I904	N905	N906	H907	P908	G909	I910	Q911	A912	E913	L914	R915	I916	R917	E918	G919	S920	G921	V922	F923	F924	L925	N926	T927	S928	T929	A930	D931	V932	V933	K934	V935	A936	Y937	Q938	E939	A940	R941	G942	V943	A944	M945	V946	H947	P948	L949	I950	P951	G952	S953	E954	V955	R956	V957	I958	H959	E960
G841	L842	Q843	A844	I845	L846	V847	H848	E849	A850	S851	G852	T853	T854	A855	I856	T857	A858	T859	A860	T861	G862	Y863	Q864	E865	S866	H867	L868	S869	S870	A871	R872	T873	K874	Q875	P876	H877	D878	P879	L880	V881	P882	L883	S884	A885	S886	I887	E888	L889	I890	L891	V892	E893	V895	R896	V897	K898	L899	E900	
H781	H782	R783	N784	P785	R786	L787	D788	L789	A790	A791	Y792	D793	Q794	E795	G796	R797	R798	F799	D800	N801	F802	S803	S804	L805	S806	I807	Q808	W809	E810	S811	T812	R813	R814	V815	L816	A817	S818	I819	E820	P821	E822	L823	P824	M825	Q826	L827	V828	S829	Q830	D831	D832	S833	G835	Q836	K837	L838	L839	H840	

L1141	F1081	L1021	E501	G841	S781	A721	E611	G601	A541	G481	I421
V1142	R1082	R1022	V902	L842	H782	L722	M622	S602	P542	S482	D422
Q1143	L1083	A1023	T903	Q843	R783	S723	L633	E603	C543	G483	A423
A1144	M1084	A1024	I904	A844	N784	V724	F644	H604	Q544	N484	A424
V1145	P1085	S1025	Y905	L845	P785	G725	E655	C605	V545	F485	L425
D1146	R1086	P1026	N906	L846	R786	N726	G666	S606	E546	S486	L426
A1147	K1087	I1027	H907	V847	L787	K727	G667	G607	A547	W487	S427
E1148	V1088	I1028	P908	H848	D788	P728	P668	I608	R548	S488	V428
T1149	T1089	T1029	G909	E849	L789	S729	R669	R609	V549	S489	V429
G1150	A969	K970	I910	A850	A790	L730	P670	V610	G550	S490	D430
K1151	A971	A971	Q911	S851	A791	T731	W671	K611	Q551	S491	Q431
V1152	I1092	A1032	A912	G852	V792	N732	I672	A612	A552	H492	D432
V1153	G1093	L1033	E913	T853	D793	P733	L673	E613	L553	L493	G433
I1154	A1094	D1034	L914	T854	Q794	F734	E674	A614	E554	V494	G434
I1155	T1095	E1035	R915	A855	E795	P735	P675	Q615	L555	A495	V435
S1156	M1096	A1036	I916	T856	G796	A736	S676	G616	P556	T496	H436
L1157	Q1097	D1037	R917	T857	R797	V737	K677	S617	L557	V497	I437
D1158	V1098	I1038	E918	A858	R798	E738	P678	T618	R558	T498	L438
L1159	T1099	M1039	G919	T859	F799	P739	F679	T619	I559	V499	Q439
V1160	S1100	Y1040	S920	A860	D800	A740	Q680	L620	S560	K500	V440
Q1161	E1101	T1041	G921	T861	N801	V741	N681	L621	G561	G501	P441
V1162	G1102	I1042	Y922	G862	F802	V742	V682	V622	V562	V502	V442
E1163	G1103	T1043	F923	Y863	S803	K743	T683	S623	M563	M503	W443
V1164	P1104	F1044	F924	Q864	S804	F744	A684	Y624	P564	T504	N444
L1165	Q1105	V1045	L925	E865	L805	V745	E685	R625	G565	T505	Q445
L1166	P1106	I1046	N926	S866	S806	C746	D686	H626	G566	G506	Q446
L1167	R1047	D1047	T927	H867	I807	A747	T687	G627	A567	S507	E447
R1168	S1108	G1048	S928	L868	Q808	P748	D688	H628	S568	D508	V448
A1169	N1109	V1049	T929	S869	W809	P749	S689	V629	E569	I509	E449
V1170	E990	A1050	A930	S970	E810	S750	I690	H630	V570	G510	I450
R1171	I991	I1051	D931	A871	S811	R751	G891	L631	V571	F511	H451
I1172	G992	G1052	V932	R872	T812	L752	L692	S632	T572	S512	I452
R1173	K993	Q1053	Y933	T873	R613	T753	A693	A633	L573	V513	P453
A1174	T994	T1054	K934	K874	P814	L754	L694	K634	S574	I514	I454
P1175	V995	S1055	V935	Q875	W815	A755	F695	I635	D575	Q515	T455
I1176	N1116	L1056	A936	P876	L816	P756	A696	T636	C576	A516	L456
M1177	E1117	T1057	Y937	H877	A817	V757	P697	I637	S577	H517	Y457
R1178	S1118	A1058	Q938	D878	S818	V758	H698	A638	D518	P458	P458
M1179	V1119	S1059	E939	P879	I819	T759	S699	A639	V519	S459	S459
R1180	A1120	V1060	A940	L880	E820	S760	S700	Y640	Q520	I460	I460
T1181	L1121	T1061	R941	V881	P821	P761	R701	L641	N521	L461	L461
G1182	V1122	N1062	G942	P882	E822	Q762	N702	P642	A582	P522	T462
T1183	S1123	K1063	V943	L883	L823	L763	V703	L643	V583	L523	F463
Q1184	A1124	A1064	A944	S884	P824	D764	Q704	K644	E584	H524	P464
M1185	A1125	H1005	N945	A885	W825	N765	Q705	A645	V585	F525	W465
P1186	G1126	K1006	V946	S886	Q826	S766	H706	V646	E586	G526	Q466
I1187	L1127	R1067	H947	I887	L827	C767	V707	D647	N587	E527	P467
V1188	V1128	I1068	P948	E888	V828	P768	I708	P648	Q588	M528	K468
I1189	Q1129	M1069	L949	L889	S829	L769	L709	S949	G589	K529	T469
T1190	L1010	S1070	L950	T890	Q830	L770	V710	S650	V590	G470	T469
G1191	A1011	A1071	P951	L891	D831	Q771	T711	V651	F591	Y531	A471
I1192	K1012	P1072	G952	V892	D832	Q772	C712	A652	Q592	V532	Y472
I1193	Y1013	Q1073	S953	E893	E833	N773	Q713	L653	P593	I533	Q473
M1194	G1134	Q1074	S954	D894	S834	K774	A714	V654	L594	E534	Y474
H1195	N1135	I1075	T955	V895	G835	Q775	L715	T855	P595	P535	T475
Q1196	G1136	E1076	T956	R896	Q836	V776	G716	L656	G596	H536	I476
M1197	T1137	V1077	N957	V897	K837	V777	E717	G657	R597	S537	R477
P1198	V1138	F1078	T958	S898	K838	P778	Q718	S658	L598	M538	A478
F1199	S1139	P1079	H959	P899	L839	V779	V719	S659	P599	E539	H479
S1200	G1140	P1080	D960	E900	H840	S780	I720	K660	P600	F540	G480

PRO	THR	PRO	ASN	ALA	LEU	PRO	PRO	ALA	ARG	LYS	ALA	SER	PRO	PRO	SER	GLY	LEU	TRP	SER	ALA	TYR	ALA	SER	HIS																																			
W1741	P1742	S1743	F1744	I1745	T1746	Y1747	T1748	V1749	G1750	L1751	L1752	D1753	P1754	A1755	A1756	G1757	S1758	Q1759	G1760	P1761	L1762	S1763	T1764	T1765	L1766	L1767	F1768	S1769	S1770	P1771	V1772	T1773	M1774	Q1775	A1776	I1777	L1778	I1779	P1780	V1781	T1782	V1783	A1784	F1785	V1786	V1787	D1788	A1789	G1791	P1792	G1793	P1794	Y1795	G1796	A1797	S1798	L1799	F1800	
Q1801	H1802	F1803	L1804	D1805	S1806	Y1807	Q1808	V1809	M1810	F1811	F1812	T1813	L1814	F1815	A1816	L1817	L1818	A1819	G1820	T1821	A1822	V1823	M1824	L1825	L1826	A1827	Y1828	H1829	T1830	V1831	G1832	THR	PRO	ARG	ASP	LEU	ALA	VAL	PRO	ALA	LEU	THR	PRO	ALA	SER	PRO	GLY	HIS	PRO	PRO	TYR	PHE	ALA	ALA	SER	SER			
F1201	G1202	M1203	A1204	V1205	P1206	G1207	L1208	T1209	L1210	H1211	W1212	S1213	V1214	T1215	K1216	R1217	V1218	V1219	L1220	D1221	L1222	R1223	G1224	R1225	H1226	H1227	E1228	A1229	S1230	I1231	R1232	L1233	P1234	S1235	Q1236	V1237	N1238	F1239	M1240	M1241	N1242	V1243	L1244	G1245	R1246	V1247	K1248	R1249	R1250	T1251	G1252	L1253	R1254	V1255	V1256	V1257	K1258	A1259	V1260
D1261	P1262	T1263	S1264	G1265	Q1266	L1267	Y1268	G1269	L1270	A1271	R1272	L1273	E1274	S1275	D1276	E1277	L1278	Q1279	V1280	Q1281	L1282	F1283	E1284	K1285	L1286	Q1287	L1288	L1289	N1290	I1291	E1292	L1293	E1294	A1295	E1296	Q1297	I1298	L1299	M1300	S1301	P1302	N1303	S1304	Y1305	I1306	K1307	L1308	Q1309	T1310	N1311	R1312	D1313	G1314	A1315	A1316	S1317	L1318	S1319	Y1320
R1321	V1322	L1323	D1324	L1325	P1326	E1327	K1328	N1329	P1330	V1331	V1332	H1333	V1334	D1335	E1336	K1337	G1338	F1339	L1340	S1341	G1342	G1343	S1344	M1345	L1346	G1347	T1348	S1349	T1350	I1351	E1352	V1353	L1354	A1355	Q1356	E1357	P1358	F1359	G1360	A1361	M1362	Q1363	T1364	L1365	I1366	V1367	A1368	V1369	K1370	V1371	S1372	P1373	V1374	S1375	Y1376	L1377	K1378	V1379	S1380
M1381	S1382	T1383	V1384	L1385	H1386	T1387	Q1388	N1389	K1390	E1391	A1392	L1393	V1394	A1395	V1396	P1397	L1398	G1399	M1400	T1401	V1402	T1403	F1404	T1405	V1406	H1407	F1408	H1409	D1410	N1411	S1412	G1413	D1414	V1415	F1416	H1417	A1418	H1419	S1420	V1421	L1422	L1423	N1424	F1425	A1426	T1427	N1428	R1429	D1430	D1431	F1432	V1433	Q1434	I1435	G1436	K1437	L1438	P1439	T1440
N1441	N1442	T1443	C1444	V1445	V1446	R1447	T1448	V1449	S1450	V1451	L1452	L1453	T1454	L1455	L1456	R1457	V1458	V1459	D1460	A1461	E1462	H1463	P1464	G1465	L1466	S1467	D1468	F1469	M1470	P1471	L1472	P1473	D1474	L1475	Q1476	A1477	I1478	S1479	P1480	E1481	L1482	S1483	G1484	A1485	M1486	V1487	L1488	G1489	D1490	V1491	L1492	C1493	L1494	A1495	T1496	V1497	L1498	T1499	S1500
L1501	E1502	G1503	L1504	S1505	G1506	T1507	W1508	S1509	S1510	S1511	A1512	M1513	S1514	I1515	L1516	H1517	L1518	D1519	P1520	K1521	L1522	G1523	V1524	A1525	V1526	A1527	R1528	A1529	V1530	G1531	S1532	T1533	V1534	V1535	V1536	Y1537	E1538	V1539	M1540	G1541	L1542	L1543	L1544	T1545	Y1546	K1547	E1548	V1549	V1550	V1551	S1552	P1553	L1554	Q1555	R1556	I1557	M1558	A1559	R1560
H1561	L1562	H1563	P1564	I1565	Q1566	T1567	S1568	F1569	Q1570	E1571	A1572	T1573	A1574	S1575	K1576	V1577	V1578	V1579	A1580	V1581	L1582	D1583	R1584	S1585	S1586	M1587	L1588	R1589	G1590	E1591	C1592	T1593	P1594	T1595	Q1596	R1597	E1598	V1599	I1600	Q1601	A1602	L1603	H1604	P1605	E1606	T1607	L1608	I1609	S1610	C1611	Q1612	S1613	Q1614	F1615	K1616	P1617	A1618	V1619	F1620
D1621	F1622	P1623	S1624	I1625	D1626	V1627	F1628	T1629	V1630	E1631	P1632	Q1633	F1634	D1635	T1636	A1637	L1638	G1639	Q1640	V1641	F1642	C1643	S1644	L1645	T1646	M1647	H1648	L1649	L1650	T1651	D1652	K1653	Q1654	R1655	K1656	H1657	L1658	S1659	M1660	K1661	L1662	T1663	A1664	L1665	V1666	V1667	S1668	A1669	S1670	L1671	S1672	S1673	S1674	H1675	F1676	T1677	T1678	E1679	Q1680
V1681	G1682	A1683	E1684	V1685	P1686	F1687	S1688	P1689	G1690	L1691	F1692	A1693	D1694	Q1695	A1696	E1697	I1698	L1699	L1700	S1701	N1702	H1703	V1704	T1705	S1706	S1707	F1708	I1709	R1710	V1711	F1712	G1713	A1714	P1715	E1716	V1717	L1718	E1719	N1720	L1721	E1722	V1723	K1724	S1725	G1726	S1727	P1728	A1729	L1731	A1732	F1733	A1734	K1735	E1736	K1737	S1738	F1739	G1740	
G1801	H1802	F1803	L1804	D1805	S1806	Y1807	Q1808	V1809	M1810	F1811	F1812	T1813	L1814	F1815	A1816	L1817	L1818	A1819	G1820	T1821	A1822	V1823	M1824	L1825	L1826	A1827	Y1828	H1829	T1830	V1831	G1832	THR	PRO	ARG	ASP	LEU	ALA	VAL	PRO	ALA	LEU	THR	PRO	ALA	SER	PRO	GLY	HIS	PRO	PRO	TYR	PHE	ALA	ALA	SER	SER			

- Molecule 2: Nuclear pore membrane glycoprotein 210

Chain 15:



MET	A2	A3	A4	A5	A6	A7	A8	A9	A10	A11	A12	A13	A14	A15	A16	A17	A18	A19	A20	A21	A22	A23	A24	A25	A26	A27	A28	A29	A30	A31	A32	A33	A34	A35	A36	A37	A38	A39	A40	A41	A42	A43	A44	A45	A46	A47	A48	A49	A50	A51	A52	A53	A54	A55	A56	A57	A58	A59	A60
P61	P62	P63	P64	P65	P66	P67	P68	P69	P70	P71	P72	P73	P74	P75	P76	P77	P78	P79	P80	P81	P82	P83	P84	P85	P86	P87	P88	P89	P90	P91	P92	P93	P94	P95	P96	P97	P98	P99	P100	P101	P102	P103	P104	P105	P106	P107	P108	P109	P110	P111	P112	P113	P114	P115	P116	P117	P118	P119	P120
I121	I122	I123	I124	I125	I126	I127	I128	I129	I130	I131	I132	I133	I134	I135	I136	I137	I138	I139	I140	I141	I142	I143	I144	I145	I146	I147	I148	I149	I150	I151	I152	I153	I154	I155	I156	I157	I158	I159	I160	I161	I162	I163	I164	I165	I166	I167	I168	I169	I170	I171	I172	I173	I174	I175	I176	I177	I178	I179	I180
T181	T182	T183	T184	T185	T186	T187	T188	T189	T190	T191	T192	T193	T194	T195	T196	T197	T198	T199	T200	T201	T202	T203	T204	T205	T206	T207	T208	T209	T210	T211	T212	T213	T214	T215	T216	T217	T218	T219	T220	T221	T222	T223	T224	T225	T226	T227	T228	T229	T230	T231	T232	T233	T234	T235	T236	T237	T238	T239	T240
E241	E242	E243	E244	E245	E246	E247	E248	E249	E250	E251	E252	E253	E254	E255	E256	E257	E258	E259	E260	E261	E262	E263	E264	E265	E266	E267	E268	E269	E270	E271	E272	E273	E274	E275	E276	E277	E278	E279	E280	E281	E282	E283	E284	E285	E286	E287	E288	E289	E290	E291	E292	E293	E294	E295	E296	E297	E298	E299	E300
A301	A302	A303	A304	A305	A306	A307	A308	A309	A310	A311	A312	A313	A314	A315	A316	A317	A318	A319	A320	A321	A322	A323	A324	A325	A326	A327	A328	A329	A330	A331	A332	A333	A334	A335	A336	A337	A338	A339	A340	A341	A342	A343	A344	A345	A346	A347	A348	A349	A350	A351	A352	A353	A354	A355	A356	A357	A358	A359	A360
E361	E362	E363	E364	E365	E366	E367	E368	E369	E370	E371	E372	E373	E374	E375	E376	E377	E378	E379	E380	E381	E382	E383	E384	E385	E386	E387	E388	E389	E390	E391	E392	E393	E394	E395	E396	E397	E398	E399	E400	E401	E402	E403	E404	E405	E406	E407	E408	E409	E410	E411	E412	E413	E414	E415	E416	E417	E418	E419	E420
I421	I422	I423	I424	I425	I426	I427	I428	I429	I430	I431	I432	I433	I434	I435	I436	I437	I438	I439	I440	I441	I442	I443	I444	I445	I446	I447	I448	I449	I450	I451	I452	I453	I454	I455	I456	I457	I458	I459	I460	I461	I462	I463	I464	I465	I466	I467	I468	I469	I470	I471	I472	I473	I474	I475	I476	I477	I478	I479	I480
G481	G482	G483	G484	G485	G486	G487	G488	G489	G490	G491	G492	G493	G494	G495	G496	G497	G498	G499	G500	G501	G502	G503	G504	G505	G506	G507	G508	G509	G510	G511	G512	G513	G514	G515	G516	G517	G518	G519	G520	G521	G522	G523	G524	G525	G526	G527	G528	G529	G530	G531	G532	G533	G534	G535	G536	G537	G538	G539	G540
A541	A542	A543	A544	A545	A546	A547	A548	A549	A550	A551	A552	A553	A554	A555	A556	A557	A558	A559	A560	A561	A562	A563	A564	A565	A566	A567	A568	A569	A570	A571	A572	A573	A574	A575	A576	A577	A578	A579	A580	A581	A582	A583	A584	A585	A586	A587	A588	A589	A590	A591	A592	A593	A594	A595	A596	A597	A598	A599	A600
G601	G602	G603	G604	G605	G606	G607	G608	G609	G610	G611	G612	G613	G614	G615	G616	G617	G618	G619	G620	G621	G622	G623	G624	G625	G626	G627	G628	G629	G630	G631	G632	G633	G634	G635	G636	G637	G638	G639	G640	G641	G642	G643	G644	G645	G646	G647	G648	G649	G650	G651	G652	G653	G654	G655	G656	G657	G658	G659	G660
E661	E662	E663	E664	E665	E666	E667	E668	E669	E670	E671	E672	E673	E674	E675	E676	E677	E678	E679	E680	E681	E682	E683	E684	E685	E686	E687	E688	E689	E690	E691	E692	E693	E694	E695	E696	E697	E698	E699	E700	E701	E702	E703	E704	E705	E706	E707	E708	E709	E710	E711	E712	E713	E714	E715	E716	E717	E718	E719	E720
A721	A722	A723	A724	A725	A726	A727	A728	A729	A730	A731	A732	A733	A734	A735	A736	A737	A738	A739	A740	A741	A742	A743	A744	A745	A746	A747	A748	A749	A750	A751	A752	A753	A754	A755	A756	A757	A758	A759	A760	A761	A762	A763	A764	A765	A766	A767	A768	A769	A770	A771	A772	A773	A774	A775	A776	A777	A778	A779	A780
S781	S782	S783	S784	S785	S786	S787	S788	S789	S790	S791	S792	S793	S794	S795	S796	S797	S798	S799	S800	S801	S802	S803	S804	S805	S806	S807	S808	S809	S810	S811	S812	S813	S814	S815	S816	S817	S818	S819	S820	S821	S822	S823	S824	S825	S826	S827	S828	S829	S830	S831	S832	S833	S834	S835	S836	S837	S838	S839	S840
H841	H842	H843	H844	H845	H846	H847	H848	H849	H850	H851	H852	H853	H854	H855	H856	H857	H858	H859	H860	H861	H862	H863	H864	H865	H866	H867	H868	H869	H870	H871	H872	H873	H874	H875	H876	H877	H878	H879	H880	H881	H882	H883	H884	H885	H886	H887	H888	H889	H890	H891	H892	H893	H894	H895	H896	H897	H898	H899	H900

H1561	L1501	M1381	R1321	D1261	F1201	L1141	F1081	L1021	L961	E901	G841
L1562	E1502	S1382	V1322	P1262	G1202	V1142	R1082	R1022	C962	V902	L842
H1563	G1503	P1383	L1323	T1263	M1203	Q1143	L1083	A1023	L963	T903	Q843
P1564	L1504	V1384	D1324	S1264	A1204	A1144	M1084	A1024	V964	I904	A844
I1565	S1505	L1385	G1325	G1265	V1205	V1145	P1085	S1025	P965	Y905	I845
Q1566	G1506	H1386	P1326	Q1266	P1206	D1146	R1086	P1026	P966	N906	L846
T1567	T1507	T1387	E1327	L1267	G1207	A1147	K1087	I1027	A967	H907	V847
S1568	W1508	Q1388	K1328	Y1268	L1208	E1148	V1088	I1028	P968	P908	H848
F1569	S1509	M1389	V1329	G1269	T1209	T1149	T1089	T1029	G969	G909	E849
Q1570	S1510	K1390	P1330	L1270	F1210	G1150	L1090	L1030	K970	I910	A850
E1571	V1511	E1391	V1331	A1271	H1211	K1151	L1091	V1031	A971	Q911	S851
A1572	A1512	A1392	V1332	R1272	W1212	V1152	I1092	A1032	V972	A912	G852
T1573	M1513	L1393	G1333	E1273	S1213	V1153	G1093	L1033	V973	E913	T853
S1574	S1514	V1394	V1334	L1274	V1214	T1154	A1094	D1034	V974	L914	T854
S1575	I1515	A1395	D1335	S1275	T1215	I1155	T1095	E1035	V975	R915	A855
K1576	L1516	V1396	E1336	D1276	K1216	S1156	M1096	A1036	S976	I916	I856
V1577	H1517	P1397	K1337	E1277	R1217	A1157	Q1097	L1037	D977	R917	T857
T1578	I1518	L1398	G1338	I1278	D1218	D1158	V1098	D1038	V978	E918	A858
V1579	D1519	G1399	F1339	Q1279	V1219	L1159	T1099	N1039	Q979	G919	T859
A1580	P1520	M1400	L1340	V1280	L1220	V1160	S1100	V1040	E980	S920	A860
V1581	K1521	T1401	A1341	Q1281	D1221	Q1161	E1101	T1041	L981	G921	T861
G1582	T1522	V1402	S1342	V1282	L1222	V1162	G1102	I1042	V982	Y922	G862
D1583	G1523	T1403	G1343	F1283	R1223	E1163	G1103	T1043	V983	F923	Y863
R1584	V1524	F1404	S1344	E1284	G1224	V1164	P1104	F1044	R984	F924	Q864
S1585	A1525	T1405	M1345	K1285	R1225	L1165	Q1105	I1045	V985	L925	E865
S1586	V1526	V1406	I1346	L1286	H1226	L1166	P1106	I1046	V986	N926	S866
M1587	A1527	H1407	G1347	Q1287	H1227	L1167	Q1107	R1047	D987	T927	H867
L1588	R1528	F1408	T1348	L1288	E1228	R1168	S1108	G1048	K988	S928	L868
R1589	A1529	H1409	S1349	L1289	A1229	A1169	M1109	V1049	V989	T929	S869
G1590	W1530	D1410	T1350	M1290	S1230	V1170	I1110	A1050	E990	A930	S870
E1591	G1531	M1411	I1351	P1291	I1231	R1171	L1111	I1051	I991	D931	A871
C1592	S1532	S1412	E1352	E1292	R1232	T1172	F1112	G1052	Q992	V932	R872
T1593	V1533	G1413	V1353	I1293	L1233	R1173	S1113	Q1053	K993	V933	T873
P1594	T1534	D1414	I1354	E1294	P1234	A1174	I1114	T1054	T994	K934	K874
L1595	V1535	V1415	A1355	A1295	S1235	P1175	S1115	S1055	V995	V935	Q875
Y1536	Y1536	F1416	Q1356	E1296	Q1236	T1176	M1116	L1056	K996	A936	P876
Y1537	Y1537	H1417	E1357	Q1297	Y1237	R1177	E1117	T1057	A997	Y937	H877
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V1539	V1539	H1419	F1359	L1299	F1239	M1179	V1119	S1059	V999	E939	P879
A1540	A1540	S1420	G1360	M1300	A1240	R1180	A1120	V1060	R1000	A940	L880
E1481	G1541	S1421	A1361	S1301	M1241	T1181	L1121	T1061	V1001	R941	V881
H1482	H1542	V1422	N1362	P1302	N1242	G1182	V1122	N1062	L1002	G942	P882
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R1484	R1544	M1424	T1364	S1304	L1244	Q1184	A1124	A1064	L1004	A944	S884
T1485	V1545	F1425	I1365	Y1305	G1245	M1185	A1125	G1065	H1005	M945	A885
E1486	Y1546	A1426	I1366	T1306	R1246	P1186	G1126	Q1066	K1006	V946	S886
V1487	K1547	T1427	V1367	K1307	V1247	I1187	L1127	R1067	K1007	H947	I887
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G1489	V1549	R1429	V1369	Q1309	G1249	V1189	T1129	N1069	F1009	L949	L889
V1550	S1610	D1430	K1370	T1310	R1250	T1190	G1130	S1070	L1010	L950	I890
V1551	C1611	D1431	V1371	M1311	T1251	G1191	L1131	A1071	A1011	P951	L891
S1552	Q1612	F1432	S1372	R1312	G1252	T1192	A1132	Q1072	K1012	G952	V892
V1553	S1613	V1433	P1373	D1313	L1253	T1193	I1133	Q1073	Y1013	S953	E893
P1554	Q1614	Q1434	G1374	G1314	R1254	N1194	G1134	Q1074	F1014	S954	D894
Q1555	F1615	I1435	S1375	A1315	V1255	H1195	M1135	I1075	P1015	T955	V895
R1556	K1616	G1436	Y1376	A1316	V1256	Q1196	G1136	E1076	F1016	I956	R896
I1557	T1617	K1437	L1377	S1317	V1257	N1197	T1137	V1077	M017	M957	V897
M1558	A1618	G1438	R1378	S1318	V1258	P1198	L1138	F1078	D1018	I958	S898
A1559	A1559	P1439	V1379	S1319	A1259	F1199	S1139	P1079	L1019	H959	P899
F1620	R1560	Y1320	S1380	Y1320	V1260	S1200	G1140	P1080	K1020	D960	E900

G481	A541	G601	E661	A721	S781	G841	E901	L961	L1021	F1081	L1141	F1201
S482	P642	S602	M662	L722	H782	L842	V902	C962	R1022	R1082	V1142	G1202
G483	C643	E603	L663	S723	R783	Q643	T903	L963	A1023	L1083	Q1143	N1203
N484	Q644	H604	F664	V724	N784	A644	I904	V964	A1024	M1084	A1144	A1204
F485	V645	C605	E665	G725	R785	I845	Y905	P965	S1025	P1085	V1145	V1205
S486	E646	S606	G666	T726	P786	L846	N906	P966	P1026	R1086	D1146	P1206
W487	A647	G607	G667	K727	L787	V647	H907	A967	I1027	K1087	A1147	G1207
S488	R648	I608	P668	P728	D788	H848	P908	P968	T1028	V1088	E1148	L1208
S489	V649	R609	R669	S729	L789	E649	G909	A969	T1029	T1089	T1149	T1209
S490	G650	V610	P670	L730	A790	A650	I910	K970	L1030	L1090	G1150	F1210
S491	Q651	K611	W671	T731	A791	S651	Q911	A971	V1031	L1091	K1151	H1211
H492	A652	A612	I672	N732	V792	G652	A912	V972	A1032	I1092	V1152	V1212
L493	L653	E613	L673	F733	D793	T653	E913	V973	L1033	G1093	V1153	S1213
V494	E654	A614	E674	F734	Q794	T654	L914	Y974	D1034	A1094	I1154	V1214
A495	L655	Q615	P675	P735	E795	A655	R915	V975	E1035	T1095	I1155	T1215
T496	P656	G616	S676	A736	G796	I656	I916	S976	A1036	M1096	S1156	K1216
V497	L657	S617	K677	V737	R797	T657	R917	D977	L1037	Q1097	Q1157	R1217
T498	R658	T618	F678	E738	R798	A658	E918	I978	D1038	V1098	D1158	D1218
V499	I659	T619	F679	P739	F799	T659	G919	Q979	M1039	T1099	L1159	V1219
K500	S660	L620	Q680	A740	D800	A660	S920	E980	M1040	S1100	V1160	L1220
G501	G661	L621	N681	V741	N601	T661	G921	L981	T1041	E1101	Q1161	D1221
V502	L662	V622	V682	V742	F902	G662	Y922	Y982	I1042	G1102	V1162	L1222
M503	M663	S623	T683	K743	S903	Y663	F923	L983	T1043	G1103	E1163	R1223
T504	P664	Y624	A684	F744	S904	Q664	F924	R984	F1044	P1104	V1164	G1224
T505	G665	R625	E685	W745	L805	E665	L925	V985	L1045	Q1105	L1165	R1225
G506	G666	H626	S686	C746	S906	S666	N926	V986	I1046	P1106	L1166	H1226
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D508	S668	H628	D688	P748	Q908	L668	T928	K988	G1048	S1108	R1168	E1228
I509	E669	V629	S689	P749	W909	S669	T929	V989	V1049	M1109	A1169	A1229
G510	V670	H630	E690	S750	E910	S670	A930	E990	A1050	I1110	V1170	S1230
F511	V671	L631	G691	R751	S811	A671	D931	I991	I1051	L1111	R1171	I1231
S512	T672	S632	L692	L752	T912	R672	V932	G992	G1052	F1112	I1172	R1232
V513	L673	A633	A693	T753	R613	T673	K933	K993	Q1053	S1113	R1173	L1233
I514	S674	K634	L694	L754	R614	K674	V934	T994	T1054	I1114	A1174	P1234
Q515	D675	I635	F695	A755	V815	Q675	V935	V995	S1055	S1115	P1175	S1235
A516	C676	T636	A696	P756	L816	P676	A936	K996	L1056	N1116	I1176	Q1236
H517	S677	I637	P697	V757	A617	H677	Y937	A997	T1057	E1117	M1177	Y1237
D518	H678	A638	H698	V758	S818	D678	Q938	Y998	A1058	S1118	R1178	L1238
V519	F679	A639	S699	T759	I919	P679	E939	V999	S1059	V1119	M1179	F1239
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N521	L681	L641	R701	P761	P821	V681	R941	V1001	T1061	L1121	T1181	M1241
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F525	V685	A645	Q705	H765	M625	A685	N945	H1005	G1065	A1125	M1185	G1245
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E527	N687	D647	V707	C767	L827	I687	H947	K1007	R1067	L1127	I1187	V1247
M528	Q688	P648	I708	P768	V828	E688	P948	P1008	T1068	V1128	V1188	K1248
K529	G689	S649	L709	L769	S829	L889	L949	F1009	M1069	Q1129	V1189	G1249
V530	V690	V710	Q710	L770	Q830	T890	L950	L1010	S1070	L1200	T1190	R1250
Y531	F691	V651	T711	Q771	D831	L691	P951	A1011	A1071	L1131	G1191	T1251
V532	Q692	A652	C712	Q772	D832	V692	G952	K1012	P1072	I1132	I1192	G1252
I533	P693	L653	Q713	N773	E933	E693	S953	Y1013	Q1073	A1133	T1193	L1253
E534	L594	V654	A714	K774	S834	D694	S954	F1014	Q1074	G1134	M1194	R1254
P535	P695	T655	L715	Q775	G835	V695	T955	P1015	I1075	N1135	H1195	V1255
H536	G596	L656	G716	V776	Q836	R696	V956	F1016	E1076	G1136	Q1196	V1256
S537	R597	G657	E717	V777	K937	V697	N957	M1017	V1077	T1137	M1197	V1257
M538	L598	Q658	Q718	P778	K938	S698	T958	L1018	F1078	L1138	P1198	L1258
E539	P599	S659	V719	V779	L839	P699	H959	L1019	P1079	S1139	F1199	A1259
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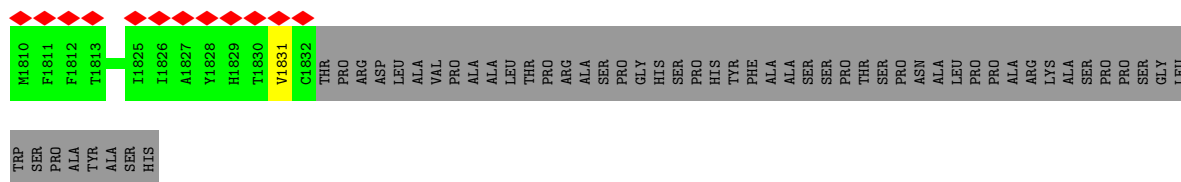
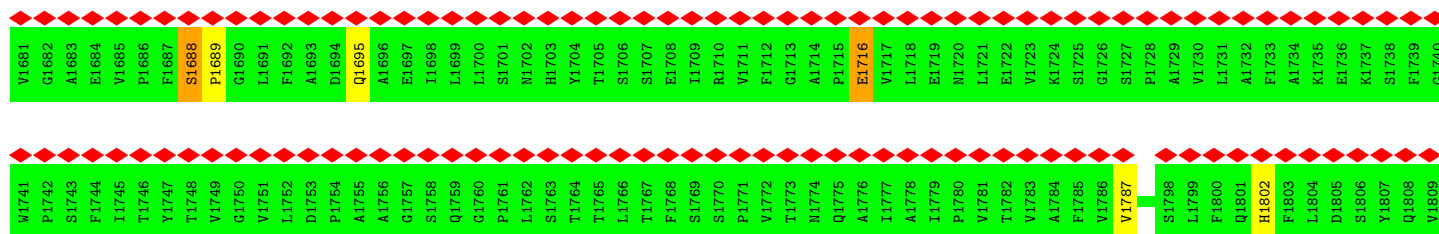
- Molecule 2: Nuclear pore membrane glycoprotein 210



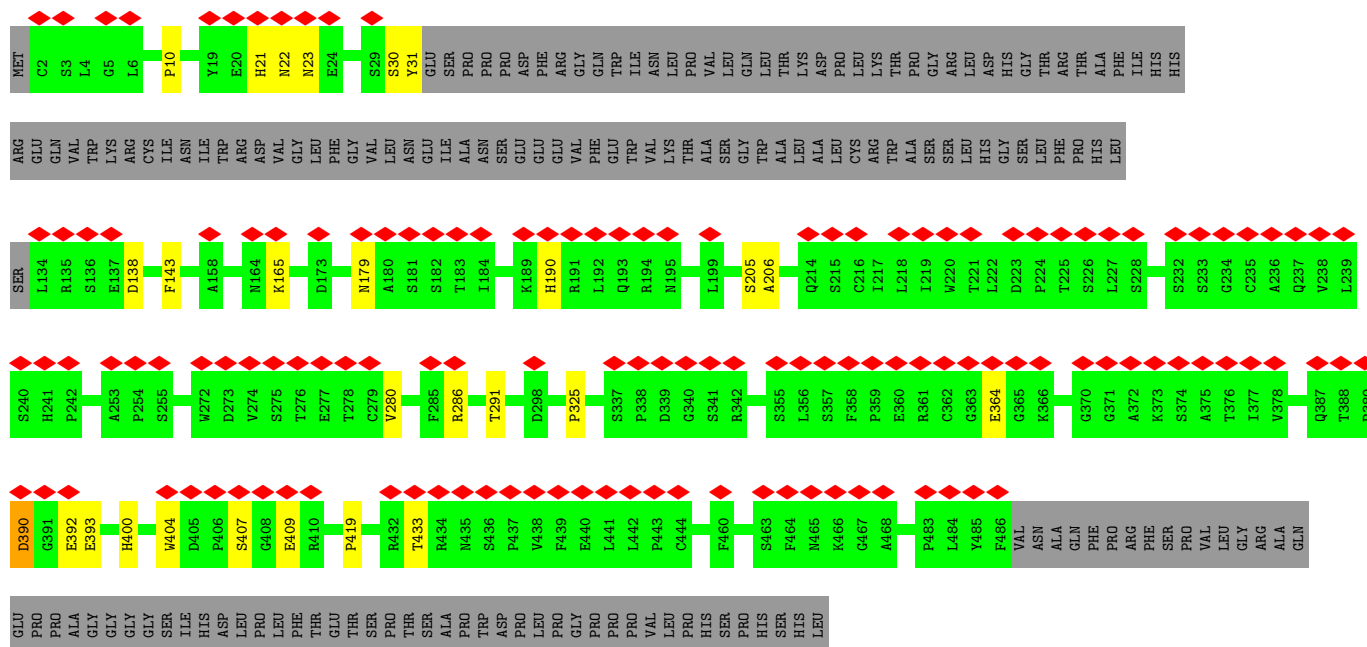
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P61	I121	T181	E241	A301	E361	I421	G481	A541	G601	E661	H781	G841
E62	V122	F182	N242	V302	T362	D422	S482	P542	S602	H662	H782	L842
V63	S123	L183	I243	L303	G363	A423	G483	C543	E603	L663	R783	Q843
A64	T124	E184	L244	A304	R364	A424	N484	Q544	H604	F664	N784	A844
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I66	R126	T186	N246	D306	V366	T426	S486	E546	S606	G666	R786	L846
E67	E127	Y187	P247	T307	E367	S427	V487	A547	G607	G667	L787	V847
P68	L128	I188	A248	S308	I368	V428	S488	R548	T608	P668	D788	H848
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G70	L130	P190	D250	V310	I370	D430	S490	G550	V610	P670	A790	A850
L71	E131	S191	V251	T311	E371	Q431	S491	Q551	K611	W671	A791	S851
D72	D132	Y192	Y252	A312	V372	D432	H492	A552	A612	L672	Y792	Q852
E73	S133	I193	L253	L313	F373	G433	L493	L553	E613	L673	D793	T853
Q74	P134	S194	M254	Q314	D374	G434	V494	E554	A614	E674	Q794	T854
Q75	L135	E195	V255	L315	K375	V435	A495	L555	Q615	P675	E795	A855
C76	E136	M196	G256	G316	F376	H436	T496	P556	G616	S676	G796	I856
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Q78	K138	K198	S258	S318	N378	L438	T498	R558	T618	F678	E798	A858
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A80	Q140	A200	H260	L320	V380	V440	K500	S560	L620	Q680	D800	A860
V81	A141	K201	Y261	V321	Y381	P441	G501	G561	L621	N681	M801	T861
V82	L142	Q202	Q262	L322	V382	V442	V502	L562	V622	L682	F802	Q862
Q83	D143	G203	V263	G323	S383	W443	M503	M563	S623	T683	S803	Y863
A84	S144	D204	Q264	H324	N384	N444	T504	P564	V624	A684	S804	Q864
R85	E145	T205	K265	R325	N385	Q445	T505	G565	R625	E685	L805	B865
L86	G146	I206	I266	S326	I386	Q446	G506	G566	H626	D686	S806	S866
T87	N147	L207	R267	I327	R387	E447	S507	A567	G627	T687	I807	H867
Q88	T148	V208	Q268	R328	I388	V448	D508	S568	H628	D688	Q808	L868
P89	F149	S209	G269	M329	E389	E449	L509	E569	V629	S689	W809	S869
A90	S150	G210	K270	Q330	T390	L450	G510	V570	H630	T690	E810	S870
R91	T151	M211	I271	G331	V391	H451	F511	V571	L631	G691	S811	A871
L92	L152	K212	T272	A332	L392	L452	S512	T572	S632	L692	T812	R872
T93	A153	T213	E273	S333	P393	P453	V513	L573	A633	A693	R813	T873
S94	G154	G214	L274	R334	A394	L454	L514	S574	K634	L694	L814	K874
I95	L155	S215	S275	L335	E395	T455	Q515	D575	L635	F695	W815	Q875
I96	V156	S216	M276	P336	F396	L456	A516	C576	T636	A696	L816	P876
F97	F157	K217	P277	N337	F397	Y457	H517	S577	L637	F697	A817	H877
A98	E158	L218	S278	S338	E398	P458	D518	H578	A638	H698	S818	D878
E99	W159	K219	D279	T339	V399	S459	V519	F579	A639	S699	I819	P879
D100	T160	A220	Q280	I340	L400	L460	Q520	D580	V640	L700	E820	L880
L101	L161	R221	Y281	Y341	S401	L461	N521	L581	L641	R701	P821	W881
T102	V162	I222	E282	V342	S402	T462	P522	A582	P642	N702	E822	P882
T103	K163	Q223	L283	V343	S403	F463	L523	V583	L643	Y703	L823	L883
G104	D164	E224	Q284	E344	Q404	P464	H524	E584	K644	Q704	P824	S884
Q105	S165	A225	L285	P345	M405	V465	F525	V585	A645	Q705	R825	A885
V106	E166	V226	Q286	G346	G406	Q466	G526	E586	V646	R706	Q826	S886
L107	A167	Y227	N287	Y347	S407	P467	E527	N587	D647	W707	L827	I887
R108	D168	K228	S288	L348	Y408	K468	N528	Q588	P648	T708	W828	E888
C109	R169	N229	I289	G349	H409	T469	K529	G589	S649	L709	S829	L889
D110	F170	Q230	P290	F350	R410	G470	V530	V590	K650	V710	Q830	L890
A111	S171	R231	G291	T351	I411	A471	Y531	F591	V651	T711	D831	L891
I112	D172	P232	P292	V352	R412	Y472	V532	Q592	A652	C712	R832	V892
V113	S173	A233	E293	H353	A413	Q473	L533	P593	L653	W713	E833	E893
D114	H174	E234	G294	P354	L414	Y474	E534	L594	V654	A714	S834	D894
L115	N175	V235	D295	G355	K415	T475	P355	P595	T655	L715	Q835	W895
I116	A176	R236	P296	D356	R416	L476	H356	G596	L656	G716	Q836	R896
H117	L177	A297	A297	R357	G417	R477	S357	R597	G657	E717	K837	R897
D118	R178	L237	Q298	K358	Q418	A478	M358	L598	S658	Q718	S838	S898
I119	L179	I239	P299	V359	T419	H479	E359	P599	S659	W719	P778	P899
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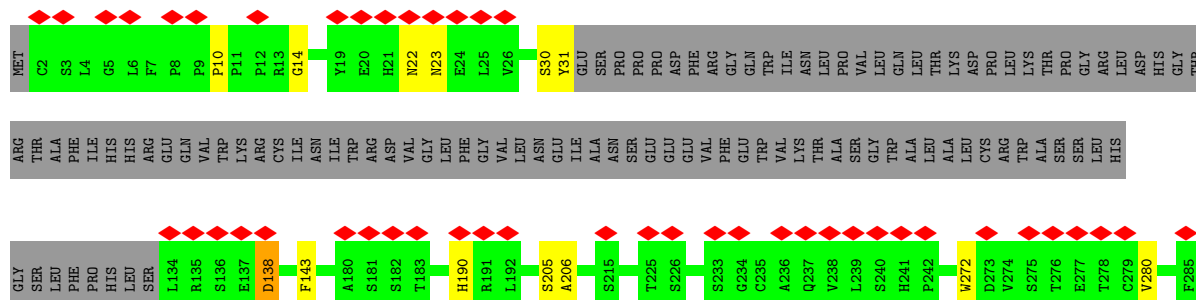
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P1623	H1563	G1503	T1443	P1383	L1323	T1263	N1203	Q1143	L1083	A1023	T903
S1624	P1564	L1504	C1444	V1384	D1324	S1264	A1204	A1144	M1084	A1024	I904
Q1625	L1565	S1505	V1445	L1385	G1325	G1265	V1205	V1145	P1085	S1025	N905
D1626	T1566	G1506	V1446	H1386	P1326	Q1266	P1206	D1146	R1086	P1026	N906
V1627	T1567	G1507	R1447	T1387	E1327	L1267	G1207	A1147	K1087	I1027	H907
F1628	S1568	W1508	T1448	Q1388	K1328	Y1268	L1208	E1148	V1088	I1028	P908
T1629	S1569	S1509	V1449	M1389	G1329	G1269	T1209	T1149	T1089	T1029	G909
V1630	Q1570	S1510	S1450	K1390	P1330	L1270	F1210	G1150	K1090	L1030	I910
E1631	E1571	S1511	V1451	E1391	V1331	A1271	H1211	K1151	L1091	V1031	Q911
P1632	A1572	A1512	G1452	A1392	V1332	R1272	W1212	V1152	I1092	A1032	A912
Q1633	T1573	L1513	L1453	L1393	H1333	E1273	S1213	V1153	G1093	L1033	E913
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D1635	S1575	I1515	L1455	A1395	D1335	S1275	T1215	I1155	T1095	E1035	R915
T1636	K1576	L1516	L1456	V1396	E1336	D1276	K1216	S1156	M1096	A1036	R916
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C1643	D1583	G1523	H1463	T1403	G1343	F1283	R1223	E1163	G1103	T1043	F923
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R1655	T1595	V1535	L1475	V1415	A1355	A1295	S1235	P1175	S1115	S1055	V935
K1656	Q1596	Y1536	Q1476	F1416	Q1356	E1296	Q1236	T1176	M1116	T1056	A936
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L1658	E1598	E1538	I1478	A1418	P1358	L1298	N1238	R1178	S1118	A1058	Q938
S1659	V1599	V1539	S1479	H1419	F1359	L1299	F1239	M1179	V1119	S1059	E939
M1660	T1600	A1540	P1480	S1420	G1360	M1300	A1240	R1180	A1120	V1060	A940
Q1661	Q1601	G1541	E1481	S1421	A1361	S1301	M1241	T1181	L1121	T1061	R941
K1662	A1602	H1542	L1482	V1422	N1362	P1302	N1242	G1182	V1122	N1062	G942
T1663	L1603	L1543	S1483	L1423	Q1363	M1303	V1243	T1183	S1123	K1063	V943
A1664	H1604	R1544	G1484	M1424	T1364	S1304	L1244	Q1184	A1124	A1064	A944
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V1667	T1607	K1547	V1487	T1427	V1367	K1307	V1247	I1187	L1127	R1067	H947
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A1669	V1609	V1549	G1489	R1429	V1369	Q1309	G1249	V1189	F1129	N1069	L949
S1670	S1610	V1550	D1490	D1430	K1370	T1310	R1250	T1190	G1130	S1070	L950
L1671	C1611	V1551	V1491	D1431	V1371	N1311	T1251	G1191	L1131	A1071	P951
S1672	S1612	S1552	L1492	F1432	S1372	R1312	G1252	T1192	A1132	P1072	G952
S1673	S1613	V1553	C1493	V1433	P1373	D1313	L1253	T1193	I1133	Q1073	S953
S1674	P1614	P1554	L1494	Q1434	V1374	G1314	R1254	N1194	G1134	Q1074	S954
H1675	F1615	Q1555	A1495	I1435	S1375	A1315	V1255	H1195	M1135	T1075	T955
F1676	K1616	T1556	T1496	G1436	Y1376	A1316	V1256	Q1196	Q1136	E1076	I956
S1677	P1617	I1557	V1497	K1437	L1377	S1317	T1257	N1197	T1137	V1077	M957
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E1679	V1619	A1559	T1499	P1439	V1379	S1319	A1259	F1199	S1139	P1079	H959
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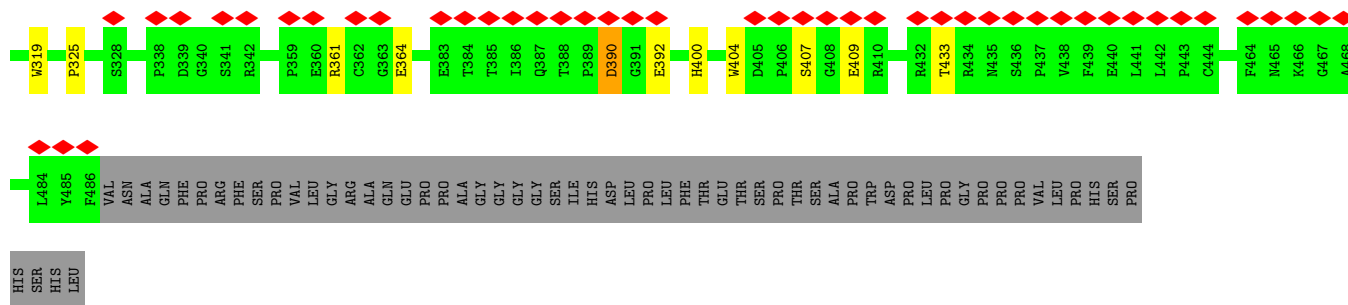


• Molecule 3: Aladin

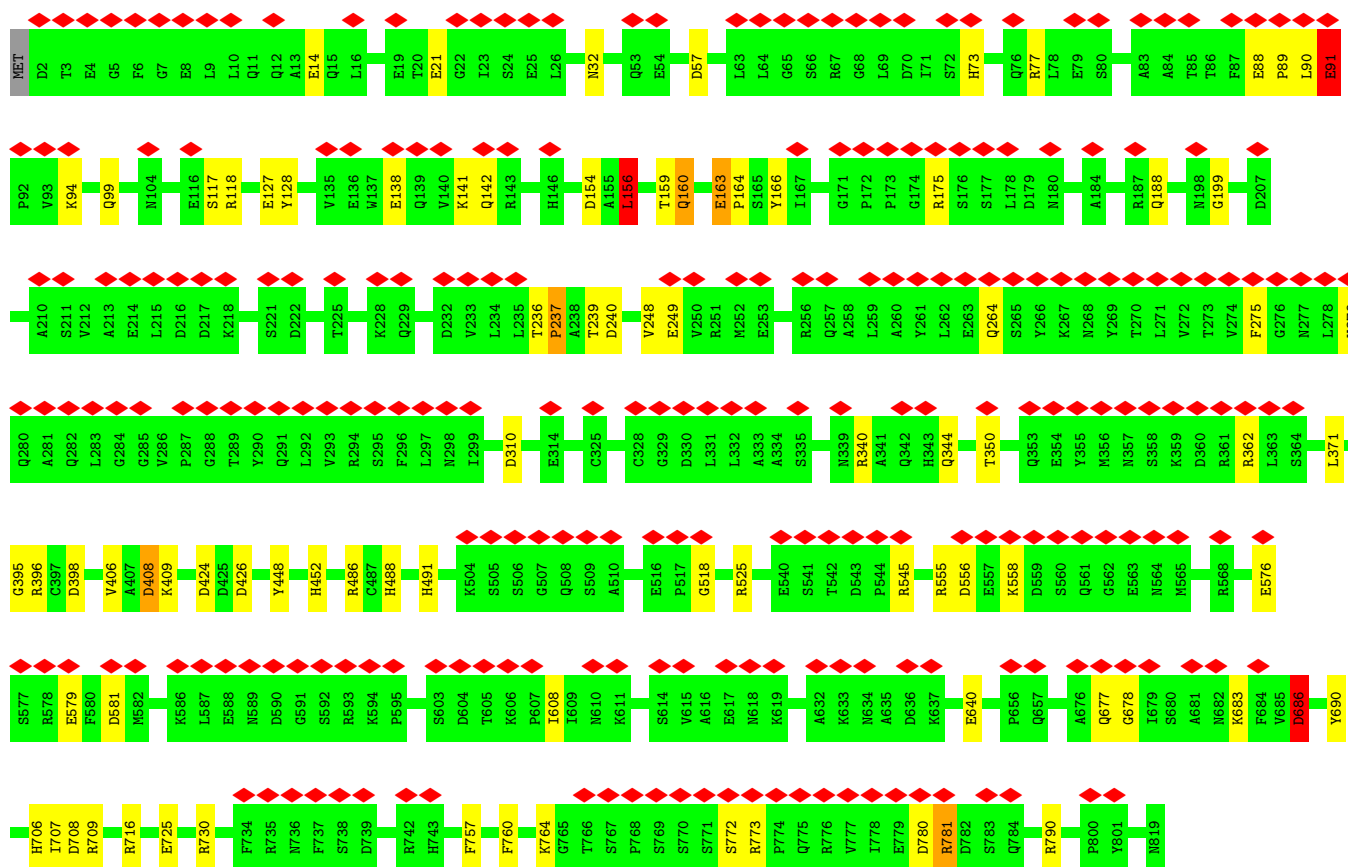
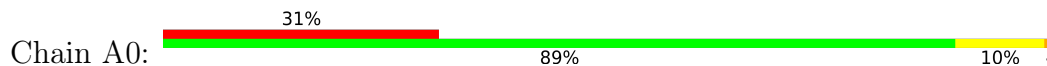


• Molecule 3: Aladin

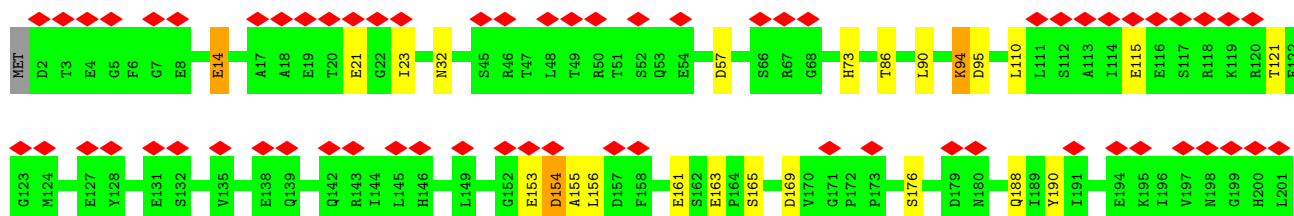
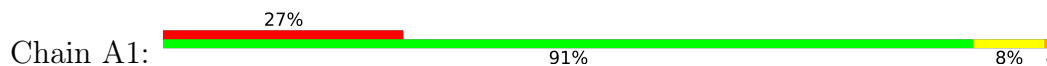




• Molecule 4: Nuclear pore complex protein Nup93

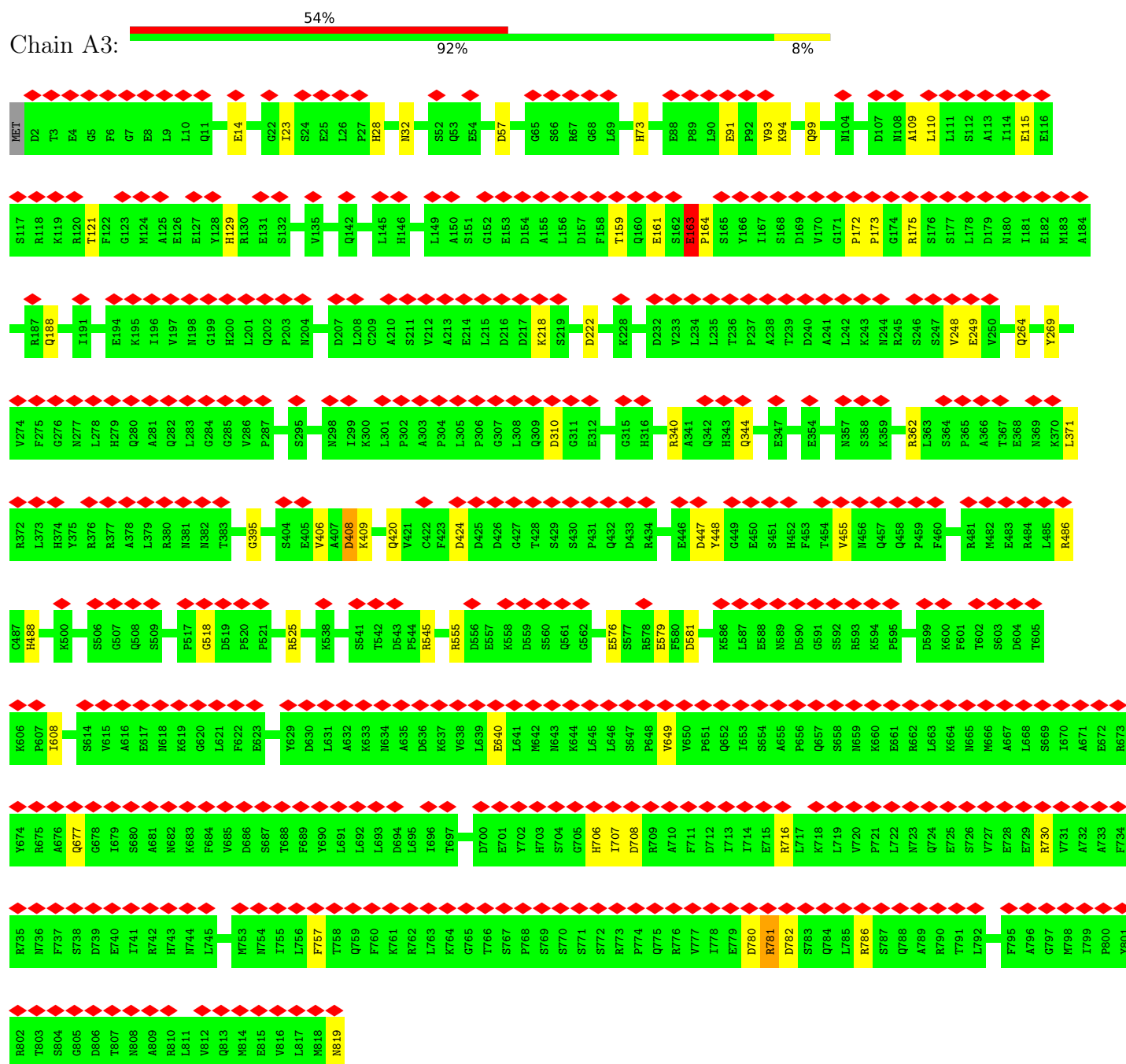


• Molecule 4: Nuclear pore complex protein Nup93



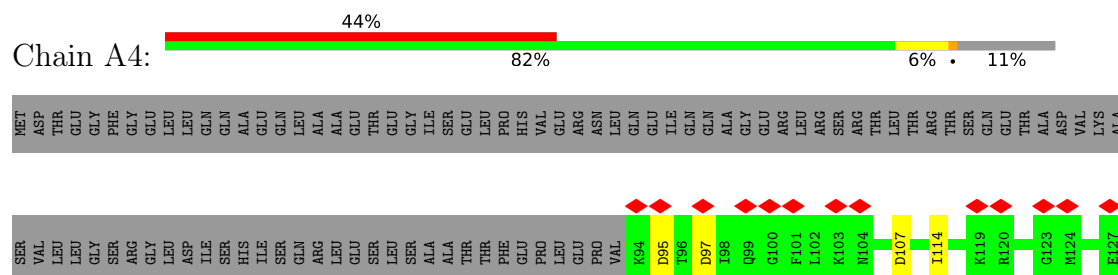
• Molecule 4: Nuclear pore complex protein Nup93

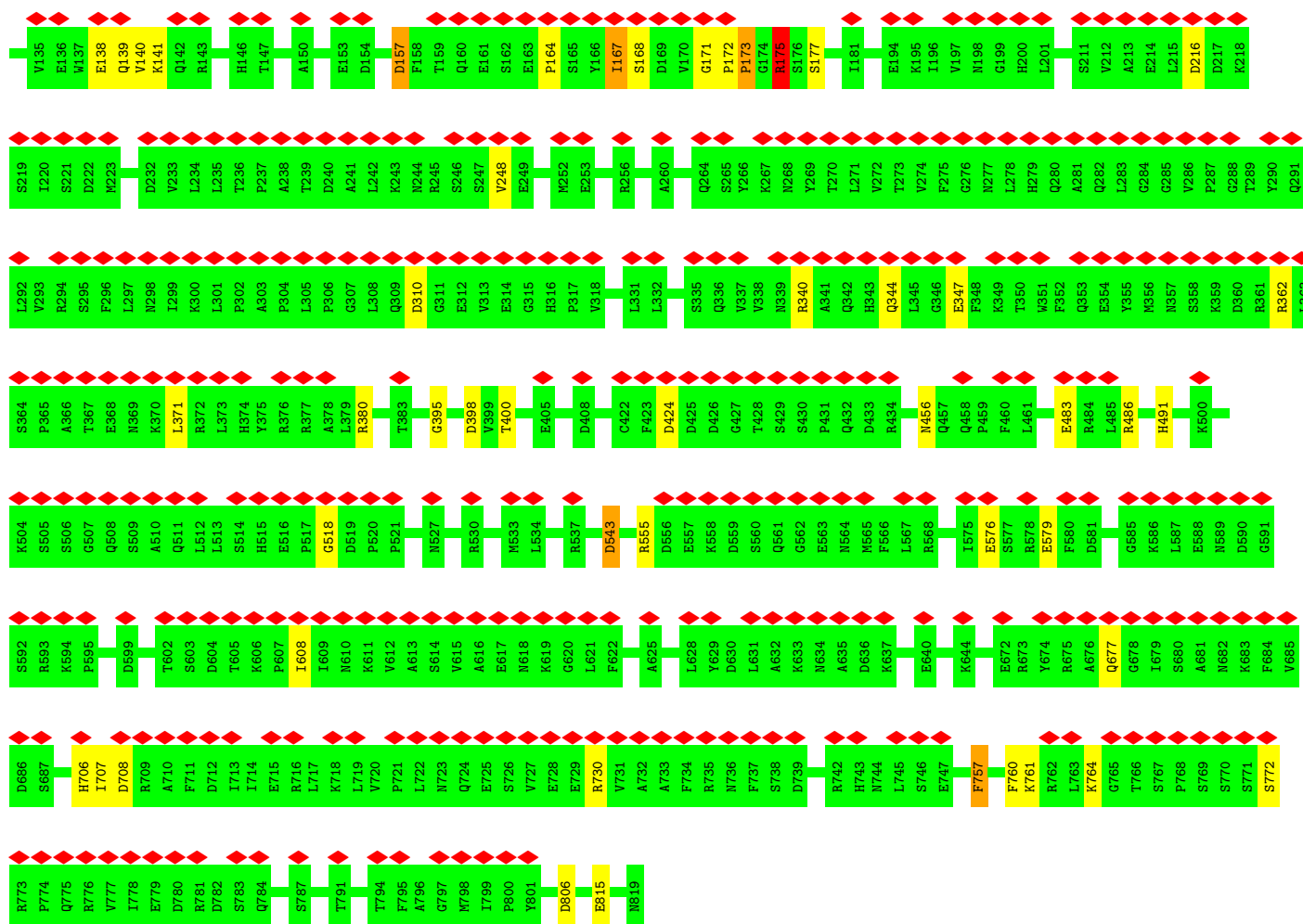
Chain A3:



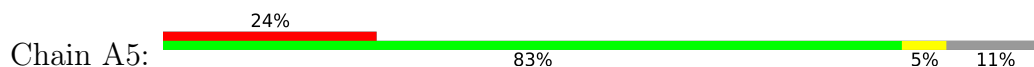
• Molecule 4: Nuclear pore complex protein Nup93

Chain A4:

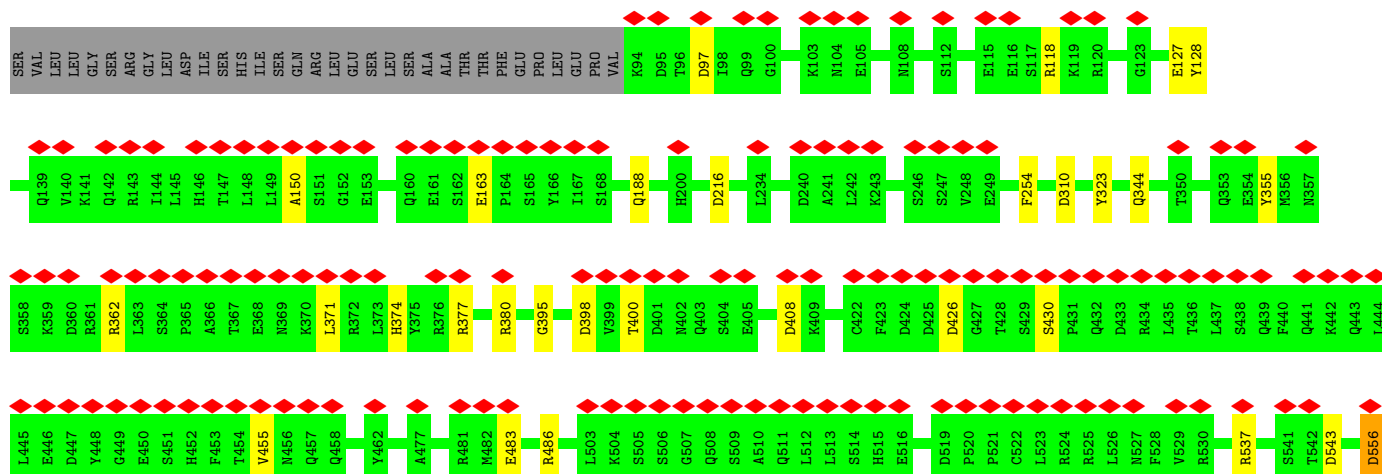


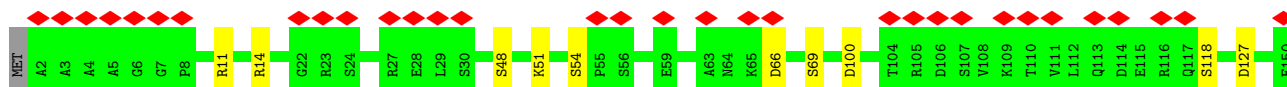


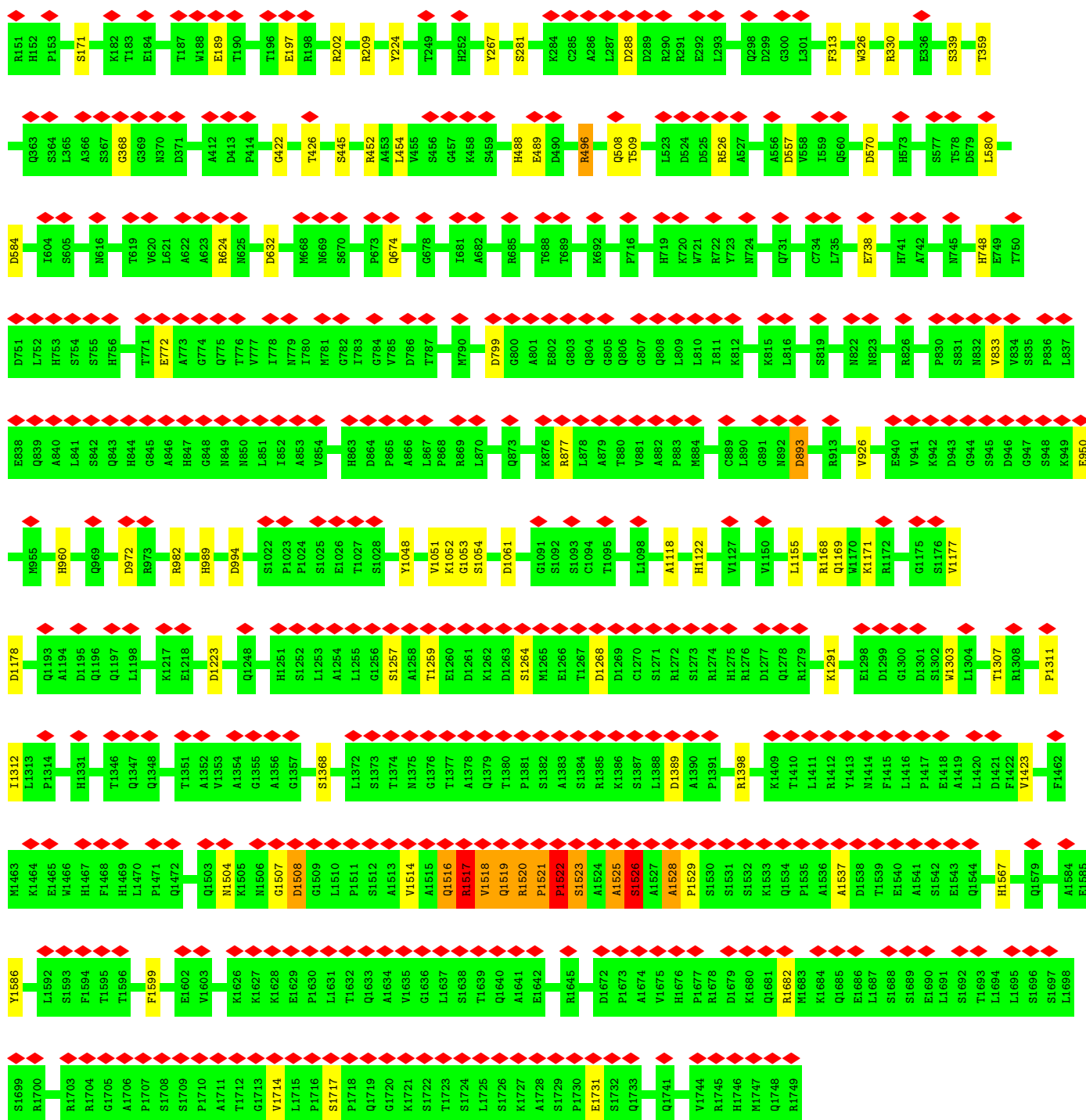
• Molecule 4: Nuclear pore complex protein Nup93



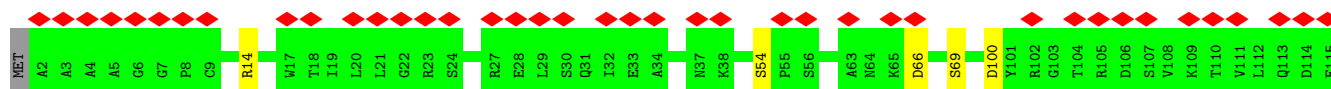
MET	ASP	THR	GLU	GLY	PHE	GLY	GLU	LEU	LEU	LEU	GLN	ALA	ALA	GLU	THR	GLU	GLY	ILE	ILE	SER	GLU	LEU	PRO	HIS	VAL	GLU	LEU	ARG	ASN	LEU	GLN	ILE	GLN	ALA	GLY	GLU	ARG	LEU	ARG	LEU	THR	THR	ARG	SER	GLN	GLU	THR	ALA	ASP	VAL	LYS	ALA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----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

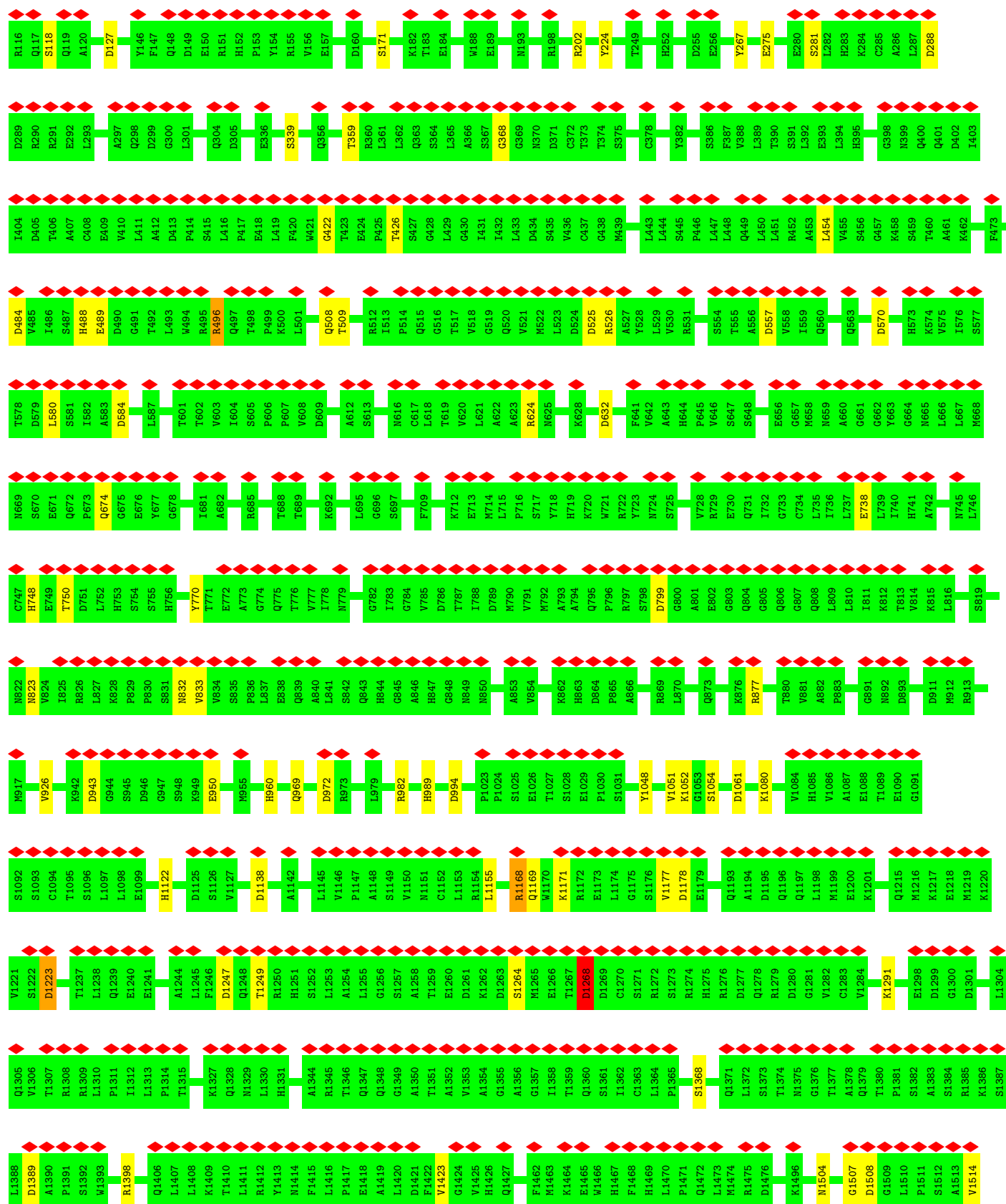


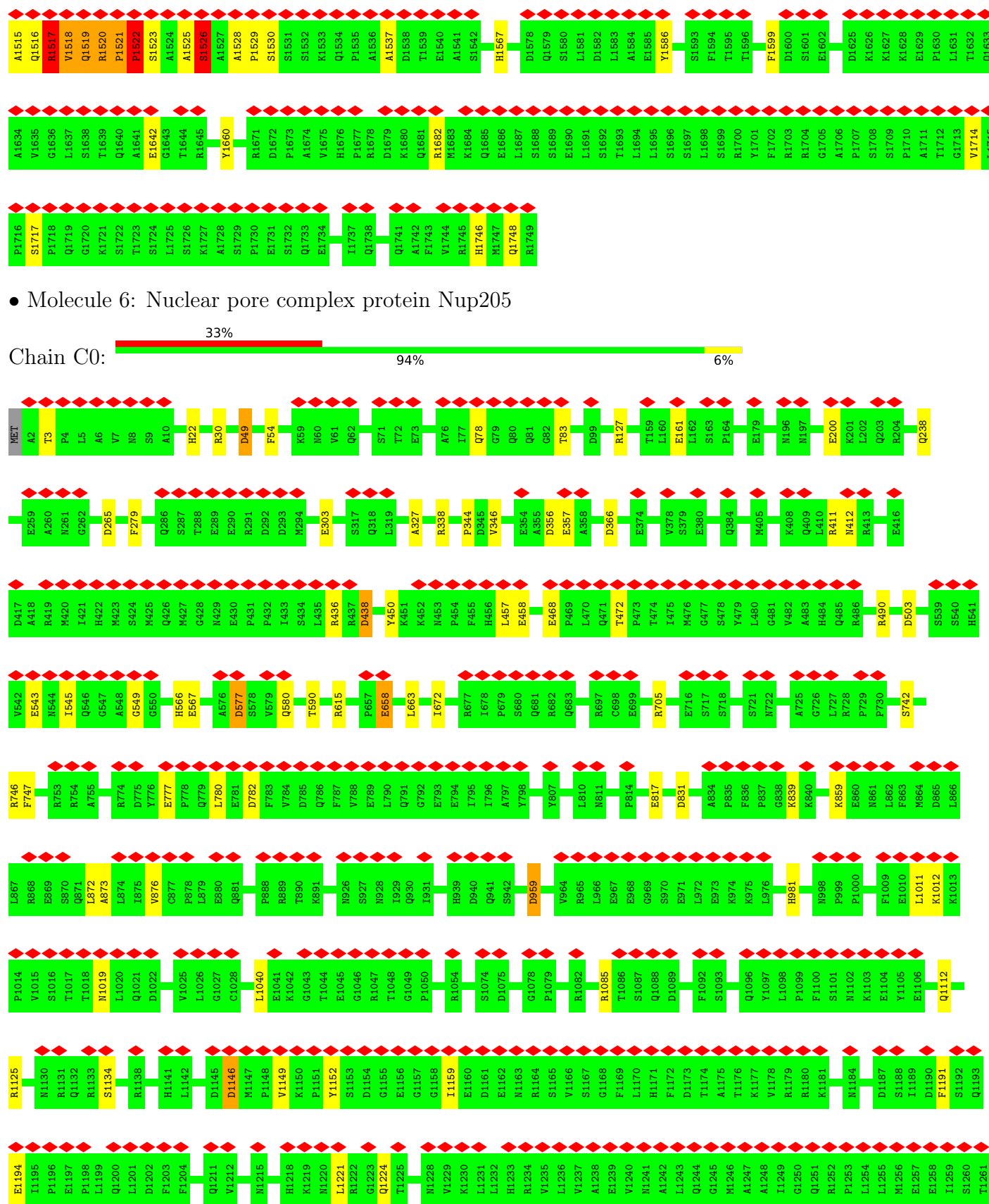


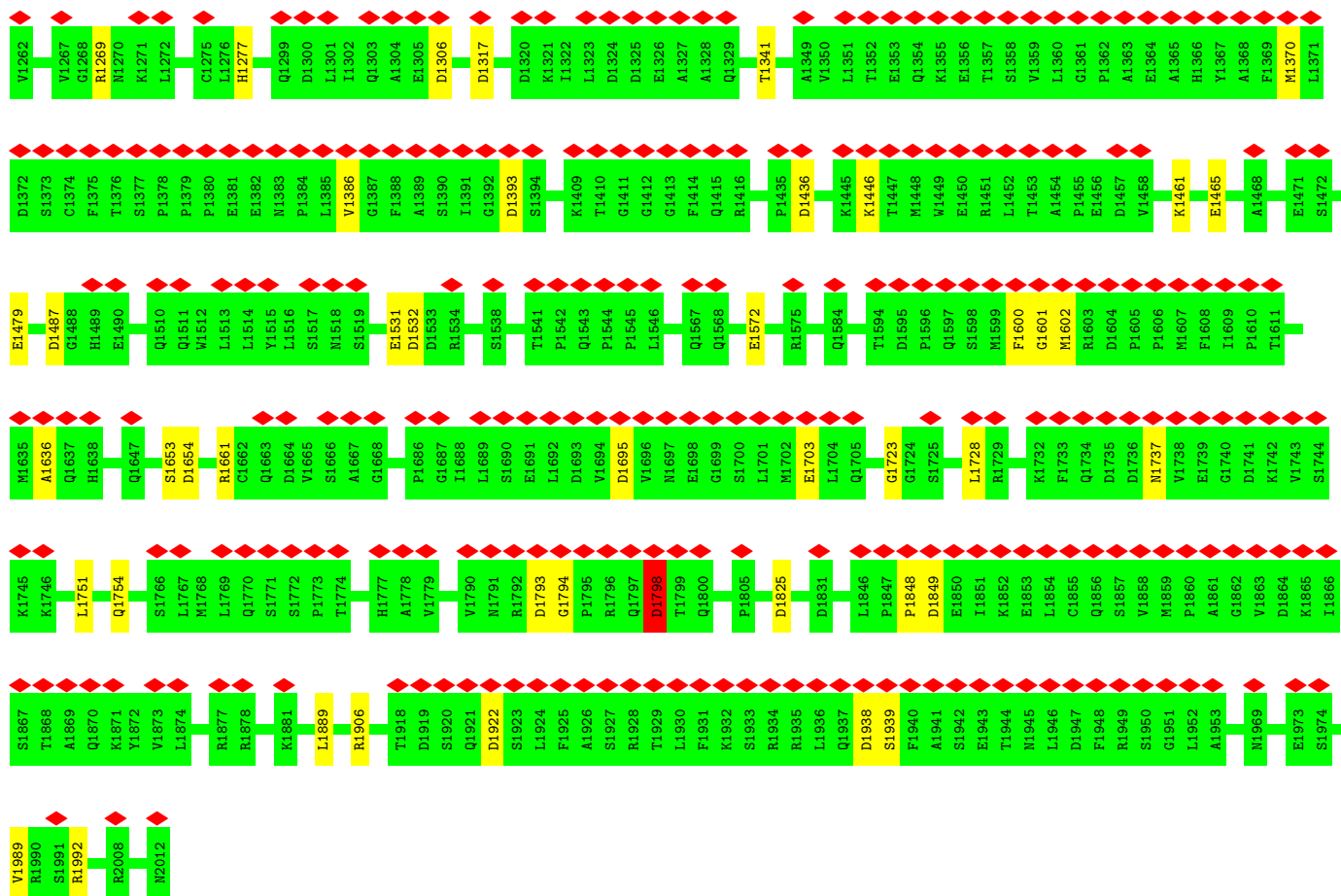


• Molecule 5: Nucleoporin NUP188 homolog

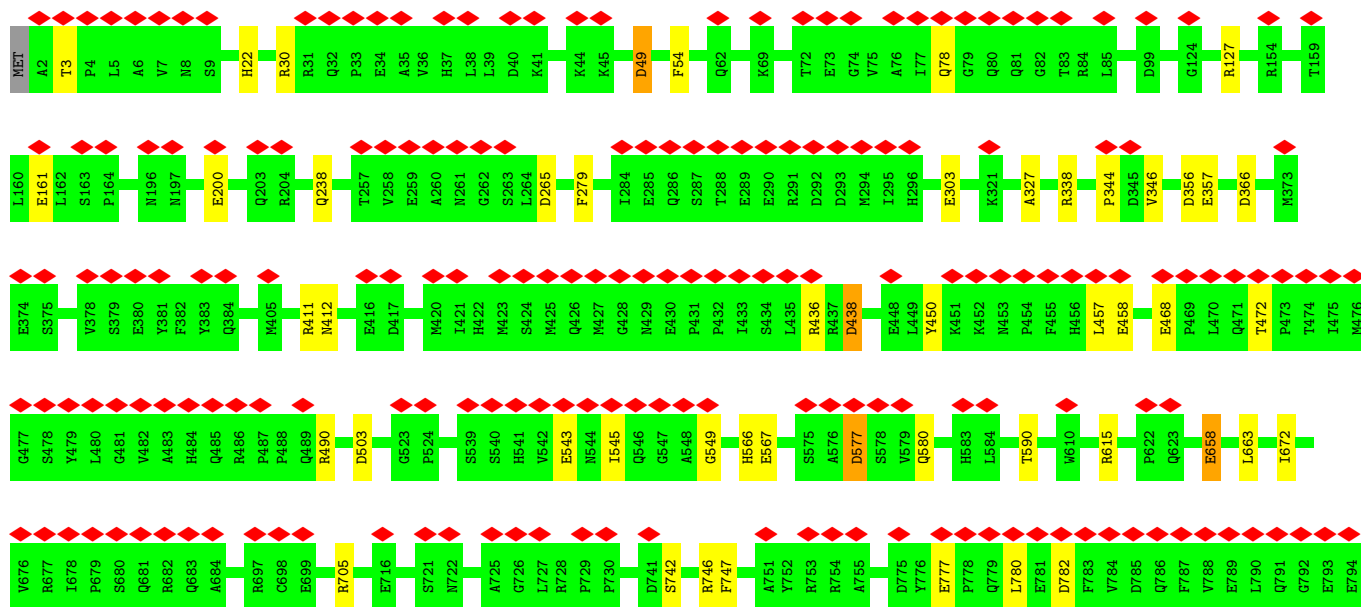


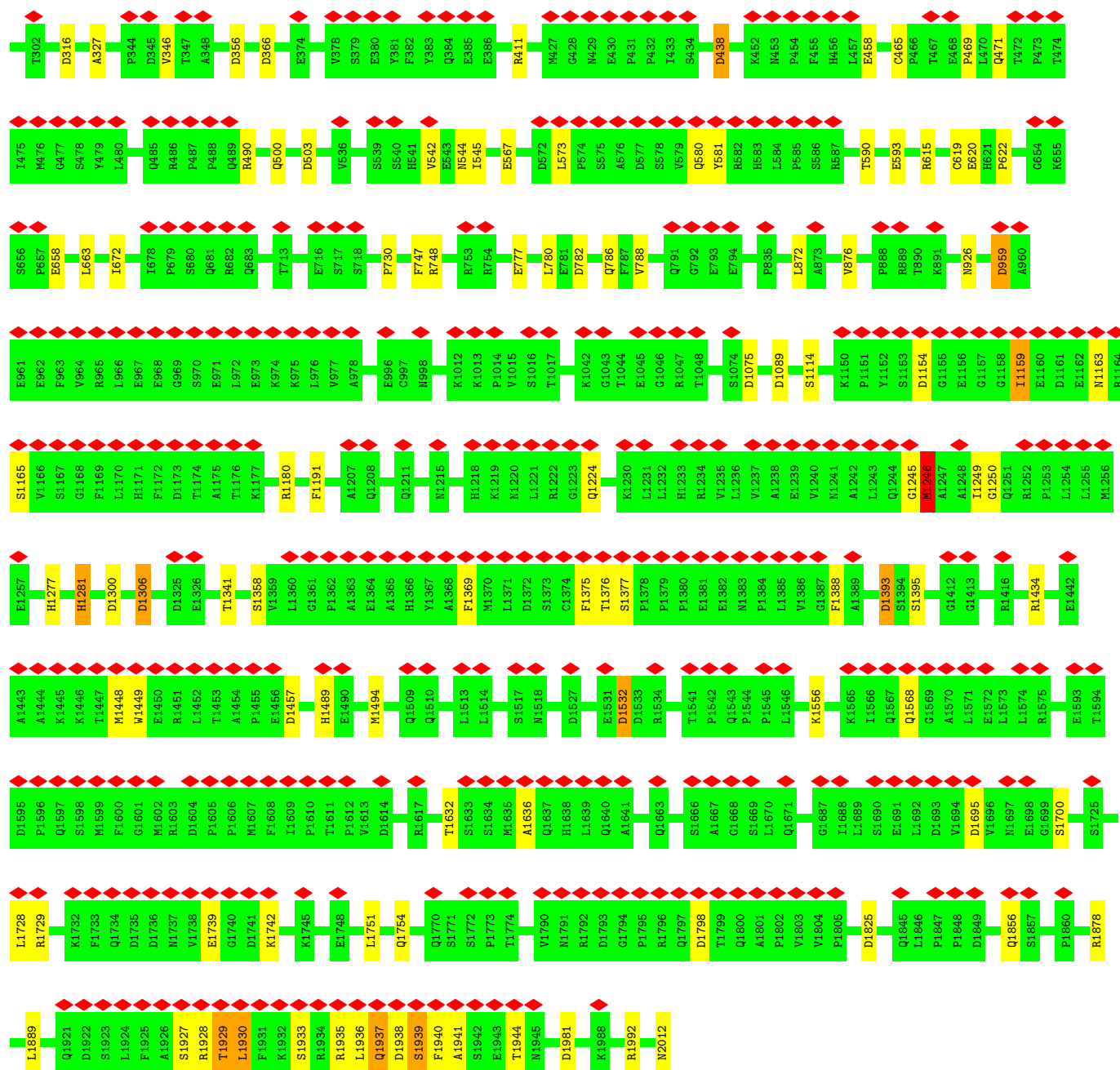




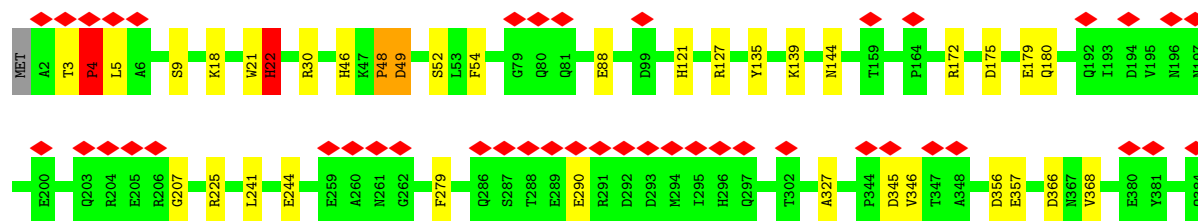
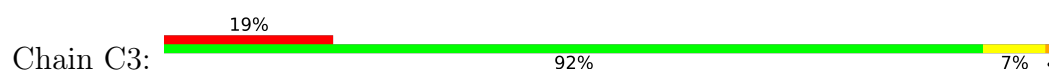


