



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2025 – 04:45 AM EDT

PDB ID : 1MVW
EMDB ID : EMD-1001
Title : MOLECULAR MODELS OF AVERAGED RIGOR CROSSBRIDGES FROM TOMOGRAMS OF INSECT FLIGHT MUSCLE
Authors : Chen, L.F.; Winkler, H.; Reedy, M.K.; Reedy, M.C.; Taylor, K.A.
Deposited on : 2002-09-26
Resolution : 70.00 Å(reported)
Based on initial models : 1ATN, 2MYS

This is a wwPDB EM Validation Summary 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:

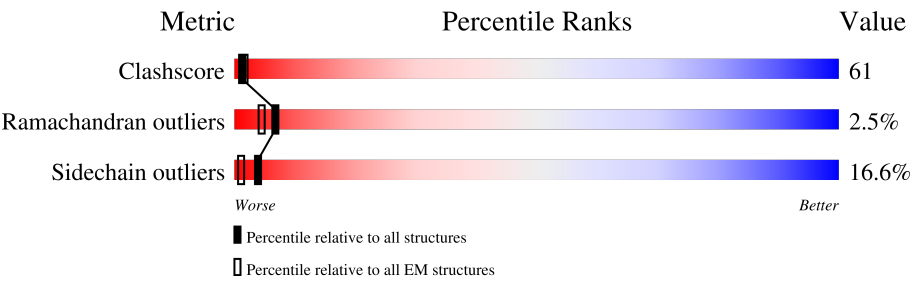
EMDB validation analysis : 0.0.1.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

1 Overall quality at a glance i

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

The reported resolution of this entry is 70.00 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	840	<div><div>100%</div><div><div></div><div>25%</div><div>51%</div><div>20%</div><div>.</div></div></div>
1	D	840	<div><div>100%</div><div><div></div><div>26%</div><div>50%</div><div>20%</div><div>.</div></div></div>
1	G	840	<div><div>100%</div><div><div></div><div>25%</div><div>52%</div><div>20%</div><div>.</div></div></div>
1	J	840	<div><div>100%</div><div><div></div><div>25%</div><div>51%</div><div>20%</div><div>.</div></div></div>
1	M	840	<div><div>100%</div><div><div></div><div>25%</div><div>50%</div><div>20%</div><div>.</div></div></div>
1	P	840	<div><div>100%</div><div><div></div><div>25%</div><div>50%</div><div>20%</div><div>.</div></div></div>
2	B	145	<div><div>100%</div><div><div></div><div>66%</div><div>25%</div><div>6%</div><div>.</div></div></div>
2	E	145	<div><div>100%</div><div><div></div><div>64%</div><div>27%</div><div>6%</div><div>.</div></div></div>

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Mol	Chain	Length	Quality of chain
2	H	145	
2	K	145	
2	N	145	
2	Q	145	
3	C	147	
3	F	147	
3	I	147	
3	L	147	
3	O	147	
3	R	147	
4	1	375	
4	2	375	
4	3	375	
4	4	375	
4	5	375	
4	6	375	
4	7	375	
4	8	375	
4	9	375	
4	V	375	
4	W	375	
4	X	375	
4	Y	375	
4	Z	375	

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

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	MLY	A	505	-	-	X	-
1	MLY	A	553	-	-	X	-
1	MLY	A	764	-	-	X	-
1	MLY	A	768	-	-	X	-
1	MLY	A	782	-	-	X	-
1	MLY	A	839	-	-	X	-
1	MLY	D	553	-	-	X	-
1	MLY	D	764	-	-	X	-
1	MLY	D	782	-	-	X	-
1	MLY	G	295	-	-	X	-
1	MLY	G	553	-	-	X	-
1	MLY	G	764	-	-	X	-
1	MLY	G	768	-	-	X	-
1	MLY	G	84	-	-	X	-
1	MLY	J	295	-	-	X	-
1	MLY	J	505	-	-	X	-
1	MLY	J	553	-	-	X	-
1	MLY	J	768	-	-	X	-
1	MLY	J	839	-	-	X	-
1	MLY	J	84	-	-	X	-
1	MLY	M	505	-	-	X	-
1	MLY	M	764	-	-	X	-
1	MLY	M	768	-	-	X	-
1	MLY	M	839	-	-	X	-
1	MLY	P	505	-	-	X	-
1	MLY	P	768	-	-	X	-
1	MLY	P	839	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 94966 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 SKELETAL MUSCLE MYOSIN II.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	840	Total	C	N	O	S	0	0
			6797	4382	1135	1243	37		
1	D	840	Total	C	N	O	S	0	0
			6797	4382	1135	1243	37		
1	G	840	Total	C	N	O	S	0	0
			6797	4382	1135	1243	37		
1	J	840	Total	C	N	O	S	0	0
			6797	4382	1135	1243	37		
1	M	840	Total	C	N	O	S	0	0
			6797	4382	1135	1243	37		
1	P	840	Total	C	N	O	S	0	0
			6797	4382	1135	1243	37		

- Molecule 2 is a protein called SKELETAL MUSCLE MYOSIN II REGULATORY; LIGHT CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	145	Total	C	N	O	S	0	0
			1127	717	177	227	6		
2	E	145	Total	C	N	O	S	0	0
			1127	717	177	227	6		
2	H	145	Total	C	N	O	S	0	0
			1127	717	177	227	6		
2	K	145	Total	C	N	O	S	0	0
			1127	717	177	227	6		
2	N	145	Total	C	N	O	S	0	0
			1127	717	177	227	6		
2	Q	145	Total	C	N	O	S	0	0
			1127	717	177	227	6		

- Molecule 3 is a protein called SKELETAL MUSCLE MYOSIN II ESSENTIAL; LIGHT CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	147	Total	C	N	O	S	0	0
			1123	698	188	230	7		
3	F	147	Total	C	N	O	S	0	0
			1123	698	188	230	7		
3	I	147	Total	C	N	O	S	0	0
			1123	698	188	230	7		
3	L	147	Total	C	N	O	S	0	0
			1123	698	188	230	7		
3	O	147	Total	C	N	O	S	0	0
			1123	698	188	230	7		
3	R	147	Total	C	N	O	S	0	0
			1123	698	188	230	7		

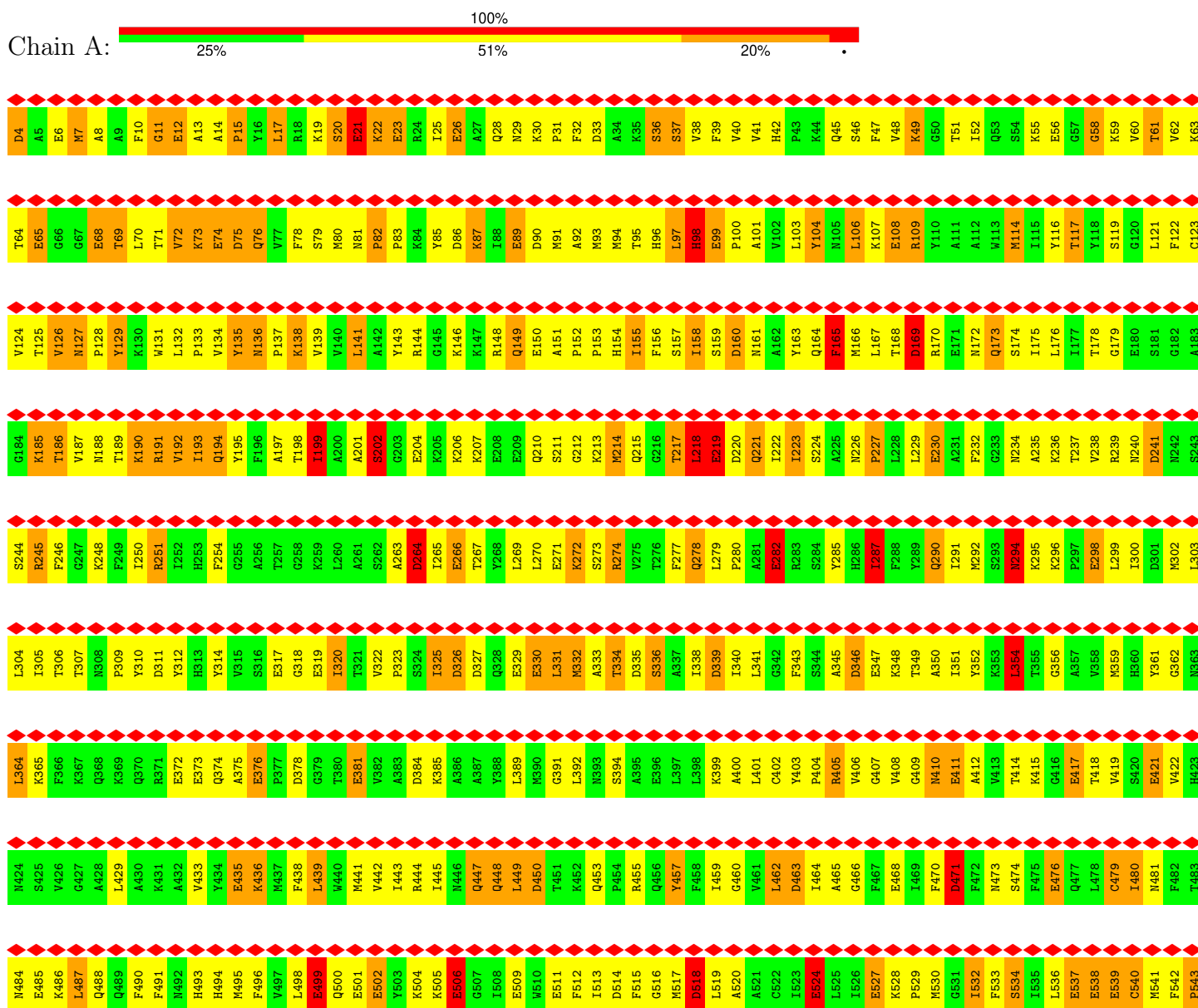
- Molecule 4 is a protein called RABBIT SKELETAL MUSCLE ACTIN.

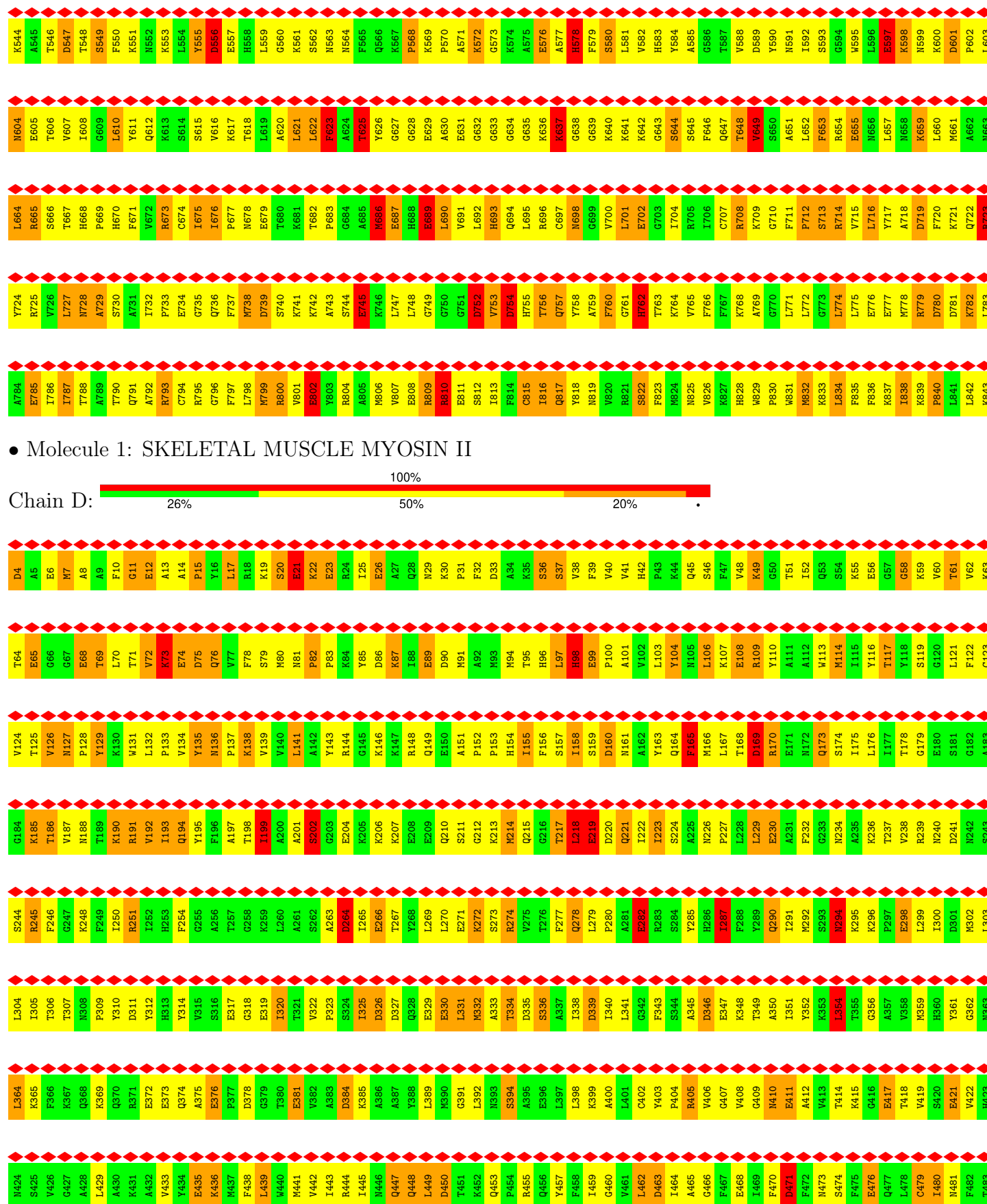
Mol	Chain	Residues	Atoms					AltConf	Trace
4	1	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	2	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	3	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	4	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	5	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	6	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	7	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	8	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	9	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	V	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	W	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	X	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	Y	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		
4	Z	372	Total	C	N	O	S	0	0
			2906	1836	489	561	20		

3 Residue-property plots

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

• Molecule 1: SKELETAL MUSCLE MYOSIN II





N484	E485	K486	L487	Q488	Q489	F490	F491	N492	H493	H494	M495	F496	F497	L498	E499	Q500	E501	E502	Y503	K504	K505	E506	G507	I508	E509	W510	E511	F512	I513	D514	F515	G516	M517	D518	L519	A520	A521	C522	I523	E524	L525	I526	E527	K528	P529	M530	G531	I532	F533	S534	I535	L536	E537	E538	E539	C540	M541	F542	P543	
K544	A545	T546	D547	T548	S549	F550	K551	N552	K553	L554	Y555	D556	E557	H558	L559	G560	K561	S562	N563	N564	F565	Q566	K567	P568	K569	P570	A571	K572	G573	K574	A575	E576	A577	H578	F579	S580	L581	V582	H583	Y584	A585	G586	T587	V588	D589	Y590	N591	I592	F593	G594	V595	L596	E597	K598	N599	K600	D601	P602	L603	
N604	E605	T606	V607	I608	G609	L610	Y611	Q612	K613	S614	S615	V616	K617	T618	L619	A620	L621	L622	F623	A624	T625	Y626	G627	G628	E629	A630	E631	G632	G633	G634	G635	K636	K637	G638	G639	K640	K641	K642	G643	S644	R645	F646	Q647	T648	V649	S650	A651	L652	F653	F654	R654	E655	N656	L657	N658	K659	L660	M661	A662	N663
L664	R665	S666	T667	H668	P669	H670	F671	V672	H673	C674	I675	I676	P677	N678	E679	T680	K681	T682	P683	G684	A685	M686	H687	H688	E689	L690	V691	L692	H693	Q694	L695	R696	C697	M698	G699	V700	L701	K702	G703	I704	R705	I706	C707	R708	K709	G710	F711	L712	S713	R714	V715	L716	T717	A718	D719	F720	T721	Q722	R723	
Y724	R725	V726	L727	M728	A729	S730	A731	I732	P733	E734	G735	Q736	F737	M738	D739	S740	K741	K742	A743	S744	E745	K746	L747	L748	G749	G750	G751	D752	V753	D754	H755	T756	C757	Y758	A759	F760	G761	H762	T763	K764	V765	F766	F767	K768	A769	G770	L771	L772	G773	L774	L775	E776	E777	M778	R779	D780	T781	K782	L783	
A784	E785	I786	T787	T788	A789	T790	Q791	A792	H793	C794	R795	G796	F797	L798	M799	R800	V801	E802	Y803	R804	A805	M806	V807	E808	R809	R810	E811	S812	I813	F814	C815	I816	Q817	Y818	N819	V820	R821	S822	F823	M824	N825	V826	K827	H828	M829	P830	M831	M832	K833	L834	F835	F836	K837	T838	K839	P840	L841	L842	K843	

● Molecule 1: SKELETAL MUSCLE MYOSIN II



L364	L365	F366	K367	Q368	K369	Q370	R371	E372	E373	Q374	A375	E376	P377	D378	G379	T380	E381	Y382	A383	D384	K385	A386	A387	Y388	L389	N390	G391	L392	N393	S394	A395	E396	L397	L398	K399	A400	L401	C402	Y403	P404	A405	V406	G407	V408	G409	N410	E411	A412	V413	T414	K415	G416	E417	T418	V419	S420	E421	V422	H423
L304	I305	T306	T307	N308	P309	Y310	D311	Y312	H313	Y314	V315	S316	E317	G318	E319	I320	T321	V322	S323	S324	I325	D326	D327	Q328	E329	E330	L331	M332	A333	T334	D335	S336	A337	I338	D339	I340	L341	G342	F343	S344	A345	D346	E347	K348	T349	A350	I351	Y352	K353	L354	T355	G356	A357	V358	N359	H360	Y361	G362	N363
S244	R245	F246	G247	K248	F249	L250	R251	L252	H253	F254	G255	A256	T257	G258	K259	L260	A261	S262	A263	D264	I265	E266	T267	Y268	L269	L270	E271	K272	S273	R274	V275	T276	F277	Q278	L279	L279	A281	E282	R283	S284	Y285	H286	I287	F288	Y289	Q290	I291	M292	S293	K294	K295	K296	E298	L299	I300	D301	M302	L303	
G184	K185	T186	V187	M188	T189	K190	R191	I192	I193	Q194	Y195	F196	A197	T198	I199	A200	A201	S202	G203	E204	K205	K206	K207	E208	E209	Q210	S211	G212	K213	M214	Q215	G216	L217	L218	E219	D220	Q221	I222	I223	S224	A225	N226	P227	F228	Y229	Q230	A231	M232	G233	N234	A235	K236	T237	V238	R239	D240	N241	M242	S243
V124	T125	V126	N127	P128	Y129	K130	V131	L132	P133	V134	Y135	N136	P137	K138	V139	Y140	L141	A142	Y143	R144	G145	K146	K147	R148	Q149	E150	A151	P152	P153	H154	I155	F156	S157	I158	S159	D160	N161	A162	Q163	Q164	F165	M166	L167	T168	D169	R170	E171	N172	Q173	S174	L175	L176	I177	T178	G179	E180	L181	G182	A183
T64	E65	G66	G67	E68	T69	L70	T71	V72	K73	E74	D75	Y76	V77	F78	S79	M80	N81	P82	P83	R24	Y85	D86	K87	I88	E89	D90	N91	A92	M93	M94	T95	H96	L97	H98	E99	P100	A101	Y102	L103	Y104	N105	L106	K107	E108	R109	Y110	A111	A112	M113	M114	I115	Y116	T117	Y118	G119	G120	L121	F122	C123
D4	A5	E6	M7	A8	A9	F10	G11	E12	A13	A14	P15	Y16	L17	R18	K19	S20	E21	K22	E23	R24	I25	E26	A27	Q28	N29	K30	P31	F32	D33	A34	K35	S36	S37	V38	F39	V40	V41	H42	K43	Q44	Q45	S46	F47	V48	K49	G50	T51	I52	Q53	S54	K55	E56	G57	G58	K59	V60	T61	V62	K63

N424	N484	K544	N604	L664	Y724	A784	N424	N484	K544	N604	L664	Y724	A784
S425	E485	A545	E505	R665	R725	E785	S425	E485	A545	E505	R665	R725	E785
V426	K486	T546	T606	S666	V726	I786	V426	K486	T546	T606	S666	V726	I786
G427	L487	D547	V607	T667	L727	T787	G427	L487	D547	V607	T667	L727	T787
A428	Q488	T548	I608	H668	A728	T788	A428	Q488	T548	I608	H668	A728	T788
L429	Q489	S549	G609	P669	A729	A789	L429	Q489	S549	G609	P669	A729	A789
A430	F490	F550	L610	H670	S730	T790	A430	F490	F550	L610	H670	S730	T790
K431	F491	K551	Y611	F671	A731	Q791	K431	F491	K551	Y611	F671	A731	Q791
A432	N492	N552	Q612	F672	I732	A792	A432	N492	N552	Q612	F672	I732	A792
V433	H493	K553	K613	R673	I733	R793	V433	H493	K553	K613	R673	I733	R793
Y434	H494	L554	S614	C674	E734	C794	Y434	H494	L554	S614	C674	E734	C794
E435	M495	Y555	S615	I675	G735	R795	E435	M495	Y555	S615	I675	G735	R795
K436	F496	D556	V616	I676	Q736	G796	K436	F496	D556	V616	I676	Q736	G796
M437	V497	V557	K617	P677	F737	F797	M437	V497	V557	K617	P677	F737	F797
F438	L498	H558	T618	N678	M738	L798	F438	L498	H558	T618	N678	M738	L798
L439	E499	L559	L619	E679	D739	M799	L439	E499	L559	L619	E679	D739	M799
V440	Q500	G560	A620	T680	S740	R800	V440	Q500	G560	A620	T680	S740	R800
M441	E501	K561	L621	K681	K741	V601	M441	E501	K561	L621	K681	K741	V601
V442	E502	S562	L622	T682	K742	E502	V442	E502	S562	L622	T682	K742	E502
I443	Y503	N563	F623	P683	A743	R503	I443	Y503	N563	F623	P683	A743	R503
R444	K504	N564	A624	G684	S744	R504	R444	K504	N564	A624	G684	S744	R504
I445	K505	F565	T625	A685	E745	A605	I445	K505	F565	T625	A685	E745	A605
N446	E506	Q566	Y626	M686	K746	M606	N446	E506	Q566	Y626	M686	K746	M606
Q447	G507	K567	G627	H687	L747	V607	Q447	G507	K567	G627	H687	L747	V607
Q448	I508	P568	G628	H688	L748	E508	Q448	I508	P568	G628	H688	L748	E508
L449	E509	K569	E629	E689	G749	R609	L449	E509	K569	E629	E689	G749	R609
D450	W510	P570	A630	L690	G750	R610	D450	W510	P570	A630	L690	G750	R610
T451	E511	A571	E631	V691	G751	E611	T451	E511	A571	E631	V691	G751	E611
K452	F512	K572	G632	L692	D752	S612	K452	F512	K572	G632	L692	D752	S612
Q453	I513	G573	G633	H693	V753	L613	Q453	I513	G573	G633	H693	V753	L613
P454	D514	K574	G634	Q694	D754	F614	P454	D514	K574	G634	Q694	D754	F614
R455	F515	A575	G635	L695	H755	C615	R455	F515	A575	G635	L695	H755	C615
Q456	G516	E576	K636	R696	T756	I616	Q456	G516	E576	K636	R696	T756	I616
Y457	M517	A577	K637	C697	Q757	Q617	Y457	M517	A577	K637	C697	Q757	Q617
F458	D518	H578	G638	N698	Y758	Y618	F458	D518	H578	G638	N698	Y758	Y618
I459	L519	F579	K639	G699	A759	N619	I459	L519	F579	K639	G699	A759	N619
G460	A520	S580	K640	V700	F760	W620	G460	A520	S580	K640	V700	F760	W620
V461	E521	L581	K641	L701	G761	R621	V461	E521	L581	K641	L701	G761	R621
L462	C522	V582	K642	E702	H762	S622	L462	C522	V582	K642	E702	H762	S622
D463	I523	H583	G643	G703	T763	F623	D463	I523	H583	G643	G703	T763	F623
I464	E524	Y584	S644	I704	K764	M624	I464	E524	Y584	S644	I704	K764	M624
A465	L525	A585	S645	R705	V765	N625	A465	L525	A585	S645	R705	V765	N625
G466	I526	G586	F646	I706	F766	V626	G466	I526	G586	F646	I706	F766	V626
F467	E527	T587	Q647	C707	F767	K627	F467	E527	T587	Q647	C707	F767	K627
E468	K528	V588	T648	R708	K768	H628	E468	K528	V588	T648	R708	K768	H628
I469	P529	D589	V649	K709	A769	W629	I469	P529	D589	V649	K709	A769	W629
F470	M530	Y590	S550	G710	G770	P630	F470	M530	Y590	S550	G710	G770	P630
D471	G531	N591	A651	F711	L771	W631	D471	G531	N591	A651	F711	L771	W631
F472	I532	L592	L652	P712	L772	M632	F472	I532	L592	L652	P712	L772	M632
N473	F533	S593	F653	S713	G773	K633	N473	F533	S593	F653	S713	G773	K633
S474	S534	G594	R654	R714	L774	L634	S474	S534	G594	R654	R714	L774	L634
F475	I535	W595	E655	V715	L775	P635	F475	I535	W595	E655	V715	L775	P635
E476	L536	L596	M656	L716	E776	F636	E476	L536	L596	M656	L716	E776	F636
Q477	E537	R597	L657	A718	M778	T638	Q477	E537	R597	L657	A718	M778	T638
L478	E538	K598	M558	D719	R779	K639	L478	E538	K598	M558	D719	R779	K639
C479	E539	N599	K659	F720	D780	P640	C479	E539	N599	K659	F720	D780	P640
I480	C540	K600	L660	W720	D781	L641	I480	C540	K600	L660	W720	D781	L641
N481	M541	D601	M661	K721	Q781	L642	N481	M541	D601	M661	K721	Q781	L642
F482	F542	P602	A662	Q722	K782	L643	F482	F542	P602	A662	Q722	K782	L643
T483	P543	L603	N663	R723	L783	K843	T483	P543	L603	N663	R723	L783	K843

● Molecule 1: SKELETAL MUSCLE MYOSIN II



D4	T64	V124	G184	S244	L304
A5	E65	T125	K185	R245	I305
E6	G66	V126	T186	F246	T306
M7	G67	M127	V187	G247	T307
A8	E68	P128	N188	K248	N308
A9	T69	Y129	T189	F249	P309
F10	L70	K130	K190	L250	Y310
G11	T71	W131	R191	R251	D311
E12	V72	L132	V192	L252	Y312
A13	K73	P133	I193	H253	H313
A14	E74	V134	Q194	F254	Y314
P15	D75	Y135	Y195	G255	V315
Y16	Q76	M136	F196	A256	S316
L17	V77	P137	A197	T257	E317
R18	F78	K138	T198	G258	G318
K19	S79	V139	I199	K259	E319
S20	M80	Y140	A200	L260	I320
E21	N81	L141	A201	A261	T321
K22	P82	A142	S202	S262	V322
P23	K84	Y143	G203	A263	P323
R24	D86	G145	E204	D264	S324
I25	Y85	R146	K206	L265	I325
E26	K87	K147	K207	E266	D326
A27	T88	L148	E208	T267	D327
Q28	E89	Q149	E209	T268	Q328
N29	D90	E150	Q210	L269	E329
K30	M91	A151	S211	L270	E330
P31	A92	P152	G212	E271	L331
F32	M93	P153	K213	K272	K332
D33	M94	H154	M214	S273	A333
A34	T95	I155	Q215	R274	T334
K35	H96	F156	Q216	V275	D335
S36	L97	S157	G217	T276	S336
S37	H98	I158	T217	F277	A337
V38	E99	S159	L218	Q278	I338
F39	P100	D160	E219	L279	D339
V40	A101	D161	D220	P280	I340
V41	Y102	M161	Q221	A281	L341
H42	L103	A162	I222	E282	G342
P43	Y104	Y163	I223	R283	F343
K44	F164	Q165	S224	S284	S344
Q45	N105	F165	A225	Y285	A345
S46	L106	M166	N226	H286	D346
V47	K107	L167	P227	T287	E347
F48	E108	T168	L228	F288	K348
R49	R109	D169	L229	Y289	T349
Y110	Y110	R170	E230	Q290	A350
T51	A111	E171	A231	T291	I351
I52	A112	M172	F232	M292	Y352
Q53	V113	Q173	G233	S293	K353
S54	M114	S174	N234	D294	L354
K55	I115	T175	A235	K295	T355
E56	Y116	L176	K236	K296	G356
G57	T117	I177	T237	P297	A357
G58	Y118	T178	V238	E298	V358
S59	S119	G179	R239	L299	K359
V60	G120	E180	N240	I300	H360
T61	L121	S181	D241	D301	Y361
V62	F122	G182	N242	K302	G362
K63	C123	A183	S243	L303	N363

L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821	L822	L823	L824	L825	L826	L827	L828	L829	L830	L831	L832	L833	L834	L835	L836	L837	L838	L839	L840	L841	L842	L843	L844
Y724	R725	V726	L727	N728	A729	S730	A731	I732	P733	E734	G735	Q736	F737	N738	D739	K740	K741	K742	A743	S744	E745	K746	L747	L748	G749	G750	G751	D752	V753	Q754	H755	T756	Q757	N758	A759	F760	G761	R762	T763	K764	V765	F766	F767	R768	A769	G770	L771	P712	S713	R714	V715	L716	Y717	A718	D719	F720	K721	Q722	R723	
L664	R665	S666	T667	H668	P669	H670	F671	V672	R673	C674	L675	L676	P677	N678	E679	T680	K681	T682	P683	G684	A685	M686	E687	H688	E689	L690	V691	L692	H693	Q694	L695	R696	G697	N698	G699	V700	L701	E702	G703	I704	R705	I706	C707	R708	K709	G710	F711	P712	S713	R714	V715	L716	Y717	A718	D719	F720	K721	Q722		
N604	E605	T606	V607	I608	G609	L610	Y611	Q612	K613	S614	S615	V616	K617	T618	L619	A620	L621	L622	F623	A624	T625	Y626	G627	G628	E629	A630	E631	G632	G633	G634	G635	K636	K637	G638	G639	K640	K641	K642	G643	S644	S645	F646	Q647	T648	V649	S650	A651	L652	F653	R654	E655	N656	L657	N658	K659	L660	M661	A662	N663	
K544	A545	T546	D547	T548	S549	F550	K551	N552	K553	L554	Y555	D556	E557	H558	L559	G560	K561	S562	N563	N564	F565	Q566	K567	P568	K569	P570	A571	K572	G573	K574	A575	E576	A577	H578	F579	S580	L581	V582	H583	Y584	A585	G586	T587	V588	D589	Y590	N591	I592	S593	G594	N595	L596	E597	K598	N599	K600	D601	P602	L603	
N484	E485	K486	L487	Q488	Q489	F490	F491	M492	H493	H494	M495	F496	V497	L498	E499	Q500	E501	E502	Y503	K504	K505	E506	I507	I508	E509	M510	F511	F512	I513	D514	F515	G516	M517	D518	L519	A520	A521	C522	I523	E524	L525	I526	E527	K528	P529	M530	G531	I532	F533	S534	I535	L536	E537	E538	E539	C540	M541	F542	P543	
N424	A425	V426	G427	A428	L429	A430	K431	A432	V433	Y434	E435	K436	M437	F438	L439	Q440	M441	V442	I443	R444	I445	M446	Q447	Q448	L449	D450	T451	K452	Q453	P454	R455	Q456	G457	F458	I459	G460	V461	L462	D463	I464	A465	G466	F467	E468	I469	F470	D471	F472	K473	S474	F475	E476	Q477	L478	C479	I480	N481	F482	T483	
L364	K365	F366	K367	Q368	K369	Q370	R371	E372	E373	Q374	A375	E376	P377	D378	G379	T380	E381	V382	A383	D384	K385	A386	A387	Y388	L389	M390	E391	L392	N393	S394	A395	E396	G397	L398	I399	A400	L401	C402	Y403	P404	R405	V406	G407	V408	G409	N410	E411	A412	T413	K415	G416	A417	T418	V419	S420	H421	V422	H423		
L304	L305	T306	T307	N308	P309	Y310	D311	Y312	H313	Y314	V315	S316	E317	G318	E319	I320	T321	V322	P323	S324	I325	D326	D327	Q328	E329	E330	L331	M332	A333	T334	D335	S336	A337	I338	D339	I340	L341	G342	F343	S344	A345	D346	E347	K348	T349	A350	I351	Y352	K353	L354	T355	G356	A357	V358	M359	H360	Y361	G362	N363	