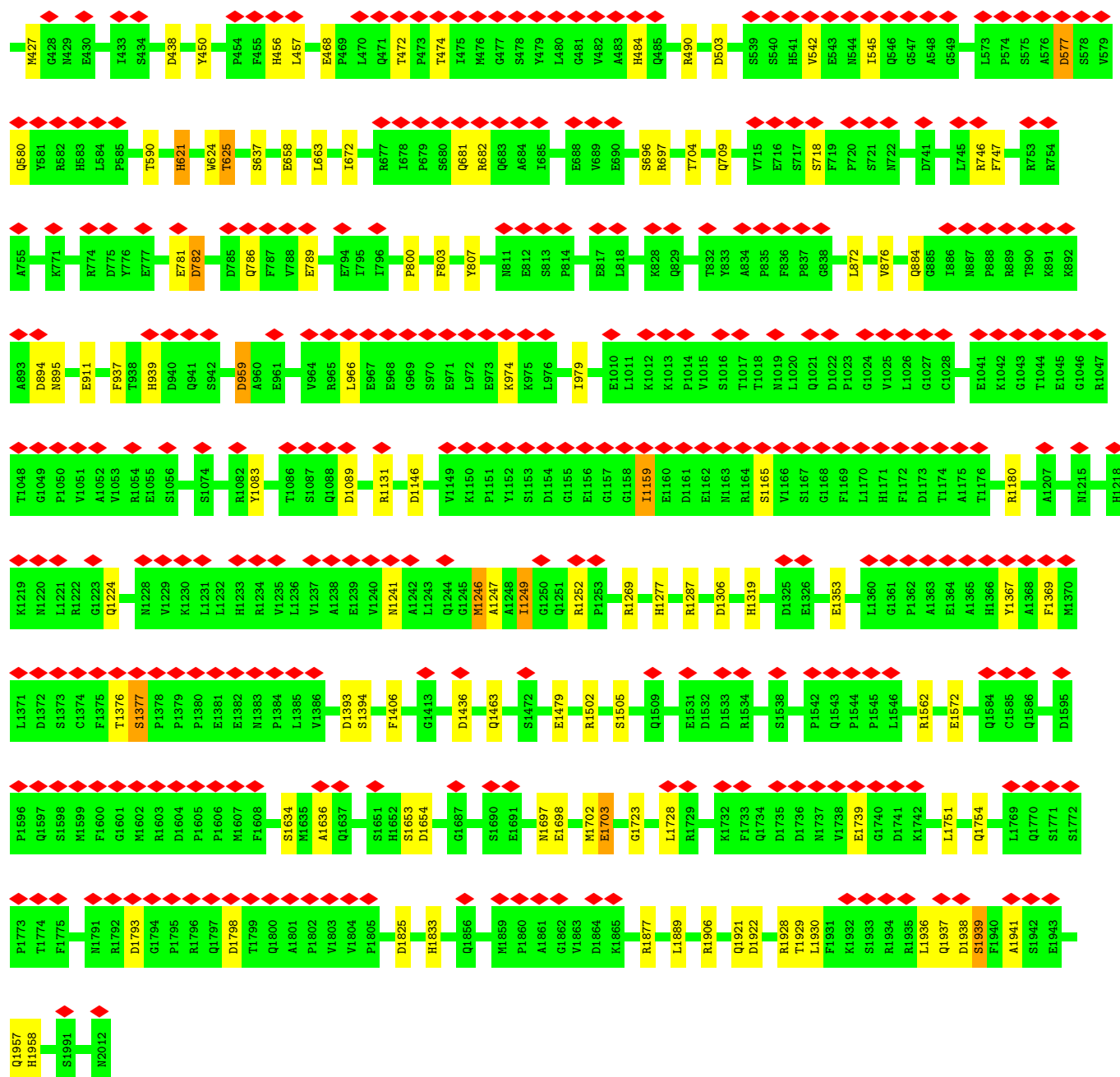
• Molecule 6: Nuclear pore complex protein Nup205





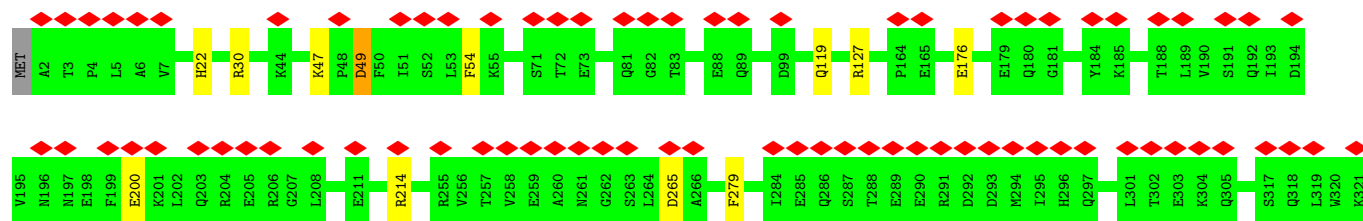
• Molecule 6: Nuclear pore complex protein Nup205

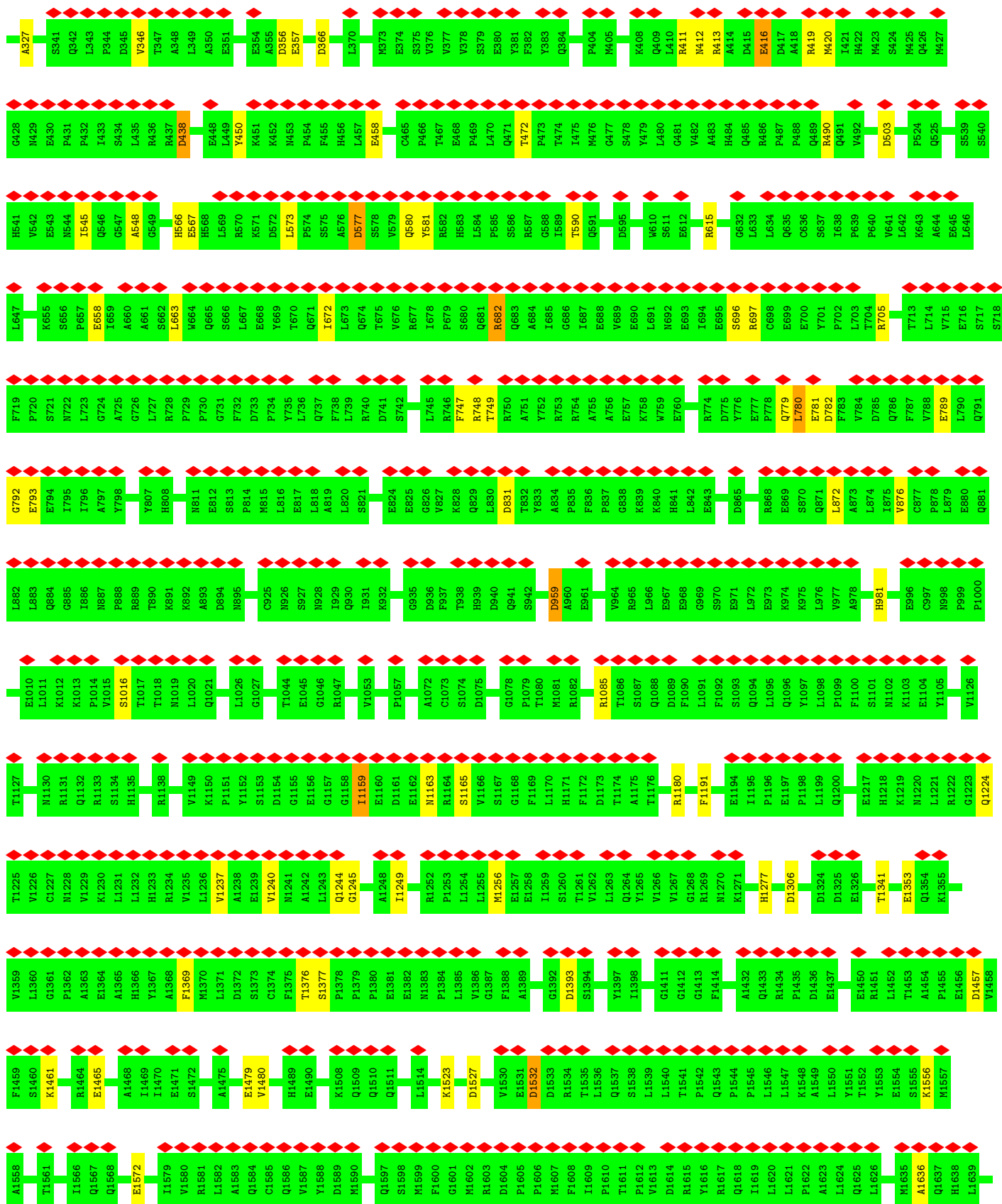




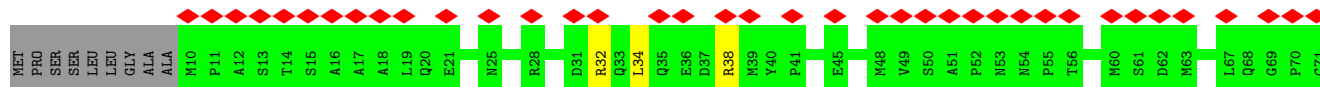
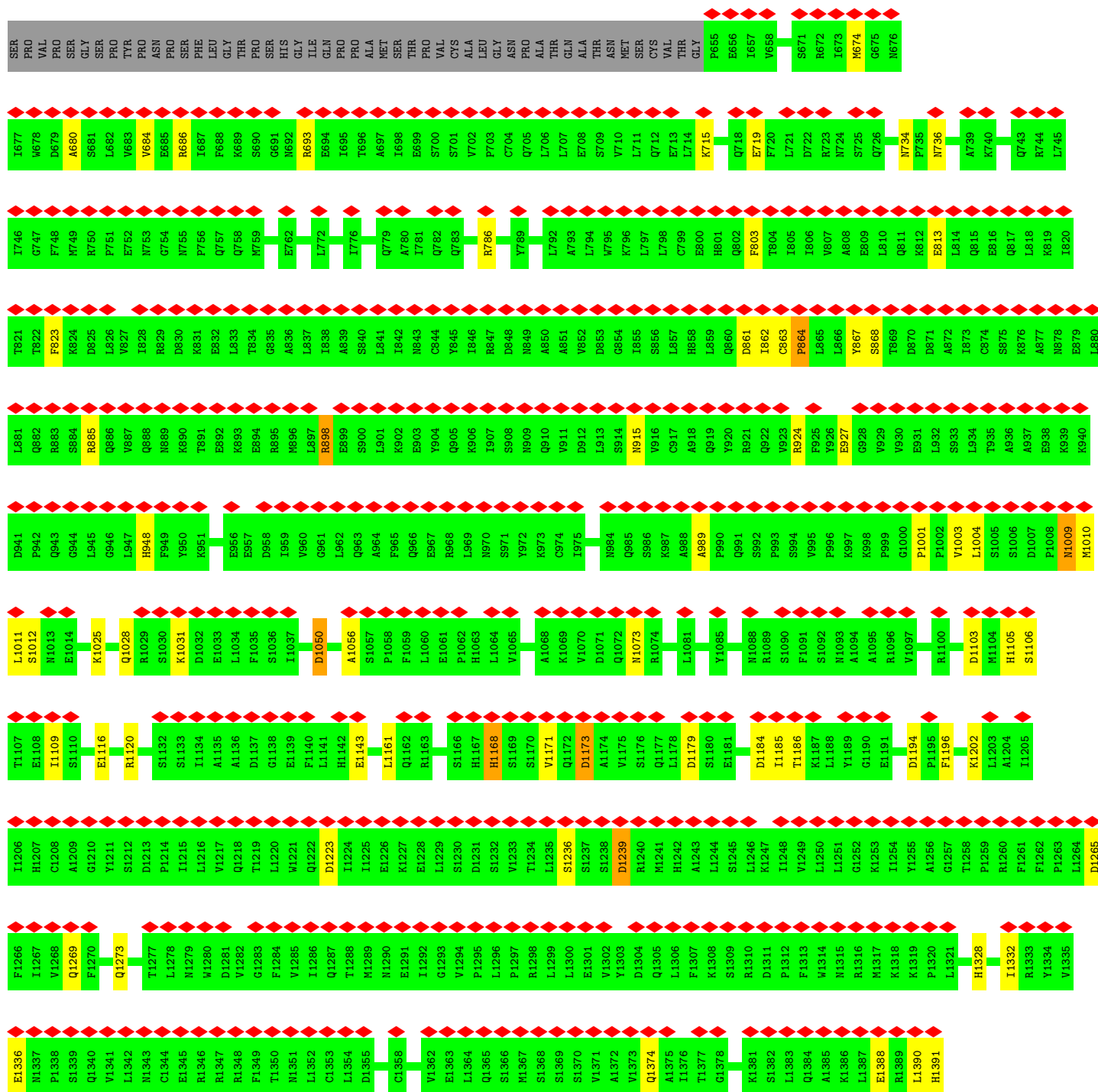
• Molecule 6: Nuclear pore complex protein Nup205

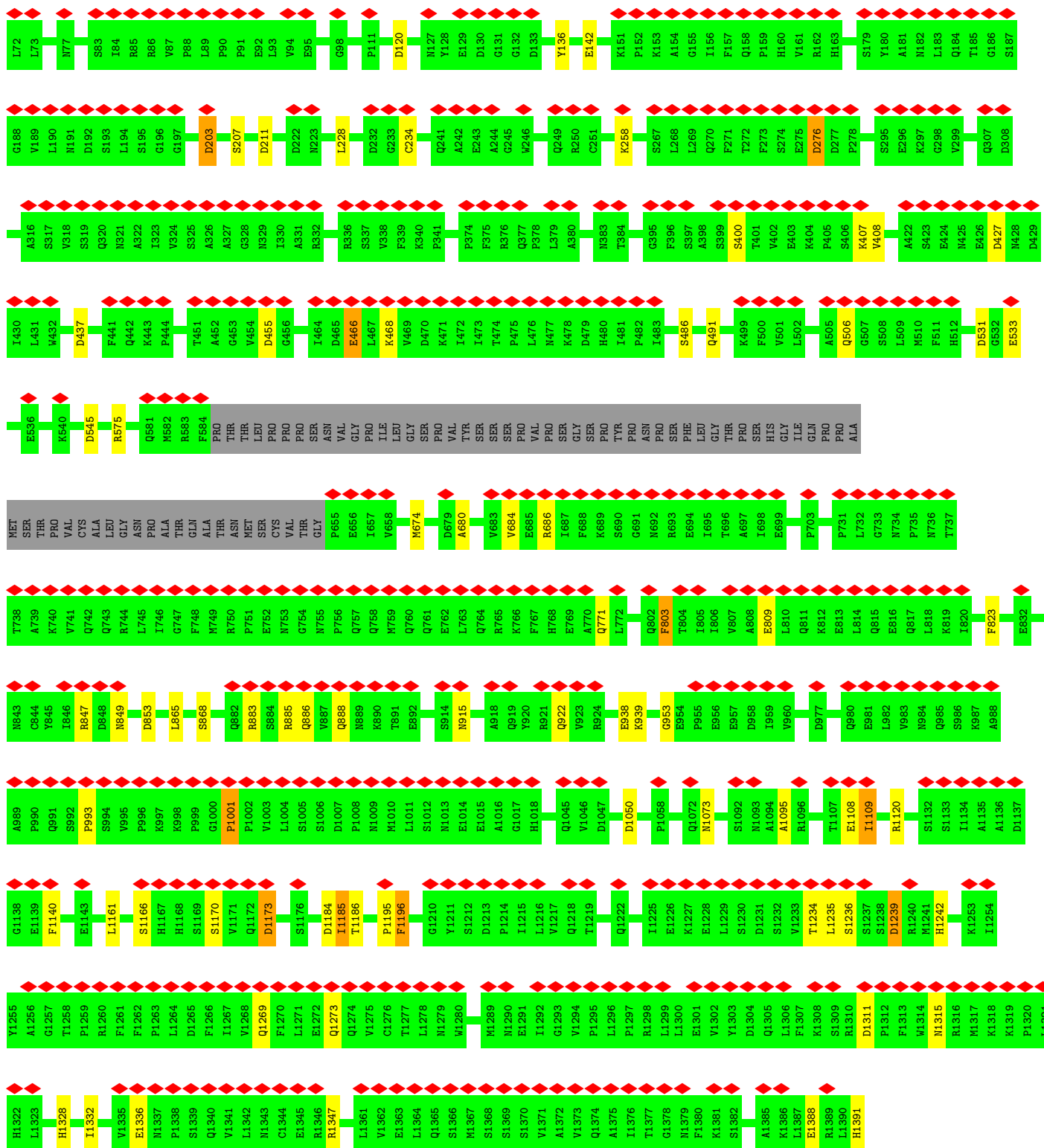
Chain C4: 39% 94% 5% •



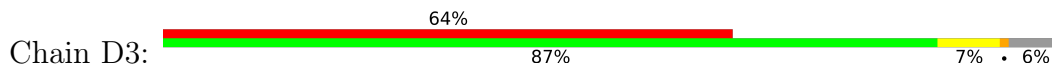


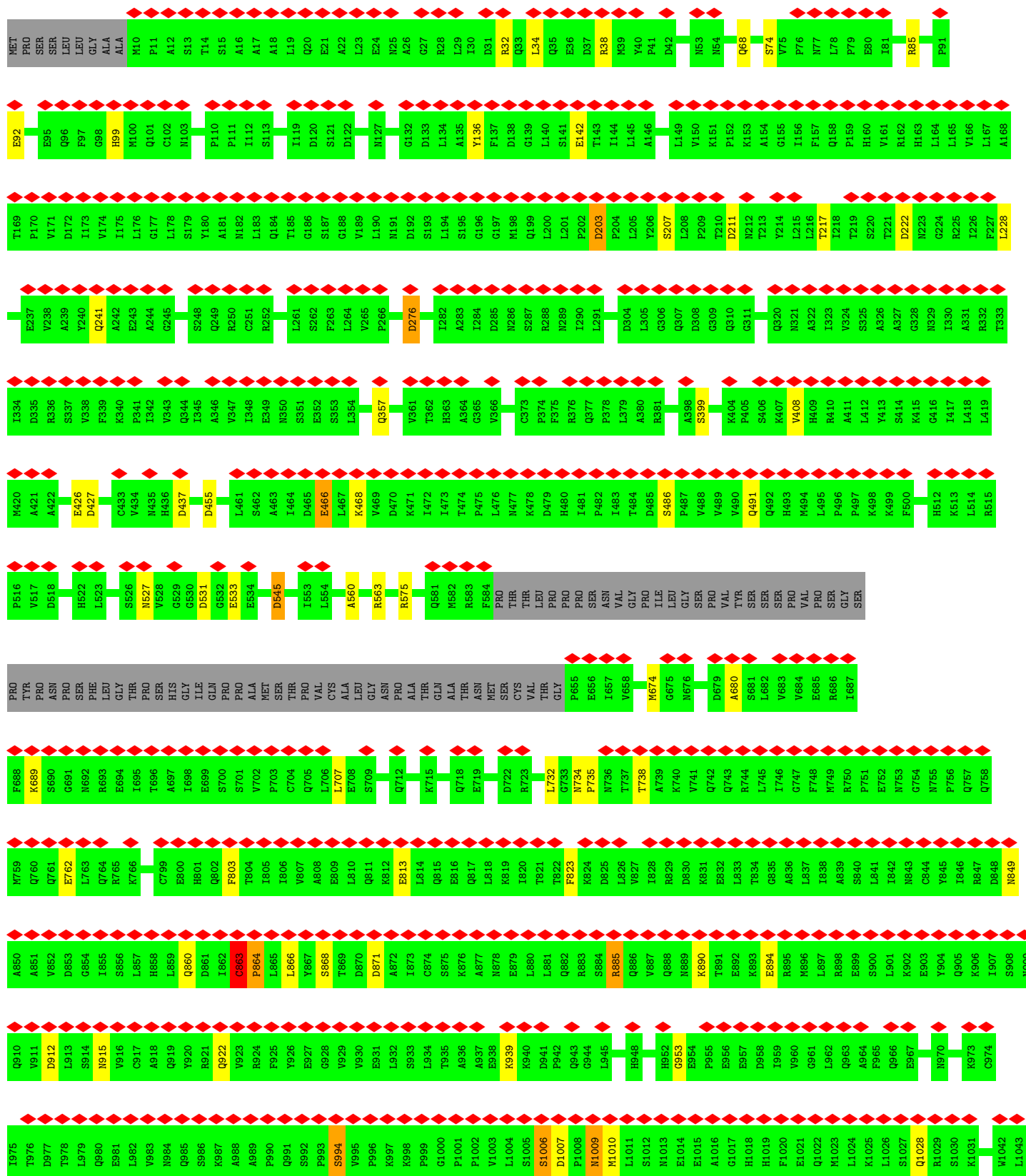


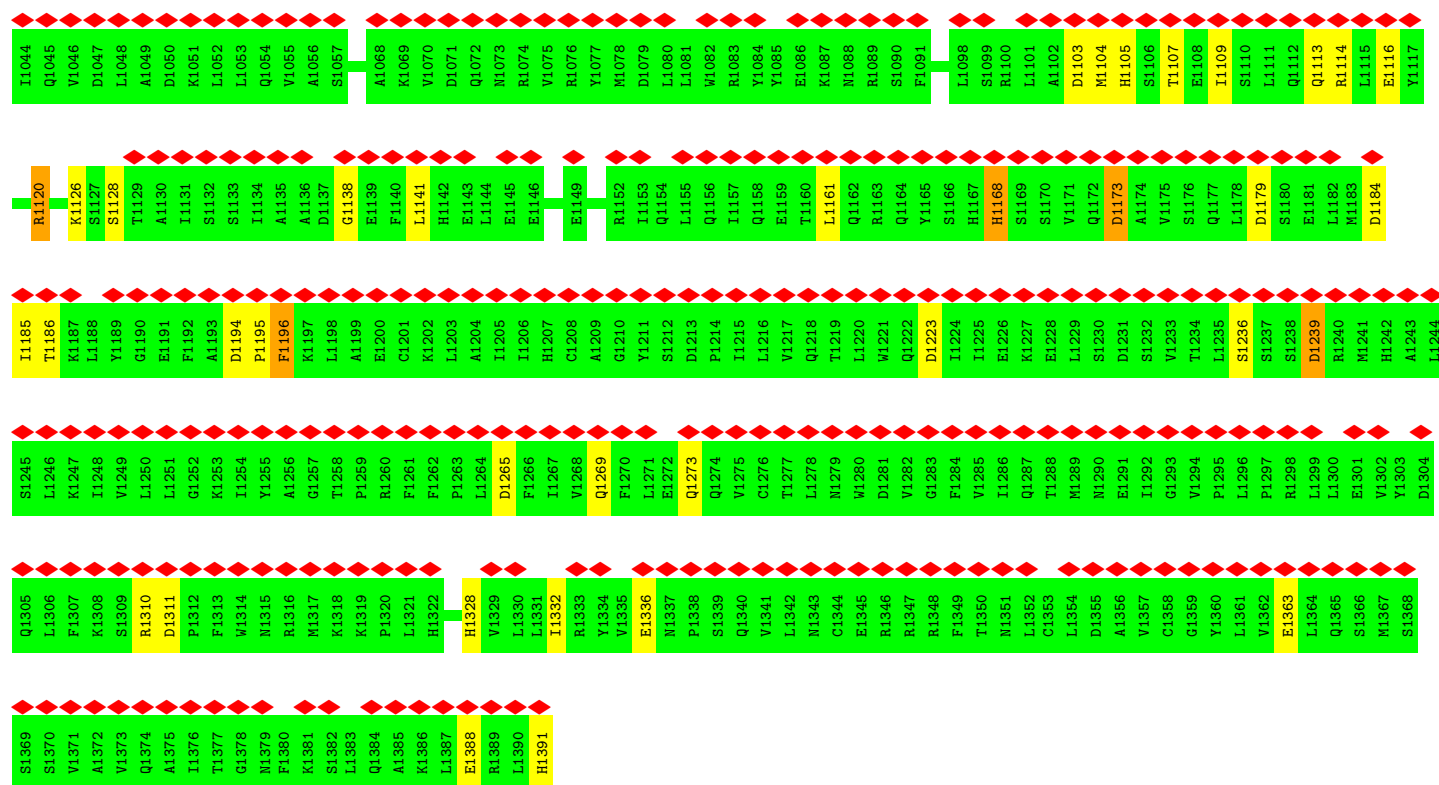




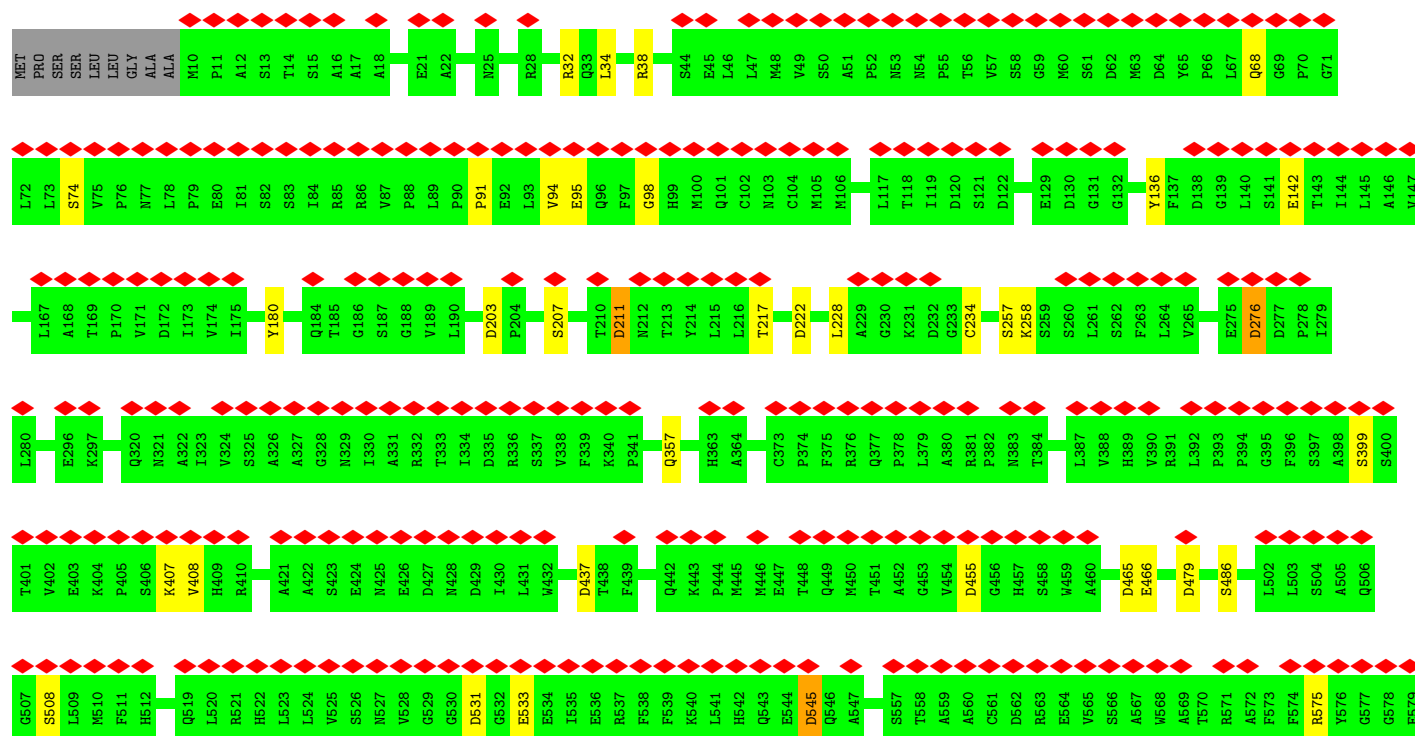
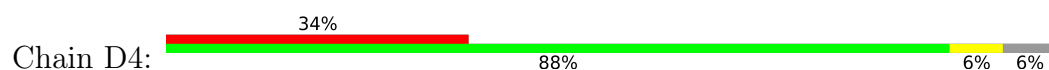
• Molecule 7: Nuclear pore complex protein Nup155







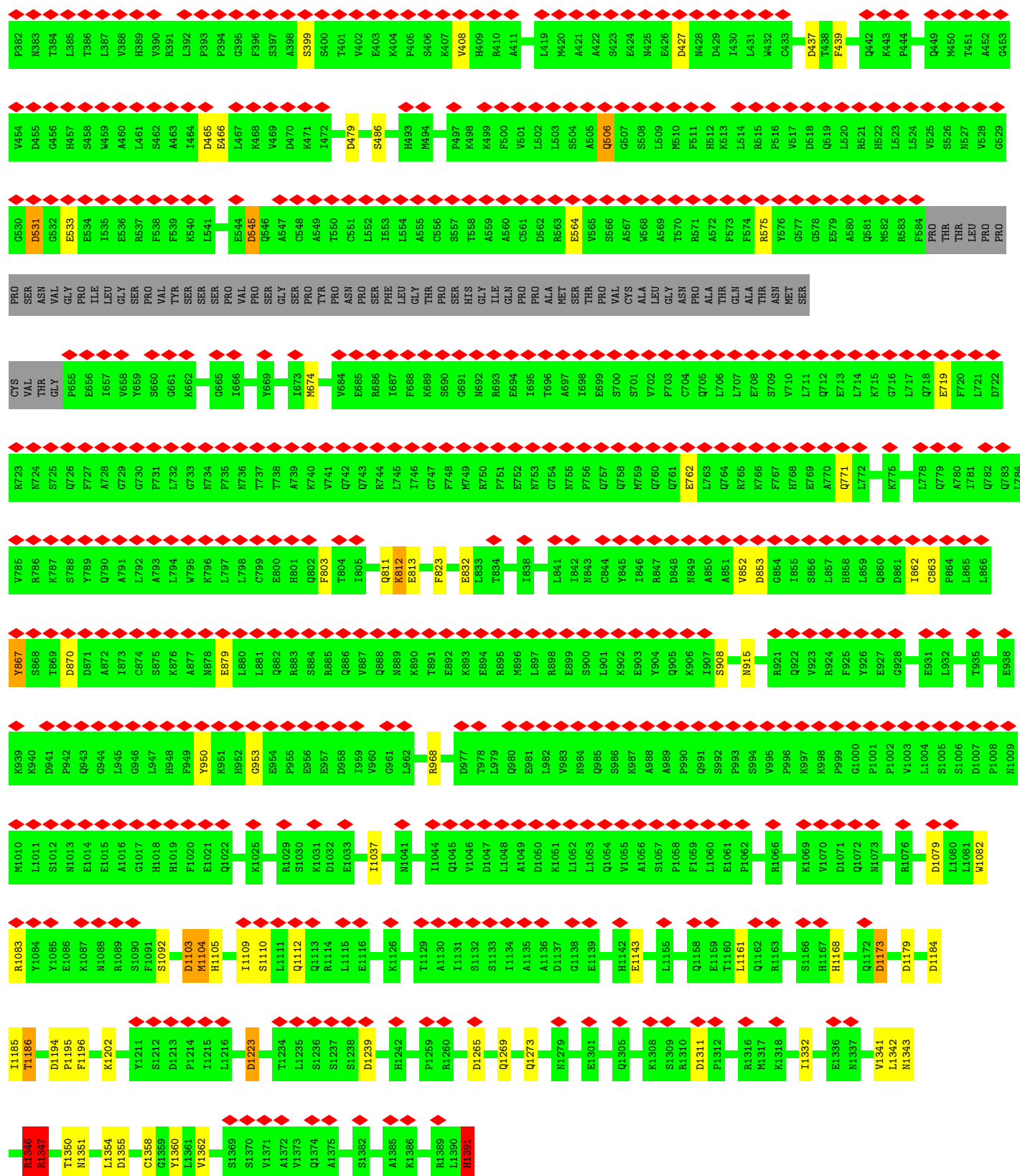
• Molecule 7: Nuclear pore complex protein Nup155

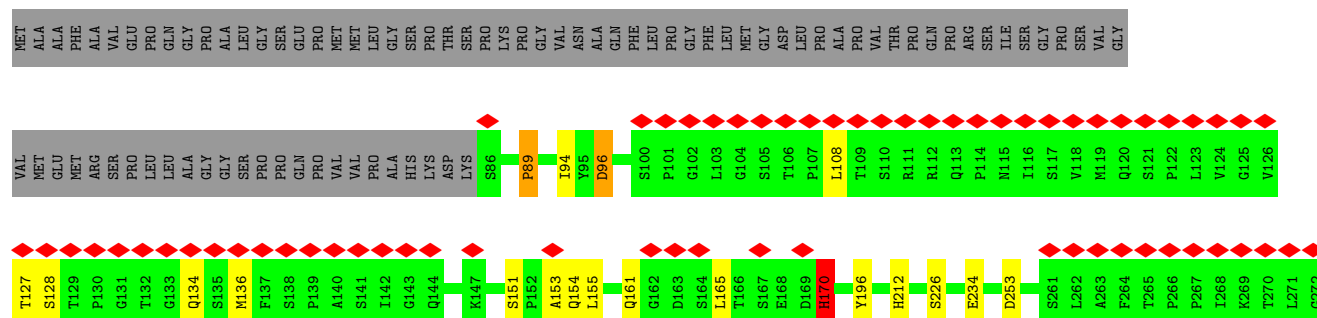


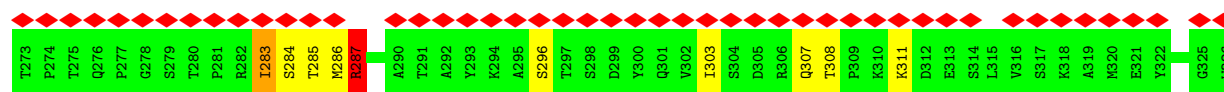


Service	Percentage
Red bar	56%
Green bar	87%
Yellow bar	6%
Grey bar	6%

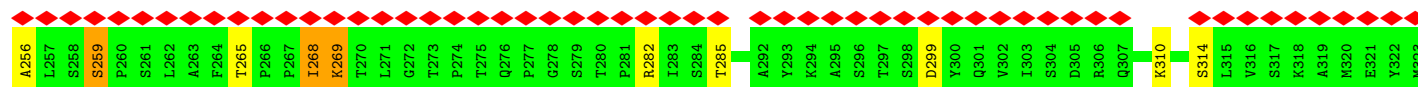
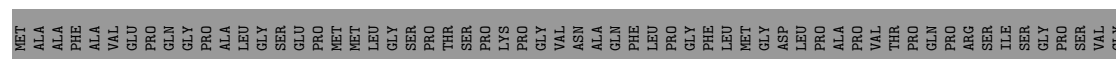
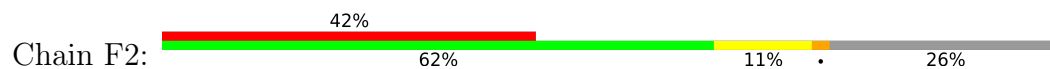




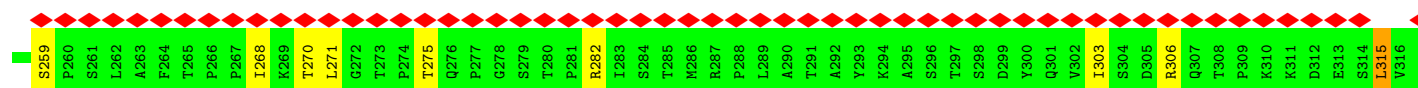
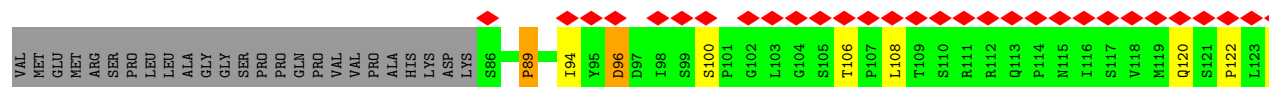
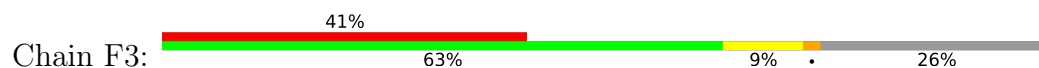




• Molecule 9: Nucleoporin NUP35

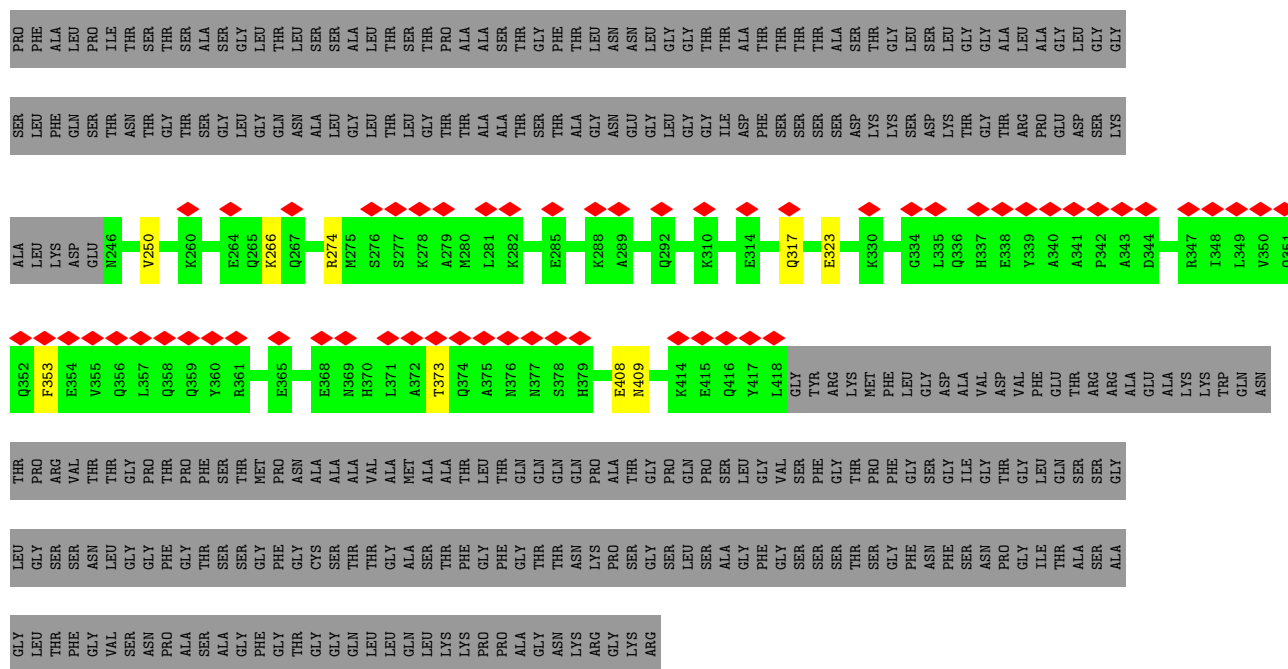


• Molecule 9: Nucleoporin NUP35

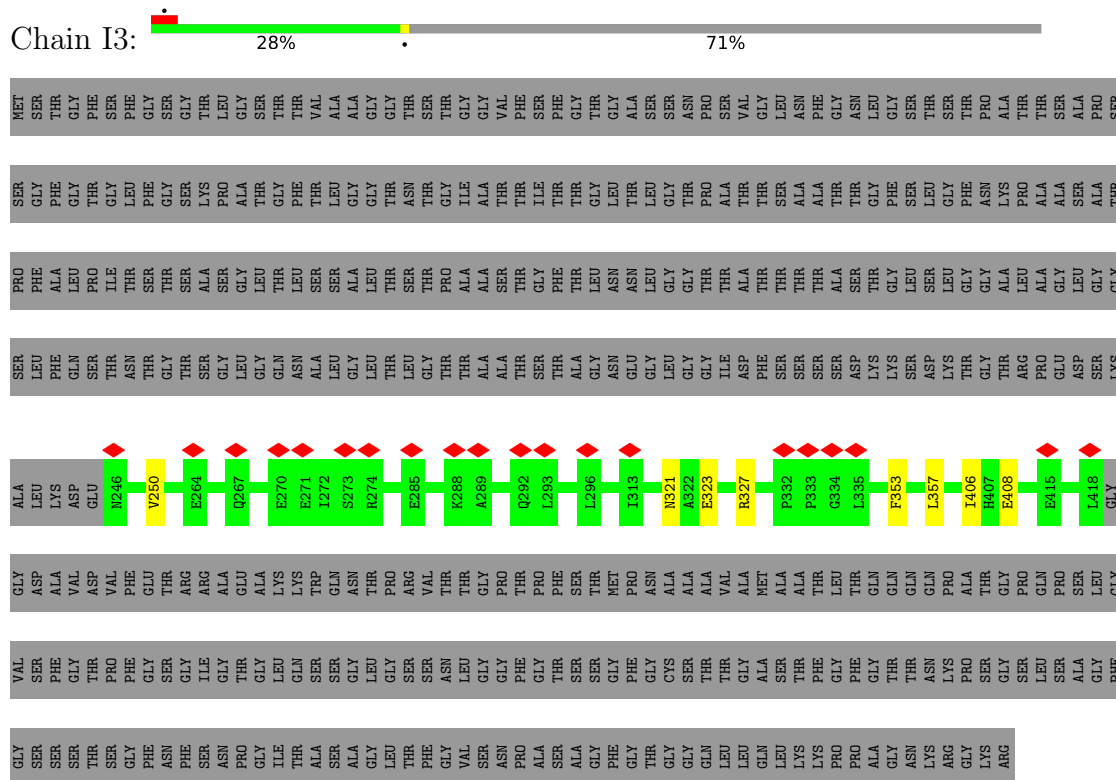


• Molecule 10: Nucleoporin p54

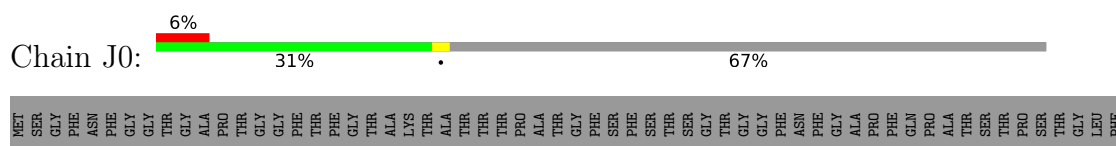


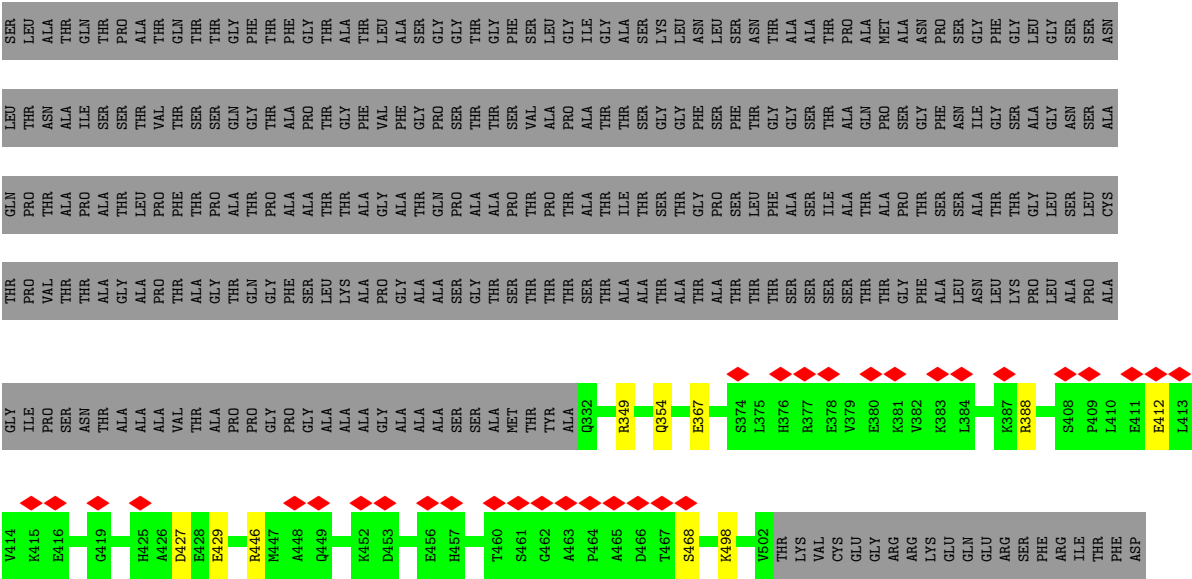


• Molecule 11: Nucleoprotein p58/p45

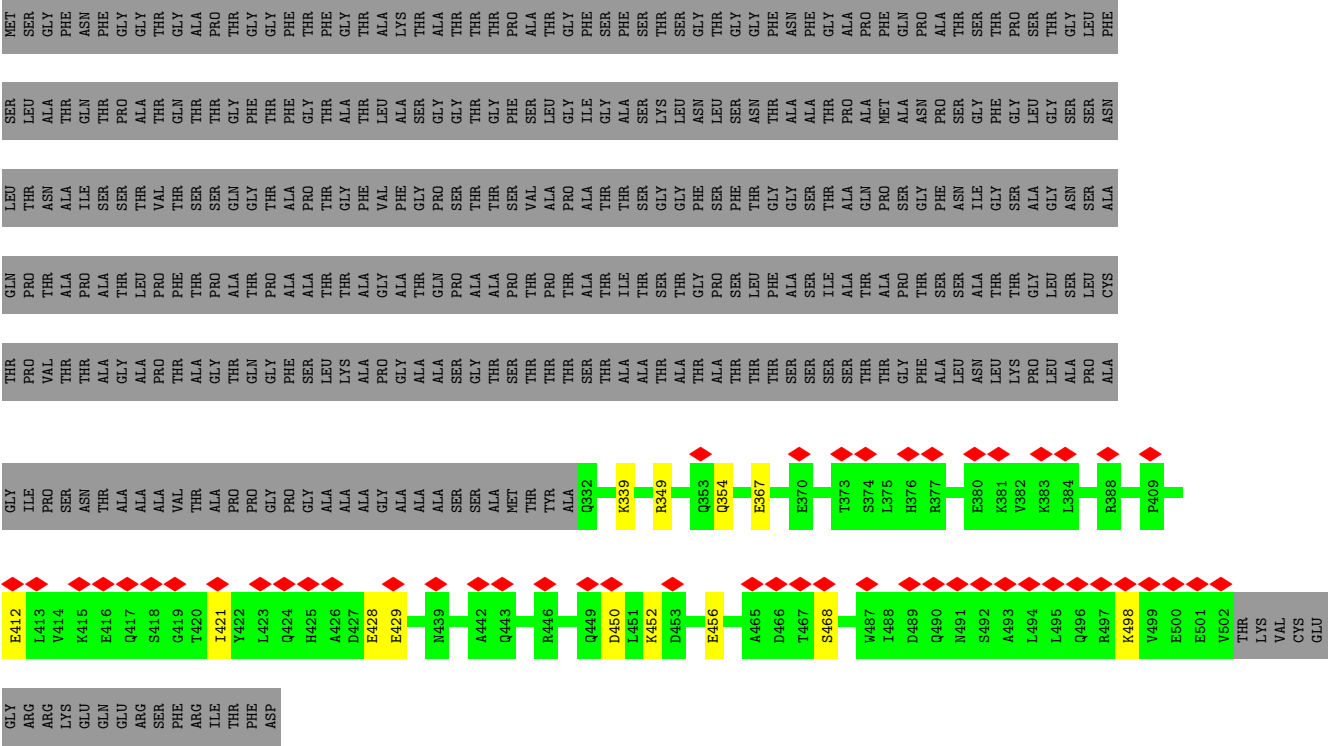


• Molecule 12: Nuclear pore glycoprotein p62

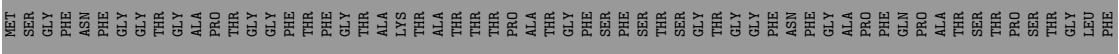


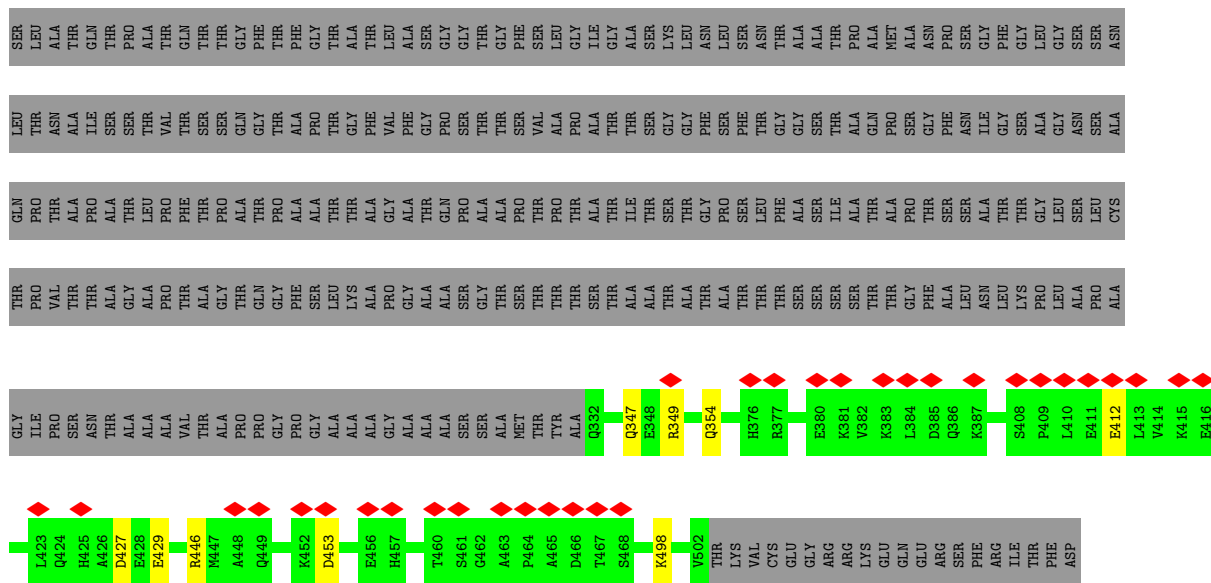


• Molecule 12: Nuclear pore glycoprotein p62

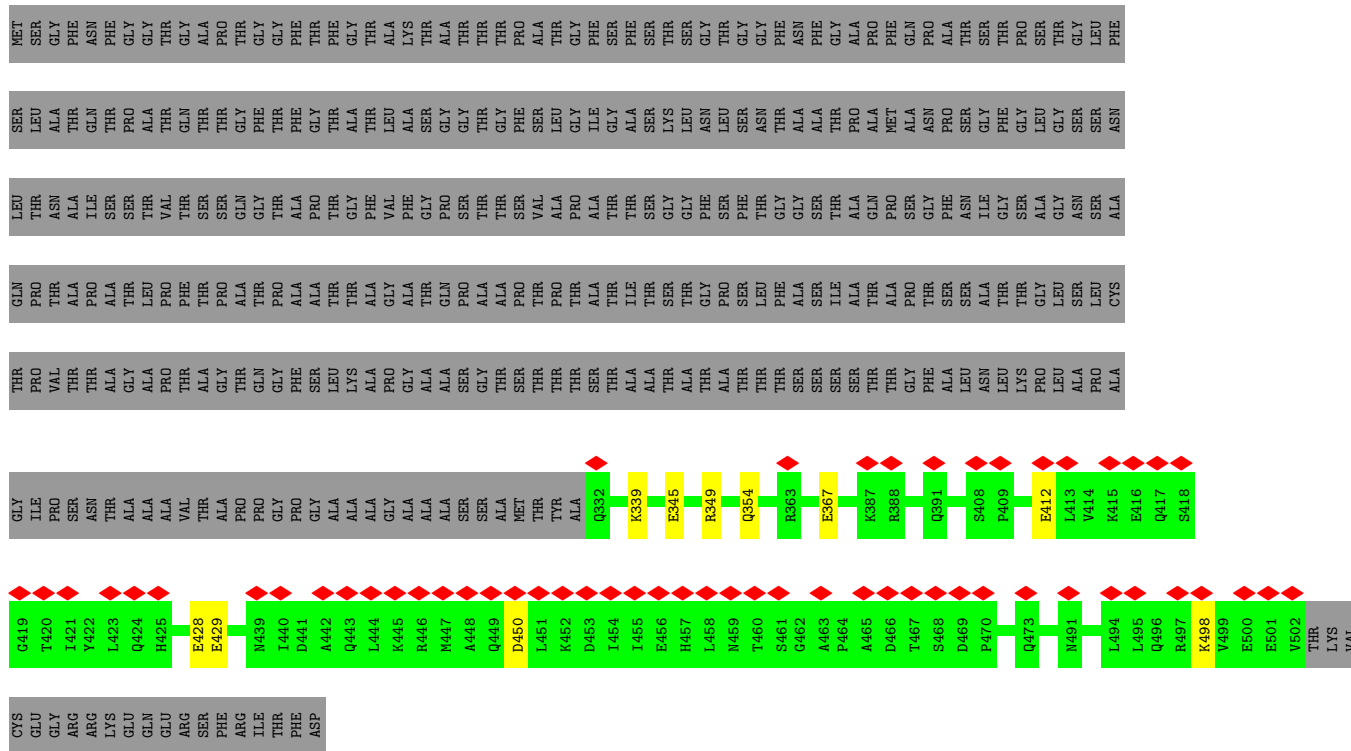


• Molecule 12: Nuclear pore glycoprotein p62

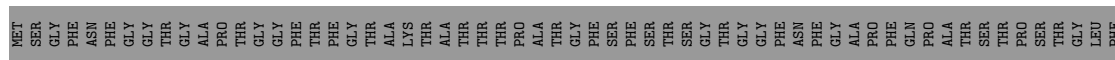


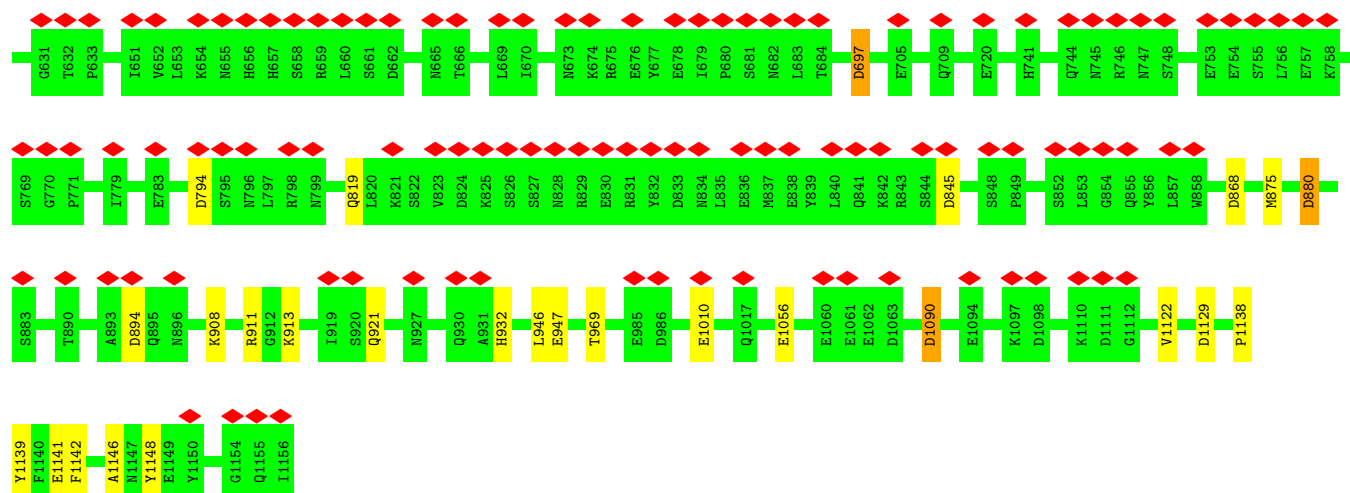


- Molecule 12: Nuclear pore glycoprotein p62

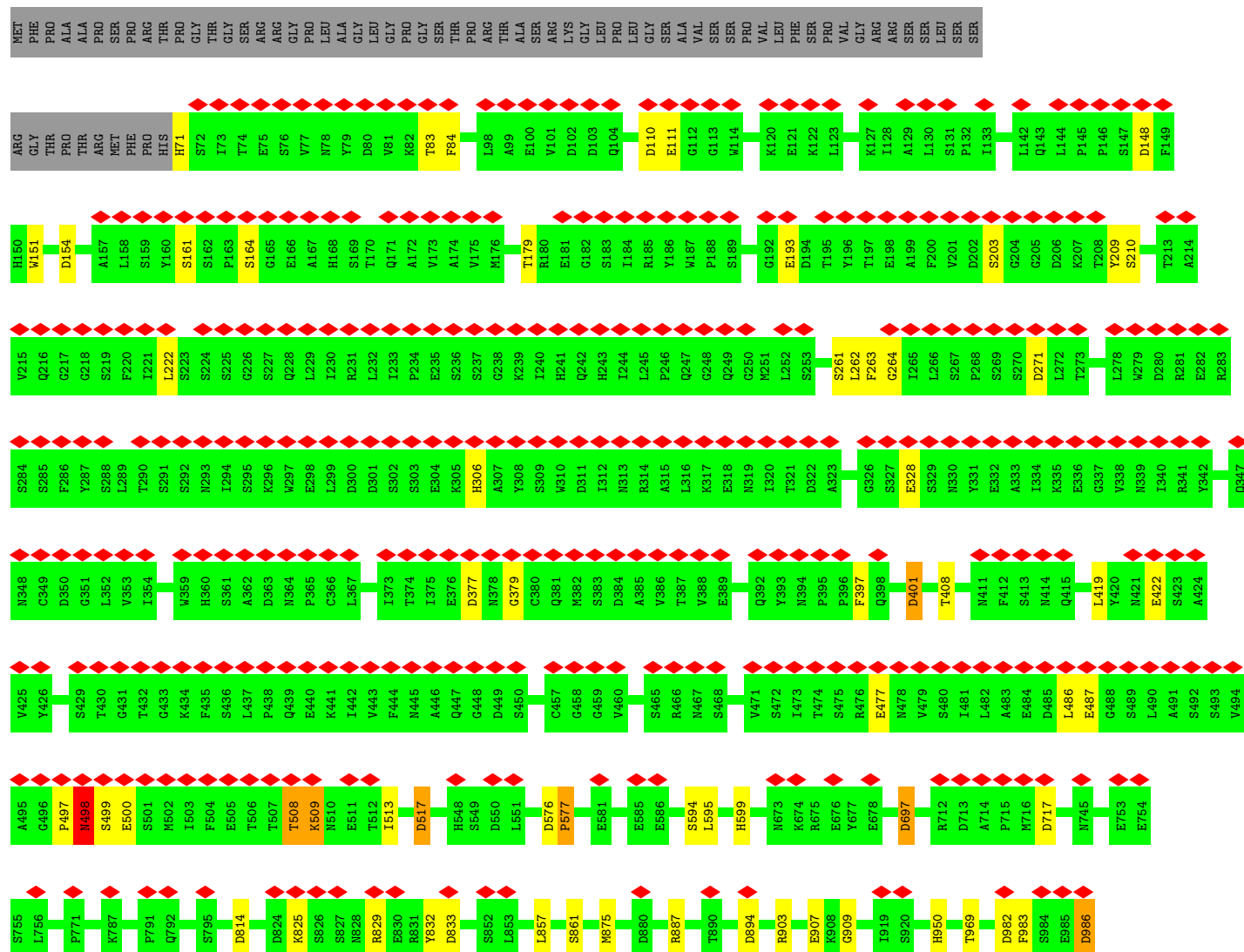
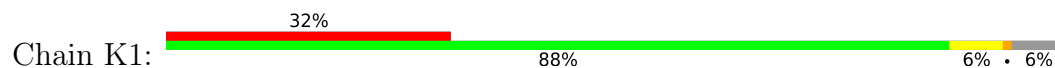


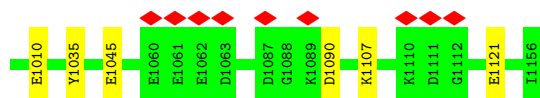
- Molecule 12: Nuclear pore glycoprotein p62





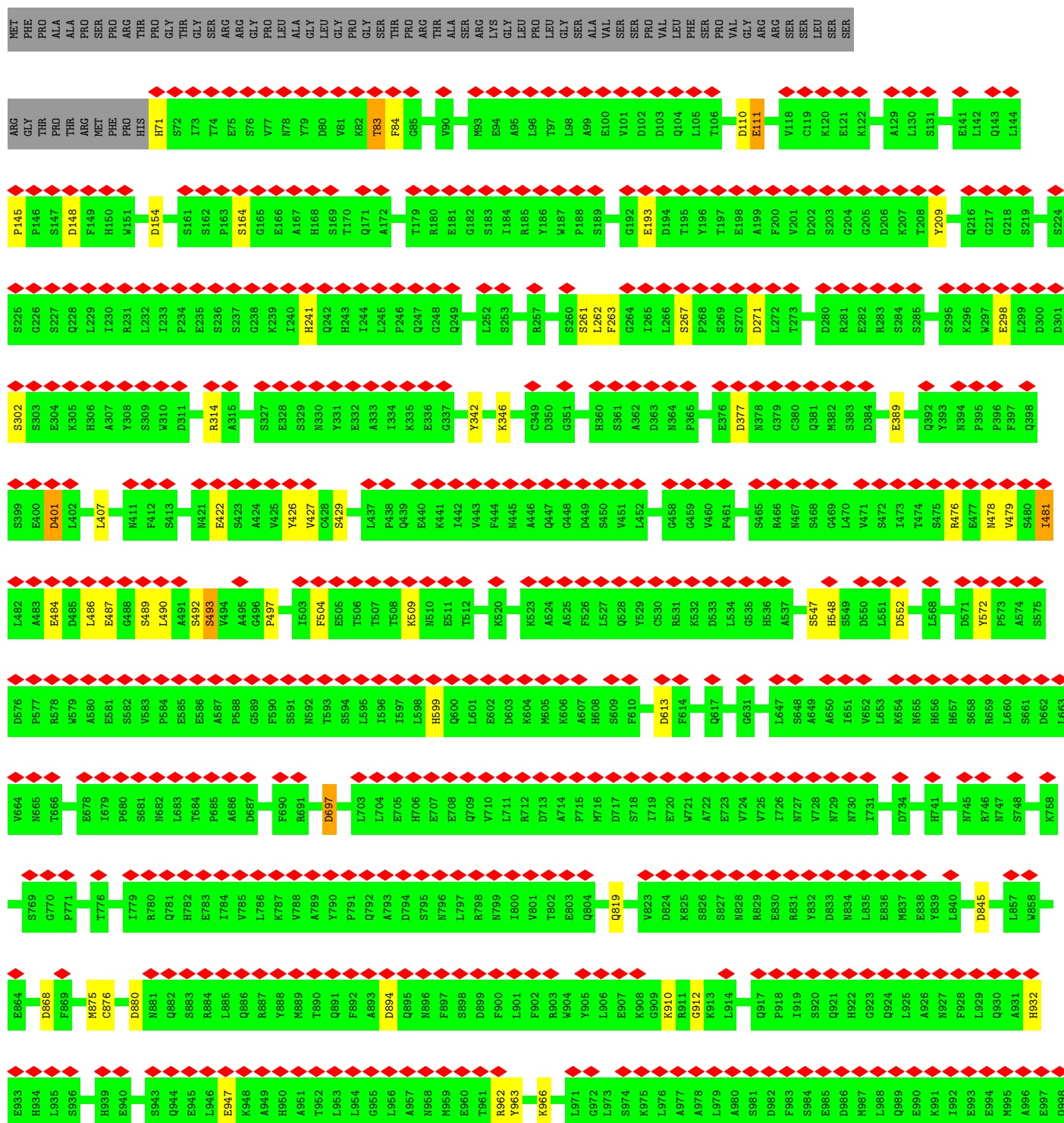
• Molecule 13: Nuclear pore complex protein Nup133

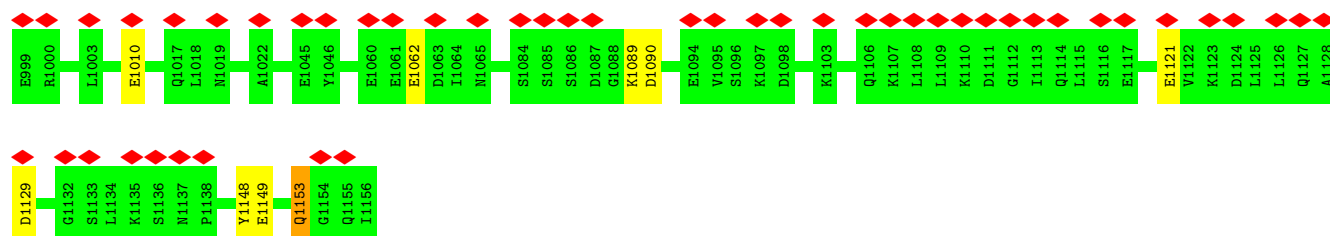




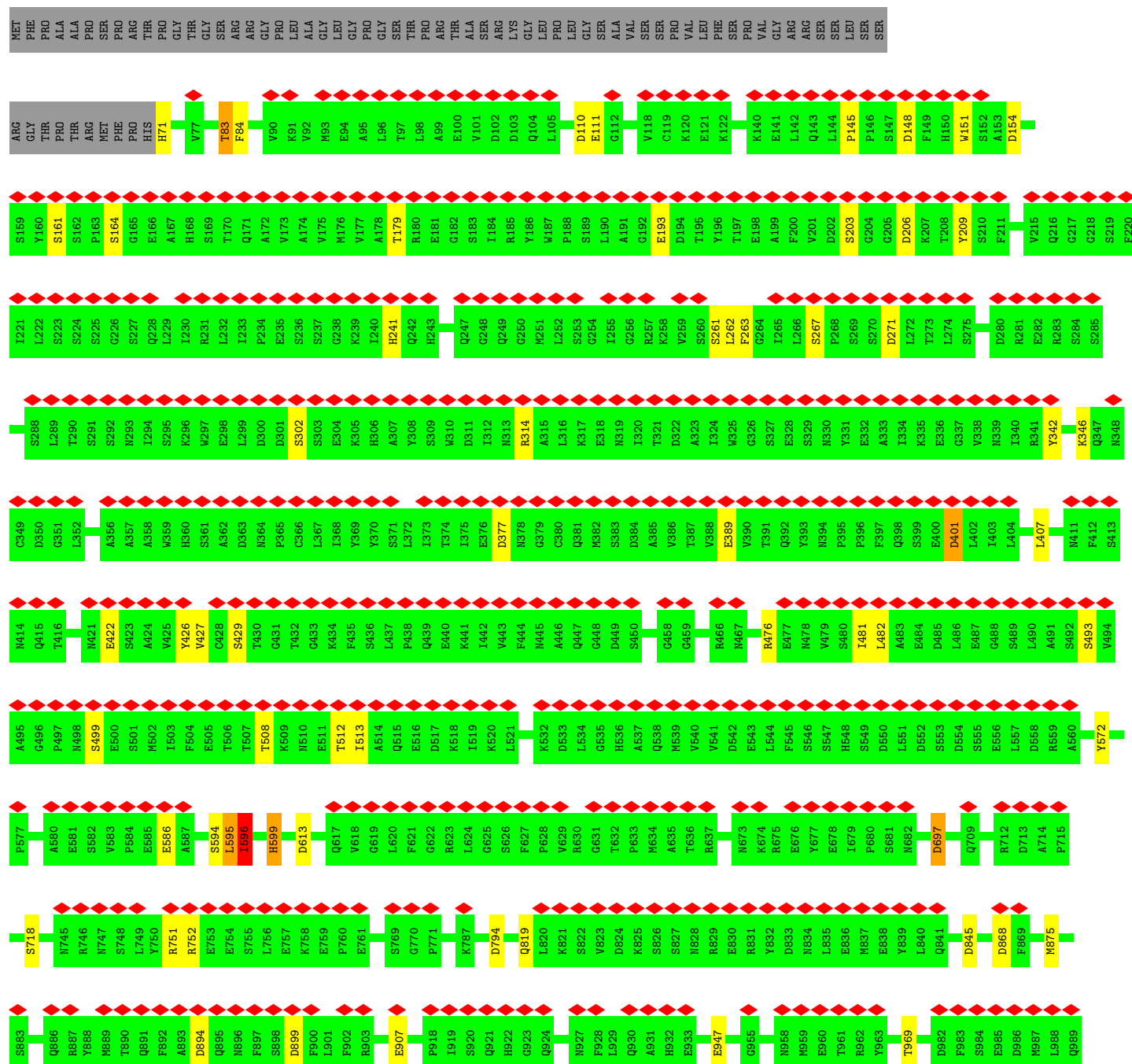
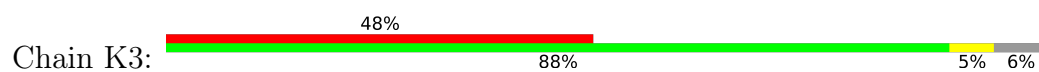
• Molecule 13: Nuclear pore complex protein Nup133

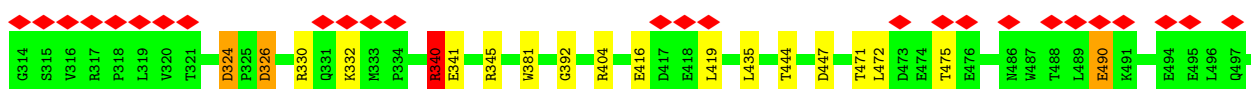
Chain K2: 51% 88% 6% • 6%

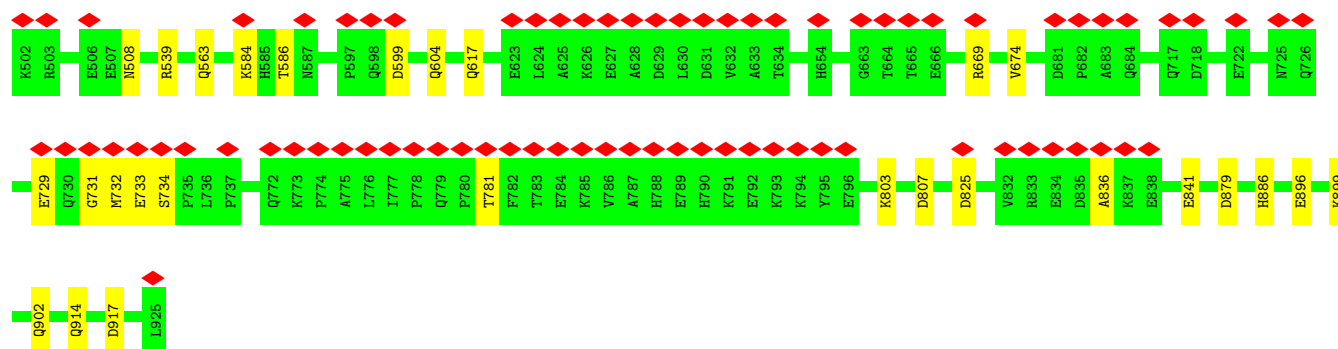




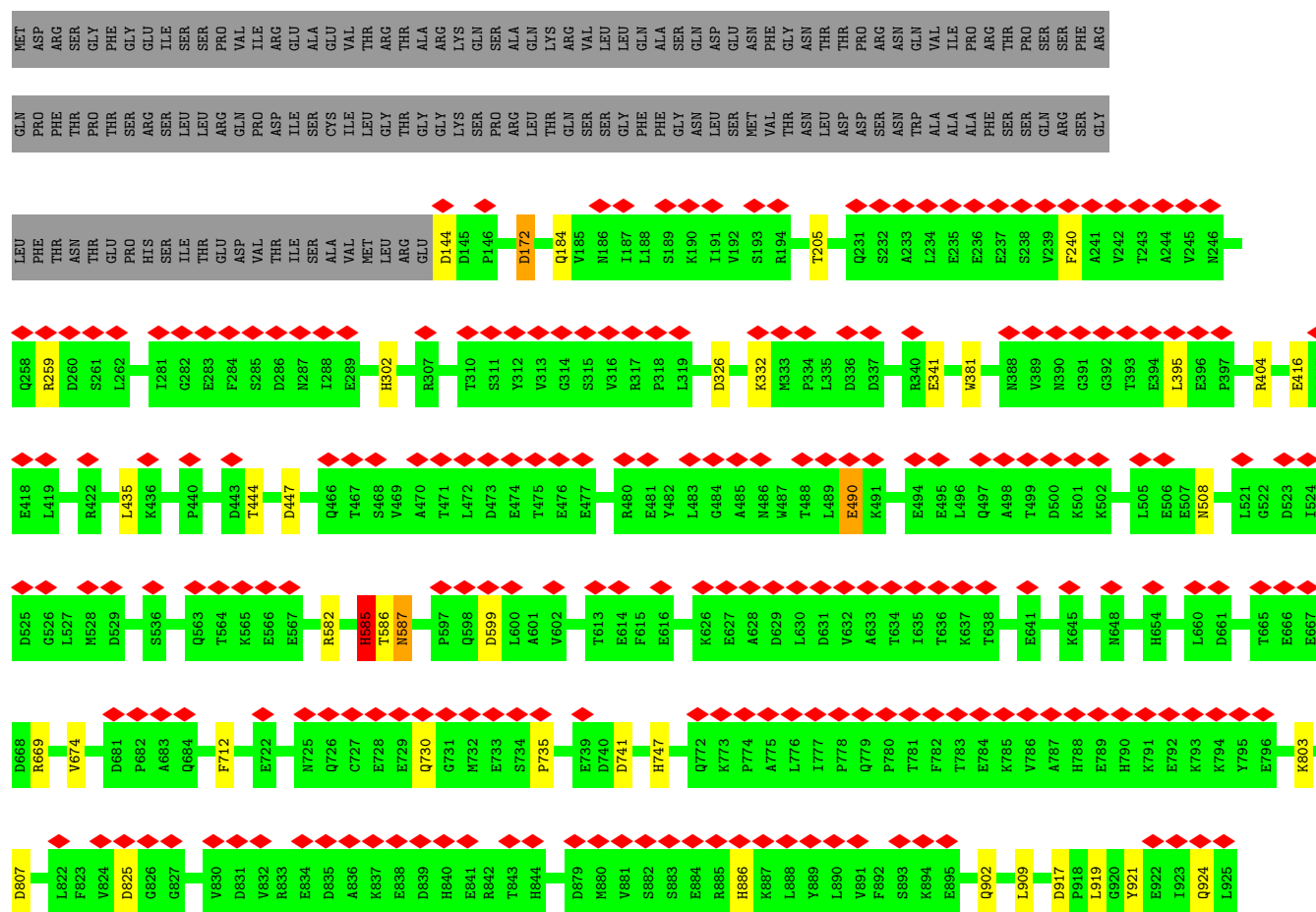
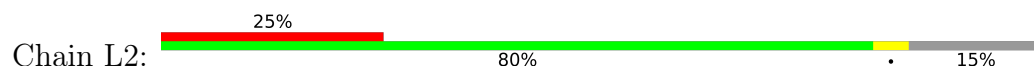
• Molecule 13: Nuclear pore complex protein Nup133



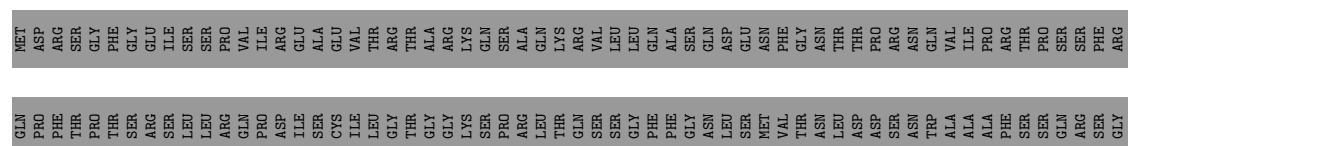
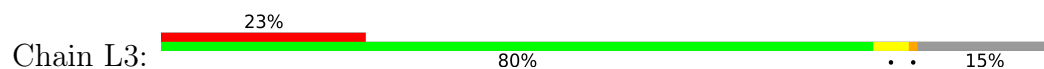