● Molecule 1: SKELETAL MUSCLE MYOSIN II



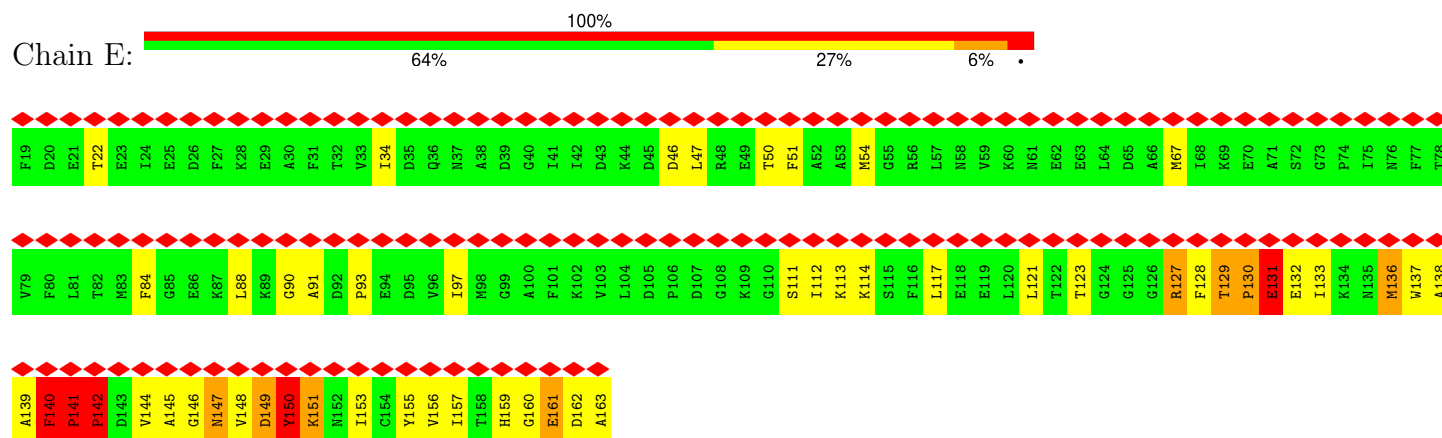
G184	K185	T186	V187	T189	K190	R191	V192	I193	Q194	Y195	F196	A197	I199	A200	A201	S202	G203	E204	K205	K206	K207	E208	E209	Q210	S211	G212	K213	M214	Q215	G216	T217	L218	E219	D220	Q221	I222	I223	S224	A225	N226	P227	L228	L229	E230	A231	F232	G233	N234	A235	K236	T237	V238	R239	N240	D241	N242	S243		
V124	T125	V126	N127	P128	Y129	K130	V131	L132	P133	V134	Y135	N136	P137	K138	V139	V140	L141	A142	Y143	R144	G145	K146	L147	R148	Q149	E150	A151	P152	P153	H154	I155	F156	S157	I158	S159	D160	N161	A162	Y163	Q164	F165	M166	L167	T168	D169	R170	E171	N172	Q173	S174	I175	L176	T177	T178	G179	E180	L181	G182	
T64	E65	G66	G67	E68	T69	L70	T71	V72	K73	E74	D75	Q76	V77	F78	S79	M80	N81	P82	P83	G84	H85	D86	K87	T88	E89	D90	N91	A92	M93	N94	T95	H96	L97	H98	E99	P100	A101	V102	L103	Y104	N105	L106	K107	E108	R109	Y110	A111	A112	Q113	M114	I115	Y116	T117	Y118	S119	G120	L121	F122	C123
D4	A5	E6	M7	A8	A9	F10	G11	E12	A13	A14	P15	Y16	L17	R18	K19	S20	E21	K22	E23	R24	I25	E26	A27	Q28	N29	K30	P31	F32	D33	A34	K35	S36	S37	V38	F39	V40	V41	H42	P43	K44	Q45	S46	F47	V48	K49	G50	T51	I52	Q53	S54	K55	E56	G57	G58	K59	V60	T61	V62	K63



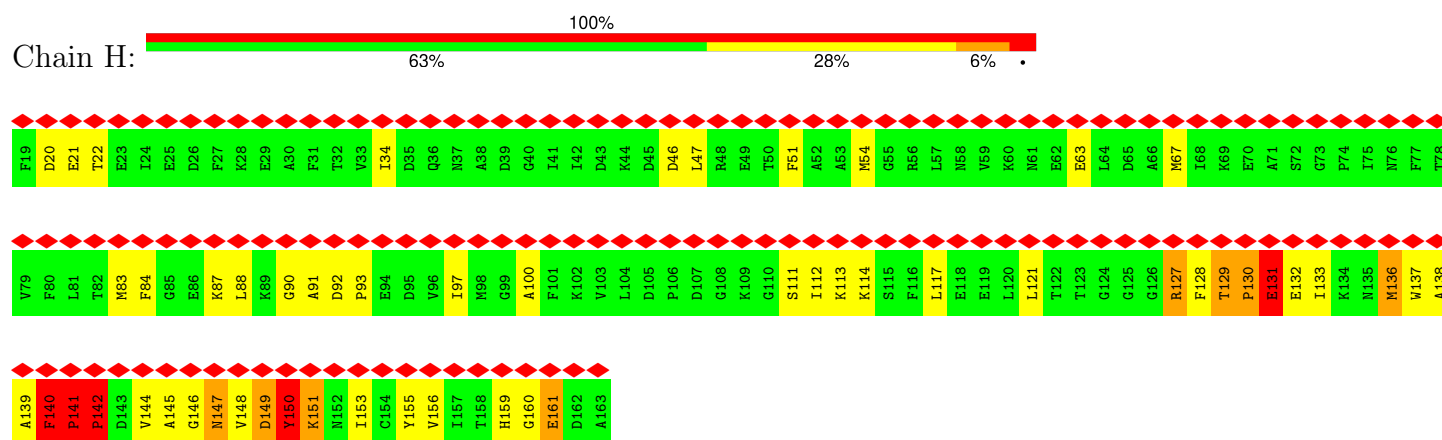
Device Type	Percentage
Smartphones	100%
Tablets	66%
Smart TVs	25%
Smart Speakers	6%



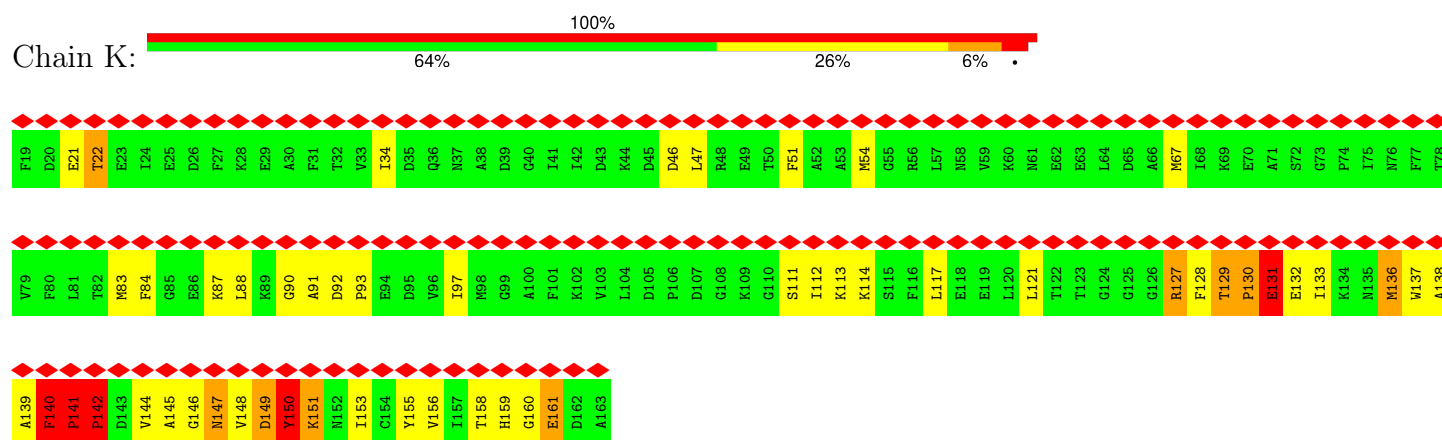
• Molecule 2: SKELETAL MUSCLE MYOSIN II REGULATORY; LIGHT CHAIN



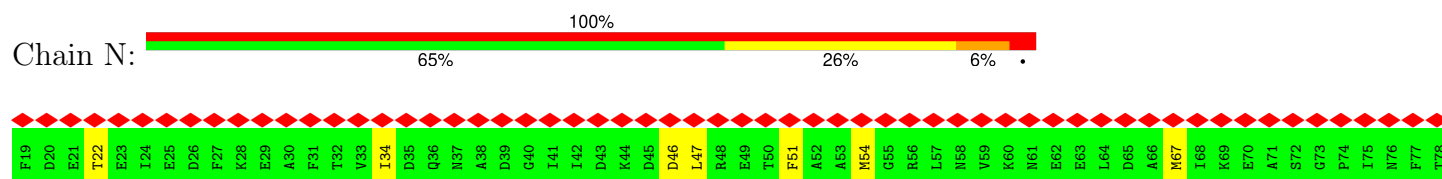
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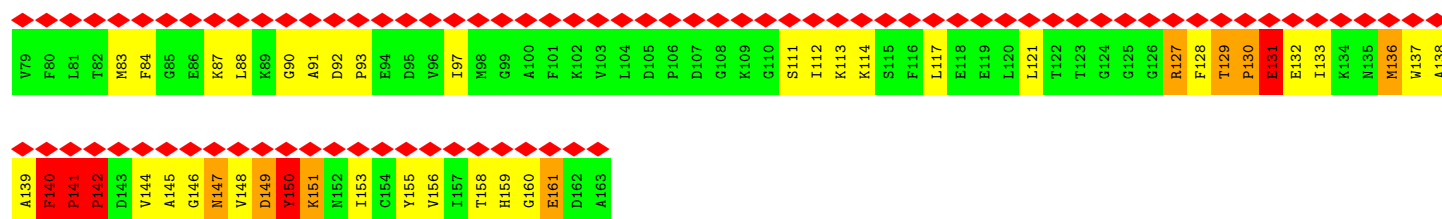


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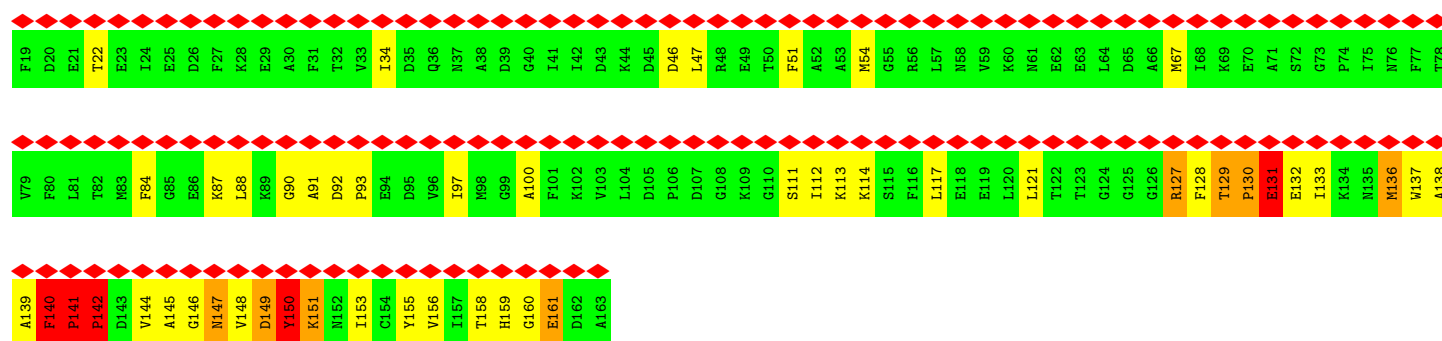


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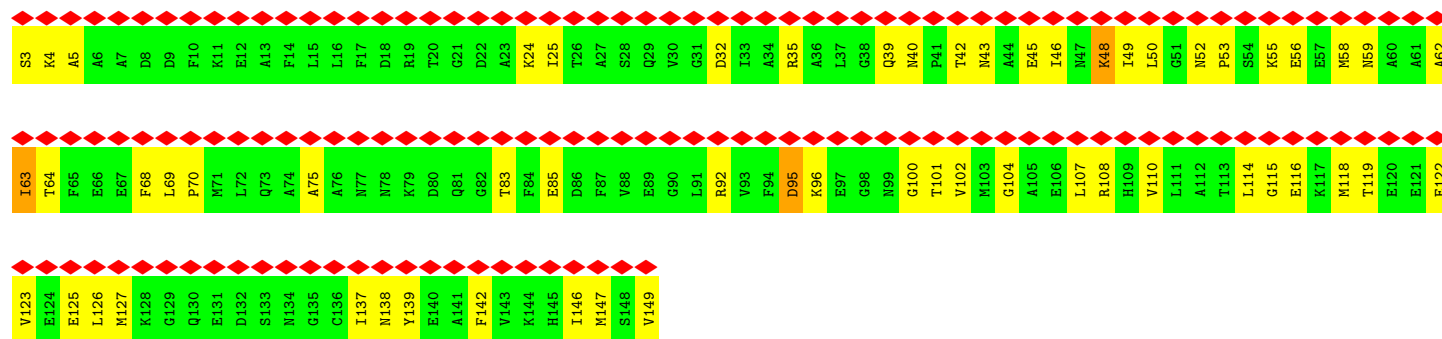




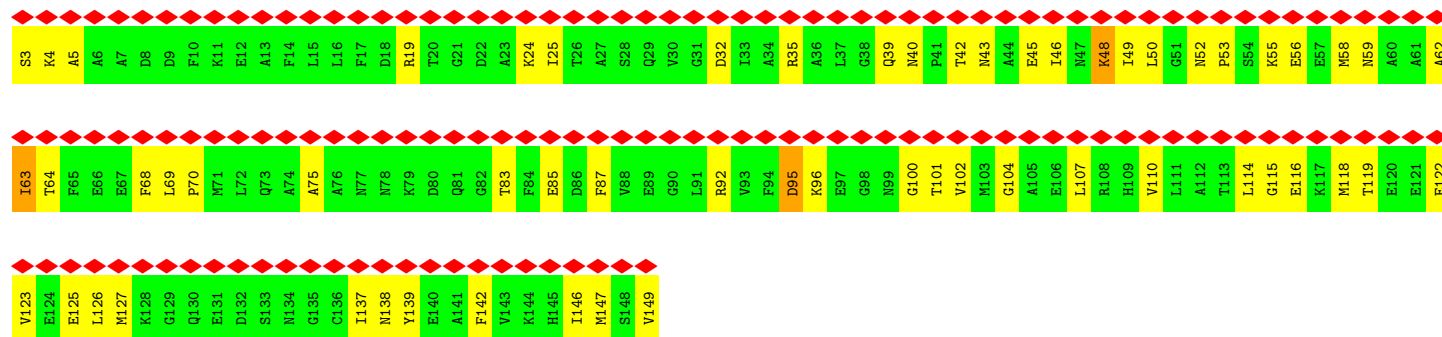
• Molecule 2: SKELETAL MUSCLE MYOSIN II REGULATORY; LIGHT CHAIN



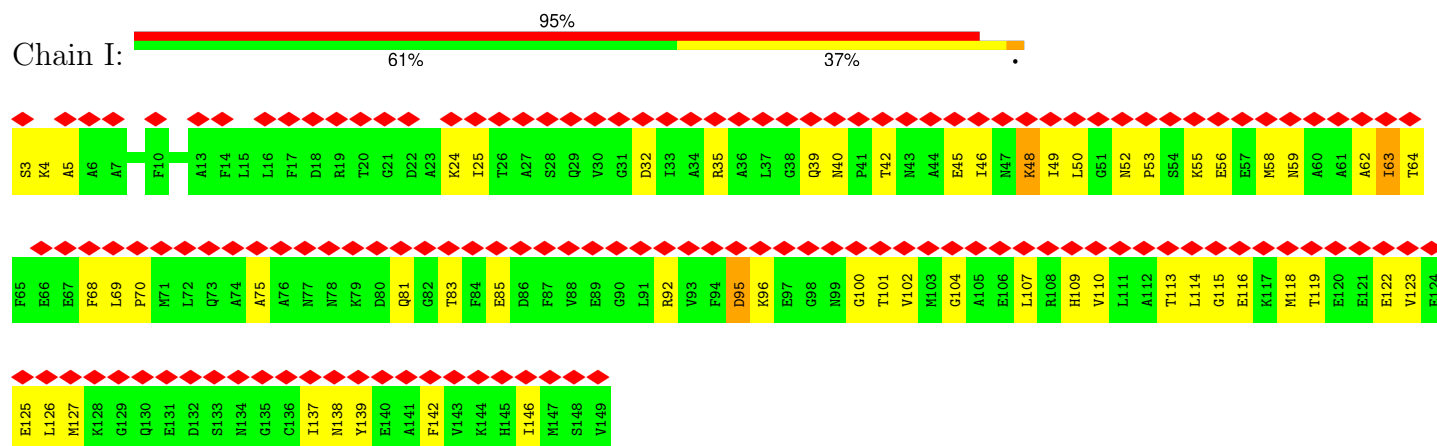
• Molecule 3: SKELETAL MUSCLE MYOSIN II ESSENTIAL; LIGHT CHAIN



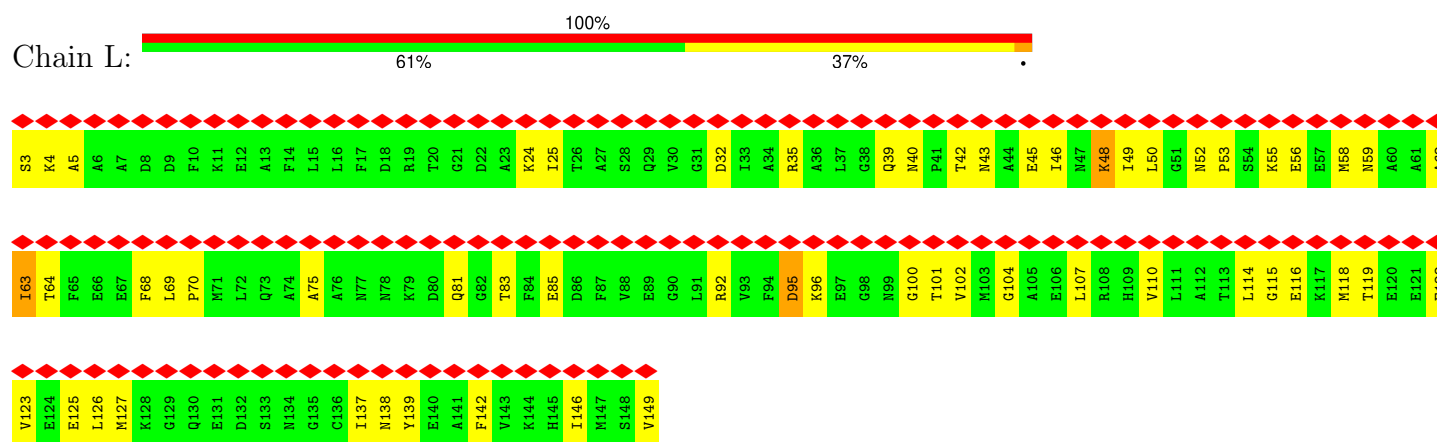
• Molecule 3: SKELETAL MUSCLE MYOSIN II ESSENTIAL; LIGHT CHAIN