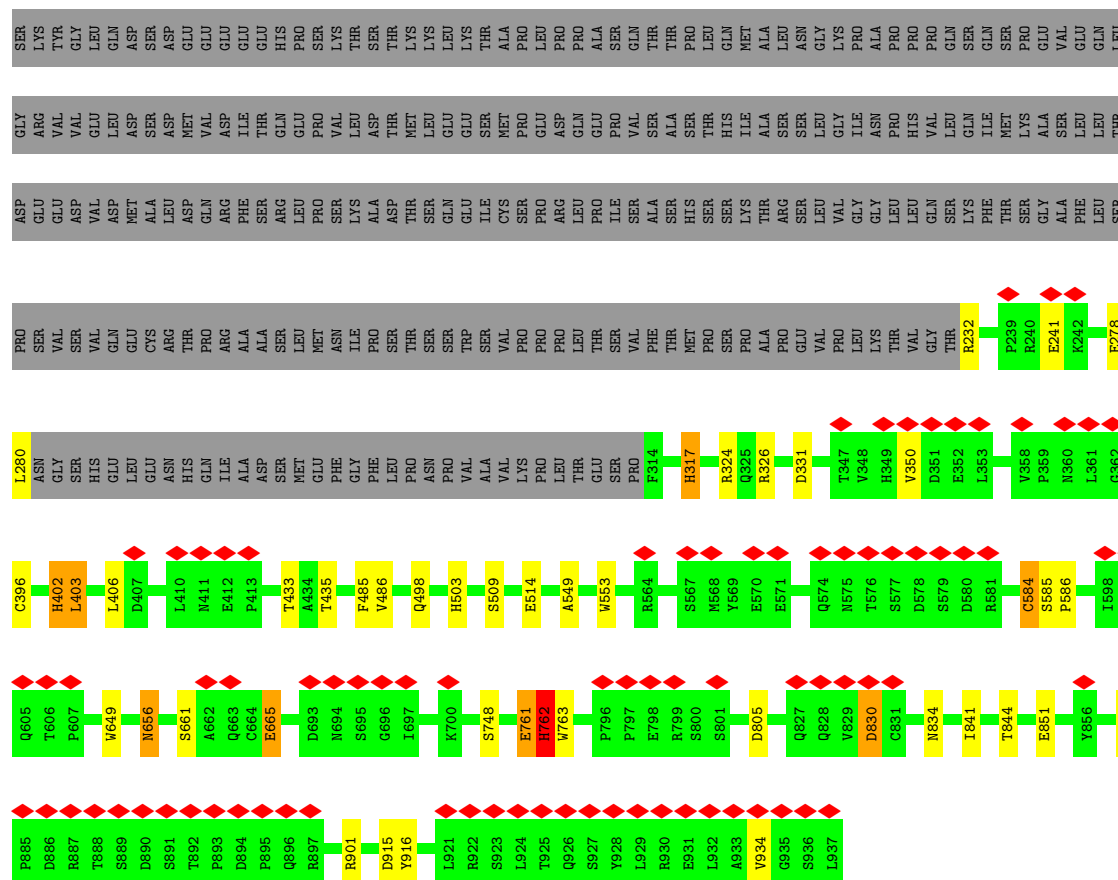


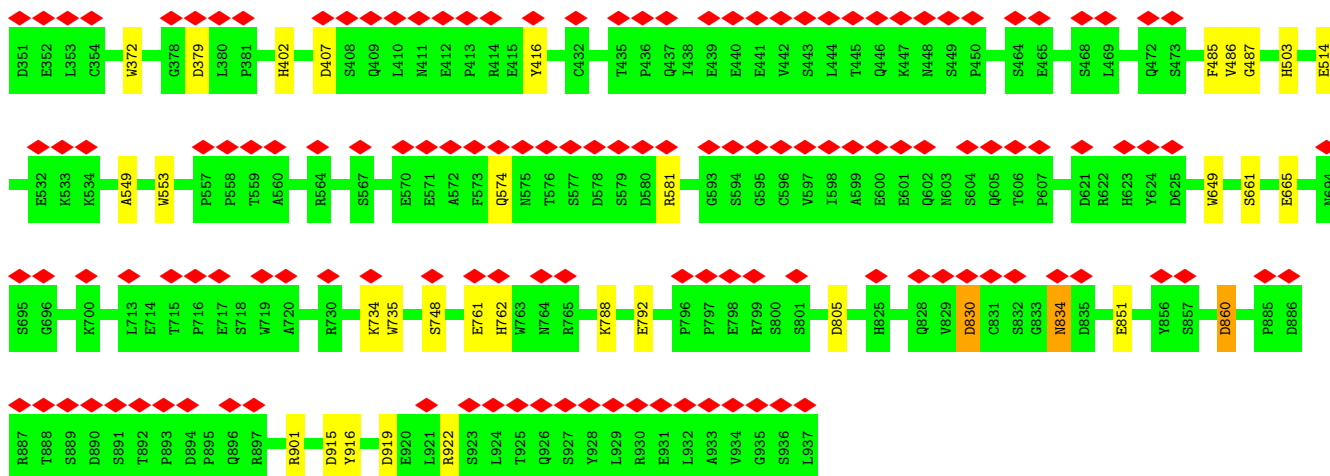
• Molecule 14: Nuclear pore complex protein Nup107



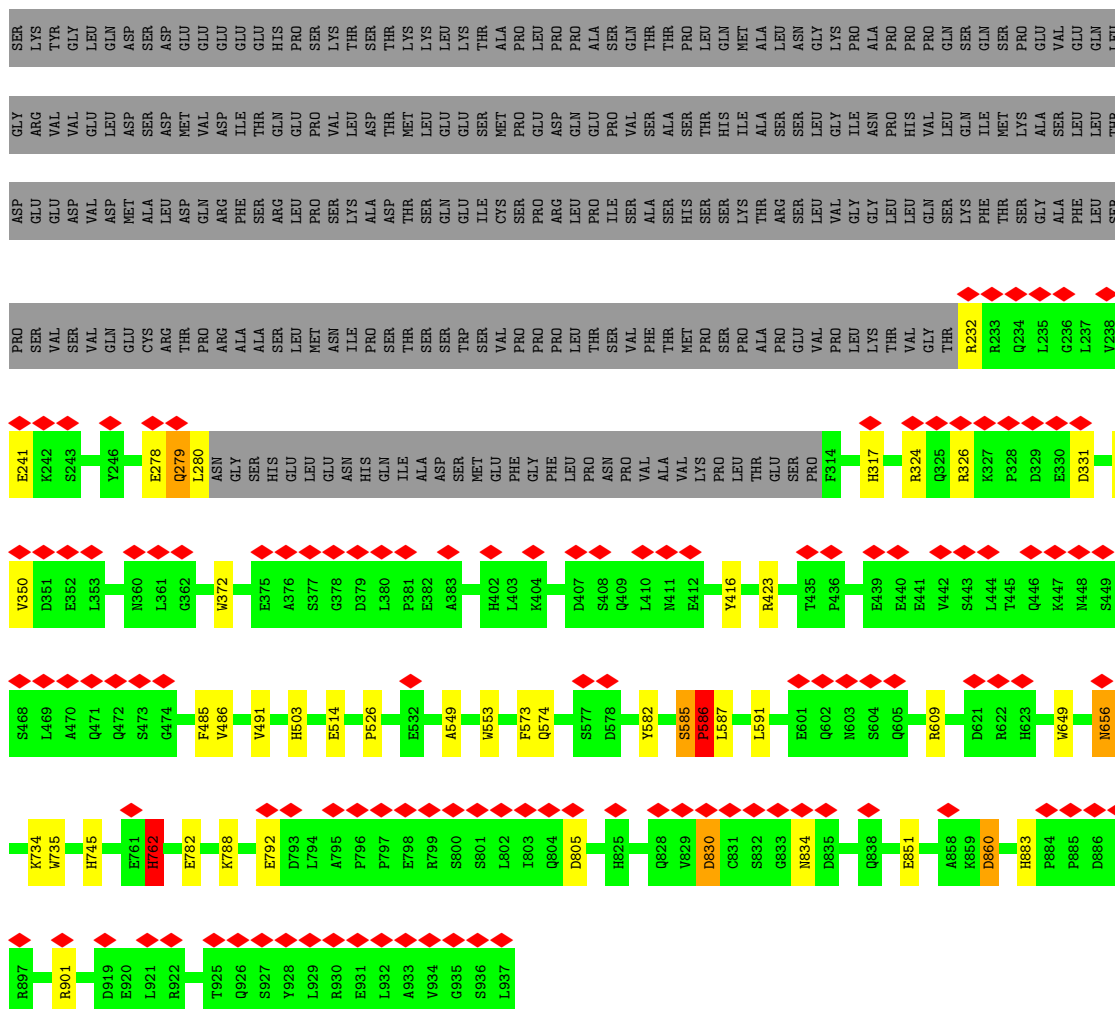
• Molecule 14: Nuclear pore complex protein Nup107



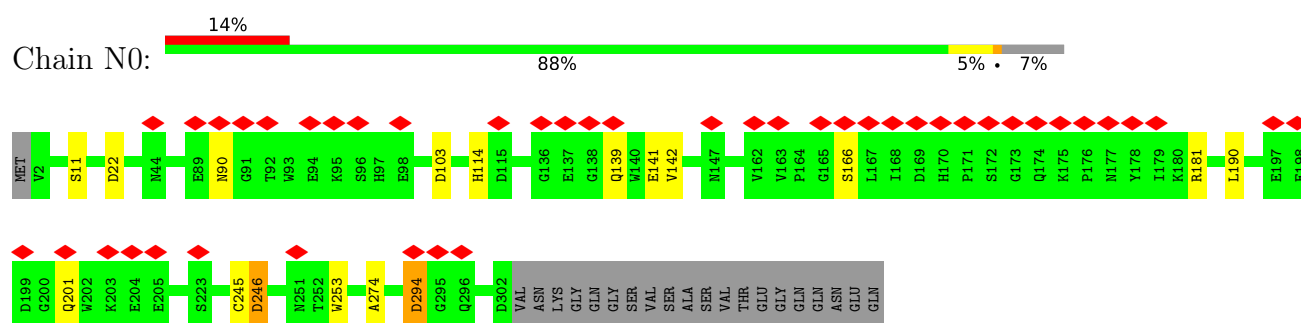




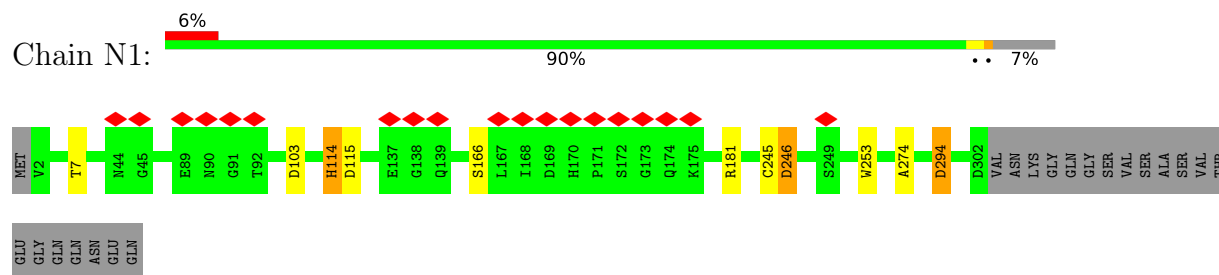
• Molecule 15: Nuclear pore complex protein Nup96



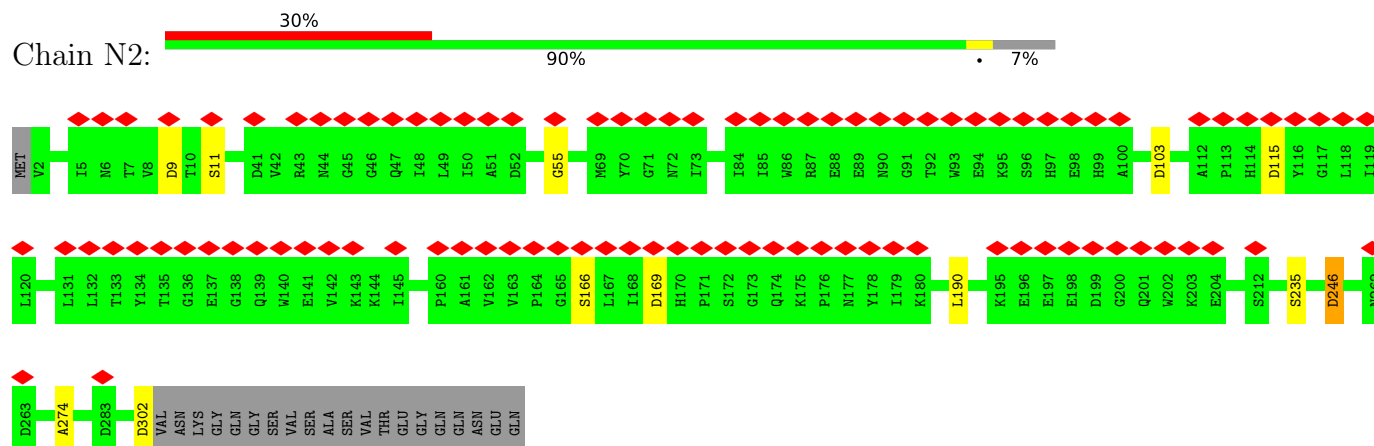
• Molecule 16: Protein SEC13 homolog



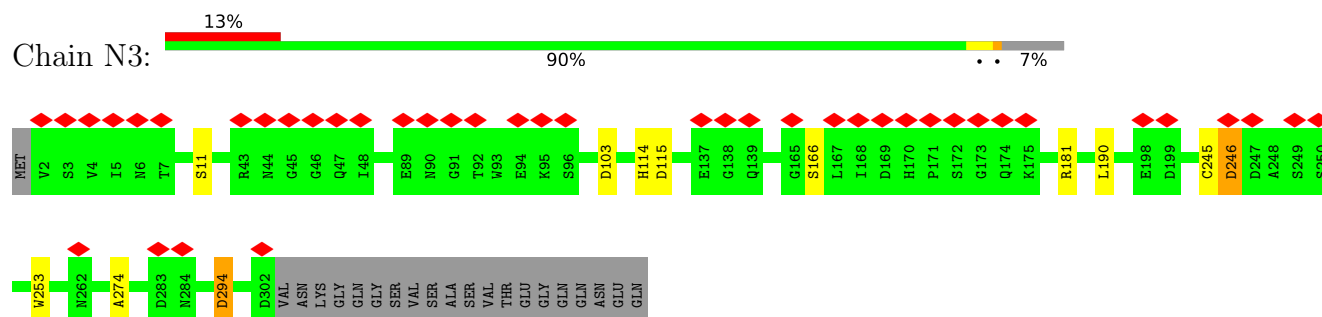
- Molecule 16: Protein SEC13 homolog



- Molecule 16: Protein SEC13 homolog

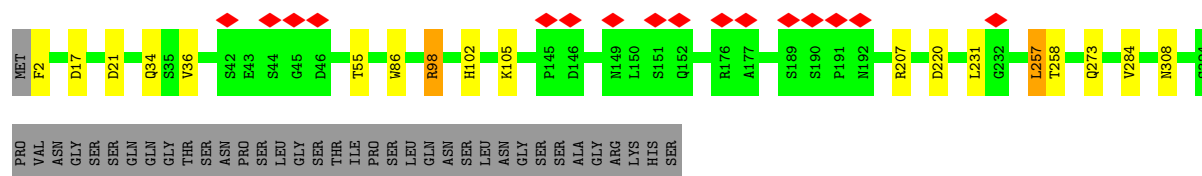


- Molecule 16: Protein SEC13 homolog

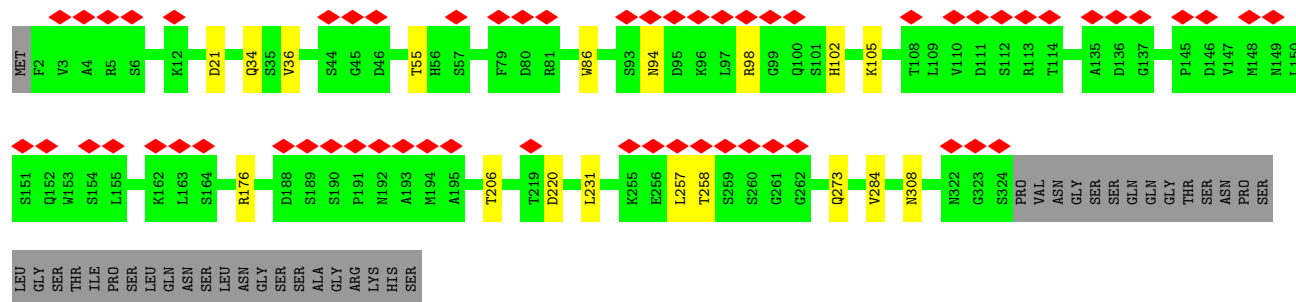
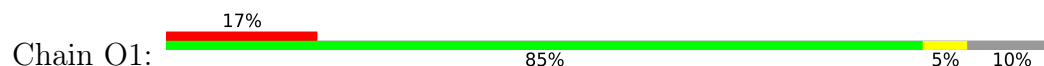


- Molecule 17: Nucleoporin SEH1

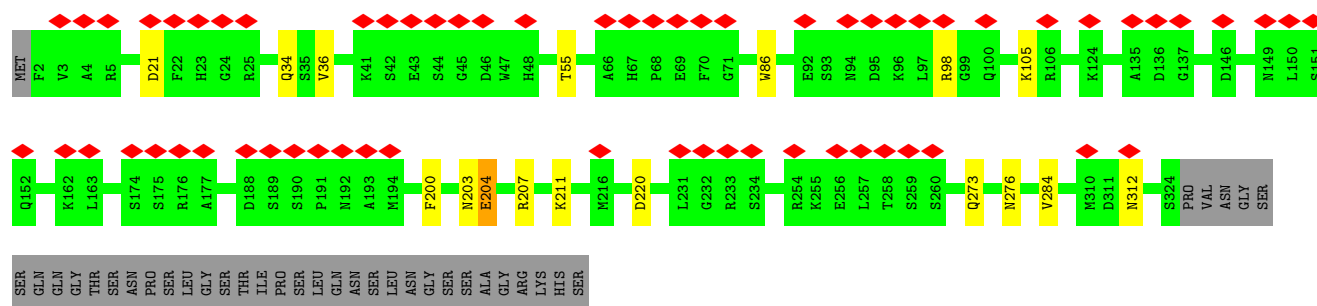
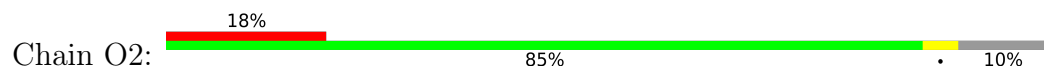




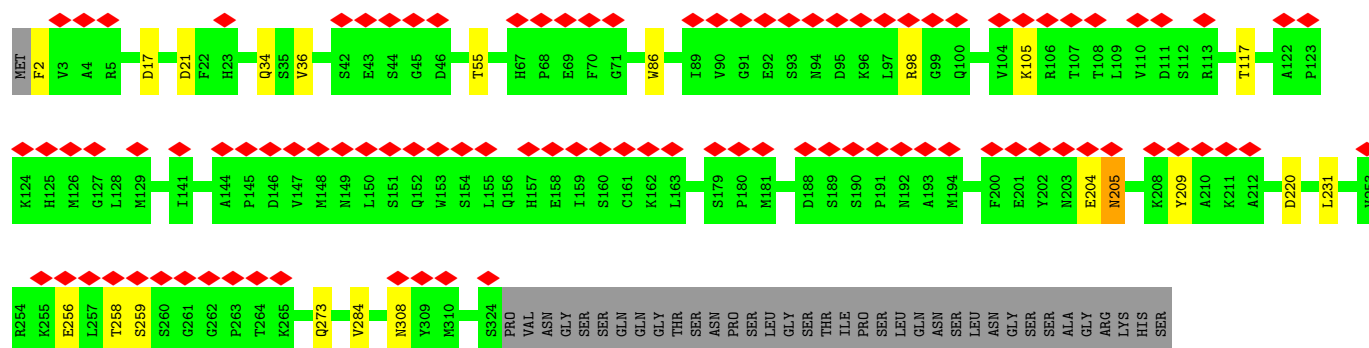
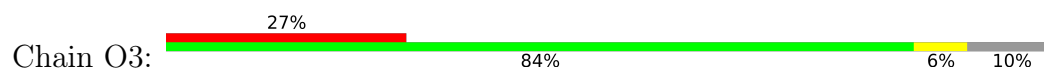
• Molecule 17: Nucleoporin SEH1



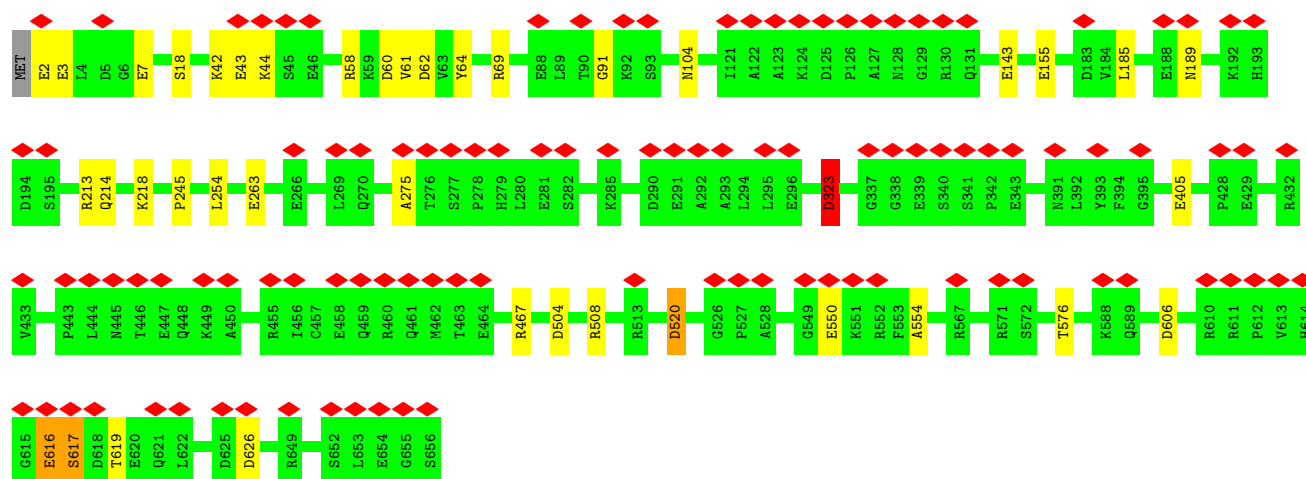
• Molecule 17: Nucleoporin SEH1



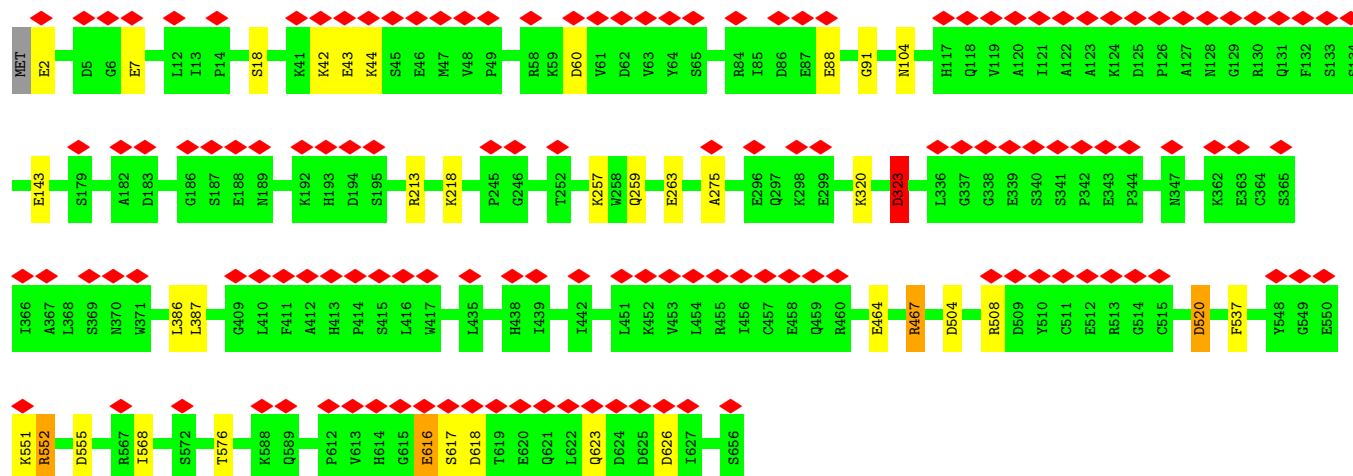
• Molecule 17: Nucleoporin SEH1



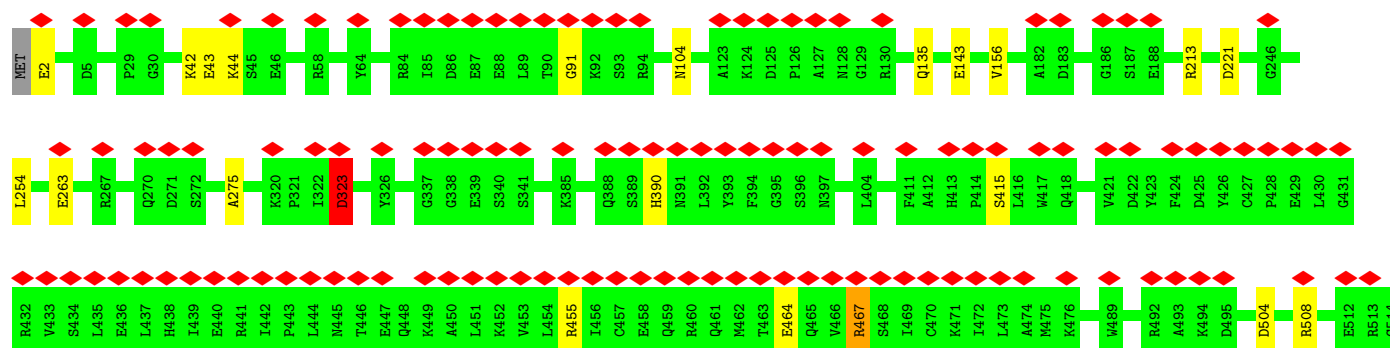
• Molecule 18: Nuclear pore complex protein Nup85

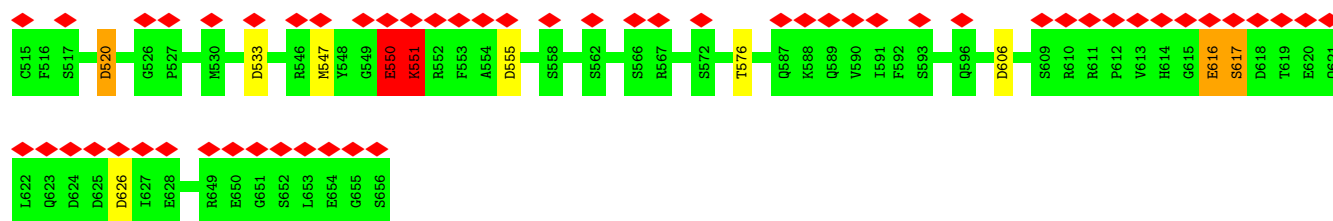


• Molecule 18: Nuclear pore complex protein Nup85

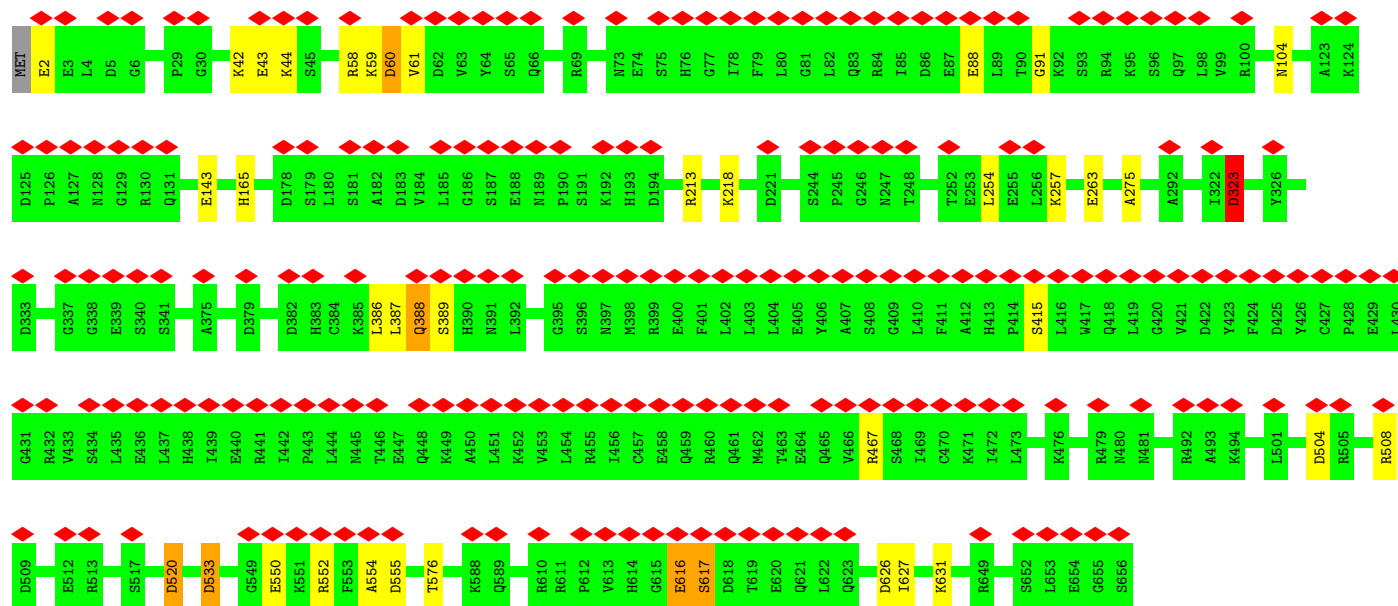


• Molecule 18: Nuclear pore complex protein Nup85

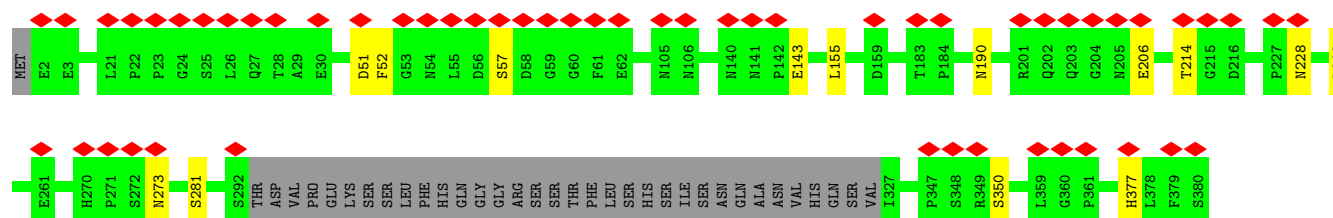
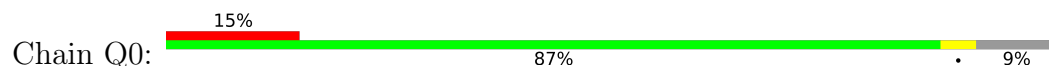




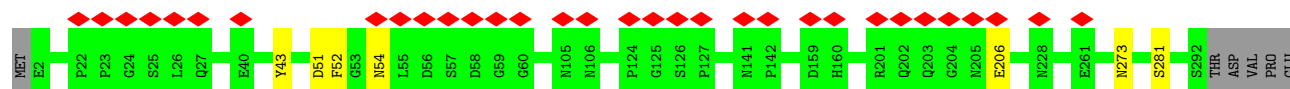
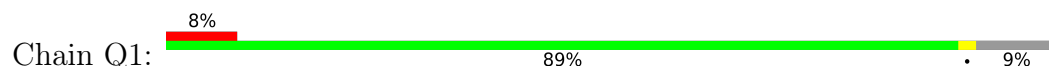
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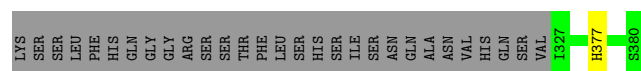


• Molecule 19: Nucleoporin Nup43

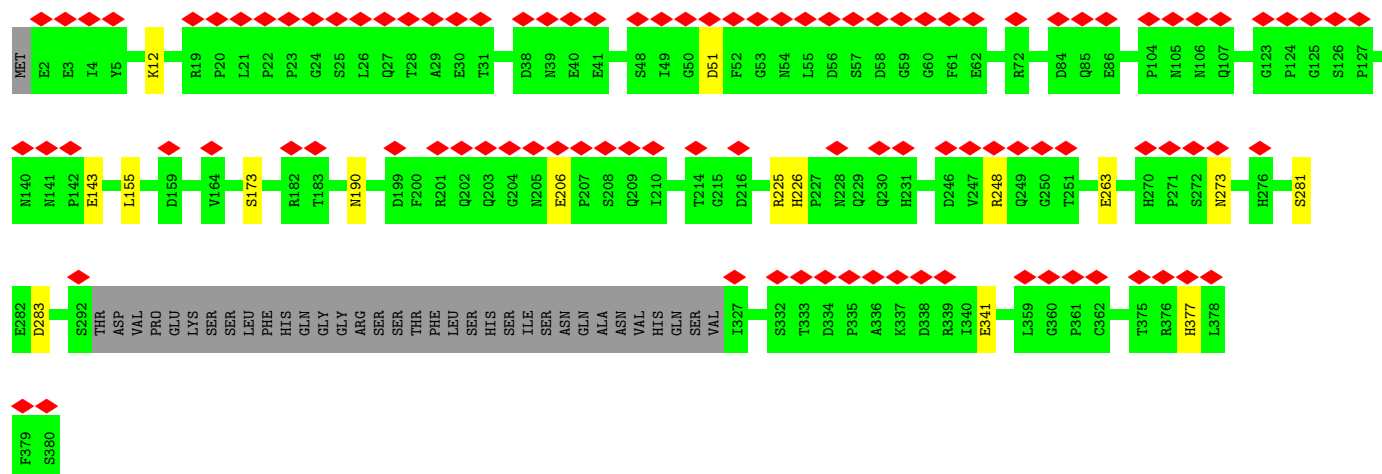
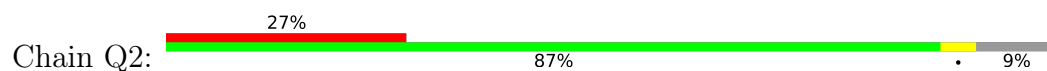


• Molecule 19: Nucleoporin Nup43

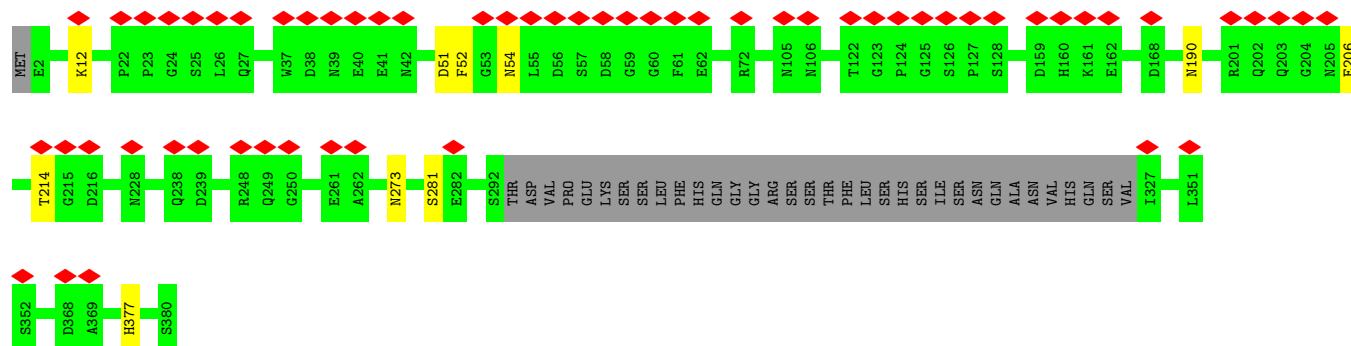
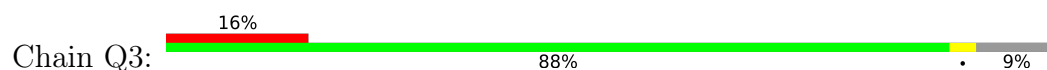




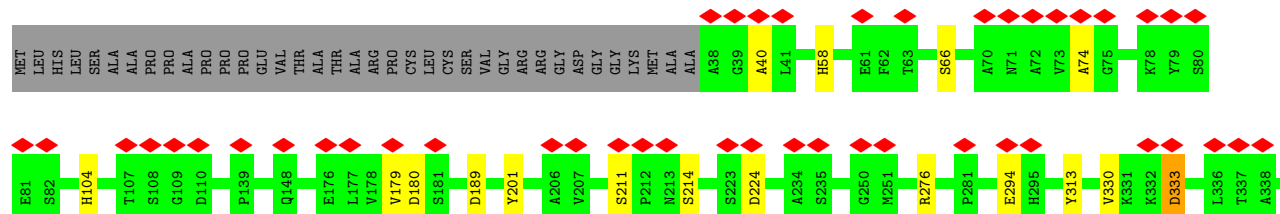
• Molecule 19: Nucleoporin Nup43

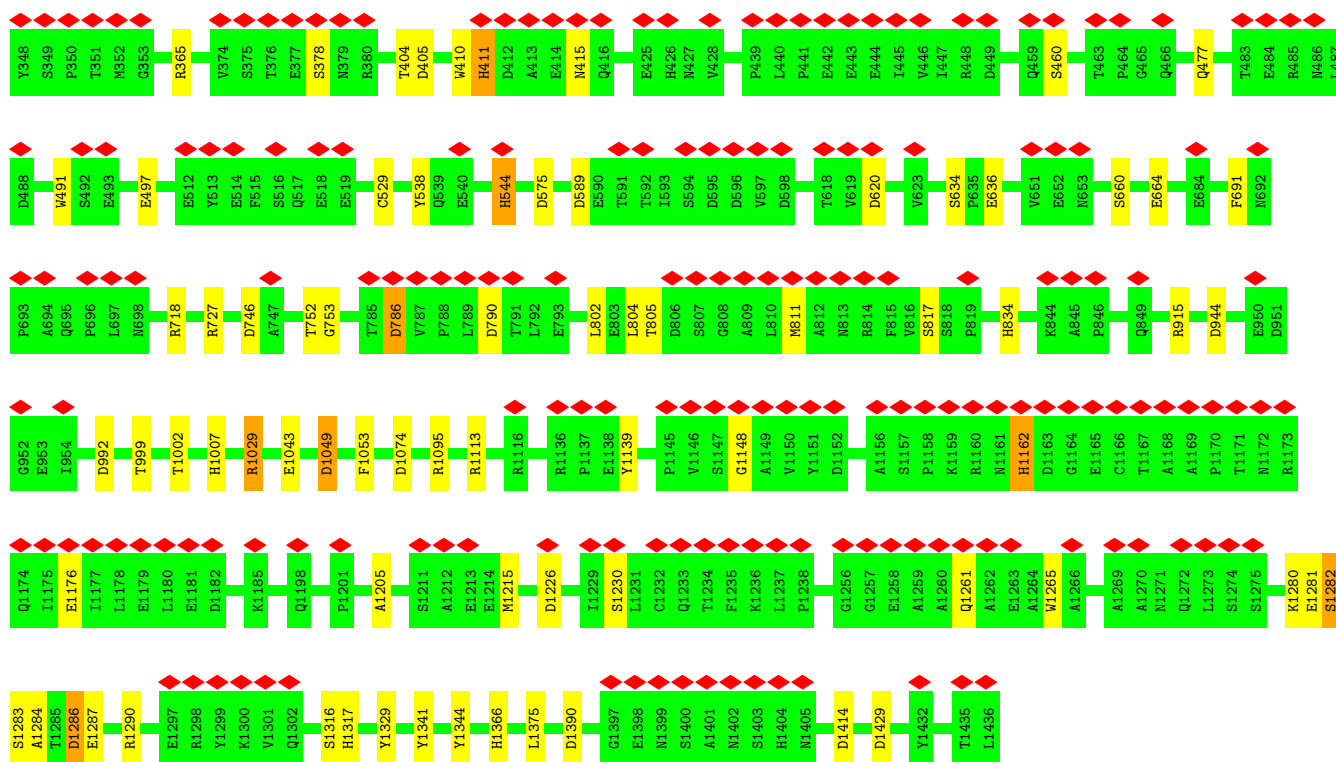


• Molecule 19: Nucleoporin Nup43

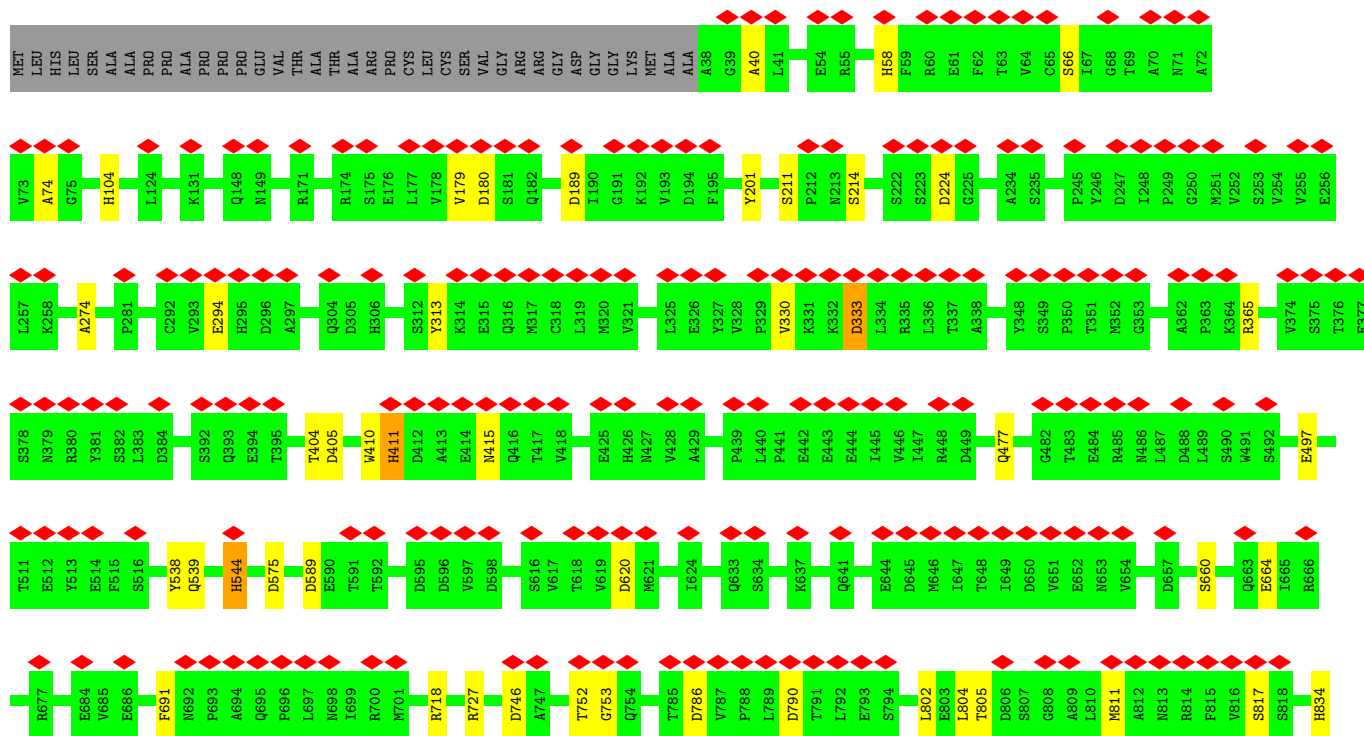


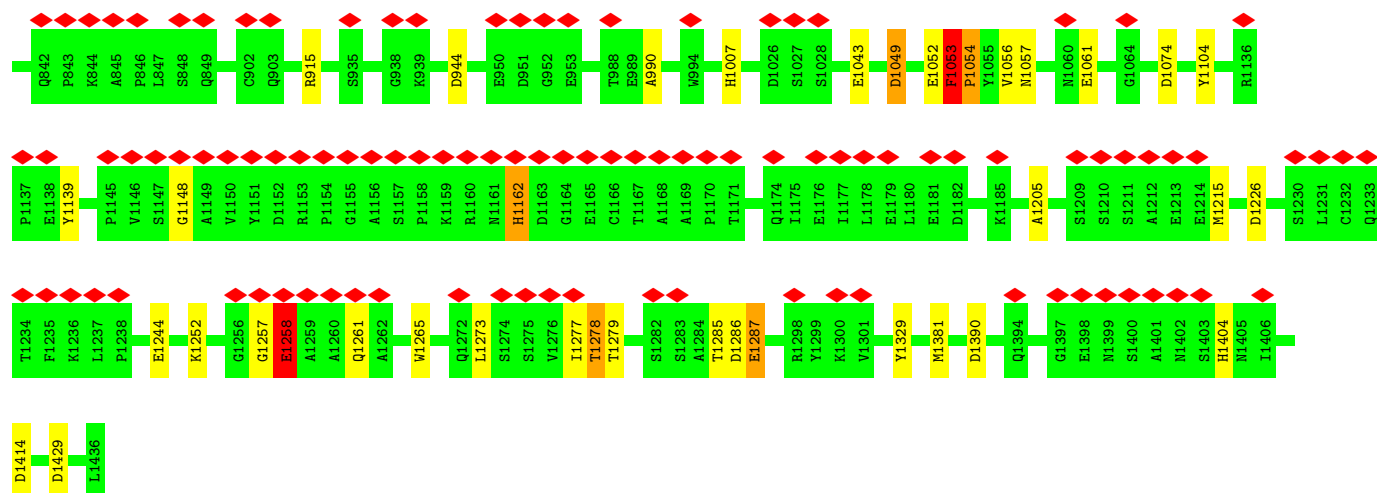
• Molecule 20: Nuclear pore complex protein Nup160



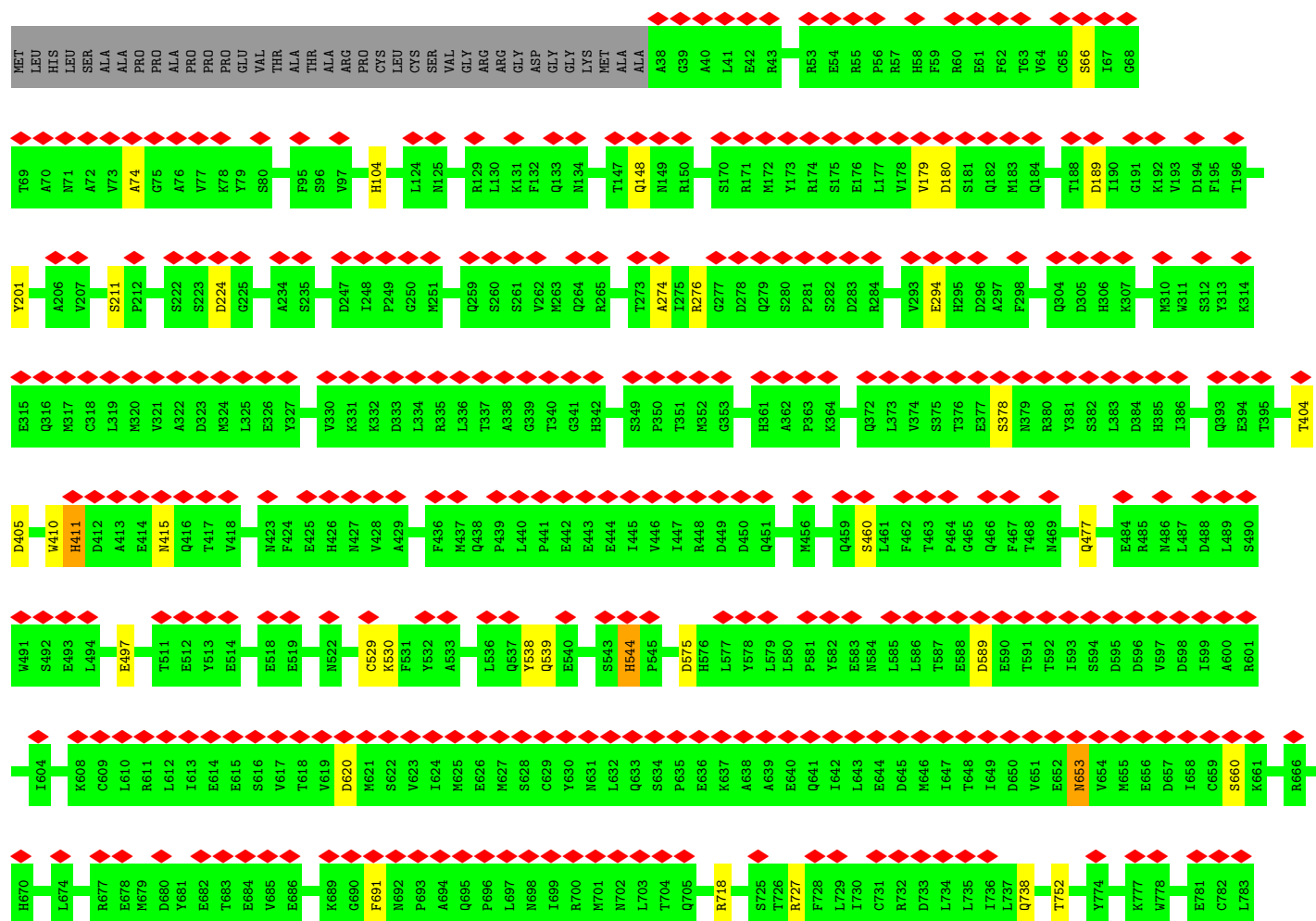


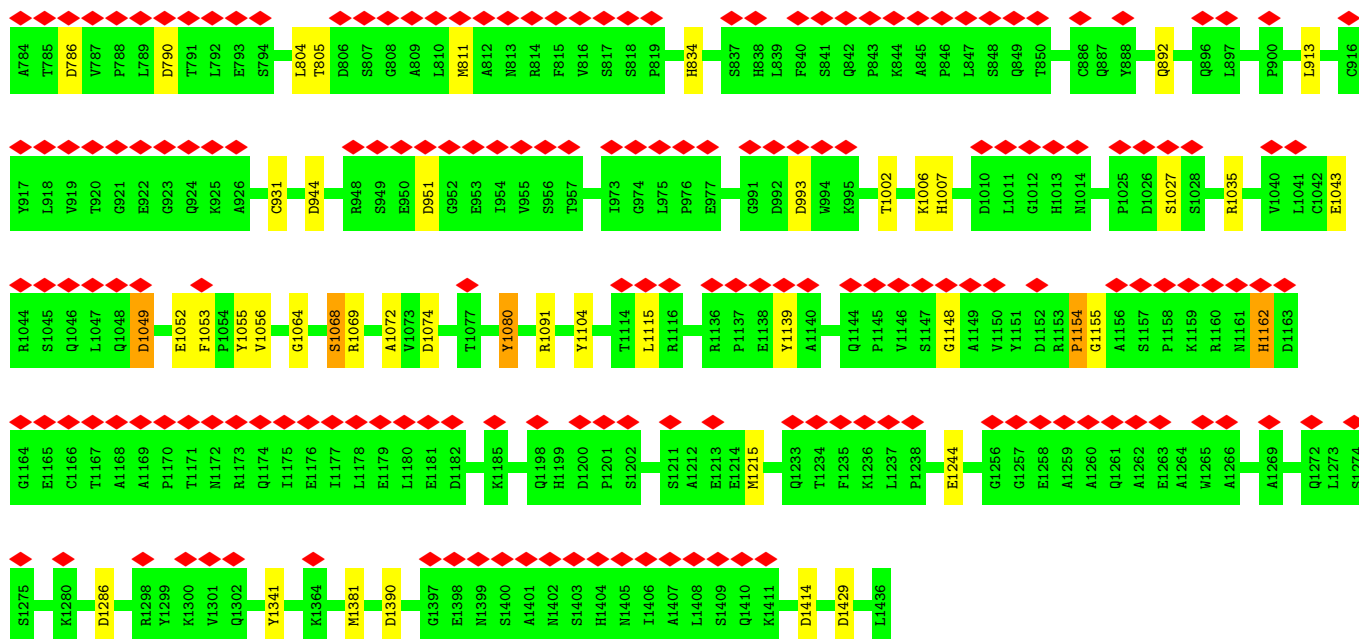
• Molecule 20: Nuclear pore complex protein Nup160



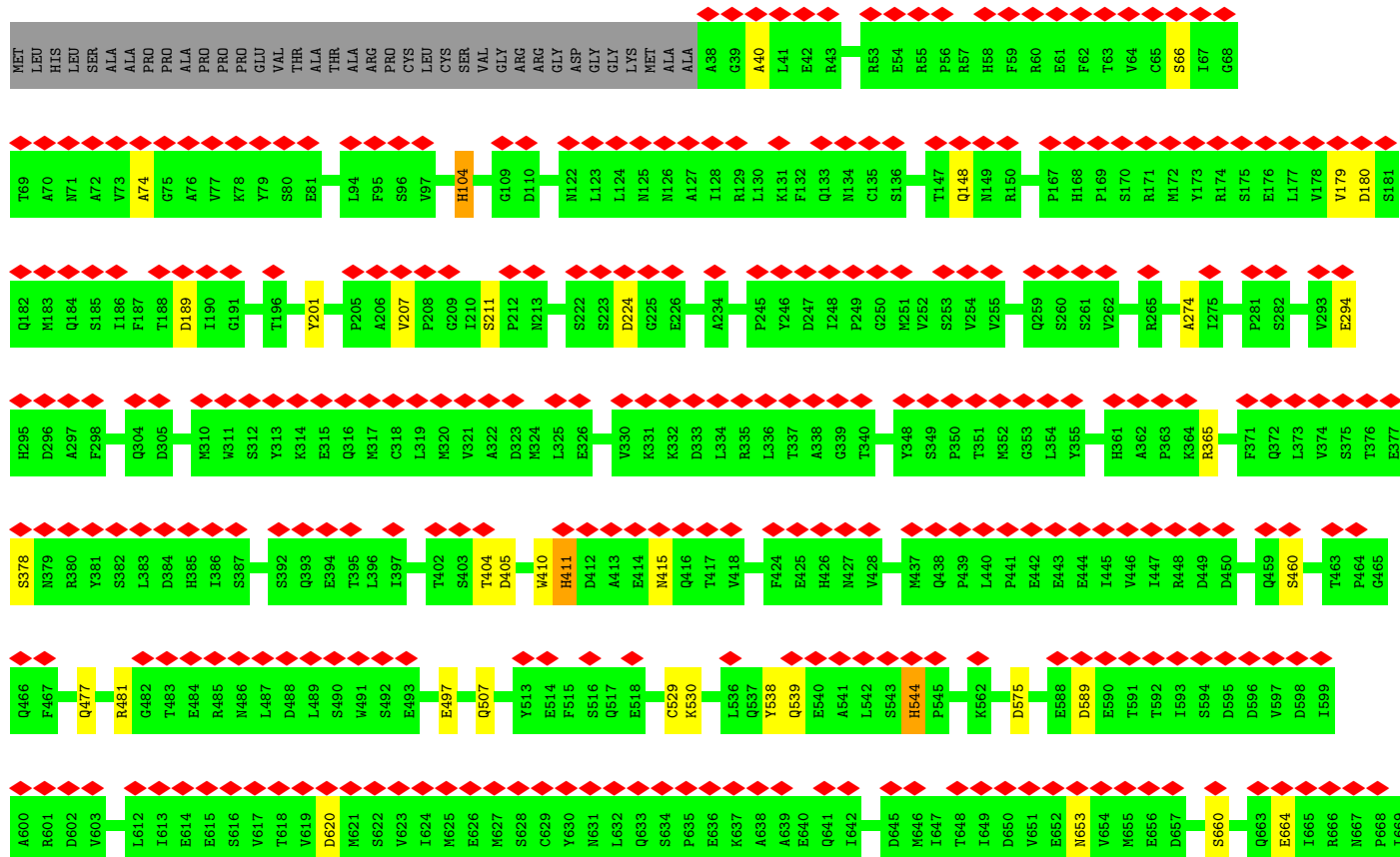
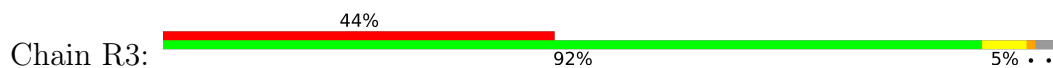


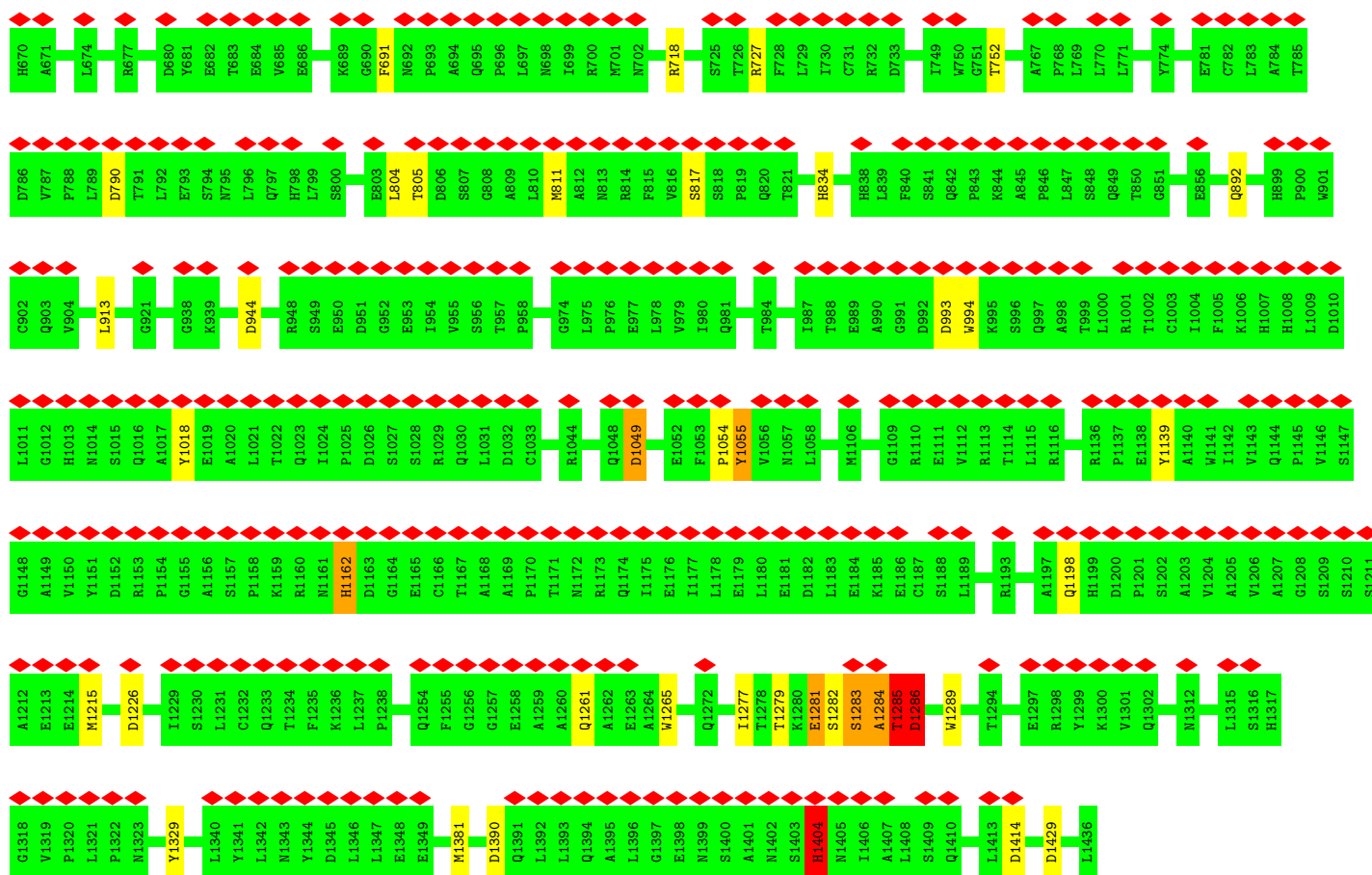
• Molecule 20: Nuclear pore complex protein Nup160





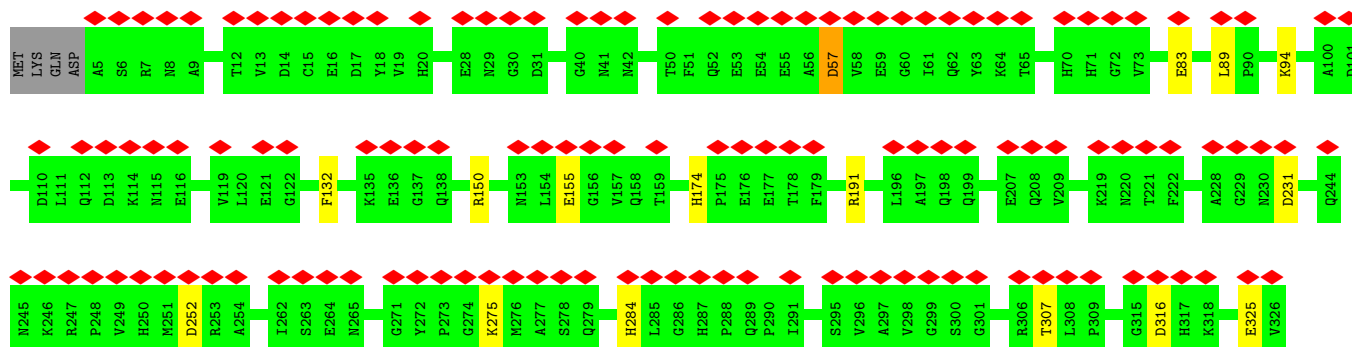
• Molecule 20: Nuclear pore complex protein Nup160





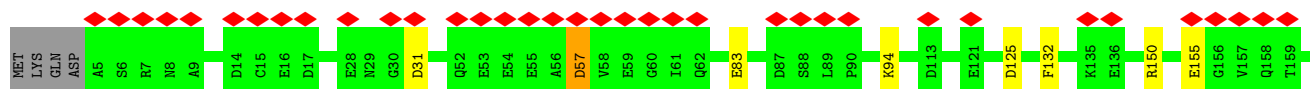
• Molecule 21: Nucleoporin Nup37

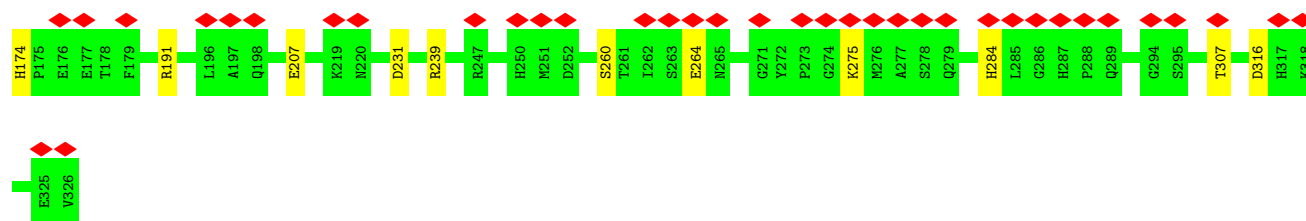
Chain S0: 40% 94% 5%



• Molecule 21: Nucleoporin Nup37

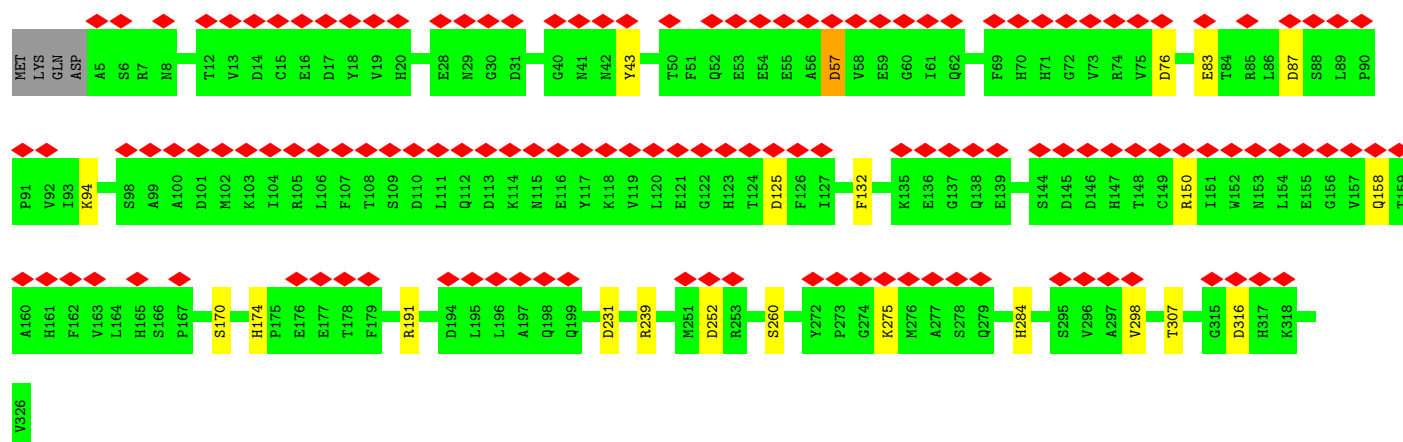
Chain S1: 22% 93% 6%





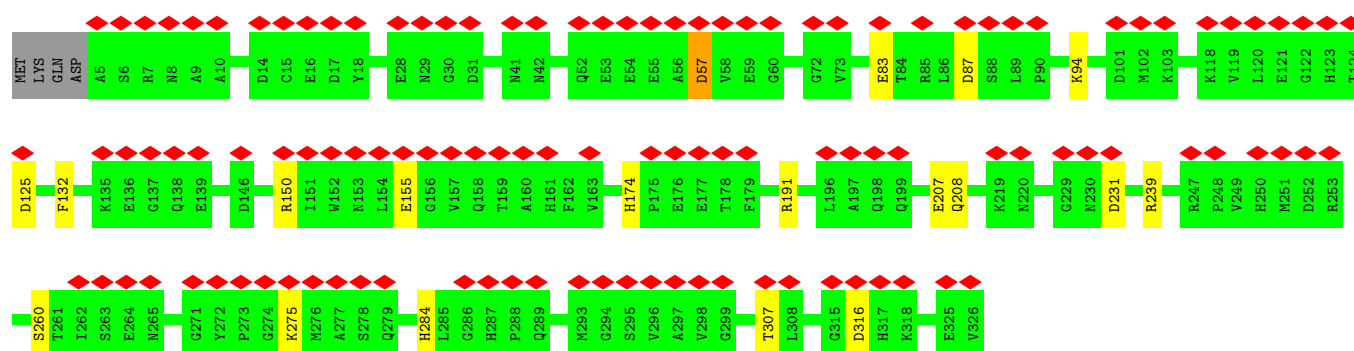
• Molecule 21: Nucleoporin Nup37

Chain S2: 41% 92% 6%



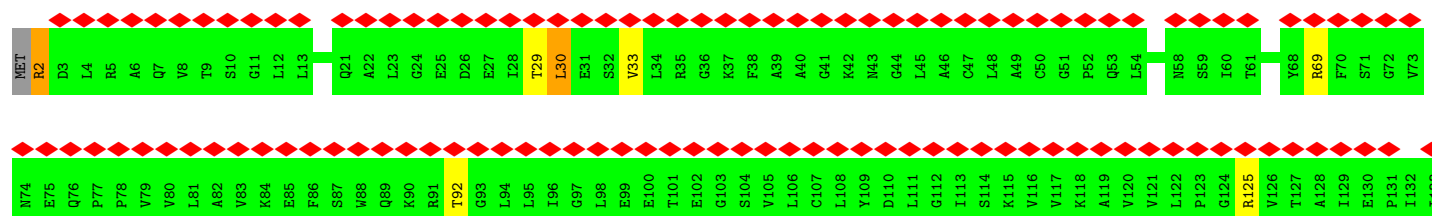
• Molecule 21: Nucleoporin Nup37

Chain S3: 36% 93% 6%



• Molecule 22: Protein ELYS

Chain T0: 25% 42% 56%





- Molecule 22: Protein ELYS

V79	V80	L81	A82	V83	K84	E85	F86	S87	W88	Q89	K90	R91	T92	G93	L94	L95	I96	G97	L98	E99	E100	T101	E102	G103	S104	V105	L106	C107	L108	V109	D110	L111	G112	I113	S114	K115	V116	V117	K118	A119	V120	V121	L122	P123	G124	R125	V126	A128	I129	E130	P131	I132	I133	M134	H135	G136	A138
ME1	R2	D3	L4	R5	A6	Q7	V8	T9	S10	G11	L12	L13	P14	E17	L20	Q21	A22	L23	G24	E25	D26	E27	T28	T29	L30	E31	S32	V33	L34	R35	A39	A40	G41	K42	N43	G44	L45	A49	C50	G51	P52	P53	Q53	L54	V68	R69	F70	S71	G72	V73	N74	E75	Q76	P77	P78		



- Molecule 23: Nuclear pore complex protein Nup98



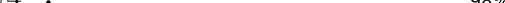
- [illegible]





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ARG	LEU	LEU	ALA	THR	ASN	ASN	ASN	GLU	ILE	PRO	L602		LYS
ALA	ASP	ASN	ASN	THR	ASN	ASN	ASN	ASN	ALA	ALA	L603		ALA
ILE	ILE	LEU	LEU	THR	SER	SER	PRO	SER	LYS	PRO	L604		THR
ASN	ASN	ASN	ASN	THR	THR	ILE	ILE	ILE	ILE	THR	L605		THR
TYR	TYR	LEU	LEU	ASP	HIS	HIS	PRO	HIS	THR	PRO	N606		HIS
GLU	GLU	ASP	ASP	ASP	MET	MET	GLN	GLN	GLN	GLN	N607		THR
GLY	GLY	ASP	ASP	ASP	HIS	HIS	THR	THR	THR	THR	N608		TYR
ARG	ARG	ILE	ILE	ILE	PRO	PRO	PRO	ALA	ALA	GLU	N609		LYS
LEU	LEU	VAL	VAL	VAL	ALA	GLY	SER	GLY	SER	SER	L610		LEU
GLU	GLU	ALA	ALA	ILE	ILE	ILE	ALA	GLY	GLY	GLY	F611		THR
VAL	VAL	ARG	ARG	ARG	ILE	ILE	ILE	ALA	VAL	VAL	S612		ARG
SER	SER	ARG	ARG	ARG	THR	THR	LYS	LYS	LYS	LYS	F613		ALA
ARG	ARG	LYS	LYS	LYS	THR	LYS	LYS	HIS	SER	SER	V614		THR
LYS	GLN	GLY	VAL	VAL	VAL	VAL	VAL	GLY	GLY	ASN	N615		ARG
GLN	ALA	VAL	VAL	VAL	TYR	TYR	TYR	TYR	SER	SER	ASP	ASP	
PHE	PHE	LEU	LEU	LEU	THR	THR	THR	THR	SER	SER	GLU	GLY	
LYS	LYS	ASP	ASP	ASP	ILE	ILE	ILE	ILE	VAL	VAL	ASN	LYS	
GLU	GLU	ASP	ASP	ASP	PRO	PRO	PRO	PRO	LEU	LEU	ASN	GLN	
GLY	GLY	VAL	VAL	VAL	ASN	ASN	ASN	ASN	ALA	ALA	GLY	PHE	
SER	SER	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LEU	LEU	ARG	ASP	
SER	SER	ALA	ALA	ALA	GLU	GLU	GLU	GLU	ASN	ASN	PHE	GLY	
PHE	PHE	GLU	GLU	GLU	CYS	CYS	ILE	ILE	GLY	GLY	PHE	ASP	
		VAL	THR	THR	VAL	VAL	VAL	VAL	LEU	LEU	LEU	ASP	
		LEU	LEU	LEU	SER	SER	SER	SER	GLY	GLY	LYS	ASP	
		GLY	GLY	GLY	PHE	PHE	SER	SER	VAL	VAL	PRO	SER	
		VAL	VAL	VAL	THR	THR	THR	THR	GLU	GLU	ASP	LEU	
		TRP	TRP	TRP	ILE	ILE	ILE	ILE	GLU	GLU	ASP	ALA	
		PRO	PRO	PRO	GLY	GLY	GLY	GLY	THR	THR	ASN	ASN	
		THR	THR	THR	THR	THR	THR	THR	ARG	ARG	HIS	ALA	
		ASP	ASP	ASP	LYS	LYS	LYS	LYS	PHE	PHE	GLN	PHE	
		THR	THR	THR	THR	THR	THR	THR	ASP	ASP	GLN	MET	
		SER	SER	SER	GLY	GLY	GLY	GLY	GLU	GLU	LYS	PRO	
		ARG	ARG	ARG	TYR	TYR	TYR	TYR	SER	SER	LYS	LYS	
		CYS	CYS	CYS	ILE	ILE	ILE	ILE	GLY	GLY	ASP	THR	
		LEU	LEU	LEU	THR	THR	THR	THR	LEU	LEU	GLU	THR	
		ILE	ILE	ILE	PHE	PHE	PHE	PHE	ASP	ASP	SER	SER	
		LYS	LYS	LYS	GLY	GLY	GLY	GLY	ASP	ASP	LYS	LYS	
		SER	SER	SER	THR	THR	THR	THR	GLU	GLU	THR	THR	
		THR	THR	THR	THR	THR	THR	THR	GLY	GLY	ASP	ASP	
		VAL	VAL	VAL	THR	THR	THR	THR	GLY	GLY	SER	SER	
		ASP	ASP	ASP	THR	THR	THR	THR	GLY	GLY	VAL	VAL	
		THR	THR	THR	THR	THR	THR	THR	GLY	GLY	SER	SER	
		ILE	ILE	ILE	THR	THR	THR	THR	ASP	ASP	HIS	HIS	
		LYS	LYS	LYS	GLY	GLY	GLY	GLY	ASP	ASP	PHE	PHE	
		SER	SER	SER	THR	THR	THR	THR	GLU	GLU	TYR	TYR	
		PRO	PRO	PRO	ASP	ASP	ASP	ASP	GLU	GLU	THR	THR	

- Molecule 23: Nuclear pore complex protein Nup98

Chain U4:  98%

[illegible]

- Molecule 23: Nuclear pore complex protein Nup98

Chain U6: 98%

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

GLY	THR	SER	THR	SER	SER	GLY	LEU	PHE	GLY	THR	THR	ASN	THR	SER	ASN	PRO	PHE	GLY	SER	SER	THR	SER	GLY	SER	SER	PHE	LEU	GLY	PRO	SER	SER	PHE	THR	ALA	ALA	PRO	THR	GLY	THR	THR	THR	LEU	LYS	PHE	ASN	PRO	PRO	THR	THR	GLY	VAL	LYS	ALA	GLY	VAL	SER	THR
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ASN	ILE	SER	THR	LYS	HIS	GLN	CYS	ILE	THR	ALA	MET	LYS	GLU	TYR	GLU	SER	LYS	SER	LEU	GLU	GLU	LEU	ARG	LEU	GLU	TYR	GLN	ALA	ASN	ARG	LYS	GLY	PRO	GLN	ASN	ASN	VAL	GLN	GLY	ALA	GLY	THR	THR	GLY	LEU	PHE	GLY	SER	SER	PRO	ALA	ALA	THR	SER	GLY	LEU
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PHE	SER	SER	SER	THR	THR	ASN	ASN	GLY	GLY	ALA	TYR	GLY	GLN	ASN	LYS	THR	ALA	PHE	GLY	THR	SER	SER	THR	THR	THR	GLY	GLY	PHE	GLY	GLY	THR	THR	ASN	PRO	GLY	GLY	LEU	PHE	PHE	GLY	GLN	GLN	ASN	GLN	GLN	THR	THR	THR	THR	GLN	GLN	GLN	GLN	GLY	PHE
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SER	PHE	GLY	GLY	ASN	THR	THR	SER	THR	THR	ILE	GLY	GLN	PRO	SER	SER	THR	THR	MET	GLY	LEU	PHE	GLY	VAL	THR	THR	GLN	ALA	ALA	SER	GLN	PRO	GLY	GLY	GLY	LEU	PHE	GLY	ALA	ALA	THR	THR	ASN	THR	THR	SER	SER	THR	THR	GLY	GLY	THR	THR	ALA	ALA	PHE	GLY	THR	GLY	GLY	THR	GLY	THR	LEU	PHE	GLY	GLY	GLN	GLN	THR	THR	ASN	THR	THR	GLY	GLY	ALA	ALA	VAL
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GLY	SER	THR	LEU	PHE	GLY	ASN	ASN	LYS	LEU	THR	THR	PHE	GLY	SER	SER	THR	THR	SER	ALA	PRO	SER	SER	PHE	GLY	THR	THR	SER	SER	GLY	LEU	PHE	GLY	ASN	LYS	PRO	THR	THR	LEU	THR	THR	GLY	LEU	THR	THR	ASN	THR	THR	ASN	THR	SER	PHE	GLY	GLY	THR	THR	ASN	THR	THR	GLY	GLY	ILE	SER	PHE
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GLY	SER	LYS	PRO	ALA	PRO	GLY	THR	LEU	LEU	GLY	THR	GLY	LEU	LEU	GLY	ALA	ALA	ALA	LEU	GLY	GLY	GLY	GLN	GLN	SER	SER	PHE	PHE	GLY	ASN	ASN	GLN	PRO	PRO	LYS	ILE	GLY	GLY	GLY	PRO	PRO	LEU	LEU	GLY	THR	THR	GLY	ALA	ALA	ALA	THR	ALA	THR	LEU	LEU	GLY	PHE	PHE	GLY
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ALA	PRO	GLN	PRO	ALA	VAL	ALA	LEU	THR	ASP	PRO	ASN	ALA	ALA	SER	ALA	ALA	GLN	GLN	ALA	LEU	GLN	HIS	ILE	ASN	SER	SER	THR	TYR	PRO	PRO	PHE	ASP	SER	PRO	PHE	ARG	ASN	PRO	MET	SER	ASP	PRO	LYS	LYS	LYS	GLU	LEU	ARG	LEU	LYS	PRO	THR	ASN	PRO	ALA
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G	L	I	L	L	A	A	A	L	L	T	T	F	F	F	F	F	L	L	L	L	L	S	
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V601	L602	K603	M604	L605	M606	M607	S608	M609	L610	F611	S612	P613	M614	M615	ARG	ASP	SER	GLU	ASN	LEU	ALA	SER	PRO	SER	GLY	GLY	ARG	PHE	SER	PHE	LEU	SER	LYS	PRO	VAL	ASP	GLU	ASN	ASN	HIS	GLN	GLN	ASP	GLY	ASP	GLU	ASP	SER	SER	LEU	VAL	SER	HIS	PHE	HIS	TYR
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ASN	PRO	ILE	ALA	LYS	PRO	ILE	PRO	GLN	THR	PRO	GLU	SER	ALA	GLY	ASN	LYS	HIS	SER	ASN	SER	SER	SER	VAL	ASP	ASP	THR	THR	ILE	ILE	ALA	LEU	ASN	MET	ARG	ALA	ALA	LEU	ARG	ASN	GLY	GLY	LEU	GLU	GLY	SER	SER	PHE	HIS	ASP	GLU	GLY	SER	LEU	GLN	ASP	ASP	ARG	GLU
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GLU	ILE	GLU	ASN	ASN	SER	TYR	HIS	MET	HIS	PRO	ALA	GLY	ILE	ILE	LEU	THR	LYS	VAL	GLY	TYR	TYR	THR	THR	ILE	PRO	SER	MET	ASP	ASP	LEU	ALA	LYS	ILE	THR	THR	ASN	GLU	LYS	GLY	GLU	CYS	CYS	ILE	VAL	SER	ASP	PHE	THR	THR	THR	ILE	GLY	ARG	LYS	LYS	TYR	TYR	PHE	GLU	GLY	GLY
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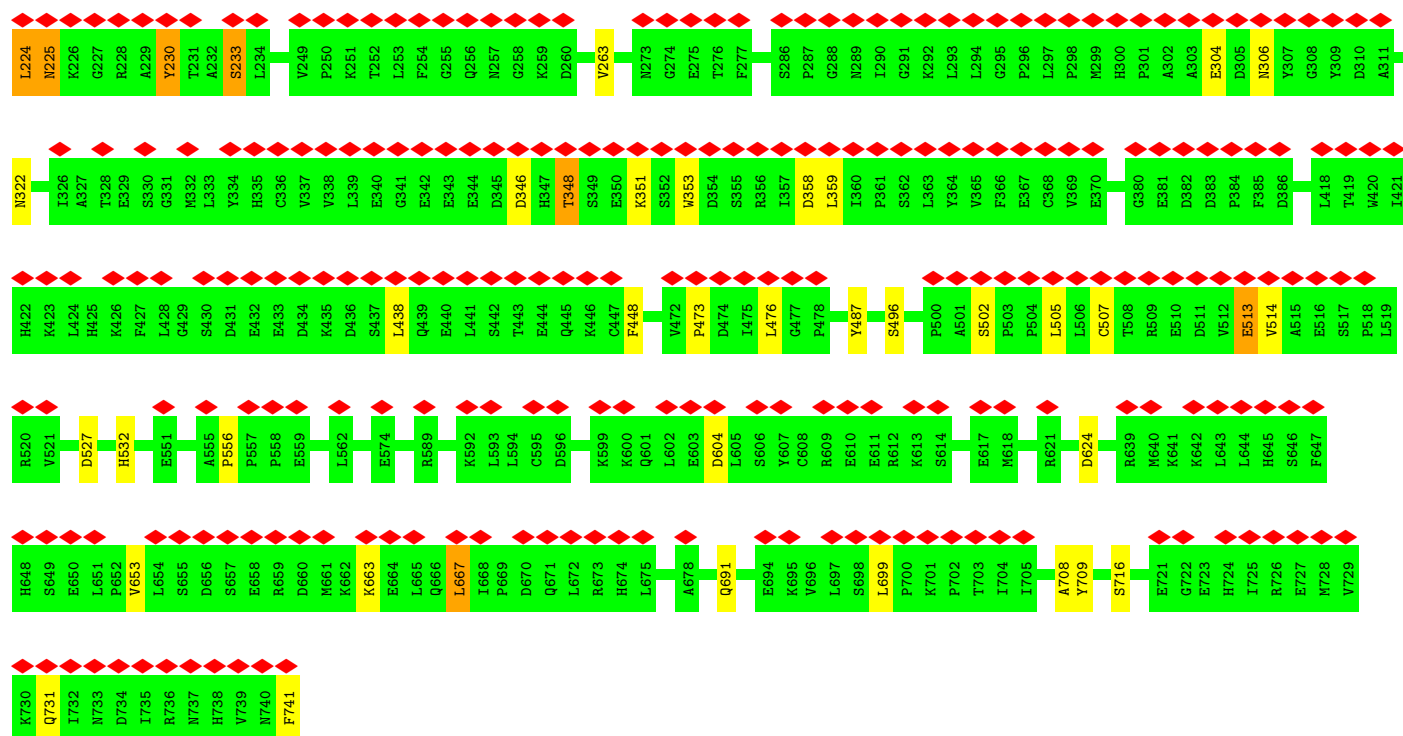
VAL	ASN	LEU	THR	ASN	LEU	ASN	LEU	ASP	ASP	ILE	VAL	HIS	ILE	ARG	ARG	LYS	GLU	VAL	VAL	VAL	TYR	LEU	ASP	ASP	ASN	ASN	GLN	LYS	PRO	PRO	VAL	GLY	GLU	GLY	LEU	ASN	ARG	LYS	ALA	ALA	GLU	VAL	THR	LEU	ASP	GLY	TRP	PRO	THR	THR	ASP	LYS	THR	SER	ARG	CYS	LEU	ILE	LYS	SER	PRO
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ASP	ARG	LEU	ALA	ASP	ILE	ASN	TYR	GLU	GLY	ARG	LEU	GLU	ALA	VAL	SER	ARG	LYS	GLN	GLY	ALA	GLN	PHE	LYS	GLU	TYR	ARG	PRO	GLU	THR	GLY	SER	TRP	VAL	PHE	LYS	VAL	SER	HIS	PHE
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- Molecule 24: Nuclear pore complex protein Nup214