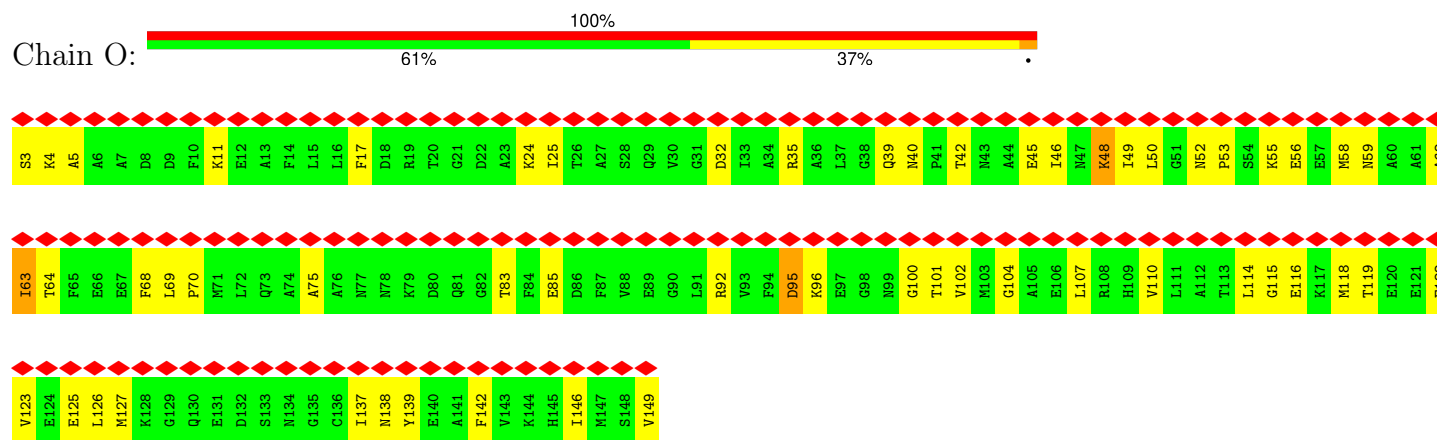
• Molecule 3: SKELETAL MUSCLE MYOSIN II ESSENTIAL; LIGHT CHAIN



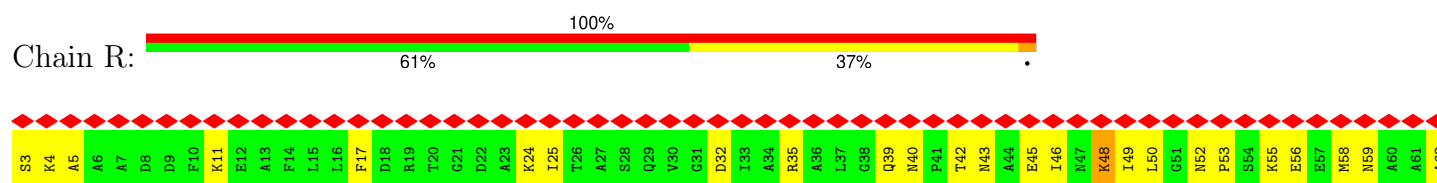
• Molecule 3: SKELETAL MUSCLE MYOSIN II ESSENTIAL; LIGHT CHAIN