Chain V0:  8% 12% 87%

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	7711	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	120	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	82.185	Depositor
Minimum map value	-69.686	Depositor
Average map value	0.077	Depositor
Map value standard deviation	0.791	Depositor
Recommended contour level	3.5	Depositor
Map size ($\text{\AA}$)	1941.1199, 1941.1199, 1941.1199	wwPDB
Map dimensions	576, 576, 576	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	3.37, 3.37, 3.37	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	00	0.84	0/6212	1.44	24/8405 (0.3%)
1	01	0.83	0/6212	1.41	20/8405 (0.2%)
1	02	0.83	0/6212	1.41	17/8405 (0.2%)
1	03	0.84	0/6212	1.41	21/8405 (0.2%)
1	04	0.83	0/6212	1.41	18/8405 (0.2%)
2	10	0.81	0/14350	1.36	30/19560 (0.2%)
2	11	0.81	0/14350	1.37	25/19560 (0.1%)
2	12	0.81	0/14350	1.36	27/19560 (0.1%)
2	13	0.81	0/14350	1.36	26/19560 (0.1%)
2	14	0.81	0/14350	1.36	30/19560 (0.2%)
2	15	0.81	0/14350	1.36	30/19560 (0.2%)
2	16	0.81	0/14350	1.36	27/19560 (0.1%)
2	17	0.81	0/14350	1.36	22/19560 (0.1%)
3	40	0.86	1/3007 (0.0%)	1.33	7/4114 (0.2%)
3	41	0.86	1/3007 (0.0%)	1.33	6/4114 (0.1%)
4	A0	0.85	0/6687	1.42	21/9036 (0.2%)
4	A1	0.84	0/6687	1.41	25/9036 (0.3%)
4	A2	0.85	0/6687	1.41	22/9036 (0.2%)
4	A3	0.83	0/6687	1.39	25/9036 (0.3%)
4	A4	0.83	0/5972	1.39	17/8068 (0.2%)
4	A5	0.82	0/5972	1.41	12/8068 (0.1%)
4	A6	0.83	1/5972 (0.0%)	1.37	13/8068 (0.2%)
5	B0	0.85	1/14018 (0.0%)	1.40	46/19022 (0.2%)
5	B1	0.85	1/14018 (0.0%)	1.40	44/19022 (0.2%)
6	C0	0.85	0/16330	1.40	44/22131 (0.2%)
6	C1	0.85	1/16330 (0.0%)	1.40	38/22131 (0.2%)
6	C2	0.84	0/16330	1.38	41/22131 (0.2%)
6	C3	0.84	1/16330 (0.0%)	1.42	57/22131 (0.3%)
6	C4	0.84	0/16330	1.38	30/22131 (0.1%)
7	D0	0.82	0/10568	1.40	23/14320 (0.2%)
7	D1	0.83	2/10568 (0.0%)	1.40	28/14320 (0.2%)
7	D2	0.82	0/10568	1.39	25/14320 (0.2%)
7	D3	0.83	0/10568	1.42	33/14320 (0.2%)
7	D4	0.81	0/10568	1.38	23/14320 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	D5	0.82	0/10568	1.41	39/14320 (0.3%)
8	E0	0.84	0/4563	1.34	6/6214 (0.1%)
8	E1	0.84	0/4563	1.33	4/6214 (0.1%)
9	F0	0.91	0/1882	1.49	9/2556 (0.4%)
9	F1	0.88	0/1882	1.44	6/2556 (0.2%)
9	F2	0.91	0/1882	1.50	7/2556 (0.3%)
9	F3	0.89	1/1882 (0.1%)	1.45	8/2556 (0.3%)
10	H0	0.82	1/3114 (0.0%)	1.40	12/4211 (0.3%)
10	H1	0.81	0/3114	1.40	13/4211 (0.3%)
10	H2	0.81	0/3114	1.40	13/4211 (0.3%)
10	H3	0.81	0/3114	1.41	15/4211 (0.4%)
11	I0	0.81	0/1416	1.42	3/1911 (0.2%)
11	I1	0.81	0/1416	1.42	6/1911 (0.3%)
11	I2	0.81	0/1416	1.42	3/1911 (0.2%)
11	I3	0.81	0/1416	1.41	4/1911 (0.2%)
12	J0	0.80	0/1420	1.40	4/1915 (0.2%)
12	J1	0.80	0/1420	1.39	5/1915 (0.3%)
12	J2	0.80	0/1420	1.37	2/1915 (0.1%)
12	J3	0.80	0/1420	1.39	3/1915 (0.2%)
12	J4	0.80	0/1420	1.44	2/1915 (0.1%)
13	K0	0.84	0/8740	1.40	32/11848 (0.3%)
13	K1	0.83	1/8740 (0.0%)	1.43	23/11848 (0.2%)
13	K2	0.83	0/8740	1.37	19/11848 (0.2%)
13	K3	0.83	1/8740 (0.0%)	1.37	16/11848 (0.1%)
14	L0	0.85	0/6518	1.39	16/8819 (0.2%)
14	L1	0.85	0/6518	1.41	21/8819 (0.2%)
14	L2	0.84	0/6518	1.39	15/8819 (0.2%)
14	L3	0.88	3/6518 (0.0%)	1.44	33/8819 (0.4%)
15	M0	0.87	0/5588	1.43	18/7581 (0.2%)
15	M1	0.87	0/5588	1.42	12/7581 (0.2%)
15	M2	0.87	0/5588	1.41	9/7581 (0.1%)
15	M3	0.86	0/5588	1.41	21/7581 (0.3%)
16	N0	0.84	0/2419	1.35	3/3301 (0.1%)
16	N1	0.84	0/2419	1.33	3/3301 (0.1%)
16	N2	0.85	0/2419	1.35	5/3301 (0.2%)
16	N3	0.83	0/2419	1.33	3/3301 (0.1%)
17	O0	0.83	0/2593	1.32	4/3520 (0.1%)
17	O1	0.83	0/2593	1.32	6/3520 (0.2%)
17	O2	0.84	0/2593	1.34	5/3520 (0.1%)
17	O3	0.83	0/2593	1.33	3/3520 (0.1%)
18	P0	0.85	0/5365	1.39	17/7257 (0.2%)
18	P1	0.85	0/5365	1.39	10/7257 (0.1%)
18	P2	0.85	0/5365	1.39	12/7257 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
18	P3	0.85	0/5365	1.39	15/7257 (0.2%)
19	Q0	0.86	0/2775	1.36	4/3786 (0.1%)
19	Q1	0.85	0/2775	1.35	3/3786 (0.1%)
19	Q2	0.86	0/2775	1.39	6/3786 (0.2%)
19	Q3	0.85	0/2775	1.36	4/3786 (0.1%)
20	R0	0.85	0/11371	1.38	29/15446 (0.2%)
20	R1	0.85	1/11371 (0.0%)	1.39	36/15446 (0.2%)
20	R2	0.85	0/11371	1.38	28/15446 (0.2%)
20	R3	0.84	0/11371	1.38	34/15446 (0.2%)
21	S0	0.83	0/2623	1.32	3/3568 (0.1%)
21	S1	0.82	0/2623	1.31	5/3568 (0.1%)
21	S2	0.83	0/2623	1.33	7/3568 (0.2%)
21	S3	0.83	0/2623	1.32	7/3568 (0.2%)
22	T0	0.84	0/8141	1.38	20/11065 (0.2%)
22	T1	0.83	0/8141	1.36	19/11065 (0.2%)
23	U0	0.85	0/1217	1.34	2/1644 (0.1%)
23	U1	0.87	0/152	1.91	6/204 (2.9%)
23	U2	1.05	0/152	2.09	7/204 (3.4%)
23	U3	1.20	1/152 (0.7%)	2.02	6/204 (2.9%)
23	U4	1.21	2/152 (1.3%)	2.09	10/204 (4.9%)
23	U5	1.07	1/152 (0.7%)	1.82	4/204 (2.0%)
23	U6	0.86	0/152	1.84	4/204 (2.0%)
24	V0	0.86	0/2240	1.47	7/3019 (0.2%)
25	W0	0.84	1/5972 (0.0%)	1.38	18/8105 (0.2%)
All	All	0.84	22/630097 (0.0%)	1.39	1651/855041 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	00	0	6
1	01	0	3
1	02	0	4
1	03	0	5
1	04	0	4
2	10	0	11
2	11	0	13
2	12	0	10
2	13	0	13
2	14	0	11

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	15	0	13
2	16	0	10
2	17	0	13
3	40	0	4
3	41	0	6
4	A0	1	23
4	A1	0	16
4	A2	0	17
4	A3	0	14
4	A4	0	9
4	A5	0	9
4	A6	0	6
5	B0	0	28
5	B1	0	26
6	C0	1	15
6	C1	1	16
6	C2	1	18
6	C3	1	23
6	C4	1	15
7	D0	0	7
7	D1	0	14
7	D2	0	12
7	D3	0	14
7	D4	0	7
7	D5	0	16
8	E0	0	2
8	E1	0	2
9	F0	0	6
9	F1	0	3
9	F2	0	3
9	F3	0	2
10	H0	0	6
10	H1	0	3
10	H2	0	3
10	H3	0	4
12	J0	0	2
12	J1	0	1
12	J2	0	2
12	J3	0	1
12	J4	0	1
13	K0	0	12
13	K1	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	K2	0	13
13	K3	0	10
14	L0	0	6
14	L1	0	6
14	L2	0	7
14	L3	0	5
15	M0	0	9
15	M1	0	9
15	M2	0	7
15	M3	0	6
16	N0	0	2
16	N1	0	2
16	N2	0	2
16	N3	0	2
17	O3	0	1
18	P0	0	7
18	P1	1	9
18	P2	0	8
18	P3	0	8
19	Q0	0	1
19	Q1	0	2
19	Q2	0	2
19	Q3	0	1
20	R0	0	14
20	R1	0	13
20	R2	0	17
20	R3	0	18
21	S0	0	4
21	S1	0	5
21	S2	0	6
21	S3	0	5
22	T0	2	11
22	T1	2	9
23	U0	0	1
24	V0	0	1
25	W0	0	10
All	All	11	728

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	L3	727	CYS	CA-C	9.14	1.64	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	U3	610	LEU	N-CA	-8.09	1.36	1.46
14	L3	731	GLY	CA-C	7.49	1.62	1.51
14	L3	731	GLY	N-CA	7.03	1.55	1.45
6	C1	1379	PRO	CA-C	6.18	1.55	1.51
20	R1	1052	GLU	CA-C	6.18	1.55	1.52
5	B0	1521	PRO	CA-C	6.09	1.57	1.52
5	B1	1521	PRO	CA-C	5.91	1.57	1.52
23	U4	610	LEU	N-CA	-5.75	1.39	1.46
23	U5	610	LEU	N-CA	-5.73	1.38	1.46
7	D1	90	PRO	CA-C	5.48	1.54	1.51
23	U4	610	LEU	C-N	-5.46	1.26	1.33
4	A6	215	LEU	CA-C	5.39	1.55	1.52
25	W0	556	PRO	CA-C	5.39	1.55	1.52
6	C3	4	PRO	N-CD	-5.29	1.40	1.47
3	40	10	PRO	CA-C	5.26	1.54	1.51
13	K3	596	ILE	N-CA	-5.19	1.39	1.46
10	H0	160	PRO	CA-C	5.17	1.54	1.51
9	F3	89	PRO	CA-C	5.16	1.54	1.51
7	D1	1001	PRO	CA-C	5.13	1.54	1.51
13	K1	577	PRO	N-CD	-5.10	1.40	1.47
3	41	10	PRO	CA-C	5.01	1.54	1.51

All (1651) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	15	5	GLY	O-C-N	-38.98	78.22	123.44
2	10	5	GLY	O-C-N	-38.55	78.72	123.44
2	13	5	GLY	O-C-N	-38.52	78.75	123.44
2	14	5	GLY	O-C-N	-38.46	78.83	123.44
2	17	5	GLY	O-C-N	-38.45	78.84	123.44
2	12	5	GLY	O-C-N	-38.41	78.88	123.44
2	11	5	GLY	O-C-N	-38.38	78.92	123.44
2	16	5	GLY	O-C-N	-38.34	78.96	123.44
2	15	5	GLY	CA-C-O	-35.62	84.21	121.61
2	16	5	GLY	CA-C-O	-35.45	84.39	121.61
2	12	5	GLY	CA-C-O	-35.43	84.41	121.61
2	14	5	GLY	CA-C-O	-35.43	84.41	121.61
2	13	5	GLY	CA-C-O	-35.42	84.42	121.61
2	10	5	GLY	CA-C-O	-35.39	84.45	121.61
2	11	5	GLY	CA-C-O	-35.36	84.48	121.61
2	17	5	GLY	CA-C-O	-35.34	84.50	121.61
6	C1	1379	PRO	O-C-N	-20.16	112.03	121.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	K1	986	ASP	CB-CG-OD1	19.54	163.34	118.40
13	K1	986	ASP	OD1-CG-OD2	-18.32	78.94	122.90
23	U2	610	LEU	CD1-CG-CD2	14.99	143.77	110.80
13	K1	986	ASP	CB-CG-OD2	-14.78	84.40	118.40
13	K3	596	ILE	CA-CB-CG1	14.69	135.37	110.40
4	A4	167	ILE	CB-CA-C	14.02	131.43	110.96
23	U3	610	LEU	CD1-CG-CD2	13.54	140.59	110.80
23	U1	610	LEU	CB-CA-C	13.18	132.69	110.94
23	U4	610	LEU	CD1-CG-CD2	13.10	139.61	110.80
23	U6	610	LEU	CB-CA-C	13.04	132.45	110.94
4	A0	686	ASP	CA-CB-CG	13.03	125.62	112.60
2	11	1106	PRO	CA-C-N	-12.96	102.58	121.24
2	11	1106	PRO	C-N-CA	-12.96	102.58	121.24
7	D5	1355	ASP	CA-CB-CG	12.52	125.11	112.60
13	K1	576	ASP	O-C-N	-11.21	110.66	121.19
7	D5	1347	ARG	CB-CA-C	11.00	128.92	110.44
23	U5	610	LEU	CD1-CG-CD2	10.78	134.51	110.80
4	A1	408	ASP	CA-CB-CG	10.64	123.24	112.60
2	11	1176	ILE	O-C-N	-10.64	111.62	123.00
4	A2	408	ASP	CA-CB-CG	10.63	123.23	112.60
1	00	375	THR	CA-C-N	10.38	141.36	122.06
1	00	375	THR	C-N-CA	10.38	141.36	122.06
4	A0	408	ASP	CA-CB-CG	10.34	122.94	112.60
4	A3	408	ASP	CA-CB-CG	9.91	122.51	112.60
4	A6	154	ASP	CA-CB-CG	9.80	122.40	112.60
7	D3	1103	ASP	CA-CB-CG	9.54	122.14	112.60
6	C2	619	CYS	CA-C-N	9.26	133.07	120.38
6	C2	619	CYS	C-N-CA	9.26	133.07	120.38
4	A5	556	ASP	CA-CB-CG	9.20	121.80	112.60
4	A1	780	ASP	CA-CB-CG	9.17	121.77	112.60
6	C1	1380	PRO	CA-N-CD	-9.12	99.23	112.00
14	L3	732	MET	N-CA-C	9.07	126.00	114.31
20	R3	1286	ASP	N-CA-C	8.97	124.98	107.57
4	A0	237	PRO	CB-CA-C	8.93	125.23	113.09
18	P2	520	ASP	CA-CB-CG	8.84	121.44	112.60
4	A4	175	ARG	CD-NE-CZ	8.78	136.70	124.40
5	B1	1268	ASP	CA-CB-CG	8.78	121.38	112.60
4	A4	172	PRO	O-C-N	-8.75	111.14	121.46
4	A1	154	ASP	CA-CB-CG	8.71	121.31	112.60
7	D0	203	ASP	CA-CB-CG	8.70	121.30	112.60
6	C3	1939	SER	N-CA-C	8.64	121.82	111.02
18	P1	520	ASP	CA-CB-CG	8.62	121.22	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	R1	1258	GLU	CA-C-N	8.62	132.16	120.44
20	R1	1258	GLU	C-N-CA	8.62	132.16	120.44
15	M3	762	HIS	CA-CB-CG	8.60	122.40	113.80
6	C4	1393	ASP	CA-CB-CG	8.60	121.19	112.60
20	R3	1286	ASP	CA-CB-CG	-8.51	104.09	112.60
20	R2	653	ASN	CA-CB-CG	8.49	121.09	112.60
21	S3	57	ASP	CA-CB-CG	8.38	120.98	112.60
5	B0	1525	ALA	CA-C-N	8.36	136.74	121.70
5	B0	1525	ALA	C-N-CA	8.36	136.74	121.70
4	A0	780	ASP	CA-CB-CG	8.34	120.94	112.60
3	41	390	ASP	CA-CB-CG	8.34	120.94	112.60
14	L2	172	ASP	CA-CB-CG	8.25	120.85	112.60
7	D3	203	ASP	CA-CB-CG	8.24	120.84	112.60
4	A3	172	PRO	N-CA-C	8.23	120.74	110.70
5	B0	632	ASP	CA-CB-CG	8.21	120.81	112.60
21	S0	57	ASP	CA-CB-CG	8.20	120.80	112.60
2	11	164	ASP	CA-CB-CG	8.19	120.78	112.60
2	15	164	ASP	CA-CB-CG	8.18	120.78	112.60
21	S1	57	ASP	CA-CB-CG	8.18	120.78	112.60
6	C2	1393	ASP	CA-CB-CG	8.17	120.77	112.60
7	D0	1239	ASP	CA-CB-CG	8.17	120.77	112.60
14	L3	730	GLN	CB-CA-C	8.16	125.61	110.10
7	D1	1239	ASP	CA-CB-CG	8.15	120.75	112.60
18	P2	323	ASP	CA-CB-CG	8.14	120.75	112.60
18	P3	323	ASP	CA-CB-CG	8.14	120.74	112.60
25	W0	225	ASN	N-CA-C	8.13	121.19	111.02
14	L1	172	ASP	CA-CB-CG	8.12	120.72	112.60
3	40	390	ASP	CA-CB-CG	8.11	120.71	112.60
14	L0	172	ASP	CA-CB-CG	8.10	120.70	112.60
18	P3	520	ASP	CA-CB-CG	8.10	120.70	112.60
7	D1	531	ASP	CA-CB-CG	8.09	120.69	112.60
4	A3	780	ASP	CA-CB-CG	8.07	120.67	112.60
7	D2	1239	ASP	CA-CB-CG	8.07	120.67	112.60
6	C0	1939	SER	CA-C-N	8.05	136.20	121.70
6	C0	1939	SER	C-N-CA	8.05	136.20	121.70
7	D0	531	ASP	CA-CB-CG	8.04	120.64	112.60
7	D3	1239	ASP	CA-CB-CG	8.05	120.65	112.60
14	L1	324	ASP	CA-CB-CG	8.04	120.64	112.60
23	U2	609	ASN	CA-C-N	-8.04	109.99	120.44
23	U2	609	ASN	C-N-CA	-8.04	109.99	120.44
18	P0	323	ASP	CA-CB-CG	8.02	120.62	112.60
14	L3	172	ASP	CA-CB-CG	8.02	120.62	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	L3	730	GLN	CA-C-O	-8.00	107.20	120.80
20	R2	1049	ASP	CA-CB-CG	7.99	120.58	112.60
2	16	164	ASP	CA-CB-CG	7.96	120.56	112.60
6	C2	1159	ILE	CA-C-N	7.95	136.01	121.70
6	C2	1159	ILE	C-N-CA	7.95	136.01	121.70
6	C4	1159	ILE	CA-C-N	7.95	136.01	121.70
6	C4	1159	ILE	C-N-CA	7.95	136.01	121.70
6	C3	1246	MET	CB-CA-C	-7.93	98.12	110.81
18	P1	323	ASP	CA-CB-CG	7.92	120.52	112.60
7	D5	1342	LEU	CA-C-N	7.90	131.92	120.38
7	D5	1342	LEU	C-N-CA	7.90	131.92	120.38
7	D1	1050	ASP	CA-CB-CG	7.85	120.45	112.60
14	L3	729	GLU	CA-C-N	7.83	135.80	121.70
14	L3	729	GLU	C-N-CA	7.83	135.80	121.70
7	D3	915	ASN	CA-CB-CG	7.79	120.39	112.60
13	K1	401	ASP	CA-CB-CG	7.78	120.38	112.60
7	D2	203	ASP	CA-CB-CG	7.78	120.38	112.60
1	00	125	PHE	CA-CB-CG	7.75	121.55	113.80
13	K0	599	HIS	CB-CG-CD2	-7.74	121.14	131.20
13	K3	596	ILE	CB-CG1-CD1	7.72	130.01	113.80
7	D4	531	ASP	CA-CB-CG	7.67	120.27	112.60
7	D2	531	ASP	CA-CB-CG	7.65	120.25	112.60
4	A0	236	THR	O-C-N	-7.62	114.68	121.31
18	P0	520	ASP	CA-CB-CG	7.62	120.22	112.60
7	D0	1050	ASP	CA-CB-CG	7.59	120.19	112.60
13	K2	1153	GLN	CA-CB-CG	-7.59	98.92	114.10
20	R3	653	ASN	CA-CB-CG	7.57	120.17	112.60
6	C2	1246	MET	CA-C-N	7.56	130.27	120.44
6	C2	1246	MET	C-N-CA	7.56	130.27	120.44
18	P1	104	ASN	CA-CB-CG	7.56	120.16	112.60
18	P3	104	ASN	CA-CB-CG	7.56	120.16	112.60
6	C2	542	VAL	CA-C-N	7.55	135.97	121.54
6	C2	542	VAL	C-N-CA	7.55	135.97	121.54
13	K1	982	ASP	CA-CB-CG	7.55	120.16	112.60
20	R1	1277	ILE	CA-C-N	7.54	135.94	121.54
20	R1	1277	ILE	C-N-CA	7.54	135.94	121.54
2	14	164	ASP	CA-CB-CG	7.53	120.13	112.60
18	P0	104	ASN	CA-CB-CG	7.51	120.11	112.60
2	12	164	ASP	CA-CB-CG	7.48	120.08	112.60
7	D1	1103	ASP	CA-CB-CG	7.48	120.08	112.60
6	C1	1393	ASP	CA-CB-CG	7.46	120.06	112.60
2	10	164	ASP	CA-CB-CG	7.45	120.05	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	F3	253	ASP	CA-CB-CG	7.45	120.05	112.60
6	C0	1939	SER	O-C-N	-7.42	112.72	122.59
7	D1	1168	HIS	CB-CG-CD2	-7.40	121.58	131.20
2	10	1626	ASP	CA-CB-CG	7.40	120.00	112.60
7	D2	915	ASN	CA-CB-CG	7.39	119.99	112.60
7	D1	1168	HIS	CB-CA-C	7.37	121.91	109.75
6	C0	1393	ASP	CA-CB-CG	7.35	119.95	112.60
7	D0	915	ASN	CA-CB-CG	7.35	119.95	112.60
7	D5	531	ASP	CA-CB-CG	7.33	119.93	112.60
13	K2	697	ASP	CA-CB-CG	7.32	119.92	112.60
2	11	1626	ASP	CA-CB-CG	7.30	119.91	112.60
6	C3	577	ASP	CA-CB-CG	7.29	119.89	112.60
13	K3	697	ASP	CA-CB-CG	7.28	119.88	112.60
13	K1	814	ASP	CA-CB-CG	7.27	119.87	112.60
1	00	331	ILE	CA-C-N	7.26	132.94	122.85
1	00	331	ILE	C-N-CA	7.26	132.94	122.85
6	C2	1306	ASP	CA-CB-CG	7.25	119.85	112.60
20	R3	1049	ASP	CA-CB-CG	7.24	119.83	112.60
14	L3	728	GLU	CA-CB-CG	7.23	128.56	114.10
2	12	1626	ASP	CA-CB-CG	7.22	119.83	112.60
2	13	1626	ASP	CA-CB-CG	7.21	119.81	112.60
6	C4	1939	SER	N-CA-C	7.20	121.01	111.28
7	D3	1168	HIS	CB-CA-C	7.20	121.63	109.75
4	A4	543	ASP	CA-CB-CG	7.20	119.80	112.60
20	R0	1049	ASP	CA-CB-CG	7.18	119.78	112.60
9	F1	89	PRO	N-CA-CB	7.18	107.21	103.19
14	L3	731	GLY	N-CA-C	7.16	130.16	113.18
2	17	1626	ASP	CA-CB-CG	7.16	119.76	112.60
14	L3	727	CYS	O-C-N	-7.16	114.29	122.09
4	A2	237	PRO	CA-C-N	7.16	131.56	120.75
4	A2	237	PRO	C-N-CA	7.16	131.56	120.75
20	R3	1429	ASP	CA-CB-CG	7.16	119.75	112.60
4	A1	14	GLU	CA-CB-CG	7.12	128.34	114.10
5	B1	632	ASP	CA-CB-CG	7.12	119.72	112.60
7	D3	531	ASP	CA-CB-CG	7.12	119.72	112.60
2	17	164	ASP	CA-CB-CG	7.11	119.71	112.60
4	A2	14	GLU	CA-CB-CG	7.11	128.32	114.10
15	M0	317	HIS	CB-CG-CD2	-7.10	121.96	131.20
2	15	1626	ASP	CA-CB-CG	7.10	119.70	112.60
5	B0	1520	ARG	CA-C-N	7.09	127.69	120.38
5	B0	1520	ARG	C-N-CA	7.09	127.69	120.38
6	C1	279	PHE	CA-CB-CG	7.09	120.89	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	F2	89	PRO	N-CA-CB	7.08	107.16	103.19
4	A0	14	GLU	CA-CB-CG	7.08	128.25	114.10
18	P3	626	ASP	CA-CB-CG	7.05	119.65	112.60
5	B1	1520	ARG	CA-C-N	7.03	127.62	120.38
5	B1	1520	ARG	C-N-CA	7.03	127.62	120.38
14	L3	727	CYS	N-CA-CB	-7.01	100.07	111.01
6	C0	279	PHE	CA-CB-CG	7.01	120.81	113.80
2	16	1626	ASP	CA-CB-CG	7.00	119.60	112.60
18	P2	104	ASN	CA-CB-CG	6.99	119.59	112.60
7	D1	915	ASN	CA-CB-CG	6.99	119.59	112.60
6	C3	54	PHE	CA-CB-CG	6.97	120.77	113.80
2	13	164	ASP	CA-CB-CG	6.97	119.57	112.60
6	C3	4	PRO	CA-C-N	6.96	134.83	121.54
6	C3	4	PRO	C-N-CA	6.96	134.83	121.54
1	00	332	LYS	N-CA-CB	-6.96	98.91	110.39
2	14	1626	ASP	CA-CB-CG	6.96	119.56	112.60
4	A3	14	GLU	CA-CB-CG	6.92	127.95	114.10
15	M3	317	HIS	CB-CG-CD2	-6.92	122.20	131.20
6	C3	4	PRO	N-CD-CG	-6.92	95.49	103.80
7	D5	870	ASP	CA-C-N	6.92	129.44	120.44
7	D5	870	ASP	C-N-CA	6.92	129.44	120.44
13	K1	697	ASP	CA-CB-CG	6.91	119.51	112.60
2	13	984	ARG	CD-NE-CZ	6.89	134.04	124.40
2	10	984	ARG	CD-NE-CZ	6.88	134.04	124.40
7	D5	1223	ASP	CA-CB-CG	6.88	119.48	112.60
15	M3	762	HIS	CB-CG-CD2	-6.88	122.26	131.20
14	L0	467	THR	CA-CB-CG2	6.87	122.18	110.50
14	L3	730	GLN	CA-C-N	6.86	134.86	121.41
14	L3	730	GLN	C-N-CA	6.86	134.86	121.41
2	17	984	ARG	CD-NE-CZ	6.86	134.01	124.40
22	T0	186	ASP	CA-CB-CG	6.85	119.45	112.60
13	K0	697	ASP	CA-CB-CG	6.84	119.44	112.60
23	U6	606	ASN	CA-CB-CG	6.84	119.44	112.60
13	K1	986	ASP	CA-CB-CG	6.83	119.43	112.60
15	M2	317	HIS	CB-CG-CD2	-6.82	122.33	131.20
23	U5	606	ASN	CA-CB-CG	6.82	119.42	112.60
23	U1	606	ASN	CA-CB-CG	6.80	119.40	112.60
22	T1	186	ASP	CA-CB-CG	6.79	119.39	112.60
7	D5	1103	ASP	CA-CB-CG	6.78	119.38	112.60
20	R1	746	ASP	CA-CB-CG	6.78	119.38	112.60
13	K0	484	GLU	CA-C-N	6.78	133.39	121.80
13	K0	484	GLU	C-N-CA	6.78	133.39	121.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C3	450	TYR	CA-C-N	6.78	130.27	120.38
6	C3	450	TYR	C-N-CA	6.78	130.27	120.38
4	A4	167	ILE	N-CA-CB	-6.77	102.93	111.46
7	D4	1173	ASP	CA-CB-CG	6.76	119.36	112.60
20	R1	1287	GLU	CB-CA-C	6.76	121.41	109.65
25	W0	667	LEU	CA-C-N	6.75	124.50	120.24
25	W0	667	LEU	C-N-CA	6.75	124.50	120.24
6	C2	1825	ASP	CA-CB-CG	6.75	119.35	112.60
2	11	984	ARG	CD-NE-CZ	6.75	133.85	124.40
23	U4	606	ASN	CA-CB-CG	6.75	119.35	112.60
1	03	183	ASP	CA-CB-CG	6.74	119.34	112.60
2	12	1217	ARG	CA-C-N	6.74	129.21	120.44
2	12	1217	ARG	C-N-CA	6.74	129.21	120.44
18	P2	626	ASP	CA-CB-CG	6.74	119.34	112.60
2	12	984	ARG	CD-NE-CZ	6.73	133.82	124.40
2	14	984	ARG	CD-NE-CZ	6.73	133.82	124.40
4	A4	173	PRO	CB-CA-C	6.72	122.66	111.56
2	16	984	ARG	CD-NE-CZ	6.71	133.80	124.40
23	U2	606	ASN	CA-CB-CG	6.71	119.31	112.60
22	T0	29	THR	CA-C-N	6.71	134.35	121.54
22	T0	29	THR	C-N-CA	6.71	134.35	121.54
23	U3	606	ASN	CA-CB-CG	6.69	119.29	112.60
9	F0	89	PRO	N-CA-CB	6.69	106.94	103.19
6	C4	279	PHE	CA-CB-CG	6.68	120.48	113.80
20	R2	1429	ASP	CA-CB-CG	6.68	119.28	112.60
7	D2	1173	ASP	CA-CB-CG	6.67	119.27	112.60
23	U5	606	ASN	OD1-CG-ND2	-6.67	115.93	122.60
14	L3	727	CYS	N-CA-C	6.67	124.42	114.09
20	R0	746	ASP	CA-CB-CG	6.65	119.25	112.60
6	C2	49	ASP	CA-CB-CG	6.64	119.24	112.60
2	10	1217	ARG	CA-C-N	6.63	129.06	120.44
2	10	1217	ARG	C-N-CA	6.63	129.06	120.44
5	B1	972	ASP	CA-CB-CG	6.63	119.23	112.60
4	A6	107	ASP	CA-CB-CG	6.62	119.22	112.60
1	01	183	ASP	CA-CB-CG	6.62	119.22	112.60
6	C1	54	PHE	CA-CB-CG	6.62	120.42	113.80
15	M1	317	HIS	CB-CG-CD2	-6.62	122.60	131.20
22	T0	867	LYS	CB-CA-C	6.61	115.89	111.20
4	A5	254	PHE	CA-CB-CG	6.61	120.41	113.80
23	U1	606	ASN	OD1-CG-ND2	-6.60	116.00	122.60
4	A5	581	ASP	CA-CB-CG	6.60	119.20	112.60
25	W0	141	GLY	CA-C-N	6.59	130.01	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	W0	141	GLY	C-N-CA	6.59	130.01	120.38
7	D3	276	ASP	CA-CB-CG	6.59	119.19	112.60
23	U2	606	ASN	OD1-CG-ND2	-6.58	116.02	122.60
6	C0	577	ASP	CA-CB-CG	6.58	119.18	112.60
7	D5	1173	ASP	CA-CB-CG	6.57	119.17	112.60
18	P1	626	ASP	CA-CB-CG	6.57	119.17	112.60
2	15	984	ARG	CD-NE-CZ	6.56	133.59	124.40
9	F0	233	GLY	CA-C-N	6.56	134.07	121.54
9	F0	233	GLY	C-N-CA	6.56	134.07	121.54
13	K2	504	PHE	CA-CB-CG	6.56	120.36	113.80
5	B1	1523	SER	CA-C-N	6.55	133.49	121.70
5	B1	1523	SER	C-N-CA	6.55	133.49	121.70
20	R1	1257	GLY	CA-C-N	6.55	134.04	121.54
20	R1	1257	GLY	C-N-CA	6.55	134.04	121.54
23	U6	606	ASN	OD1-CG-ND2	-6.55	116.05	122.60
13	K2	599	HIS	CB-CG-CD2	-6.54	122.70	131.20
10	H3	315	ASP	CA-CB-CG	6.53	119.13	112.60
13	K1	262	LEU	CA-C-N	6.53	133.45	121.70
13	K1	262	LEU	C-N-CA	6.53	133.45	121.70
6	C0	54	PHE	CA-CB-CG	6.52	120.32	113.80
5	B0	1525	ALA	O-C-N	-6.52	115.82	123.25
9	F3	89	PRO	N-CA-CB	6.52	106.84	103.19
7	D0	1173	ASP	CA-CB-CG	6.51	119.11	112.60
10	H0	415	ASP	CA-CB-CG	6.51	119.11	112.60
6	C2	959	ASP	CA-CB-CG	6.50	119.10	112.60
6	C3	1159	ILE	CA-C-N	6.50	133.40	121.70
6	C3	1159	ILE	C-N-CA	6.50	133.40	121.70
1	02	183	ASP	CA-CB-CG	6.49	119.08	112.60
4	A1	757	PHE	CA-CB-CG	6.48	120.28	113.80
7	D3	1168	HIS	CB-CG-CD2	-6.47	122.78	131.20
5	B1	1526	SER	CA-C-N	6.47	133.35	121.70
5	B1	1526	SER	C-N-CA	6.47	133.35	121.70
6	C0	1532	ASP	CA-CB-CG	6.47	119.07	112.60
10	H1	315	ASP	CA-CB-CG	6.47	119.07	112.60
2	10	1177	MET	CB-CA-C	6.46	120.19	109.80
2	11	1463	HIS	CA-CB-CG	6.46	120.26	113.80
6	C4	1825	ASP	CA-CB-CG	6.46	119.06	112.60
7	D4	1213	ASP	CA-CB-CG	6.46	119.06	112.60
10	H2	315	ASP	CA-CB-CG	6.45	119.05	112.60
18	P0	189	ASN	CA-CB-CG	6.45	119.05	112.60
13	K3	599	HIS	CB-CG-CD2	-6.45	122.82	131.20
6	C4	54	PHE	CA-CB-CG	6.44	120.24	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	U3	606	ASN	OD1-CG-ND2	-6.43	116.17	122.60
1	01	553	LEU	CB-CA-C	6.43	122.06	109.72
7	D5	1347	ARG	NE-CZ-NH2	-6.42	113.42	119.20
6	C1	577	ASP	CA-CB-CG	6.42	119.02	112.60
14	L3	731	GLY	CA-C-N	6.42	132.31	122.24
14	L3	731	GLY	C-N-CA	6.42	132.31	122.24
10	H2	415	ASP	CA-CB-CG	6.41	119.01	112.60
20	R2	1068	SER	CA-CB-OG	6.41	123.92	111.10
5	B0	972	ASP	CA-CB-CG	6.41	119.01	112.60
6	C2	2012	ASN	CA-CB-CG	6.41	119.01	112.60
23	U4	606	ASN	OD1-CG-ND2	-6.40	116.20	122.60
20	R1	1049	ASP	CA-CB-CG	6.39	118.99	112.60
13	K2	486	LEU	CA-C-N	6.39	131.28	121.83
13	K2	486	LEU	C-N-CA	6.39	131.28	121.83
20	R2	1154	PRO	O-C-N	6.38	130.63	122.85
6	C3	1393	ASP	CA-CB-CG	6.37	118.97	112.60
7	D0	99	HIS	CB-CG-CD2	-6.37	122.93	131.20
10	H0	483	ASP	CA-CB-CG	6.35	118.95	112.60
4	A1	73	HIS	CB-CG-CD2	-6.33	122.97	131.20
6	C4	1532	ASP	CA-CB-CG	6.32	118.92	112.60
2	I3	783	ARG	NE-CZ-NH1	6.31	127.81	121.50
20	R0	1074	ASP	CA-C-N	6.30	129.58	120.38
20	R0	1074	ASP	C-N-CA	6.30	129.58	120.38
13	K2	401	ASP	CA-CB-CG	6.30	118.90	112.60
13	K3	401	ASP	CA-CB-CG	6.27	118.87	112.60
14	L1	471	THR	CA-C-N	6.27	132.65	122.81
14	L1	471	THR	C-N-CA	6.27	132.65	122.81
6	C1	1825	ASP	CA-CB-CG	6.26	118.86	112.60
13	K0	498	ASN	N-CA-C	6.26	116.54	108.34
13	K2	262	LEU	CA-C-N	6.25	132.96	121.70
13	K2	262	LEU	C-N-CA	6.25	132.96	121.70
7	D3	1173	ASP	CA-CB-CG	6.25	118.85	112.60
2	I3	1217	ARG	CA-C-N	6.25	128.97	120.54
2	I3	1217	ARG	C-N-CA	6.25	128.97	120.54
6	C0	1825	ASP	CA-CB-CG	6.25	118.85	112.60
4	A2	757	PHE	CA-CB-CG	6.25	120.05	113.80
7	D1	563	ARG	NE-CZ-NH2	6.24	124.82	119.20
2	I2	700	SER	CB-CA-C	6.24	118.96	111.22
14	L0	447	ASP	CA-CB-CG	6.24	118.84	112.60
17	O2	276	ASN	CA-CB-CG	6.24	118.84	112.60
7	D5	1346	ARG	CD-NE-CZ	6.23	133.12	124.40
20	R2	1074	ASP	CA-C-N	6.23	129.25	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	R2	1074	ASP	C-N-CA	6.23	129.25	120.28
4	A4	248	VAL	CA-C-N	6.21	128.52	120.44
4	A4	248	VAL	C-N-CA	6.21	128.52	120.44
2	15	747	ALA	N-CA-C	6.21	113.60	108.07
6	C3	175	ASP	CA-CB-CG	6.21	118.81	112.60
18	P3	533	ASP	CA-CB-CG	6.21	118.81	112.60
1	04	183	ASP	CA-CB-CG	6.21	118.81	112.60
13	K0	262	LEU	CA-C-N	6.21	132.87	121.70
13	K0	262	LEU	C-N-CA	6.21	132.87	121.70
13	K3	262	LEU	CA-C-N	6.21	132.87	121.70
13	K3	262	LEU	C-N-CA	6.21	132.87	121.70
14	L2	447	ASP	CA-CB-CG	6.19	118.79	112.60
9	F0	96	ASP	CA-CB-CG	6.18	118.78	112.60
25	W0	348	THR	N-CA-C	6.18	120.61	113.38
21	S2	57	ASP	CA-CB-CG	6.17	118.77	112.60
5	B1	288	ASP	CA-CB-CG	6.17	118.77	112.60
2	12	2	ALA	CA-C-N	6.17	132.80	121.70
2	12	2	ALA	C-N-CA	6.17	132.80	121.70
4	A4	107	ASP	CA-CB-CG	6.17	118.77	112.60
5	B0	288	ASP	CA-CB-CG	6.17	118.77	112.60
13	K0	1090	ASP	CA-CB-CG	6.16	118.76	112.60
14	L1	447	ASP	CA-CB-CG	6.16	118.76	112.60
9	F1	170	HIS	CB-CG-CD2	-6.16	123.19	131.20
12	J3	450	ASP	CA-CB-CG	6.15	118.75	112.60
14	L3	447	ASP	CA-CB-CG	6.15	118.75	112.60
6	C3	49	ASP	CA-CB-CG	6.14	118.74	112.60
9	F0	310	LYS	CA-C-N	6.14	129.55	120.95
9	F0	310	LYS	C-N-CA	6.14	129.55	120.95
10	H2	439	ARG	NE-CZ-NH2	6.14	124.72	119.20
1	00	396	LYS	CA-C-N	6.13	128.50	120.28
1	00	396	LYS	C-N-CA	6.13	128.50	120.28
14	L0	730	GLN	CB-CA-C	6.12	122.61	110.42
8	E0	599	GLN	OE1-CD-NE2	-6.12	116.48	122.60
12	J1	450	ASP	CA-CB-CG	6.12	118.72	112.60
18	P0	254	LEU	CA-C-N	6.12	128.39	120.44
18	P0	254	LEU	C-N-CA	6.12	128.39	120.44
20	R2	1390	ASP	CA-CB-CG	6.11	118.71	112.60
7	D0	437	ASP	CA-CB-CG	6.10	118.70	112.60
7	D5	437	ASP	CA-CB-CG	6.09	118.69	112.60
6	C4	959	ASP	CA-CB-CG	6.08	118.68	112.60
6	C2	1754	GLN	OE1-CD-NE2	-6.08	116.52	122.60
5	B0	1311	PRO	CA-C-N	6.08	129.10	120.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B0	1311	PRO	C-N-CA	6.08	129.10	120.53
7	D2	437	ASP	CA-CB-CG	6.08	118.68	112.60
15	M3	585	SER	CA-C-N	6.07	127.43	119.84
15	M3	585	SER	C-N-CA	6.07	127.43	119.84
8	E0	6	SER	N-CA-C	6.07	120.48	113.38
4	A4	173	PRO	N-CA-CB	6.07	109.62	103.25
8	E1	599	GLN	OE1-CD-NE2	-6.06	116.54	122.60
1	00	651	HIS	CB-CG-CD2	-6.05	123.33	131.20
1	01	396	LYS	CA-C-N	6.05	128.39	120.28
1	01	396	LYS	C-N-CA	6.05	128.39	120.28
5	B0	893	ASP	CA-CB-CG	6.04	118.64	112.60
4	A6	706	HIS	CA-C-N	6.04	132.85	121.97
4	A6	706	HIS	C-N-CA	6.04	132.85	121.97
13	K0	401	ASP	CA-CB-CG	6.04	118.64	112.60
6	C4	1697	ASN	CA-CB-CG	6.04	118.64	112.60
20	R3	1404	HIS	CB-CA-C	6.04	121.31	109.72
7	D4	437	ASP	CA-CB-CG	6.04	118.64	112.60
21	S3	174	HIS	CB-CG-CD2	-6.04	123.35	131.20
2	13	783	ARG	CD-NE-CZ	6.03	132.84	124.40
6	C2	1532	ASP	CA-CB-CG	6.03	118.63	112.60
23	U4	609	ASN	CA-C-N	-6.03	112.60	120.44
23	U4	609	ASN	C-N-CA	-6.03	112.60	120.44
13	K3	613	ASP	CA-CB-CG	6.03	118.63	112.60
20	R3	1285	THR	CA-CB-OG1	6.03	118.64	109.60
21	S0	174	HIS	CB-CG-CD2	-6.03	123.37	131.20
6	C4	782	ASP	CA-CB-CG	6.02	118.62	112.60
13	K1	517	ASP	CA-CB-CG	6.01	118.61	112.60
20	R1	1279	THR	CA-C-N	6.01	129.66	120.82
20	R1	1279	THR	C-N-CA	6.01	129.66	120.82
1	01	651	HIS	CB-CG-CD2	-6.01	123.39	131.20
1	03	651	HIS	CB-CG-CD2	-6.01	123.39	131.20
21	S1	174	HIS	CB-CG-CD2	-6.00	123.39	131.20
4	A2	780	ASP	CA-CB-CG	6.00	118.60	112.60
20	R3	1284	ALA	CA-C-N	6.00	133.00	121.54
20	R3	1284	ALA	C-N-CA	6.00	133.00	121.54
11	I3	353	PHE	CA-CB-CG	6.00	119.80	113.80
20	R1	179	VAL	CA-C-N	6.00	129.88	121.24
20	R1	179	VAL	C-N-CA	6.00	129.88	121.24
22	T1	821	ASN	CA-CB-CG	6.00	118.60	112.60
6	C4	577	ASP	CA-CB-CG	5.99	118.59	112.60
21	S2	174	HIS	CB-CG-CD2	-5.99	123.41	131.20
20	R0	179	VAL	CA-C-N	5.99	129.87	121.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	R0	179	VAL	C-N-CA	5.99	129.87	121.24
12	J0	427	ASP	CA-CB-CG	5.99	118.59	112.60
13	K3	596	ILE	CA-CB-CG2	-5.99	100.32	110.50
19	Q2	273	ASN	CA-CB-CG	5.99	118.59	112.60
10	H0	315	ASP	CA-CB-CG	5.98	118.58	112.60
7	D1	1173	ASP	CA-CB-CG	5.98	118.58	112.60
20	R0	1429	ASP	CA-CB-CG	5.98	118.58	112.60
18	P3	554	ALA	CA-C-N	5.98	128.61	120.54
18	P3	554	ALA	C-N-CA	5.98	128.61	120.54
2	15	1217	ARG	CA-C-N	5.97	128.77	120.29
2	15	1217	ARG	C-N-CA	5.97	128.77	120.29
20	R1	1429	ASP	CA-CB-CG	5.97	118.57	112.60
23	U3	610	LEU	CA-CB-CG	-5.97	95.40	116.30
20	R3	1390	ASP	CA-CB-CG	5.97	118.57	112.60
6	C1	1798	ASP	CA-CB-CG	5.97	118.57	112.60
20	R0	1390	ASP	CA-CB-CG	5.97	118.57	112.60
25	W0	7	PRO	CA-N-CD	-5.96	103.65	112.00
7	D2	276	ASP	CA-CB-CG	5.96	118.56	112.60
6	C0	782	ASP	CA-CB-CG	5.96	118.56	112.60
18	P1	618	ASP	CA-C-N	5.96	129.08	120.38
18	P1	618	ASP	C-N-CA	5.96	129.08	120.38
4	A1	169	ASP	CA-CB-CG	5.96	118.56	112.60
6	C3	1249	ILE	CA-C-N	5.95	127.78	120.22
6	C3	1249	ILE	C-N-CA	5.95	127.78	120.22
4	A4	757	PHE	CA-CB-CG	5.95	119.75	113.80
7	D3	1223	ASP	CA-CB-CG	5.95	118.55	112.60
9	F2	173	ASP	CA-CB-CG	5.95	118.55	112.60
6	C3	503	ASP	CA-CB-CG	5.95	118.55	112.60
7	D3	32	ARG	CD-NE-CZ	5.94	132.71	124.40
4	A5	408	ASP	CA-CB-CG	5.93	118.53	112.60
20	R1	1390	ASP	CA-CB-CG	5.93	118.53	112.60
2	16	1410	ASP	CA-CB-CG	5.93	118.53	112.60
11	I2	353	PHE	CA-CB-CG	5.93	119.73	113.80
2	15	783	ARG	NE-CZ-NH1	5.93	127.43	121.50
20	R2	1068	SER	CB-CA-C	5.93	120.34	110.92
7	D3	734	ASN	O-C-N	5.92	126.57	121.30
4	A3	73	HIS	CB-CG-CD2	-5.92	123.50	131.20
7	D1	545	ASP	CA-CB-CG	5.92	118.52	112.60
4	A6	757	PHE	CA-CB-CG	5.91	119.71	113.80
5	B0	1526	SER	CA-C-N	5.91	132.34	121.70
5	B0	1526	SER	C-N-CA	5.91	132.34	121.70
15	M0	761	GLU	CA-C-N	5.91	132.82	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	M0	761	GLU	C-N-CA	5.91	132.82	121.54
2	15	1410	ASP	CA-CB-CG	5.90	118.50	112.60
13	K2	613	ASP	CA-CB-CG	5.90	118.50	112.60
1	03	83	TYR	CA-C-N	5.90	128.11	120.44
1	03	83	TYR	C-N-CA	5.90	128.11	120.44
7	D1	1223	ASP	CA-CB-CG	5.90	118.50	112.60
11	I1	353	PHE	CA-CB-CG	5.89	119.69	113.80
5	B1	1155	LEU	CA-C-N	5.89	126.48	120.00
5	B1	1155	LEU	C-N-CA	5.89	126.48	120.00
22	T1	465	PRO	N-CA-CB	5.88	106.28	103.22
14	L3	332	LYS	CB-CA-C	5.88	119.74	111.86
2	15	1633	GLN	OE1-CD-NE2	-5.87	116.73	122.60
6	C0	49	ASP	CA-CB-CG	5.86	118.46	112.60
6	C1	1754	GLN	OE1-CD-NE2	-5.86	116.74	122.60
20	R1	333	ASP	CA-CB-CG	5.86	118.46	112.60
5	B0	1155	LEU	CA-C-N	5.85	126.44	120.00
5	B0	1155	LEU	C-N-CA	5.85	126.44	120.00
12	J4	443	GLN	OE1-CD-NE2	-5.85	116.75	122.60
20	R1	990	ALA	CA-C-N	5.85	128.53	120.92
20	R1	990	ALA	C-N-CA	5.85	128.53	120.92
15	M0	406	LEU	CA-C-N	5.85	130.05	120.63
15	M0	406	LEU	C-N-CA	5.85	130.05	120.63
7	D1	437	ASP	CA-CB-CG	5.85	118.45	112.60
20	R2	179	VAL	CA-C-N	5.85	129.66	121.24
20	R2	179	VAL	C-N-CA	5.85	129.66	121.24
1	02	651	HIS	CB-CG-CD2	-5.84	123.60	131.20
6	C1	959	ASP	CA-CB-CG	5.84	118.44	112.60
4	A0	757	PHE	CA-CB-CG	5.84	119.64	113.80
6	C1	782	ASP	CA-CB-CG	5.84	118.44	112.60
22	T0	821	ASN	CA-CB-CG	5.84	118.44	112.60
6	C2	542	VAL	O-C-N	5.83	129.03	122.67
7	D4	1110	SER	CA-C-N	5.83	128.89	120.38
7	D4	1110	SER	C-N-CA	5.83	128.89	120.38
20	R3	179	VAL	CA-C-N	5.83	129.63	121.24
20	R3	179	VAL	C-N-CA	5.83	129.63	121.24
2	11	132	ASP	CA-CB-CG	5.83	118.43	112.60
14	L0	435	LEU	CA-C-N	5.83	128.67	120.28
14	L0	435	LEU	C-N-CA	5.83	128.67	120.28
7	D4	1074	ARG	CA-C-N	5.83	127.90	120.56
7	D4	1074	ARG	C-N-CA	5.83	127.90	120.56
6	C1	356	ASP	CA-CB-CG	5.82	118.42	112.60
6	C4	1754	GLN	OE1-CD-NE2	-5.82	116.78	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	14	132	ASP	CA-CB-CG	5.82	118.42	112.60
6	C1	412	ASN	CA-CB-CG	5.82	118.42	112.60
1	00	183	ASP	CA-CB-CG	5.82	118.42	112.60
7	D1	32	ARG	CD-NE-CZ	5.82	132.54	124.40
1	01	83	TYR	CA-C-N	5.81	128.00	120.44
1	01	83	TYR	C-N-CA	5.81	128.00	120.44
9	F2	310	LYS	CA-C-N	5.81	129.09	120.95
9	F2	310	LYS	C-N-CA	5.81	129.09	120.95
15	M2	834	ASN	CA-CB-CG	5.81	118.41	112.60
6	C3	800	PRO	N-CA-CB	5.81	106.44	103.19
6	C1	49	ASP	CA-CB-CG	5.81	118.41	112.60
7	D3	437	ASP	CA-CB-CG	5.81	118.41	112.60
14	L1	836	ALA	CA-C-N	5.80	129.51	120.75
14	L1	836	ALA	C-N-CA	5.80	129.51	120.75
20	R3	365	ARG	CD-NE-CZ	5.80	132.52	124.40
4	A6	248	VAL	CA-C-N	5.80	128.33	120.44
4	A6	248	VAL	C-N-CA	5.80	128.33	120.44
10	H1	415	ASP	CA-CB-CG	5.80	118.40	112.60
6	C1	438	ASP	CA-CB-CG	5.80	118.40	112.60
10	H0	443	HIS	CB-CG-CD2	-5.80	123.66	131.20
10	H2	357	ASP	CA-CB-CG	5.79	118.39	112.60
2	14	1217	ARG	CA-C-N	5.79	128.51	120.29
2	14	1217	ARG	C-N-CA	5.79	128.51	120.29
1	03	125	PHE	CA-CB-CG	5.79	119.59	113.80
6	C0	959	ASP	CA-CB-CG	5.79	118.39	112.60
23	U4	610	LEU	CA-CB-CG	-5.79	96.04	116.30
6	C0	1487	ASP	CA-CB-CG	5.78	118.38	112.60
20	R3	1162	HIS	CB-CG-CD2	-5.78	123.69	131.20
7	D3	1009	ASN	CA-CB-CG	5.78	118.38	112.60
16	N0	294	ASP	CA-CB-CG	5.78	118.38	112.60
6	C0	1754	GLN	OE1-CD-NE2	-5.78	116.83	122.60
1	04	396	LYS	CA-C-N	5.77	128.02	120.28
1	04	396	LYS	C-N-CA	5.77	128.02	120.28
6	C4	49	ASP	CA-CB-CG	5.77	118.37	112.60
1	04	651	HIS	CB-CG-CD2	-5.77	123.70	131.20
2	15	132	ASP	CA-CB-CG	5.77	118.37	112.60
6	C2	503	ASP	CA-CB-CG	5.77	118.37	112.60
15	M3	762	HIS	CB-CA-C	5.77	120.00	111.17
22	T1	29	THR	CA-C-N	5.77	132.56	121.54
22	T1	29	THR	C-N-CA	5.77	132.56	121.54
23	U4	610	LEU	N-CA-CB	-5.77	101.65	110.01
6	C3	786	GLN	OE1-CD-NE2	-5.76	116.83	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	T0	161	ASP	CA-CB-CG	5.76	118.36	112.60
6	C3	625	THR	CA-C-N	5.76	125.44	119.05
6	C3	625	THR	C-N-CA	5.76	125.44	119.05
6	C2	54	PHE	CA-CB-CG	5.76	119.56	113.80
2	17	1410	ASP	CA-CB-CG	5.75	118.35	112.60
7	D3	545	ASP	CA-CB-CG	5.75	118.35	112.60
6	C0	438	ASP	CA-CB-CG	5.75	118.35	112.60
14	L2	184	GLN	OE1-CD-NE2	-5.75	116.85	122.60
5	B0	1523	SER	N-CA-C	5.75	123.04	110.80
6	C0	412	ASN	CA-CB-CG	5.75	118.35	112.60
13	K0	548	HIS	CB-CG-CD2	-5.74	123.73	131.20
5	B0	1522	PRO	CA-N-CD	-5.74	103.47	111.50
14	L2	585	HIS	CB-CG-CD2	-5.74	123.74	131.20
14	L2	435	LEU	CA-C-N	5.74	128.54	120.28
14	L2	435	LEU	C-N-CA	5.74	128.54	120.28
22	T0	305	GLN	OE1-CD-NE2	-5.74	116.86	122.60
6	C3	48	PRO	CB-CA-C	-5.74	103.95	112.55
11	I0	353	PHE	CA-CB-CG	5.73	119.53	113.80
1	01	125	PHE	CA-CB-CG	5.73	119.53	113.80
7	D2	427	ASP	CA-CB-CG	5.73	118.33	112.60
6	C0	1938	ASP	CB-CA-C	5.73	120.70	111.36
19	Q0	273	ASN	CA-CB-CG	5.72	118.32	112.60
9	F2	249	MET	CA-C-N	5.72	128.73	120.38
9	F2	249	MET	C-N-CA	5.72	128.73	120.38
14	L0	184	GLN	OE1-CD-NE2	-5.71	116.89	122.60
7	D5	811	GLN	OE1-CD-NE2	-5.71	116.89	122.60
14	L3	184	GLN	OE1-CD-NE2	-5.71	116.89	122.60
20	R0	333	ASP	CA-CB-CG	5.71	118.31	112.60
19	Q3	273	ASN	CA-CB-CG	5.71	118.31	112.60
4	A0	426	ASP	CA-CB-CG	5.71	118.31	112.60
14	L1	435	LEU	CA-C-N	5.71	128.50	120.28
14	L1	435	LEU	C-N-CA	5.71	128.50	120.28
13	K2	819	GLN	OE1-CD-NE2	-5.71	116.89	122.60
7	D1	276	ASP	CA-CB-CG	5.70	118.30	112.60
18	P0	617	SER	CA-C-N	5.70	131.97	121.70
18	P0	617	SER	C-N-CA	5.70	131.97	121.70
7	D0	889	ASN	CA-CB-CG	-5.70	106.90	112.60
20	R2	529	CYS	CA-C-N	5.70	128.49	120.28
20	R2	529	CYS	C-N-CA	5.70	128.49	120.28
21	S1	284	HIS	CB-CG-CD2	-5.70	123.79	131.20
2	13	1657	HIS	CB-CG-CD2	-5.70	123.79	131.20
6	C0	356	ASP	CA-CB-CG	5.70	118.30	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	R1	1162	HIS	CB-CG-CD2	-5.70	123.79	131.20
7	D3	1107	THR	N-CA-C	5.69	117.64	110.24
22	T0	465	PRO	N-CA-CB	5.69	106.18	103.22
6	C3	937	PHE	CA-CB-CG	5.69	119.49	113.80
20	R3	1286	ASP	N-CA-CB	-5.69	101.08	110.53
23	U4	610	LEU	CA-C-O	5.69	126.79	120.82
20	R3	529	CYS	CA-C-N	5.68	128.47	120.28
20	R3	529	CYS	C-N-CA	5.68	128.47	120.28
4	A5	216	ASP	CA-CB-CG	5.68	118.28	112.60
5	B0	1518	VAL	N-CA-C	5.68	121.16	109.34
7	D4	1103	ASP	CA-CB-CG	5.68	118.28	112.60
4	A1	94	LYS	CA-C-N	5.68	132.39	121.54
4	A1	94	LYS	C-N-CA	5.68	132.39	121.54
7	D5	852	VAL	CA-C-N	5.68	128.46	120.28
7	D5	852	VAL	C-N-CA	5.68	128.46	120.28
14	L1	184	GLN	OE1-CD-NE2	-5.68	116.92	122.60
20	R2	1162	HIS	CB-CG-CD2	-5.68	123.82	131.20
22	T0	377	ASP	CA-CB-CG	5.68	118.28	112.60
5	B0	1312	ILE	N-CA-C	5.67	117.09	110.62
7	D5	32	ARG	CD-NE-CZ	5.67	132.34	124.40
4	A0	556	ASP	CA-CB-CG	5.67	118.27	112.60
22	T0	30	LEU	N-CA-C	5.67	122.88	110.80
2	15	747	ALA	N-CA-CB	-5.67	105.45	111.29
3	40	190	HIS	CB-CG-CD2	-5.67	123.83	131.20
6	C3	356	ASP	CA-CB-CG	5.67	118.27	112.60
2	10	132	ASP	CA-CB-CG	5.67	118.27	112.60
6	C2	279	PHE	CA-CB-CG	5.67	119.47	113.80
20	R0	1162	HIS	CB-CG-CD2	-5.67	123.83	131.20
2	13	2	ALA	CA-C-N	5.67	131.90	121.70
2	13	2	ALA	C-N-CA	5.67	131.90	121.70
4	A2	723	ASN	CA-CB-CG	5.67	118.27	112.60
5	B0	1223	ASP	CA-CB-CG	5.67	118.27	112.60
2	10	2	ALA	CA-C-N	5.66	131.89	121.70
2	10	2	ALA	C-N-CA	5.66	131.89	121.70
1	03	28	LYS	CA-C-N	5.66	126.27	119.98
1	03	28	LYS	C-N-CA	5.66	126.27	119.98
1	03	396	LYS	CA-C-N	5.66	128.33	120.29
1	03	396	LYS	C-N-CA	5.66	128.33	120.29
2	16	1217	ARG	CA-C-N	5.66	128.33	120.29
2	16	1217	ARG	C-N-CA	5.66	128.33	120.29
2	17	1217	ARG	CA-C-N	5.66	128.33	120.29
2	17	1217	ARG	C-N-CA	5.66	128.33	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C1	1532	ASP	CA-CB-CG	5.66	118.26	112.60
9	F3	254	ARG	CD-NE-CZ	5.66	132.32	124.40
13	K2	868	ASP	CA-CB-CG	-5.66	106.94	112.60
1	00	28	LYS	CA-C-N	5.65	126.26	119.98
1	00	28	LYS	C-N-CA	5.65	126.26	119.98
3	41	190	HIS	CB-CG-CD2	-5.65	123.85	131.20
3	40	419	PRO	CA-C-N	5.65	132.33	121.54
3	40	419	PRO	C-N-CA	5.65	132.33	121.54
4	A1	153	GLU	CA-C-N	5.65	127.85	120.28
4	A1	153	GLU	C-N-CA	5.65	127.85	120.28
5	B0	1268	ASP	N-CA-C	5.65	119.48	112.47
1	03	84	ARG	NE-CZ-NH2	5.65	124.28	119.20
6	C3	279	PHE	CA-CB-CG	5.65	119.45	113.80
14	L2	332	LYS	CB-CA-C	5.65	119.43	111.86
14	L3	435	LEU	CA-C-N	5.65	128.41	120.28
14	L3	435	LEU	C-N-CA	5.65	128.41	120.28
12	J0	468	SER	CA-C-N	5.64	128.33	120.65
12	J0	468	SER	C-N-CA	5.64	128.33	120.65
2	17	2	ALA	CA-C-N	5.64	131.86	121.70
2	17	2	ALA	C-N-CA	5.64	131.86	121.70
7	D0	276	ASP	CA-CB-CG	5.64	118.24	112.60
13	K0	1141	GLU	O-C-N	-5.64	116.26	122.07
1	04	164	ASP	CA-CB-CG	5.64	118.24	112.60
20	R0	365	ARG	CD-NE-CZ	5.64	132.30	124.40
2	16	132	ASP	CA-CB-CG	5.64	118.24	112.60
1	00	83	TYR	CA-C-N	5.64	127.77	120.44
1	00	83	TYR	C-N-CA	5.64	127.77	120.44
4	A6	97	ASP	CA-CB-CG	5.64	118.24	112.60
13	K0	819	GLN	OE1-CD-NE2	-5.64	116.96	122.60
22	T0	843	HIS	CB-CG-CD2	-5.64	123.87	131.20
6	C1	1600	PHE	CA-CB-CG	5.63	119.43	113.80
7	D5	99	HIS	CB-CG-CD2	-5.63	123.88	131.20
2	12	132	ASP	CA-CB-CG	5.63	118.23	112.60
2	14	2	ALA	CA-C-N	5.63	131.84	121.70
2	14	2	ALA	C-N-CA	5.63	131.84	121.70
6	C2	1159	ILE	O-C-N	-5.63	115.53	122.57
15	M0	762	HIS	CA-C-N	5.63	132.30	121.54
15	M0	762	HIS	C-N-CA	5.63	132.30	121.54
6	C1	450	TYR	CA-C-N	5.63	129.69	120.63
6	C1	450	TYR	C-N-CA	5.63	129.69	120.63
7	D2	1001	PRO	N-CA-C	5.63	117.57	110.70
21	S3	284	HIS	CB-CG-CD2	-5.63	123.88	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	41	22	ASN	CA-CB-CG	5.63	118.23	112.60
6	C0	450	TYR	CA-C-N	5.62	129.69	120.63
6	C0	450	TYR	C-N-CA	5.62	129.69	120.63
6	C3	121	HIS	CB-CG-CD2	-5.62	123.89	131.20
14	L0	332	LYS	CB-CA-C	5.62	119.88	111.89
22	T0	413	PRO	CA-C-N	5.62	128.28	120.29
22	T0	413	PRO	C-N-CA	5.62	128.28	120.29
7	D0	1269	GLN	OE1-CD-NE2	-5.62	116.98	122.60
23	U4	610	LEU	O-C-N	-5.62	116.29	122.07
4	A2	73	HIS	CB-CG-CD2	-5.61	123.90	131.20
17	O1	34	GLN	OE1-CD-NE2	-5.61	116.99	122.60
2	11	2	ALA	CA-C-N	5.61	131.80	121.70
2	11	2	ALA	C-N-CA	5.61	131.80	121.70
10	H0	147	PHE	CA-CB-CG	5.61	119.41	113.80
1	04	83	TYR	CA-C-N	5.61	127.73	120.44
1	04	83	TYR	C-N-CA	5.61	127.73	120.44
7	D0	1105	HIS	CB-CG-CD2	-5.61	123.91	131.20
8	E1	322	ASN	CB-CA-C	5.61	115.88	111.00
13	K0	509	LYS	CA-C-N	5.61	132.26	121.54
13	K0	509	LYS	C-N-CA	5.61	132.26	121.54
13	K3	868	ASP	CA-CB-CG	-5.61	106.99	112.60
20	R3	1286	ASP	CA-C-N	5.61	130.36	121.44
20	R3	1286	ASP	C-N-CA	5.61	130.36	121.44
2	16	2	ALA	CA-C-N	5.60	131.79	121.70
2	16	2	ALA	C-N-CA	5.60	131.79	121.70
7	D4	32	ARG	CD-NE-CZ	5.60	132.25	124.40
13	K0	868	ASP	CA-CB-CG	-5.60	107.00	112.60
2	15	1414	ASP	CA-CB-CG	5.60	118.20	112.60
21	S3	87	ASP	CA-CB-CG	5.60	118.20	112.60
6	C3	1739	GLU	N-CA-C	5.60	117.06	111.07
4	A5	374	HIS	CA-CB-CG	5.60	119.40	113.80
6	C2	1300	ASP	CA-CB-CG	5.59	118.19	112.60
7	D2	32	ARG	CD-NE-CZ	5.59	132.23	124.40
13	K0	613	ASP	CA-CB-CG	5.59	118.19	112.60
18	P1	387	LEU	N-CA-C	5.59	117.74	109.69
5	B0	1519	GLN	N-CA-C	5.59	122.70	110.80
6	C4	1159	ILE	O-C-N	-5.59	115.59	122.57
21	S2	284	HIS	CB-CG-CD2	-5.58	123.94	131.20
7	D0	32	ARG	CD-NE-CZ	5.58	132.22	124.40
21	S0	284	HIS	CB-CG-CD2	-5.58	123.94	131.20
4	A1	110	LEU	CA-C-N	5.58	128.08	120.54
4	A1	110	LEU	C-N-CA	5.58	128.08	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	L2	395	LEU	CA-C-N	5.58	129.16	120.68
14	L2	395	LEU	C-N-CA	5.58	129.16	120.68
9	F1	307	GLN	CA-C-N	5.58	128.60	120.51
9	F1	307	GLN	C-N-CA	5.58	128.60	120.51
5	B1	1518	VAL	N-CA-C	5.58	120.94	109.34
1	02	28	LYS	CA-C-N	5.58	126.17	119.98
1	02	28	LYS	C-N-CA	5.58	126.17	119.98
2	15	783	ARG	CD-NE-CZ	5.58	132.21	124.40
2	17	132	ASP	CA-CB-CG	5.58	118.17	112.60
24	V0	839	HIS	CB-CG-CD2	-5.57	123.95	131.20
1	02	83	TYR	CA-C-N	5.57	127.68	120.44
1	02	83	TYR	C-N-CA	5.57	127.68	120.44
2	13	132	ASP	CA-CB-CG	5.57	118.17	112.60
6	C4	356	ASP	CA-CB-CG	5.57	118.17	112.60
9	F0	306	ARG	N-CA-C	5.57	115.90	108.38
2	15	2	ALA	CA-C-N	5.57	131.72	121.70
2	15	2	ALA	C-N-CA	5.57	131.72	121.70
13	K1	861	SER	CA-C-N	5.57	128.20	120.63
13	K1	861	SER	C-N-CA	5.57	128.20	120.63
2	11	1695	GLN	OE1-CD-NE2	-5.56	117.04	122.60
4	A2	556	ASP	CA-CB-CG	5.56	118.16	112.60
13	K1	833	ASP	CA-CB-CG	5.56	118.16	112.60
6	C3	709	GLN	OE1-CD-NE2	-5.56	117.04	122.60
4	A5	97	ASP	CA-CB-CG	5.56	118.16	112.60
7	D5	211	ASP	CA-CB-CG	5.56	118.16	112.60
25	W0	604	ASP	CA-CB-CG	5.56	118.16	112.60
8	E0	322	ASN	CB-CA-C	5.56	115.84	111.00
16	N3	294	ASP	CA-CB-CG	5.56	118.16	112.60
18	P1	616	GLU	N-CA-C	5.56	119.35	112.24
10	H0	388	GLN	OE1-CD-NE2	-5.55	117.05	122.60
4	A0	248	VAL	CA-C-N	5.55	127.66	120.44
4	A0	248	VAL	C-N-CA	5.55	127.66	120.44
20	R2	944	ASP	CA-C-N	5.55	129.97	120.71
20	R2	944	ASP	C-N-CA	5.55	129.97	120.71
22	T0	881	THR	CA-C-N	5.55	128.35	120.53
22	T0	881	THR	C-N-CA	5.55	128.35	120.53
6	C3	782	ASP	CA-CB-CG	5.54	118.14	112.60
22	T0	683	ILE	N-CA-C	5.54	112.14	106.21
22	T1	377	ASP	CA-CB-CG	5.54	118.14	112.60
15	M2	901	ARG	CD-NE-CZ	5.54	132.15	124.40
4	A3	110	LEU	CA-C-N	5.53	128.01	120.54
4	A3	110	LEU	C-N-CA	5.53	128.01	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	M1	614	HIS	CB-CG-CD2	-5.53	124.01	131.20
1	O2	125	PHE	CA-CB-CG	5.53	119.33	113.80
17	O2	273	GLN	OE1-CD-NE2	-5.53	117.07	122.60
4	A1	447	ASP	CA-CB-CG	5.53	118.13	112.60
10	H3	470	GLN	OE1-CD-NE2	-5.53	117.07	122.60
13	K0	110	ASP	CA-C-N	5.53	132.10	121.54
13	K0	110	ASP	C-N-CA	5.53	132.10	121.54
18	P3	254	LEU	CA-C-N	5.53	127.95	120.65
18	P3	254	LEU	C-N-CA	5.53	127.95	120.65
2	I2	1657	HIS	CB-CG-CD2	-5.53	124.02	131.20
6	C1	1317	ASP	CA-CB-CG	5.53	118.13	112.60
6	C2	1981	ASP	CA-CB-CG	5.53	118.12	112.60
5	B0	1537	ALA	CA-C-N	5.52	128.23	120.28
5	B0	1537	ALA	C-N-CA	5.52	128.23	120.28
18	P2	254	LEU	CA-C-N	5.52	127.94	120.65
18	P2	254	LEU	C-N-CA	5.52	127.94	120.65
6	C3	959	ASP	CA-CB-CG	5.52	118.12	112.60
18	P2	221	ASP	CA-CB-CG	5.52	118.12	112.60
7	D5	1347	ARG	N-CA-CB	-5.52	102.11	111.27
6	C0	503	ASP	CA-CB-CG	5.52	118.12	112.60
6	C0	1600	PHE	CA-CB-CG	5.52	119.32	113.80
13	K1	983	PHE	CA-CB-CG	5.52	119.32	113.80
15	M1	503	HIS	CB-CG-CD2	-5.52	124.03	131.20
15	M2	860	ASP	CA-CB-CG	5.51	118.11	112.60
5	B1	1537	ALA	CA-C-N	5.51	128.22	120.28
5	B1	1537	ALA	C-N-CA	5.51	128.22	120.28
20	R3	1055	TYR	CB-CA-C	5.51	118.71	109.89
25	W0	624	ASP	CA-CB-CG	5.51	118.11	112.60
1	O1	84	ARG	NE-CZ-NH2	5.51	124.16	119.20
6	C0	78	GLN	OE1-CD-NE2	-5.51	117.09	122.60
7	D4	211	ASP	CA-CB-CG	5.51	118.11	112.60
4	A6	780	ASP	CA-CB-CG	5.50	118.11	112.60
14	L1	302	HIS	CB-CG-CD2	-5.50	124.04	131.20
15	M3	586	PRO	N-CA-C	5.50	123.81	112.47
6	C4	450	TYR	CA-C-N	5.50	129.49	120.63
6	C4	450	TYR	C-N-CA	5.50	129.49	120.63
16	N2	246	ASP	CA-CB-CG	5.50	118.10	112.60
22	T1	843	HIS	CB-CG-CD2	-5.50	124.05	131.20
6	C3	939	HIS	CB-CG-CD2	-5.50	124.06	131.20
4	A4	157	ASP	CA-CB-CG	5.50	118.09	112.60
7	D2	1269	GLN	OE1-CD-NE2	-5.50	117.11	122.60
7	D5	545	ASP	CA-CB-CG	5.50	118.09	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	17	1003	ASP	CA-CB-CG	5.49	118.09	112.60
5	B1	570	ASP	CA-CB-CG	5.49	118.09	112.60
6	C4	503	ASP	CA-CB-CG	5.49	118.09	112.60
6	C1	78	GLN	OE1-CD-NE2	-5.49	117.11	122.60
9	F1	96	ASP	CA-CB-CG	5.49	118.09	112.60
2	16	1695	GLN	OE1-CD-NE2	-5.49	117.11	122.60
14	L3	728	GLU	N-CA-CB	5.48	120.09	110.27
6	C0	1317	ASP	CA-CB-CG	5.48	118.08	112.60
6	C1	1012	LYS	CA-C-N	5.48	129.96	122.07
6	C1	1012	LYS	C-N-CA	5.48	129.96	122.07
15	M3	745	HIS	CB-CG-CD2	-5.48	124.07	131.20
1	04	125	PHE	CA-CB-CG	5.48	119.28	113.80
13	K2	110	ASP	CA-C-N	5.48	132.00	121.54
13	K2	110	ASP	C-N-CA	5.48	132.00	121.54
22	T1	413	PRO	CA-C-N	5.48	128.07	120.29
22	T1	413	PRO	C-N-CA	5.48	128.07	120.29
4	A4	175	ARG	NE-CZ-NH1	5.48	126.98	121.50
18	P0	626	ASP	CA-CB-CG	5.48	118.08	112.60
5	B1	1223	ASP	CA-CB-CG	5.47	118.07	112.60
10	H2	147	PHE	CA-CB-CG	5.47	119.27	113.80
6	C3	803	PHE	CA-CB-CG	5.47	119.27	113.80
10	H3	443	HIS	CB-CG-CD2	-5.47	124.09	131.20
2	10	1793	GLY	O-C-N	-5.47	116.30	121.77
24	V0	846	GLN	OE1-CD-NE2	-5.47	117.13	122.60
2	16	1003	ASP	CA-CB-CG	5.47	118.07	112.60
4	A3	706	HIS	CA-C-N	5.47	131.81	121.97
4	A3	706	HIS	C-N-CA	5.47	131.81	121.97
17	O1	308	ASN	CA-CB-CG	5.47	118.07	112.60
18	P2	616	GLU	N-CA-C	5.47	119.12	111.74
15	M2	331	ASP	CA-CB-CG	5.46	118.06	112.60
17	O3	34	GLN	OE1-CD-NE2	-5.46	117.14	122.60
23	U2	610	LEU	CA-CB-CG	-5.46	97.19	116.30
6	C2	782	ASP	CA-CB-CG	5.46	118.06	112.60
19	Q1	273	ASN	CA-CB-CG	5.46	118.06	112.60
3	40	22	ASN	CA-CB-CG	5.46	118.06	112.60
7	D2	506	GLN	OE1-CD-NE2	-5.46	117.14	122.60
12	J3	339	LYS	CG-CD-CE	-5.46	98.75	111.30
7	D4	545	ASP	CA-CB-CG	5.46	118.06	112.60
18	P0	616	GLU	N-CA-C	5.46	119.10	111.74
7	D3	1113	GLN	OE1-CD-NE2	-5.45	117.15	122.60
5	B1	1177	VAL	CA-C-O	5.45	123.70	118.90
7	D5	1083	ARG	CD-NE-CZ	5.45	132.03	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	J1	339	LYS	CG-CD-CE	-5.45	98.77	111.30
6	C3	22	HIS	CB-CG-CD2	-5.45	124.12	131.20
5	B1	1526	SER	N-CA-C	5.44	122.40	110.80
23	U3	609	ASN	CA-C-N	-5.44	113.46	120.65
23	U3	609	ASN	C-N-CA	-5.44	113.46	120.65
4	A3	99	GLN	CA-C-N	5.44	126.02	119.98
4	A3	99	GLN	C-N-CA	5.44	126.02	119.98
18	P3	387	LEU	N-CA-C	5.44	117.53	109.69
22	T1	683	ILE	N-CA-C	5.44	112.03	106.21
2	14	688	ASP	CA-CB-CG	5.44	118.04	112.60
7	D4	276	ASP	CA-CB-CG	5.44	118.04	112.60
9	F0	134	GLN	CA-C-N	5.44	127.57	120.28
9	F0	134	GLN	C-N-CA	5.44	127.57	120.28
2	16	713	GLN	OE1-CD-NE2	-5.44	117.16	122.60
7	D2	1073	ASN	CA-C-N	5.44	127.83	120.38
7	D2	1073	ASN	C-N-CA	5.44	127.83	120.38
18	P3	616	GLU	N-CA-C	5.44	119.13	111.52
2	17	1695	GLN	OE1-CD-NE2	-5.44	117.16	122.60
4	A2	248	VAL	CA-C-N	5.44	127.83	120.44
4	A2	248	VAL	C-N-CA	5.44	127.83	120.44
13	K0	241	HIS	CB-CG-CD2	-5.44	124.13	131.20
17	O0	308	ASN	CA-CB-CG	5.44	118.04	112.60
2	10	1695	GLN	OE1-CD-NE2	-5.43	117.17	122.60
6	C1	503	ASP	CA-CB-CG	5.43	118.03	112.60
6	C3	345	ASP	CA-CB-CG	5.43	118.03	112.60
7	D3	1269	GLN	OE1-CD-NE2	-5.43	117.17	122.60
13	K3	819	GLN	OE1-CD-NE2	-5.43	117.17	122.60
2	12	1695	GLN	OE1-CD-NE2	-5.43	117.17	122.60
10	H3	415	ASP	CA-CB-CG	5.43	118.03	112.60
6	C3	681	GLN	CA-C-N	5.43	128.00	120.29
6	C3	681	GLN	C-N-CA	5.43	128.00	120.29
4	A5	188	GLN	OE1-CD-NE2	-5.43	117.17	122.60
4	A0	188	GLN	OE1-CD-NE2	-5.42	117.17	122.60
6	C3	1653	SER	N-CA-C	5.42	117.62	111.11
20	R0	805	THR	N-CA-C	5.42	117.18	107.80
6	C1	566	HIS	CB-CG-CD2	-5.42	124.15	131.20
6	C3	1793	ASP	CA-CB-CG	5.42	118.02	112.60
2	11	353	HIS	CB-CG-CD2	-5.42	124.15	131.20
10	H0	357	ASP	CA-CB-CG	5.42	118.02	112.60
2	15	353	HIS	CB-CG-CD2	-5.42	124.16	131.20
4	A0	73	HIS	CB-CG-CD2	-5.42	124.16	131.20
7	D4	1113	GLN	OE1-CD-NE2	-5.42	117.19	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	12	117	HIS	CB-CG-CD2	-5.41	124.16	131.20
7	D5	276	ASP	CA-CB-CG	5.41	118.01	112.60
17	O3	273	GLN	OE1-CD-NE2	-5.41	117.19	122.60
15	M3	586	PRO	CA-C-N	5.41	131.44	121.70
15	M3	586	PRO	C-N-CA	5.41	131.44	121.70
2	12	353	HIS	CB-CG-CD2	-5.41	124.17	131.20
2	15	688	ASP	CA-CB-CG	5.41	118.01	112.60
5	B0	1177	VAL	CA-C-O	5.41	123.83	119.29
5	B0	1520	ARG	N-CA-C	5.41	121.77	109.81
10	H1	468	LYS	CG-CD-CE	-5.41	98.86	111.30
20	R1	365	ARG	CD-NE-CZ	5.41	131.97	124.40
2	10	353	HIS	CB-CG-CD2	-5.41	124.17	131.20
2	12	1788	ASP	CA-CB-CG	-5.41	107.19	112.60
7	D5	771	GLN	OE1-CD-NE2	-5.41	117.19	122.60
24	V0	923	THR	CA-CB-CG2	5.41	119.69	110.50
6	C0	566	HIS	CB-CG-CD2	-5.40	124.17	131.20
11	I1	379	HIS	CB-CG-CD2	-5.40	124.17	131.20
1	04	410	ASP	CA-CB-CG	5.40	118.00	112.60
14	L2	587	ASN	N-CA-C	5.40	122.30	110.80
2	11	1414	ASP	CA-CB-CG	5.40	118.00	112.60
1	02	396	LYS	CA-C-N	5.40	127.95	120.29
1	02	396	LYS	C-N-CA	5.40	127.95	120.29
15	M0	584	CYS	CA-C-N	5.40	131.42	121.70
15	M0	584	CYS	C-N-CA	5.40	131.42	121.70
17	O0	34	GLN	OE1-CD-NE2	-5.40	117.20	122.60
7	D3	1009	ASN	OD1-CG-ND2	-5.40	117.20	122.60
4	A3	248	VAL	CA-C-N	5.39	127.78	120.44
4	A3	248	VAL	C-N-CA	5.39	127.78	120.44
20	R1	1414	ASP	CA-CB-CG	5.39	118.00	112.60
20	R3	944	ASP	CA-C-N	5.39	129.72	120.71
20	R3	944	ASP	C-N-CA	5.39	129.72	120.71
1	00	410	ASP	CA-CB-CG	5.39	117.99	112.60
1	03	251	ASP	CA-C-N	5.39	127.46	120.56
1	03	251	ASP	C-N-CA	5.39	127.46	120.56
2	10	117	HIS	CB-CG-CD2	-5.39	124.19	131.20
2	17	117	HIS	CB-CG-CD2	-5.39	124.19	131.20
18	P0	619	THR	CA-C-N	5.39	131.83	121.54
18	P0	619	THR	C-N-CA	5.39	131.83	121.54
25	W0	224	LEU	CA-C-N	5.39	130.97	122.78
25	W0	224	LEU	C-N-CA	5.39	130.97	122.78
2	16	353	HIS	CB-CG-CD2	-5.39	124.19	131.20
14	L3	302	HIS	CB-CG-CD2	-5.39	124.20	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A1	248	VAL	CA-C-N	5.39	127.77	120.44
4	A1	248	VAL	C-N-CA	5.39	127.77	120.44
7	D0	1311	ASP	CA-CB-CG	5.39	117.99	112.60
19	Q2	190	ASN	N-CA-C	5.39	116.46	108.86
4	A0	99	GLN	OE1-CD-NE2	-5.38	117.22	122.60
14	L0	302	HIS	CB-CG-CD2	-5.38	124.20	131.20
6	C1	1191	PHE	CA-CB-CG	5.38	119.18	113.80
1	01	410	ASP	CA-CB-CG	5.38	117.98	112.60
10	H0	453	TYR	N-CA-C	5.38	116.89	110.44
17	O0	273	GLN	OE1-CD-NE2	-5.38	117.22	122.60
15	M0	834	ASN	CA-CB-CG	5.38	117.97	112.60
2	14	1633	GLN	OE1-CD-NE2	-5.37	117.23	122.60
20	R1	1052	GLU	N-CA-C	5.37	116.67	108.12
20	R2	834	HIS	CB-CG-CD2	-5.37	124.21	131.20
6	C0	1798	ASP	CA-CB-CG	5.37	117.97	112.60
15	M1	402	HIS	CB-CA-C	5.37	121.11	110.42
18	P1	617	SER	CA-C-N	5.37	131.37	121.70
18	P1	617	SER	C-N-CA	5.37	131.37	121.70
19	Q2	51	ASP	CA-CB-CG	-5.37	107.23	112.60
20	R0	1414	ASP	CA-CB-CG	5.37	117.97	112.60
2	16	117	HIS	CB-CG-CD2	-5.37	124.22	131.20
5	B1	1177	VAL	CA-C-N	5.36	129.80	120.68
5	B1	1177	VAL	C-N-CA	5.36	129.80	120.68
2	15	298	ARG	CD-NE-CZ	5.36	131.91	124.40
24	V0	796	HIS	CB-CG-CD2	-5.36	124.23	131.20
7	D3	994	SER	CA-C-N	5.36	123.62	120.24
7	D3	994	SER	C-N-CA	5.36	123.62	120.24
14	L1	199	LEU	CA-C-N	5.36	127.72	120.38
14	L1	199	LEU	C-N-CA	5.36	127.72	120.38
5	B1	1714	VAL	CA-C-N	5.36	126.44	120.06
5	B1	1714	VAL	C-N-CA	5.36	126.44	120.06
6	C2	1281	HIS	CA-CB-CG	5.36	119.16	113.80
7	D4	1391	HIS	CB-CG-CD2	-5.36	124.23	131.20
2	11	117	HIS	CB-CG-CD2	-5.36	124.24	131.20
15	M1	745	HIS	CB-CG-CD2	-5.36	124.24	131.20
2	17	353	HIS	CB-CG-CD2	-5.35	124.24	131.20
4	A0	491	HIS	CA-CB-CG	-5.35	108.45	113.80
5	B0	570	ASP	CA-CB-CG	5.35	117.95	112.60
2	14	117	HIS	CB-CG-CD2	-5.35	124.24	131.20
2	15	1695	GLN	OE1-CD-NE2	-5.35	117.25	122.60
7	D4	771	GLN	OE1-CD-NE2	-5.35	117.25	122.60
9	F2	259	SER	CB-CA-C	5.35	120.71	110.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B0	1169	GLN	OE1-CD-NE2	-5.35	117.25	122.60
15	M0	503	HIS	CB-CG-CD2	-5.35	124.25	131.20
2	15	117	HIS	CB-CG-CD2	-5.35	124.25	131.20
6	C0	1012	LYS	CA-C-N	5.35	129.81	122.06
6	C0	1012	LYS	C-N-CA	5.35	129.81	122.06
7	D0	1315	ASN	CA-C-N	5.35	127.44	120.28
7	D0	1315	ASN	C-N-CA	5.35	127.44	120.28
7	D3	1273	GLN	OE1-CD-NE2	-5.35	117.25	122.60
2	14	1657	HIS	CB-CG-CD2	-5.35	124.25	131.20
7	D2	1273	GLN	OE1-CD-NE2	-5.35	117.25	122.60
20	R0	544	HIS	CB-CG-CD2	-5.35	124.25	131.20
2	13	117	HIS	CB-CG-CD2	-5.34	124.25	131.20
17	O1	273	GLN	OE1-CD-NE2	-5.34	117.26	122.60
5	B0	1567	HIS	CB-CG-CD2	-5.34	124.25	131.20
4	A2	88	GLU	CB-CA-C	5.34	120.69	110.17
5	B0	1714	VAL	CA-C-N	5.34	126.42	120.06
5	B0	1714	VAL	C-N-CA	5.34	126.42	120.06
6	C2	438	ASP	CA-CB-CG	5.34	117.94	112.60
6	C4	1245	GLY	CA-C-N	5.34	127.75	120.54
6	C4	1245	GLY	C-N-CA	5.34	127.75	120.54
7	D1	1273	GLN	OE1-CD-NE2	-5.34	117.26	122.60
14	L2	302	HIS	CB-CG-CD2	-5.34	124.26	131.20
1	04	28	LYS	CA-C-N	5.34	125.91	119.98
1	04	28	LYS	C-N-CA	5.34	125.91	119.98
2	16	298	ARG	CD-NE-CZ	5.34	131.87	124.40
6	C3	1958	HIS	CB-CG-CD2	-5.34	124.26	131.20
6	C3	1825	ASP	CA-CB-CG	5.33	117.94	112.60
13	K3	145	PRO	N-CA-CB	5.33	105.99	103.22
5	B1	1519	GLN	N-CA-C	5.33	122.16	110.80
7	D3	1196	PHE	CA-CB-CG	5.33	119.13	113.80
22	T1	161	ASP	CA-CB-CG	5.33	117.93	112.60
1	02	410	ASP	CA-CB-CG	5.33	117.93	112.60
4	A3	757	PHE	CA-CB-CG	5.33	119.13	113.80
6	C4	416	GLU	CB-CG-CD	5.33	121.66	112.60
2	15	1657	HIS	CB-CG-CD2	-5.33	124.27	131.20
20	R3	834	HIS	CB-CG-CD2	-5.33	124.27	131.20
7	D0	1273	GLN	OE1-CD-NE2	-5.33	117.27	122.60
9	F1	212	HIS	CB-CG-CD2	-5.33	124.28	131.20
19	Q2	281	SER	N-CA-C	5.33	116.94	108.79
2	14	831	ASP	CA-CB-CG	5.32	117.92	112.60
20	R1	544	HIS	CB-CG-CD2	-5.32	124.28	131.20
14	L0	259	ARG	CD-NE-CZ	5.32	131.85	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	R3	805	THR	N-CA-C	5.32	117.01	107.80
5	B0	1523	SER	CA-C-N	5.32	131.28	121.70
5	B0	1523	SER	C-N-CA	5.32	131.28	121.70
6	C2	119	GLN	OE1-CD-NE2	-5.32	117.28	122.60
17	O2	34	GLN	OE1-CD-NE2	-5.32	117.28	122.60
2	17	508	ASP	CA-CB-CG	5.32	117.92	112.60
2	11	298	ARG	CD-NE-CZ	5.32	131.84	124.40
2	13	688	ASP	CA-CB-CG	5.32	117.92	112.60
2	13	1695	GLN	OE1-CD-NE2	-5.32	117.28	122.60
2	16	1633	GLN	OE1-CD-NE2	-5.32	117.28	122.60
4	A0	237	PRO	CA-C-N	5.32	129.85	120.87
4	A0	237	PRO	C-N-CA	5.32	129.85	120.87
10	H1	470	GLN	OE1-CD-NE2	-5.32	117.28	122.60
10	H3	493	HIS	CB-CG-CD2	-5.32	124.29	131.20
16	N0	246	ASP	CA-CB-CG	5.31	117.91	112.60
2	14	353	HIS	CB-CG-CD2	-5.31	124.30	131.20
7	D5	1273	GLN	OE1-CD-NE2	-5.31	117.29	122.60
15	M3	331	ASP	CA-CB-CG	5.31	117.91	112.60
20	R0	834	HIS	CB-CG-CD2	-5.31	124.30	131.20
1	03	262	PHE	CA-CB-CG	5.30	119.10	113.80
6	C4	412	ASN	CA-CB-CG	5.30	117.90	112.60
9	F3	96	ASP	CA-CB-CG	5.30	117.90	112.60
1	00	262	PHE	CA-CB-CG	5.30	119.10	113.80
7	D1	1073	ASN	CA-C-N	5.30	127.64	120.38
7	D1	1073	ASN	C-N-CA	5.30	127.64	120.38
5	B1	1567	HIS	CB-CG-CD2	-5.30	124.31	131.20
20	R2	1068	SER	N-CA-CB	-5.30	101.77	109.82
25	W0	358	ASP	CA-CB-CG	5.30	117.90	112.60
1	01	201	LEU	CA-C-N	5.30	127.33	120.44
1	01	201	LEU	C-N-CA	5.30	127.33	120.44
22	T1	30	LEU	N-CA-C	5.30	122.08	110.80
1	01	28	LYS	CA-C-N	5.29	125.86	119.98
1	01	28	LYS	C-N-CA	5.29	125.86	119.98
9	F3	212	HIS	CB-CG-CD2	-5.29	124.32	131.20
6	C1	1378	PRO	CA-C-N	5.29	123.52	119.66
6	C1	1378	PRO	C-N-CA	5.29	123.52	119.66
16	N1	114	HIS	CB-CG-CD2	-5.29	124.32	131.20
2	13	1414	ASP	CA-CB-CG	5.29	117.89	112.60
1	01	262	PHE	CA-CB-CG	5.29	119.09	113.80
7	D1	1269	GLN	OE1-CD-NE2	-5.29	117.31	122.60
2	12	699	SER	O-C-N	-5.29	116.93	123.33
5	B0	748	HIS	CB-CG-CD2	-5.29	124.33	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C2	1568	GLN	OE1-CD-NE2	-5.29	117.31	122.60
1	00	163	ASP	CA-CB-CG	5.28	117.88	112.60
7	D4	852	VAL	CA-C-N	5.28	127.89	120.28
7	D4	852	VAL	C-N-CA	5.28	127.89	120.28
15	M3	503	HIS	CB-CG-CD2	-5.28	124.33	131.20
20	R3	1414	ASP	CA-CB-CG	5.28	117.88	112.60
22	T1	998	ASP	CA-CB-CG	5.28	117.88	112.60
14	L3	729	GLU	O-C-N	-5.28	115.98	122.11
1	03	410	ASP	CA-CB-CG	5.28	117.88	112.60
5	B0	1517	ARG	N-CA-C	5.28	122.04	110.80
15	M3	573	PHE	CA-CB-CG	5.28	119.08	113.80
15	M1	834	ASN	CA-CB-CG	5.28	117.88	112.60
1	04	201	LEU	CA-C-N	5.27	127.29	120.44
1	04	201	LEU	C-N-CA	5.27	127.29	120.44
7	D4	1273	GLN	OE1-CD-NE2	-5.27	117.33	122.60
15	M2	503	HIS	CB-CG-CD2	-5.27	124.34	131.20
6	C3	1754	GLN	OE1-CD-NE2	-5.27	117.33	122.60
4	A4	97	ASP	CA-CB-CG	5.26	117.86	112.60
2	10	1414	ASP	CA-CB-CG	5.26	117.86	112.60
5	B1	1520	ARG	N-CA-C	5.26	121.44	109.81
13	K0	145	PRO	N-CA-CB	5.26	105.96	103.22
19	Q1	281	SER	N-CA-C	5.26	116.52	108.42
2	12	688	ASP	CA-CB-CG	5.26	117.86	112.60
10	H3	147	PHE	CA-CB-CG	5.26	119.06	113.80
18	P2	617	SER	CA-C-N	5.26	131.17	121.70
18	P2	617	SER	C-N-CA	5.26	131.17	121.70
4	A2	188	GLN	OE1-CD-NE2	-5.26	117.34	122.60
2	15	1694	ASP	CA-CB-CG	5.26	117.86	112.60
2	17	1633	GLN	OE1-CD-NE2	-5.26	117.34	122.60
4	A2	491	HIS	CA-CB-CG	-5.26	108.54	113.80
16	N3	114	HIS	CB-CG-CD2	-5.25	124.37	131.20
20	R1	834	HIS	CB-CG-CD2	-5.25	124.37	131.20
22	T1	305	GLN	OE1-CD-NE2	-5.25	117.34	122.60
2	10	688	ASP	CA-CB-CG	5.25	117.85	112.60
20	R3	544	HIS	CB-CG-CD2	-5.25	124.37	131.20
18	P3	388	GLN	OE1-CD-NE2	-5.25	117.35	122.60
1	03	663	ASN	OD1-CG-ND2	-5.25	117.35	122.60
5	B1	508	GLN	CA-C-N	5.25	131.56	121.54
5	B1	508	GLN	C-N-CA	5.25	131.56	121.54
6	C2	1191	PHE	CA-CB-CG	5.25	119.05	113.80
6	C2	1939	SER	N-CA-C	5.25	121.98	110.80
1	01	145	ASP	CA-C-N	5.25	125.76	119.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	01	145	ASP	C-N-CA	5.25	125.76	119.94
13	K0	466	ARG	CD-NE-CZ	5.25	131.75	124.40
13	K1	498	ASN	CA-CB-CG	5.25	117.85	112.60
14	L1	886	HIS	CB-CG-CD2	-5.25	124.38	131.20
15	M0	396	CYS	CA-C-N	5.25	127.62	120.54
15	M0	396	CYS	C-N-CA	5.25	127.62	120.54
24	V0	958	PRO	CA-C-N	5.25	128.25	122.22
24	V0	958	PRO	C-N-CA	5.25	128.25	122.22
2	10	783	ARG	NE-CZ-NH1	5.25	126.75	121.50
6	C2	1941	ALA	N-CA-C	5.24	118.36	111.28
6	C3	48	PRO	N-CA-CB	5.24	109.31	103.44
7	D4	357	GLN	OE1-CD-NE2	-5.24	117.36	122.60
9	F3	234	GLU	CB-CA-C	5.24	119.90	111.36
15	M1	331	ASP	CA-CB-CG	5.24	117.84	112.60
1	04	145	ASP	CA-C-N	5.24	125.76	119.94
1	04	145	ASP	C-N-CA	5.24	125.76	119.94
4	A1	677	GLN	OE1-CD-NE2	-5.24	117.36	122.60
4	A2	677	GLN	OE1-CD-NE2	-5.24	117.36	122.60
5	B1	1522	PRO	CA-N-CD	-5.24	104.16	111.50
15	M1	901	ARG	CD-NE-CZ	5.24	131.74	124.40
6	C2	356	ASP	CA-CB-CG	5.24	117.84	112.60
2	13	353	HIS	CB-CG-CD2	-5.24	124.39	131.20
5	B0	1118	ALA	CA-C-N	5.24	128.27	120.31
5	B0	1118	ALA	C-N-CA	5.24	128.27	120.31
14	L2	886	HIS	CB-CG-CD2	-5.24	124.39	131.20
6	C4	265	ASP	CA-CB-CG	5.23	117.83	112.60
20	R3	411	HIS	CB-CG-CD2	-5.23	124.39	131.20
5	B1	1169	GLN	OE1-CD-NE2	-5.23	117.37	122.60
10	H1	493	HIS	CB-CG-CD2	-5.23	124.40	131.20
4	A3	129	HIS	CA-C-N	5.23	127.29	120.28
4	A3	129	HIS	C-N-CA	5.23	127.29	120.28
7	D1	1168	HIS	CA-C-N	5.23	127.24	120.44
7	D1	1168	HIS	C-N-CA	5.23	127.24	120.44
10	H2	493	HIS	CB-CG-CD2	-5.23	124.40	131.20
20	R0	1290	ARG	NE-CZ-NH2	5.23	123.91	119.20
20	R2	805	THR	N-CA-C	5.23	116.85	107.80
20	R2	1414	ASP	CA-CB-CG	5.23	117.83	112.60
6	C4	1191	PHE	CA-CB-CG	5.23	119.03	113.80
11	I3	406	ILE	CA-C-N	5.23	127.29	120.28
11	I3	406	ILE	C-N-CA	5.23	127.29	120.28
12	J3	354	GLN	OE1-CD-NE2	-5.23	117.37	122.60
1	00	201	LEU	CA-C-N	5.23	127.24	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	00	201	LEU	C-N-CA	5.23	127.24	120.44
5	B1	1530	SER	CA-C-N	5.23	131.11	121.70
5	B1	1530	SER	C-N-CA	5.23	131.11	121.70
13	K0	599	HIS	CA-CB-CG	-5.23	108.57	113.80
13	K3	241	HIS	CB-CG-CD2	-5.23	124.41	131.20
15	M0	331	ASP	CA-CB-CG	5.22	117.82	112.60
19	Q2	377	HIS	CB-CG-CD2	-5.22	124.41	131.20
1	02	262	PHE	CA-CB-CG	5.22	119.02	113.80
6	C3	621	HIS	CB-CG-CD2	-5.22	124.41	131.20
4	A1	649	VAL	CA-C-N	5.22	125.44	120.43
4	A1	649	VAL	C-N-CA	5.22	125.44	120.43
14	L3	385	HIS	CB-CG-CD2	-5.22	124.41	131.20
2	15	508	ASP	CA-CB-CG	5.22	117.82	112.60
7	D0	863	CYS	CB-CA-C	5.22	120.45	110.17
4	A4	491	HIS	CA-CB-CG	-5.22	108.58	113.80
7	D4	915	ASN	CA-CB-CG	5.22	117.82	112.60
14	L3	886	HIS	CB-CG-CD2	-5.21	124.42	131.20
6	C2	78	GLN	OE1-CD-NE2	-5.21	117.39	122.60
13	K1	71	HIS	CB-CG-CD2	-5.21	124.42	131.20
20	R2	544	HIS	CB-CG-CD2	-5.21	124.42	131.20
7	D0	771	GLN	OE1-CD-NE2	-5.21	117.39	122.60
4	A3	447	ASP	CA-CB-CG	5.21	117.81	112.60
20	R1	1074	ASP	CA-C-N	5.21	128.93	120.60
20	R1	1074	ASP	C-N-CA	5.21	128.93	120.60
6	C2	465	CYS	N-CA-C	5.20	121.31	109.81
10	H3	348	GLN	OE1-CD-NE2	-5.20	117.40	122.60
13	K0	1090	ASP	CA-C-N	5.20	127.64	120.67
13	K0	1090	ASP	C-N-CA	5.20	127.64	120.67
2	14	1695	GLN	OE1-CD-NE2	-5.20	117.40	122.60
22	T1	743	ASP	CA-CB-CG	5.20	117.80	112.60
23	U4	610	LEU	CB-CG-CD1	-5.20	95.09	110.70
2	17	688	ASP	CA-CB-CG	5.20	117.80	112.60
7	D5	357	GLN	OE1-CD-NE2	-5.20	117.40	122.60
1	00	663	ASN	OD1-CG-ND2	-5.20	117.40	122.60
2	12	1694	ASP	CA-CB-CG	5.20	117.80	112.60
4	A4	140	VAL	N-CA-C	5.20	115.41	110.42
6	C2	265	ASP	CA-CB-CG	5.20	117.80	112.60
7	D5	1110	SER	CA-C-N	5.20	129.00	120.63
7	D5	1110	SER	C-N-CA	5.20	129.00	120.63
8	E0	570	HIS	CB-CG-CD2	-5.20	124.44	131.20
14	L1	259	ARG	CD-NE-CZ	5.20	131.68	124.40
18	P3	617	SER	CA-C-N	5.20	131.06	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	P3	617	SER	C-N-CA	5.20	131.06	121.70
13	K2	145	PRO	N-CA-CB	5.19	105.92	103.22
2	10	1196	GLN	OE1-CD-NE2	-5.19	117.41	122.60
4	A3	649	VAL	CA-C-N	5.19	125.42	120.43
4	A3	649	VAL	C-N-CA	5.19	125.42	120.43
10	H2	348	GLN	OE1-CD-NE2	-5.19	117.41	122.60
20	R3	530	LYS	N-CA-CB	-5.19	102.23	110.22
1	03	260	GLN	OE1-CD-NE2	-5.19	117.41	122.60
4	A0	488	HIS	CB-CG-CD2	-5.19	124.46	131.20
1	02	260	GLN	OE1-CD-NE2	-5.18	117.42	122.60
2	13	930	ALA	CA-C-N	5.18	129.49	120.68
2	13	930	ALA	C-N-CA	5.18	129.49	120.68
15	M2	919	ASP	CA-CB-CG	5.18	117.78	112.60
4	A5	757	PHE	CA-CB-CG	5.18	118.98	113.80
14	L3	727	CYS	CA-C-N	5.18	130.45	122.42
14	L3	727	CYS	C-N-CA	5.18	130.45	122.42
6	C2	1940	PHE	N-CA-C	5.18	121.84	110.80
1	02	663	ASN	OD1-CG-ND2	-5.18	117.42	122.60
2	10	832	ASP	CA-CB-CG	5.18	117.78	112.60
13	K0	845	ASP	CA-CB-CG	5.18	117.78	112.60
6	C4	119	GLN	OE1-CD-NE2	-5.18	117.42	122.60
15	M2	761	GLU	N-CA-C	5.18	119.18	112.86
2	14	744	PHE	CA-C-N	5.17	130.61	122.33
2	14	744	PHE	C-N-CA	5.17	130.61	122.33
10	H1	295	GLN	OE1-CD-NE2	-5.17	117.42	122.60
20	R2	411	HIS	CB-CG-CD2	-5.17	124.47	131.20
20	R2	530	LYS	N-CA-CB	-5.17	102.25	110.22
11	I0	409	ASN	CA-CB-CG	5.17	117.77	112.60
13	K1	110	ASP	CA-C-N	5.17	131.42	121.54
13	K1	110	ASP	C-N-CA	5.17	131.42	121.54
14	L2	902	GLN	OE1-CD-NE2	-5.17	117.43	122.60
20	R3	539	GLN	OE1-CD-NE2	-5.17	117.43	122.60
21	S2	76	ASP	CA-CB-CG	5.17	117.77	112.60
12	J1	468	SER	CA-C-N	5.17	128.22	120.83
12	J1	468	SER	C-N-CA	5.17	128.22	120.83
20	R2	477	GLN	OE1-CD-NE2	-5.17	117.43	122.60
1	02	145	ASP	CA-C-N	5.17	125.68	119.94
1	02	145	ASP	C-N-CA	5.17	125.68	119.94
5	B0	960	HIS	CB-CG-CD2	-5.17	124.48	131.20
6	C3	241	LEU	CA-C-N	5.17	126.07	120.44
6	C3	241	LEU	C-N-CA	5.17	126.07	120.44
10	H3	484	ASP	CA-CB-CG	5.17	117.77	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	L1	326	ASP	CA-CB-CG	5.17	117.77	112.60
25	W0	691	GLN	OE1-CD-NE2	-5.17	117.43	122.60
6	C3	1921	GLN	OE1-CD-NE2	-5.17	117.43	122.60
5	B1	748	HIS	CB-CG-CD2	-5.17	124.48	131.20
6	C3	1833	HIS	CB-CG-CD2	-5.17	124.48	131.20
15	M3	834	ASN	CA-CB-CG	5.17	117.77	112.60
2	15	1802	HIS	CB-CG-CD2	-5.16	124.49	131.20
5	B1	1518	VAL	CA-C-N	5.16	131.40	121.54
5	B1	1518	VAL	C-N-CA	5.16	131.40	121.54
10	H0	493	HIS	CB-CG-CD2	-5.16	124.49	131.20
14	L3	584	LYS	CA-C-N	5.16	131.40	121.54
14	L3	584	LYS	C-N-CA	5.16	131.40	121.54
19	Q3	190	ASN	N-CA-C	5.16	116.14	108.86
1	04	262	PHE	CA-CB-CG	5.16	118.96	113.80
15	M1	423	ARG	NE-CZ-NH2	5.16	123.84	119.20
15	M3	860	ASP	CA-CB-CG	5.16	117.76	112.60
4	A5	724	GLN	CA-C-N	5.16	127.91	120.38
4	A5	724	GLN	C-N-CA	5.16	127.91	120.38
5	B1	1525	ALA	N-CA-C	5.16	115.85	107.23
6	C4	438	ASP	CA-CB-CG	5.16	117.76	112.60
15	M0	656	ASN	CA-CB-CG	5.16	117.76	112.60
20	R0	944	ASP	CA-C-N	5.16	129.32	120.71
20	R0	944	ASP	C-N-CA	5.16	129.32	120.71
20	R1	944	ASP	CA-C-N	5.16	129.33	120.71
20	R1	944	ASP	C-N-CA	5.16	129.33	120.71
4	A5	374	HIS	CB-CG-CD2	-5.16	124.50	131.20
4	A6	677	GLN	OE1-CD-NE2	-5.16	117.44	122.60
7	D2	1311	ASP	CA-CB-CG	5.16	117.76	112.60
7	D2	1347	ARG	CD-NE-CZ	5.16	131.62	124.40
7	D3	863	CYS	N-CA-C	5.16	121.21	109.81
2	16	1414	ASP	CA-CB-CG	5.15	117.75	112.60
5	B0	799	ASP	CA-CB-CG	5.15	117.75	112.60
22	T1	554	GLN	OE1-CD-NE2	-5.15	117.45	122.60
6	C4	566	HIS	CB-CG-CD2	-5.15	124.50	131.20
20	R3	477	GLN	OE1-CD-NE2	-5.15	117.45	122.60
23	U1	609	ASN	CA-C-N	-5.15	114.44	122.73
23	U1	609	ASN	C-N-CA	-5.15	114.44	122.73
9	F3	150	LEU	CA-C-N	5.15	129.49	122.07
9	F3	150	LEU	C-N-CA	5.15	129.49	122.07
16	N2	302	ASP	CA-CB-CG	5.15	117.75	112.60
6	C1	1040	LEU	CA-C-N	5.15	127.60	120.29
6	C1	1040	LEU	C-N-CA	5.15	127.60	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C3	894	ASP	CA-CB-CG	5.15	117.75	112.60
6	C3	1723	GLY	CA-C-N	5.15	126.75	122.17
6	C3	1723	GLY	C-N-CA	5.15	126.75	122.17
7	D3	707	LEU	CA-C-N	5.15	127.13	120.44
7	D3	707	LEU	C-N-CA	5.15	127.13	120.44
11	I2	409	ASN	CA-CB-CG	5.15	117.75	112.60
20	R0	1007	HIS	CB-CG-CD2	-5.15	124.51	131.20
15	M3	609	ARG	NE-CZ-NH2	5.14	123.83	119.20
1	00	260	GLN	OE1-CD-NE2	-5.14	117.46	122.60
2	14	1410	ASP	CA-CB-CG	5.14	117.74	112.60
2	16	688	ASP	CA-CB-CG	5.14	117.74	112.60
2	16	1074	GLN	OE1-CD-NE2	-5.14	117.46	122.60
10	H0	348	GLN	OE1-CD-NE2	-5.14	117.46	122.60
23	U0	790	ASP	CA-CB-CG	5.14	117.74	112.60
2	13	745	VAL	N-CA-C	5.14	116.31	108.80
2	16	508	ASP	CA-CB-CG	5.14	117.74	112.60
8	E0	635	ARG	CD-NE-CZ	5.14	131.60	124.40
4	A6	142	GLN	OE1-CD-NE2	-5.14	117.46	122.60
10	H1	388	GLN	OE1-CD-NE2	-5.14	117.46	122.60
14	L0	914	GLN	OE1-CD-NE2	-5.14	117.46	122.60
1	01	260	GLN	OE1-CD-NE2	-5.14	117.46	122.60
7	D5	915	ASN	CA-CB-CG	5.14	117.74	112.60
7	D1	898	ARG	CG-CD-NE	5.14	123.30	112.00
13	K1	950	HIS	CB-CG-CD2	-5.14	124.52	131.20
14	L3	835	ASP	CA-CB-CG	5.14	117.74	112.60
16	N1	246	ASP	CA-CB-CG	5.14	117.74	112.60
5	B1	1517	ARG	N-CA-C	5.13	121.73	110.80
10	H3	388	GLN	OE1-CD-NE2	-5.13	117.47	122.60
13	K2	241	HIS	CB-CG-CD2	-5.13	124.53	131.20
14	L0	497	GLN	OE1-CD-NE2	-5.13	117.47	122.60
19	Q2	283	ASP	CA-CB-CG	5.13	117.73	112.60
20	R0	411	HIS	CB-CG-CD2	-5.13	124.53	131.20
20	R0	477	GLN	OE1-CD-NE2	-5.13	117.47	122.60
2	11	508	ASP	CA-CB-CG	5.13	117.73	112.60
15	M1	656	ASN	CA-CB-CG	5.13	117.73	112.60
2	16	1802	HIS	CB-CG-CD2	-5.13	124.53	131.20
6	C3	484	HIS	CB-CG-CD2	-5.13	124.53	131.20
25	W0	532	HIS	CB-CG-CD2	-5.13	124.53	131.20
2	12	1414	ASP	CA-CB-CG	5.13	117.73	112.60
10	H1	111	PRO	CA-N-CD	-5.13	104.82	112.00
20	R0	786	ASP	CA-CB-CG	5.13	117.73	112.60
20	R2	1154	PRO	CA-C-N	5.13	129.92	122.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	R2	1154	PRO	C-N-CA	5.13	129.92	122.28
11	I2	317	GLN	OE1-CD-NE2	-5.13	117.47	122.60
15	M3	656	ASN	CA-CB-CG	5.13	117.73	112.60
7	D5	1347	ARG	N-CA-C	5.12	120.66	113.02
22	T0	160	THR	N-CA-C	5.12	116.78	109.14
2	17	1802	HIS	CB-CG-CD2	-5.12	124.54	131.20
14	L0	886	HIS	CB-CG-CD2	-5.12	124.54	131.20
15	M3	901	ARG	CD-NE-CZ	5.12	131.57	124.40
20	R2	539	GLN	OE1-CD-NE2	-5.12	117.48	122.60
2	12	298	ARG	CD-NE-CZ	5.12	131.57	124.40
6	C3	290	GLU	CA-C-N	5.12	127.45	120.54
6	C3	290	GLU	C-N-CA	5.12	127.45	120.54
10	H2	286	THR	CA-C-N	5.12	128.12	120.90
10	H2	286	THR	C-N-CA	5.12	128.12	120.90
13	K1	599	HIS	CB-CG-CD2	-5.12	124.54	131.20
2	15	1074	GLN	OE1-CD-NE2	-5.12	117.48	122.60
12	J2	427	ASP	CA-CB-CG	5.12	117.72	112.60
13	K2	548	HIS	CB-CG-CD2	-5.12	124.54	131.20
16	N0	114	HIS	CB-CG-CD2	-5.12	124.54	131.20
1	O2	201	LEU	CA-C-N	5.12	127.09	120.44
1	O2	201	LEU	C-N-CA	5.12	127.09	120.44
2	10	713	GLN	OE1-CD-NE2	-5.12	117.48	122.60
5	B0	1518	VAL	CA-C-N	5.12	131.32	121.54
5	B0	1518	VAL	C-N-CA	5.12	131.32	121.54
5	B1	960	HIS	CB-CG-CD2	-5.12	124.55	131.20
7	D4	1269	GLN	OE1-CD-NE2	-5.12	117.48	122.60
7	D5	1269	GLN	OE1-CD-NE2	-5.12	117.48	122.60
10	H3	468	LYS	CG-CD-CE	-5.12	99.53	111.30
13	K2	552	ASP	CA-CB-CG	5.12	117.72	112.60
17	O1	206	THR	CA-C-N	5.12	129.39	122.07
17	O1	206	THR	C-N-CA	5.12	129.39	122.07
6	C3	1319	HIS	CA-CB-CG	5.12	118.92	113.80
2	12	713	GLN	OE1-CD-NE2	-5.11	117.49	122.60
10	H0	111	PRO	N-CA-CB	5.11	108.62	103.00
25	W0	130	GLY	N-CA-C	5.11	118.04	110.42
2	17	930	ALA	CA-C-N	5.11	129.37	120.68
2	17	930	ALA	C-N-CA	5.11	129.37	120.68
7	D2	803	PHE	CA-C-N	5.11	127.84	120.38
7	D2	803	PHE	C-N-CA	5.11	127.84	120.38
15	M3	423	ARG	NE-CZ-NH2	5.11	123.80	119.20
19	Q3	377	HIS	CB-CG-CD2	-5.11	124.55	131.20
22	T0	998	ASP	CA-CB-CG	5.11	117.71	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	10	930	ALA	CA-C-N	5.11	129.37	120.68
2	10	930	ALA	C-N-CA	5.11	129.37	120.68
4	A1	86	THR	CA-C-N	5.11	128.11	120.90
4	A1	86	THR	C-N-CA	5.11	128.11	120.90
6	C0	839	LYS	CG-CD-CE	-5.11	99.55	111.30
7	D5	812	LYS	CA-C-N	5.11	127.13	120.28
7	D5	812	LYS	C-N-CA	5.11	127.13	120.28
15	M3	574	GLN	OE1-CD-NE2	-5.11	117.49	122.60
22	T0	173	ASP	CA-CB-CG	5.11	117.71	112.60
16	N1	294	ASP	CA-CB-CG	5.11	117.71	112.60
1	01	663	ASN	OD1-CG-ND2	-5.11	117.49	122.60
13	K2	845	ASP	CA-CB-CG	5.11	117.71	112.60
5	B1	674	GLN	OE1-CD-NE2	-5.11	117.50	122.60
7	D1	1105	HIS	CB-CG-CD2	-5.11	124.56	131.20
7	D3	241	GLN	OE1-CD-NE2	-5.11	117.49	122.60
11	I0	317	GLN	OE1-CD-NE2	-5.11	117.49	122.60
2	12	930	ALA	CA-C-N	5.10	129.36	120.68
2	12	930	ALA	C-N-CA	5.10	129.36	120.68
4	A0	142	GLN	OE1-CD-NE2	-5.10	117.50	122.60
16	N2	169	ASP	CA-CB-CG	5.10	117.70	112.60
2	11	1196	GLN	OE1-CD-NE2	-5.10	117.50	122.60
2	14	298	ARG	CD-NE-CZ	5.10	131.54	124.40
5	B0	674	GLN	OE1-CD-NE2	-5.10	117.50	122.60
6	C1	265	ASP	CA-CB-CG	5.10	117.70	112.60
8	E0	348	GLU	CA-CB-CG	5.10	124.30	114.10
20	R1	1007	HIS	CB-CG-CD2	-5.10	124.57	131.20
24	V0	812	GLN	OE1-CD-NE2	-5.10	117.50	122.60
6	C1	839	LYS	CG-CD-CE	-5.10	99.57	111.30
20	R1	411	HIS	CB-CG-CD2	-5.10	124.57	131.20
4	A2	99	GLN	OE1-CD-NE2	-5.10	117.50	122.60
10	H1	348	GLN	OE1-CD-NE2	-5.10	117.50	122.60
16	N3	246	ASP	CA-CB-CG	5.10	117.70	112.60
1	00	145	ASP	CA-C-N	5.10	125.64	119.98
1	00	145	ASP	C-N-CA	5.10	125.64	119.98
2	14	578	HIS	CB-CG-CD2	-5.10	124.57	131.20
4	A6	581	ASP	CA-CB-CG	5.10	117.70	112.60
6	C3	1406	PHE	CA-CB-CG	5.10	118.90	113.80
2	14	930	ALA	CA-C-N	5.10	129.34	120.68
2	14	930	ALA	C-N-CA	5.10	129.34	120.68
6	C4	981	HIS	CB-CG-CD2	-5.09	124.58	131.20
7	D3	357	GLN	OE1-CD-NE2	-5.09	117.51	122.60
11	I1	406	ILE	CA-C-N	5.09	127.11	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	I1	406	ILE	C-N-CA	5.09	127.11	120.28
15	M0	915	ASP	CA-CB-CG	5.09	117.69	112.60
23	U5	609	ASN	OD1-CG-ND2	-5.09	117.50	122.60
20	R2	738	GLN	OE1-CD-NE2	-5.09	117.51	122.60
1	O4	260	GLN	OE1-CD-NE2	-5.09	117.51	122.60
7	D1	1328	HIS	CB-CG-CD2	-5.09	124.58	131.20
13	K3	110	ASP	CA-C-N	5.09	131.26	121.54
13	K3	110	ASP	C-N-CA	5.09	131.26	121.54
22	T1	173	ASP	CA-CB-CG	5.09	117.69	112.60
1	O3	201	LEU	CA-C-N	5.09	127.06	120.44
1	O3	201	LEU	C-N-CA	5.09	127.06	120.44
10	H2	470	GLN	OE1-CD-NE2	-5.09	117.51	122.60
14	L2	259	ARG	CD-NE-CZ	5.09	131.53	124.40
16	N2	235	SER	CA-C-N	5.09	128.74	120.60
16	N2	235	SER	C-N-CA	5.09	128.74	120.60
14	L3	259	ARG	CD-NE-CZ	5.09	131.52	124.40
6	C2	1856	GLN	OE1-CD-NE2	-5.09	117.51	122.60
7	D2	1328	HIS	CB-CG-CD2	-5.09	124.59	131.20
10	H2	388	GLN	OE1-CD-NE2	-5.09	117.51	122.60
15	M1	609	ARG	NE-CZ-NH2	5.08	123.78	119.20
2	10	508	ASP	CA-CB-CG	5.08	117.68	112.60
3	41	138	ASP	CA-CB-CG	5.08	117.68	112.60
6	C0	1112	GLN	OE1-CD-NE2	-5.08	117.52	122.60
7	D4	1083	ARG	CD-NE-CZ	5.08	131.52	124.40
22	T1	686	SER	N-CA-C	5.08	121.63	110.80
2	10	524	HIS	CB-CG-CD2	-5.08	124.59	131.20
4	A0	452	HIS	CB-CG-CD2	-5.08	124.59	131.20
17	O2	203	ASN	CA-C-N	5.08	127.34	120.38
17	O2	203	ASN	C-N-CA	5.08	127.34	120.38
4	A3	677	GLN	OE1-CD-NE2	-5.08	117.52	122.60
10	H3	396	GLN	OE1-CD-NE2	-5.08	117.52	122.60
12	J2	354	GLN	OE1-CD-NE2	-5.08	117.52	122.60
4	A0	264	GLN	OE1-CD-NE2	-5.08	117.52	122.60
6	C0	1848	PRO	CA-C-N	5.08	127.50	120.29
6	C0	1848	PRO	C-N-CA	5.08	127.50	120.29
15	M0	901	ARG	CD-NE-CZ	5.08	131.51	124.40
23	U2	609	ASN	OD1-CG-ND2	-5.08	117.52	122.60
5	B1	823	ASN	OD1-CG-ND2	-5.08	117.52	122.60
7	D0	491	GLN	OE1-CD-NE2	-5.08	117.52	122.60
11	I1	321	ASN	CA-CB-CG	5.08	117.68	112.60
7	D3	491	GLN	OE1-CD-NE2	-5.08	117.53	122.60
2	14	892	VAL	CA-C-N	5.07	130.21	120.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	14	892	VAL	C-N-CA	5.07	130.21	120.97
4	A2	142	GLN	OE1-CD-NE2	-5.07	117.53	122.60
5	B1	1515	ALA	N-CA-C	5.07	117.14	108.67
6	C1	1921	GLN	CA-C-N	5.07	127.33	120.38
6	C1	1921	GLN	C-N-CA	5.07	127.33	120.38
15	M2	574	GLN	OE1-CD-NE2	-5.07	117.53	122.60
18	P2	135	GLN	OE1-CD-NE2	-5.07	117.53	122.60
23	U1	609	ASN	OD1-CG-ND2	-5.07	117.53	122.60
1	O1	267	GLN	OE1-CD-NE2	-5.07	117.53	122.60
7	D1	491	GLN	OE1-CD-NE2	-5.07	117.53	122.60
7	D1	506	GLN	OE1-CD-NE2	-5.07	117.53	122.60
7	D3	1328	HIS	CB-CG-CD2	-5.07	124.61	131.20
8	E1	635	ARG	CD-NE-CZ	5.07	131.50	124.40
18	P0	554	ALA	CA-C-N	5.07	127.39	120.54
18	P0	554	ALA	C-N-CA	5.07	127.39	120.54
23	U6	609	ASN	OD1-CG-ND2	-5.07	117.53	122.60
4	A1	264	GLN	OE1-CD-NE2	-5.07	117.53	122.60
6	C1	1112	GLN	OE1-CD-NE2	-5.07	117.53	122.60
7	D2	491	GLN	OE1-CD-NE2	-5.07	117.53	122.60
12	J4	464	PRO	N-CA-CB	5.07	106.62	103.23
18	P2	390	HIS	CB-CG-CD2	-5.07	124.61	131.20
19	Q0	190	ASN	N-CA-C	5.07	116.00	108.86
22	T1	792	ASP	CA-CB-CG	5.07	117.67	112.60
3	40	400	HIS	CB-CG-CD2	-5.07	124.61	131.20
7	D5	1311	ASP	CA-CB-CG	5.06	117.66	112.60
10	H0	404	GLN	OE1-CD-NE2	-5.06	117.54	122.60
18	P0	61	VAL	CA-C-N	5.06	131.21	121.54
18	P0	61	VAL	C-N-CA	5.06	131.21	121.54
2	12	831	ASP	CA-CB-CG	5.06	117.66	112.60
2	13	1074	GLN	OE1-CD-NE2	-5.06	117.54	122.60
7	D0	1328	HIS	CB-CG-CD2	-5.06	124.62	131.20
7	D3	1138	GLY	CA-C-N	5.06	127.02	120.44
7	D3	1138	GLY	C-N-CA	5.06	127.02	120.44
7	D3	1311	ASP	CA-CB-CG	5.06	117.66	112.60
13	K0	932	HIS	CB-CG-CD2	-5.06	124.62	131.20
20	R1	805	THR	N-CA-C	5.06	117.03	108.02
20	R3	507	GLN	OE1-CD-NE2	-5.06	117.54	122.60
22	T0	207	GLN	OE1-CD-NE2	-5.06	117.54	122.60
1	O3	145	ASP	CA-C-N	5.06	125.56	119.94
1	O3	145	ASP	C-N-CA	5.06	125.56	119.94
6	C0	265	ASP	CA-CB-CG	5.06	117.66	112.60
7	D5	506	GLN	OE1-CD-NE2	-5.06	117.54	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	S2	158	GLN	OE1-CD-NE2	-5.06	117.54	122.60
4	A3	188	GLN	OE1-CD-NE2	-5.06	117.54	122.60
6	C2	1489	HIS	CB-CG-CD2	-5.06	124.62	131.20
13	K0	921	GLN	OE1-CD-NE2	-5.06	117.54	122.60
21	S2	260	SER	CA-C-N	5.06	127.77	120.38
21	S2	260	SER	C-N-CA	5.06	127.77	120.38
2	10	1074	GLN	OE1-CD-NE2	-5.06	117.54	122.60
2	10	1802	HIS	CB-CG-CD2	-5.06	124.62	131.20
2	16	264	GLN	OE1-CD-NE2	-5.06	117.54	122.60
7	D5	122	ASP	CA-CB-CG	5.06	117.66	112.60
7	D5	1391	HIS	CB-CG-CD2	-5.06	124.63	131.20
8	E1	570	HIS	CB-CG-CD2	-5.06	124.62	131.20
11	I1	317	GLN	OE1-CD-NE2	-5.06	117.54	122.60
2	10	298	ARG	CD-NE-CZ	5.06	131.48	124.40
2	13	578	HIS	CB-CG-CD2	-5.06	124.63	131.20
4	A3	28	HIS	CB-CG-CD2	-5.06	124.63	131.20
5	B1	525	ASP	CA-CB-CG	5.06	117.66	112.60
11	I3	321	ASN	CA-CB-CG	5.06	117.66	112.60
2	11	1074	GLN	OE1-CD-NE2	-5.05	117.55	122.60
5	B0	508	GLN	CA-C-N	5.05	131.19	121.54
5	B0	508	GLN	C-N-CA	5.05	131.19	121.54
5	B1	1122	HIS	CB-CG-CD2	-5.05	124.63	131.20
6	C2	544	ASN	CA-CB-CG	-5.05	107.55	112.60
13	K1	306	HIS	CB-CG-CD2	-5.05	124.63	131.20
19	Q3	281	SER	N-CA-C	5.05	116.52	108.79
2	13	1802	HIS	CB-CG-CD2	-5.05	124.63	131.20
2	14	1802	HIS	CB-CG-CD2	-5.05	124.63	131.20
7	D2	1315	ASN	CA-C-N	5.05	127.05	120.28
7	D2	1315	ASN	C-N-CA	5.05	127.05	120.28
2	10	1177	MET	N-CA-CB	-5.05	103.13	111.01
2	13	947	HIS	CB-CG-CD2	-5.05	124.63	131.20
4	A3	420	GLN	OE1-CD-NE2	-5.05	117.55	122.60
6	C2	500	GLN	OE1-CD-NE2	-5.05	117.55	122.60
20	R3	207	VAL	CA-C-O	-5.05	117.31	119.94
3	41	319	TRP	CB-CA-C	5.05	118.63	111.86
4	A1	188	GLN	OE1-CD-NE2	-5.05	117.55	122.60
7	D1	357	GLN	OE1-CD-NE2	-5.05	117.55	122.60
12	J1	354	GLN	OE1-CD-NE2	-5.05	117.55	122.60
3	41	400	HIS	CB-CG-CD2	-5.05	124.64	131.20
4	A2	593	ARG	CA-C-N	5.05	128.27	121.20
4	A2	593	ARG	C-N-CA	5.05	128.27	121.20
20	R0	1366	HIS	CA-C-N	5.05	127.75	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	R0	1366	HIS	C-N-CA	5.05	127.75	120.38
19	Q0	377	HIS	CB-CG-CD2	-5.05	124.64	131.20
2	12	524	HIS	CB-CG-CD2	-5.04	124.64	131.20
14	L1	332	LYS	CB-CA-C	5.04	119.17	111.80
1	04	663	ASN	OD1-CG-ND2	-5.04	117.56	122.60
2	15	800	ASP	CA-CB-CG	5.04	117.64	112.60
2	17	1074	GLN	OE1-CD-NE2	-5.04	117.56	122.60
3	40	21	HIS	CB-CG-CD2	-5.04	124.64	131.20
2	15	264	GLN	OE1-CD-NE2	-5.04	117.56	122.60
2	16	930	ALA	CA-C-N	5.04	129.25	120.68
2	16	930	ALA	C-N-CA	5.04	129.25	120.68
4	A2	236	THR	CA-CB-CG2	5.04	119.07	110.50
6	C2	619	CYS	O-C-N	5.04	128.47	122.27
10	H3	286	THR	CA-C-N	5.04	128.01	120.90
10	H3	286	THR	C-N-CA	5.04	128.01	120.90
14	L0	620	HIS	CB-CG-CD2	-5.04	124.65	131.20
20	R1	313	TYR	CA-C-N	5.04	127.31	120.65
20	R1	313	TYR	C-N-CA	5.04	127.31	120.65
20	R1	477	GLN	OE1-CD-NE2	-5.04	117.56	122.60
7	D0	707	LEU	CA-C-N	5.04	126.99	120.44
7	D0	707	LEU	C-N-CA	5.04	126.99	120.44
12	J0	354	GLN	OE1-CD-NE2	-5.04	117.56	122.60
6	C0	1191	PHE	CA-CB-CG	5.04	118.84	113.80
17	O1	102	HIS	CB-CG-CD2	-5.04	124.65	131.20
20	R3	1198	GLN	OE1-CD-NE2	-5.04	117.56	122.60
6	C0	1798	ASP	CA-C-N	5.04	128.00	120.90
6	C0	1798	ASP	C-N-CA	5.04	128.00	120.90
6	C1	1848	PRO	CA-C-N	5.04	127.44	120.29
6	C1	1848	PRO	C-N-CA	5.04	127.44	120.29
6	C3	884	GLN	OE1-CD-NE2	-5.04	117.56	122.60
15	M1	501	ASP	CA-CB-CG	5.04	117.64	112.60
7	D2	1196	PHE	CA-CB-CG	5.03	118.83	113.80
20	R0	313	TYR	CA-C-N	5.03	127.29	120.65
20	R0	313	TYR	C-N-CA	5.03	127.29	120.65
6	C0	238	GLN	OE1-CD-NE2	-5.03	117.57	122.60
7	D5	1355	ASP	CB-CA-C	-5.03	102.92	110.92
14	L1	902	GLN	OE1-CD-NE2	-5.03	117.57	122.60
2	11	930	ALA	CA-C-N	5.03	129.23	120.68
2	11	930	ALA	C-N-CA	5.03	129.23	120.68
2	12	1074	GLN	OE1-CD-NE2	-5.03	117.57	122.60
6	C0	1040	LEU	CA-C-N	5.03	127.43	120.29
6	C0	1040	LEU	C-N-CA	5.03	127.43	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C0	1723	GLY	CA-C-N	5.03	126.05	121.82
6	C0	1723	GLY	C-N-CA	5.03	126.05	121.82
20	R1	58	HIS	CB-CG-CD2	-5.03	124.66	131.20
21	S3	260	SER	CA-C-N	5.03	127.72	120.38
21	S3	260	SER	C-N-CA	5.03	127.72	120.38
6	C0	859	LYS	CA-C-N	5.03	126.98	120.44
6	C0	859	LYS	C-N-CA	5.03	126.98	120.44
4	A2	264	GLN	OE1-CD-NE2	-5.03	117.57	122.60
5	B1	799	ASP	CA-CB-CG	5.03	117.63	112.60
10	H1	111	PRO	N-CA-CB	5.03	108.53	103.00
13	K0	243	HIS	CB-CG-CD2	-5.03	124.67	131.20
13	K0	946	LEU	CA-C-N	5.03	127.02	120.28
13	K0	946	LEU	C-N-CA	5.03	127.02	120.28
20	R0	58	HIS	CB-CG-CD2	-5.03	124.67	131.20
21	S3	208	GLN	OE1-CD-NE2	-5.03	117.57	122.60
25	W0	731	GLN	OE1-CD-NE2	-5.03	117.57	122.60
2	11	264	GLN	OE1-CD-NE2	-5.03	117.57	122.60
6	C1	238	GLN	OE1-CD-NE2	-5.03	117.58	122.60
6	C3	1957	GLN	OE1-CD-NE2	-5.03	117.58	122.60
10	H2	111	PRO	N-CA-CB	5.03	108.53	103.00
1	03	267	GLN	OE1-CD-NE2	-5.02	117.58	122.60
2	14	700	SER	CA-C-N	5.02	131.31	122.42
2	14	700	SER	C-N-CA	5.02	131.31	122.42
7	D5	1112	GLN	OE1-CD-NE2	-5.02	117.58	122.60
13	K3	845	ASP	CA-CB-CG	5.02	117.62	112.60
1	00	267	GLN	OE1-CD-NE2	-5.02	117.58	122.60
5	B0	1122	HIS	CB-CG-CD2	-5.02	124.67	131.20
14	L0	902	GLN	OE1-CD-NE2	-5.02	117.58	122.60
14	L2	741	ASP	CA-CB-CG	5.02	117.62	112.60
2	14	893	GLU	N-CA-CB	-5.02	103.18	110.36
4	A4	677	GLN	OE1-CD-NE2	-5.02	117.58	122.60
21	S1	260	SER	CA-C-N	5.02	127.71	120.38
21	S1	260	SER	C-N-CA	5.02	127.71	120.38
7	D2	771	GLN	OE1-CD-NE2	-5.02	117.58	122.60
14	L1	471	THR	O-C-N	5.02	128.51	122.79
10	H1	396	GLN	OE1-CD-NE2	-5.02	117.58	122.60
10	H2	111	PRO	CA-N-CD	-5.02	104.98	112.00
17	O3	308	ASN	CA-CB-CG	5.02	117.62	112.60
18	P0	617	SER	O-C-N	-5.02	118.00	123.52
2	11	1217	ARG	CA-C-N	5.02	127.41	120.29
2	11	1217	ARG	C-N-CA	5.02	127.41	120.29
4	A3	488	HIS	CB-CG-CD2	-5.02	124.68	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A2	28	HIS	CB-CG-CD2	-5.01	124.68	131.20
4	A6	264	GLN	OE1-CD-NE2	-5.01	117.58	122.60
5	B0	313	PHE	CA-CB-CG	5.01	118.81	113.80
10	H3	111	PRO	CA-N-CD	-5.01	104.98	112.00
14	L3	732	MET	CA-C-N	5.01	131.12	121.54
14	L3	732	MET	C-N-CA	5.01	131.12	121.54
2	15	436	HIS	CB-CG-CD2	-5.01	124.68	131.20
13	K0	532	LYS	CA-C-N	5.01	129.63	122.21
13	K0	532	LYS	C-N-CA	5.01	129.63	122.21
4	A3	264	GLN	OE1-CD-NE2	-5.01	117.59	122.60
10	H3	393	GLN	OE1-CD-NE2	-5.01	117.59	122.60
19	Q1	377	HIS	CB-CG-CD2	-5.01	124.69	131.20
20	R0	529	CYS	CA-C-N	5.01	128.62	120.60
20	R0	529	CYS	C-N-CA	5.01	128.62	120.60
25	W0	741	PHE	CA-CB-CG	5.01	118.81	113.80
2	10	830	GLN	OE1-CD-NE2	-5.01	117.59	122.60
6	C0	981	HIS	CB-CG-CD2	-5.01	124.69	131.20
7	D1	1374	GLN	OE1-CD-NE2	-5.01	117.59	122.60
10	H1	286	THR	CA-C-N	5.01	128.21	121.05
10	H1	286	THR	C-N-CA	5.01	128.21	121.05
14	L0	844	HIS	CB-CG-CD2	-5.01	124.69	131.20
19	Q0	281	SER	N-CA-C	5.01	116.45	108.79
25	W0	322	ASN	CA-CB-CG	5.01	117.61	112.60
7	D1	122	ASP	CA-CB-CG	5.01	117.61	112.60
14	L1	617	GLN	OE1-CD-NE2	-5.01	117.59	122.60
2	16	832	ASP	CA-CB-CG	5.01	117.61	112.60
14	L1	914	GLN	OE1-CD-NE2	-5.01	117.59	122.60
18	P3	165	HIS	CB-CG-CD2	-5.01	124.69	131.20
20	R3	104	HIS	CB-CG-CD2	-5.01	124.69	131.20
15	M3	883	HIS	CB-CG-CD2	-5.00	124.69	131.20
17	O0	102	HIS	CB-CG-CD2	-5.00	124.69	131.20
2	13	626	HIS	CB-CG-CD2	-5.00	124.70	131.20
4	A1	706	HIS	CA-C-N	5.00	130.98	121.97
4	A1	706	HIS	C-N-CA	5.00	130.98	121.97
15	M0	883	HIS	CB-CG-CD2	-5.00	124.69	131.20
20	R1	539	GLN	OE1-CD-NE2	-5.00	117.60	122.60
6	C4	1737	ASN	N-CA-C	5.00	117.84	111.69
23	U0	793	HIS	CB-CG-CD2	-5.00	124.70	131.20