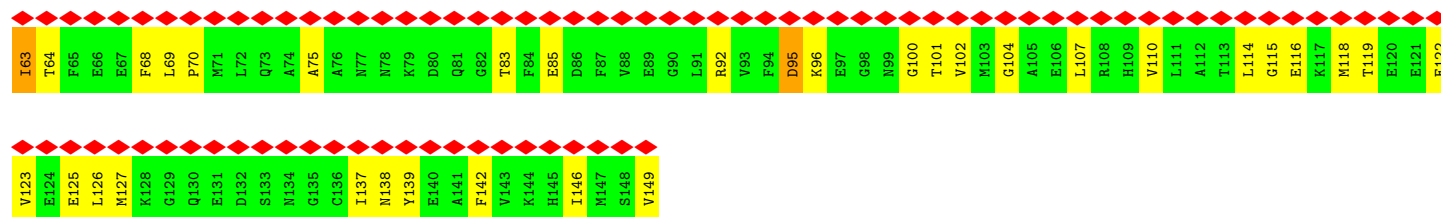


• Molecule 3: SKELETAL MUSCLE MYOSIN II ESSENTIAL; LIGHT CHAIN

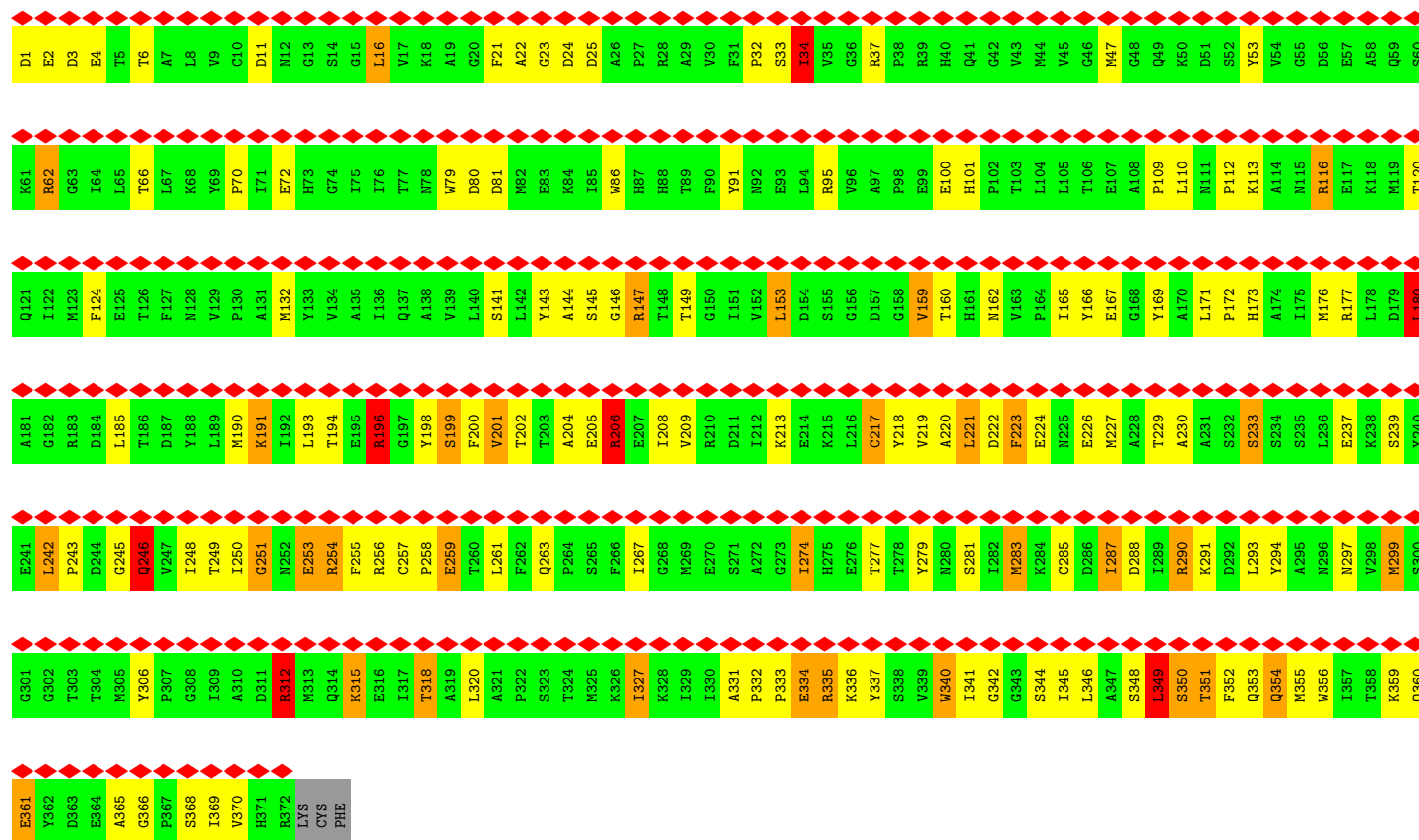


• Molecule 3: SKELETAL MUSCLE MYOSIN II ESSENTIAL; LIGHT CHAIN

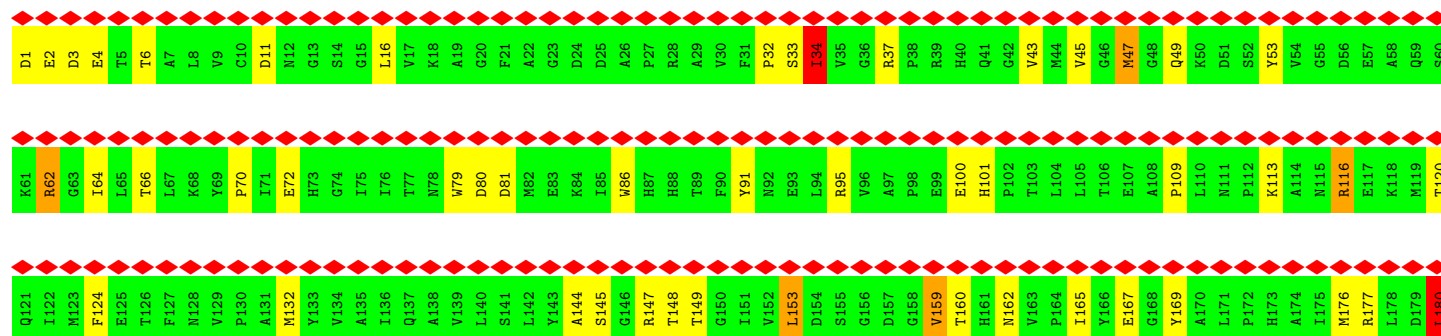


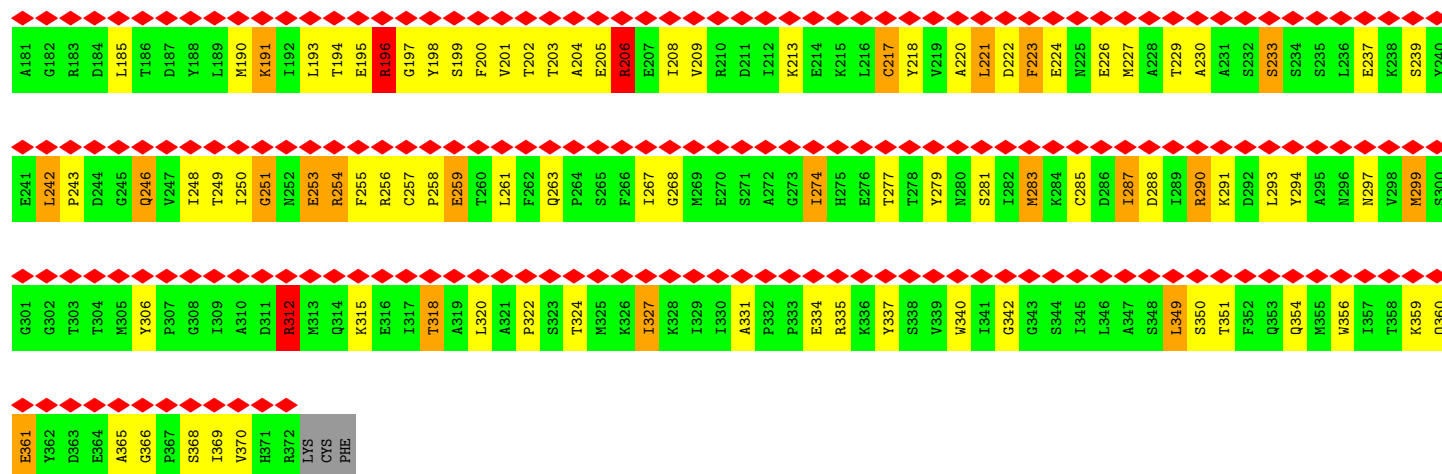


• Molecule 4: RABBIT SKELETAL MUSCLE ACTIN

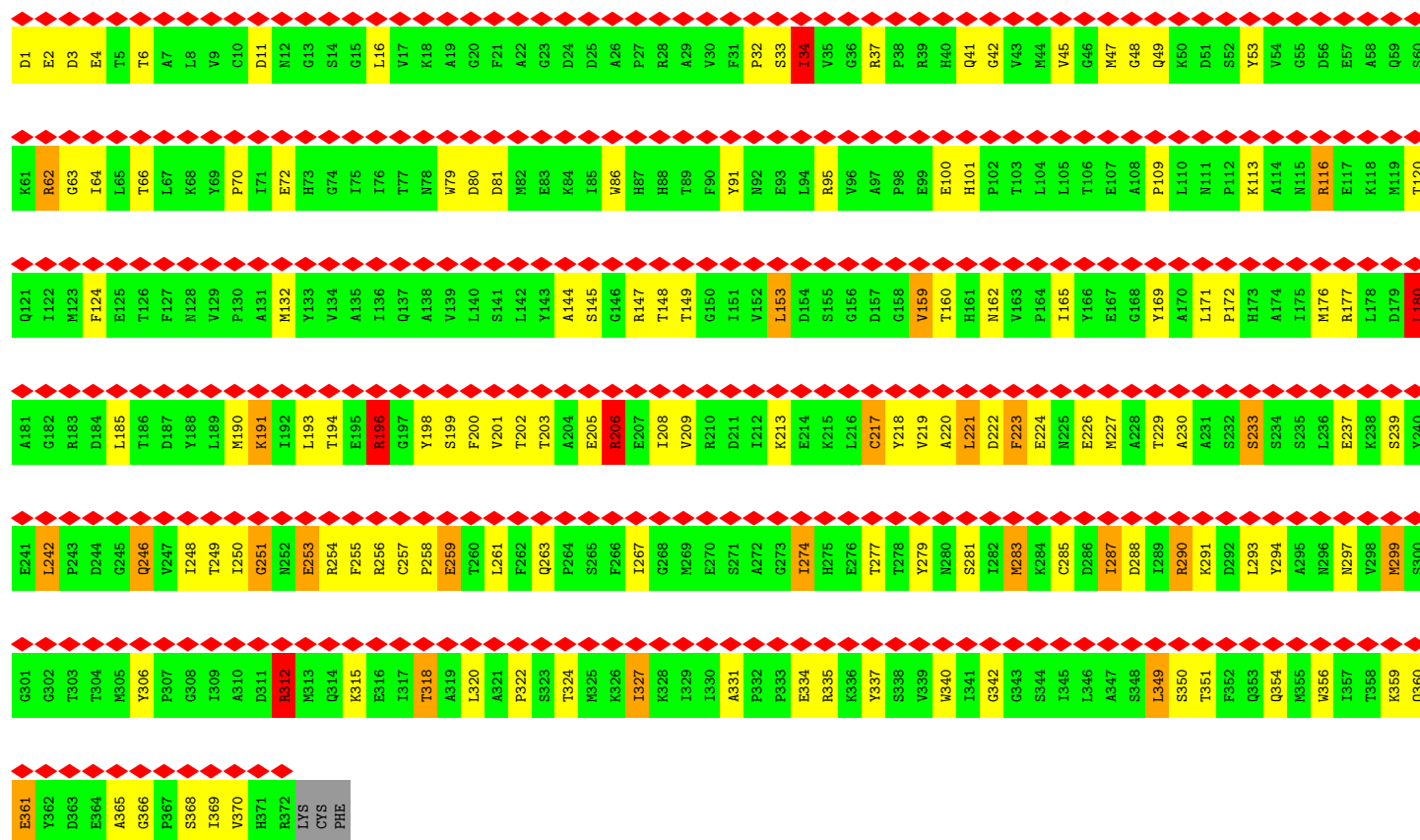


• Molecule 4: RABBIT SKELETAL MUSCLE ACTIN

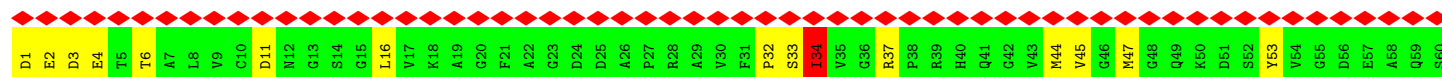


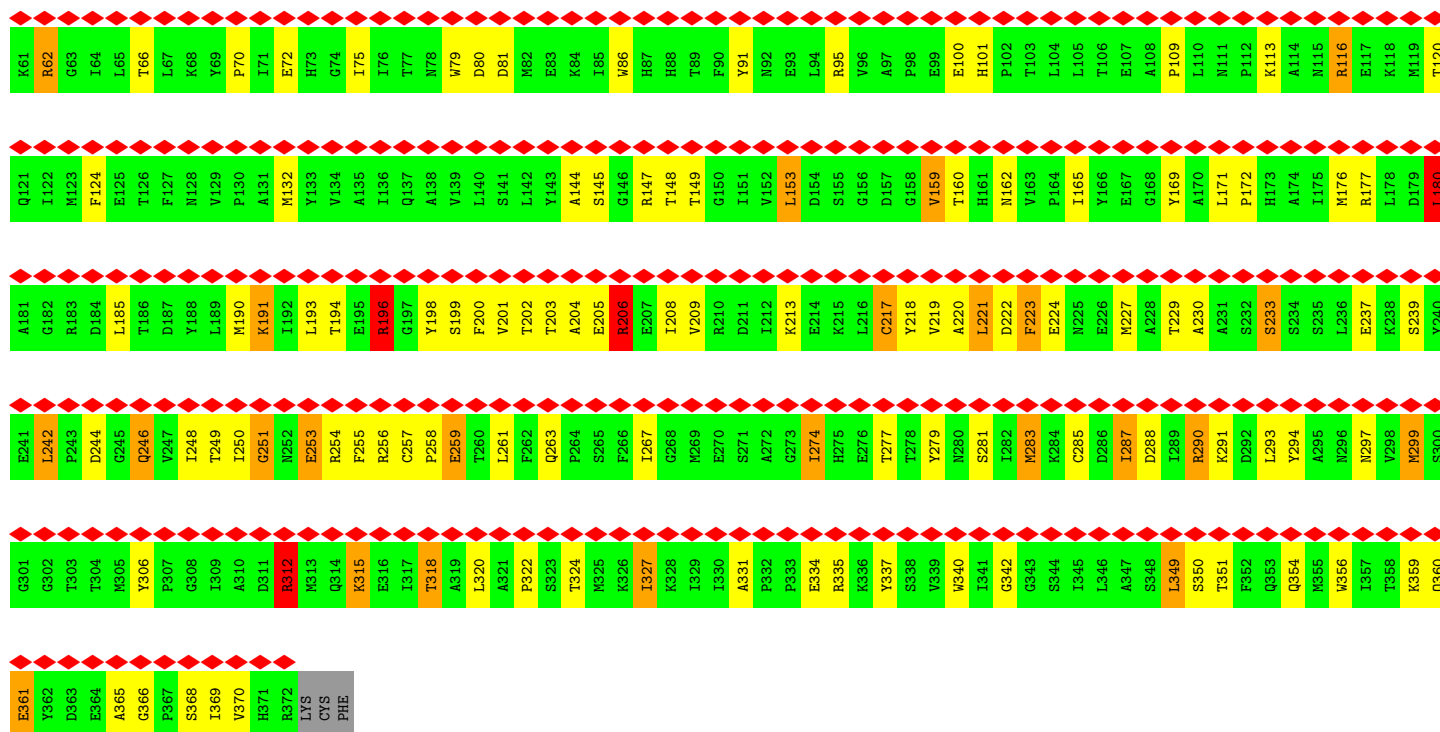


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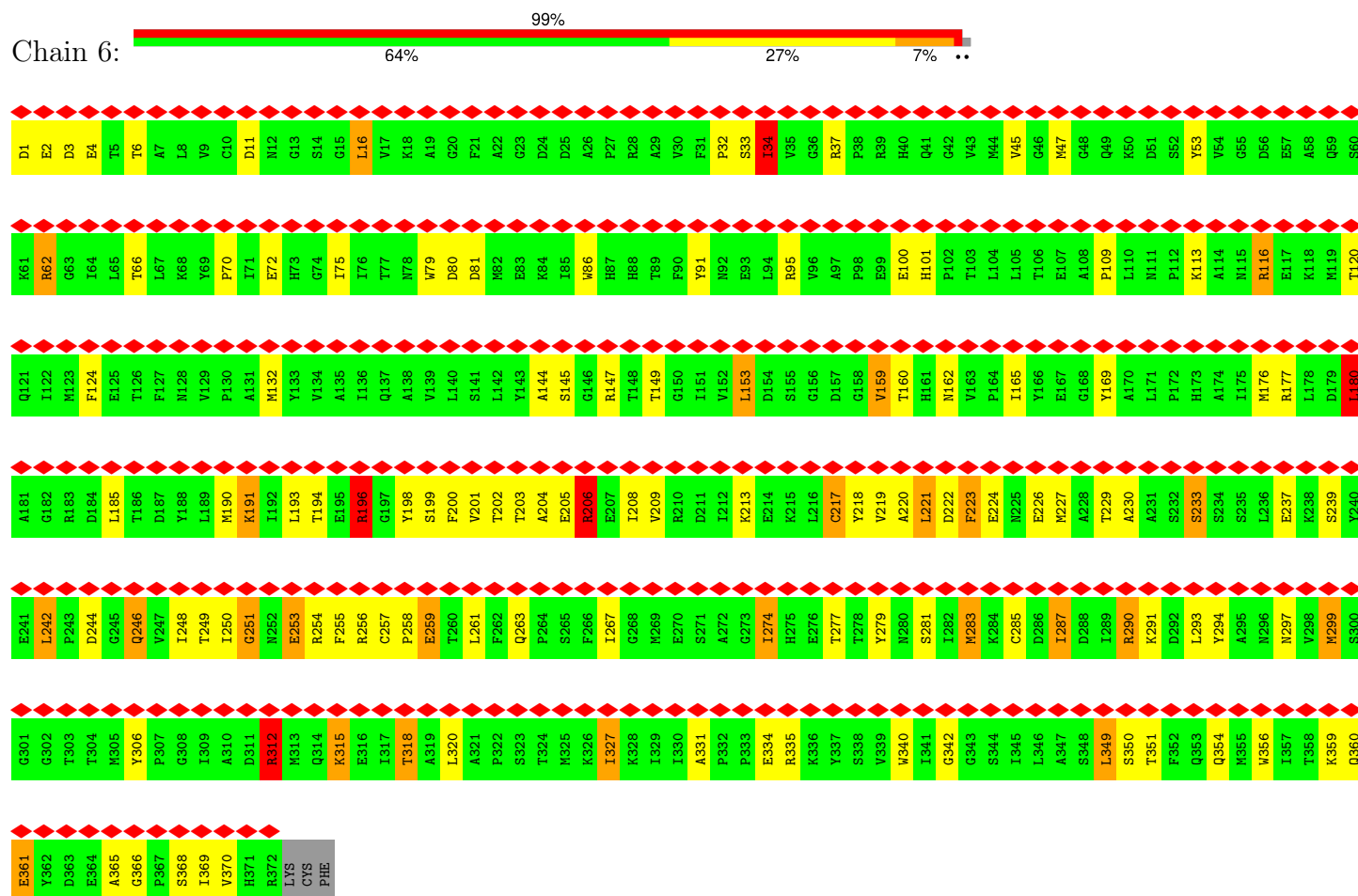


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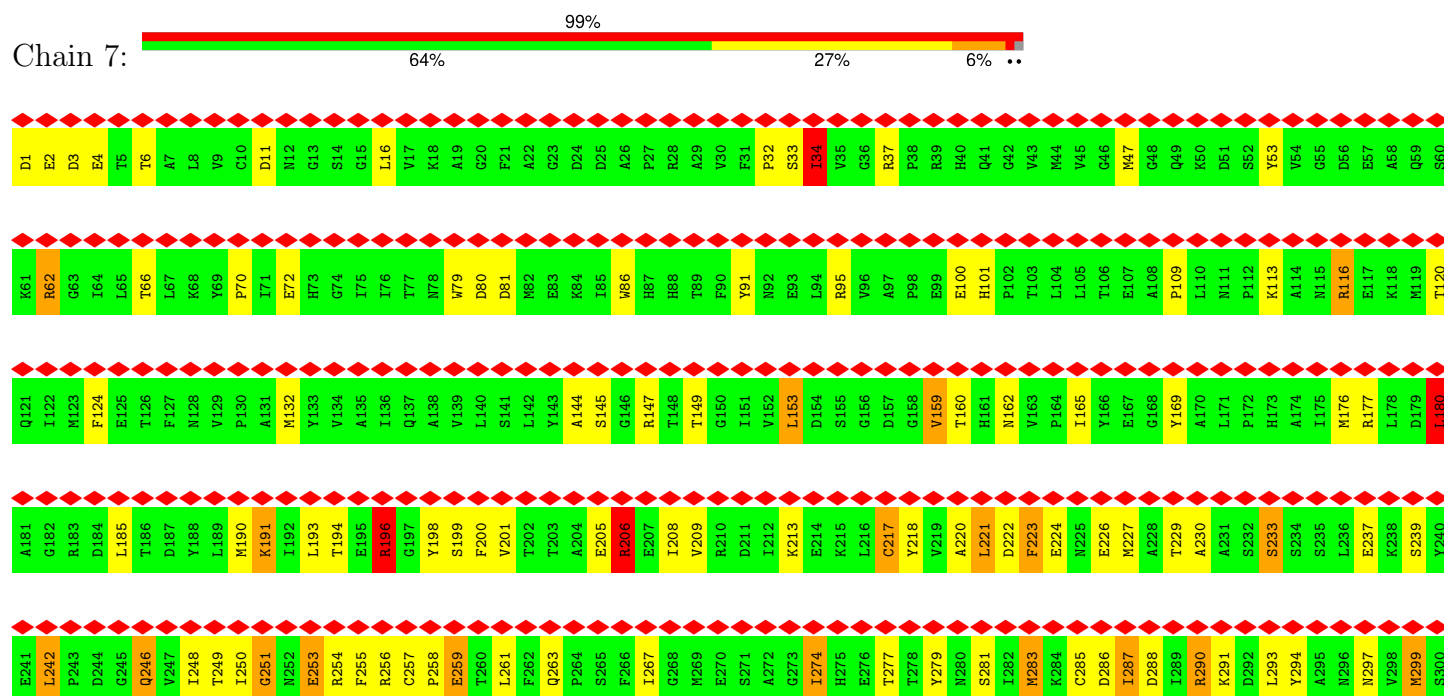


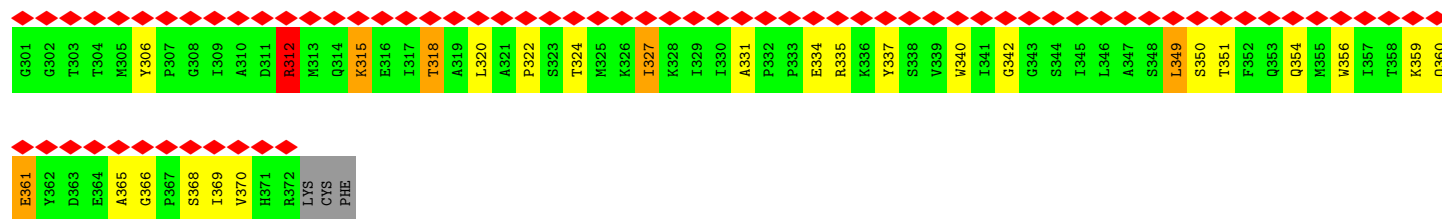


• Molecule 4: RABBIT SKELETAL MUSCLE ACTIN

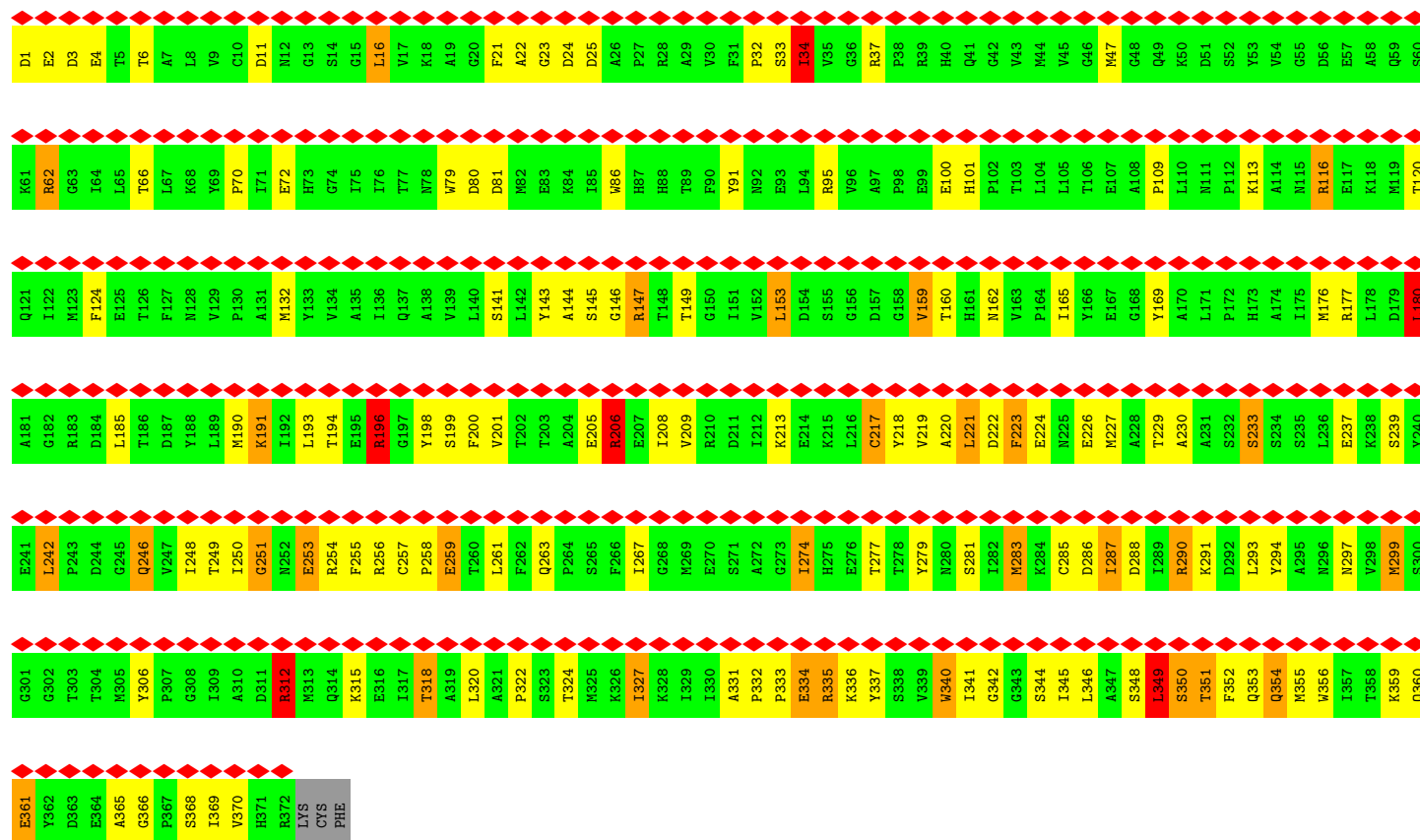


• Molecule 4: RABBIT SKELETAL MUSCLE ACTIN

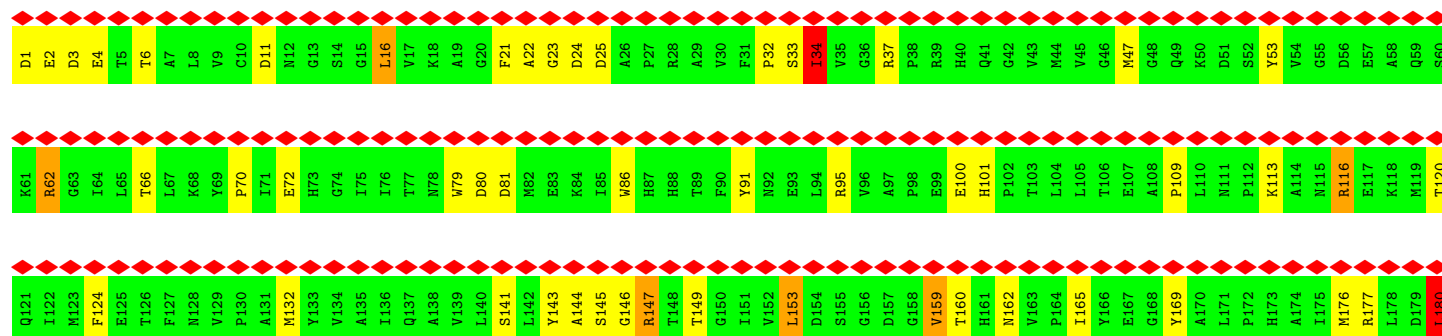


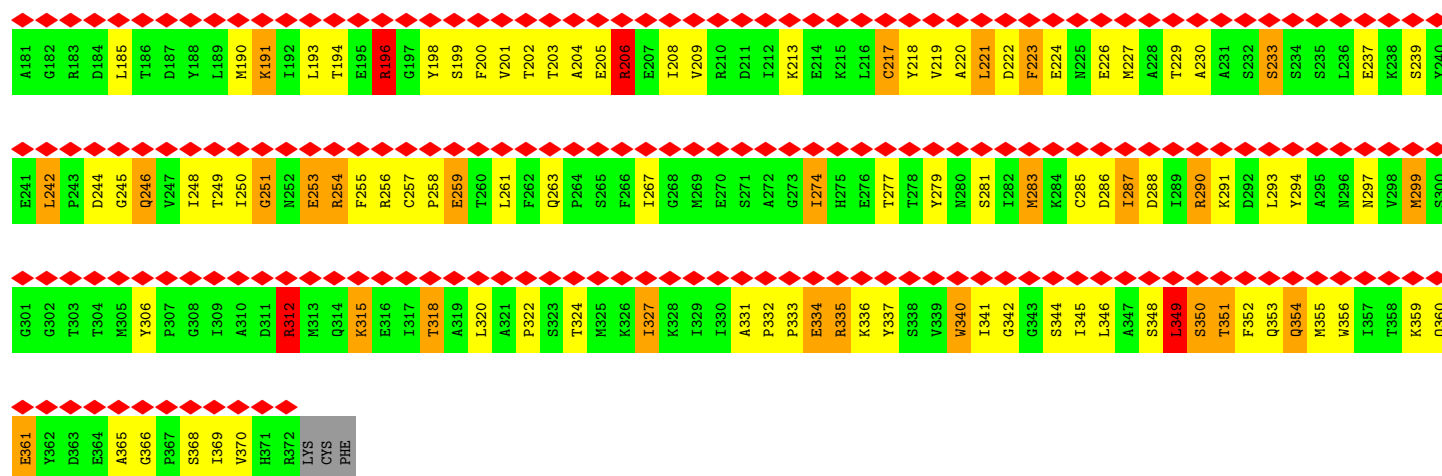


• Molecule 4: RABBIT SKELETAL MUSCLE ACTIN

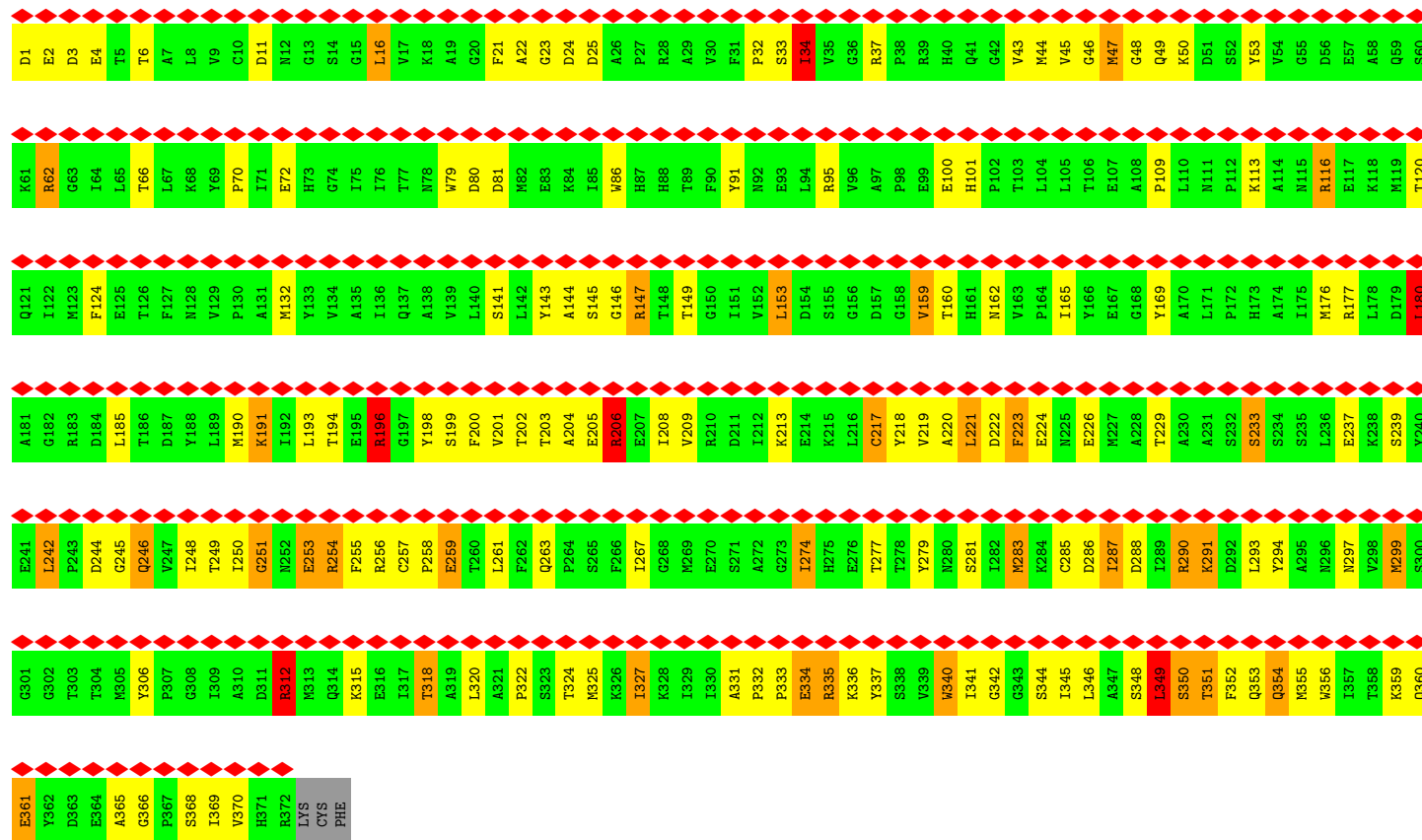


• Molecule 4: RABBIT SKELETAL MUSCLE ACTIN

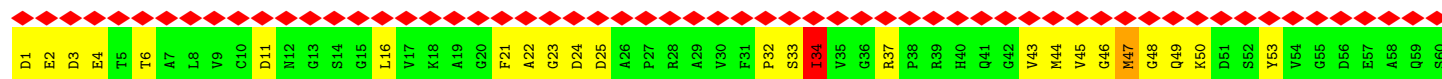




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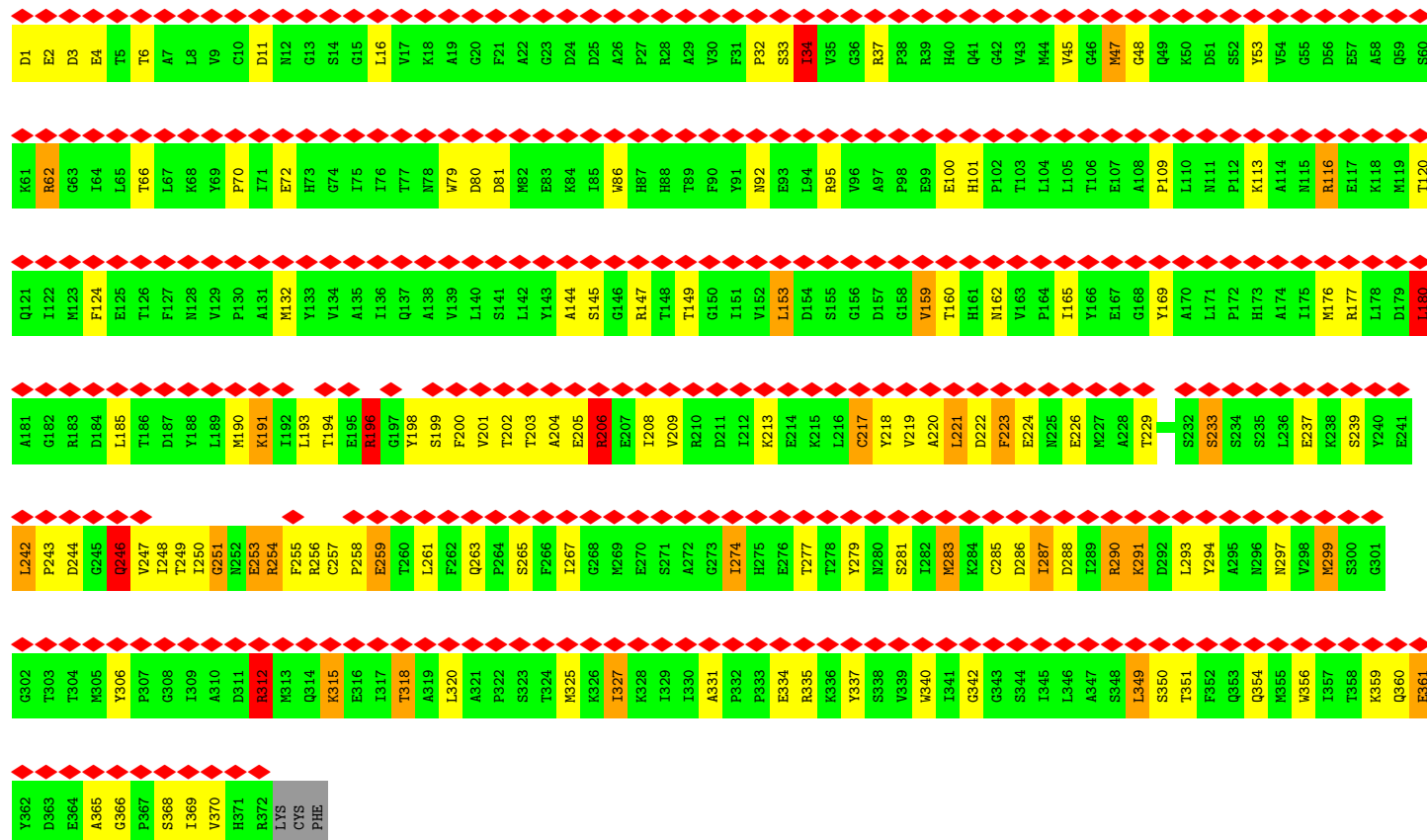


• Molecule 4: RABBIT SKELETAL MUSCLE ACTIN



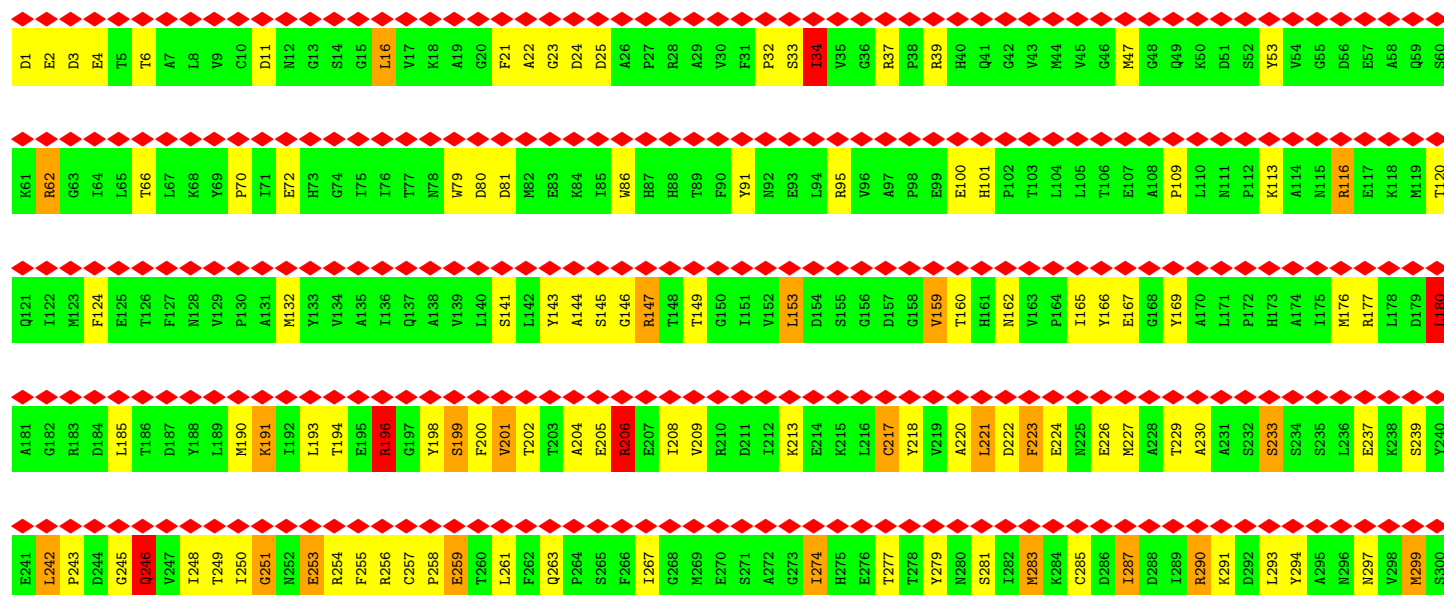
● Molecule 4: RABBIT SKELETAL MUSCLE ACTIN

Chain Y: 



● Molecule 4: RABBIT SKELETAL MUSCLE ACTIN

Chain Z: 





4 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of tilted images used	Not provided	
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI/PHILIPS EM400	Depositor
Voltage (kV)	100	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	17000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum voxel value	366.680	Depositor
Minimum voxel value	-417.992	Depositor
Average voxel value	1.860	Depositor
Voxel value standard deviation	47.792	Depositor
Recommended contour level	81.2	Depositor
Tomogram size (\AA)	9280, 9280, 464	wwPDB
Tomogram dimensions	600, 600, 30	wwPDB
Tomogram angles ($^\circ$)	90, 90, 90	wwPDB
Grid spacing (\AA)	15.4667, 15.4667, 15.4667	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.77	67/6448 (1.0%)	1.82	116/8729 (1.3%)
1	D	1.77	63/6448 (1.0%)	1.82	114/8729 (1.3%)
1	G	1.77	66/6449 (1.0%)	1.82	118/8732 (1.4%)
1	J	1.78	68/6449 (1.1%)	1.87	118/8732 (1.4%)
1	M	1.78	65/6448 (1.0%)	1.90	122/8729 (1.4%)
1	P	1.82	68/6448 (1.1%)	1.86	119/8729 (1.4%)
2	B	1.22	10/1148 (0.9%)	1.61	16/1548 (1.0%)
2	E	1.22	10/1148 (0.9%)	1.62	16/1548 (1.0%)
2	H	1.22	10/1148 (0.9%)	1.62	16/1548 (1.0%)
2	K	1.22	10/1148 (0.9%)	1.61	16/1548 (1.0%)
2	N	1.22	10/1148 (0.9%)	1.61	16/1548 (1.0%)
2	Q	1.22	10/1148 (0.9%)	1.61	16/1548 (1.0%)
3	C	0.80	0/1136	0.95	4/1525 (0.3%)
3	F	0.80	0/1136	0.95	4/1525 (0.3%)
3	I	0.80	0/1136	0.95	4/1525 (0.3%)
3	L	0.79	0/1136	0.94	4/1525 (0.3%)
3	O	0.79	0/1136	0.95	4/1525 (0.3%)
3	R	0.79	0/1136	0.95	4/1525 (0.3%)
4	1	0.89	2/2968 (0.1%)	1.64	51/4023 (1.3%)
4	2	0.89	2/2968 (0.1%)	1.64	50/4023 (1.2%)
4	3	0.89	1/2968 (0.0%)	1.64	52/4023 (1.3%)
4	4	0.89	2/2968 (0.1%)	1.64	51/4023 (1.3%)
4	5	0.89	2/2968 (0.1%)	1.64	51/4023 (1.3%)
4	6	0.89	1/2968 (0.0%)	1.64	49/4023 (1.2%)
4	7	0.89	2/2968 (0.1%)	1.64	51/4023 (1.3%)
4	8	0.89	2/2968 (0.1%)	1.64	51/4023 (1.3%)
4	9	0.89	2/2968 (0.1%)	1.64	52/4023 (1.3%)
4	V	0.89	2/2968 (0.1%)	1.64	52/4023 (1.3%)
4	W	0.89	1/2968 (0.0%)	1.64	52/4023 (1.3%)
4	X	0.89	2/2968 (0.1%)	1.64	52/4023 (1.3%)
4	Y	0.89	2/2968 (0.1%)	1.64	51/4023 (1.3%)
4	Z	0.89	2/2968 (0.1%)	1.64	51/4023 (1.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	1.35	482/93946 (0.5%)	1.69	1543/127140 (1.2%)

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	A	1	4
1	D	1	4
1	G	1	4
1	J	1	6
1	M	1	5
1	P	1	4
2	B	0	3
2	E	0	3
2	H	0	3
2	K	0	3
2	N	0	3
2	Q	0	3
3	C	0	2
3	F	0	2
3	I	0	2
3	L	0	2
3	O	0	2
3	R	0	2
4	1	0	1
4	2	0	1
4	3	0	1
4	4	0	1
4	5	0	1
4	6	0	1
4	7	0	1
4	8	0	1
4	9	0	1
4	V	0	1
4	W	0	1
4	X	0	1
4	Y	0	1
4	Z	0	1
All	All	6	71

The worst 5 of 482 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	649	VAL	CB-CG1	53.31	2.64	1.52
1	J	649	VAL	CB-CG1	53.28	2.64	1.52
1	G	649	VAL	CB-CG1	53.26	2.64	1.52
1	P	649	VAL	CB-CG1	53.24	2.64	1.52
1	A	649	VAL	CB-CG1	53.20	2.64	1.52

The worst 5 of 1543 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	637	LYS	O-C-N	-58.48	23.78	123.20
1	D	637	LYS	O-C-N	-58.48	23.78	123.20
1	J	637	LYS	O-C-N	-58.47	23.80	123.20
1	M	637	LYS	O-C-N	-58.47	23.81	123.20
1	P	637	LYS	O-C-N	-58.46	23.82	123.20

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	648	THR	CB
1	D	648	THR	CB
1	G	648	THR	CB
1	J	648	THR	CB
1	M	648	THR	CB

5 of 71 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	623	PHE	Sidechain
1	A	637	LYS	Mainchain
1	A	649	VAL	Mainchain
1	A	98	HIS	Mainchain
2	B	22	THR	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6797	0	6753	1482	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	6797	0	6757	1507	0
1	G	6797	0	6765	1499	0
1	J	6797	0	6761	1459	0
1	M	6797	0	6759	1617	0
1	P	6797	0	6759	1556	0
2	B	1127	0	1085	233	0
2	E	1127	0	1087	278	0
2	H	1127	0	1087	274	0
2	K	1127	0	1089	284	0
2	N	1127	0	1089	261	0
2	Q	1127	0	1088	260	0
3	C	1123	0	1083	188	0
3	F	1123	0	1084	192	0
3	I	1123	0	1082	185	0
3	L	1123	0	1082	159	0
3	O	1123	0	1084	193	0
3	R	1123	0	1083	170	0
4	1	2906	0	2856	425	0
4	2	2906	0	2860	217	0
4	3	2906	0	2864	161	0
4	4	2906	0	2863	181	0
4	5	2906	0	2865	95	0
4	6	2906	0	2865	100	0
4	7	2906	0	2866	76	0
4	8	2906	0	2857	316	0
4	9	2906	0	2855	347	0
4	V	2906	0	2851	381	0
4	W	2906	0	2851	395	0
4	X	2906	0	2863	181	0
4	Y	2906	0	2864	183	0
4	Z	2906	0	2855	379	0
All	All	94966	0	93612	11529	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 61.