All (11) chirality outliers are listed below:

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Mol	Chain	Res	Type	Atom
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Mol	Chain	Res	Type	Atom
4	A0	156	LEU	CA
6	C0	174	THR	CB
6	C1	174	THR	CB
6	C2	174	THR	CB
6	C3	174	THR	CB
6	C4	174	THR	CB
18	P1	552	ARG	CA
22	T0	856	HIS	CA
22	T0	882	VAL	CA
22	T1	856	HIS	CA
22	T1	882	VAL	CA

All (728) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	00	132	TYR	Sidechain
1	00	175	TYR	Sidechain
1	00	193	ARG	Sidechain
1	00	375	THR	Peptide,Mainchain
1	00	710	TYR	Sidechain
1	01	132	TYR	Sidechain
1	01	193	ARG	Sidechain
1	01	710	TYR	Sidechain
1	02	132	TYR	Sidechain
1	02	161	ARG	Peptide
1	02	193	ARG	Sidechain
1	02	710	TYR	Sidechain
1	03	10	ARG	Sidechain
1	03	132	TYR	Sidechain
1	03	166	HIS	Sidechain
1	03	193	ARG	Sidechain
1	03	710	TYR	Sidechain
1	04	161	ARG	Peptide
1	04	165	VAL	Peptide
1	04	193	ARG	Sidechain
1	04	710	TYR	Sidechain
2	10	1176	ILE	Mainchain
2	10	1180	ARG	Sidechain
2	10	1537	TYR	Sidechain
2	10	1788	ASP	Peptide
2	10	236	ARG	Sidechain

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Mol	Chain	Res	Type	Group
2	10	24	ALA	Peptide
2	10	334	ARG	Sidechain
2	10	42	ARG	Sidechain
2	10	5	GLY	Mainchain
2	10	644	LYS	Peptide
2	10	698	HIS	Peptide
2	11	1176	ILE	Mainchain
2	11	1180	ARG	Sidechain
2	11	1537	TYR	Sidechain
2	11	1786	VAL	Peptide
2	11	236	ARG	Sidechain
2	11	24	ALA	Peptide
2	11	334	ARG	Sidechain
2	11	42	ARG	Sidechain
2	11	472	TYR	Sidechain
2	11	5	GLY	Mainchain
2	11	698	HIS	Peptide
2	11	742	VAL	Peptide
2	11	743	LYS	Peptide
2	12	1178	ARG	Sidechain
2	12	1180	ARG	Sidechain
2	12	1537	TYR	Sidechain
2	12	1789	ARG	Sidechain
2	12	236	ARG	Sidechain
2	12	24	ALA	Peptide
2	12	334	ARG	Sidechain
2	12	42	ARG	Sidechain
2	12	5	GLY	Mainchain
2	12	698	HIS	Peptide
2	13	1165	LEU	Peptide
2	13	1180	ARG	Sidechain
2	13	1537	TYR	Sidechain
2	13	1788	ASP	Peptide
2	13	1789	ARG	Peptide
2	13	236	ARG	Sidechain
2	13	24	ALA	Peptide
2	13	334	ARG	Sidechain
2	13	42	ARG	Sidechain
2	13	5	GLY	Mainchain
2	13	644	LYS	Peptide
2	13	669	ARG	Sidechain
2	13	698	HIS	Peptide

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Mol	Chain	Res	Type	Group
2	14	1180	ARG	Sidechain
2	14	1537	TYR	Sidechain
2	14	1556	ARG	Sidechain
2	14	1584	ARG	Sidechain
2	14	236	ARG	Sidechain
2	14	24	ALA	Peptide
2	14	334	ARG	Sidechain
2	14	42	ARG	Sidechain
2	14	5	GLY	Mainchain
2	14	698	HIS	Peptide
2	14	746	CYS	Peptide
2	15	1180	ARG	Sidechain
2	15	1537	TYR	Sidechain
2	15	1556	ARG	Sidechain
2	15	1584	ARG	Sidechain
2	15	236	ARG	Sidechain
2	15	24	ALA	Peptide
2	15	334	ARG	Sidechain
2	15	42	ARG	Sidechain
2	15	472	TYR	Sidechain
2	15	5	GLY	Mainchain
2	15	698	HIS	Peptide
2	15	746	CYS	Peptide
2	15	747	ALA	Peptide
2	16	1180	ARG	Sidechain
2	16	1537	TYR	Sidechain
2	16	1584	ARG	Sidechain
2	16	236	ARG	Sidechain
2	16	24	ALA	Peptide
2	16	334	ARG	Sidechain
2	16	42	ARG	Sidechain
2	16	472	TYR	Sidechain
2	16	5	GLY	Mainchain
2	16	698	HIS	Peptide
2	17	1180	ARG	Sidechain
2	17	1537	TYR	Sidechain
2	17	1556	ARG	Sidechain
2	17	1584	ARG	Sidechain
2	17	1688	SER	Peptide
2	17	236	ARG	Sidechain
2	17	24	ALA	Peptide
2	17	252	TYR	Sidechain

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Mol	Chain	Res	Type	Group
2	17	334	ARG	Sidechain
2	17	42	ARG	Sidechain
2	17	5	GLY	Mainchain
2	17	644	LYS	Peptide
2	17	698	HIS	Peptide
3	40	206	ALA	Peptide
3	40	286	ARG	Peptide
3	40	30	SER	Peptide
3	40	392	GLU	Peptide
3	41	206	ALA	Peptide
3	41	272	TRP	Peptide
3	41	286	ARG	Peptide,Sidechain
3	41	30	SER	Peptide
3	41	392	GLU	Peptide
4	A0	118	ARG	Sidechain
4	A0	128	TYR	Sidechain
4	A0	154	ASP	Peptide
4	A0	156	LEU	Peptide
4	A0	166	TYR	Sidechain
4	A0	175	ARG	Peptide
4	A0	340	ARG	Sidechain
4	A0	362	ARG	Sidechain
4	A0	396	ARG	Sidechain
4	A0	486	ARG	Sidechain
4	A0	525	ARG	Sidechain
4	A0	545	ARG	Sidechain
4	A0	555	ARG	Sidechain
4	A0	706	HIS	Peptide
4	A0	709	ARG	Sidechain
4	A0	716	ARG	Sidechain
4	A0	730	ARG	Sidechain
4	A0	77	ARG	Sidechain
4	A0	773	ARG	Peptide
4	A0	781	ARG	Sidechain
4	A0	790	ARG	Sidechain
4	A0	88	GLU	Peptide
4	A0	91	GLU	Peptide
4	A1	155	ALA	Peptide
4	A1	165	SER	Peptide
4	A1	190	TYR	Sidechain
4	A1	269	TYR	Sidechain
4	A1	340	ARG	Sidechain

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Mol	Chain	Res	Type	Group
4	A1	362	ARG	Sidechain
4	A1	486	ARG	Sidechain
4	A1	525	ARG	Sidechain
4	A1	545	ARG	Sidechain
4	A1	555	ARG	Sidechain
4	A1	716	ARG	Sidechain
4	A1	730	ARG	Sidechain
4	A1	767	SER	Peptide
4	A1	781	ARG	Sidechain
4	A1	790	ARG	Sidechain
4	A1	802	ARG	Peptide
4	A2	118	ARG	Sidechain
4	A2	128	TYR	Sidechain
4	A2	157	ASP	Peptide
4	A2	158	PHE	Peptide
4	A2	269	TYR	Sidechain
4	A2	340	ARG	Sidechain
4	A2	362	ARG	Sidechain
4	A2	525	ARG	Sidechain
4	A2	545	ARG	Sidechain
4	A2	555	ARG	Sidechain
4	A2	706	HIS	Peptide
4	A2	709	ARG	Sidechain
4	A2	716	ARG	Sidechain
4	A2	730	ARG	Sidechain
4	A2	77	ARG	Sidechain
4	A2	781	ARG	Sidechain
4	A2	802	ARG	Peptide
4	A3	159	THR	Peptide
4	A3	175	ARG	Peptide
4	A3	269	TYR	Sidechain
4	A3	340	ARG	Sidechain
4	A3	362	ARG	Sidechain
4	A3	486	ARG	Sidechain
4	A3	525	ARG	Sidechain
4	A3	545	ARG	Sidechain
4	A3	555	ARG	Sidechain
4	A3	716	ARG	Sidechain
4	A3	730	ARG	Sidechain
4	A3	781	ARG	Sidechain
4	A3	786	ARG	Sidechain
4	A3	91	GLU	Peptide

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Mol	Chain	Res	Type	Group
4	A4	128	TYR	Sidechain
4	A4	175	ARG	Peptide
4	A4	340	ARG	Sidechain
4	A4	362	ARG	Sidechain
4	A4	380	ARG	Sidechain
4	A4	486	ARG	Sidechain
4	A4	555	ARG	Sidechain
4	A4	706	HIS	Peptide
4	A4	730	ARG	Sidechain
4	A5	118	ARG	Sidechain
4	A5	128	TYR	Sidechain
4	A5	323	TYR	Sidechain
4	A5	355	TYR	Sidechain
4	A5	362	ARG	Sidechain
4	A5	377	ARG	Sidechain
4	A5	380	ARG	Sidechain
4	A5	486	ARG	Sidechain
4	A5	730	ARG	Sidechain
4	A6	118	ARG	Sidechain
4	A6	362	ARG	Sidechain
4	A6	380	ARG	Sidechain
4	A6	486	ARG	Sidechain
4	A6	555	ARG	Sidechain
4	A6	730	ARG	Sidechain
5	B0	1048	TYR	Sidechain
5	B0	11	ARG	Sidechain
5	B0	1168	ARG	Sidechain
5	B0	1257	SER	Peptide
5	B0	1398	ARG	Sidechain
5	B0	1507	GLY	Peptide
5	B0	1508	ASP	Peptide
5	B0	1516	GLN	Peptide
5	B0	1517	ARG	Peptide,Mainchain
5	B0	1519	GLN	Peptide
5	B0	1522	PRO	Peptide
5	B0	1525	ALA	Peptide
5	B0	1528	ALA	Peptide
5	B0	1586	TYR	Sidechain
5	B0	1599	PHE	Peptide
5	B0	1682	ARG	Sidechain
5	B0	1731	GLU	Peptide
5	B0	209	ARG	Sidechain

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Mol	Chain	Res	Type	Group
5	B0	224	TYR	Sidechain
5	B0	267	TYR	Sidechain
5	B0	368	GLY	Peptide
5	B0	452	ARG	Sidechain
5	B0	496	ARG	Sidechain
5	B0	526	ARG	Sidechain
5	B0	624	ARG	Sidechain
5	B0	877	ARG	Sidechain
5	B0	989	HIS	Sidechain
5	B1	1048	TYR	Sidechain
5	B1	1168	ARG	Sidechain
5	B1	1398	ARG	Sidechain
5	B1	1507	GLY	Peptide
5	B1	1508	ASP	Peptide
5	B1	1516	GLN	Peptide
5	B1	1517	ARG	Peptide,Mainchain
5	B1	1519	GLN	Peptide,Mainchain
5	B1	1522	PRO	Peptide
5	B1	1526	SER	Peptide
5	B1	1586	TYR	Sidechain
5	B1	1599	PHE	Peptide
5	B1	1660	TYR	Sidechain
5	B1	1682	ARG	Sidechain
5	B1	1748	GLN	Peptide
5	B1	224	TYR	Sidechain
5	B1	267	TYR	Sidechain
5	B1	368	GLY	Peptide
5	B1	496	ARG	Sidechain
5	B1	526	ARG	Sidechain
5	B1	624	ARG	Sidechain
5	B1	750	THR	Peptide
5	B1	877	ARG	Sidechain
5	B1	989	HIS	Sidechain
6	C0	1085	ARG	Sidechain
6	C0	1125	ARG	Sidechain
6	C0	1146	ASP	Peptide
6	C0	1269	ARG	Sidechain
6	C0	127	ARG	Sidechain
6	C0	1601	GLY	Peptide
6	C0	30	ARG	Sidechain
6	C0	338	ARG	Sidechain
6	C0	411	ARG	Sidechain

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Mol	Chain	Res	Type	Group
6	C0	436	ARG	Sidechain
6	C0	490	ARG	Sidechain
6	C0	615	ARG	Sidechain
6	C0	672	ILE	Peptide
6	C0	705	ARG	Sidechain
6	C0	746	ARG	Sidechain
6	C1	1085	ARG	Sidechain
6	C1	1146	ASP	Peptide
6	C1	1269	ARG	Sidechain
6	C1	127	ARG	Sidechain
6	C1	1483	ARG	Sidechain
6	C1	1534	ARG	Sidechain
6	C1	1601	GLY	Peptide
6	C1	30	ARG	Sidechain
6	C1	338	ARG	Sidechain
6	C1	411	ARG	Sidechain
6	C1	436	ARG	Sidechain
6	C1	490	ARG	Sidechain
6	C1	615	ARG	Sidechain
6	C1	672	ILE	Peptide
6	C1	705	ARG	Sidechain
6	C1	746	ARG	Sidechain
6	C2	1089	ASP	Peptide
6	C2	1180	ARG	Sidechain
6	C2	1245	GLY	Peptide
6	C2	127	ARG	Sidechain
6	C2	1375	PHE	Peptide
6	C2	1434	ARG	Sidechain
6	C2	1729	ARG	Sidechain
6	C2	1798	ASP	Peptide
6	C2	1878	ARG	Sidechain
6	C2	1927	SER	Peptide
6	C2	1929	THR	Peptide
6	C2	1935	ARG	Peptide
6	C2	1939	SER	Peptide
6	C2	411	ARG	Sidechain
6	C2	490	ARG	Sidechain
6	C2	615	ARG	Sidechain
6	C2	672	ILE	Peptide
6	C2	748	ARG	Sidechain
6	C3	1083	TYR	Sidechain
6	C3	1089	ASP	Peptide

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Mol	Chain	Res	Type	Group
6	C3	1131	ARG	Sidechain
6	C3	1180	ARG	Sidechain
6	C3	1269	ARG	Sidechain
6	C3	127	ARG	Sidechain
6	C3	1287	ARG	Sidechain
6	C3	1367	TYR	Sidechain
6	C3	172	ARG	Sidechain
6	C3	1798	ASP	Peptide
6	C3	1877	ARG	Sidechain
6	C3	1906	ARG	Sidechain
6	C3	1939	SER	Peptide
6	C3	1941	ALA	Peptide
6	C3	225	ARG	Sidechain
6	C3	30	ARG	Sidechain
6	C3	4	PRO	Mainchain
6	C3	413	ARG	Sidechain
6	C3	490	ARG	Sidechain
6	C3	625	THR	Peptide
6	C3	672	ILE	Peptide
6	C3	682	ARG	Sidechain
6	C3	807	TYR	Sidechain
6	C4	1085	ARG	Sidechain
6	C4	1180	ARG	Sidechain
6	C4	127	ARG	Sidechain
6	C4	1798	ASP	Peptide
6	C4	1939	SER	Peptide
6	C4	214	ARG	Sidechain
6	C4	30	ARG	Sidechain
6	C4	411	ARG	Sidechain
6	C4	413	ARG	Sidechain
6	C4	490	ARG	Sidechain
6	C4	615	ARG	Sidechain
6	C4	672	ILE	Peptide
6	C4	682	ARG	Sidechain
6	C4	705	ARG	Sidechain
6	C4	748	ARG	Sidechain
7	D0	1114	ARG	Sidechain
7	D0	1196	PHE	Sidechain
7	D0	136	TYR	Sidechain
7	D0	38	ARG	Sidechain
7	D0	466	GLU	Peptide
7	D0	575	ARG	Sidechain

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Mol	Chain	Res	Type	Group
7	D0	680	ALA	Peptide
7	D1	1168	HIS	Sidechain
7	D1	1336	GLU	Peptide
7	D1	136	TYR	Sidechain
7	D1	38	ARG	Sidechain
7	D1	466	GLU	Peptide
7	D1	575	ARG	Sidechain
7	D1	680	ALA	Peptide
7	D1	74	SER	Peptide
7	D1	786	ARG	Sidechain
7	D1	861	ASP	Peptide
7	D1	863	CYS	Peptide
7	D1	868	SER	Peptide
7	D1	885	ARG	Sidechain
7	D1	924	ARG	Sidechain
7	D2	1120	ARG	Sidechain
7	D2	1234	THR	Mainchain
7	D2	1336	GLU	Peptide
7	D2	136	TYR	Sidechain
7	D2	38	ARG	Sidechain
7	D2	466	GLU	Peptide
7	D2	575	ARG	Sidechain
7	D2	680	ALA	Peptide
7	D2	849	ASN	Peptide
7	D2	865	LEU	Peptide
7	D2	883	ARG	Sidechain
7	D2	885	ARG	Sidechain
7	D3	1006	SER	Peptide
7	D3	1114	ARG	Sidechain
7	D3	1168	HIS	Sidechain
7	D3	1336	GLU	Peptide
7	D3	136	TYR	Sidechain
7	D3	38	ARG	Sidechain
7	D3	466	GLU	Peptide
7	D3	563	ARG	Sidechain
7	D3	575	ARG	Sidechain
7	D3	680	ALA	Peptide
7	D3	74	SER	Peptide
7	D3	860	GLN	Peptide
7	D3	863	CYS	Peptide
7	D3	885	ARG	Sidechain
7	D4	136	TYR	Sidechain

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Mol	Chain	Res	Type	Group
7	D4	180	TYR	Sidechain
7	D4	38	ARG	Sidechain
7	D4	466	GLU	Peptide
7	D4	575	ARG	Sidechain
7	D4	74	SER	Peptide
7	D4	885	ARG	Sidechain
7	D5	1104	MET	Peptide
7	D5	1346	ARG	Sidechain
7	D5	1347	ARG	Peptide,Mainchain,Sidechain
7	D5	136	TYR	Sidechain
7	D5	1360	TYR	Sidechain
7	D5	180	TYR	Sidechain
7	D5	38	ARG	Sidechain
7	D5	439	PHE	Peptide
7	D5	466	GLU	Peptide
7	D5	531	ASP	Peptide
7	D5	575	ARG	Sidechain
7	D5	74	SER	Peptide
7	D5	867	TYR	Peptide
7	D5	968	ARG	Sidechain
8	E0	49	ILE	Peptide
8	E0	665	ARG	Sidechain
8	E1	49	ILE	Peptide
8	E1	665	ARG	Sidechain
9	F0	132	THR	Peptide
9	F0	151	SER	Peptide
9	F0	159	TYR	Peptide
9	F0	161	GLN	Peptide
9	F0	301	GLN	Peptide
9	F0	306	ARG	Sidechain
9	F1	165	LEU	Peptide
9	F1	170	HIS	Sidechain
9	F1	196	TYR	Sidechain
9	F2	159	TYR	Sidechain
9	F2	252	SER	Peptide
9	F2	282	ARG	Peptide
9	F3	161	GLN	Peptide
9	F3	196	TYR	Sidechain
10	H0	178	TYR	Sidechain
10	H0	350	ARG	Sidechain
10	H0	411	ARG	Sidechain
10	H0	426	GLN	Peptide

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Mol	Chain	Res	Type	Group
10	H0	450	GLU	Peptide
10	H0	452	ARG	Sidechain
10	H1	178	TYR	Sidechain
10	H1	411	ARG	Sidechain
10	H1	439	ARG	Sidechain
10	H2	178	TYR	Sidechain
10	H2	350	ARG	Sidechain
10	H2	411	ARG	Sidechain
10	H3	178	TYR	Sidechain
10	H3	411	ARG	Sidechain
10	H3	443	HIS	Sidechain
10	H3	448	ARG	Peptide
12	J0	349	ARG	Sidechain
12	J0	446	ARG	Sidechain
12	J1	349	ARG	Sidechain
12	J2	349	ARG	Sidechain
12	J2	446	ARG	Sidechain
12	J3	349	ARG	Sidechain
12	J4	430	ARG	Sidechain
13	K0	1148	TYR	Sidechain
13	K0	209	TYR	Sidechain
13	K0	267	SER	Peptide
13	K0	314	ARG	Sidechain
13	K0	342	TYR	Sidechain
13	K0	480	SER	Peptide
13	K0	482	LEU	Peptide
13	K0	487	GLU	Peptide
13	K0	533	ASP	Peptide
13	K0	548	HIS	Sidechain
13	K0	572	TYR	Sidechain
13	K0	599	HIS	Sidechain
13	K1	1035	TYR	Sidechain
13	K1	477	GLU	Peptide
13	K1	497	PRO	Peptide
13	K1	829	ARG	Sidechain
13	K1	903	ARG	Sidechain
13	K2	1089	LYS	Peptide
13	K2	1148	TYR	Sidechain
13	K2	209	TYR	Sidechain
13	K2	267	SER	Peptide
13	K2	314	ARG	Sidechain
13	K2	342	TYR	Sidechain

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Mol	Chain	Res	Type	Group
13	K2	426	TYR	Sidechain
13	K2	476	ARG	Sidechain
13	K2	487	GLU	Peptide
13	K2	490	LEU	Peptide
13	K2	493	SER	Peptide
13	K2	497	PRO	Peptide
13	K2	572	TYR	Sidechain
13	K3	1089	LYS	Peptide
13	K3	1148	TYR	Sidechain
13	K3	209	TYR	Sidechain
13	K3	267	SER	Peptide
13	K3	314	ARG	Sidechain
13	K3	342	TYR	Sidechain
13	K3	426	TYR	Sidechain
13	K3	476	ARG	Sidechain
13	K3	572	TYR	Sidechain
13	K3	595	LEU	Mainchain
14	L0	144	ASP	Peptide
14	L0	404	ARG	Sidechain
14	L0	582	ARG	Sidechain
14	L0	583	GLU	Peptide
14	L0	586	THR	Peptide
14	L0	669	ARG	Sidechain
14	L1	144	ASP	Peptide
14	L1	330	ARG	Sidechain
14	L1	340	ARG	Sidechain
14	L1	404	ARG	Sidechain
14	L1	586	THR	Peptide
14	L1	669	ARG	Sidechain
14	L2	144	ASP	Peptide
14	L2	404	ARG	Sidechain
14	L2	582	ARG	Peptide
14	L2	585	HIS	Peptide
14	L2	586	THR	Peptide
14	L2	669	ARG	Sidechain
14	L2	735	PRO	Peptide
14	L3	144	ASP	Peptide
14	L3	586	THR	Peptide
14	L3	669	ARG	Sidechain
14	L3	733	GLU	Peptide
14	L3	735	PRO	Peptide
15	M0	232	ARG	Peptide

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Mol	Chain	Res	Type	Group
15	M0	278	GLU	Peptide
15	M0	279	GLN	Peptide
15	M0	317	HIS	Peptide
15	M0	402	HIS	Peptide
15	M0	586	PRO	Peptide
15	M0	762	HIS	Peptide
15	M0	861	ARG	Sidechain
15	M0	916	TYR	Sidechain
15	M1	232	ARG	Peptide
15	M1	279	GLN	Peptide
15	M1	416	TYR	Sidechain
15	M1	477	ARG	Sidechain
15	M1	515	ARG	Sidechain
15	M1	584	CYS	Peptide
15	M1	586	PRO	Peptide
15	M1	761	GLU	Peptide
15	M1	930	ARG	Sidechain
15	M2	232	ARG	Peptide
15	M2	278	GLU	Peptide
15	M2	279	GLN	Peptide
15	M2	317	HIS	Peptide
15	M2	581	ARG	Sidechain
15	M2	916	TYR	Sidechain
15	M2	922	ARG	Sidechain
15	M3	232	ARG	Peptide
15	M3	278	GLU	Peptide
15	M3	279	GLN	Peptide
15	M3	416	TYR	Sidechain
15	M3	586	PRO	Peptide
15	M3	762	HIS	Sidechain
16	N0	181	ARG	Sidechain
16	N0	190	LEU	Peptide
16	N1	114	HIS	Sidechain
16	N1	181	ARG	Sidechain
16	N2	190	LEU	Peptide
16	N2	55	GLY	Peptide
16	N3	181	ARG	Sidechain
16	N3	190	LEU	Peptide
17	O3	209	TYR	Sidechain
18	P0	213	ARG	Sidechain
18	P0	323	ASP	Peptide
18	P0	467	ARG	Sidechain

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Mol	Chain	Res	Type	Group
18	P0	504	ASP	Peptide
18	P0	508	ARG	Sidechain
18	P0	616	GLU	Peptide
18	P0	69	ARG	Sidechain
18	P1	213	ARG	Sidechain
18	P1	323	ASP	Peptide
18	P1	386	LEU	Peptide
18	P1	467	ARG	Sidechain
18	P1	504	ASP	Peptide
18	P1	508	ARG	Sidechain
18	P1	552	ARG	Sidechain
18	P1	60	ASP	Peptide
18	P1	616	GLU	Peptide
18	P2	213	ARG	Sidechain
18	P2	323	ASP	Peptide
18	P2	455	ARG	Sidechain
18	P2	467	ARG	Sidechain
18	P2	504	ASP	Peptide
18	P2	508	ARG	Sidechain
18	P2	550	GLU	Peptide
18	P2	616	GLU	Peptide
18	P3	213	ARG	Sidechain
18	P3	323	ASP	Peptide
18	P3	386	LEU	Peptide
18	P3	467	ARG	Sidechain
18	P3	504	ASP	Peptide
18	P3	508	ARG	Sidechain
18	P3	59	LYS	Peptide
18	P3	616	GLU	Peptide
19	Q0	350	SER	Peptide
19	Q1	43	TYR	Sidechain
19	Q1	54	ASN	Peptide
19	Q2	225	ARG	Sidechain
19	Q2	341	GLU	Peptide
19	Q3	54	ASN	Peptide
20	R0	1029	ARG	Sidechain
20	R0	1095	ARG	Sidechain
20	R0	1139	TYR	Sidechain
20	R0	1162	HIS	Sidechain
20	R0	1280	LYS	Peptide
20	R0	1329	TYR	Sidechain
20	R0	1341	TYR	Sidechain

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Mol	Chain	Res	Type	Group
20	R0	40	ALA	Peptide
20	R0	410	TRP	Peptide
20	R0	538	TYR	Sidechain
20	R0	544	HIS	Sidechain
20	R0	718	ARG	Sidechain
20	R0	727	ARG	Sidechain
20	R0	804	LEU	Peptide
20	R1	1053	PHE	Peptide
20	R1	1104	TYR	Sidechain
20	R1	1139	TYR	Sidechain
20	R1	1162	HIS	Sidechain
20	R1	1285	THR	Peptide
20	R1	1329	TYR	Sidechain
20	R1	40	ALA	Peptide
20	R1	410	TRP	Peptide
20	R1	538	TYR	Sidechain
20	R1	544	HIS	Sidechain
20	R1	718	ARG	Sidechain
20	R1	727	ARG	Sidechain
20	R1	804	LEU	Peptide
20	R2	1007	HIS	Sidechain
20	R2	1043	GLU	Peptide
20	R2	1053	PHE	Peptide
20	R2	1055	TYR	Peptide,Sidechain
20	R2	1080	TYR	Sidechain
20	R2	1104	TYR	Sidechain
20	R2	1139	TYR	Sidechain
20	R2	1162	HIS	Sidechain
20	R2	1341	TYR	Sidechain
20	R2	410	TRP	Peptide
20	R2	538	TYR	Sidechain
20	R2	544	HIS	Sidechain
20	R2	718	ARG	Sidechain
20	R2	727	ARG	Sidechain
20	R2	804	LEU	Peptide
20	R2	993	ASP	Peptide
20	R3	1018	TYR	Sidechain
20	R3	1054	PRO	Peptide
20	R3	1055	TYR	Peptide,Sidechain
20	R3	1139	TYR	Sidechain
20	R3	1162	HIS	Sidechain
20	R3	1285	THR	Peptide,Mainchain

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Mol	Chain	Res	Type	Group
20	R3	1286	ASP	Peptide
20	R3	1329	TYR	Sidechain
20	R3	40	ALA	Peptide
20	R3	410	TRP	Peptide
20	R3	481	ARG	Peptide
20	R3	538	TYR	Sidechain
20	R3	544	HIS	Sidechain
20	R3	718	ARG	Sidechain
20	R3	727	ARG	Sidechain
20	R3	804	LEU	Peptide
21	S0	132	PHE	Peptide
21	S0	150	ARG	Sidechain
21	S0	191	ARG	Sidechain
21	S0	231	ASP	Peptide
21	S1	132	PHE	Peptide
21	S1	150	ARG	Sidechain
21	S1	191	ARG	Sidechain
21	S1	231	ASP	Peptide
21	S1	239	ARG	Sidechain
21	S2	132	PHE	Peptide
21	S2	150	ARG	Sidechain
21	S2	191	ARG	Sidechain
21	S2	231	ASP	Peptide
21	S2	239	ARG	Sidechain
21	S2	43	TYR	Sidechain
21	S3	132	PHE	Peptide
21	S3	150	ARG	Sidechain
21	S3	191	ARG	Sidechain
21	S3	231	ASP	Peptide
21	S3	239	ARG	Sidechain
22	T0	125	ARG	Sidechain
22	T0	2	ARG	Peptide
22	T0	254	ARG	Sidechain
22	T0	441	SER	Peptide
22	T0	457	ARG	Peptide
22	T0	685	ASP	Peptide
22	T0	69	ARG	Sidechain
22	T0	712	ARG	Sidechain
22	T0	764	LEU	Peptide
22	T0	823	TYR	Sidechain
22	T0	832	HIS	Peptide
22	T1	125	ARG	Sidechain

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Mol	Chain	Res	Type	Group
22	T1	2	ARG	Peptide
22	T1	441	SER	Peptide
22	T1	457	ARG	Peptide
22	T1	685	ASP	Peptide
22	T1	69	ARG	Sidechain
22	T1	712	ARG	Sidechain
22	T1	764	LEU	Peptide
22	T1	887	ARG	Sidechain
23	U0	772	TYR	Sidechain
24	V0	851	VAL	Peptide
25	W0	219	GLU	Peptide
25	W0	224	LEU	Peptide
25	W0	225	ASN	Peptide
25	W0	230	TYR	Sidechain
25	W0	353	TRP	Peptide
25	W0	40	GLU	Peptide
25	W0	476	LEU	Peptide
25	W0	487	TYR	Sidechain
25	W0	513	GLU	Peptide
25	W0	709	TYR	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	00	6085	0	6080	38	0
1	01	6085	0	6080	27	0
1	02	6085	0	6080	10	0
1	03	6085	0	6080	40	0
1	04	6085	0	6080	12	0
2	10	14046	0	14194	21	0
2	11	14046	0	14194	27	0
2	12	14046	0	14194	33	0
2	13	14046	0	14194	22	0
2	14	14046	0	14194	26	0
2	15	14046	0	14194	16	0
2	16	14046	0	14194	12	0
2	17	14046	0	14194	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	40	2922	0	2899	4	0
3	41	2922	0	2899	3	0
4	A0	6568	0	6527	70	0
4	A1	6568	0	6527	11	0
4	A2	6568	0	6527	24	0
4	A3	6568	0	6527	10	0
4	A4	5860	0	5828	25	0
4	A5	5860	0	5828	5	0
4	A6	5860	0	5828	7	0
5	B0	13746	0	13949	7	0
5	B1	13746	0	13949	10	0
6	C0	16013	0	16224	13	0
6	C1	16013	0	16224	14	0
6	C2	16013	0	16224	94	0
6	C3	16013	0	16224	72	0
6	C4	16013	0	16224	62	0
7	D0	10363	0	10400	50	0
7	D1	10363	0	10400	118	0
7	D2	10363	0	10400	58	0
7	D3	10363	0	10400	70	0
7	D4	10363	0	10400	59	0
7	D5	10363	0	10400	59	0
8	E0	4432	0	4472	14	0
8	E1	4432	0	4472	1	0
9	F0	1837	0	1825	13	0
9	F1	1837	0	1825	5	0
9	F2	1837	0	1825	3	0
9	F3	1837	0	1825	11	0
10	H0	3066	0	3103	26	0
10	H1	3066	0	3103	5	0
10	H2	3066	0	3103	2	0
10	H3	3066	0	3103	4	0
11	I0	1398	0	1431	26	0
11	I1	1398	0	1431	3	0
11	I2	1398	0	1431	2	0
11	I3	1398	0	1431	2	0
12	J0	1403	0	1391	2	0
12	J1	1403	0	1391	3	0
12	J2	1403	0	1391	1	0
12	J3	1403	0	1391	0	0
12	J4	1403	0	1391	0	0
13	K0	8574	0	8438	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	K1	8574	0	8438	17	0
13	K2	8574	0	8438	22	0
13	K3	8574	0	8438	21	0
14	L0	6383	0	6313	24	0
14	L1	6383	0	6313	36	0
14	L2	6383	0	6313	13	0
14	L3	6383	0	6313	12	0
15	M0	5461	0	5443	11	0
15	M1	5461	0	5443	14	0
15	M2	5461	0	5443	6	0
15	M3	5461	0	5443	8	0
16	N0	2352	0	2220	17	0
16	N1	2352	0	2220	2	0
16	N2	2352	0	2220	0	0
16	N3	2352	0	2220	1	0
17	O0	2528	0	2444	45	0
17	O1	2528	0	2444	6	0
17	O2	2528	0	2444	6	0
17	O3	2528	0	2444	18	0
18	P0	5257	0	5249	9	0
18	P1	5257	0	5249	8	0
18	P2	5257	0	5249	4	0
18	P3	5257	0	5249	11	0
19	Q0	2703	0	2555	16	0
19	Q1	2703	0	2555	0	0
19	Q2	2703	0	2555	5	0
19	Q3	2703	0	2555	1	0
20	R0	11132	0	11066	74	0
20	R1	11132	0	11066	19	0
20	R2	11132	0	11066	23	0
20	R3	11132	0	11066	27	0
21	S0	2552	0	2452	5	0
21	S1	2552	0	2452	1	0
21	S2	2552	0	2452	2	0
21	S3	2552	0	2452	1	0
22	T0	7960	0	7896	6	0
22	T1	7960	0	7896	4	0
23	U0	1193	0	1188	7	0
23	U1	151	0	167	25	0
23	U2	151	0	167	25	0
23	U3	151	0	167	20	0
23	U4	151	0	167	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	U5	151	0	167	25	0
23	U6	151	0	167	26	0
24	V0	2203	0	2226	21	0
25	W0	5836	0	5850	14	0
All	All	617133	0	616873	1222	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 1.