The worst 5 of 11529 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:84:MLY:HD3	1:J:724:TYR:CE2	1.23	1.69
1:D:797:PHE:CE2	3:F:126:LEU:HD22	1.22	1.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:508:ILE:CD1	1:D:766:PHE:CE1	1.74	1.68
1:P:149:GLN:CG	1:P:716:LEU:HD23	1.21	1.68
4:2:287:ILE:CG2	4:4:202:THR:HB	1.23	1.66

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	789/840 (94%)	651 (82%)	112 (14%)	26 (3%)	3	21
1	D	789/840 (94%)	651 (82%)	112 (14%)	26 (3%)	3	21
1	G	791/840 (94%)	651 (82%)	113 (14%)	27 (3%)	3	21
1	J	791/840 (94%)	651 (82%)	113 (14%)	27 (3%)	3	21
1	M	789/840 (94%)	650 (82%)	111 (14%)	28 (4%)	3	20
1	P	789/840 (94%)	651 (82%)	111 (14%)	27 (3%)	3	21
2	B	143/145 (99%)	126 (88%)	9 (6%)	8 (6%)	1	14
2	E	143/145 (99%)	126 (88%)	9 (6%)	8 (6%)	1	14
2	H	143/145 (99%)	126 (88%)	9 (6%)	8 (6%)	1	14
2	K	143/145 (99%)	126 (88%)	9 (6%)	8 (6%)	1	14
2	N	143/145 (99%)	126 (88%)	9 (6%)	8 (6%)	1	14
2	Q	143/145 (99%)	126 (88%)	9 (6%)	8 (6%)	1	14
3	C	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
3	F	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
3	I	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
3	L	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
3	O	143/147 (97%)	133 (93%)	10 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	R	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
4	1	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	8	38
4	2	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	8	38
4	3	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	8	38
4	4	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	8	38
4	5	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	8	38
4	6	370/375 (99%)	335 (90%)	29 (8%)	6 (2%)	8	38
4	7	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	8	38
4	8	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	8	38
4	9	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	8	38
4	V	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	8	38
4	W	370/375 (99%)	335 (90%)	29 (8%)	6 (2%)	8	38
4	X	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	8	38
4	Y	370/375 (99%)	334 (90%)	30 (8%)	6 (2%)	8	38
4	Z	370/375 (99%)	335 (90%)	29 (8%)	6 (2%)	8	38
All	All	11634/12042 (97%)	10138 (87%)	1203 (10%)	293 (2%)	7	26

5 of 293 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	73	LYS
1	A	202	SER
1	A	572	LYS
1	A	712	PRO
1	A	729	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	672/672 (100%)	512 (76%)	160 (24%)	0	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	672/672 (100%)	515 (77%)	157 (23%)	0	4
1	G	672/672 (100%)	513 (76%)	159 (24%)	0	3
1	J	672/672 (100%)	514 (76%)	158 (24%)	0	4
1	M	672/672 (100%)	514 (76%)	158 (24%)	0	4
1	P	672/672 (100%)	514 (76%)	158 (24%)	0	4
2	B	120/120 (100%)	119 (99%)	1 (1%)	79	85
2	E	120/120 (100%)	119 (99%)	1 (1%)	79	85
2	H	120/120 (100%)	119 (99%)	1 (1%)	79	85
2	K	120/120 (100%)	119 (99%)	1 (1%)	79	85
2	N	120/120 (100%)	119 (99%)	1 (1%)	79	85
2	Q	120/120 (100%)	119 (99%)	1 (1%)	79	85
3	C	117/117 (100%)	112 (96%)	5 (4%)	25	46
3	F	117/117 (100%)	112 (96%)	5 (4%)	25	46
3	I	117/117 (100%)	112 (96%)	5 (4%)	25	46
3	L	117/117 (100%)	112 (96%)	5 (4%)	25	46
3	O	117/117 (100%)	112 (96%)	5 (4%)	25	46
3	R	117/117 (100%)	112 (96%)	5 (4%)	25	46
4	1	315/318 (99%)	268 (85%)	47 (15%)	2	11
4	2	315/318 (99%)	269 (85%)	46 (15%)	2	12
4	3	315/318 (99%)	269 (85%)	46 (15%)	2	12
4	4	315/318 (99%)	269 (85%)	46 (15%)	2	12
4	5	315/318 (99%)	269 (85%)	46 (15%)	2	12
4	6	315/318 (99%)	268 (85%)	47 (15%)	2	11
4	7	315/318 (99%)	269 (85%)	46 (15%)	2	12
4	8	315/318 (99%)	268 (85%)	47 (15%)	2	11
4	9	315/318 (99%)	268 (85%)	47 (15%)	2	11
4	V	315/318 (99%)	268 (85%)	47 (15%)	2	11
4	W	315/318 (99%)	269 (85%)	46 (15%)	2	12
4	X	315/318 (99%)	268 (85%)	47 (15%)	2	11
4	Y	315/318 (99%)	269 (85%)	46 (15%)	2	12
4	Z	315/318 (99%)	268 (85%)	47 (15%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	9864/9906 (100%)	8227 (83%)	1637 (17%)	4 9

5 of 1637 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	561	LYS
4	4	239	SER
4	Z	116	ARG
1	P	714	ARG
1	P	549	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 238 such sidechains are listed below:

Mol	Chain	Res	Type
1	M	368	GLN
4	X	87	HIS
1	P	424	ASN
4	W	263	GLN
4	Z	252	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