All (1222) 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)
6:C2:1249:ILE:HG21	20:R0:1284:ALA:CB	1.29	1.54
6:C2:622:PRO:HB3	20:R0:1316:SER:CB	1.44	1.47
6:C2:788:VAL:CG2	17:O0:258:THR:HG21	1.53	1.39
6:C2:1249:ILE:CG2	20:R0:1284:ALA:HB2	1.58	1.33
6:C2:622:PRO:CB	20:R0:1316:SER:HB3	1.56	1.33
2:12:776:VAL:HG21	2:13:700:SER:OG	1.31	1.26
1:03:78:LYS:CE	17:O0:98:ARG:HH11	1.50	1.24
10:H0:427:PHE:CZ	11:I0:361:ARG:HB2	1.72	1.24
10:H0:427:PHE:CE1	11:I0:361:ARG:NH2	2.06	1.22
6:C3:468:GLU:CD	20:R1:1205:ALA:HB1	1.66	1.20
10:H0:427:PHE:CE2	11:I0:361:ARG:HB2	1.78	1.18
6:C2:1249:ILE:HG22	20:R0:1265:TRP:NE1	1.57	1.18
14:L1:419:LEU:HD23	16:N0:139:GLN:NE2	1.58	1.18
1:00:28:LYS:HE2	14:L0:472:LEU:CD1	1.71	1.18
7:D4:1184:ASP:CB	23:U1:597:ILE:CG2	2.21	1.18
10:H0:427:PHE:CZ	11:I0:361:ARG:NE	2.12	1.18
1:00:28:LYS:HE2	14:L0:472:LEU:HD11	1.18	1.18
4:A0:558:LYS:HE3	7:D1:1031:LYS:CD	1.74	1.17
7:D4:1184:ASP:HB2	23:U1:597:ILE:CG2	1.73	1.15
1:03:78:LYS:HE2	17:O0:98:ARG:HH11	1.01	1.15
7:D4:1184:ASP:HB3	23:U1:597:ILE:HG22	1.25	1.14
18:P0:185:LEU:HD12	25:W0:708:ALA:HB1	1.30	1.13
7:D4:1184:ASP:CB	23:U1:597:ILE:HG22	1.77	1.13
7:D2:1184:ASP:HB2	23:U4:597:ILE:HG23	1.31	1.12
7:D5:1358:CYS:SG	20:R2:1035:ARG:HB3	1.89	1.12
4:A0:279:HIS:NE2	7:D2:886:GLN:HB3	1.64	1.12
7:D0:1184:ASP:HB2	23:U2:597:ILE:HG23	1.19	1.12
7:D5:1184:ASP:CB	23:U6:597:ILE:CG2	2.28	1.12
10:H0:427:PHE:HD2	11:I0:364:ILE:HD12	1.08	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D2:1184:ASP:HB3	23:U4:597:ILE:HG22	1.30	1.11
7:D0:1184:ASP:HB3	23:U2:597:ILE:HG22	1.21	1.11
7:D1:1184:ASP:HB3	23:U3:597:ILE:HG22	1.31	1.11
2:12:1177:MET:HG3	2:13:1108:SER:HA	1.30	1.10
6:C2:1249:ILE:CB	20:R0:1265:TRP:HE1	1.62	1.10
7:D5:1184:ASP:HB2	23:U6:597:ILE:HG23	1.22	1.10
4:A0:558:LYS:HE3	7:D1:1031:LYS:HD3	1.17	1.10
4:A0:239:THR:CG2	7:D1:1028:GLN:HB3	1.82	1.09
6:C2:788:VAL:HG21	17:O0:258:THR:CG2	1.81	1.09
7:D0:1184:ASP:CB	23:U2:597:ILE:CG2	2.31	1.08
7:D3:1184:ASP:HB3	23:U5:597:ILE:HG22	1.36	1.08
7:D1:1184:ASP:HB2	23:U3:597:ILE:HG23	1.35	1.08
7:D3:1184:ASP:HB2	23:U5:597:ILE:HG23	1.35	1.07
1:00:92:THR:CG2	14:L0:262:LEU:HD23	1.84	1.06
7:D5:1184:ASP:HB2	23:U6:597:ILE:CG2	1.83	1.06
7:D4:1184:ASP:HB2	23:U1:597:ILE:HG23	1.11	1.06
6:C2:1249:ILE:CG2	20:R0:1265:TRP:HE1	1.69	1.06
7:D5:1184:ASP:CB	23:U6:597:ILE:HG22	1.84	1.06
10:H0:427:PHE:CE2	11:I0:361:ARG:CB	2.38	1.06
10:H0:427:PHE:CD2	11:I0:364:ILE:HD12	1.90	1.06
1:00:92:THR:HG22	14:L0:262:LEU:HD23	1.28	1.06
7:D4:1366:SER:HB2	20:R0:999:THR:CG2	1.86	1.06
6:C2:788:VAL:CG2	17:O0:258:THR:CG2	2.33	1.05
6:C2:622:PRO:CB	20:R0:1316:SER:CB	2.21	1.05
7:D5:1184:ASP:HB3	23:U6:597:ILE:HG22	1.35	1.05
1:03:78:LYS:CD	17:O0:98:ARG:HH11	1.70	1.04
9:F0:162:GLY:HA3	9:F0:165:LEU:HD12	1.36	1.04
10:H0:427:PHE:HD2	11:I0:364:ILE:CD1	1.71	1.03
4:A0:683:LYS:NZ	7:D1:567:ALA:HB2	1.73	1.03
7:D0:1184:ASP:CB	23:U2:597:ILE:HG23	1.87	1.03
2:14:1831:VAL:CG1	7:D3:689:LYS:NZ	2.22	1.02
6:C2:622:PRO:HB3	20:R0:1316:SER:HB3	1.03	1.02
6:C2:1249:ILE:HG22	20:R0:1265:TRP:CD1	1.96	1.01
7:D0:1184:ASP:HB3	23:U2:597:ILE:CG2	1.87	1.01
1:03:78:LYS:HE2	17:O0:98:ARG:NH1	1.75	1.00
2:10:1761:PRO:O	8:E0:157:ALA:HB1	1.61	1.00
4:A0:558:LYS:CE	7:D1:1031:LYS:HD3	1.91	1.00
6:C2:1249:ILE:CG2	20:R0:1284:ALA:CB	2.25	1.00
7:D1:1196:PHE:CE2	23:U3:610:LEU:HD11	1.96	1.00
6:C4:1249:ILE:HD11	20:R3:1284:ALA:CA	1.91	0.99
7:D2:1184:ASP:CB	23:U4:597:ILE:CG2	2.40	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A0:683:LYS:HZ2	7:D1:567:ALA:HB2	1.23	0.99
1:00:92:THR:HG22	14:L0:262:LEU:CD2	1.92	0.99
2:12:1346:ILE:HD11	2:13:1074:GLN:OE1	1.62	0.98
7:D4:1184:ASP:CB	23:U1:597:ILE:HG23	1.89	0.98
6:C2:788:VAL:HG22	17:O0:258:THR:OG1	1.64	0.98
6:C3:658:GLU:CB	20:R1:1252:LYS:HE2	1.93	0.98
1:03:78:LYS:NZ	17:O0:98:ARG:HD3	1.78	0.98
2:15:700:SER:OG	2:16:776:VAL:HG21	1.63	0.97
6:C4:1695:ASP:HB2	18:P3:257:LYS:HG2	1.42	0.97
6:C3:658:GLU:HB3	20:R1:1252:LYS:HE2	1.00	0.97
18:P0:185:LEU:CD1	25:W0:708:ALA:HB1	1.95	0.97
4:A0:239:THR:HG21	7:D1:1028:GLN:HB3	1.45	0.97
6:C2:1249:ILE:CG2	20:R0:1265:TRP:NE1	2.25	0.97
6:C4:1249:ILE:HD11	20:R3:1284:ALA:HA	1.44	0.96
6:C3:1703:GLU:OE2	24:V0:800:LYS:HD2	1.65	0.96
10:H0:427:PHE:HE2	11:I0:361:ARG:CB	1.75	0.96
7:D1:1184:ASP:CB	23:U3:597:ILE:HG22	1.95	0.96
7:D1:1184:ASP:CB	23:U3:597:ILE:CG2	2.42	0.96
10:H0:427:PHE:HE1	11:I0:361:ARG:NH2	1.62	0.95
6:C2:1249:ILE:HD13	20:R0:1284:ALA:HB3	1.48	0.95
6:C2:471:GLN:NE2	20:R0:1205:ALA:CB	2.29	0.95
6:C3:658:GLU:HB3	20:R1:1252:LYS:CE	1.94	0.95
6:C2:471:GLN:HE21	20:R0:1205:ALA:HB1	1.29	0.95
6:C4:1244:GLN:HE22	17:O3:205:ASN:HD21	0.96	0.95
6:C2:1249:ILE:C	20:R0:1265:TRP:CD1	2.45	0.94
7:D3:1184:ASP:CB	23:U5:597:ILE:CG2	2.45	0.94
6:C2:471:GLN:HE21	20:R0:1205:ALA:CB	1.80	0.94
6:C2:1250:GLY:HA2	20:R0:1265:TRP:CD1	2.02	0.94
1:03:78:LYS:CD	17:O0:98:ARG:NH1	2.30	0.94
1:00:334:ILE:HG12	14:L0:731:GLY:HA2	1.49	0.94
6:C2:788:VAL:HG21	17:O0:258:THR:HG21	0.96	0.93
7:D0:1241:MET:SD	7:D1:734:ASN:ND2	2.42	0.93
1:03:78:LYS:CE	17:O0:98:ARG:HD3	1.98	0.93
7:D5:1184:ASP:CB	23:U6:597:ILE:HG23	1.94	0.93
10:H0:427:PHE:CE1	11:I0:361:ARG:CZ	2.52	0.92
7:D2:1196:PHE:CE2	23:U4:610:LEU:HD11	2.04	0.92
4:A2:712:ASP:OD1	7:D3:85:ARG:HD2	1.70	0.92
13:K2:1153:GLN:CD	13:K3:596:ILE:HG23	1.94	0.92
19:Q0:57:SER:OG	24:V0:851:VAL:HG21	1.68	0.92
2:12:1279:GLN:HE22	2:13:1125:ALA:HB2	1.35	0.91
7:D3:1184:ASP:CB	23:U5:597:ILE:HG22	2.00	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C2:1249:ILE:HD12	20:R0:1284:ALA:H	1.35	0.91
6:C3:746:ARG:HG2	19:Q0:228:ASN:OD1	1.71	0.91
6:C3:468:GLU:CD	20:R1:1205:ALA:CB	2.43	0.90
14:L1:419:LEU:CD2	16:N0:139:GLN:NE2	2.33	0.90
4:A0:239:THR:HG22	7:D1:1028:GLN:HB3	1.53	0.90
7:D0:1184:ASP:CB	23:U2:597:ILE:HG22	1.98	0.90
7:D1:1184:ASP:HB2	23:U3:597:ILE:CG2	2.00	0.90
7:D0:1184:ASP:HB2	23:U2:597:ILE:CG2	1.97	0.90
7:D2:1184:ASP:CB	23:U4:597:ILE:HG22	1.98	0.89
19:Q0:57:SER:HB3	24:V0:851:VAL:HG11	1.54	0.89
6:C4:1244:GLN:NE2	17:O3:205:ASN:HD21	1.70	0.89
7:D1:1196:PHE:CE1	23:U3:610:LEU:HD21	2.07	0.89
7:D3:1184:ASP:HB2	23:U5:597:ILE:CG2	2.02	0.89
1:00:28:LYS:CE	14:L0:472:LEU:CD1	2.51	0.89
6:C0:83:THR:O	12:J1:421:ILE:HD12	1.73	0.88
7:D2:1184:ASP:HB2	23:U4:597:ILE:CG2	2.01	0.88
2:14:1831:VAL:HG12	7:D3:689:LYS:HZ1	1.37	0.88
2:15:700:SER:OG	2:16:776:VAL:CG2	2.21	0.88
7:D4:1366:SER:CB	20:R0:999:THR:CG2	2.51	0.88
6:C3:781:GLU:OE2	17:O1:258:THR:HG22	1.74	0.88
7:D2:1184:ASP:CB	23:U4:597:ILE:HG23	2.02	0.88
2:12:776:VAL:CG2	2:13:700:SER:OG	2.22	0.87
6:C3:427:MET:HE3	21:S0:89:LEU:CD1	2.04	0.87
4:A0:239:THR:CG2	7:D1:1028:GLN:CB	2.53	0.86
2:14:1831:VAL:CG1	7:D3:689:LYS:HZ1	1.85	0.86
6:C3:468:GLU:CG	20:R1:1205:ALA:HB1	2.06	0.86
7:D2:1242:HIS:CE1	7:D3:732:LEU:CD2	2.59	0.86
6:C2:1250:GLY:HA2	20:R0:1265:TRP:CG	2.09	0.86
2:14:1831:VAL:CG1	7:D3:689:LYS:HZ3	1.86	0.85
7:D0:1186:THR:HG23	23:U2:601:VAL:O	1.76	0.85
6:C2:1249:ILE:HB	20:R0:1265:TRP:HE1	1.42	0.85
4:A0:239:THR:HG21	7:D1:1028:GLN:CB	2.05	0.85
14:L1:345:ARG:NH2	16:N0:201:GLN:CG	2.38	0.85
14:L1:419:LEU:HD23	16:N0:139:GLN:HE21	1.38	0.85
14:L1:419:LEU:HD23	16:N0:139:GLN:HE22	1.39	0.84
6:C4:1695:ASP:HB2	18:P3:257:LYS:CG	2.06	0.84
7:D1:693:ARG:NH2	9:F3:315:LEU:HG	1.92	0.84
6:C2:622:PRO:HB3	20:R0:1316:SER:OG	1.78	0.84
6:C2:1249:ILE:C	20:R0:1265:TRP:NE1	2.36	0.84
7:D2:1184:ASP:HB3	23:U4:597:ILE:CG2	2.02	0.83
1:00:733:LYS:NZ	14:L1:781:THR:HG22	1.93	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q0:57:SER:CB	24:V0:851:VAL:HG21	2.06	0.83
6:C2:1249:ILE:HG21	20:R0:1284:ALA:HB1	1.58	0.83
4:A4:483:GLU:HG2	6:C3:180:GLN:HA	1.60	0.83
6:C2:1249:ILE:CD1	20:R0:1284:ALA:H	1.91	0.83
6:C3:746:ARG:HG2	19:Q0:228:ASN:CG	2.04	0.83
6:C3:781:GLU:OE2	17:O1:258:THR:CG2	2.26	0.83
7:D2:1242:HIS:CE1	7:D3:732:LEU:HD22	2.13	0.83
6:C3:746:ARG:CG	19:Q0:228:ASN:OD1	2.26	0.83
6:C2:1250:GLY:N	20:R0:1265:TRP:CD1	2.46	0.83
6:C2:1249:ILE:HG21	20:R0:1284:ALA:HB2	0.83	0.82
8:E0:165:TYR:CE2	8:E0:258:LEU:HD11	2.14	0.82
1:O3:78:LYS:HG2	17:O0:98:ARG:NH1	1.94	0.82
6:C2:1250:GLY:CA	20:R0:1265:TRP:CD1	2.62	0.82
6:C4:1244:GLN:HB2	17:O3:204:GLU:OE2	1.79	0.82
7:D0:1196:PHE:CZ	23:U2:610:LEU:HD11	2.15	0.81
6:C2:1249:ILE:HD13	20:R0:1284:ALA:CB	2.10	0.81
7:D2:1196:PHE:CD1	23:U4:610:LEU:HD21	2.13	0.81
7:D3:1196:PHE:CD2	23:U5:610:LEU:HD11	2.14	0.81
4:A0:239:THR:HG21	7:D1:1028:GLN:CG	2.10	0.81
10:H0:427:PHE:HE2	11:I0:361:ARG:CA	1.93	0.81
2:12:776:VAL:HG21	2:13:700:SER:CB	2.11	0.81
6:C2:1249:ILE:HG21	20:R0:1284:ALA:HB3	1.57	0.80
6:C4:1249:ILE:CD1	20:R3:1285:THR:H	1.95	0.80
7:D1:1184:ASP:HB3	23:U3:597:ILE:CG2	2.07	0.80
6:C4:1244:GLN:HG2	20:R3:1283:SER:OG	1.80	0.80
1:O1:745:MET:HE3	1:O4:10:ARG:NH2	1.97	0.80
10:H0:427:PHE:HZ	11:I0:361:ARG:HB2	1.35	0.80
6:C2:469:PRO:HB3	20:R0:1113:ARG:NH1	1.96	0.80
10:H0:427:PHE:CZ	11:I0:361:ARG:CZ	2.65	0.80
7:D3:1184:ASP:HB3	23:U5:597:ILE:CG2	2.10	0.79
6:C3:1703:GLU:OE2	24:V0:800:LYS:CD	2.31	0.78
1:O0:28:LYS:HE2	14:L0:472:LEU:HD13	1.63	0.78
7:D4:1365:GLN:C	20:R0:1029:ARG:HH22	1.91	0.78
1:O3:78:LYS:NZ	17:O0:98:ARG:CD	2.46	0.78
6:C2:622:PRO:HA	20:R0:1316:SER:HB2	1.64	0.78
6:C2:1250:GLY:N	20:R0:1265:TRP:NE1	2.31	0.78
8:E0:165:TYR:CZ	8:E0:258:LEU:HD11	2.19	0.78
7:D2:1196:PHE:CZ	23:U4:610:LEU:HD11	2.19	0.77
1:O1:549:ALA:HB1	14:L1:233:ALA:CB	2.13	0.77
6:C2:788:VAL:HG22	17:O0:258:THR:CG2	2.14	0.77
6:C4:1695:ASP:HB2	18:P3:257:LYS:CD	2.14	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K2:1153:GLN:OE1	13:K3:596:ILE:HG23	1.85	0.77
1:00:28:LYS:CG	14:L0:472:LEU:HD21	2.15	0.77
13:K3:969:THR:HA	14:L3:879:ASP:OD2	1.84	0.77
7:D1:693:ARG:HH21	9:F3:315:LEU:HG	1.48	0.77
1:00:28:LYS:CE	14:L0:472:LEU:HD13	2.14	0.77
6:C2:730:PRO:HG3	17:O0:258:THR:HG22	1.67	0.76
4:A0:558:LYS:CE	7:D1:1031:LYS:HZ2	1.98	0.76
10:H0:427:PHE:CE2	11:I0:361:ARG:CG	2.69	0.76
6:C2:622:PRO:CA	20:R0:1316:SER:HB2	2.16	0.76
10:H0:427:PHE:CZ	11:I0:361:ARG:CB	2.61	0.75
10:H0:427:PHE:CE1	11:I0:361:ARG:NE	2.53	0.75
4:A4:141:LYS:HE3	6:C2:1992:ARG:HH11	1.51	0.75
7:D4:1362:VAL:HG11	20:R0:1002:THR:HG21	1.68	0.75
7:D5:1391:HIS:O	20:R2:1154:PRO:HB3	1.86	0.75
6:C2:622:PRO:HB2	20:R0:1316:SER:HB3	1.66	0.75
6:C4:1695:ASP:CB	18:P3:257:LYS:HG2	2.16	0.75
4:A0:239:THR:CG2	7:D1:1028:GLN:CD	2.59	0.75
7:D2:1195:PRO:O	23:U4:611:PHE:CE2	2.39	0.75
14:L3:728:GLU:H	14:L3:731:GLY:CA	2.00	0.75
2:17:1831:VAL:HG22	7:D2:1001:PRO:HG3	1.69	0.74
7:D4:1196:PHE:CG	23:U1:610:LEU:HD21	2.22	0.74
4:A4:167:ILE:HG23	6:C3:4:PRO:HD2	1.69	0.74
4:A4:483:GLU:CD	6:C3:179:GLU:O	2.30	0.74
13:K3:596:ILE:HG21	13:K3:599:HIS:ND1	2.00	0.74
14:L3:728:GLU:H	14:L3:731:GLY:HA3	1.52	0.74
2:11:1177:MET:H	2:12:1106:PRO:HB3	1.51	0.74
1:03:78:LYS:CG	17:O0:98:ARG:NH1	2.50	0.74
4:A0:239:THR:HG23	7:D1:1028:GLN:CD	2.13	0.74
6:C4:1244:GLN:HE22	17:O3:205:ASN:ND2	1.80	0.74
2:10:1761:PRO:O	8:E0:157:ALA:CB	2.36	0.74
19:Q0:57:SER:HB3	24:V0:851:VAL:HG21	1.70	0.73
7:D0:1195:PRO:O	23:U2:611:PHE:CE2	2.40	0.73
1:03:78:LYS:CE	17:O0:98:ARG:NH1	2.36	0.73
1:03:78:LYS:HZ1	17:O0:98:ARG:HD3	1.51	0.73
6:C3:1703:GLU:OE2	24:V0:800:LYS:CG	2.36	0.73
7:D2:1196:PHE:CE1	23:U4:610:LEU:HD21	2.22	0.73
1:03:78:LYS:HD3	17:O0:98:ARG:NH1	2.03	0.73
6:C3:427:MET:HE3	21:S0:89:LEU:HD11	1.69	0.73
7:D1:1196:PHE:CD1	23:U3:610:LEU:HD21	2.24	0.73
1:03:78:LYS:HE2	17:O0:98:ARG:HD3	1.70	0.72
7:D4:1366:SER:HB2	20:R0:999:THR:HG23	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q0:57:SER:CB	24:V0:851:VAL:HG11	2.19	0.72
2:12:1279:GLN:NE2	2:13:1125:ALA:HB2	2.03	0.72
4:A0:558:LYS:HG3	7:D1:1031:LYS:NZ	2.05	0.72
7:D5:1196:PHE:CD2	23:U6:610:LEU:HD11	2.24	0.72
1:01:116:TYR:HE2	15:M0:841:ILE:HD13	1.54	0.72
6:C4:781:GLU:HB2	17:O3:258:THR:OG1	1.88	0.72
1:01:543:ALA:O	14:L1:563:GLN:NE2	2.23	0.72
7:D2:1186:THR:HG23	23:U4:601:VAL:O	1.88	0.72
7:D3:885:ARG:HD3	7:D5:506:GLN:HE21	1.55	0.72
1:00:733:LYS:HZ2	14:L1:781:THR:HG22	1.54	0.72
7:D2:1196:PHE:CD1	23:U4:610:LEU:CD2	2.72	0.72
9:F0:164:SER:O	9:F0:165:LEU:HG	1.90	0.71
4:A0:199:GLY:HA3	7:D1:898:ARG:CD	2.19	0.71
6:C3:746:ARG:CD	19:Q0:228:ASN:OD1	2.38	0.71
3:40:165:LYS:HG2	3:40:179:ASN:HB2	1.72	0.71
7:D4:1206:ILE:HG22	23:U1:600:LEU:CD2	2.21	0.71
7:D0:1186:THR:HG21	23:U2:601:VAL:HB	1.70	0.71
6:C2:622:PRO:CA	20:R0:1316:SER:CB	2.68	0.71
14:L1:345:ARG:NH2	16:N0:201:GLN:HG2	2.04	0.71
7:D3:1196:PHE:CG	23:U5:610:LEU:HD11	2.26	0.71
15:M0:391:LEU:HD22	15:M0:433:THR:HG22	1.73	0.71
6:C4:1249:ILE:HD11	20:R3:1285:THR:H	1.56	0.70
6:C4:1249:ILE:HD11	20:R3:1284:ALA:CB	2.20	0.70
2:14:1831:VAL:HG13	7:D3:689:LYS:NZ	2.05	0.70
2:14:1831:VAL:HG13	7:D3:689:LYS:HZ3	1.56	0.70
7:D4:1366:SER:CB	20:R0:999:THR:HG22	2.21	0.70
6:C3:468:GLU:HG2	20:R1:1205:ALA:HB1	1.73	0.70
1:03:14:SER:HB2	15:M1:444:LEU:HD22	1.75	0.69
6:C2:788:VAL:HG22	17:O0:258:THR:CB	2.22	0.69
7:D3:1196:PHE:CE2	23:U5:610:LEU:HD11	2.27	0.69
6:C3:468:GLU:CG	20:R1:1205:ALA:CB	2.70	0.69
6:C3:468:GLU:HG2	20:R1:1205:ALA:CB	2.22	0.69
7:D1:989:ALA:HB1	7:D4:91:PRO:HG3	1.74	0.69
1:03:78:LYS:CE	17:O0:98:ARG:CD	2.69	0.69
2:12:1346:ILE:CD1	2:13:1074:GLN:OE1	2.39	0.69
6:C4:1249:ILE:HG23	20:R3:1261:GLN:HB3	1.75	0.69
4:A0:199:GLY:HA3	7:D1:898:ARG:HD3	1.75	0.69
6:C2:1249:ILE:CB	20:R0:1265:TRP:NE1	2.47	0.69
14:L1:345:ARG:HH21	16:N0:201:GLN:CG	2.06	0.69
6:C3:427:MET:HE3	21:S0:89:LEU:HD13	1.74	0.68
13:K2:1153:GLN:HG2	13:K3:596:ILE:HD12	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D0:1196:PHE:CD1	23:U2:610:LEU:HD22	2.29	0.68
7:D1:1011:LEU:HD13	7:D4:95:GLU:HG2	1.75	0.68
6:C2:788:VAL:CG2	17:O0:258:THR:CB	2.71	0.68
7:D1:1161:LEU:HD21	7:D1:1196:PHE:CD2	2.29	0.68
7:D2:1161:LEU:HD21	7:D2:1196:PHE:CD2	2.29	0.68
4:A4:456:ASN:CG	6:C3:244:GLU:OE1	2.36	0.68
7:D5:1196:PHE:CG	23:U6:610:LEU:HD21	2.29	0.68
13:K0:1139:TYR:HA	13:K1:595:LEU:HD13	1.75	0.68
6:C2:1249:ILE:CB	20:R0:1284:ALA:HB2	2.24	0.67
1:O3:626:ILE:HG23	15:M1:497:MET:HE1	1.75	0.67
7:D4:1186:THR:HG23	23:U1:601:VAL:HB	1.75	0.67
6:C4:779:GLN:OE1	17:O3:258:THR:HG23	1.95	0.67
7:D0:1196:PHE:CD1	23:U2:610:LEU:CD2	2.77	0.67
4:A0:279:HIS:NE2	7:D2:886:GLN:CB	2.51	0.67
6:C3:1703:GLU:OE2	24:V0:800:LYS:CB	2.42	0.67
14:L1:419:LEU:CD2	16:N0:139:GLN:HE21	2.00	0.67
7:D4:1196:PHE:CD2	23:U1:610:LEU:HD11	2.30	0.67
6:C0:83:THR:O	12:J1:421:ILE:CD1	2.42	0.67
6:C0:1134:SER:OG	10:H1:411:ARG:NH2	2.27	0.67
6:C2:1249:ILE:O	20:R0:1265:TRP:CD1	2.48	0.67
6:C3:427:MET:CE	21:S0:89:LEU:HD13	2.25	0.67
7:D4:1366:SER:HB2	20:R0:999:THR:HG21	1.72	0.67
4:A0:199:GLY:CA	7:D1:898:ARG:HD3	2.26	0.66
10:H0:427:PHE:CE1	11:I0:357:LEU:HD22	2.29	0.66
7:D4:1186:THR:CG2	23:U1:601:VAL:HB	2.25	0.66
4:A0:683:LYS:HA	7:D1:563:ARG:HH12	1.60	0.66
7:D0:1161:LEU:HD22	7:D0:1196:PHE:CE1	2.30	0.66
6:C4:1249:ILE:HG22	20:R3:1265:TRP:HE1	1.61	0.66
4:A0:279:HIS:HE2	7:D2:886:GLN:HB3	1.56	0.65
7:D4:1206:ILE:HG22	23:U1:600:LEU:HD22	1.78	0.65
7:D2:1196:PHE:CD2	23:U4:610:LEU:HD11	2.31	0.65
7:D2:1095:ALA:HB1	7:D2:1140:PHE:CE2	2.30	0.65
1:O1:745:MET:CE	1:O4:10:ARG:NH2	2.58	0.65
4:A0:199:GLY:CA	7:D1:898:ARG:CD	2.74	0.65
7:D2:1186:THR:HG21	23:U4:601:VAL:HB	1.78	0.65
7:D4:1196:PHE:CE2	23:U1:610:LEU:HG	2.31	0.65
1:O0:28:LYS:HG2	14:L0:472:LEU:HD21	1.79	0.65
7:D2:888:GLN:NE2	9:F3:124:VAL:O	2.23	0.65
2:12:1279:GLN:HE22	2:13:1125:ALA:CB	2.09	0.65
7:D0:1196:PHE:CZ	23:U2:610:LEU:CD1	2.80	0.65
2:12:1278:ILE:HG22	2:13:1109:ASN:HD21	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D5:1196:PHE:CE2	23:U6:610:LEU:HG	2.31	0.64
4:A0:558:LYS:HE3	7:D1:1031:LYS:HD2	1.76	0.64
7:D1:1196:PHE:CZ	23:U3:610:LEU:HD11	2.32	0.64
1:00:28:LYS:HE3	14:L0:472:LEU:HD22	1.79	0.64
14:L1:345:ARG:HH21	16:N0:201:GLN:HG2	1.60	0.64
6:C3:1703:GLU:OE2	24:V0:800:LYS:HB3	1.98	0.64
7:D3:1184:ASP:CB	23:U5:597:ILE:HG23	2.10	0.64
6:C2:1448:MET:HE1	6:C3:88:GLU:OE1	1.98	0.64
7:D1:693:ARG:HH21	9:F3:315:LEU:CG	2.11	0.63
2:12:1373:PRO:HB3	2:13:1074:GLN:OE1	1.98	0.63
6:C2:471:GLN:NE2	20:R0:1205:ALA:HB3	2.12	0.63
4:A0:558:LYS:HE2	7:D1:1031:LYS:HZ2	1.62	0.63
4:A0:279:HIS:CE1	7:D2:886:GLN:HB3	2.32	0.63
7:D5:1186:THR:CG2	23:U6:601:VAL:HB	2.28	0.63
6:C2:1249:ILE:C	20:R0:1265:TRP:HE1	2.06	0.63
2:12:1177:MET:CG	2:13:1108:SER:HA	2.17	0.63
4:A0:558:LYS:CD	7:D1:1031:LYS:HD3	2.28	0.63
7:D0:1186:THR:HA	23:U2:600:LEU:HD12	1.80	0.63
2:10:1177:MET:HG3	2:11:1106:PRO:CA	2.28	0.63
7:D2:1161:LEU:HD21	7:D2:1196:PHE:CG	2.34	0.62
7:D3:1196:PHE:CD1	23:U5:610:LEU:HD21	2.34	0.62
7:D5:1347:ARG:HH22	20:R2:1068:SER:HA	1.63	0.62
17:O2:86:TRP:CZ2	17:O2:105:LYS:HE2	2.34	0.62
6:C4:1249:ILE:HD11	20:R3:1285:THR:N	2.14	0.62
7:D0:1196:PHE:CE1	23:U2:610:LEU:CD2	2.83	0.62
4:A0:239:THR:HG23	7:D1:1028:GLN:OE1	2.00	0.62
7:D5:1354:LEU:HB3	20:R2:1035:ARG:HD3	1.81	0.62
7:D3:1161:LEU:HD21	7:D3:1196:PHE:CG	2.33	0.62
10:H0:427:PHE:CD2	11:I0:364:ILE:CD1	2.64	0.62
14:L3:727:CYS:H	14:L3:731:GLY:C	2.08	0.62
4:A0:690:TYR:CG	7:D1:560:ALA:CB	2.83	0.62
7:D2:1242:HIS:CE1	7:D3:732:LEU:HD23	2.35	0.62
4:A2:690:TYR:HB2	7:D3:560:ALA:CB	2.30	0.61
7:D4:1362:VAL:O	20:R0:1029:ARG:NH1	2.33	0.61
17:O3:86:TRP:CZ2	17:O3:105:LYS:HE2	2.35	0.61
7:D1:1003:VAL:HG13	7:D4:95:GLU:CD	2.26	0.61
7:D1:1003:VAL:C	7:D4:95:GLU:OE2	2.42	0.61
7:D4:1165:TYR:CE1	23:U1:611:PHE:HE1	2.19	0.61
8:E0:165:TYR:CD2	8:E0:269:LEU:HD22	2.36	0.61
7:D4:1195:PRO:HB2	23:U1:610:LEU:HD22	1.80	0.61
7:D5:1347:ARG:NE	20:R2:1072:ALA:HB2	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E0:165:TYR:HE1	8:E0:255:HIS:HD2	1.49	0.61
6:C2:622:PRO:CB	20:R0:1316:SER:HB2	2.26	0.61
6:C2:1249:ILE:CG2	20:R0:1261:GLN:O	2.48	0.61
7:D0:1196:PHE:CE1	23:U2:610:LEU:HD21	2.36	0.61
7:D2:1186:THR:HA	23:U4:600:LEU:HD12	1.82	0.61
1:00:733:LYS:HZ3	14:L1:781:THR:HG22	1.65	0.61
14:L1:345:ARG:NH2	16:N0:201:GLN:CD	2.59	0.61
18:P1:259:GLN:OE1	25:W0:653:VAL:HG13	2.01	0.61
6:C3:1698:GLU:CB	24:V0:796:HIS:NE2	2.64	0.61
2:14:171:SER:HB3	2:15:440:VAL:HG11	1.81	0.61
10:H0:427:PHE:CE2	11:I0:361:ARG:HG3	2.34	0.61
14:L1:345:ARG:HH22	16:N0:201:GLN:CD	2.09	0.61
4:A0:279:HIS:CD2	7:D2:886:GLN:HB3	2.34	0.61
11:I0:305:THR:HG23	12:J0:388:ARG:HH22	1.64	0.61
1:01:745:MET:HE3	1:04:10:ARG:HH21	1.65	0.60
7:D5:1362:VAL:HG13	20:R2:1002:THR:HG22	1.83	0.60
9:F0:164:SER:C	9:F0:165:LEU:HG	2.26	0.60
17:O0:86:TRP:CZ2	17:O0:105:LYS:HE2	2.35	0.60
1:03:78:LYS:HG2	17:O0:98:ARG:HH12	1.64	0.60
6:C3:1698:GLU:HB3	24:V0:796:HIS:NE2	2.15	0.60
6:C4:1695:ASP:HB2	18:P3:257:LYS:HD3	1.83	0.60
7:D4:1196:PHE:CD2	23:U1:610:LEU:HD21	2.36	0.60
2:11:990:GLU:CD	2:11:993:LYS:HE3	2.26	0.60
4:A1:409:LYS:HD3	9:F2:94:ILE:HG22	1.83	0.60
13:K2:912:GLY:HA2	14:L2:909:LEU:HD22	1.83	0.60
1:01:88:GLU:OE1	15:M0:844:THR:HG22	2.02	0.60
6:C4:1249:ILE:HD11	20:R3:1284:ALA:HB1	1.84	0.60
2:10:1291:PRO:HD3	2:14:1306:ILE:HD13	1.83	0.60
2:12:1176:ILE:HG22	2:13:1106:PRO:HG3	1.84	0.60
6:C4:1244:GLN:OE1	17:O3:204:GLU:HB2	2.02	0.60
7:D5:1347:ARG:HH22	20:R2:1068:SER:CA	2.15	0.60
6:C2:1249:ILE:O	20:R0:1265:TRP:HD1	1.84	0.60
2:10:1306:ILE:HD13	2:14:1291:PRO:HD3	1.83	0.59
7:D5:1186:THR:HG23	23:U6:601:VAL:HB	1.84	0.59
4:A0:690:TYR:CG	7:D1:560:ALA:HB2	2.37	0.59
7:D2:1161:LEU:HD22	7:D2:1196:PHE:CE1	2.37	0.59
7:D1:1010:MET:O	7:D4:98:GLY:HA3	2.03	0.59
20:R3:1282:SER:HG	20:R3:1289:TRP:CD1	2.20	0.59
4:A0:558:LYS:CG	7:D1:1031:LYS:NZ	2.65	0.59
7:D1:1011:LEU:HD11	7:D4:95:GLU:OE2	2.02	0.59
4:A2:199:GLY:C	7:D3:939:LYS:HE2	2.27	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:10:1177:MET:HG3	2:11:1106:PRO:HA	1.83	0.58
4:A0:686:ASP:HB3	7:D1:563:ARG:NH1	2.18	0.58
6:C4:1249:ILE:CG1	20:R3:1284:ALA:HB1	2.32	0.58
7:D0:1161:LEU:HD21	7:D0:1196:PHE:CD2	2.38	0.58
13:K0:1138:PRO:CB	13:K1:577:PRO:CD	2.81	0.58
4:A0:199:GLY:HA3	7:D1:898:ARG:HD2	1.84	0.58
6:C3:1241:ASN:HA	6:C3:1252:ARG:HH21	1.69	0.58
2:14:212:LYS:NZ	2:15:443:TRP:CH2	2.68	0.58
8:E0:165:TYR:CD2	8:E0:258:LEU:HD21	2.39	0.58
13:K2:962:ARG:NH2	14:L2:924:GLN:NE2	2.51	0.58
7:D0:1161:LEU:HD21	7:D0:1196:PHE:CG	2.39	0.58
7:D0:1186:THR:CG2	23:U2:601:VAL:HB	2.33	0.58
7:D3:1196:PHE:CE1	23:U5:610:LEU:HD11	2.39	0.58
7:D5:1347:ARG:HH21	20:R2:1154:PRO:HG2	1.67	0.58
7:D3:1161:LEU:HD21	7:D3:1196:PHE:CD2	2.38	0.58
1:00:28:LYS:HG3	14:L0:472:LEU:HD21	1.84	0.58
4:A0:279:HIS:CD2	7:D2:886:GLN:CB	2.87	0.58
6:C3:1249:ILE:HG22	20:R1:1265:TRP:CD1	2.39	0.58
1:00:454:ARG:HE	1:00:466:HIS:CE1	2.22	0.58
1:01:116:TYR:CE2	15:M0:841:ILE:HD13	2.38	0.58
1:01:454:ARG:HE	1:01:466:HIS:CE1	2.22	0.58
4:A4:483:GLU:HG3	6:C3:180:GLN:OE1	2.04	0.58
6:C4:1249:ILE:HG12	20:R3:1284:ALA:HB1	1.85	0.58
6:C4:780:LEU:HB3	17:O3:256:GLU:CD	2.28	0.57
7:D1:1196:PHE:CD1	23:U3:610:LEU:CD2	2.87	0.57
2:16:1716:GLU:CD	2:16:1716:GLU:H	2.12	0.57
13:K2:1149:GLU:HG3	13:K2:1153:GLN:CD	2.29	0.57
2:14:1716:GLU:H	2:14:1716:GLU:CD	2.13	0.57
2:10:1176:ILE:C	2:10:1177:MET:HG2	2.28	0.57
6:C4:696:SER:O	19:Q2:248:ARG:NH1	2.37	0.57
7:D3:1196:PHE:CZ	23:U5:610:LEU:HD11	2.38	0.57
1:03:454:ARG:HE	1:03:466:HIS:CE1	2.22	0.57
1:04:454:ARG:HE	1:04:466:HIS:CE1	2.23	0.57
4:A2:690:TYR:CB	7:D3:560:ALA:CB	2.82	0.57
6:C4:1244:GLN:CG	20:R3:1283:SER:OG	2.53	0.57
13:K2:966:LYS:HG3	14:L2:919:LEU:HD12	1.86	0.57
10:H0:427:PHE:HE2	11:I0:361:ARG:HA	1.67	0.57
2:15:1716:GLU:CD	2:15:1716:GLU:H	2.13	0.57
4:A2:141:LYS:HE3	6:C1:1992:ARG:HH11	1.70	0.57
4:A4:167:ILE:HG23	6:C3:4:PRO:CD	2.34	0.57
4:A6:141:LYS:HE3	6:C4:1992:ARG:HH11	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C4:1244:GLN:HB3	20:R3:1283:SER:HA	1.87	0.56
7:D1:1196:PHE:CD2	23:U3:610:LEU:HD11	2.40	0.56
1:03:626:ILE:CG2	15:M1:497:MET:HE1	2.35	0.56
6:C3:696:SER:O	19:Q0:248:ARG:NH1	2.39	0.56
6:C4:781:GLU:OE1	17:O3:259:SER:HB3	2.04	0.56
6:C2:730:PRO:HG3	17:O0:258:THR:CG2	2.34	0.56
6:C2:1250:GLY:CA	20:R0:1265:TRP:CG	2.85	0.56
7:D0:1196:PHE:CE2	23:U2:610:LEU:HD13	2.41	0.56
13:K2:912:GLY:CA	14:L2:909:LEU:HD22	2.36	0.56
1:03:78:LYS:HZ3	17:O0:98:ARG:CD	2.17	0.56
6:C0:1661:ARG:NH2	6:C1:1807:TRP:HE1	2.03	0.56
7:D0:1161:LEU:HD22	7:D0:1196:PHE:CZ	2.39	0.56
4:A0:558:LYS:HG3	7:D1:1031:LYS:HZ3	1.69	0.56
7:D2:1161:LEU:CD2	7:D2:1196:PHE:CD1	2.89	0.56
2:10:1290:ASN:ND2	2:14:1307:LYS:O	2.37	0.56
3:40:165:LYS:HG2	3:40:179:ASN:CB	2.35	0.56
17:O1:86:TRP:CZ2	17:O1:105:LYS:HE2	2.41	0.56
2:11:747:ALA:HB1	2:11:748:PRO:HD2	1.88	0.56
2:12:1373:PRO:HB3	2:13:1074:GLN:CD	2.31	0.56
2:10:1716:GLU:CD	2:10:1716:GLU:H	2.14	0.55
4:A2:409:LYS:HD3	9:F1:94:ILE:HG22	1.88	0.55
7:D4:1195:PRO:O	23:U1:611:PHE:CE2	2.59	0.55
2:17:1716:GLU:H	2:17:1716:GLU:CD	2.14	0.55
7:D5:1161:LEU:HD22	7:D5:1196:PHE:CD2	2.41	0.55
1:02:454:ARG:HE	1:02:466:HIS:CE1	2.24	0.55
4:A3:409:LYS:HD3	9:F0:94:ILE:HG22	1.89	0.55
7:D1:1196:PHE:CE2	23:U3:610:LEU:CD1	2.83	0.55
1:01:11:TYR:CE1	14:L1:245:VAL:CG1	2.89	0.55
7:D0:1237:SER:OG	7:D1:736:ASN:CB	2.54	0.55
6:C2:1249:ILE:CA	20:R0:1265:TRP:HE1	2.18	0.55
2:11:745:VAL:HG12	2:11:746:CYS:H	1.72	0.55
1:01:11:TYR:CE1	14:L1:245:VAL:HG11	2.42	0.55
2:13:1716:GLU:H	2:13:1716:GLU:CD	2.15	0.55
4:A3:163:GLU:H	4:A3:164:PRO:HD2	1.71	0.55
7:D5:674:MET:HE2	7:D5:823:PHE:CE2	2.42	0.55
13:K1:969:THR:HA	14:L1:879:ASP:OD2	2.06	0.55
6:C2:786:GLN:NE2	17:O0:257:LEU:CD1	2.70	0.55
6:C2:786:GLN:HE22	17:O0:257:LEU:HD13	1.72	0.55
6:C4:1249:ILE:CD1	20:R3:1284:ALA:HA	2.29	0.55
9:F0:164:SER:O	9:F0:165:LEU:CG	2.55	0.55
1:00:28:LYS:HE3	14:L0:472:LEU:CD2	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:14:1831:VAL:HG11	7:D3:689:LYS:HZ3	1.69	0.55
4:A3:218:LYS:HZ1	4:A3:222:ASP:CG	2.16	0.55
6:C4:1249:ILE:CD1	20:R3:1284:ALA:HB1	2.37	0.55
6:C2:788:VAL:HG22	17:O0:258:THR:HG1	1.71	0.54
7:D1:1186:THR:CG2	23:U3:601:VAL:HB	2.37	0.54
7:D2:1196:PHE:CD2	23:U4:610:LEU:CD1	2.90	0.54
7:D3:1196:PHE:CD1	23:U5:610:LEU:HD11	2.42	0.54
7:D5:1184:ASP:CG	23:U6:597:ILE:CG2	2.79	0.54
7:D0:1161:LEU:CD2	7:D0:1196:PHE:CD1	2.91	0.54
7:D5:1195:PRO:HB2	23:U6:610:LEU:HD22	1.89	0.54
1:O1:549:ALA:HB1	14:L1:233:ALA:HB1	1.89	0.54
4:A0:239:THR:HG21	7:D1:1028:GLN:CD	2.31	0.54
7:D0:674:MET:HE2	7:D0:823:PHE:CE2	2.42	0.54
7:D4:1161:LEU:CD2	7:D4:1196:PHE:CD2	2.91	0.54
7:D1:1161:LEU:HD21	7:D1:1196:PHE:CG	2.42	0.54
7:D1:1161:LEU:HD22	7:D1:1196:PHE:CZ	2.42	0.54
7:D5:1184:ASP:HB3	23:U6:597:ILE:CG2	2.12	0.54
7:D5:1362:VAL:HG11	20:R2:1006:LYS:HB2	1.89	0.54
6:C2:788:VAL:CG2	17:O0:258:THR:OG1	2.48	0.54
6:C2:1249:ILE:HB	20:R0:1265:TRP:NE1	2.15	0.54
7:D0:1238:SER:HB2	7:D1:734:ASN:HB2	1.90	0.54
7:D1:1196:PHE:CD2	23:U3:610:LEU:CD1	2.90	0.54
20:R3:1282:SER:H	20:R3:1286:ASP:CG	2.15	0.54
7:D5:1161:LEU:CD2	7:D5:1196:PHE:CD2	2.90	0.54
4:A4:168:SER:O	6:C3:4:PRO:HG3	2.08	0.54
13:K2:1153:GLN:CD	13:K3:596:ILE:CG2	2.74	0.54
1:O3:78:LYS:HD3	17:O0:98:ARG:CD	2.38	0.54
6:C3:1246:MET:CG	20:R1:1287:GLU:HG3	2.38	0.54
21:S0:83:GLU:CD	21:S0:94:LYS:HZ2	2.16	0.53
2:12:1716:GLU:CD	2:12:1716:GLU:H	2.17	0.53
2:13:1290:ASN:ND2	2:17:1307:LYS:O	2.40	0.53
18:P0:245:PRO:O	24:V0:923:THR:HG22	2.09	0.53
21:S3:83:GLU:CD	21:S3:94:LYS:HZ2	2.17	0.53
23:U0:823:LEU:HD12	25:W0:230:TYR:CE1	2.43	0.53
4:A0:690:TYR:CB	7:D1:560:ALA:HB1	2.38	0.53
7:D4:1195:PRO:CB	23:U1:610:LEU:HD22	2.38	0.53
1:O1:688:HIS:CE1	1:O4:4:SER:CB	2.92	0.53
7:D5:1184:ASP:HB3	23:U6:597:ILE:N	2.24	0.53
1:O0:375:THR:HB	1:O0:376:PHE:CD2	2.44	0.53
2:11:443:TRP:HZ2	2:12:212:LYS:HZ1	1.56	0.53
7:D2:1235:LEU:CD1	7:D3:735:PRO:CB	2.87	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K0:947:GLU:H	13:K0:947:GLU:CD	2.17	0.53
1:02:202:GLU:CD	1:02:202:GLU:H	2.17	0.53
2:10:1177:MET:CB	2:11:1106:PRO:HA	2.38	0.53
7:D0:1196:PHE:CE2	23:U2:610:LEU:CD1	2.91	0.53
7:D1:1161:LEU:HD22	7:D1:1196:PHE:CE1	2.44	0.53
2:11:1105:GLN:HA	2:11:1106:PRO:C	2.34	0.53
6:C3:1698:GLU:HB2	24:V0:796:HIS:CE1	2.44	0.53
4:A2:448:TYR:CZ	9:F1:89:PRO:HD3	2.44	0.53
7:D2:993:PRO:HG3	7:D3:426:GLU:OE2	2.09	0.53
7:D2:1161:LEU:HD22	7:D2:1196:PHE:CD1	2.44	0.53
7:D4:1161:LEU:HD22	7:D4:1196:PHE:CD2	2.44	0.53
4:A0:141:LYS:HE3	6:C0:1992:ARG:HH11	1.74	0.53
4:A0:239:THR:HG22	7:D1:1028:GLN:CB	2.27	0.53
4:A1:448:TYR:CZ	9:F2:89:PRO:HD3	2.44	0.53
6:C4:792:GLY:HA3	20:R3:1404:HIS:CD2	2.44	0.53
18:P0:185:LEU:HD13	25:W0:708:ALA:O	2.08	0.53
2:13:1307:LYS:O	2:17:1290:ASN:ND2	2.42	0.52
6:C3:781:GLU:OE2	17:O1:258:THR:HG23	2.07	0.52
7:D2:1186:THR:CG2	23:U4:601:VAL:HB	2.39	0.52
15:M1:317:HIS:CE1	16:N1:7:THR:HG23	2.44	0.52
7:D4:674:MET:HE2	7:D4:823:PHE:CE2	2.44	0.52
7:D5:1184:ASP:CB	23:U6:597:ILE:N	2.72	0.52
20:R1:1053:PHE:H	20:R1:1054:PRO:HD2	1.73	0.52
20:R2:1064:GLY:O	20:R2:1068:SER:HB2	2.09	0.52
2:13:1306:ILE:HD13	2:17:1291:PRO:HD3	1.90	0.52
6:C2:730:PRO:CG	17:O0:258:THR:HG22	2.38	0.52
6:C2:1249:ILE:CD1	20:R0:1284:ALA:CB	2.86	0.52
14:L1:419:LEU:CD2	16:N0:139:GLN:HE22	2.09	0.52
2:11:1716:GLU:CD	2:11:1716:GLU:H	2.17	0.52
2:14:1831:VAL:HG11	7:D3:689:LYS:NZ	2.18	0.52
7:D0:1279:ASN:O	7:D1:736:ASN:ND2	2.40	0.52
7:D1:674:MET:HE2	7:D1:823:PHE:CE2	2.44	0.52
7:D3:1186:THR:CG2	23:U5:601:VAL:HB	2.39	0.52
13:K2:1153:GLN:HG2	13:K3:596:ILE:CD1	2.40	0.52
13:K2:947:GLU:CD	13:K2:947:GLU:H	2.17	0.52
6:C4:1695:ASP:O	18:P3:257:LYS:HG2	2.10	0.52
21:S2:83:GLU:CD	21:S2:94:LYS:HZ2	2.17	0.52
1:03:31:TYR:OH	15:M1:541:GLN:HG2	2.09	0.52
2:11:1346:ILE:HD12	2:12:1024:ALA:HB1	1.92	0.52
4:A0:239:THR:CG2	7:D1:1028:GLN:CG	2.79	0.52
4:A0:371:LEU:HD22	4:A0:395:GLY:HA3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D0:1389:ARG:NH1	7:D1:948:HIS:CE1	2.77	0.52
15:M1:549:ALA:HB1	15:M1:553:TRP:CZ3	2.44	0.52
17:O2:204:GLU:CD	17:O2:204:GLU:H	2.17	0.52
4:A4:371:LEU:HD22	4:A4:395:GLY:HA3	1.92	0.52
7:D0:1185:ILE:CG2	23:U2:600:LEU:HB2	2.40	0.52
7:D5:1347:ARG:HA	7:D5:1350:THR:H	1.74	0.52
4:A1:218:LYS:HZ1	4:A1:222:ASP:CG	2.17	0.52
18:P1:259:GLN:OE1	25:W0:653:VAL:CG1	2.58	0.52
6:C2:620:GLU:HA	20:R0:1317:HIS:CE1	2.44	0.51
6:C4:1240:VAL:HG11	6:C4:1256:MET:HE2	1.92	0.51
19:Q0:57:SER:OG	24:V0:851:VAL:CG2	2.50	0.51
4:A4:167:ILE:CG2	6:C3:4:PRO:HD2	2.38	0.51
6:C4:1237:VAL:HG22	6:C4:1256:MET:HE1	1.92	0.51
7:D0:1389:ARG:HD3	7:D1:948:HIS:NE2	2.25	0.51
10:H0:427:PHE:CE2	11:I0:361:ARG:NE	2.72	0.51
2:13:1291:PRO:HD3	2:17:1306:ILE:HD13	1.93	0.51
13:K0:1138:PRO:CB	13:K1:577:PRO:HD3	2.40	0.51
2:14:171:SER:HB3	2:15:440:VAL:CG1	2.41	0.51
2:14:171:SER:CB	2:15:440:VAL:HG11	2.40	0.51
1:03:78:LYS:HD3	17:O0:98:ARG:CZ	2.39	0.51
4:A4:456:ASN:CB	6:C3:244:GLU:OE1	2.59	0.51
6:C3:18:LYS:HE3	6:C3:22:HIS:CE1	2.45	0.51
20:R3:1281:GLU:H	20:R3:1281:GLU:CD	2.19	0.51
7:D2:1161:LEU:CD2	7:D2:1196:PHE:CG	2.94	0.51
1:00:24:GLN:NE2	14:L0:473:ASP:OD1	2.43	0.51
1:02:454:ARG:HH21	1:02:466:HIS:CG	2.28	0.51
6:C3:1702:MET:HE2	24:V0:797:LEU:HD11	1.92	0.51
15:M0:584:CYS:HB2	15:M0:585:SER:HA	1.92	0.51
21:S1:83:GLU:CD	21:S1:94:LYS:HZ2	2.19	0.51
7:D0:1238:SER:HB2	7:D1:734:ASN:CB	2.41	0.51
4:A0:690:TYR:CG	7:D1:560:ALA:HB1	2.45	0.51
4:A4:175:ARG:HG3	4:A4:175:ARG:HH11	1.75	0.51
23:U1:610:LEU:C	23:U1:610:LEU:HD23	2.36	0.51
1:04:454:ARG:HH21	1:04:466:HIS:CG	2.28	0.51
14:L1:305:LYS:HE2	15:M1:510:PHE:CZ	2.46	0.51
4:A0:275:PHE:CE1	9:F3:122:PRO:HA	2.46	0.50
7:D4:1184:ASP:CG	23:U1:597:ILE:CG2	2.84	0.50
1:00:202:GLU:CD	1:00:202:GLU:H	2.19	0.50
6:C4:780:LEU:HB3	17:O3:256:GLU:OE1	2.11	0.50
7:D0:1237:SER:HB2	7:D1:736:ASN:HB2	1.92	0.50
13:K2:966:LYS:CG	14:L2:919:LEU:HD12	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O0:207:ARG:HE	20:R0:1286:ASP:CG	2.19	0.50
2:11:1177:MET:N	2:12:1106:PRO:HB3	2.23	0.50
6:C2:1249:ILE:HG23	20:R0:1261:GLN:O	2.10	0.50
6:C4:781:GLU:CB	17:O3:258:THR:OG1	2.58	0.50
8:E0:165:TYR:HD2	8:E0:269:LEU:HD22	1.76	0.50
14:L3:322:GLU:CD	14:L3:330:ARG:HH21	2.19	0.50
13:K0:1142:PHE:CZ	13:K0:1146:ALA:HB2	2.47	0.50
7:D1:1011:LEU:CD1	7:D4:95:GLU:OE2	2.59	0.50
23:U0:842:ARG:O	23:U0:846:ILE:HG23	2.12	0.50
4:A0:683:LYS:HZ3	7:D1:567:ALA:HB2	1.71	0.50
6:C2:1249:ILE:HG23	20:R0:1261:GLN:C	2.37	0.50
13:K2:71:HIS:N	13:K2:83:THR:HG1	2.09	0.50
25:W0:513:GLU:O	25:W0:514:VAL:HG23	2.12	0.50
4:A3:819:ASN:HA	7:D3:1120:ARG:HH21	1.77	0.50
6:C1:658:GLU:H	6:C1:658:GLU:CD	2.19	0.50
13:K3:71:HIS:N	13:K3:83:THR:HG1	2.09	0.50
4:A6:371:LEU:HD22	4:A6:395:GLY:HA3	1.92	0.50
6:C3:468:GLU:OE2	20:R1:1205:ALA:CB	2.60	0.50
7:D2:674:MET:HE2	7:D2:823:PHE:CE2	2.47	0.50
7:D3:1161:LEU:CD2	7:D3:1196:PHE:CD1	2.95	0.50
19:Q0:57:SER:HB3	24:V0:851:VAL:CG1	2.33	0.50
1:01:57:GLU:H	1:01:57:GLU:CD	2.20	0.50
6:C4:780:LEU:HB3	17:O3:256:GLU:OE2	2.12	0.50
10:H1:468:LYS:HE3	10:H1:472:GLU:CD	2.37	0.50
7:D0:1237:SER:CB	7:D1:736:ASN:HB2	2.42	0.49
1:04:202:GLU:CD	1:04:202:GLU:H	2.19	0.49
2:17:1012:LYS:HE3	2:17:1013:TYR:CE1	2.47	0.49
6:C0:1370:MET:SD	6:C0:1446:LYS:HE3	2.52	0.49
17:O1:86:TRP:CH2	17:O1:105:LYS:HE2	2.47	0.49
1:00:57:GLU:H	1:00:57:GLU:CD	2.20	0.49
1:03:334:ILE:HG22	1:03:335:LYS:H	1.77	0.49
6:C4:327:ALA:HB2	6:C4:366:ASP:HB2	1.94	0.49
7:D3:674:MET:HE2	7:D3:823:PHE:CE2	2.48	0.49
1:01:202:GLU:CD	1:01:202:GLU:H	2.20	0.49
6:C0:658:GLU:CD	6:C0:658:GLU:H	2.20	0.49
6:C4:420:MET:HE1	21:S2:87:ASP:HB2	1.93	0.49
7:D3:1196:PHE:CG	23:U5:610:LEU:CD1	2.94	0.49
7:D5:1346:ARG:HD2	20:R2:1155:GLY:HA3	1.95	0.49
7:D5:1346:ARG:HD2	20:R2:1155:GLY:CA	2.42	0.49
15:M1:587:LEU:HB3	15:M1:588:PRO:HD2	1.94	0.49
6:C3:1463:GLN:NE2	6:C3:1502:ARG:HH22	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D0:1389:ARG:HH11	7:D1:948:HIS:CE1	2.30	0.49
1:03:57:GLU:CD	1:03:57:GLU:H	2.20	0.49
2:12:1306:ILE:HD13	2:16:1291:PRO:HD3	1.94	0.49
6:C3:1698:GLU:HB2	24:V0:796:HIS:NE2	2.27	0.49
7:D2:1196:PHE:CE1	23:U4:610:LEU:CD2	2.94	0.49
4:A0:558:LYS:HG3	7:D1:1031:LYS:CE	2.43	0.49
4:A4:129:HIS:HA	6:C2:1632:THR:HG21	1.95	0.49
17:O2:200:PHE:CZ	17:O2:211:LYS:HE2	2.48	0.49
1:00:334:ILE:HG22	1:00:335:LYS:H	1.77	0.49
1:03:202:GLU:H	1:03:202:GLU:CD	2.21	0.49
2:10:1176:ILE:C	2:10:1177:MET:CG	2.86	0.49
4:A2:690:TYR:CD2	7:D3:560:ALA:HB2	2.47	0.49
6:C2:622:PRO:HB2	20:R0:1344:TYR:OH	2.12	0.49
6:C4:1244:GLN:NE2	17:O3:205:ASN:ND2	2.49	0.49
7:D5:1343:ASN:HA	7:D5:1346:ARG:HH12	1.77	0.49
13:K3:947:GLU:CD	13:K3:947:GLU:H	2.21	0.49
15:M1:788:LYS:HE3	15:M1:792:GLU:HG3	1.95	0.49
6:C1:1224:GLN:HE21	6:C1:1277:HIS:CG	2.30	0.49
7:D1:1003:VAL:CG1	7:D4:95:GLU:OE2	2.61	0.49
4:A3:448:TYR:CZ	9:F0:89:PRO:HD3	2.47	0.49
6:C1:1370:MET:SD	6:C1:1446:LYS:HE3	2.52	0.49
13:K0:1138:PRO:HB3	13:K1:577:PRO:HD3	1.95	0.49
14:L0:490:GLU:CD	14:L0:490:GLU:H	2.21	0.49
14:L1:291:TYR:CE1	16:N0:201:GLN:OE1	2.66	0.49
6:C0:1751:LEU:HA	6:C0:1889:LEU:HD21	1.95	0.48
1:03:78:LYS:HZ3	17:O0:98:ARG:HD2	1.78	0.48
2:12:990:GLU:CD	2:12:993:LYS:HE3	2.38	0.48
4:A2:760:PHE:CE1	4:A2:764:LYS:HE3	2.48	0.48
13:K3:595:LEU:C	13:K3:596:ILE:HD13	2.38	0.48
1:02:708:LYS:HE2	1:02:756:TYR:CG	2.48	0.48
4:A2:371:LEU:HD22	4:A2:395:GLY:HA3	1.94	0.48
4:A6:249:GLU:H	4:A6:249:GLU:CD	2.22	0.48
6:C2:622:PRO:HA	20:R0:1316:SER:CB	2.32	0.48
9:F0:100:SER:HA	9:F0:101:PRO:C	2.39	0.48
14:L1:490:GLU:CD	14:L1:490:GLU:H	2.21	0.48
14:L3:734:SER:HB3	14:L3:735:PRO:HD3	1.94	0.48
2:12:1291:PRO:HD3	2:16:1306:ILE:HD13	1.95	0.48
6:C2:1448:MET:HE1	6:C3:88:GLU:CD	2.38	0.48
7:D2:922:GLN:HG2	9:F3:268:ILE:HD12	1.95	0.48
7:D3:1161:LEU:CD2	7:D3:1196:PHE:CG	2.96	0.48
7:D4:1366:SER:HB3	20:R0:999:THR:HG22	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D5:1347:ARG:HE	20:R2:1154:PRO:HB2	1.78	0.48
15:M3:788:LYS:HE3	15:M3:792:GLU:HG3	1.95	0.48
1:00:375:THR:O	1:00:378:ASN:ND2	2.46	0.48
2:10:1012:LYS:HE3	2:10:1013:TYR:CE1	2.48	0.48
6:C2:327:ALA:HB2	6:C2:366:ASP:HB2	1.96	0.48
6:C4:1751:LEU:HA	6:C4:1889:LEU:HD21	1.96	0.48
7:D5:1195:PRO:CB	23:U6:610:LEU:HD22	2.43	0.48
13:K2:966:LYS:HG3	14:L2:919:LEU:CD1	2.43	0.48
1:01:88:GLU:CD	15:M0:844:THR:HG22	2.38	0.48
4:A2:690:TYR:CB	7:D3:560:ALA:HB2	2.44	0.48
6:C2:1114:SER:HB3	6:C2:1281:HIS:CD2	2.49	0.48
7:D1:563:ARG:HH11	7:D1:563:ARG:CG	2.27	0.48
7:D1:715:LYS:HE3	7:D1:864:PRO:HG3	1.96	0.48
10:H3:468:LYS:HE3	10:H3:472:GLU:CD	2.38	0.48
1:04:708:LYS:HE2	1:04:756:TYR:CG	2.48	0.48
4:A1:371:LEU:HD22	4:A1:395:GLY:HA3	1.95	0.48
5:B1:833:VAL:HG21	6:C1:1380:PRO:HD2	1.96	0.48
7:D1:1171:VAL:HG22	7:D1:1196:PHE:CE1	2.48	0.48
22:T0:741:LYS:HE3	22:T0:748:GLY:HA3	1.96	0.48
6:C2:786:GLN:NE2	17:O0:257:LEU:HD12	2.29	0.48
7:D1:134:LEU:HD21	9:F1:287:ARG:HH12	1.78	0.48
4:A4:175:ARG:HD2	6:C3:48:PRO:HD3	1.96	0.48
6:C4:781:GLU:HG3	17:O3:256:GLU:HB2	1.96	0.48
23:U4:610:LEU:HD23	23:U4:611:PHE:CD1	2.49	0.48
1:03:454:ARG:HH21	1:03:466:HIS:CG	2.32	0.48
2:10:1307:LYS:O	2:14:1290:ASN:ND2	2.44	0.48
2:11:1788:ASP:CG	2:11:1789:ARG:H	2.21	0.48
4:A3:371:LEU:HD22	4:A3:395:GLY:HA3	1.95	0.48
6:C0:1224:GLN:HE21	6:C0:1277:HIS:CG	2.31	0.48
6:C4:1249:ILE:HD11	20:R3:1284:ALA:C	2.36	0.48
14:L3:490:GLU:H	14:L3:490:GLU:CD	2.22	0.48
1:03:78:LYS:HZ1	17:O0:98:ARG:HB3	1.78	0.47
2:11:1290:ASN:ND2	2:15:1307:LYS:O	2.44	0.47
1:03:78:LYS:CD	17:O0:98:ARG:CD	2.92	0.47
4:A0:91:GLU:CD	10:H0:453:TYR:H	2.21	0.47
6:C4:749:THR:HB	19:Q2:226:HIS:CE1	2.48	0.47
4:A2:287:PRO:HG2	8:E0:652:HIS:CD2	2.49	0.47
4:A2:690:TYR:CG	7:D3:560:ALA:HB2	2.50	0.47
6:C2:471:GLN:NE2	20:R0:1205:ALA:HB1	2.03	0.47
14:L2:490:GLU:H	14:L2:490:GLU:CD	2.22	0.47
15:M0:549:ALA:HB1	15:M0:553:TRP:CZ3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P1:320:LYS:HE2	25:W0:663:LYS:HG2	1.97	0.47
1:03:78:LYS:HD3	17:O0:98:ARG:HD2	1.95	0.47
2:17:576:CYS:HB2	2:17:579:PHE:CE1	2.49	0.47
6:C1:1751:LEU:HA	6:C1:1889:LEU:HD21	1.96	0.47
7:D1:1186:THR:HA	23:U3:600:LEU:HD12	1.96	0.47
14:L1:340:ARG:NH2	16:N0:142:VAL:H	2.12	0.47
1:01:454:ARG:HH21	1:01:466:HIS:CG	2.33	0.47
1:01:607:LYS:HE3	1:01:654:PHE:CE1	2.50	0.47
2:10:672:ILE:H	2:10:672:ILE:HD12	1.79	0.47
2:11:1291:PRO:HD3	2:15:1306:ILE:HD13	1.96	0.47
4:A4:168:SER:O	6:C3:4:PRO:CG	2.62	0.47
20:R2:1064:GLY:O	20:R2:1068:SER:CB	2.62	0.47
1:04:607:LYS:HE3	1:04:654:PHE:CE1	2.50	0.47
2:11:1306:ILE:HD13	2:15:1291:PRO:HD3	1.97	0.47
4:A0:448:TYR:CZ	9:F3:89:PRO:HD3	2.50	0.47
13:K0:71:HIS:N	13:K0:83:THR:HG1	2.12	0.47
15:M3:549:ALA:HB1	15:M3:553:TRP:CZ3	2.49	0.47
22:T1:741:LYS:HE3	22:T1:748:GLY:HA3	1.96	0.47
1:01:18:SER:O	14:L1:472:LEU:HD21	2.14	0.47
4:A0:558:LYS:HD2	7:D1:1031:LYS:HD3	1.95	0.47
4:A2:690:TYR:HB2	7:D3:560:ALA:HB1	1.96	0.47
4:A4:760:PHE:CE1	4:A4:764:LYS:HE3	2.50	0.47
6:C3:1751:LEU:HA	6:C3:1889:LEU:HD21	1.96	0.47
6:C4:658:GLU:CD	6:C4:658:GLU:H	2.23	0.47
7:D3:890:LYS:HE2	7:D3:894:GLU:OE2	2.14	0.47
7:D3:1195:PRO:O	23:U5:610:LEU:HB2	2.15	0.47
7:D5:1347:ARG:NH1	20:R2:1068:SER:C	2.72	0.47
8:E0:165:TYR:HE1	8:E0:255:HIS:CD2	2.31	0.47
12:J1:452:LYS:HZ1	12:J1:456:GLU:CD	2.23	0.47
13:K1:825:LYS:HE2	13:K1:832:TYR:CE1	2.50	0.47
13:K3:596:ILE:HG22	13:K3:599:HIS:H	1.80	0.47
1:00:607:LYS:HE3	1:00:654:PHE:CE1	2.50	0.47
3:40:143:PHE:CE1	3:40:291:THR:HG21	2.50	0.47
6:C3:46:HIS:C	6:C3:48:PRO:HD2	2.40	0.47
1:01:688:HIS:CE1	1:04:4:SER:OG	2.68	0.47
4:A0:199:GLY:CA	7:D1:898:ARG:HD2	2.43	0.47
4:A0:409:LYS:HD3	9:F3:94:ILE:HG22	1.96	0.47
7:D0:1196:PHE:CD2	23:U2:610:LEU:HD13	2.50	0.47
7:D3:922:GLN:HG2	7:D5:86:ARG:NE	2.30	0.47
2:17:672:ILE:HD12	2:17:672:ILE:H	1.80	0.47
4:A5:757:PHE:CE1	4:A5:761:LYS:HE3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C2:1224:GLN:HE21	6:C2:1277:HIS:CD2	2.33	0.47
7:D1:898:ARG:NE	7:D1:927:GLU:OE1	2.48	0.47
7:D1:1161:LEU:CD2	7:D1:1196:PHE:CD1	2.98	0.47
9:F0:308:THR:HB	9:F0:309:PRO:CD	2.45	0.47
15:M1:402:HIS:CB	15:M1:403:LEU:HA	2.46	0.47
1:00:454:ARG:HH21	1:00:466:HIS:CG	2.33	0.46
1:02:334:ILE:HG22	1:02:335:LYS:H	1.79	0.46
4:A2:199:GLY:O	7:D3:939:LYS:HE2	2.15	0.46
4:A2:757:PHE:CE1	4:A2:761:LYS:HE3	2.49	0.46
5:B1:833:VAL:HG21	6:C1:1380:PRO:CD	2.45	0.46
6:C4:1224:GLN:HE21	6:C4:1277:HIS:CG	2.33	0.46
7:D4:1185:ILE:HG23	23:U1:600:LEU:HD13	1.96	0.46
13:K0:1142:PHE:CE2	13:K1:594:SER:HA	2.51	0.46
13:K1:261:SER:C	13:K1:263:PHE:HA	2.40	0.46
17:O3:2:PHE:HA	18:P3:58:ARG:O	2.15	0.46
23:U0:827:TRP:CZ3	23:U0:838:LYS:HE2	2.49	0.46
23:U6:610:LEU:HD23	23:U6:610:LEU:C	2.40	0.46
1:00:28:LYS:CE	14:L0:472:LEU:CD2	2.93	0.46
1:03:607:LYS:HE3	1:03:654:PHE:CE1	2.50	0.46
4:A0:199:GLY:HA2	7:D1:898:ARG:HD3	1.96	0.46
7:D1:1186:THR:HG21	23:U3:601:VAL:HB	1.96	0.46
7:D5:1351:ASN:HD21	20:R2:1069:ARG:HD2	1.80	0.46
13:K0:1138:PRO:HB3	13:K1:577:PRO:CD	2.45	0.46
23:U2:609:ASN:O	23:U2:610:LEU:C	2.56	0.46
1:00:607:LYS:HE3	1:00:654:PHE:CD1	2.51	0.46
2:11:672:ILE:HD12	2:11:672:ILE:H	1.80	0.46
1:02:607:LYS:HE3	1:02:654:PHE:CE1	2.49	0.46
4:A0:279:HIS:CD2	7:D2:886:GLN:HB2	2.50	0.46
6:C0:327:ALA:HB2	6:C0:366:ASP:HB2	1.96	0.46
7:D2:1170:SER:OG	23:U4:610:LEU:O	2.34	0.46
7:D4:813:GLU:CD	7:D4:813:GLU:H	2.24	0.46
13:K0:346:LYS:HE2	13:K0:407:LEU:O	2.16	0.46
19:Q2:143:GLU:CG	19:Q2:155:LEU:HD11	2.46	0.46
2:12:672:ILE:HD12	2:12:672:ILE:H	1.80	0.46
4:A4:141:LYS:CE	6:C2:1992:ARG:HH11	2.25	0.46
9:F0:196:TYR:CE1	9:F0:227:LYS:HE2	2.50	0.46
22:T0:2:ARG:HA	22:T0:423:HIS:O	2.16	0.46
1:01:607:LYS:HE3	1:01:654:PHE:CD1	2.51	0.46
1:01:708:LYS:HE2	1:01:756:TYR:CG	2.51	0.46
1:03:607:LYS:HE3	1:03:654:PHE:CD1	2.51	0.46
4:A0:558:LYS:CG	7:D1:1031:LYS:HZ2	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C3:1697:ASN:HD21	18:P1:257:LYS:HG3	1.80	0.46
9:F0:164:SER:O	9:F0:165:LEU:CD2	2.63	0.46
6:C4:793:GLU:HG3	20:R3:1404:HIS:HB2	1.97	0.46
6:C4:1249:ILE:HG22	20:R3:1265:TRP:NE1	2.27	0.46
13:K0:1142:PHE:HB3	13:K1:595:LEU:HD11	1.96	0.46
13:K2:346:LYS:HE2	13:K2:407:LEU:O	2.16	0.46
13:K2:912:GLY:HA2	14:L2:909:LEU:CD2	2.46	0.46
13:K2:963:TYR:CE2	14:L2:921:TYR:HB3	2.51	0.46
13:K2:1149:GLU:HG3	13:K2:1153:GLN:NE2	2.30	0.46
14:L0:322:GLU:CD	14:L0:330:ARG:HH21	2.23	0.46
1:00:708:LYS:HE2	1:00:756:TYR:CG	2.51	0.46
1:03:708:LYS:HE2	1:03:756:TYR:CG	2.51	0.46
2:11:776:VAL:HG22	2:11:888:GLU:HB2	1.98	0.46
2:14:171:SER:CB	2:15:440:VAL:CG1	2.94	0.46
6:C3:327:ALA:HB2	6:C3:366:ASP:HB2	1.98	0.46
6:C3:1252:ARG:HH11	20:R1:1261:GLN:HB2	1.80	0.46
9:F3:254:ARG:HH11	9:F3:254:ARG:HG3	1.81	0.46
6:C1:327:ALA:HB2	6:C1:366:ASP:HB2	1.96	0.46
7:D4:1161:LEU:HD21	7:D4:1196:PHE:CD2	2.51	0.46
7:D5:1341:VAL:CG1	7:D5:1346:ARG:HA	2.46	0.46
13:K0:1139:TYR:HA	13:K1:595:LEU:CD1	2.43	0.46
13:K3:969:THR:CA	14:L3:879:ASP:OD2	2.61	0.46
2:10:1291:PRO:HD3	2:14:1306:ILE:CD1	2.45	0.46
2:10:1306:ILE:CD1	2:14:1291:PRO:HD3	2.45	0.46
2:11:747:ALA:HB1	2:11:748:PRO:CD	2.46	0.46
7:D2:1185:ILE:CG2	23:U4:600:LEU:HB2	2.46	0.46
2:14:672:ILE:H	2:14:672:ILE:HD12	1.81	0.45
4:A0:240:ASP:HB2	7:D1:1056:ALA:HB3	1.97	0.45
5:B1:832:ASN:C	5:B1:833:VAL:HG23	2.40	0.45
7:D5:1343:ASN:HA	7:D5:1346:ARG:NH1	2.31	0.45
15:M0:402:HIS:CG	15:M0:403:LEU:HA	2.50	0.45
4:A4:175:ARG:CZ	4:A4:177:SER:HA	2.47	0.45
6:C4:697:ARG:HA	19:Q2:248:ARG:HD2	1.99	0.45
7:D0:1185:ILE:HG23	23:U2:600:LEU:HD13	1.98	0.45
7:D4:1366:SER:CB	20:R0:999:THR:HG21	2.36	0.45
19:Q0:143:GLU:CG	19:Q0:155:LEU:HD11	2.46	0.45
23:U0:855:VAL:HG11	25:W0:233:SER:HA	1.96	0.45
1:02:708:LYS:HE2	1:02:756:TYR:CD1	2.52	0.45
1:04:708:LYS:HE2	1:04:756:TYR:CD1	2.51	0.45
4:A0:371:LEU:C	4:A0:371:LEU:HD23	2.42	0.45
6:C4:1765:GLN:HE21	6:C4:1899:THR:HG23	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D1:1196:PHE:CE1	23:U3:610:LEU:CD2	2.92	0.45
13:K3:346:LYS:HE2	13:K3:407:LEU:O	2.17	0.45
4:A5:760:PHE:CZ	4:A5:764:LYS:HE3	2.52	0.45
6:C2:1532:ASP:CG	6:C2:1556:LYS:HZ2	2.25	0.45
6:C3:1463:GLN:HE21	6:C3:1502:ARG:HH22	1.63	0.45
6:C4:1532:ASP:CG	6:C4:1556:LYS:HZ2	2.24	0.45
7:D4:1165:TYR:CE1	23:U1:611:PHE:CE1	3.04	0.45
13:K3:595:LEU:HB2	13:K3:596:ILE:HD13	1.97	0.45
17:O1:36:VAL:HG23	17:O1:55:THR:HG21	1.99	0.45
2:15:672:ILE:HD12	2:15:672:ILE:H	1.82	0.45
6:C2:1246:MET:HE1	20:R0:1287:GLU:CG	2.47	0.45
2:16:672:ILE:HD12	2:16:672:ILE:H	1.81	0.45
4:A6:760:PHE:CE1	4:A6:764:LYS:HE3	2.51	0.45
7:D0:1389:ARG:HD3	7:D1:948:HIS:CE1	2.51	0.45
7:D2:993:PRO:CB	7:D3:426:GLU:OE2	2.65	0.45
7:D5:1196:PHE:CD2	23:U6:610:LEU:HD21	2.50	0.45
7:D5:1185:ILE:CG2	23:U6:600:LEU:HB2	2.46	0.45
15:M2:734:LYS:HE3	15:M2:735:TRP:CE2	2.52	0.45
17:O2:36:VAL:HG23	17:O2:55:THR:HG21	1.99	0.45
3:41:143:PHE:CE1	3:41:291:THR:HG21	2.52	0.45
4:A2:249:GLU:H	4:A2:249:GLU:CD	2.25	0.45
7:D2:1161:LEU:HD22	7:D2:1196:PHE:CZ	2.51	0.45
7:D3:1161:LEU:HD22	7:D3:1196:PHE:CE1	2.52	0.45
7:D5:1354:LEU:HB3	20:R2:1035:ARG:CD	2.45	0.45
4:A1:760:PHE:CE1	4:A1:764:LYS:HE3	2.51	0.45
4:A4:757:PHE:CE1	4:A4:761:LYS:HE3	2.52	0.45
7:D1:715:LYS:HE3	7:D1:719:GLU:OE2	2.17	0.45
22:T1:864:GLN:O	22:T1:867:LYS:HE3	2.16	0.45
24:V0:894:TRP:CG	24:V0:895:SER:H	2.35	0.45
6:C2:620:GLU:HA	20:R0:1317:HIS:NE2	2.32	0.45
7:D0:1196:PHE:CE1	23:U2:610:LEU:CG	3.00	0.45
7:D5:813:GLU:CD	7:D5:813:GLU:H	2.25	0.45
7:D5:1195:PRO:O	23:U6:611:PHE:CE2	2.69	0.45
6:C1:1461:LYS:HE2	6:C1:1465:GLU:CD	2.42	0.44
7:D4:1365:GLN:O	20:R0:1029:ARG:NH2	2.50	0.44
15:M3:514:GLU:H	15:M3:514:GLU:CD	2.25	0.44
1:O1:571:GLN:NE2	1:O1:633:PHE:H	2.16	0.44
4:A2:371:LEU:C	4:A2:371:LEU:HD23	2.42	0.44
4:A5:371:LEU:C	4:A5:371:LEU:HD23	2.43	0.44
5:B0:488:HIS:CD2	5:B0:489:GLU:H	2.35	0.44
6:C3:1697:ASN:OD1	18:P1:257:LYS:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D3:922:GLN:HG2	7:D5:86:ARG:HE	1.83	0.44
17:O0:2:PHE:HA	18:P0:60:ASP:OD2	2.17	0.44
18:P1:320:LYS:CE	25:W0:663:LYS:HE2	2.47	0.44
4:A5:371:LEU:HD22	4:A5:395:GLY:HA3	1.99	0.44
5:B1:488:HIS:CD2	5:B1:489:GLU:H	2.36	0.44
6:C0:1461:LYS:HE2	6:C0:1465:GLU:CD	2.43	0.44
13:K2:1153:GLN:NE2	13:K3:596:ILE:HA	2.33	0.44
20:R2:1052:GLU:C	20:R2:1091:ARG:HH22	2.26	0.44
22:T1:2:ARG:HA	22:T1:423:HIS:O	2.17	0.44
4:A1:371:LEU:C	4:A1:371:LEU:HD23	2.43	0.44
4:A3:249:GLU:CD	4:A3:249:GLU:H	2.26	0.44
4:A4:371:LEU:C	4:A4:371:LEU:HD23	2.43	0.44
7:D0:1161:LEU:HD22	7:D0:1196:PHE:CD1	2.51	0.44
7:D2:684:VAL:HG23	7:D2:686:ARG:HE	1.83	0.44
14:L0:491:LYS:HE2	14:L0:495:GLU:OE2	2.18	0.44
15:M0:649:TRP:HE1	15:M0:665:GLU:CD	2.26	0.44
17:O3:36:VAL:HG23	17:O3:55:THR:HG21	2.00	0.44
1:O0:92:THR:HG22	14:L0:262:LEU:HD22	1.93	0.44
2:10:1177:MET:CG	2:11:1106:PRO:HA	2.47	0.44
7:D5:1347:ARG:HH22	20:R2:1068:SER:CB	2.30	0.44
10:H2:342:GLN:HE21	10:H2:346:GLN:NE2	2.15	0.44
1:O0:571:GLN:NE2	1:O0:633:PHE:H	2.16	0.44
2:13:672:ILE:HD12	2:13:672:ILE:H	1.81	0.44
5:B0:14:ARG:HH22	5:B0:100:ASP:CG	2.26	0.44
5:B1:14:ARG:HH22	5:B1:100:ASP:CG	2.26	0.44
6:C3:746:ARG:NE	19:Q0:228:ASN:OD1	2.51	0.44
6:C3:966:LEU:O	6:C3:974:LYS:HE2	2.18	0.44
6:C3:1224:GLN:HE21	6:C3:1277:HIS:CD2	2.36	0.44
7:D1:1161:LEU:CD2	7:D1:1196:PHE:CG	3.01	0.44
7:D4:1161:LEU:HD22	7:D4:1196:PHE:CE2	2.52	0.44
18:P0:155:GLU:OE2	24:V0:920:LEU:HD13	2.18	0.44
2:11:783:ARG:HH22	2:11:894:ASP:CG	2.26	0.44
6:C2:469:PRO:HB3	20:R0:1113:ARG:HH11	1.78	0.44
7:D0:1237:SER:OG	7:D1:736:ASN:HB2	2.17	0.44
7:D3:1186:THR:HA	23:U5:600:LEU:HD12	2.00	0.44
10:H1:342:GLN:HE21	10:H1:346:GLN:NE2	2.16	0.44
13:K3:595:LEU:CA	13:K3:596:ILE:HD13	2.48	0.44
17:O2:200:PHE:CE1	17:O2:211:LYS:HE2	2.53	0.44
4:A0:138:GLU:HA	6:C0:1992:ARG:NH1	2.32	0.44
7:D2:1235:LEU:HD13	7:D3:735:PRO:HA	1.99	0.44
7:D4:1194:ASP:HA	7:D4:1202:LYS:HE2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D5:1194:ASP:HA	7:D5:1202:LYS:HE2	1.99	0.44
14:L3:728:GLU:N	14:L3:730:GLN:O	2.51	0.44
18:P0:214:GLN:OE1	25:W0:716:SER:HB2	2.18	0.44
1:01:596:ARG:CZ	1:01:661:ASN:HA	2.48	0.43
6:C3:135:TYR:CZ	6:C3:139:LYS:HE3	2.52	0.43
7:D3:1186:THR:HG21	23:U5:601:VAL:HB	1.99	0.43
9:F1:234:GLU:N	9:F1:234:GLU:CD	2.76	0.43
10:H3:342:GLN:HE21	10:H3:346:GLN:NE2	2.15	0.43
2:11:1346:ILE:CD1	2:12:1024:ALA:HB1	2.48	0.43
4:A0:683:LYS:HA	7:D1:563:ARG:NH1	2.29	0.43
7:D0:938:GLU:OE1	7:D0:939:LYS:HE3	2.18	0.43
9:F3:234:GLU:CD	9:F3:234:GLU:N	2.76	0.43
1:03:571:GLN:NE2	1:03:633:PHE:H	2.16	0.43
2:11:1012:LYS:HE3	2:11:1013:TYR:CE1	2.52	0.43
4:A1:757:PHE:CE1	4:A1:761:LYS:HE3	2.53	0.43
5:B1:832:ASN:C	5:B1:833:VAL:CG2	2.90	0.43
10:H0:342:GLN:HE21	10:H0:346:GLN:NE2	2.16	0.43
15:M3:526:PRO:HB2	15:M3:582:TYR:CE1	2.53	0.43
17:O0:36:VAL:HG23	17:O0:55:THR:HG21	2.00	0.43
18:P2:415:SER:HB2	19:Q2:12:LYS:HE3	2.00	0.43
1:00:708:LYS:HE2	1:00:756:TYR:CD1	2.54	0.43
7:D2:1195:PRO:HB2	23:U4:610:LEU:HD13	1.99	0.43
7:D2:1242:HIS:ND1	7:D3:732:LEU:HD23	2.32	0.43
7:D5:1362:VAL:HG11	20:R2:1006:LYS:CB	2.48	0.43
8:E0:165:TYR:CE2	8:E0:269:LEU:HD22	2.53	0.43
15:M0:514:GLU:H	15:M0:514:GLU:CD	2.26	0.43
20:R2:1069:ARG:HD3	20:R2:1080:TYR:CE1	2.53	0.43
23:U0:873:TRP:CE3	25:W0:230:TYR:CZ	3.07	0.43
6:C3:1247:ALA:HB2	20:R1:1278:THR:HG21	2.01	0.43
7:D3:1195:PRO:C	23:U5:610:LEU:HD13	2.44	0.43
7:D5:1161:LEU:HD22	7:D5:1196:PHE:CE2	2.54	0.43
13:K1:151:TRP:CH2	13:K1:179:THR:HB	2.53	0.43
1:00:596:ARG:CZ	1:00:661:ASN:HA	2.48	0.43
1:01:708:LYS:HE2	1:01:756:TYR:CD1	2.53	0.43
1:03:596:ARG:CZ	1:03:661:ASN:HA	2.49	0.43
2:13:1366:ILE:HG21	2:17:1350:THR:CG2	2.48	0.43
3:40:280:VAL:HG13	8:E0:207:ARG:HH12	1.83	0.43
4:A6:371:LEU:C	4:A6:371:LEU:HD23	2.43	0.43
7:D0:1237:SER:HB2	7:D1:734:ASN:OD1	2.18	0.43
7:D1:1186:THR:HG23	23:U3:601:VAL:HB	2.00	0.43
7:D2:993:PRO:CG	7:D3:426:GLU:OE2	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D5:1186:THR:HG21	23:U6:601:VAL:HB	2.01	0.43
10:H2:468:LYS:HE3	10:H2:472:GLU:CD	2.43	0.43
13:K1:209:TYR:CE1	13:K1:222:LEU:HB3	2.54	0.43
14:L1:340:ARG:CZ	14:L1:340:ARG:HB3	2.48	0.43
18:P1:537:PHE:HB2	18:P1:568:ILE:HG22	2.01	0.43
4:A3:371:LEU:HD23	4:A3:371:LEU:C	2.43	0.43
4:A4:114:ILE:CD1	6:C2:1494:MET:HE3	2.48	0.43
6:C3:621:HIS:CD2	6:C3:624:TRP:CE3	3.07	0.43
6:C4:1694:VAL:HG12	18:P3:257:LYS:HE2	2.01	0.43
7:D1:234:CYS:SG	7:D1:258:LYS:HE3	2.59	0.43
4:A2:218:LYS:HZ1	4:A2:222:ASP:CG	2.26	0.43
7:D1:1194:ASP:HA	7:D1:1202:LYS:HE2	2.00	0.43
7:D2:1196:PHE:CE1	23:U4:610:LEU:CG	3.01	0.43
14:L3:728:GLU:N	14:L3:732:MET:H	2.16	0.43
4:A0:249:GLU:CD	4:A0:249:GLU:H	2.27	0.43
7:D1:1003:VAL:HG12	7:D4:95:GLU:OE2	2.19	0.43
7:D5:1161:LEU:HD21	7:D5:1196:PHE:CD2	2.54	0.43
7:D5:1168:HIS:HE2	23:U6:611:PHE:C	2.26	0.43
14:L0:712:PHE:CE2	14:L0:747:HIS:CE1	3.07	0.43
14:L1:381:TRP:CD1	14:L1:381:TRP:H	2.37	0.43
18:P1:464:GLU:CD	18:P1:467:ARG:HH12	2.26	0.43
2:11:443:TRP:HZ2	2:12:212:LYS:NZ	2.15	0.43
2:12:1012:LYS:HE3	2:12:1013:TYR:CE1	2.54	0.43
2:16:745:VAL:HG22	2:16:746:CYS:H	1.83	0.43
4:A0:686:ASP:CB	7:D1:563:ARG:NH1	2.82	0.43
4:A1:249:GLU:CD	4:A1:249:GLU:H	2.26	0.43
4:A2:138:GLU:HA	6:C1:1992:ARG:NH1	2.32	0.43
4:A2:448:TYR:CE2	9:F1:89:PRO:HD3	2.54	0.43
15:M3:734:LYS:HE3	15:M3:735:TRP:CE2	2.53	0.43
23:U4:609:ASN:O	23:U4:610:LEU:C	2.60	0.43
2:10:1177:MET:HB2	2:11:1106:PRO:HA	2.01	0.42
2:16:1285:LYS:HZ3	2:16:1294:GLU:CD	2.26	0.42
4:A0:159:THR:HG23	4:A0:160:GLN:H	1.84	0.42
6:C1:1461:LYS:HE2	6:C1:1465:GLU:OE1	2.19	0.42
6:C3:1505:SER:HB3	6:C3:1562:ARG:CZ	2.49	0.42
14:L1:340:ARG:HH12	16:N0:141:GLU:HG3	1.84	0.42
14:L3:727:CYS:HB3	14:L3:733:GLU:N	2.33	0.42
15:M1:402:HIS:CG	15:M1:403:LEU:HA	2.54	0.42
1:03:708:LYS:HE2	1:03:756:TYR:CD1	2.53	0.42
4:A1:448:TYR:CE2	9:F2:89:PRO:HD3	2.53	0.42
6:C4:1694:VAL:CG1	18:P3:257:LYS:NZ	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D4:1185:ILE:CG2	23:U1:600:LEU:HD13	2.48	0.42
8:E0:72:PHE:CD2	8:E0:72:PHE:C	2.96	0.42
15:M2:514:GLU:CD	15:M2:514:GLU:H	2.27	0.42
1:02:57:GLU:CD	1:02:57:GLU:H	2.27	0.42
2:10:1366:ILE:HG21	2:14:1350:THR:CG2	2.50	0.42
6:C2:281:ILE:HG23	6:C2:284:ILE:HD12	2.01	0.42
6:C4:1461:LYS:HE2	6:C4:1465:GLU:OE2	2.19	0.42
7:D1:1186:THR:HG23	23:U3:601:VAL:O	2.19	0.42
7:D2:809:GLU:CD	7:D2:847:ARG:HH12	2.26	0.42
7:D3:1195:PRO:HB2	23:U5:610:LEU:HD13	2.02	0.42
7:D4:234:CYS:SG	7:D4:258:LYS:HE3	2.59	0.42
4:A0:91:GLU:H	10:H0:454:TYR:H	1.68	0.42
7:D0:234:CYS:SG	7:D0:258:LYS:HE3	2.60	0.42
7:D2:234:CYS:SG	7:D2:258:LYS:HE3	2.59	0.42
10:H3:417:ILE:HG23	11:I3:357:LEU:HD11	2.02	0.42
19:Q0:57:SER:HB3	24:V0:851:VAL:CG2	2.44	0.42
2:16:1012:LYS:HE3	2:16:1013:TYR:CE1	2.55	0.42
4:A0:558:LYS:HE3	7:D1:1031:LYS:HZ2	1.81	0.42
4:A1:760:PHE:CZ	4:A1:818:MET:HA	2.53	0.42
7:D3:1186:THR:HG23	23:U5:601:VAL:HB	2.01	0.42
4:A0:237:PRO:HB2	7:D1:1025:LYS:HD3	2.01	0.42
4:A3:448:TYR:CE2	9:F0:89:PRO:HD3	2.55	0.42
6:C3:1246:MET:HG3	20:R1:1287:GLU:HG3	2.01	0.42
7:D1:813:GLU:CD	7:D1:813:GLU:H	2.27	0.42
7:D1:1003:VAL:CG1	7:D4:95:GLU:CD	2.93	0.42
20:R0:636:GLU:CD	20:R0:636:GLU:H	2.27	0.42
6:C3:1247:ALA:H	20:R1:1278:THR:HB	1.84	0.42
7:D0:1003:VAL:HG13	7:D1:101:GLN:HB3	2.01	0.42
7:D5:234:CYS:SG	7:D5:258:LYS:HE3	2.59	0.42
11:I2:266:LYS:NZ	11:I3:327:ARG:NH2	2.68	0.42
13:K1:508:THR:O	13:K1:509:LYS:HE2	2.20	0.42
17:O2:207:ARG:NH1	20:R2:1286:ASP:HA	2.35	0.42
18:P0:185:LEU:CD1	25:W0:708:ALA:O	2.68	0.42
1:00:92:THR:HG21	14:L0:262:LEU:HD23	1.89	0.42
1:00:387:ASP:HB3	13:K1:887:ARG:HD2	2.02	0.42
2:14:580:ASP:HA	2:14:597:ARG:HH21	1.84	0.42
4:A4:141:LYS:HE3	6:C2:1992:ARG:HD3	2.01	0.42
6:C0:1461:LYS:HE2	6:C0:1465:GLU:OE1	2.20	0.42
6:C2:1751:LEU:HA	6:C2:1889:LEU:HD21	2.02	0.42
6:C4:1249:ILE:HD13	20:R3:1285:THR:H	1.77	0.42
13:K0:880:ASP:CG	13:K0:913:LYS:HZ1	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K3:261:SER:C	13:K3:263:PHE:HA	2.45	0.42
15:M3:338:PRO:HG3	15:M3:372:TRP:CH2	2.55	0.42
1:03:78:LYS:CD	17:O0:98:ARG:HD2	2.49	0.42
2:14:1789:ARG:NH2	2:15:1728:PRO:HG3	2.34	0.42
6:C2:1739:GLU:HA	6:C2:1742:LYS:HE3	2.02	0.42
7:D4:950:TYR:CE2	7:D4:1037:ILE:HD13	2.54	0.42
7:D5:1168:HIS:NE2	23:U6:611:PHE:HA	2.34	0.42
10:H1:448:ARG:HH12	11:I1:378:SER:CB	2.33	0.42
11:I0:305:THR:CG2	12:J0:388:ARG:HH22	2.32	0.42
13:K2:1153:GLN:HG2	13:K3:596:ILE:CG1	2.50	0.42
13:K3:594:SER:HB3	13:K3:596:ILE:HB	2.01	0.42
15:M2:788:LYS:HE3	15:M2:792:GLU:HG3	2.01	0.42
18:P2:550:GLU:HG2	18:P2:551:LYS:H	1.85	0.42
7:D1:1161:LEU:CD2	7:D1:1196:PHE:CE2	3.03	0.42
7:D3:92:GLU:CD	7:D3:92:GLU:H	2.28	0.42
7:D5:1186:THR:HG23	23:U6:601:VAL:H	1.84	0.42
7:D5:1196:PHE:HD2	23:U6:610:LEU:HD11	1.80	0.42
18:P0:58:ARG:HD3	18:P0:64:TYR:CE2	2.55	0.42
6:C4:47:LYS:HZ2	6:C4:176:GLU:CD	2.28	0.41
7:D5:1079:ASP:HA	7:D5:1082:TRP:CD1	2.55	0.41
10:H1:417:ILE:HG23	11:I1:357:LEU:HD11	2.02	0.41
14:L1:345:ARG:NH2	16:N0:201:GLN:HG3	2.27	0.41
1:01:147:TRP:CZ2	1:01:178:THR:HG21	2.55	0.41
2:14:1012:LYS:HE3	2:14:1013:TYR:CE1	2.55	0.41
6:C2:788:VAL:HG21	17:O0:258:THR:CB	2.40	0.41
6:C4:1249:ILE:CD1	20:R3:1284:ALA:CB	2.95	0.41
7:D0:809:GLU:CD	7:D0:847:ARG:HH12	2.28	0.41
1:00:370:LYS:HE3	1:00:374:GLU:OE1	2.19	0.41
2:12:1290:ASN:ND2	2:16:1307:LYS:O	2.47	0.41
6:C3:911:GLU:HG2	6:C3:979:ILE:HD13	2.02	0.41
7:D4:1186:THR:HG21	23:U1:601:VAL:HB	2.01	0.41
15:M1:338:PRO:HG3	15:M1:372:TRP:CH2	2.56	0.41
15:M2:549:ALA:HB1	15:M2:553:TRP:CZ3	2.55	0.41
20:R0:802:LEU:HD11	20:R0:915:ARG:HH21	1.83	0.41
1:02:607:LYS:HE3	1:02:654:PHE:CD1	2.55	0.41
2:10:1171:ARG:HG3	2:11:1145:VAL:HG21	2.02	0.41
4:A2:199:GLY:O	7:D3:939:LYS:CE	2.68	0.41
7:D1:563:ARG:NH1	7:D1:563:ARG:HG3	2.35	0.41
14:L1:164:LYS:HZ2	14:L1:176:GLU:CD	2.29	0.41
23:U0:803:LEU:HD12	23:U0:803:LEU:N	2.35	0.41
2:12:1056:LEU:O	2:12:1072:PRO:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:17:1266:GLN:H	2:17:1266:GLN:CD	2.29	0.41
4:A0:678:GLY:HA2	7:D1:558:THR:HG21	2.02	0.41
7:D3:1126:LYS:HE3	7:D3:1141:LEU:HD21	2.01	0.41
13:K0:261:SER:C	13:K0:263:PHE:HA	2.45	0.41
14:L0:803:LYS:HE3	14:L0:807:ASP:OD1	2.21	0.41
15:M1:649:TRP:HE1	15:M1:665:GLU:CD	2.28	0.41
16:N3:245:CYS:HB2	16:N3:253:TRP:CD2	2.55	0.41
20:R3:993:ASP:CG	20:R3:994:TRP:H	2.28	0.41
2:12:1366:ILE:HG21	2:16:1350:THR:CG2	2.51	0.41
4:A2:287:PRO:HG2	8:E0:652:HIS:NE2	2.35	0.41
4:A6:138:GLU:HA	6:C4:1992:ARG:NH1	2.36	0.41
5:B0:1303:TRP:CZ2	5:B0:1307:THR:HG21	2.56	0.41
10:H0:427:PHE:CE2	11:I0:361:ARG:CA	2.84	0.41
18:P3:627:ILE:HG22	18:P3:631:LYS:HE3	2.03	0.41
22:T0:970:LEU:C	22:T0:970:LEU:HD23	2.45	0.41
2:11:1194:ASN:OD1	2:12:1150:GLY:CA	2.68	0.41
4:A0:760:PHE:CE1	4:A0:764:LYS:HE3	2.54	0.41
4:A2:652:GLN:HE22	6:C1:1694:VAL:HG13	1.86	0.41
4:A6:757:PHE:CE1	4:A6:761:LYS:HE3	2.56	0.41
7:D0:1310:ARG:HH21	7:D0:1363:GLU:CD	2.29	0.41
7:D1:684:VAL:HG23	7:D1:686:ARG:HE	1.86	0.41
7:D1:1161:LEU:HD22	7:D1:1196:PHE:CE2	2.55	0.41
7:D5:950:TYR:CE2	7:D5:1037:ILE:HD13	2.55	0.41
9:F0:112:ARG:HH22	9:F0:119:MET:HA	1.86	0.41
13:K3:751:ARG:HG2	13:K3:752:ARG:N	2.35	0.41
15:M3:587:LEU:HD13	15:M3:591:LEU:CB	2.51	0.41
18:P3:415:SER:HB2	19:Q3:12:LYS:HE3	2.03	0.41
1:01:549:ALA:HB1	14:L1:233:ALA:HB2	1.96	0.41
2:12:1105:GLN:HA	2:12:1106:PRO:HA	1.92	0.41
5:B1:127:ASP:CG	5:B1:202:ARG:HH22	2.29	0.41
5:B1:770:TYR:CD1	6:C1:1382:GLU:HG2	2.55	0.41
5:B1:1080:LYS:HE3	5:B1:1138:ASP:HB2	2.02	0.41
6:C2:1393:ASP:HB3	6:C2:1395:SER:H	1.86	0.41
7:D2:1235:LEU:HD13	7:D3:735:PRO:CA	2.51	0.41
14:L1:803:LYS:HE3	14:L1:807:ASP:OD1	2.21	0.41
14:L2:803:LYS:HE2	14:L2:807:ASP:OD2	2.21	0.41
14:L2:803:LYS:HE3	14:L2:807:ASP:OD1	2.20	0.41
15:M2:338:PRO:HG3	15:M2:372:TRP:CH2	2.55	0.41
15:M2:649:TRP:HE1	15:M2:665:GLU:CD	2.28	0.41
1:03:454:ARG:HH21	1:03:466:HIS:CD2	2.38	0.41
2:10:783:ARG:HH22	2:10:894:ASP:CG	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:12:580:ASP:HA	2:12:597:ARG:HH21	1.85	0.41
2:12:1266:GLN:CD	2:12:1266:GLN:H	2.29	0.41
2:13:27:LYS:HZ2	2:13:51:GLU:CD	2.29	0.41
2:14:990:GLU:CD	2:14:993:LYS:HE3	2.46	0.41
4:A0:239:THR:HG21	7:D1:1028:GLN:HG2	2.00	0.41
4:A0:448:TYR:CE2	9:F3:89:PRO:HD3	2.55	0.41
4:A4:171:GLY:O	4:A4:173:PRO:HD3	2.21	0.41
5:B0:48:SER:O	5:B0:51:LYS:HE3	2.20	0.41
6:C4:416:GLU:HG2	6:C4:419:ARG:CZ	2.51	0.41
7:D3:1196:PHE:CD2	23:U5:610:LEU:CD1	2.95	0.41
7:D3:1196:PHE:CD1	23:U5:610:LEU:CD2	3.04	0.41
7:D3:1310:ARG:HH21	7:D3:1363:GLU:CD	2.29	0.41
7:D4:1366:SER:N	20:R0:1029:ARG:HH22	2.16	0.41
11:I0:310:LYS:HE2	11:I0:314:GLU:OE1	2.21	0.41
13:K0:151:TRP:CH2	13:K0:179:THR:HB	2.56	0.41
13:K2:261:SER:C	13:K2:263:PHE:HA	2.45	0.41
13:K3:151:TRP:CH2	13:K3:179:THR:HB	2.56	0.41
15:M0:391:LEU:CD2	15:M0:433:THR:HG22	2.48	0.41
15:M1:734:LYS:HE3	15:M1:735:TRP:CE2	2.56	0.41
15:M3:649:TRP:HE1	15:M3:665:GLU:CD	2.29	0.41
18:P2:550:GLU:C	18:P2:551:LYS:HG3	2.46	0.41
20:R1:802:LEU:HD11	20:R1:915:ARG:HH21	1.85	0.41
20:R2:892:GLN:HE21	20:R2:913:LEU:CD1	2.34	0.41
23:U0:846:ILE:HG22	25:W0:304:GLU:O	2.21	0.41
1:02:412:ARG:HH21	1:02:415:GLU:CD	2.29	0.41
2:15:1266:GLN:CD	2:15:1266:GLN:H	2.29	0.41
5:B0:326:TRP:CZ2	5:B0:330:ARG:HD3	2.56	0.41
6:C2:658:GLU:H	6:C2:658:GLU:CD	2.27	0.41
6:C4:1523:LYS:HE2	6:C4:1527:ASP:OD2	2.21	0.41
14:L2:712:PHE:CE2	14:L2:747:HIS:CE1	3.09	0.41
14:L3:803:LYS:HE2	14:L3:807:ASP:OD2	2.21	0.41
1:00:730:SER:CB	14:L1:781:THR:HG21	2.51	0.40
1:04:607:LYS:HE3	1:04:654:PHE:CD1	2.56	0.40
2:15:1012:LYS:HE3	2:15:1013:TYR:CE1	2.57	0.40
3:41:280:VAL:HG13	8:E1:207:ARG:HH12	1.86	0.40
6:C3:697:ARG:HA	19:Q0:248:ARG:HH11	1.86	0.40
7:D2:466:GLU:OE1	7:D2:468:LYS:HE2	2.22	0.40
7:D4:1168:HIS:CE1	23:U1:611:PHE:HA	2.56	0.40
7:D4:1227:LYS:HE2	7:D4:1231:ASP:OD2	2.21	0.40
13:K0:969:THR:HA	14:L0:879:ASP:OD2	2.21	0.40
13:K1:1045:GLU:CG	13:K1:1107:LYS:HE3	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T0:864:GLN:O	22:T0:867:LYS:HE3	2.21	0.40
4:A5:746:SER:HB2	4:A5:807:THR:HG21	2.03	0.40
6:C2:47:LYS:HZ2	6:C2:176:GLU:CD	2.30	0.40
6:C2:1937:GLN:HA	6:C2:1938:ASP:HA	2.01	0.40
6:C3:327:ALA:HB1	6:C3:368:VAL:HB	2.03	0.40
7:D3:466:GLU:OE1	7:D3:468:LYS:HE2	2.21	0.40
7:D3:813:GLU:H	7:D3:813:GLU:CD	2.29	0.40
14:L2:381:TRP:CD1	14:L2:381:TRP:H	2.39	0.40
18:P2:464:GLU:CD	18:P2:467:ARG:HH12	2.29	0.40
2:15:1105:GLN:HA	2:15:1106:PRO:C	2.46	0.40
2:16:1266:GLN:H	2:16:1266:GLN:CD	2.30	0.40
4:A3:109:ALA:HA	5:B1:1168:ARG:HD2	2.02	0.40
5:B0:127:ASP:CG	5:B0:202:ARG:HH22	2.28	0.40
6:C2:1249:ILE:HD13	20:R0:1284:ALA:H	1.80	0.40
6:C3:21:TRP:CH2	6:C3:144:ASN:HB3	2.56	0.40
7:D1:1012:SER:OG	7:D4:94:VAL:HG12	2.21	0.40
7:D3:1126:LYS:HE3	7:D3:1141:LEU:HD11	2.04	0.40
7:D4:1228:GLU:CD	7:D4:1247:LYS:HE2	2.46	0.40
13:K2:1149:GLU:HG3	13:K2:1153:GLN:OE1	2.21	0.40
14:L1:803:LYS:HE2	14:L1:807:ASP:OD2	2.21	0.40
16:N0:245:CYS:HB2	16:N0:253:TRP:CD2	2.56	0.40
22:T1:221:THR:HG21	22:T1:241:ASP:CG	2.47	0.40
4:A4:139:GLN:C	6:C2:1992:ARG:HH22	2.29	0.40
4:A4:167:ILE:HG12	6:C3:4:PRO:HG2	2.03	0.40
5:B0:197:GLU:H	5:B0:197:GLU:CD	2.29	0.40
7:D0:40:TYR:HA	7:D0:41:PRO:HD3	1.95	0.40
7:D2:938:GLU:OE1	7:D2:939:LYS:HE3	2.21	0.40
10:H3:167:GLU:H	10:H3:167:GLU:CD	2.29	0.40
11:I2:266:LYS:HE2	12:J2:347:GLN:NE2	2.36	0.40
14:L1:896:GLU:HA	14:L1:899:LYS:HB3	2.04	0.40
22:T0:221:THR:HG21	22:T0:241:ASP:CG	2.47	0.40
1:00:376:PHE:HA	13:K1:857:LEU:CD1	2.52	0.40
3:41:315:GLU:CD	3:41:361:ARG:HH22	2.30	0.40
4:A0:677:GLN:O	7:D1:715:LYS:HD3	2.22	0.40
4:A0:690:TYR:CD2	7:D1:560:ALA:CB	3.05	0.40
4:A1:14:GLU:HB3	11:I1:303:ARG:HH22	1.86	0.40
6:C3:1252:ARG:CZ	20:R1:1258:GLU:HA	2.52	0.40
7:D3:1195:PRO:O	23:U5:610:LEU:CB	2.70	0.40
7:D4:1366:SER:HB3	20:R0:1029:ARG:NH1	2.35	0.40
9:F0:148:THR:HB	9:F0:153:ALA:HB3	2.03	0.40
13:K0:481:ILE:O	13:K0:539:MET:HE3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N1:245:CYS:HB2	16:N1:253:TRP:CD2	2.57	0.40
17:O3:86:TRP:CH2	17:O3:105:LYS:HE2	2.57	0.40
20:R3:892:GLN:HE21	20:R3:913:LEU:CD1	2.35	0.40
22:T0:595:LYS:HZ2	22:T0:599:ASP:CG	2.29	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	00	754/3224 (23%)	703 (93%)	43 (6%)	8 (1%)	11	46
1	01	754/3224 (23%)	706 (94%)	42 (6%)	6 (1%)	16	54
1	02	754/3224 (23%)	707 (94%)	44 (6%)	3 (0%)	30	67
1	03	754/3224 (23%)	700 (93%)	45 (6%)	9 (1%)	10	44
1	04	754/3224 (23%)	702 (93%)	49 (6%)	3 (0%)	30	67
2	10	1829/1887 (97%)	1726 (94%)	94 (5%)	9 (0%)	24	63
2	11	1829/1887 (97%)	1725 (94%)	93 (5%)	11 (1%)	21	59
2	12	1829/1887 (97%)	1724 (94%)	95 (5%)	10 (0%)	24	63
2	13	1829/1887 (97%)	1711 (94%)	107 (6%)	11 (1%)	21	59
2	14	1829/1887 (97%)	1731 (95%)	90 (5%)	8 (0%)	30	67
2	15	1829/1887 (97%)	1733 (95%)	87 (5%)	9 (0%)	24	63
2	16	1829/1887 (97%)	1734 (95%)	86 (5%)	9 (0%)	24	63
2	17	1829/1887 (97%)	1724 (94%)	95 (5%)	10 (0%)	24	63
3	40	379/546 (69%)	350 (92%)	28 (7%)	1 (0%)	36	72
3	41	379/546 (69%)	348 (92%)	29 (8%)	2 (0%)	24	63
4	A0	816/819 (100%)	741 (91%)	65 (8%)	10 (1%)	10	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A1	816/819 (100%)	753 (92%)	54 (7%)	9 (1%)	11	46
4	A2	816/819 (100%)	756 (93%)	50 (6%)	10 (1%)	10	44
4	A3	816/819 (100%)	755 (92%)	55 (7%)	6 (1%)	18	56
4	A4	724/819 (88%)	680 (94%)	40 (6%)	4 (1%)	21	59
4	A5	724/819 (88%)	688 (95%)	31 (4%)	5 (1%)	18	56
4	A6	724/819 (88%)	674 (93%)	47 (6%)	3 (0%)	30	67
5	B0	1746/1749 (100%)	1634 (94%)	93 (5%)	19 (1%)	11	46
5	B1	1746/1749 (100%)	1626 (93%)	103 (6%)	17 (1%)	12	49
6	C0	2009/2012 (100%)	1878 (94%)	111 (6%)	20 (1%)	12	49
6	C1	2009/2012 (100%)	1879 (94%)	109 (5%)	21 (1%)	12	49
6	C2	2009/2012 (100%)	1886 (94%)	106 (5%)	17 (1%)	16	54
6	C3	2009/2012 (100%)	1876 (93%)	118 (6%)	15 (1%)	18	56
6	C4	2009/2012 (100%)	1873 (93%)	123 (6%)	13 (1%)	21	59
7	D0	1308/1391 (94%)	1207 (92%)	89 (7%)	12 (1%)	14	51
7	D1	1308/1391 (94%)	1209 (92%)	88 (7%)	11 (1%)	16	54
7	D2	1308/1391 (94%)	1218 (93%)	81 (6%)	9 (1%)	18	56
7	D3	1308/1391 (94%)	1210 (92%)	85 (6%)	13 (1%)	12	49
7	D4	1308/1391 (94%)	1221 (93%)	77 (6%)	10 (1%)	16	54
7	D5	1308/1391 (94%)	1233 (94%)	65 (5%)	10 (1%)	16	54
8	E0	544/674 (81%)	516 (95%)	26 (5%)	2 (0%)	30	67
8	E1	544/674 (81%)	514 (94%)	29 (5%)	1 (0%)	43	78
9	F0	239/326 (73%)	189 (79%)	33 (14%)	17 (7%)	1	11
9	F1	239/326 (73%)	192 (80%)	33 (14%)	14 (6%)	1	13
9	F2	239/326 (73%)	177 (74%)	45 (19%)	17 (7%)	1	11
9	F3	239/326 (73%)	188 (79%)	39 (16%)	12 (5%)	1	16
10	H0	381/507 (75%)	365 (96%)	16 (4%)	0	100	100
10	H1	381/507 (75%)	364 (96%)	16 (4%)	1 (0%)	36	72
10	H2	381/507 (75%)	366 (96%)	15 (4%)	0	100	100
10	H3	381/507 (75%)	363 (95%)	16 (4%)	2 (0%)	24	63
11	I0	171/599 (28%)	168 (98%)	3 (2%)	0	100	100
11	I1	171/599 (28%)	167 (98%)	3 (2%)	1 (1%)	21	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	I2	171/599 (28%)	167 (98%)	4 (2%)	0	100	100
11	I3	171/599 (28%)	167 (98%)	4 (2%)	0	100	100
12	J0	169/522 (32%)	166 (98%)	3 (2%)	0	100	100
12	J1	169/522 (32%)	168 (99%)	1 (1%)	0	100	100
12	J2	169/522 (32%)	167 (99%)	2 (1%)	0	100	100
12	J3	169/522 (32%)	166 (98%)	2 (1%)	1 (1%)	21	59
12	J4	169/522 (32%)	168 (99%)	1 (1%)	0	100	100
13	K0	1084/1156 (94%)	985 (91%)	85 (8%)	14 (1%)	9	42
13	K1	1084/1156 (94%)	990 (91%)	78 (7%)	16 (2%)	8	40
13	K2	1084/1156 (94%)	992 (92%)	82 (8%)	10 (1%)	14	51
13	K3	1084/1156 (94%)	1001 (92%)	70 (6%)	13 (1%)	10	44
14	L0	780/925 (84%)	734 (94%)	42 (5%)	4 (0%)	24	63
14	L1	780/925 (84%)	734 (94%)	38 (5%)	8 (1%)	12	49
14	L2	780/925 (84%)	732 (94%)	45 (6%)	3 (0%)	30	67
14	L3	780/925 (84%)	731 (94%)	43 (6%)	6 (1%)	16	54
15	M0	669/937 (71%)	609 (91%)	50 (8%)	10 (2%)	8	40
15	M1	669/937 (71%)	613 (92%)	48 (7%)	8 (1%)	10	44
15	M2	669/937 (71%)	618 (92%)	45 (7%)	6 (1%)	14	51
15	M3	669/937 (71%)	612 (92%)	50 (8%)	7 (1%)	12	49
16	N0	299/322 (93%)	277 (93%)	19 (6%)	3 (1%)	12	49
16	N1	299/322 (93%)	277 (93%)	20 (7%)	2 (1%)	18	56
16	N2	299/322 (93%)	277 (93%)	19 (6%)	3 (1%)	12	49
16	N3	299/322 (93%)	278 (93%)	18 (6%)	3 (1%)	12	49
17	O0	321/360 (89%)	304 (95%)	14 (4%)	3 (1%)	14	51
17	O1	321/360 (89%)	302 (94%)	15 (5%)	4 (1%)	10	44
17	O2	321/360 (89%)	302 (94%)	18 (6%)	1 (0%)	36	72
17	O3	321/360 (89%)	299 (93%)	19 (6%)	3 (1%)	14	51
18	P0	653/656 (100%)	607 (93%)	40 (6%)	6 (1%)	14	51
18	P1	653/656 (100%)	612 (94%)	35 (5%)	6 (1%)	14	51
18	P2	653/656 (100%)	610 (93%)	36 (6%)	7 (1%)	11	46
18	P3	653/656 (100%)	611 (94%)	35 (5%)	7 (1%)	11	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	Q0	341/380 (90%)	320 (94%)	20 (6%)	1 (0%)	36	72
19	Q1	341/380 (90%)	322 (94%)	18 (5%)	1 (0%)	36	72
19	Q2	341/380 (90%)	320 (94%)	20 (6%)	1 (0%)	36	72
19	Q3	341/380 (90%)	323 (95%)	17 (5%)	1 (0%)	36	72
20	R0	1397/1436 (97%)	1288 (92%)	93 (7%)	16 (1%)	11	46
20	R1	1397/1436 (97%)	1285 (92%)	94 (7%)	18 (1%)	9	42
20	R2	1397/1436 (97%)	1298 (93%)	87 (6%)	12 (1%)	14	51
20	R3	1397/1436 (97%)	1294 (93%)	93 (7%)	10 (1%)	18	56
21	S0	320/326 (98%)	292 (91%)	26 (8%)	2 (1%)	21	59
21	S1	320/326 (98%)	293 (92%)	24 (8%)	3 (1%)	14	51
21	S2	320/326 (98%)	290 (91%)	28 (9%)	2 (1%)	21	59
21	S3	320/326 (98%)	292 (91%)	25 (8%)	3 (1%)	14	51
22	T0	1002/2266 (44%)	927 (92%)	62 (6%)	13 (1%)	9	42
22	T1	1002/2266 (44%)	931 (93%)	58 (6%)	13 (1%)	9	42
23	U0	148/880 (17%)	140 (95%)	8 (5%)	0	100	100
23	U1	17/880 (2%)	16 (94%)	1 (6%)	0	100	100
23	U2	17/880 (2%)	15 (88%)	2 (12%)	0	100	100
23	U3	17/880 (2%)	15 (88%)	1 (6%)	1 (6%)	1	13
23	U4	17/880 (2%)	15 (88%)	2 (12%)	0	100	100
23	U5	17/880 (2%)	14 (82%)	2 (12%)	1 (6%)	1	13
23	U6	17/880 (2%)	16 (94%)	1 (6%)	0	100	100
24	V0	271/2090 (13%)	255 (94%)	12 (4%)	4 (2%)	8	40
25	W0	733/741 (99%)	688 (94%)	40 (6%)	5 (1%)	18	56
All	All	77792/109146 (71%)	72515 (93%)	4606 (6%)	671 (1%)	16	51

All (671) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	O2	165	VAL
4	A1	90	LEU
4	A1	95	ASP
4	A2	88	GLU
4	A2	167	ILE
4	A4	707	ILE

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Mol	Chain	Res	Type
4	A6	707	ILE
5	B0	1522	PRO
5	B0	1529	PRO
5	B1	1051	VAL
5	B1	1522	PRO
6	C0	1146	ASP
6	C0	1149	VAL
6	C1	1146	ASP
6	C1	1149	VAL
6	C1	1636	ALA
6	C2	458	GLU
6	C2	581	TYR
6	C2	1246	MET
6	C2	1377	SER
6	C2	1933	SER
6	C2	1936	LEU
6	C3	5	LEU
6	C3	1636	ALA
6	C3	1928	ARG
6	C4	458	GLU
6	C4	1377	SER
6	C4	1636	ALA
6	C4	1928	ARG
7	D0	408	VAL
7	D0	803	PHE
7	D0	863	CYS
7	D1	408	VAL
7	D1	803	PHE
7	D2	803	PHE
7	D3	408	VAL
7	D3	803	PHE
7	D3	863	CYS
7	D3	864	PRO
7	D4	408	VAL
7	D4	803	PHE
7	D4	1213	ASP
7	D5	408	VAL
7	D5	803	PHE
9	F0	101	PRO
9	F1	287	ARG
9	F2	259	SER
9	F3	169	ASP

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Mol	Chain	Res	Type
9	F3	253	ASP
13	K0	111	GLU
13	K0	193	GLU
13	K0	477	GLU
13	K0	483	ALA
13	K0	510	ASN
13	K0	911	ARG
13	K1	397	PHE
13	K1	500	GLU
13	K2	193	GLU
13	K3	193	GLU
14	L0	825	ASP
14	L1	729	GLU
14	L1	825	ASP
14	L2	587	ASN
14	L2	825	ASP
14	L3	733	GLU
14	L3	734	SER
14	L3	825	ASP
15	M0	763	TRP
15	M1	586	PRO
15	M3	586	PRO
18	P0	42	LYS
20	R1	1056	VAL
20	R2	1056	VAL
20	R3	1285	THR
22	T0	30	LEU
22	T0	418	SER
22	T1	30	LEU
24	V0	852	PRO
24	V0	907	HIS
25	W0	36	PRO
1	00	20	PRO
1	01	20	PRO
1	02	20	PRO
1	03	20	PRO
1	03	164	ASP
1	04	20	PRO
1	04	163	ASP
2	10	499	VAL
2	10	815	VAL
2	11	499	VAL

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Mol	Chain	Res	Type
2	11	747	ALA
2	12	499	VAL
2	12	1789	ARG
2	13	499	VAL
2	13	815	VAL
2	14	499	VAL
2	15	499	VAL
2	15	906	ASN
2	16	499	VAL
2	17	499	VAL
2	17	815	VAL
4	A0	21	GLU
4	A0	89	PRO
4	A0	156	LEU
4	A0	164	PRO
4	A0	707	ILE
4	A1	23	ILE
4	A1	176	SER
4	A2	21	GLU
4	A3	23	ILE
4	A3	163	GLU
5	B0	1051	VAL
5	B0	1264	SER
5	B0	1514	VAL
5	B0	1518	VAL
5	B0	1717	SER
5	B1	1052	LYS
5	B1	1268	ASP
5	B1	1518	VAL
5	B1	1526	SER
5	B1	1717	SER
6	C0	458	GLU
6	C0	1636	ALA
6	C1	458	GLU
6	C2	1159	ILE
6	C2	1165	SER
6	C2	1636	ALA
6	C2	1928	ARG
6	C3	457	LEU
6	C3	1159	ILE
6	C3	1165	SER
6	C3	1377	SER

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Mol	Chain	Res	Type
6	C3	1936	LEU
6	C4	1159	ILE
6	C4	1695	ASP
7	D0	1166	SER
7	D1	862	ILE
7	D1	867	TYR
7	D1	1106	SER
7	D2	408	VAL
7	D2	1166	SER
7	D3	1105	HIS
7	D4	1105	HIS
7	D4	1210	GLY
7	D5	908	SER
7	D5	1109	ILE
9	F0	147	LYS
9	F0	151	SER
9	F0	234	GLU
9	F0	294	LYS
9	F0	308	THR
9	F1	128	SER
9	F1	134	GLN
9	F1	170	HIS
9	F1	284	SER
9	F1	303	ILE
9	F2	129	THR
10	H3	427	PHE
10	H3	449	SER
13	K0	148	ASP
13	K0	302	SER
13	K1	111	GLU
13	K1	164	SER
13	K1	193	GLU
13	K1	203	SER
13	K1	513	ILE
13	K1	907	GLU
13	K1	909	GLY
13	K2	111	GLU
13	K2	148	ASP
13	K2	302	SER
13	K2	493	SER
13	K3	148	ASP
13	K3	302	SER

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Mol	Chain	Res	Type
13	K3	481	ILE
13	K3	493	SER
15	M0	279	GLN
15	M0	326	ARG
15	M0	762	HIS
15	M1	326	ARG
15	M1	851	GLU
15	M2	326	ARG
15	M2	487	GLY
15	M2	851	GLU
15	M3	326	ARG
15	M3	851	GLU
17	O0	98	ARG
17	O1	231	LEU
17	O3	98	ARG
17	O3	205	ASN
18	P0	62	ASP
18	P1	42	LYS
18	P2	42	LYS
18	P2	551	LYS
18	P3	42	LYS
19	Q1	52	PHE
19	Q3	52	PHE
20	R0	294	GLU
20	R1	294	GLU
20	R1	1278	THR
20	R2	294	GLU
20	R3	294	GLU
20	R3	1283	SER
22	T0	365	ASP
22	T0	558	LEU
22	T1	418	SER
24	V0	925	ILE
25	W0	351	LYS
25	W0	505	LEU
1	00	375	THR
1	03	159	TYR
2	10	940	ALA
2	11	940	ALA
2	11	1798	SER
2	12	906	ASN
2	12	940	ALA

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Mol	Chain	Res	Type
2	13	849	GLU
2	13	940	ALA
2	13	1674	SER
2	14	940	ALA
2	14	1787	VAL
2	15	172	ASP
2	15	743	LYS
2	15	940	ALA
2	16	580	ASP
2	16	815	VAL
2	16	940	ALA
2	17	940	ALA
2	17	1688	SER
2	17	1689	PRO
4	A0	94	LYS
4	A0	772	SER
4	A1	518	GLY
4	A1	780	ASP
4	A2	169	ASP
4	A2	200	HIS
4	A2	707	ILE
4	A2	772	SER
4	A3	173	PRO
4	A3	707	ILE
4	A5	150	ALA
4	A5	588	GLU
5	B0	454	LEU
5	B0	1052	LYS
5	B0	1053	GLY
5	B1	454	LEU
5	B1	1264	SER
5	B1	1514	VAL
6	C0	161	GLU
6	C0	545	ILE
6	C0	873	ALA
6	C0	1152	TYR
6	C0	1159	ILE
6	C0	1798	ASP
6	C1	161	GLU
6	C1	545	ILE
6	C1	1152	TYR
6	C1	1159	ILE

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Mol	Chain	Res	Type
6	C2	1695	ASP
6	C4	581	TYR
6	C4	1165	SER
6	C4	1936	LEU
7	D1	1004	LEU
7	D3	868	SER
7	D3	912	ASP
7	D3	1010	MET
9	F0	105	SER
9	F0	115	ASN
9	F0	305	ASP
9	F1	283	ILE
9	F1	285	THR
9	F2	170	HIS
9	F3	108	LEU
9	F3	161	GLN
9	F3	167	SER
11	I1	377	ASN
12	J3	345	GLU
13	K1	161	SER
13	K1	498	ASN
13	K1	499	SER
13	K2	880	ASP
13	K3	111	GLU
13	K3	499	SER
14	L1	392	GLY
15	M0	830	ASP
15	M1	404	LYS
15	M2	279	GLN
15	M3	830	ASP
16	N0	274	ALA
16	N1	274	ALA
16	N2	11	SER
16	N2	274	ALA
16	N3	11	SER
17	O1	98	ARG
17	O1	257	LEU
17	O2	98	ARG
18	P3	61	VAL
18	P3	552	ARG
19	Q0	52	PHE
20	R0	66	SER

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Mol	Chain	Res	Type
20	R0	415	ASN
20	R0	691	PHE
20	R0	786	ASP
20	R0	992	ASP
20	R0	1281	GLU
20	R1	415	ASN
20	R1	691	PHE
20	R1	786	ASP
20	R1	1053	PHE
20	R1	1057	ASN
20	R1	1258	GLU
20	R2	66	SER
20	R2	691	PHE
20	R2	786	ASP
20	R2	951	ASP
20	R3	415	ASN
20	R3	691	PHE
21	S0	275	LYS
21	S1	275	LYS
21	S2	275	LYS
21	S3	275	LYS
22	T0	684	ASP
22	T0	686	SER
22	T0	902	ARG
22	T1	343	ARG
22	T1	684	ASP
22	T1	686	SER
22	T1	902	ARG
24	V0	904	SER
25	W0	473	PRO
1	00	164	ASP
1	00	504	ASN
1	00	696	ASN
1	01	504	ASN
1	01	696	ASN
1	03	504	ASN
1	03	696	ASN
2	10	172	ASP
2	10	650	SER
2	10	1674	SER
2	11	172	ASP
2	11	580	ASP

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Mol	Chain	Res	Type
2	11	1483	SER
2	11	1674	SER
2	12	172	ASP
2	12	650	SER
2	12	849	GLU
2	12	1674	SER
2	12	1798	SER
2	13	172	ASP
2	13	650	SER
2	13	1789	ARG
2	14	172	ASP
2	14	650	SER
2	14	849	GLU
2	15	580	ASP
2	15	849	GLU
2	16	172	ASP
2	16	849	GLU
2	17	849	GLU
4	A1	161	GLU
4	A2	152	GLY
4	A5	426	ASP
5	B0	509	THR
5	B0	1171	LYS
5	B0	1523	SER
5	B0	1526	SER
5	B1	509	THR
5	B1	1171	LYS
5	B1	1520	ARG
6	C0	457	LEU
6	C0	1011	LEU
6	C0	1221	LEU
6	C0	1386	VAL
6	C1	457	LEU
6	C1	1011	LEU
6	C1	1386	VAL
6	C1	1798	ASP
6	C1	1938	ASP
6	C1	1940	PHE
6	C2	4	PRO
6	C3	346	VAL
6	C3	718	SER
6	C4	545	ILE

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Mol	Chain	Res	Type
6	C4	548	ALA
6	C4	1937	GLN
7	D0	953	GLY
7	D0	1003	VAL
7	D0	1104	MET
7	D1	68	GLN
7	D1	407	LYS
7	D1	1388	GLU
7	D2	407	LYS
7	D3	68	GLN
7	D3	1028	GLN
7	D3	1388	GLU
7	D4	68	GLN
7	D4	407	LYS
7	D4	908	SER
7	D5	68	GLN
7	D5	867	TYR
7	D5	953	GLY
8	E1	154	GLY
9	F1	127	THR
9	F1	136	MET
9	F1	226	SER
9	F1	253	ASP
9	F1	311	LYS
9	F2	149	THR
9	F2	226	SER
9	F3	120	GLN
9	F3	171	LEU
13	K0	164	SER
13	K0	203	SER
13	K1	508	THR
13	K3	161	SER
13	K3	164	SER
13	K3	203	SER
15	M0	851	GLU
15	M1	477	ARG
15	M1	587	LEU
15	M1	830	ASP
15	M2	748	SER
15	M2	830	ASP
16	N0	90	ASN
16	N1	166	SER

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Mol	Chain	Res	Type
16	N3	166	SER
16	N3	274	ALA
17	O0	231	LEU
17	O1	176	ARG
17	O3	231	LEU
18	P1	275	ALA
18	P1	552	ARG
18	P2	44	LYS
18	P3	44	LYS
18	P3	60	ASP
20	R0	74	ALA
20	R0	752	THR
20	R0	1282	SER
20	R1	66	SER
20	R1	74	ALA
20	R1	752	THR
20	R1	753	GLY
20	R1	1054	PRO
20	R2	74	ALA
20	R2	274	ALA
20	R2	415	ASN
20	R2	752	THR
20	R3	66	SER
20	R3	274	ALA
20	R3	752	THR
21	S1	316	ASP
22	T0	485	SER
22	T0	572	GLU
22	T1	344	GLY
22	T1	572	GLU
22	T1	647	GLU
1	00	729	LEU
1	01	165	VAL
1	01	729	LEU
1	02	504	ASN
1	03	729	LEU
1	04	504	ASN
2	10	700	SER
2	10	1483	SER
2	11	700	SER
2	11	815	VAL
2	12	815	VAL

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Mol	Chain	Res	Type
2	13	580	ASP
2	13	1483	SER
2	14	815	VAL
2	15	700	SER
2	16	650	SER
2	16	700	SER
2	17	172	ASP
2	17	650	SER
2	17	700	SER
2	17	1787	VAL
3	40	325	PRO
4	A0	518	GLY
4	A1	21	GLU
4	A2	176	SER
4	A3	93	VAL
4	A3	518	GLY
4	A4	164	PRO
4	A4	772	SER
4	A5	163	GLU
4	A5	537	ARG
4	A6	170	VAL
5	B0	1516	GLN
5	B0	1517	ARG
5	B1	1517	ARG
6	C0	543	GLU
6	C0	549	GLY
6	C0	1737	ASN
6	C1	543	GLU
6	C1	549	GLY
6	C1	1221	LEU
6	C1	1737	ASN
6	C2	346	VAL
6	C2	545	ILE
6	C2	1358	SER
6	C2	1930	LEU
6	C2	1937	GLN
6	C3	456	HIS
6	C3	1146	ASP
6	C3	1937	GLN
7	D0	120	ASP
7	D0	938	GLU
7	D1	864	PRO

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Mol	Chain	Res	Type
7	D1	1009	ASN
7	D2	868	SER
7	D2	1109	ILE
7	D4	953	GLY
7	D5	863	CYS
8	E0	154	GLY
9	F0	112	ARG
9	F0	114	PRO
9	F0	146	ARG
9	F0	259	SER
9	F0	269	LYS
9	F0	271	LEU
9	F0	296	SER
9	F0	298	SER
9	F1	153	ALA
9	F2	99	SER
9	F2	152	PRO
9	F2	157	PRO
9	F2	268	ILE
9	F2	269	LYS
9	F3	159	TYR
9	F3	226	SER
9	F3	251	SER
10	H1	427	PHE
13	K0	161	SER
13	K0	487	GLU
13	K2	164	SER
13	K2	479	VAL
13	K2	481	ILE
13	K2	489	SER
13	K3	512	THR
13	K3	513	ILE
13	K3	596	ILE
14	L0	508	ASN
14	L0	595	HIS
14	L1	508	ASN
14	L1	539	ARG
14	L2	508	ASN
15	M0	486	VAL
15	M0	748	SER
15	M1	487	GLY
15	M3	279	GLN

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Mol	Chain	Res	Type
16	N0	166	SER
16	N2	166	SER
17	O0	257	LEU
18	P0	18	SER
18	P0	44	LYS
18	P0	91	GLY
18	P0	275	ALA
18	P1	18	SER
18	P1	44	LYS
18	P2	275	ALA
18	P2	547	MET
18	P3	275	ALA
19	Q2	263	GLU
20	R0	634	SER
20	R0	1053	PHE
20	R1	1148	GLY
20	R2	148	GLN
20	R3	74	ALA
20	R3	148	GLN
21	S0	316	ASP
21	S3	316	ASP
22	T0	141	SER
22	T0	484	ASN
22	T1	141	SER
22	T1	484	ASN
22	T1	485	SER
23	U3	611	PHE
23	U5	611	PHE
25	W0	346	ASP
1	03	166	HIS
2	10	906	ASN
2	11	650	SER
2	13	764	ASP
2	14	700	SER
2	15	1674	SER
2	16	1674	SER
4	A0	163	GLU
4	A2	518	GLY
5	B1	1528	ALA
6	C3	545	ILE
6	C4	346	VAL
7	D0	407	LYS

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Mol	Chain	Res	Type
7	D0	1388	GLU
7	D2	120	ASP
7	D2	953	GLY
7	D2	1388	GLU
7	D3	953	GLY
7	D3	1006	SER
7	D5	120	ASP
9	F2	113	GLN
9	F2	256	ALA
13	K0	880	ASP
13	K1	148	ASP
14	L0	587	ASN
14	L1	731	GLY
14	L1	734	SER
14	L3	508	ASN
14	L3	539	ARG
15	M0	509	SER
15	M3	585	SER
18	P1	91	GLY
18	P2	91	GLY
18	P3	91	GLY
20	R0	1375	LEU
20	R1	274	ALA
20	R1	1273	LEU
21	S1	207	GLU
21	S2	316	ASP
21	S3	207	GLU
22	T0	33	VAL
22	T0	344	GLY
1	00	165	VAL
1	03	165	VAL
3	41	14	GLY
4	A4	518	GLY
5	B0	422	GLY
5	B0	1520	ARG
6	C0	346	VAL
6	C1	346	VAL
13	K1	379	GLY
14	L3	736	LEU
15	M0	934	VAL
20	R0	753	GLY
22	T1	33	VAL

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Mol	Chain	Res	Type
3	41	325	PRO
4	A0	91	GLU
4	A6	152	GLY
6	C0	344	PRO
6	C1	344	PRO
6	C3	207	GLY
7	D0	864	PRO
7	D4	863	CYS
8	E0	156	PRO
9	F3	157	PRO
13	K1	264	GLY
15	M3	486	VAL
20	R2	1148	GLY
9	F2	162	GLY
9	F2	265	THR
14	L1	313	VAL
20	R0	330	VAL
20	R1	330	VAL
1	00	628	PRO
1	01	628	PRO
1	03	628	PRO
4	A1	707	ILE
5	B0	1528	ALA
5	B1	422	GLY
6	C0	1794	GLY
7	D5	862	ILE
9	F2	116	ILE
9	F3	100	SER
13	K0	379	GLY
20	R0	1148	GLY
6	C1	1794	GLY
9	F2	131	GLY
9	F2	139	PRO
18	P2	156	VAL
5	B1	1529	PRO

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	00	675/2818 (24%)	655 (97%)	20 (3%)	36	57
1	01	675/2818 (24%)	656 (97%)	19 (3%)	38	60
1	02	675/2818 (24%)	654 (97%)	21 (3%)	35	56
1	03	675/2818 (24%)	655 (97%)	20 (3%)	36	57
1	04	675/2818 (24%)	654 (97%)	21 (3%)	35	56
2	10	1565/1608 (97%)	1543 (99%)	22 (1%)	59	72
2	11	1565/1608 (97%)	1535 (98%)	30 (2%)	50	67
2	12	1565/1608 (97%)	1541 (98%)	24 (2%)	57	72
2	13	1565/1608 (97%)	1535 (98%)	30 (2%)	50	67
2	14	1565/1608 (97%)	1543 (99%)	22 (1%)	59	72
2	15	1565/1608 (97%)	1539 (98%)	26 (2%)	53	69
2	16	1565/1608 (97%)	1539 (98%)	26 (2%)	53	69
2	17	1565/1608 (97%)	1542 (98%)	23 (2%)	57	72
3	40	323/463 (70%)	312 (97%)	11 (3%)	32	54
3	41	323/463 (70%)	313 (97%)	10 (3%)	35	56
4	A0	725/726 (100%)	700 (97%)	25 (3%)	32	54
4	A1	725/726 (100%)	705 (97%)	20 (3%)	38	60
4	A2	725/726 (100%)	700 (97%)	25 (3%)	32	54
4	A3	725/726 (100%)	704 (97%)	21 (3%)	37	58
4	A4	647/726 (89%)	629 (97%)	18 (3%)	38	60
4	A5	647/726 (89%)	633 (98%)	14 (2%)	45	64
4	A6	647/726 (89%)	629 (97%)	18 (3%)	38	60
5	B0	1540/1541 (100%)	1504 (98%)	36 (2%)	44	64
5	B1	1540/1541 (100%)	1502 (98%)	38 (2%)	42	63
6	C0	1776/1777 (100%)	1732 (98%)	44 (2%)	42	63
6	C1	1776/1777 (100%)	1737 (98%)	39 (2%)	45	64
6	C2	1776/1777 (100%)	1742 (98%)	34 (2%)	50	67
6	C3	1776/1777 (100%)	1736 (98%)	40 (2%)	44	64
6	C4	1776/1777 (100%)	1740 (98%)	36 (2%)	48	66
7	D0	1157/1222 (95%)	1128 (98%)	29 (2%)	42	63
7	D1	1157/1222 (95%)	1126 (97%)	31 (3%)	39	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	D2	1157/1222 (95%)	1135 (98%)	22 (2%)	50	67
7	D3	1157/1222 (95%)	1117 (96%)	40 (4%)	32	53
7	D4	1157/1222 (95%)	1125 (97%)	32 (3%)	38	60
7	D5	1157/1222 (95%)	1117 (96%)	40 (4%)	32	53
8	E0	489/604 (81%)	484 (99%)	5 (1%)	68	78
8	E1	489/604 (81%)	484 (99%)	5 (1%)	68	78
9	F0	210/277 (76%)	195 (93%)	15 (7%)	13	35
9	F1	210/277 (76%)	199 (95%)	11 (5%)	21	42
9	F2	210/277 (76%)	192 (91%)	18 (9%)	10	29
9	F3	210/277 (76%)	196 (93%)	14 (7%)	15	36
10	H0	345/425 (81%)	340 (99%)	5 (1%)	59	72
10	H1	345/425 (81%)	339 (98%)	6 (2%)	53	69
10	H2	345/425 (81%)	339 (98%)	6 (2%)	53	69
10	H3	345/425 (81%)	338 (98%)	7 (2%)	48	66
11	I0	155/459 (34%)	151 (97%)	4 (3%)	40	62
11	I1	155/459 (34%)	152 (98%)	3 (2%)	50	67
11	I2	155/459 (34%)	150 (97%)	5 (3%)	34	56
11	I3	155/459 (34%)	152 (98%)	3 (2%)	50	67
12	J0	158/401 (39%)	154 (98%)	4 (2%)	42	63
12	J1	158/401 (39%)	153 (97%)	5 (3%)	34	56
12	J2	158/401 (39%)	154 (98%)	4 (2%)	42	63
12	J3	158/401 (39%)	153 (97%)	5 (3%)	34	56
12	J4	158/401 (39%)	155 (98%)	3 (2%)	50	67
13	K0	958/1013 (95%)	924 (96%)	34 (4%)	32	53
13	K1	958/1013 (95%)	934 (98%)	24 (2%)	42	63
13	K2	958/1013 (95%)	929 (97%)	29 (3%)	36	57
13	K3	958/1013 (95%)	932 (97%)	26 (3%)	39	61
14	L0	701/827 (85%)	682 (97%)	19 (3%)	39	61
14	L1	701/827 (85%)	680 (97%)	21 (3%)	36	57
14	L2	701/827 (85%)	688 (98%)	13 (2%)	50	67
14	L3	701/827 (85%)	686 (98%)	15 (2%)	47	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	M0	602/840 (72%)	586 (97%)	16 (3%)	39	61
15	M1	602/840 (72%)	583 (97%)	19 (3%)	34	56
15	M2	602/840 (72%)	585 (97%)	17 (3%)	38	60
15	M3	602/840 (72%)	588 (98%)	14 (2%)	44	64
16	N0	255/272 (94%)	250 (98%)	5 (2%)	48	66
16	N1	255/272 (94%)	251 (98%)	4 (2%)	55	70
16	N2	255/272 (94%)	251 (98%)	4 (2%)	55	70
16	N3	255/272 (94%)	251 (98%)	4 (2%)	55	70
17	O0	279/310 (90%)	275 (99%)	4 (1%)	59	72
17	O1	279/310 (90%)	275 (99%)	4 (1%)	59	72
17	O2	279/310 (90%)	274 (98%)	5 (2%)	51	68
17	O3	279/310 (90%)	274 (98%)	5 (2%)	51	68
18	P0	584/585 (100%)	570 (98%)	14 (2%)	43	64
18	P1	584/585 (100%)	571 (98%)	13 (2%)	45	64
18	P2	584/585 (100%)	571 (98%)	13 (2%)	45	64
18	P3	584/585 (100%)	568 (97%)	16 (3%)	39	61
19	Q0	303/335 (90%)	300 (99%)	3 (1%)	68	78
19	Q1	303/335 (90%)	301 (99%)	2 (1%)	76	81
19	Q2	303/335 (90%)	301 (99%)	2 (1%)	76	81
19	Q3	303/335 (90%)	300 (99%)	3 (1%)	68	78
20	R0	1233/1259 (98%)	1200 (97%)	33 (3%)	39	61
20	R1	1233/1259 (98%)	1204 (98%)	29 (2%)	43	64
20	R2	1233/1259 (98%)	1206 (98%)	27 (2%)	45	64
20	R3	1233/1259 (98%)	1205 (98%)	28 (2%)	44	64
21	S0	278/282 (99%)	273 (98%)	5 (2%)	51	68
21	S1	278/282 (99%)	272 (98%)	6 (2%)	45	64
21	S2	278/282 (99%)	272 (98%)	6 (2%)	45	64
21	S3	278/282 (99%)	274 (99%)	4 (1%)	59	72
22	T0	891/2037 (44%)	878 (98%)	13 (2%)	57	72
22	T1	891/2037 (44%)	874 (98%)	17 (2%)	50	67
23	U0	131/703 (19%)	127 (97%)	4 (3%)	35	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	U1	19/703 (3%)	16 (84%)	3 (16%)	2	11
23	U2	19/703 (3%)	18 (95%)	1 (5%)	20	41
23	U3	19/703 (3%)	18 (95%)	1 (5%)	20	41
23	U4	19/703 (3%)	18 (95%)	1 (5%)	20	41
23	U5	19/703 (3%)	18 (95%)	1 (5%)	20	41
23	U6	19/703 (3%)	17 (90%)	2 (10%)	6	21
24	V0	249/1685 (15%)	237 (95%)	12 (5%)	23	44
25	W0	661/663 (100%)	643 (97%)	18 (3%)	39	61
All	All	68601/94353 (73%)	66987 (98%)	1614 (2%)	43	64

All (1614) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	00	57	GLU
1	00	102	GLU
1	00	107	ASN
1	00	119	GLU
1	00	161	ARG
1	00	183	ASP
1	00	202	GLU
1	00	224	ASP
1	00	251	ASP
1	00	275	ASN
1	00	277	GLU
1	00	397	ASP
1	00	408	ASN
1	00	411	VAL
1	00	418	ASP
1	00	485	GLU
1	00	566	GLU
1	00	677	VAL
1	00	740	GLU
1	00	756	TYR
1	01	57	GLU
1	01	102	GLU
1	01	107	ASN
1	01	119	GLU
1	01	183	ASP
1	01	202	GLU

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Mol	Chain	Res	Type
1	01	224	ASP
1	01	251	ASP
1	01	275	ASN
1	01	277	GLU
1	01	397	ASP
1	01	408	ASN
1	01	411	VAL
1	01	418	ASP
1	01	485	GLU
1	01	566	GLU
1	01	677	VAL
1	01	740	GLU
1	01	756	TYR
1	02	57	GLU
1	02	102	GLU
1	02	107	ASN
1	02	119	GLU
1	02	183	ASP
1	02	202	GLU
1	02	224	ASP
1	02	251	ASP
1	02	275	ASN
1	02	333	LEU
1	02	335	LYS
1	02	397	ASP
1	02	408	ASN
1	02	411	VAL
1	02	418	ASP
1	02	485	GLU
1	02	520	CYS
1	02	566	GLU
1	02	677	VAL
1	02	740	GLU
1	02	756	TYR
1	03	57	GLU
1	03	102	GLU
1	03	107	ASN
1	03	119	GLU
1	03	165	VAL
1	03	183	ASP
1	03	202	GLU
1	03	224	ASP

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Mol	Chain	Res	Type
1	03	251	ASP
1	03	275	ASN
1	03	277	GLU
1	03	397	ASP
1	03	408	ASN
1	03	411	VAL
1	03	418	ASP
1	03	485	GLU
1	03	566	GLU
1	03	677	VAL
1	03	740	GLU
1	03	756	TYR
1	04	30	PHE
1	04	57	GLU
1	04	107	ASN
1	04	119	GLU
1	04	163	ASP
1	04	164	ASP
1	04	183	ASP
1	04	202	GLU
1	04	224	ASP
1	04	251	ASP
1	04	275	ASN
1	04	397	ASP
1	04	408	ASN
1	04	411	VAL
1	04	418	ASP
1	04	485	GLU
1	04	566	GLU
1	04	677	VAL
1	04	706	GLU
1	04	740	GLU
1	04	756	TYR
2	10	51	GLU
2	10	102	THR
2	10	278	SER
2	10	339	THR
2	10	605	CYS
2	10	619	THR
2	10	681	ASN
2	10	851	SER
2	10	918	GLU

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Mol	Chain	Res	Type
2	10	931	ASP
2	10	1149	THR
2	10	1195	HIS
2	10	1297	GLN
2	10	1335	ASP
2	10	1421	SER
2	10	1534	THR
2	10	1619	VAL
2	10	1626	ASP
2	10	1673	SER
2	10	1716	GLU
2	10	1788	ASP
2	10	1789	ARG
2	11	9	LEU
2	11	51	GLU
2	11	102	THR
2	11	278	SER
2	11	339	THR
2	11	343	VAL
2	11	605	CYS
2	11	619	THR
2	11	681	ASN
2	11	745	VAL
2	11	831	ASP
2	11	918	GLU
2	11	931	ASP
2	11	1034	ASP
2	11	1109	ASN
2	11	1149	THR
2	11	1166	LEU
2	11	1195	HIS
2	11	1218	ASP
2	11	1297	GLN
2	11	1335	ASP
2	11	1421	SER
2	11	1463	HIS
2	11	1534	THR
2	11	1619	VAL
2	11	1626	ASP
2	11	1643	CYS
2	11	1673	SER
2	11	1788	ASP

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Mol	Chain	Res	Type
2	11	1789	ARG
2	12	51	GLU
2	12	102	THR
2	12	278	SER
2	12	339	THR
2	12	343	VAL
2	12	605	CYS
2	12	619	THR
2	12	681	ASN
2	12	700	SER
2	12	743	LYS
2	12	831	ASP
2	12	918	GLU
2	12	931	ASP
2	12	1149	THR
2	12	1166	LEU
2	12	1297	GLN
2	12	1335	ASP
2	12	1421	SER
2	12	1534	THR
2	12	1619	VAL
2	12	1626	ASP
2	12	1662	LYS
2	12	1673	SER
2	12	1786	VAL
2	13	102	THR
2	13	205	THR
2	13	278	SER
2	13	339	THR
2	13	452	ILE
2	13	580	ASP
2	13	605	CYS
2	13	619	THR
2	13	681	ASN
2	13	717	GLU
2	13	743	LYS
2	13	745	VAL
2	13	783	ARG
2	13	893	GLU
2	13	918	GLU
2	13	929	THR
2	13	1149	THR

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Mol	Chain	Res	Type
2	13	1166	LEU
2	13	1297	GLN
2	13	1335	ASP
2	13	1421	SER
2	13	1534	THR
2	13	1619	VAL
2	13	1626	ASP
2	13	1643	CYS
2	13	1673	SER
2	13	1697	GLU
2	13	1716	GLU
2	13	1743	SER
2	13	1789	ARG
2	14	51	GLU
2	14	102	THR
2	14	278	SER
2	14	339	THR
2	14	605	CYS
2	14	619	THR
2	14	681	ASN
2	14	743	LYS
2	14	831	ASP
2	14	918	GLU
2	14	931	ASP
2	14	1034	ASP
2	14	1149	THR
2	14	1297	GLN
2	14	1335	ASP
2	14	1421	SER
2	14	1534	THR
2	14	1569	PHE
2	14	1619	VAL
2	14	1626	ASP
2	14	1631	GLU
2	14	1716	GLU
2	15	9	LEU
2	15	51	GLU
2	15	102	THR
2	15	278	SER
2	15	339	THR
2	15	528	MET
2	15	605	CYS

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Mol	Chain	Res	Type
2	15	681	ASN
2	15	743	LYS
2	15	745	VAL
2	15	783	ARG
2	15	831	ASP
2	15	918	GLU
2	15	931	ASP
2	15	1034	ASP
2	15	1149	THR
2	15	1195	HIS
2	15	1218	ASP
2	15	1335	ASP
2	15	1534	THR
2	15	1619	VAL
2	15	1626	ASP
2	15	1631	GLU
2	15	1716	GLU
2	15	1790	ARG
2	15	1802	HIS
2	16	9	LEU
2	16	51	GLU
2	16	102	THR
2	16	278	SER
2	16	339	THR
2	16	605	CYS
2	16	619	THR
2	16	681	ASN
2	16	783	ARG
2	16	831	ASP
2	16	851	SER
2	16	918	GLU
2	16	931	ASP
2	16	1034	ASP
2	16	1149	THR
2	16	1195	HIS
2	16	1218	ASP
2	16	1297	GLN
2	16	1335	ASP
2	16	1421	SER
2	16	1534	THR
2	16	1569	PHE
2	16	1619	VAL

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Mol	Chain	Res	Type
2	16	1626	ASP
2	16	1631	GLU
2	16	1716	GLU
2	17	51	GLU
2	17	102	THR
2	17	278	SER
2	17	528	MET
2	17	605	CYS
2	17	619	THR
2	17	681	ASN
2	17	918	GLU
2	17	929	THR
2	17	1149	THR
2	17	1195	HIS
2	17	1203	ASN
2	17	1297	GLN
2	17	1335	ASP
2	17	1421	SER
2	17	1534	THR
2	17	1569	PHE
2	17	1571	GLU
2	17	1619	VAL
2	17	1626	ASP
2	17	1631	GLU
2	17	1643	CYS
2	17	1716	GLU
3	40	23	ASN
3	40	31	TYR
3	40	138	ASP
3	40	205	SER
3	40	364	GLU
3	40	390	ASP
3	40	393	GLU
3	40	404	TRP
3	40	407	SER
3	40	409	GLU
3	40	433	THR
3	41	23	ASN
3	41	31	TYR
3	41	138	ASP
3	41	205	SER
3	41	364	GLU

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Mol	Chain	Res	Type
3	41	390	ASP
3	41	404	TRP
3	41	407	SER
3	41	409	GLU
3	41	433	THR
4	A0	32	ASN
4	A0	57	ASP
4	A0	90	LEU
4	A0	91	GLU
4	A0	117	SER
4	A0	127	GLU
4	A0	156	LEU
4	A0	160	GLN
4	A0	163	GLU
4	A0	310	ASP
4	A0	344	GLN
4	A0	350	THR
4	A0	398	ASP
4	A0	406	VAL
4	A0	408	ASP
4	A0	424	ASP
4	A0	576	GLU
4	A0	579	GLU
4	A0	581	ASP
4	A0	608	ILE
4	A0	640	GLU
4	A0	686	ASP
4	A0	708	ASP
4	A0	725	GLU
4	A0	781	ARG
4	A1	32	ASN
4	A1	57	ASP
4	A1	94	LYS
4	A1	115	GLU
4	A1	121	THR
4	A1	154	ASP
4	A1	156	LEU
4	A1	163	GLU
4	A1	310	ASP
4	A1	344	GLN
4	A1	408	ASP
4	A1	424	ASP

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Mol	Chain	Res	Type
4	A1	455	VAL
4	A1	483	GLU
4	A1	576	GLU
4	A1	579	GLU
4	A1	581	ASP
4	A1	608	ILE
4	A1	771	SER
4	A1	782	ASP
4	A2	32	ASN
4	A2	57	ASP
4	A2	85	THR
4	A2	91	GLU
4	A2	117	SER
4	A2	138	GLU
4	A2	159	THR
4	A2	160	GLN
4	A2	161	GLU
4	A2	168	SER
4	A2	175	ARG
4	A2	310	ASP
4	A2	344	GLN
4	A2	406	VAL
4	A2	408	ASP
4	A2	424	ASP
4	A2	455	VAL
4	A2	579	GLU
4	A2	581	ASP
4	A2	608	ILE
4	A2	623	GLU
4	A2	640	GLU
4	A2	708	ASP
4	A2	777	VAL
4	A2	782	ASP
4	A3	32	ASN
4	A3	57	ASP
4	A3	94	LYS
4	A3	115	GLU
4	A3	121	THR
4	A3	161	GLU
4	A3	163	GLU
4	A3	310	ASP
4	A3	344	GLN

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Mol	Chain	Res	Type
4	A3	406	VAL
4	A3	408	ASP
4	A3	424	ASP
4	A3	455	VAL
4	A3	576	GLU
4	A3	579	GLU
4	A3	581	ASP
4	A3	608	ILE
4	A3	640	GLU
4	A3	708	ASP
4	A3	781	ARG
4	A3	782	ASP
4	A4	95	ASP
4	A4	138	GLU
4	A4	157	ASP
4	A4	175	ARG
4	A4	216	ASP
4	A4	310	ASP
4	A4	344	GLN
4	A4	347	GLU
4	A4	398	ASP
4	A4	400	THR
4	A4	424	ASP
4	A4	543	ASP
4	A4	576	GLU
4	A4	579	GLU
4	A4	608	ILE
4	A4	708	ASP
4	A4	806	ASP
4	A4	815	GLU
4	A5	127	GLU
4	A5	310	ASP
4	A5	344	GLN
4	A5	398	ASP
4	A5	400	THR
4	A5	430	SER
4	A5	455	VAL
4	A5	483	GLU
4	A5	543	ASP
4	A5	556	ASP
4	A5	576	GLU
4	A5	608	ILE

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Mol	Chain	Res	Type
4	A5	787	SER
4	A5	806	ASP
4	A6	95	ASP
4	A6	127	GLU
4	A6	138	GLU
4	A6	154	ASP
4	A6	176	SER
4	A6	177	SER
4	A6	310	ASP
4	A6	344	GLN
4	A6	398	ASP
4	A6	400	THR
4	A6	424	ASP
4	A6	483	GLU
4	A6	537	ARG
4	A6	576	GLU
4	A6	608	ILE
4	A6	640	GLU
4	A6	806	ASP
4	A6	815	GLU
5	B0	54	SER
5	B0	66	ASP
5	B0	69	SER
5	B0	118	SER
5	B0	171	SER
5	B0	189	GLU
5	B0	281	SER
5	B0	339	SER
5	B0	359	THR
5	B0	426	THR
5	B0	445	SER
5	B0	496	ARG
5	B0	557	ASP
5	B0	580	LEU
5	B0	584	ASP
5	B0	738	GLU
5	B0	772	GLU
5	B0	833	VAL
5	B0	893	ASP
5	B0	926	VAL
5	B0	950	GLU
5	B0	982	ARG

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Mol	Chain	Res	Type
5	B0	994	ASP
5	B0	1054	SER
5	B0	1061	ASP
5	B0	1178	ASP
5	B0	1259	THR
5	B0	1291	LYS
5	B0	1368	SER
5	B0	1389	ASP
5	B0	1423	VAL
5	B0	1504	ASN
5	B0	1508	ASP
5	B0	1521	PRO
5	B0	1522	PRO
5	B0	1526	SER
5	B1	54	SER
5	B1	66	ASP
5	B1	69	SER
5	B1	118	SER
5	B1	171	SER
5	B1	275	GLU
5	B1	281	SER
5	B1	339	SER
5	B1	359	THR
5	B1	426	THR
5	B1	484	ASP
5	B1	496	ARG
5	B1	557	ASP
5	B1	580	LEU
5	B1	584	ASP
5	B1	738	GLU
5	B1	926	VAL
5	B1	943	ASP
5	B1	950	GLU
5	B1	969	GLN
5	B1	982	ARG
5	B1	994	ASP
5	B1	1054	SER
5	B1	1061	ASP
5	B1	1178	ASP
5	B1	1223	ASP
5	B1	1247	ASP
5	B1	1249	THR

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Mol	Chain	Res	Type
5	B1	1268	ASP
5	B1	1291	LYS
5	B1	1368	SER
5	B1	1389	ASP
5	B1	1423	VAL
5	B1	1504	ASN
5	B1	1521	PRO
5	B1	1522	PRO
5	B1	1642	GLU
5	B1	1746	HIS
6	C0	3	THR
6	C0	22	HIS
6	C0	49	ASP
6	C0	200	GLU
6	C0	303	GLU
6	C0	357	GLU
6	C0	438	ASP
6	C0	468	GLU
6	C0	472	THR
6	C0	567	GLU
6	C0	577	ASP
6	C0	580	GLN
6	C0	590	THR
6	C0	658	GLU
6	C0	663	LEU
6	C0	742	SER
6	C0	747	PHE
6	C0	777	GLU
6	C0	780	LEU
6	C0	817	GLU
6	C0	831	ASP
6	C0	872	LEU
6	C0	876	VAL
6	C0	959	ASP
6	C0	1019	ASN
6	C0	1194	GLU
6	C0	1306	ASP
6	C0	1341	THR
6	C0	1436	ASP
6	C0	1479	GLU
6	C0	1531	GLU
6	C0	1572	GLU

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Mol	Chain	Res	Type
6	C0	1602	MET
6	C0	1653	SER
6	C0	1654	ASP
6	C0	1695	ASP
6	C0	1703	GLU
6	C0	1728	LEU
6	C0	1793	ASP
6	C0	1798	ASP
6	C0	1849	ASP
6	C0	1906	ARG
6	C0	1922	ASP
6	C0	1989	VAL
6	C1	3	THR
6	C1	22	HIS
6	C1	49	ASP
6	C1	200	GLU
6	C1	303	GLU
6	C1	357	GLU
6	C1	438	ASP
6	C1	468	GLU
6	C1	472	THR
6	C1	567	GLU
6	C1	577	ASP
6	C1	580	GLN
6	C1	590	THR
6	C1	658	GLU
6	C1	663	LEU
6	C1	742	SER
6	C1	747	PHE
6	C1	777	GLU
6	C1	780	LEU
6	C1	817	GLU
6	C1	831	ASP
6	C1	872	LEU
6	C1	876	VAL
6	C1	959	ASP
6	C1	1019	ASN
6	C1	1194	GLU
6	C1	1306	ASP
6	C1	1341	THR
6	C1	1436	ASP
6	C1	1572	GLU

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Mol	Chain	Res	Type
6	C1	1576	SER
6	C1	1602	MET
6	C1	1654	ASP
6	C1	1703	GLU
6	C1	1728	LEU
6	C1	1793	ASP
6	C1	1798	ASP
6	C1	1849	ASP
6	C1	1989	VAL
6	C2	22	HIS
6	C2	49	ASP
6	C2	200	GLU
6	C2	316	ASP
6	C2	438	ASP
6	C2	567	GLU
6	C2	573	LEU
6	C2	580	GLN
6	C2	590	THR
6	C2	593	GLU
6	C2	663	LEU
6	C2	747	PHE
6	C2	777	GLU
6	C2	780	LEU
6	C2	872	LEU
6	C2	876	VAL
6	C2	926	ASN
6	C2	959	ASP
6	C2	1075	ASP
6	C2	1154	ASP
6	C2	1163	ASN
6	C2	1246	MET
6	C2	1306	ASP
6	C2	1341	THR
6	C2	1369	PHE
6	C2	1376	THR
6	C2	1388	PHE
6	C2	1449	TRP
6	C2	1457	ASP
6	C2	1700	SER
6	C2	1728	LEU
6	C2	1929	THR
6	C2	1930	LEU

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Mol	Chain	Res	Type
6	C2	1944	THR
6	C3	3	THR
6	C3	9	SER
6	C3	22	HIS
6	C3	49	ASP
6	C3	52	SER
6	C3	357	GLU
6	C3	438	ASP
6	C3	472	THR
6	C3	474	THR
6	C3	542	VAL
6	C3	577	ASP
6	C3	580	GLN
6	C3	590	THR
6	C3	637	SER
6	C3	663	LEU
6	C3	704	THR
6	C3	747	PHE
6	C3	782	ASP
6	C3	789	GLU
6	C3	872	LEU
6	C3	876	VAL
6	C3	895	ASN
6	C3	959	ASP
6	C3	1306	ASP
6	C3	1353	GLU
6	C3	1369	PHE
6	C3	1376	THR
6	C3	1377	SER
6	C3	1394	SER
6	C3	1436	ASP
6	C3	1479	GLU
6	C3	1572	GLU
6	C3	1634	SER
6	C3	1654	ASP
6	C3	1703	GLU
6	C3	1728	LEU
6	C3	1922	ASP
6	C3	1929	THR
6	C3	1930	LEU
6	C3	1938	ASP
6	C4	22	HIS

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Mol	Chain	Res	Type
6	C4	49	ASP
6	C4	200	GLU
6	C4	357	GLU
6	C4	438	ASP
6	C4	472	THR
6	C4	567	GLU
6	C4	573	LEU
6	C4	577	ASP
6	C4	580	GLN
6	C4	590	THR
6	C4	663	LEU
6	C4	682	ARG
6	C4	747	PHE
6	C4	780	LEU
6	C4	789	GLU
6	C4	831	ASP
6	C4	872	LEU
6	C4	876	VAL
6	C4	959	ASP
6	C4	1016	SER
6	C4	1163	ASN
6	C4	1306	ASP
6	C4	1341	THR
6	C4	1353	GLU
6	C4	1369	PHE
6	C4	1376	THR
6	C4	1457	ASP
6	C4	1479	GLU
6	C4	1480	VAL
6	C4	1572	GLU
6	C4	1654	ASP
6	C4	1697	ASN
6	C4	1728	LEU
6	C4	1930	LEU
6	C4	1938	ASP
7	D0	21	GLU
7	D0	34	LEU
7	D0	99	HIS
7	D0	142	GLU
7	D0	203	ASP
7	D0	207	SER
7	D0	211	ASP

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Mol	Chain	Res	Type
7	D0	217	THR
7	D0	228	LEU
7	D0	276	ASP
7	D0	400	SER
7	D0	424	GLU
7	D0	455	ASP
7	D0	486	SER
7	D0	493	HIS
7	D0	533	GLU
7	D0	545	ASP
7	D0	853	ASP
7	D0	871	ASP
7	D0	879	GLU
7	D0	1099	SER
7	D0	1143	GLU
7	D0	1159	GLU
7	D0	1173	ASP
7	D0	1185	ILE
7	D0	1236	SER
7	D0	1239	ASP
7	D0	1332	ILE
7	D0	1391	HIS
7	D1	34	LEU
7	D1	92	GLU
7	D1	142	GLU
7	D1	203	ASP
7	D1	207	SER
7	D1	211	ASP
7	D1	217	THR
7	D1	222	ASP
7	D1	228	LEU
7	D1	276	ASP
7	D1	399	SER
7	D1	455	ASP
7	D1	486	SER
7	D1	533	GLU
7	D1	545	ASP
7	D1	563	ARG
7	D1	1009	ASN
7	D1	1050	ASP
7	D1	1109	ILE
7	D1	1116	GLU

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Mol	Chain	Res	Type
7	D1	1120	ARG
7	D1	1143	GLU
7	D1	1173	ASP
7	D1	1179	ASP
7	D1	1185	ILE
7	D1	1236	SER
7	D1	1239	ASP
7	D1	1265	ASP
7	D1	1332	ILE
7	D1	1390	LEU
7	D1	1391	HIS
7	D2	34	LEU
7	D2	142	GLU
7	D2	203	ASP
7	D2	207	SER
7	D2	211	ASP
7	D2	228	LEU
7	D2	276	ASP
7	D2	400	SER
7	D2	455	ASP
7	D2	486	SER
7	D2	533	GLU
7	D2	545	ASP
7	D2	853	ASP
7	D2	1050	ASP
7	D2	1108	GLU
7	D2	1109	ILE
7	D2	1173	ASP
7	D2	1185	ILE
7	D2	1236	SER
7	D2	1239	ASP
7	D2	1332	ILE
7	D2	1391	HIS
7	D3	34	LEU
7	D3	99	HIS
7	D3	142	GLU
7	D3	203	ASP
7	D3	207	SER
7	D3	211	ASP
7	D3	217	THR
7	D3	222	ASP
7	D3	228	LEU

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Mol	Chain	Res	Type
7	D3	276	ASP
7	D3	399	SER
7	D3	427	ASP
7	D3	455	ASP
7	D3	486	SER
7	D3	527	ASN
7	D3	533	GLU
7	D3	545	ASP
7	D3	738	THR
7	D3	762	GLU
7	D3	849	ASN
7	D3	864	PRO
7	D3	866	LEU
7	D3	871	ASP
7	D3	994	SER
7	D3	1007	ASP
7	D3	1009	ASN
7	D3	1104	MET
7	D3	1109	ILE
7	D3	1116	GLU
7	D3	1120	ARG
7	D3	1128	SER
7	D3	1173	ASP
7	D3	1179	ASP
7	D3	1185	ILE
7	D3	1194	ASP
7	D3	1236	SER
7	D3	1239	ASP
7	D3	1265	ASP
7	D3	1332	ILE
7	D3	1391	HIS
7	D4	34	LEU
7	D4	142	GLU
7	D4	203	ASP
7	D4	207	SER
7	D4	211	ASP
7	D4	217	THR
7	D4	222	ASP
7	D4	228	LEU
7	D4	257	SER
7	D4	276	ASP
7	D4	399	SER

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Mol	Chain	Res	Type
7	D4	455	ASP
7	D4	465	ASP
7	D4	479	ASP
7	D4	486	SER
7	D4	508	SER
7	D4	533	GLU
7	D4	545	ASP
7	D4	762	GLU
7	D4	832	GLU
7	D4	853	ASP
7	D4	871	ASP
7	D4	1099	SER
7	D4	1143	GLU
7	D4	1173	ASP
7	D4	1179	ASP
7	D4	1186	THR
7	D4	1213	ASP
7	D4	1239	ASP
7	D4	1265	ASP
7	D4	1332	ILE
7	D4	1391	HIS
7	D5	34	LEU
7	D5	99	HIS
7	D5	142	GLU
7	D5	193	SER
7	D5	203	ASP
7	D5	207	SER
7	D5	211	ASP
7	D5	217	THR
7	D5	222	ASP
7	D5	228	LEU
7	D5	257	SER
7	D5	276	ASP
7	D5	399	SER
7	D5	427	ASP
7	D5	465	ASP
7	D5	479	ASP
7	D5	486	SER
7	D5	533	GLU
7	D5	545	ASP
7	D5	564	GLU
7	D5	719	GLU

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Mol	Chain	Res	Type
7	D5	762	GLU
7	D5	812	LYS
7	D5	832	GLU
7	D5	853	ASP
7	D5	879	GLU
7	D5	1092	SER
7	D5	1103	ASP
7	D5	1104	MET
7	D5	1105	HIS
7	D5	1143	GLU
7	D5	1173	ASP
7	D5	1179	ASP
7	D5	1186	THR
7	D5	1223	ASP
7	D5	1239	ASP
7	D5	1265	ASP
7	D5	1332	ILE
7	D5	1347	ARG
7	D5	1391	HIS
8	E0	3	THR
8	E0	148	THR
8	E0	169	PHE
8	E0	333	GLN
8	E0	527	GLU
8	E1	3	THR
8	E1	148	THR
8	E1	309	GLU
8	E1	333	GLN
8	E1	527	GLU
9	F0	96	ASP
9	F0	101	PRO
9	F0	103	LEU
9	F0	112	ARG
9	F0	113	GLN
9	F0	136	MET
9	F0	149	THR
9	F0	159	TYR
9	F0	161	GLN
9	F0	170	HIS
9	F0	202	HIS
9	F0	206	ASN
9	F0	270	THR

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Mol	Chain	Res	Type
9	F0	297	THR
9	F0	314	SER
9	F1	96	ASP
9	F1	108	LEU
9	F1	151	SER
9	F1	154	GLN
9	F1	155	LEU
9	F1	161	GLN
9	F1	283	ILE
9	F1	286	MET
9	F1	287	ARG
9	F1	296	SER
9	F1	308	THR
9	F2	96	ASP
9	F2	112	ARG
9	F2	117	SER
9	F2	120	GLN
9	F2	123	LEU
9	F2	144	GLN
9	F2	147	LYS
9	F2	151	SER
9	F2	169	ASP
9	F2	246	LYS
9	F2	252	SER
9	F2	253	ASP
9	F2	254	ARG
9	F2	268	ILE
9	F2	269	LYS
9	F2	285	THR
9	F2	299	ASP
9	F2	314	SER
9	F3	96	ASP
9	F3	106	THR
9	F3	136	MET
9	F3	154	GLN
9	F3	156	ASP
9	F3	254	ARG
9	F3	259	SER
9	F3	270	THR
9	F3	271	LEU
9	F3	275	THR
9	F3	282	ARG

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Mol	Chain	Res	Type
9	F3	303	ILE
9	F3	306	ARG
9	F3	315	LEU
10	H0	168	ASN
10	H0	196	ASN
10	H0	211	GLU
10	H0	487	ASP
10	H0	490	LEU
10	H1	168	ASN
10	H1	196	ASN
10	H1	211	GLU
10	H1	341	ASP
10	H1	487	ASP
10	H1	490	LEU
10	H2	168	ASN
10	H2	196	ASN
10	H2	211	GLU
10	H2	341	ASP
10	H2	487	ASP
10	H2	490	LEU
10	H3	167	GLU
10	H3	168	ASN
10	H3	196	ASN
10	H3	211	GLU
10	H3	341	ASP
10	H3	487	ASP
10	H3	490	LEU
11	I0	250	VAL
11	I0	323	GLU
11	I0	373	THR
11	I0	408	GLU
11	I1	250	VAL
11	I1	323	GLU
11	I1	408	GLU
11	I2	250	VAL
11	I2	274	ARG
11	I2	323	GLU
11	I2	373	THR
11	I2	408	GLU
11	I3	250	VAL
11	I3	323	GLU
11	I3	408	GLU

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Mol	Chain	Res	Type
12	J0	367	GLU
12	J0	412	GLU
12	J0	429	GLU
12	J0	498	LYS
12	J1	367	GLU
12	J1	412	GLU
12	J1	428	GLU
12	J1	429	GLU
12	J1	498	LYS
12	J2	412	GLU
12	J2	429	GLU
12	J2	453	ASP
12	J2	498	LYS
12	J3	367	GLU
12	J3	412	GLU
12	J3	428	GLU
12	J3	429	GLU
12	J3	498	LYS
12	J4	423	LEU
12	J4	458	LEU
12	J4	471	LEU
13	K0	83	THR
13	K0	84	PHE
13	K0	154	ASP
13	K0	166	GLU
13	K0	203	SER
13	K0	206	ASP
13	K0	235	GLU
13	K0	271	ASP
13	K0	377	ASP
13	K0	389	GLU
13	K0	401	ASP
13	K0	422	GLU
13	K0	427	VAL
13	K0	429	SER
13	K0	474	THR
13	K0	475	SER
13	K0	486	LEU
13	K0	502	MET
13	K0	505	GLU
13	K0	510	ASN
13	K0	517	ASP

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Mol	Chain	Res	Type
13	K0	534	LEU
13	K0	542	ASP
13	K0	592	ASN
13	K0	697	ASP
13	K0	794	ASP
13	K0	875	MET
13	K0	894	ASP
13	K0	908	LYS
13	K0	1010	GLU
13	K0	1056	GLU
13	K0	1090	ASP
13	K0	1122	VAL
13	K0	1129	ASP
13	K1	83	THR
13	K1	84	PHE
13	K1	154	ASP
13	K1	210	SER
13	K1	271	ASP
13	K1	328	GLU
13	K1	377	ASP
13	K1	401	ASP
13	K1	408	THR
13	K1	419	LEU
13	K1	422	GLU
13	K1	486	LEU
13	K1	487	GLU
13	K1	498	ASN
13	K1	509	LYS
13	K1	517	ASP
13	K1	697	ASP
13	K1	717	ASP
13	K1	875	MET
13	K1	894	ASP
13	K1	986	ASP
13	K1	1010	GLU
13	K1	1090	ASP
13	K1	1121	GLU
13	K2	83	THR
13	K2	84	PHE
13	K2	111	GLU
13	K2	154	ASP
13	K2	271	ASP

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Mol	Chain	Res	Type
13	K2	298	GLU
13	K2	377	ASP
13	K2	389	GLU
13	K2	401	ASP
13	K2	422	GLU
13	K2	427	VAL
13	K2	429	SER
13	K2	478	ASN
13	K2	481	ILE
13	K2	484	GLU
13	K2	492	SER
13	K2	509	LYS
13	K2	547	SER
13	K2	697	ASP
13	K2	875	MET
13	K2	876	CYS
13	K2	894	ASP
13	K2	910	LYS
13	K2	932	HIS
13	K2	1010	GLU
13	K2	1062	GLU
13	K2	1090	ASP
13	K2	1121	GLU
13	K2	1129	ASP
13	K3	83	THR
13	K3	84	PHE
13	K3	154	ASP
13	K3	206	ASP
13	K3	271	ASP
13	K3	377	ASP
13	K3	389	GLU
13	K3	401	ASP
13	K3	422	GLU
13	K3	427	VAL
13	K3	429	SER
13	K3	482	LEU
13	K3	508	THR
13	K3	586	GLU
13	K3	596	ILE
13	K3	697	ASP
13	K3	718	SER
13	K3	794	ASP

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Mol	Chain	Res	Type
13	K3	875	MET
13	K3	894	ASP
13	K3	899	ASP
13	K3	907	GLU
13	K3	1010	GLU
13	K3	1090	ASP
13	K3	1121	GLU
13	K3	1129	ASP
14	L0	157	ASP
14	L0	172	ASP
14	L0	205	THR
14	L0	240	PHE
14	L0	245	VAL
14	L0	295	VAL
14	L0	326	ASP
14	L0	341	GLU
14	L0	395	LEU
14	L0	416	GLU
14	L0	444	THR
14	L0	490	GLU
14	L0	583	GLU
14	L0	584	LYS
14	L0	599	ASP
14	L0	674	VAL
14	L0	727	CYS
14	L0	736	LEU
14	L0	917	ASP
14	L1	172	ASP
14	L1	205	THR
14	L1	234	LEU
14	L1	240	PHE
14	L1	295	VAL
14	L1	324	ASP
14	L1	326	ASP
14	L1	340	ARG
14	L1	341	GLU
14	L1	416	GLU
14	L1	444	THR
14	L1	475	THR
14	L1	490	GLU
14	L1	584	LYS
14	L1	599	ASP

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Mol	Chain	Res	Type
14	L1	604	GLN
14	L1	674	VAL
14	L1	732	MET
14	L1	733	GLU
14	L1	841	GLU
14	L1	917	ASP
14	L2	172	ASP
14	L2	205	THR
14	L2	240	PHE
14	L2	326	ASP
14	L2	341	GLU
14	L2	416	GLU
14	L2	444	THR
14	L2	490	GLU
14	L2	585	HIS
14	L2	599	ASP
14	L2	674	VAL
14	L2	730	GLN
14	L2	917	ASP
14	L3	172	ASP
14	L3	205	THR
14	L3	240	PHE
14	L3	326	ASP
14	L3	341	GLU
14	L3	416	GLU
14	L3	444	THR
14	L3	490	GLU
14	L3	582	ARG
14	L3	585	HIS
14	L3	674	VAL
14	L3	728	GLU
14	L3	733	GLU
14	L3	841	GLU
14	L3	917	ASP
15	M0	241	GLU
15	M0	280	LEU
15	M0	324	ARG
15	M0	350	VAL
15	M0	403	LEU
15	M0	435	THR
15	M0	485	PHE
15	M0	498	GLN

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Mol	Chain	Res	Type
15	M0	656	ASN
15	M0	661	SER
15	M0	665	GLU
15	M0	761	GLU
15	M0	805	ASP
15	M0	830	ASP
15	M0	860	ASP
15	M0	866	ASP
15	M1	241	GLU
15	M1	280	LEU
15	M1	324	ARG
15	M1	350	VAL
15	M1	402	HIS
15	M1	403	LEU
15	M1	435	THR
15	M1	485	PHE
15	M1	486	VAL
15	M1	498	GLN
15	M1	586	PRO
15	M1	587	LEU
15	M1	656	ASN
15	M1	661	SER
15	M1	665	GLU
15	M1	761	GLU
15	M1	805	ASP
15	M1	830	ASP
15	M1	860	ASP
15	M2	241	GLU
15	M2	324	ARG
15	M2	347	THR
15	M2	350	VAL
15	M2	379	ASP
15	M2	402	HIS
15	M2	407	ASP
15	M2	416	TYR
15	M2	485	PHE
15	M2	486	VAL
15	M2	661	SER
15	M2	762	HIS
15	M2	805	ASP
15	M2	830	ASP
15	M2	834	ASN

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Mol	Chain	Res	Type
15	M2	860	ASP
15	M2	915	ASP
15	M3	241	GLU
15	M3	280	LEU
15	M3	324	ARG
15	M3	350	VAL
15	M3	485	PHE
15	M3	491	VAL
15	M3	586	PRO
15	M3	656	ASN
15	M3	661	SER
15	M3	762	HIS
15	M3	782	GLU
15	M3	805	ASP
15	M3	830	ASP
15	M3	860	ASP
16	N0	11	SER
16	N0	22	ASP
16	N0	103	ASP
16	N0	246	ASP
16	N0	294	ASP
16	N1	103	ASP
16	N1	115	ASP
16	N1	246	ASP
16	N1	294	ASP
16	N2	9	ASP
16	N2	103	ASP
16	N2	115	ASP
16	N2	246	ASP
16	N3	103	ASP
16	N3	115	ASP
16	N3	246	ASP
16	N3	294	ASP
17	O0	17	ASP
17	O0	21	ASP
17	O0	220	ASP
17	O0	284	VAL
17	O1	21	ASP
17	O1	94	ASN
17	O1	220	ASP
17	O1	284	VAL
17	O2	21	ASP

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Mol	Chain	Res	Type
17	O2	204	GLU
17	O2	220	ASP
17	O2	284	VAL
17	O2	312	ASN
17	O3	17	ASP
17	O3	21	ASP
17	O3	117	THR
17	O3	220	ASP
17	O3	284	VAL
18	P0	2	GLU
18	P0	3	GLU
18	P0	7	GLU
18	P0	43	GLU
18	P0	143	GLU
18	P0	218	LYS
18	P0	263	GLU
18	P0	323	ASP
18	P0	405	GLU
18	P0	520	ASP
18	P0	550	GLU
18	P0	576	THR
18	P0	606	ASP
18	P0	617	SER
18	P1	2	GLU
18	P1	7	GLU
18	P1	43	GLU
18	P1	88	GLU
18	P1	143	GLU
18	P1	218	LYS
18	P1	263	GLU
18	P1	323	ASP
18	P1	520	ASP
18	P1	551	LYS
18	P1	555	ASP
18	P1	576	THR
18	P1	623	GLN
18	P2	2	GLU
18	P2	43	GLU
18	P2	143	GLU
18	P2	263	GLU
18	P2	323	ASP
18	P2	520	ASP

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Mol	Chain	Res	Type
18	P2	533	ASP
18	P2	550	GLU
18	P2	551	LYS
18	P2	555	ASP
18	P2	576	THR
18	P2	606	ASP
18	P2	617	SER
18	P3	2	GLU
18	P3	43	GLU
18	P3	60	ASP
18	P3	88	GLU
18	P3	143	GLU
18	P3	218	LYS
18	P3	263	GLU
18	P3	323	ASP
18	P3	388	GLN
18	P3	389	SER
18	P3	520	ASP
18	P3	533	ASP
18	P3	550	GLU
18	P3	555	ASP
18	P3	576	THR
18	P3	617	SER
19	Q0	51	ASP
19	Q0	206	GLU
19	Q0	214	THR
19	Q1	51	ASP
19	Q1	206	GLU
19	Q2	173	SER
19	Q2	206	GLU
19	Q3	51	ASP
19	Q3	206	GLU
19	Q3	214	THR
20	R0	104	HIS
20	R0	180	ASP
20	R0	189	ASP
20	R0	201	TYR
20	R0	211	SER
20	R0	214	SER
20	R0	224	ASP
20	R0	276	ARG
20	R0	333	ASP

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Mol	Chain	Res	Type
20	R0	378	SER
20	R0	404	THR
20	R0	405	ASP
20	R0	411	HIS
20	R0	460	SER
20	R0	491	TRP
20	R0	497	GLU
20	R0	575	ASP
20	R0	589	ASP
20	R0	620	ASP
20	R0	660	SER
20	R0	664	GLU
20	R0	790	ASP
20	R0	811	MET
20	R0	817	SER
20	R0	1043	GLU
20	R0	1049	ASP
20	R0	1176	GLU
20	R0	1215	MET
20	R0	1226	ASP
20	R0	1230	SER
20	R0	1282	SER
20	R0	1283	SER
20	R0	1286	ASP
20	R1	104	HIS
20	R1	180	ASP
20	R1	189	ASP
20	R1	201	TYR
20	R1	211	SER
20	R1	214	SER
20	R1	224	ASP
20	R1	333	ASP
20	R1	404	THR
20	R1	405	ASP
20	R1	411	HIS
20	R1	497	GLU
20	R1	575	ASP
20	R1	589	ASP
20	R1	620	ASP
20	R1	660	SER
20	R1	664	GLU
20	R1	790	ASP

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Mol	Chain	Res	Type
20	R1	811	MET
20	R1	817	SER
20	R1	1043	GLU
20	R1	1049	ASP
20	R1	1061	GLU
20	R1	1215	MET
20	R1	1226	ASP
20	R1	1244	GLU
20	R1	1286	ASP
20	R1	1381	MET
20	R1	1404	HIS
20	R2	104	HIS
20	R2	180	ASP
20	R2	189	ASP
20	R2	201	TYR
20	R2	211	SER
20	R2	224	ASP
20	R2	276	ARG
20	R2	378	SER
20	R2	404	THR
20	R2	405	ASP
20	R2	411	HIS
20	R2	460	SER
20	R2	497	GLU
20	R2	575	ASP
20	R2	589	ASP
20	R2	620	ASP
20	R2	653	ASN
20	R2	660	SER
20	R2	790	ASP
20	R2	811	MET
20	R2	931	CYS
20	R2	1027	SER
20	R2	1049	ASP
20	R2	1115	LEU
20	R2	1215	MET
20	R2	1244	GLU
20	R2	1381	MET
20	R3	104	HIS
20	R3	180	ASP
20	R3	189	ASP
20	R3	201	TYR

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Mol	Chain	Res	Type
20	R3	211	SER
20	R3	224	ASP
20	R3	378	SER
20	R3	404	THR
20	R3	405	ASP
20	R3	411	HIS
20	R3	460	SER
20	R3	497	GLU
20	R3	575	ASP
20	R3	589	ASP
20	R3	620	ASP
20	R3	660	SER
20	R3	664	GLU
20	R3	790	ASP
20	R3	811	MET
20	R3	817	SER
20	R3	1049	ASP
20	R3	1215	MET
20	R3	1226	ASP
20	R3	1277	ILE
20	R3	1279	THR
20	R3	1281	GLU
20	R3	1381	MET
20	R3	1404	HIS
21	S0	57	ASP
21	S0	155	GLU
21	S0	252	ASP
21	S0	307	THR
21	S0	325	GLU
21	S1	31	ASP
21	S1	57	ASP
21	S1	125	ASP
21	S1	155	GLU
21	S1	264	GLU
21	S1	307	THR
21	S2	57	ASP
21	S2	125	ASP
21	S2	170	SER
21	S2	252	ASP
21	S2	298	VAL
21	S2	307	THR
21	S3	57	ASP

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Mol	Chain	Res	Type
21	S3	125	ASP
21	S3	155	GLU
21	S3	307	THR
22	T0	92	THR
22	T0	185	SER
22	T0	186	ASP
22	T0	293	ASP
22	T0	424	ASN
22	T0	452	GLU
22	T0	647	GLU
22	T0	684	ASP
22	T0	765	ASP
22	T0	800	THR
22	T0	821	ASN
22	T0	825	SER
22	T0	945	SER
22	T1	30	LEU
22	T1	92	THR
22	T1	186	ASP
22	T1	203	SER
22	T1	293	ASP
22	T1	375	SER
22	T1	424	ASN
22	T1	452	GLU
22	T1	498	GLU
22	T1	647	GLU
22	T1	684	ASP
22	T1	765	ASP
22	T1	800	THR
22	T1	820	HIS
22	T1	821	ASN
22	T1	825	SER
22	T1	945	SER
23	U0	766	THR
23	U0	800	VAL
23	U0	805	ASP
23	U0	846	ILE
23	U1	598	LYS
23	U1	606	ASN
23	U1	610	LEU
23	U2	606	ASN
23	U3	606	ASN

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Mol	Chain	Res	Type
23	U4	606	ASN
23	U5	606	ASN
23	U6	606	ASN
23	U6	610	LEU
24	V0	767	SER
24	V0	779	VAL
24	V0	797	LEU
24	V0	837	ASP
24	V0	840	LEU
24	V0	849	LEU
24	V0	857	LEU
24	V0	878	LEU
24	V0	926	GLU
24	V0	932	LEU
24	V0	940	SER
24	V0	962	THR
25	W0	37	THR
25	W0	45	SER
25	W0	55	LEU
25	W0	81	VAL
25	W0	223	VAL
25	W0	233	SER
25	W0	263	VAL
25	W0	306	ASN
25	W0	348	THR
25	W0	359	LEU
25	W0	438	LEU
25	W0	448	PHE
25	W0	496	SER
25	W0	502	SER
25	W0	507	CYS
25	W0	527	ASP
25	W0	667	LEU
25	W0	699	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (920) such sidechains are listed below:

Mol	Chain	Res	Type
1	00	16	GLN
1	00	408	ASN
1	00	445	ASN
1	00	496	HIS

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Mol	Chain	Res	Type
1	00	511	GLN
1	00	571	GLN
1	01	16	GLN
1	01	241	ASN
1	01	408	ASN
1	01	445	ASN
1	01	496	HIS
1	01	511	GLN
1	01	571	GLN
1	01	688	HIS
1	02	16	GLN
1	02	137	GLN
1	02	187	HIS
1	02	241	ASN
1	02	360	ASN
1	02	511	GLN
1	02	571	GLN
1	02	651	HIS
1	03	16	GLN
1	03	408	ASN
1	03	445	ASN
1	03	496	HIS
1	03	511	GLN
1	03	571	GLN
1	04	241	ASN
1	04	360	ASN
1	04	408	ASN
1	04	511	GLN
1	04	571	GLN
1	04	620	ASN
1	04	651	HIS
2	10	44	ASN
2	10	174	HIS
2	10	223	GLN
2	10	242	ASN
2	10	284	GLN
2	10	286	GLN
2	10	713	GLN
2	10	906	ASN
2	10	979	GLN
2	10	1097	GLN
2	10	1157	GLN

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Mol	Chain	Res	Type
2	10	1227	HIS
2	10	1362	ASN
2	10	1363	GLN
2	10	1517	HIS
2	10	1601	GLN
2	10	1612	GLN
2	10	1640	GLN
2	10	1695	GLN
2	11	44	ASN
2	11	223	GLN
2	11	260	HIS
2	11	284	GLN
2	11	286	GLN
2	11	713	GLN
2	11	911	GLN
2	11	979	GLN
2	11	1097	GLN
2	11	1143	GLN
2	11	1157	GLN
2	11	1203	ASN
2	11	1227	HIS
2	11	1362	ASN
2	11	1363	GLN
2	11	1601	GLN
2	11	1612	GLN
2	11	1640	GLN
2	12	44	ASN
2	12	174	HIS
2	12	223	GLN
2	12	284	GLN
2	12	286	GLN
2	12	287	ASN
2	12	911	GLN
2	12	979	GLN
2	12	1097	GLN
2	12	1135	ASN
2	12	1143	GLN
2	12	1157	GLN
2	12	1227	HIS
2	12	1279	GLN
2	12	1333	HIS
2	12	1362	ASN

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Mol	Chain	Res	Type
2	12	1363	GLN
2	12	1517	HIS
2	12	1570	GLN
2	12	1612	GLN
2	12	1640	GLN
2	12	1774	ASN
2	13	44	ASN
2	13	174	HIS
2	13	242	ASN
2	13	284	GLN
2	13	286	GLN
2	13	836	GLN
2	13	911	GLN
2	13	1097	GLN
2	13	1109	ASN
2	13	1129	GLN
2	13	1135	ASN
2	13	1143	GLN
2	13	1157	GLN
2	13	1356	GLN
2	13	1362	ASN
2	13	1363	GLN
2	13	1517	HIS
2	13	1612	GLN
2	13	1640	GLN
2	14	44	ASN
2	14	75	GLN
2	14	174	HIS
2	14	223	GLN
2	14	284	GLN
2	14	286	GLN
2	14	681	ASN
2	14	713	GLN
2	14	911	GLN
2	14	979	GLN
2	14	1097	GLN
2	14	1135	ASN
2	14	1143	GLN
2	14	1157	GLN
2	14	1184	GLN
2	14	1227	HIS
2	14	1362	ASN

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Mol	Chain	Res	Type
2	14	1363	GLN
2	14	1517	HIS
2	14	1570	GLN
2	14	1587	ASN
2	14	1601	GLN
2	14	1612	GLN
2	14	1640	GLN
2	14	1801	GLN
2	15	44	ASN
2	15	246	ASN
2	15	264	GLN
2	15	284	GLN
2	15	286	GLN
2	15	713	GLN
2	15	864	GLN
2	15	911	GLN
2	15	979	GLN
2	15	1097	GLN
2	15	1135	ASN
2	15	1143	GLN
2	15	1157	GLN
2	15	1227	HIS
2	15	1362	ASN
2	15	1517	HIS
2	15	1570	GLN
2	15	1587	ASN
2	15	1612	GLN
2	15	1640	GLN
2	16	44	ASN
2	16	174	HIS
2	16	260	HIS
2	16	284	GLN
2	16	286	GLN
2	16	864	GLN
2	16	911	GLN
2	16	979	GLN
2	16	1097	GLN
2	16	1135	ASN
2	16	1143	GLN
2	16	1157	GLN
2	16	1227	HIS
2	16	1362	ASN

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Mol	Chain	Res	Type
2	16	1517	HIS
2	16	1587	ASN
2	16	1601	GLN
2	16	1612	GLN
2	16	1640	GLN
2	17	44	ASN
2	17	174	HIS
2	17	242	ASN
2	17	246	ASN
2	17	264	GLN
2	17	284	GLN
2	17	286	GLN
2	17	911	GLN
2	17	979	GLN
2	17	1097	GLN
2	17	1333	HIS
2	17	1356	GLN
2	17	1362	ASN
2	17	1363	GLN
2	17	1517	HIS
2	17	1566	GLN
2	17	1612	GLN
2	17	1640	GLN
3	40	179	ASN
3	41	179	ASN
3	41	454	GLN
4	A0	180	ASN
4	A0	193	ASN
4	A0	279	HIS
4	A0	280	GLN
4	A0	344	GLN
4	A0	452	HIS
4	A0	457	GLN
4	A0	458	GLN
4	A0	515	HIS
4	A0	549	GLN
4	A0	723	ASN
4	A1	15	GLN
4	A1	142	GLN
4	A1	193	ASN
4	A1	280	GLN
4	A1	344	GLN

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Mol	Chain	Res	Type
4	A1	420	GLN
4	A1	456	ASN
4	A1	511	GLN
4	A1	549	GLN
4	A1	788	GLN
4	A2	15	GLN
4	A2	104	ASN
4	A2	193	ASN
4	A2	280	GLN
4	A2	344	GLN
4	A2	420	GLN
4	A2	452	HIS
4	A2	457	GLN
4	A2	549	GLN
4	A2	610	ASN
4	A2	634	ASN
4	A2	759	GLN
4	A2	784	GLN
4	A2	788	GLN
4	A3	142	GLN
4	A3	193	ASN
4	A3	344	GLN
4	A3	420	GLN
4	A3	456	ASN
4	A3	549	GLN
4	A3	724	GLN
4	A3	759	GLN
4	A3	788	GLN
4	A3	819	ASN
4	A4	193	ASN
4	A4	229	GLN
4	A4	280	GLN
4	A4	456	ASN
4	A4	457	GLN
4	A4	458	GLN
4	A4	549	GLN
4	A4	788	GLN
4	A5	193	ASN
4	A5	200	HIS
4	A5	229	GLN
4	A5	244	ASN
4	A5	264	GLN

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Mol	Chain	Res	Type
4	A5	268	ASN
4	A5	381	ASN
4	A5	403	GLN
4	A5	420	GLN
4	A5	457	GLN
4	A5	515	HIS
4	A5	549	GLN
4	A5	610	ASN
4	A5	634	ASN
4	A5	744	ASN
4	A5	788	GLN
4	A6	193	ASN
4	A6	280	GLN
4	A6	344	GLN
4	A6	381	ASN
4	A6	443	GLN
4	A6	458	GLN
4	A6	515	HIS
4	A6	549	GLN
4	A6	610	ASN
4	A6	634	ASN
4	A6	706	HIS
4	A6	788	GLN
5	B0	113	GLN
5	B0	117	GLN
5	B0	211	GLN
5	B0	248	GLN
5	B0	250	ASN
5	B0	295	GLN
5	B0	510	ASN
5	B0	616	ASN
5	B0	644	HIS
5	B0	699	GLN
5	B0	775	GLN
5	B0	779	ASN
5	B0	989	HIS
5	B0	993	GLN
5	B0	1057	GLN
5	B0	1215	GLN
5	B0	1229	GLN
5	B0	1329	ASN
5	B0	1441	GLN

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Mol	Chain	Res	Type
5	B0	1458	GLN
5	B0	1467	HIS
5	B0	1587	ASN
5	B0	1685	GLN
5	B1	113	GLN
5	B1	117	GLN
5	B1	211	GLN
5	B1	248	GLN
5	B1	250	ASN
5	B1	295	GLN
5	B1	616	ASN
5	B1	699	GLN
5	B1	775	GLN
5	B1	779	ASN
5	B1	861	HIS
5	B1	1057	GLN
5	B1	1215	GLN
5	B1	1229	GLN
5	B1	1239	GLN
5	B1	1329	ASN
5	B1	1406	GLN
5	B1	1458	GLN
5	B1	1587	ASN
5	B1	1685	GLN
5	B1	1738	GLN
6	C0	22	HIS
6	C0	26	ASN
6	C0	56	ASN
6	C0	80	GLN
6	C0	151	GLN
6	C0	412	ASN
6	C0	453	ASN
6	C0	528	HIS
6	C0	537	ASN
6	C0	613	ASN
6	C0	709	GLN
6	C0	722	ASN
6	C0	737	GLN
6	C0	895	ASN
6	C0	909	ASN
6	C0	1019	ASN
6	C0	1088	GLN

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Mol	Chain	Res	Type
6	C0	1112	GLN
6	C0	1137	GLN
6	C0	1220	ASN
6	C0	1224	GLN
6	C0	1319	HIS
6	C0	1420	HIS
6	C0	1509	GLN
6	C0	1510	GLN
6	C0	1567	GLN
6	C0	1618	GLN
6	C0	1712	GLN
6	C0	1730	GLN
6	C0	1734	GLN
6	C0	1765	GLN
6	C0	1958	HIS
6	C1	22	HIS
6	C1	26	ASN
6	C1	56	ASN
6	C1	80	GLN
6	C1	151	GLN
6	C1	412	ASN
6	C1	528	HIS
6	C1	537	ASN
6	C1	613	ASN
6	C1	709	GLN
6	C1	722	ASN
6	C1	737	GLN
6	C1	895	ASN
6	C1	905	HIS
6	C1	909	ASN
6	C1	1088	GLN
6	C1	1112	GLN
6	C1	1137	GLN
6	C1	1218	HIS
6	C1	1220	ASN
6	C1	1224	GLN
6	C1	1319	HIS
6	C1	1510	GLN
6	C1	1567	GLN
6	C1	1618	GLN
6	C1	1638	HIS
6	C1	1712	GLN

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Mol	Chain	Res	Type
6	C1	1730	GLN
6	C1	1734	GLN
6	C1	1765	GLN
6	C1	1958	HIS
6	C1	2012	ASN
6	C2	80	GLN
6	C2	119	GLN
6	C2	315	GLN
6	C2	412	ASN
6	C2	471	GLN
6	C2	484	HIS
6	C2	560	HIS
6	C2	709	GLN
6	C2	786	GLN
6	C2	808	HIS
6	C2	848	HIS
6	C2	854	ASN
6	C2	858	GLN
6	C2	909	ASN
6	C2	1021	GLN
6	C2	1111	ASN
6	C2	1137	GLN
6	C2	1251	GLN
6	C2	1277	HIS
6	C2	1281	HIS
6	C2	1319	HIS
6	C2	1329	GLN
6	C2	1430	GLN
6	C2	1510	GLN
6	C2	1567	GLN
6	C2	1730	GLN
6	C2	1856	GLN
6	C2	1957	GLN
6	C2	2012	ASN
6	C3	26	ASN
6	C3	32	GLN
6	C3	56	ASN
6	C3	68	GLN
6	C3	80	GLN
6	C3	119	GLN
6	C3	151	GLN
6	C3	342	GLN

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Mol	Chain	Res	Type
6	C3	453	ASN
6	C3	525	GLN
6	C3	560	HIS
6	C3	566	HIS
6	C3	568	HIS
6	C3	613	ASN
6	C3	674	GLN
6	C3	681	GLN
6	C3	709	GLN
6	C3	895	ASN
6	C3	898	ASN
6	C3	926	ASN
6	C3	928	ASN
6	C3	1088	GLN
6	C3	1111	ASN
6	C3	1112	GLN
6	C3	1137	GLN
6	C3	1215	ASN
6	C3	1277	HIS
6	C3	1329	GLN
6	C3	1348	GLN
6	C3	1420	HIS
6	C3	1463	GLN
6	C3	1510	GLN
6	C3	1567	GLN
6	C3	1628	GLN
6	C3	1945	ASN
6	C4	22	HIS
6	C4	26	ASN
6	C4	56	ASN
6	C4	151	GLN
6	C4	412	ASN
6	C4	491	GLN
6	C4	537	ASN
6	C4	594	GLN
6	C4	709	GLN
6	C4	848	HIS
6	C4	909	ASN
6	C4	926	ASN
6	C4	928	ASN
6	C4	1088	GLN
6	C4	1112	GLN

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Mol	Chain	Res	Type
6	C4	1137	GLN
6	C4	1218	HIS
6	C4	1220	ASN
6	C4	1224	GLN
6	C4	1251	GLN
6	C4	1288	GLN
6	C4	1319	HIS
6	C4	1329	GLN
6	C4	1430	GLN
6	C4	1509	GLN
6	C4	1510	GLN
6	C4	1511	GLN
6	C4	1567	GLN
6	C4	1618	GLN
6	C4	1628	GLN
6	C4	1697	ASN
6	C4	1712	GLN
6	C4	1730	GLN
6	C4	1734	GLN
6	C4	1765	GLN
6	C4	1962	GLN
7	D0	33	GLN
7	D0	249	GLN
7	D0	377	GLN
7	D0	718	GLN
7	D0	736	ASN
7	D0	760	GLN
7	D0	985	GLN
7	D0	1019	HIS
7	D0	1022	GLN
7	D0	1028	GLN
7	D0	1073	ASN
7	D0	1105	HIS
7	D0	1158	GLN
7	D0	1177	GLN
7	D0	1384	GLN
7	D1	310	GLN
7	D1	363	HIS
7	D1	377	GLN
7	D1	383	ASN
7	D1	428	ASN
7	D1	736	ASN

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Mol	Chain	Res	Type
7	D1	882	GLN
7	D1	915	ASN
7	D1	919	GLN
7	D1	943	GLN
7	D1	948	HIS
7	D1	1158	GLN
7	D1	1340	GLN
7	D1	1384	GLN
7	D2	33	GLN
7	D2	249	GLN
7	D2	383	ASN
7	D2	718	GLN
7	D2	760	GLN
7	D2	768	HIS
7	D2	811	GLN
7	D2	985	GLN
7	D2	1022	GLN
7	D2	1028	GLN
7	D2	1218	GLN
7	D2	1242	HIS
7	D2	1340	GLN
7	D2	1384	GLN
7	D3	96	GLN
7	D3	199	GLN
7	D3	310	GLN
7	D3	363	HIS
7	D3	377	GLN
7	D3	383	ASN
7	D3	428	ASN
7	D3	718	GLN
7	D3	724	ASN
7	D3	736	ASN
7	D3	943	GLN
7	D3	985	GLN
7	D3	1019	HIS
7	D3	1028	GLN
7	D3	1088	ASN
7	D3	1105	HIS
7	D3	1158	GLN
7	D3	1168	HIS
7	D3	1218	GLN
7	D3	1340	GLN

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Mol	Chain	Res	Type
7	D3	1384	GLN
7	D4	163	HIS
7	D4	249	GLN
7	D4	310	GLN
7	D4	383	ASN
7	D4	428	ASN
7	D4	457	HIS
7	D4	664	ASN
7	D4	718	GLN
7	D4	736	ASN
7	D4	782	GLN
7	D4	1158	GLN
7	D5	96	GLN
7	D5	163	HIS
7	D5	249	GLN
7	D5	310	GLN
7	D5	377	GLN
7	D5	383	ASN
7	D5	457	HIS
7	D5	522	HIS
7	D5	527	ASN
7	D5	664	ASN
7	D5	724	ASN
7	D5	782	GLN
7	D5	1158	GLN
7	D5	1340	GLN
8	E0	111	HIS
8	E0	113	GLN
8	E0	114	GLN
8	E0	190	ASN
8	E0	198	GLN
8	E0	340	GLN
8	E0	546	HIS
8	E1	113	GLN
8	E1	159	GLN
8	E1	190	ASN
8	E1	304	GLN
8	E1	340	GLN
8	E1	374	ASN
8	E1	546	HIS
9	F0	134	GLN
9	F0	144	GLN

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Mol	Chain	Res	Type
9	F0	206	ASN
9	F0	220	GLN
9	F0	276	GLN
9	F1	113	GLN
9	F1	192	GLN
9	F1	195	GLN
9	F1	202	HIS
9	F2	220	GLN
9	F2	301	GLN
9	F3	161	GLN
9	F3	198	ASN
9	F3	202	HIS
9	F3	216	GLN
9	F3	220	GLN
9	F3	301	GLN
10	H0	119	ASN
10	H0	275	GLN
10	H0	342	GLN
10	H0	409	GLN
10	H0	418	GLN
10	H0	437	GLN
10	H1	119	ASN
10	H1	342	GLN
10	H1	388	GLN
10	H1	409	GLN
10	H1	418	GLN
10	H1	437	GLN
10	H1	443	HIS
10	H1	465	GLN
10	H2	119	ASN
10	H2	158	ASN
10	H2	275	GLN
10	H2	342	GLN
10	H3	119	ASN
10	H3	158	ASN
10	H3	342	GLN
10	H3	388	GLN
10	H3	409	GLN
10	H3	418	GLN
11	I0	292	GLN
11	I0	337	HIS
11	I0	356	GLN

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Mol	Chain	Res	Type
11	I1	292	GLN
11	I1	299	ASN
11	I1	337	HIS
11	I1	363	GLN
11	I1	394	GLN
11	I2	292	GLN
11	I2	299	ASN
11	I2	363	GLN
11	I3	292	GLN
11	I3	363	GLN
12	J0	347	GLN
12	J0	354	GLN
12	J0	386	GLN
12	J0	439	ASN
12	J0	443	GLN
12	J0	486	GLN
12	J1	347	GLN
12	J1	354	GLN
12	J1	386	GLN
12	J1	443	GLN
12	J1	457	HIS
12	J2	347	GLN
12	J2	354	GLN
12	J2	357	GLN
12	J2	449	GLN
12	J2	472	GLN
12	J3	347	GLN
12	J3	354	GLN
12	J3	386	GLN
12	J4	347	GLN
12	J4	376	HIS
12	J4	386	GLN
12	J4	400	GLN
12	J4	424	GLN
12	J4	481	HIS
13	K0	247	GLN
13	K0	394	ASN
13	K0	415	GLN
13	K0	510	ASN
13	K0	874	GLN
13	K0	878	GLN
13	K0	895	GLN

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Mol	Chain	Res	Type
13	K0	917	GLN
13	K0	932	HIS
13	K0	950	HIS
13	K0	1030	GLN
13	K0	1067	ASN
13	K1	293	ASN
13	K1	313	ASN
13	K1	319	ASN
13	K1	478	ASN
13	K1	498	ASN
13	K1	799	ASN
13	K1	882	GLN
13	K1	886	GLN
13	K1	917	GLN
13	K1	921	GLN
13	K1	1004	HIS
13	K1	1065	ASN
13	K1	1067	ASN
13	K1	1147	ASN
13	K2	394	ASN
13	K2	592	ASN
13	K2	727	ASN
13	K2	878	GLN
13	K2	895	GLN
13	K2	1079	GLN
13	K2	1147	ASN
13	K2	1153	GLN
13	K3	394	ASN
13	K3	727	ASN
13	K3	744	GLN
13	K3	874	GLN
13	K3	878	GLN
13	K3	882	GLN
13	K3	917	GLN
13	K3	942	ASN
13	K3	950	HIS
13	K3	1030	GLN
14	L0	302	HIS
14	L0	486	ASN
14	L0	541	ASN
14	L0	604	GLN
14	L0	725	ASN

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Mol	Chain	Res	Type
14	L0	761	ASN
14	L1	302	HIS
14	L1	486	ASN
14	L1	541	ASN
14	L1	617	GLN
14	L1	757	HIS
14	L1	844	HIS
14	L2	302	HIS
14	L2	388	ASN
14	L2	541	ASN
14	L2	761	ASN
14	L2	924	GLN
14	L3	541	ASN
14	L3	705	HIS
14	L3	761	ASN
14	L3	924	GLN
15	M0	360	ASN
15	M0	367	HIS
15	M0	402	HIS
15	M0	498	GLN
15	M0	503	HIS
15	M0	535	GLN
15	M0	825	HIS
15	M0	926	GLN
15	M1	360	ASN
15	M1	409	GLN
15	M1	446	GLN
15	M1	503	HIS
15	M1	535	GLN
15	M1	781	ASN
15	M1	825	HIS
15	M1	840	HIS
15	M1	873	ASN
15	M1	926	GLN
15	M2	360	ASN
15	M2	503	HIS
15	M2	751	HIS
15	M2	762	HIS
15	M2	825	HIS
15	M2	926	GLN
15	M3	270	ASN
15	M3	360	ASN

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Mol	Chain	Res	Type
15	M3	503	HIS
15	M3	825	HIS
15	M3	926	GLN
16	N0	107	ASN
16	N0	139	GLN
16	N0	146	ASN
16	N0	154	ASN
16	N0	284	ASN
16	N1	99	HIS
16	N1	107	ASN
16	N1	146	ASN
16	N1	147	ASN
16	N1	154	ASN
16	N2	107	ASN
16	N2	146	ASN
16	N2	147	ASN
16	N2	154	ASN
16	N3	107	ASN
16	N3	146	ASN
16	N3	154	ASN
17	O0	23	HIS
17	O0	125	HIS
17	O0	205	ASN
17	O1	23	HIS
17	O1	125	HIS
17	O1	312	ASN
17	O2	23	HIS
17	O2	94	ASN
17	O2	205	ASN
17	O3	23	HIS
17	O3	125	HIS
17	O3	157	HIS
17	O3	203	ASN
17	O3	205	ASN
18	P0	73	ASN
18	P0	118	GLN
18	P0	388	GLN
18	P0	480	ASN
18	P1	118	GLN
18	P1	388	GLN
18	P1	621	GLN
18	P1	642	ASN

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Mol	Chain	Res	Type
18	P2	73	ASN
18	P2	118	GLN
18	P2	480	ASN
18	P2	621	GLN
18	P2	642	ASN
18	P3	22	GLN
18	P3	73	ASN
18	P3	118	GLN
18	P3	358	HIS
18	P3	388	GLN
18	P3	391	ASN
18	P3	480	ASN
18	P3	642	ASN
19	Q0	121	HIS
19	Q0	169	ASN
19	Q0	229	GLN
19	Q1	121	HIS
19	Q1	229	GLN
19	Q2	106	ASN
19	Q2	121	HIS
19	Q2	229	GLN
19	Q2	230	GLN
19	Q3	121	HIS
19	Q3	169	ASN
19	Q3	229	GLN
20	R0	125	ASN
20	R0	279	GLN
20	R0	411	HIS
20	R0	555	ASN
20	R0	702	ASN
20	R0	738	GLN
20	R0	760	GLN
20	R0	813	ASN
20	R0	1014	ASN
20	R0	1093	ASN
20	R0	1233	GLN
20	R0	1410	GLN
20	R1	279	GLN
20	R1	372	GLN
20	R1	411	HIS
20	R1	653	ASN
20	R1	702	ASN

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Mol	Chain	Res	Type
20	R1	738	GLN
20	R1	760	GLN
20	R1	813	ASN
20	R1	924	GLN
20	R1	1014	ASN
20	R1	1144	GLN
20	R1	1199	HIS
20	R1	1367	GLN
20	R1	1394	GLN
20	R1	1410	GLN
20	R2	125	ASN
20	R2	279	GLN
20	R2	411	HIS
20	R2	426	HIS
20	R2	555	ASN
20	R2	702	ASN
20	R2	738	GLN
20	R2	813	ASN
20	R2	849	GLN
20	R2	924	GLN
20	R2	981	GLN
20	R2	1014	ASN
20	R2	1060	ASN
20	R2	1304	ASN
20	R2	1410	GLN
20	R3	125	ASN
20	R3	279	GLN
20	R3	411	HIS
20	R3	549	HIS
20	R3	555	ASN
20	R3	702	ASN
20	R3	738	GLN
20	R3	813	ASN
20	R3	924	GLN
20	R3	1014	ASN
20	R3	1046	GLN
20	R3	1059	HIS
20	R3	1174	GLN
20	R3	1304	ASN
20	R3	1327	ASN
20	R3	1404	HIS
20	R3	1410	GLN

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Mol	Chain	Res	Type
21	S0	244	GLN
21	S0	245	ASN
21	S1	244	GLN
21	S1	245	ASN
21	S2	244	GLN
21	S3	244	GLN
22	T0	281	ASN
22	T0	392	GLN
22	T0	423	HIS
22	T0	665	GLN
22	T0	820	HIS
22	T0	864	GLN
22	T0	960	GLN
22	T1	164	GLN
22	T1	281	ASN
22	T1	310	ASN
22	T1	363	HIS
22	T1	392	GLN
22	T1	519	ASN
22	T1	665	GLN
22	T1	789	ASN
22	T1	813	GLN
22	T1	820	HIS
22	T1	899	HIS
22	T1	960	GLN
24	V0	863	ASN
24	V0	864	ASN
24	V0	928	HIS
25	W0	154	ASN
25	W0	451	HIS
25	W0	588	GLN
25	W0	601	GLN
25	W0	689	GLN
25	W0	731	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

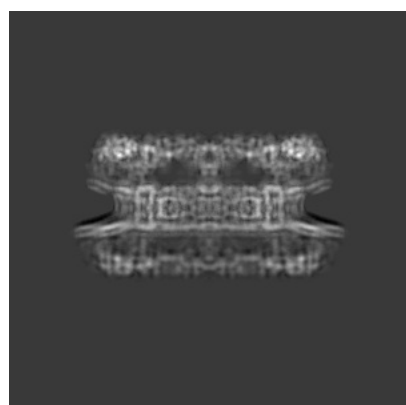
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14322. These allow visual inspection of the internal detail of the map and identification of artifacts.

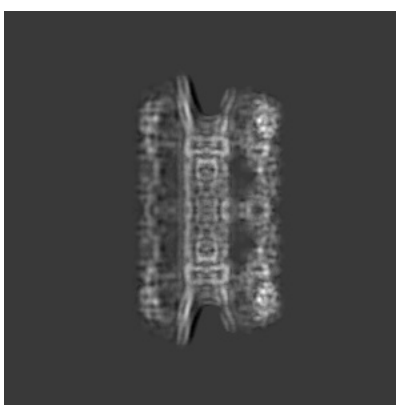
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

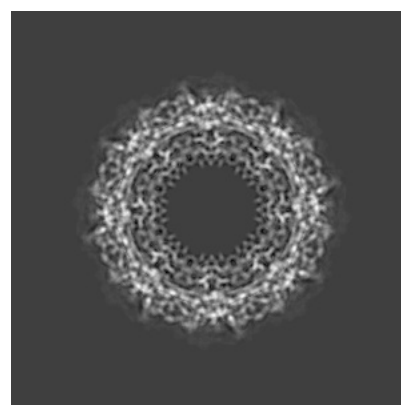
6.1.1 Primary map



X



Y

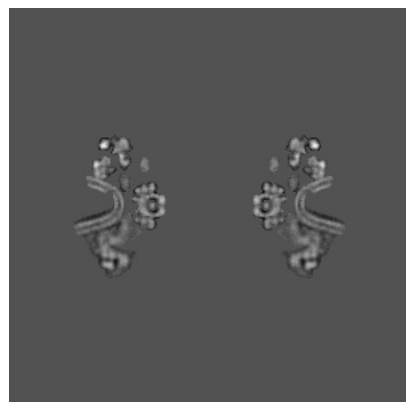


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 288



Y Index: 288



Z Index: 288

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

6.3 Largest variance slices [i](#)

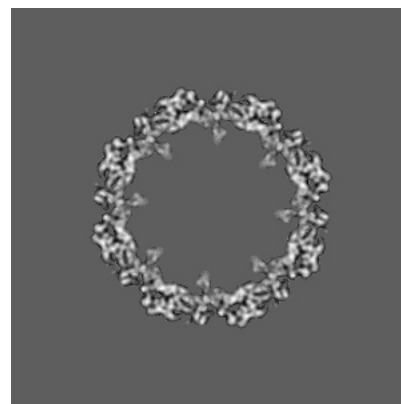
6.3.1 Primary map



X Index: 404



Y Index: 172

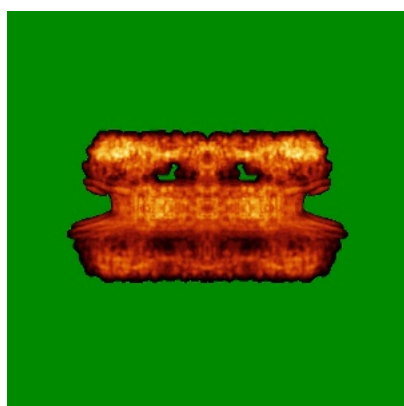


Z Index: 370

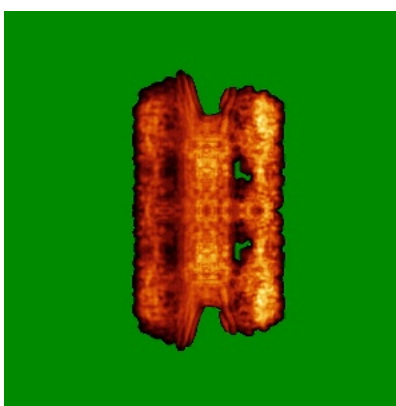
The images above show the largest variance slices of the map in three orthogonal directions.

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

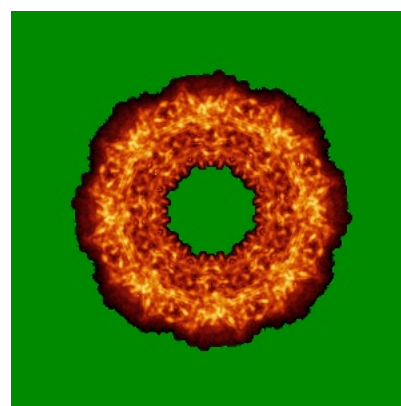
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

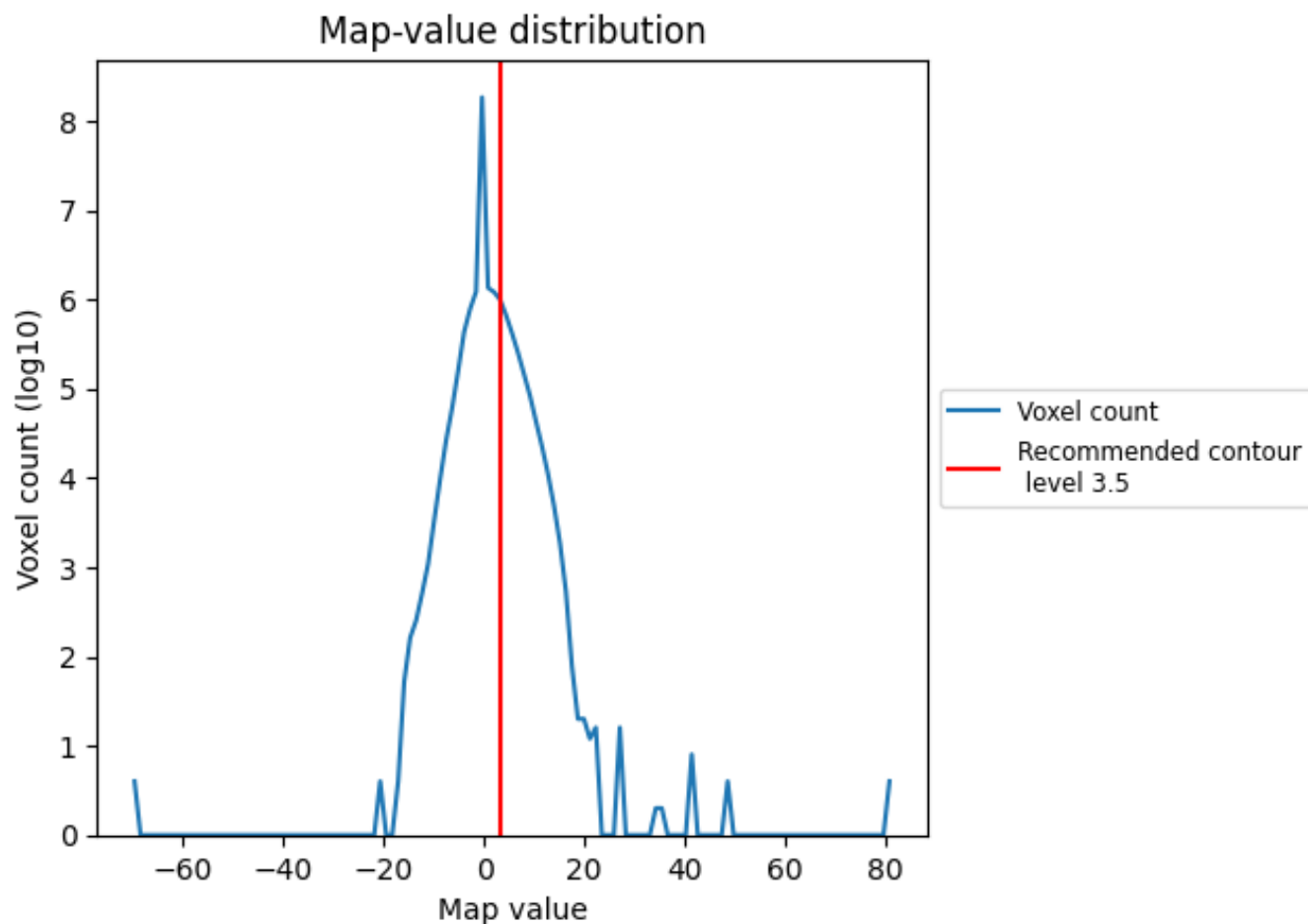
6.6 Mask visualisation

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

7 Map analysis ⓘ

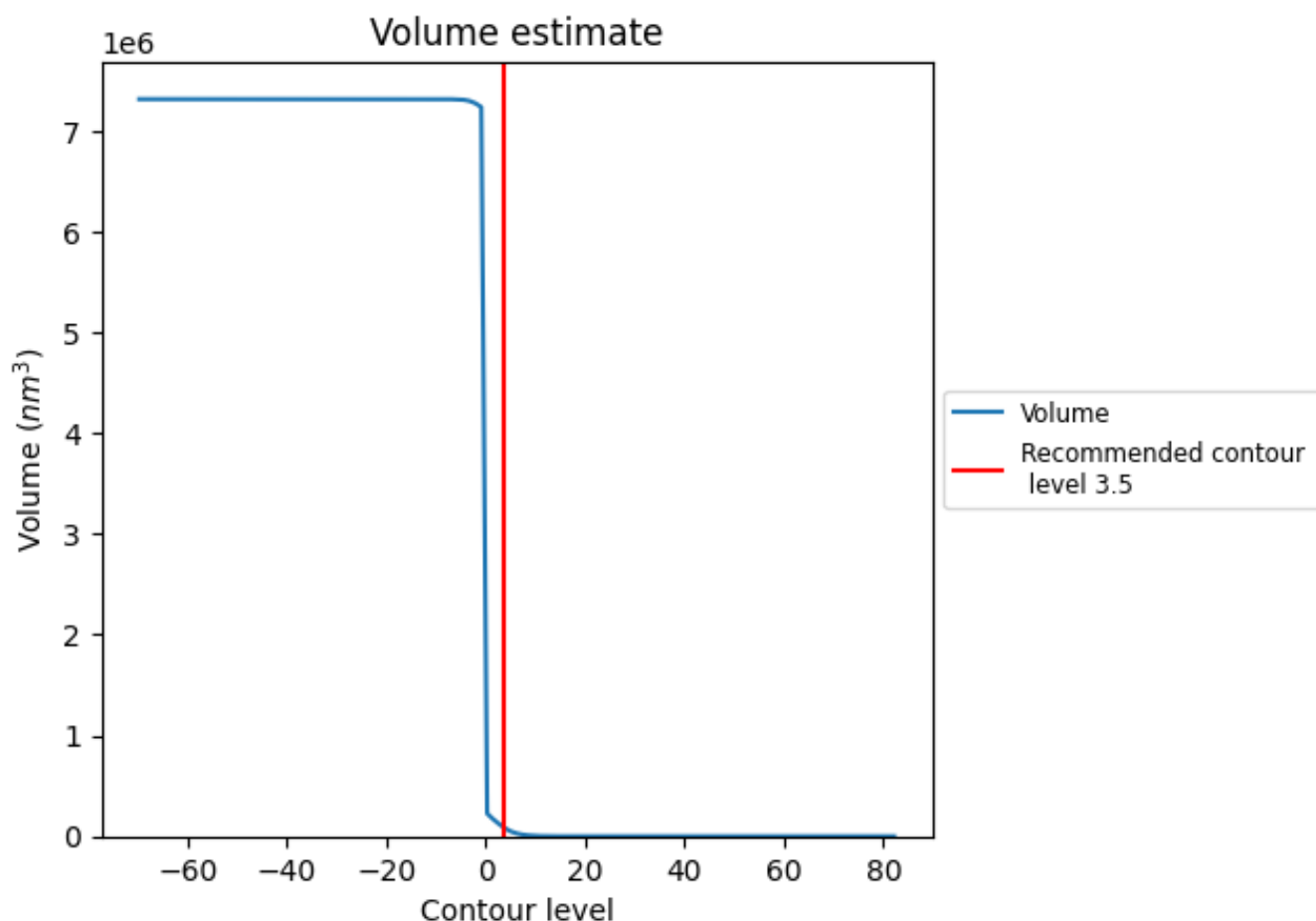
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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

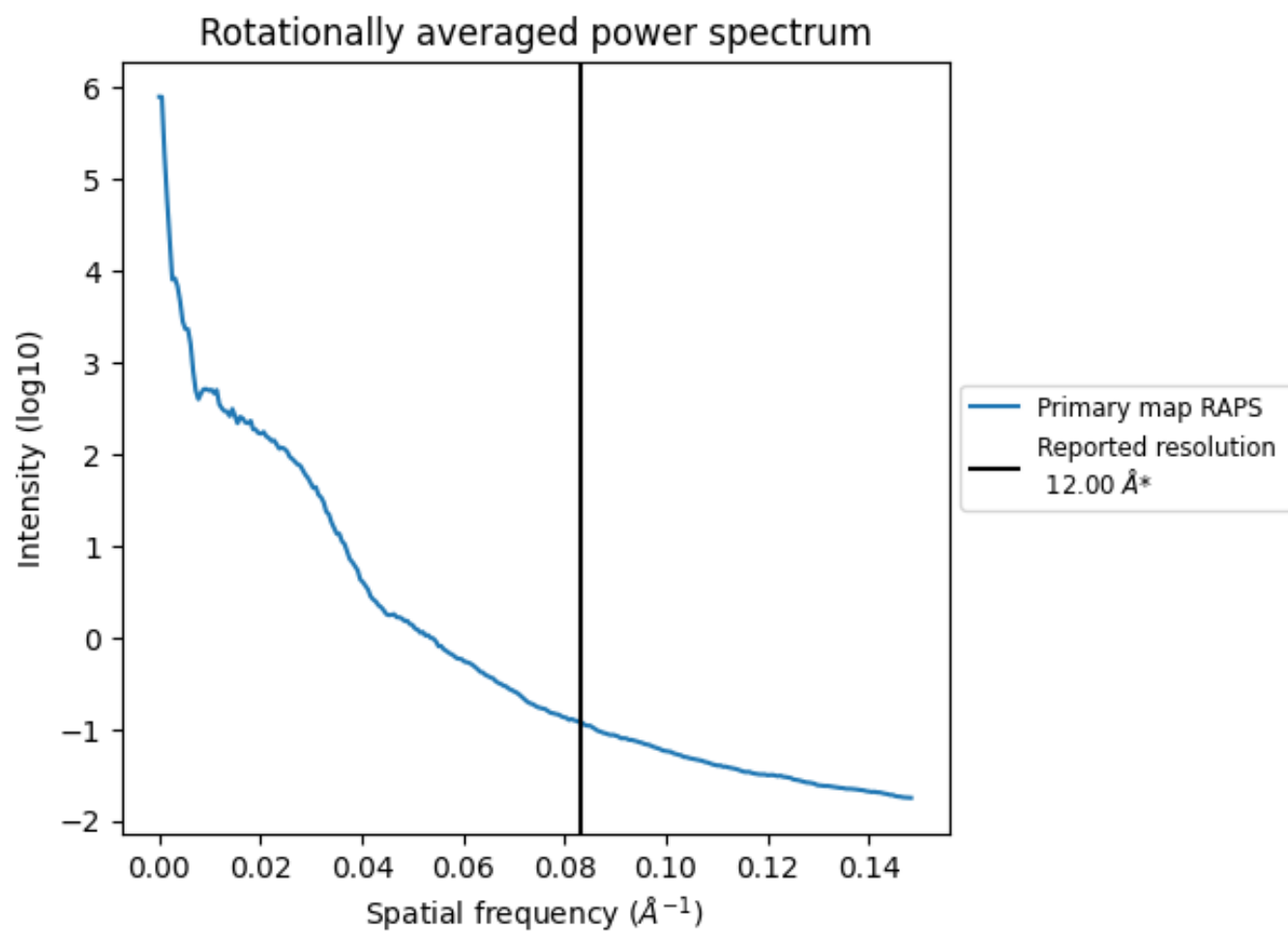
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 93549 nm³; this corresponds to an approximate mass of 84505 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 0.083 Å⁻¹

8 Fourier-Shell correlation

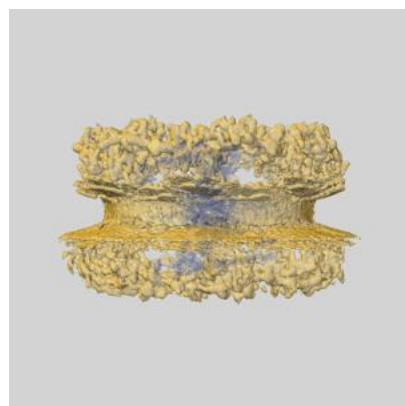
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit ⓘ

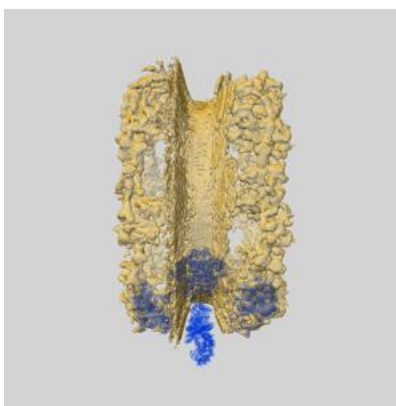
This section contains information regarding the fit between EMDB map EMD-14322 and PDB model 7R5K. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlays

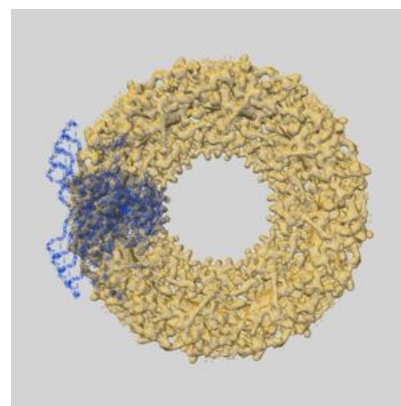
9.1.1 Map-model overlay ⓘ



X



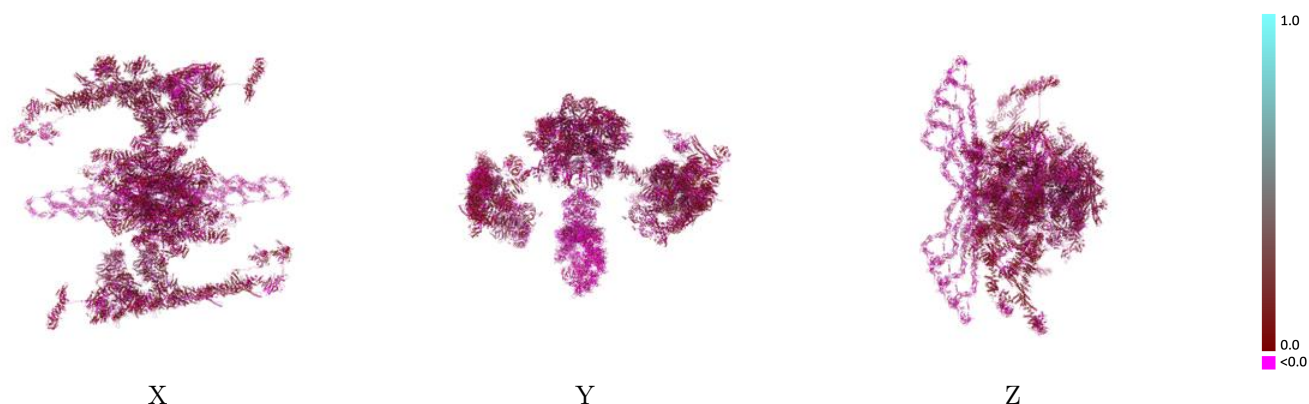
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.5 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](#)

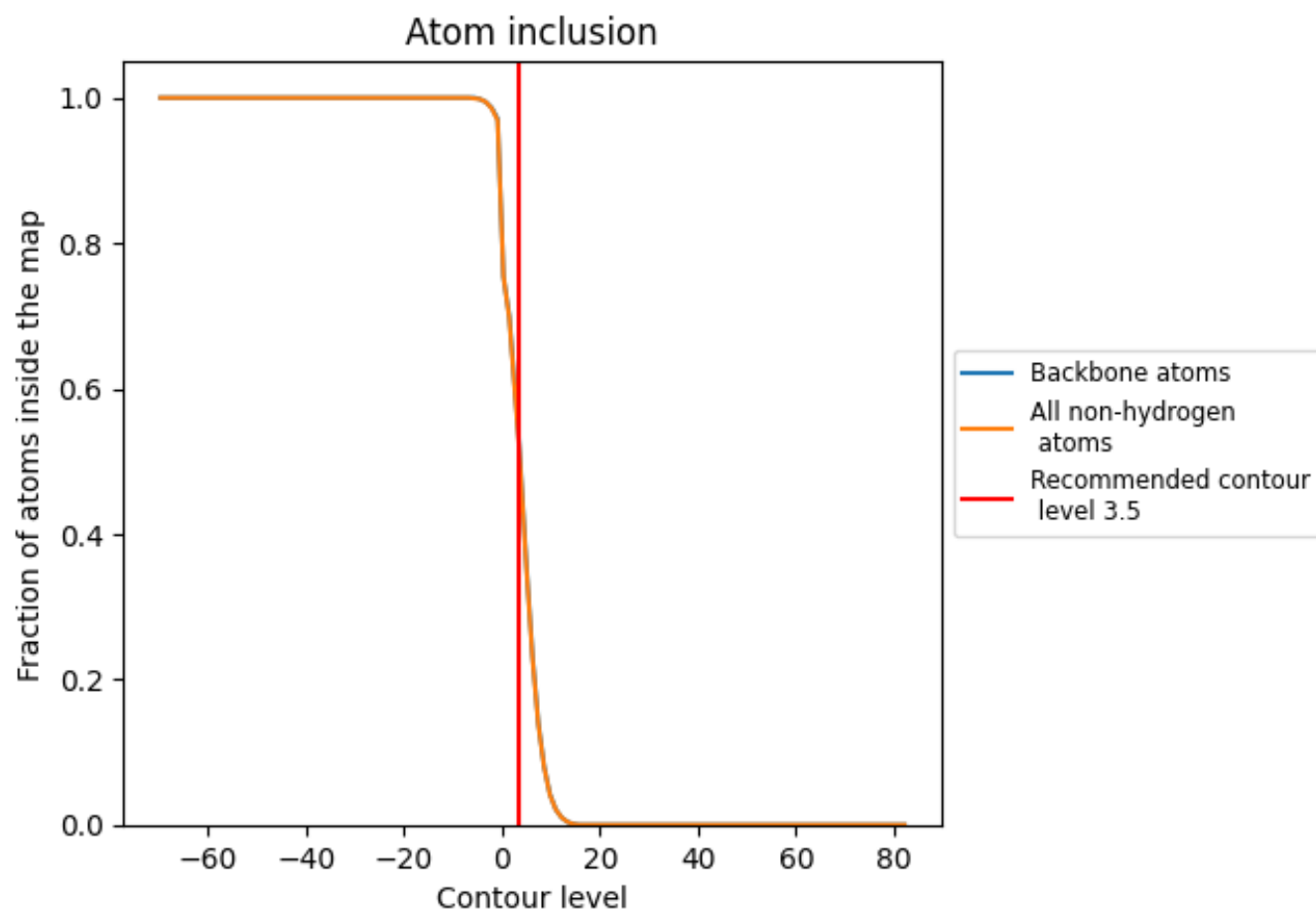


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 52% of all backbone atoms, 52% 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 (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5200	 0.0340
00	 0.7710	 0.0570
01	 0.8680	 0.0670
02	 0.7430	 0.0510
03	 0.8230	 0.0600
04	 0.7590	 0.0550
10	 0.0120	 -0.0060
11	 0.0120	 -0.0040
12	 0.0110	 0.0040
13	 0.0050	 -0.0000
14	 0.0010	 -0.0020
15	 0.0020	 0.0020
16	 0.0080	 0.0020
17	 0.0090	 0.0010
40	 0.6160	 0.0330
41	 0.7430	 0.0250
A0	 0.6740	 0.0430
A1	 0.7070	 0.0470
A2	 0.6610	 0.0350
A3	 0.4500	 0.0420
A4	 0.4880	 0.0200
A5	 0.7030	 0.0440
A6	 0.5810	 0.0430
B0	 0.7170	 0.0430
B1	 0.5480	 0.0460
C0	 0.6490	 0.0390
C1	 0.6230	 0.0380
C2	 0.7760	 0.0500
C3	 0.7830	 0.0510
C4	 0.5730	 0.0360
D0	 0.5970	 0.0340
D1	 0.3000	 0.0200
D2	 0.5780	 0.0340
D3	 0.2990	 0.0260
D4	 0.6280	 0.0360



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Chain	Atom inclusion	Q-score
D5	 0.3960	 0.0340
E0	 0.3660	 0.0300
E1	 0.4950	 0.0300
F0	 0.4030	 0.0140
F1	 0.5440	 0.0380
F2	 0.4320	 0.0080
F3	 0.4360	 0.0200
H0	 0.6290	 0.0510
H1	 0.6440	 0.0450
H2	 0.6890	 0.0530
H3	 0.6760	 0.0500
I0	 0.6100	 0.0360
I1	 0.8110	 0.0740
I2	 0.5930	 0.0350
I3	 0.8400	 0.0700
J0	 0.7640	 0.0770
J1	 0.6620	 0.0480
J2	 0.7830	 0.0580
J3	 0.6210	 0.0270
J4	 0.3930	 0.0100
K0	 0.6410	 0.0440
K1	 0.6500	 0.0460
K2	 0.4360	 0.0320
K3	 0.4760	 0.0500
L0	 0.8650	 0.0640
L1	 0.7600	 0.0530
L2	 0.6900	 0.0530
L3	 0.7000	 0.0500
M0	 0.8390	 0.0520
M1	 0.8520	 0.0520
M2	 0.7400	 0.0460
M3	 0.7740	 0.0560
N0	 0.8210	 0.0420
N1	 0.9280	 0.0520
N2	 0.6600	 0.0300
N3	 0.8470	 0.0500
O0	 0.9370	 0.0600
O1	 0.8100	 0.0420
O2	 0.7760	 0.0430
O3	 0.6630	 0.0300
P0	 0.8220	 0.0440
P1	 0.7660	 0.0420

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Chain	Atom inclusion	Q-score
P2	 0.7050	 0.0450
P3	 0.6510	 0.0390
Q0	 0.8020	 0.0550
Q1	 0.8860	 0.0590
Q2	 0.6720	 0.0420
Q3	 0.7960	 0.0480
R0	 0.8160	 0.0500
R1	 0.7570	 0.0390
R2	 0.6000	 0.0360
R3	 0.5240	 0.0350
S0	 0.5650	 0.0350
S1	 0.7370	 0.0430
S2	 0.5650	 0.0290
S3	 0.6200	 0.0350
T0	 0.4250	 0.0380
T1	 0.1950	 0.0270
U0	 0.1440	 -0.0010
U1	 1.0000	 0.0840
U2	 0.0000	 -0.0540
U3	 0.0000	 -0.0440
U4	 0.0070	 -0.0040
U5	 0.0000	 -0.0250
U6	 0.2720	 0.0500
V0	 0.3540	 0.0120
W0	 0.5130	 0.0120