270 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	MLY	D	107	1	9,10,11	0.52	0	6,11,13	0.32	0
1	MLY	G	505	1	9,10,11	0.81	0	6,11,13	0.35	0
1	MLY	A	528	1	9,10,11	0.89	0	6,11,13	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	A	87	1	9,10,11	1.10	1 (11%)	6,11,13	0.42	0
1	MLY	J	613	1	9,10,11	0.55	0	6,11,13	0.62	0
1	MLY	P	782	1	9,10,11	0.79	0	6,11,13	0.36	0
1	MLY	P	837	1	9,10,11	0.57	0	6,11,13	0.56	0
1	MLY	A	130	1	9,10,11	0.79	0	6,11,13	0.73	0
1	MLY	A	272	1	9,10,11	0.91	1 (11%)	6,11,13	0.56	0
1	MLY	J	367	1	9,10,11	0.59	0	6,11,13	0.36	0
1	MLY	M	600	1	9,10,11	0.53	0	6,11,13	0.38	0
1	MLY	M	613	1	9,10,11	0.55	0	6,11,13	0.62	0
1	MLY	J	551	1	9,10,11	0.51	0	6,11,13	0.18	0
1	MLY	D	415	1	9,10,11	0.76	0	6,11,13	0.19	0
1	MLY	P	598	1	9,10,11	0.81	0	6,11,13	0.41	0
1	MLY	A	49	1	9,10,11	0.95	1 (11%)	6,11,13	0.74	0
1	MLY	A	436	1	9,10,11	0.94	1 (11%)	6,11,13	0.47	0
1	MLY	D	130	1	9,10,11	0.78	0	6,11,13	0.72	0
1	MLY	G	84	1	9,10,11	0.49	0	6,11,13	0.81	0
1	MLY	P	486	1	9,10,11	0.66	0	6,11,13	0.40	0
1	MLY	G	59	1	9,10,11	0.82	0	6,11,13	0.48	0
1	MLY	J	19	1	9,10,11	1.08	1 (11%)	6,11,13	0.58	0
1	MLY	D	19	1	9,10,11	1.08	1 (11%)	6,11,13	0.58	0
1	MLY	P	35	1	9,10,11	0.72	0	6,11,13	0.39	0
1	MLY	P	369	1	9,10,11	0.71	0	6,11,13	0.45	0
1	MLY	A	764	1	9,10,11	0.83	0	6,11,13	0.36	0
1	MLY	A	295	1	9,10,11	0.78	0	6,11,13	0.34	0
1	MLY	A	833	1	9,10,11	1.11	1 (11%)	6,11,13	0.31	0
1	MLY	D	84	1	9,10,11	0.52	0	6,11,13	0.81	0
1	MLY	D	236	1	9,10,11	0.83	1 (11%)	6,11,13	0.48	0
1	MLY	D	600	1	9,10,11	0.51	0	6,11,13	0.38	0
1	MLY	G	504	1	9,10,11	0.89	0	6,11,13	0.22	0
1	MLY	J	138	1	9,10,11	1.21	1 (11%)	6,11,13	0.83	0
1	MLY	P	55	1	9,10,11	0.73	0	6,11,13	0.80	0
1	MLY	G	385	1	9,10,11	0.92	1 (11%)	6,11,13	0.45	0
1	MLY	A	35	1	9,10,11	0.74	0	6,11,13	0.38	0
1	MLY	J	764	1	9,10,11	0.82	0	6,11,13	0.36	0
1	MLY	P	348	1	9,10,11	0.77	0	6,11,13	0.47	0
1	MLY	P	839	1	9,10,11	0.65	0	6,11,13	0.78	0
1	MLY	A	681	1	9,10,11	0.57	0	6,11,13	0.47	0
1	MLY	D	617	1	9,10,11	0.91	1 (11%)	6,11,13	0.34	0
1	MLY	D	681	1	9,10,11	0.56	0	6,11,13	0.45	0
1	MLY	M	617	1	9,10,11	0.91	0	6,11,13	0.33	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	G	415	1	9,10,11	0.74	0	6,11,13	0.18	0
1	MLY	M	764	1	9,10,11	0.84	0	6,11,13	0.36	0
1	MLY	P	600	1	9,10,11	0.53	0	6,11,13	0.39	0
1	MLY	A	236	1	9,10,11	0.83	1 (11%)	6,11,13	0.49	0
1	MLY	G	659	1	9,10,11	0.84	1 (11%)	6,11,13	0.60	0
1	MLY	G	138	1	9,10,11	1.22	1 (11%)	6,11,13	0.82	0
1	MLY	J	236	1	9,10,11	0.83	1 (11%)	6,11,13	0.48	0
1	MLY	G	486	1	9,10,11	0.66	0	6,11,13	0.40	0
1	MLY	G	598	1	9,10,11	0.82	0	6,11,13	0.41	0
1	MLY	J	505	1	9,10,11	0.85	1 (11%)	6,11,13	0.34	0
1	MLY	G	107	1	9,10,11	0.49	0	6,11,13	0.33	0
1	MLY	P	30	1	9,10,11	0.91	0	6,11,13	0.31	0
1	MLY	J	782	1	9,10,11	0.82	0	6,11,13	0.36	0
1	MLY	P	59	1	9,10,11	0.85	0	6,11,13	0.47	0
1	MLY	D	367	1	9,10,11	0.60	0	6,11,13	0.37	0
1	MLY	G	296	1	9,10,11	0.62	0	6,11,13	0.36	0
1	MLY	P	87	1	9,10,11	1.10	1 (11%)	6,11,13	0.43	0
1	MLY	A	613	1	9,10,11	0.58	0	6,11,13	0.62	0
1	MLY	D	138	1	9,10,11	1.24	1 (11%)	6,11,13	0.82	0
1	MLY	D	768	1	9,10,11	0.75	0	6,11,13	0.41	0
1	MLY	G	87	1	9,10,11	1.14	1 (11%)	6,11,13	0.44	0
1	MLY	D	782	1	9,10,11	0.81	0	6,11,13	0.34	0
1	MLY	M	138	1	9,10,11	1.21	1 (11%)	6,11,13	0.81	0
1	MLY	D	369	1	9,10,11	0.70	0	6,11,13	0.44	0
1	MLY	J	348	1	9,10,11	0.76	0	6,11,13	0.46	0
1	MLY	J	49	1	9,10,11	1.00	1 (11%)	6,11,13	0.75	0
1	MLY	A	415	1	9,10,11	0.73	0	6,11,13	0.19	0
1	MLY	M	486	1	9,10,11	0.67	0	6,11,13	0.41	0
1	MLY	P	190	1	9,10,11	1.22	2 (22%)	6,11,13	0.52	0
1	MLY	G	19	1	9,10,11	1.04	1 (11%)	6,11,13	0.59	0
1	MLY	D	505	1	9,10,11	0.78	0	6,11,13	0.34	0
1	MLY	A	486	1	9,10,11	0.66	0	6,11,13	0.40	0
1	MLY	M	837	1	9,10,11	0.58	0	6,11,13	0.56	0
1	MLY	M	353	1	9,10,11	0.86	0	6,11,13	0.81	0
1	MLY	G	600	1	9,10,11	0.52	0	6,11,13	0.37	0
1	MLY	G	130	1	9,10,11	0.78	0	6,11,13	0.73	0
1	MLY	P	353	1	9,10,11	0.86	0	6,11,13	0.80	0
1	MLY	A	782	1	9,10,11	0.82	1 (11%)	6,11,13	0.37	0
1	MLY	G	837	1	9,10,11	0.60	0	6,11,13	0.53	0
1	MLY	D	63	1	9,10,11	0.85	0	6,11,13	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	D	431	1	9,10,11	0.51	0	6,11,13	0.46	0
1	MLY	J	768	1	9,10,11	0.77	0	6,11,13	0.43	0
1	MLY	P	659	1	9,10,11	0.84	1 (11%)	6,11,13	0.58	0
1	MLY	D	827	1	9,10,11	0.66	0	6,11,13	0.47	0
1	MLY	J	35	1	9,10,11	0.74	0	6,11,13	0.38	0
1	MLY	M	431	1	9,10,11	0.52	0	6,11,13	0.44	0
1	MLY	M	827	1	9,10,11	0.70	0	6,11,13	0.47	0
1	MLY	G	551	1	9,10,11	0.53	0	6,11,13	0.18	0
1	MLY	D	30	1	9,10,11	0.93	0	6,11,13	0.31	0
1	MLY	J	63	1	9,10,11	0.86	0	6,11,13	0.44	0
1	MLY	J	296	1	9,10,11	0.66	0	6,11,13	0.35	0
1	MLY	M	369	1	9,10,11	0.71	0	6,11,13	0.45	0
1	MLY	A	659	1	9,10,11	0.84	1 (11%)	6,11,13	0.60	0
1	MLY	J	528	1	9,10,11	0.89	0	6,11,13	0.65	0
1	MLY	D	296	1	9,10,11	0.63	0	6,11,13	0.37	0
1	MLY	G	248	1	9,10,11	0.79	0	6,11,13	0.65	0
1	MLY	A	84	1	9,10,11	0.51	0	6,11,13	0.80	0
1	MLY	P	764	1	9,10,11	0.81	0	6,11,13	0.37	0
1	MLY	D	272	1	9,10,11	0.88	1 (11%)	6,11,13	0.56	0
1	MLY	A	385	1	9,10,11	0.93	1 (11%)	6,11,13	0.44	0
1	MLY	M	348	1	9,10,11	0.77	0	6,11,13	0.47	0
1	MLY	M	272	1	9,10,11	0.92	1 (11%)	6,11,13	0.55	0
1	MLY	J	833	1	9,10,11	1.13	2 (22%)	6,11,13	0.30	0
1	MLY	M	839	1	9,10,11	0.65	0	6,11,13	0.78	0
1	MLY	G	528	1	9,10,11	0.92	0	6,11,13	0.66	0
1	MLY	J	385	1	9,10,11	0.94	1 (11%)	6,11,13	0.44	0
1	MLY	J	30	1	9,10,11	0.91	0	6,11,13	0.32	0
1	MLY	A	551	1	9,10,11	0.51	0	6,11,13	0.19	0
1	MLY	D	49	1	9,10,11	1.00	1 (11%)	6,11,13	0.76	0
1	MLY	M	436	1	9,10,11	0.98	1 (11%)	6,11,13	0.49	0
1	MLY	J	681	1	9,10,11	0.56	0	6,11,13	0.47	0
1	MLY	A	190	1	9,10,11	1.21	2 (22%)	6,11,13	0.52	0
1	MLY	M	768	1	9,10,11	0.74	0	6,11,13	0.41	0
1	MLY	G	782	1	9,10,11	0.80	0	6,11,13	0.36	0
1	MLY	D	295	1	9,10,11	0.74	0	6,11,13	0.38	0
1	MLY	J	353	1	9,10,11	0.85	0	6,11,13	0.79	0
1	MLY	A	827	1	9,10,11	0.68	0	6,11,13	0.45	0
1	MLY	M	30	1	9,10,11	0.90	0	6,11,13	0.31	0
1	MLY	P	63	1	9,10,11	0.87	0	6,11,13	0.43	0
1	MLY	P	768	1	9,10,11	0.76	0	6,11,13	0.43	0
1	MLY	G	63	1	9,10,11	0.86	0	6,11,13	0.45	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	M	295	1	9,10,11	0.74	0	6,11,13	0.36	0
1	MLY	P	19	1	9,10,11	1.06	1 (11%)	6,11,13	0.59	0
1	MLY	P	49	1	9,10,11	0.99	1 (11%)	6,11,13	0.75	0
1	MLY	A	839	1	9,10,11	0.66	0	6,11,13	0.82	0
1	MLY	J	504	1	9,10,11	0.84	0	6,11,13	0.23	0
1	MLY	A	837	1	9,10,11	0.59	0	6,11,13	0.54	0
1	MLY	A	107	1	9,10,11	0.47	0	6,11,13	0.33	0
1	MLY	G	30	1	9,10,11	0.90	0	6,11,13	0.30	0
1	MLY	J	837	1	9,10,11	0.57	0	6,11,13	0.56	0
1	MLY	G	613	1	9,10,11	0.59	0	6,11,13	0.61	0
1	MLY	G	190	1	9,10,11	1.21	2 (22%)	6,11,13	0.53	0
1	MLY	J	295	1	9,10,11	0.77	0	6,11,13	0.37	0
1	MLY	J	659	1	9,10,11	0.83	1 (11%)	6,11,13	0.58	0
1	MLY	M	385	1	9,10,11	0.93	1 (11%)	6,11,13	0.45	0
1	MLY	P	553	1	9,10,11	0.65	0	6,11,13	0.53	0
1	MLY	M	107	1	9,10,11	0.48	0	6,11,13	0.32	0
1	MLY	P	504	1	9,10,11	0.83	0	6,11,13	0.23	0
1	MLY	G	55	1	9,10,11	0.74	0	6,11,13	0.81	0
1	MLY	M	681	1	9,10,11	0.58	0	6,11,13	0.47	0
1	MLY	J	431	1	9,10,11	0.52	0	6,11,13	0.45	0
1	MLY	J	827	1	9,10,11	0.72	0	6,11,13	0.48	0
1	MLY	P	505	1	9,10,11	0.86	1 (11%)	6,11,13	0.34	0
1	MLY	G	272	1	9,10,11	0.88	1 (11%)	6,11,13	0.54	0
1	MLY	M	415	1	9,10,11	0.77	0	6,11,13	0.20	0
1	MLY	P	295	1	9,10,11	0.75	0	6,11,13	0.37	0
1	MLY	P	833	1	9,10,11	1.15	2 (22%)	6,11,13	0.30	0
1	MLY	J	190	1	9,10,11	1.21	2 (22%)	6,11,13	0.53	0
1	MLY	J	553	1	9,10,11	0.66	0	6,11,13	0.54	0
1	MLY	D	248	1	9,10,11	0.81	0	6,11,13	0.66	0
1	MLY	A	600	1	9,10,11	0.53	0	6,11,13	0.39	0
1	MLY	M	130	1	9,10,11	0.76	0	6,11,13	0.74	0
1	MLY	P	107	1	9,10,11	0.48	0	6,11,13	0.33	0
1	MLY	G	617	1	9,10,11	0.90	0	6,11,13	0.35	0
1	MLY	G	764	1	9,10,11	0.81	0	6,11,13	0.36	0
1	MLY	A	63	1	9,10,11	0.89	0	6,11,13	0.44	0
1	MLY	G	553	4,1	9,10,11	0.67	0	6,11,13	0.55	0
1	MLY	M	367	1	9,10,11	0.57	0	6,11,13	0.38	0
1	MLY	D	528	1	9,10,11	0.91	0	6,11,13	0.64	0
1	MLY	P	367	1	9,10,11	0.58	0	6,11,13	0.35	0
1	MLY	P	551	1	9,10,11	0.51	0	6,11,13	0.18	0
1	MLY	M	505	1	9,10,11	0.84	1 (11%)	6,11,13	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	D	659	1	9,10,11	0.84	1 (11%)	6,11,13	0.59	0
1	MLY	M	598	1	9,10,11	0.84	1 (11%)	6,11,13	0.42	0
1	MLY	D	385	1	9,10,11	0.91	1 (11%)	6,11,13	0.45	0
1	MLY	M	19	1	9,10,11	1.07	1 (11%)	6,11,13	0.57	0
1	MLY	M	49	1	9,10,11	1.00	1 (11%)	6,11,13	0.75	0
1	MLY	A	768	1	9,10,11	0.77	0	6,11,13	0.41	0
1	MLY	D	190	1	9,10,11	1.19	2 (22%)	6,11,13	0.53	0
1	MLY	A	553	4,1	9,10,11	0.66	0	6,11,13	0.54	0
1	MLY	D	436	1	9,10,11	1.00	1 (11%)	6,11,13	0.48	0
1	MLY	D	87	1	9,10,11	1.06	1 (11%)	6,11,13	0.43	0
1	MLY	D	551	1	9,10,11	0.52	0	6,11,13	0.20	0
1	MLY	G	431	1	9,10,11	0.51	0	6,11,13	0.46	0
1	MLY	M	236	1	9,10,11	0.84	1 (11%)	6,11,13	0.49	0
1	MLY	M	551	1	9,10,11	0.52	0	6,11,13	0.19	0
1	MLY	A	505	1	9,10,11	0.83	0	6,11,13	0.34	0
1	MLY	A	369	1	9,10,11	0.72	0	6,11,13	0.46	0
1	MLY	D	764	1	9,10,11	0.84	0	6,11,13	0.34	0
1	MLY	D	598	1	9,10,11	0.86	1 (11%)	6,11,13	0.42	0
1	MLY	M	35	1	9,10,11	0.74	0	6,11,13	0.38	0
1	MLY	P	248	1	9,10,11	0.80	0	6,11,13	0.65	0
1	MLY	A	367	1	9,10,11	0.60	0	6,11,13	0.37	0
1	MLY	G	367	1	9,10,11	0.61	0	6,11,13	0.39	0
1	MLY	A	353	1	9,10,11	0.88	0	6,11,13	0.81	0
1	MLY	G	827	1	9,10,11	0.68	0	6,11,13	0.48	0
1	MLY	A	348	1	9,10,11	0.80	0	6,11,13	0.48	0
1	MLY	M	504	1	9,10,11	0.84	0	6,11,13	0.23	0
1	MLY	P	681	1	9,10,11	0.57	0	6,11,13	0.47	0
1	MLY	P	827	1	9,10,11	0.69	0	6,11,13	0.47	0
1	MLY	P	84	1	9,10,11	0.51	0	6,11,13	0.80	0
1	MLY	A	30	1	9,10,11	0.90	0	6,11,13	0.32	0
1	MLY	G	369	1	9,10,11	0.71	0	6,11,13	0.47	0
1	MLY	A	504	1	9,10,11	0.88	0	6,11,13	0.24	0
1	MLY	J	87	1	9,10,11	1.12	1 (11%)	6,11,13	0.44	0
1	MLY	P	528	1	9,10,11	0.88	0	6,11,13	0.66	0
1	MLY	P	130	1	9,10,11	0.75	0	6,11,13	0.74	0
1	MLY	J	415	1	9,10,11	0.75	0	6,11,13	0.19	0
1	MLY	J	598	1	9,10,11	0.82	0	6,11,13	0.41	0
1	MLY	M	833	1	9,10,11	1.14	2 (22%)	6,11,13	0.30	0
1	MLY	G	348	1	9,10,11	0.80	0	6,11,13	0.47	0
1	MLY	D	837	1	9,10,11	0.59	0	6,11,13	0.58	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	G	839	1	9,10,11	0.65	0	6,11,13	0.80	0
1	MLY	P	236	1	9,10,11	0.83	1 (11%)	6,11,13	0.47	0
1	MLY	A	55	1	9,10,11	0.72	0	6,11,13	0.80	0
1	MLY	G	833	1	9,10,11	1.15	2 (22%)	6,11,13	0.31	0
1	MLY	M	296	1	9,10,11	0.64	0	6,11,13	0.35	0
1	MLY	J	55	1	9,10,11	0.73	0	6,11,13	0.79	0
1	MLY	G	436	1	9,10,11	0.95	1 (11%)	6,11,13	0.48	0
1	MLY	M	59	1	9,10,11	0.85	0	6,11,13	0.46	0
1	MLY	M	87	1	9,10,11	1.11	1 (11%)	6,11,13	0.44	0
1	MLY	A	431	1	9,10,11	0.50	0	6,11,13	0.45	0
1	MLY	A	19	1	9,10,11	1.03	1 (11%)	6,11,13	0.57	0
1	MLY	P	138	1	9,10,11	1.17	1 (11%)	6,11,13	0.82	0
1	MLY	J	272	1	9,10,11	0.90	1 (11%)	6,11,13	0.56	0
1	MLY	D	486	1	9,10,11	0.67	0	6,11,13	0.41	0
1	MLY	P	617	1	9,10,11	0.93	1 (11%)	6,11,13	0.34	0
1	MLY	J	130	1	9,10,11	0.75	0	6,11,13	0.72	0
1	MLY	D	35	1	9,10,11	0.75	0	6,11,13	0.37	0
1	MLY	J	84	1	9,10,11	0.49	0	6,11,13	0.81	0
1	MLY	A	598	1	9,10,11	0.83	1 (11%)	6,11,13	0.43	0
1	MLY	A	248	1	9,10,11	0.82	0	6,11,13	0.64	0
1	MLY	A	617	1	9,10,11	0.87	0	6,11,13	0.35	0
1	MLY	M	659	1	9,10,11	0.82	1 (11%)	6,11,13	0.58	0
1	MLY	J	107	1	9,10,11	0.49	0	6,11,13	0.34	0
1	MLY	P	296	1	9,10,11	0.67	0	6,11,13	0.36	0
1	MLY	J	617	1	9,10,11	0.92	1 (11%)	6,11,13	0.34	0
1	MLY	G	236	1	9,10,11	0.82	1 (11%)	6,11,13	0.48	0
1	MLY	J	248	1	9,10,11	0.81	0	6,11,13	0.65	0
1	MLY	P	385	1	9,10,11	0.94	1 (11%)	6,11,13	0.45	0
1	MLY	G	353	1	9,10,11	0.86	0	6,11,13	0.83	0
1	MLY	P	613	1	9,10,11	0.57	0	6,11,13	0.62	0
1	MLY	A	296	1	9,10,11	0.59	0	6,11,13	0.36	0
1	MLY	P	272	1	9,10,11	0.92	1 (11%)	6,11,13	0.57	0
1	MLY	D	833	1	9,10,11	1.13	2 (22%)	6,11,13	0.30	0
1	MLY	G	295	1	9,10,11	0.76	0	6,11,13	0.35	0
1	MLY	J	369	1	9,10,11	0.72	0	6,11,13	0.46	0
1	MLY	M	248	1	9,10,11	0.81	0	6,11,13	0.66	0
1	MLY	P	431	1	9,10,11	0.51	0	6,11,13	0.44	0
1	MLY	M	190	1	9,10,11	1.20	2 (22%)	6,11,13	0.53	0
1	MLY	D	613	1	9,10,11	0.58	0	6,11,13	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	G	681	1	9,10,11	0.58	0	6,11,13	0.45	0
1	MLY	M	55	1	9,10,11	0.73	0	6,11,13	0.80	0
1	MLY	P	436	1	9,10,11	0.94	1 (11%)	6,11,13	0.48	0
1	MLY	G	49	1	9,10,11	1.01	1 (11%)	6,11,13	0.74	0
1	MLY	M	84	1	9,10,11	0.52	0	6,11,13	0.80	0
1	MLY	D	553	4,1	9,10,11	0.67	0	6,11,13	0.55	0
1	MLY	J	59	1	9,10,11	0.85	0	6,11,13	0.47	0
1	MLY	D	504	1	9,10,11	0.86	0	6,11,13	0.20	0
1	MLY	D	59	1	9,10,11	0.85	0	6,11,13	0.48	0
1	MLY	M	528	1	9,10,11	0.89	0	6,11,13	0.65	0
1	MLY	J	486	1	9,10,11	0.67	0	6,11,13	0.40	0
1	MLY	D	55	1	9,10,11	0.73	0	6,11,13	0.81	0
1	MLY	J	839	1	9,10,11	0.66	0	6,11,13	0.77	0
1	MLY	P	415	1	9,10,11	0.76	0	6,11,13	0.19	0
1	MLY	M	553	1	9,10,11	0.63	0	6,11,13	0.54	0
1	MLY	A	138	1	9,10,11	1.21	1 (11%)	6,11,13	0.82	0
1	MLY	G	768	1	9,10,11	0.75	0	6,11,13	0.42	0
1	MLY	J	436	1	9,10,11	0.95	1 (11%)	6,11,13	0.48	0
1	MLY	J	600	1	9,10,11	0.53	0	6,11,13	0.38	0
1	MLY	M	782	1	9,10,11	0.81	0	6,11,13	0.38	0
1	MLY	G	35	1	9,10,11	0.74	0	6,11,13	0.39	0
1	MLY	D	353	1	9,10,11	0.85	0	6,11,13	0.80	0
1	MLY	A	59	1	9,10,11	0.84	0	6,11,13	0.47	0
1	MLY	D	348	1	9,10,11	0.77	0	6,11,13	0.48	0
1	MLY	M	63	1	9,10,11	0.87	0	6,11,13	0.44	0
1	MLY	D	839	1	9,10,11	0.64	0	6,11,13	0.79	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	D	107	1	-	2/8/9/11	-
1	MLY	G	505	1	-	5/8/9/11	-
1	MLY	A	528	1	-	4/8/9/11	-
1	MLY	A	87	1	-	2/8/9/11	-
1	MLY	J	613	1	-	3/8/9/11	-
1	MLY	P	782	1	-	6/8/9/11	-
1	MLY	P	837	1	-	6/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	A	130	1	-	5/8/9/11	-
1	MLY	A	272	1	-	3/8/9/11	-
1	MLY	J	367	1	-	2/8/9/11	-
1	MLY	M	600	1	-	3/8/9/11	-
1	MLY	M	613	1	-	3/8/9/11	-
1	MLY	J	551	1	-	3/8/9/11	-
1	MLY	D	415	1	-	3/8/9/11	-
1	MLY	P	598	1	-	5/8/9/11	-
1	MLY	A	49	1	-	3/8/9/11	-
1	MLY	A	436	1	-	4/8/9/11	-
1	MLY	D	130	1	-	5/8/9/11	-
1	MLY	G	84	1	-	4/8/9/11	-
1	MLY	P	486	1	-	2/8/9/11	-
1	MLY	G	59	1	-	3/8/9/11	-
1	MLY	J	19	1	-	4/8/9/11	-
1	MLY	D	19	1	-	4/8/9/11	-
1	MLY	P	35	1	-	3/8/9/11	-
1	MLY	P	369	1	-	2/8/9/11	-
1	MLY	A	764	1	-	2/8/9/11	-
1	MLY	A	295	1	-	2/8/9/11	-
1	MLY	A	833	1	-	6/8/9/11	-
1	MLY	D	84	1	-	4/8/9/11	-
1	MLY	D	236	1	-	3/8/9/11	-
1	MLY	D	600	1	-	3/8/9/11	-
1	MLY	G	504	1	-	4/8/9/11	-
1	MLY	J	138	1	-	4/8/9/11	-
1	MLY	P	55	1	-	6/8/9/11	-
1	MLY	G	385	1	-	2/8/9/11	-
1	MLY	A	35	1	-	3/8/9/11	-
1	MLY	J	764	1	-	2/8/9/11	-
1	MLY	P	348	1	-	5/8/9/11	-
1	MLY	P	839	1	-	3/8/9/11	-
1	MLY	A	681	1	-	4/8/9/11	-
1	MLY	D	617	1	-	2/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	D	681	1	-	4/8/9/11	-
1	MLY	M	617	1	-	2/8/9/11	-
1	MLY	G	415	1	-	3/8/9/11	-
1	MLY	M	764	1	-	2/8/9/11	-
1	MLY	P	600	1	-	3/8/9/11	-
1	MLY	A	236	1	-	3/8/9/11	-
1	MLY	G	659	1	-	3/8/9/11	-
1	MLY	G	138	1	-	4/8/9/11	-
1	MLY	J	236	1	-	3/8/9/11	-
1	MLY	G	486	1	-	2/8/9/11	-
1	MLY	G	598	1	-	5/8/9/11	-
1	MLY	J	505	1	-	5/8/9/11	-
1	MLY	G	107	1	-	2/8/9/11	-
1	MLY	P	30	1	-	3/8/9/11	-
1	MLY	J	782	1	-	6/8/9/11	-
1	MLY	P	59	1	-	3/8/9/11	-
1	MLY	D	367	1	-	2/8/9/11	-
1	MLY	G	296	1	-	4/8/9/11	-
1	MLY	P	87	1	-	2/8/9/11	-
1	MLY	A	613	1	-	3/8/9/11	-
1	MLY	D	138	1	-	4/8/9/11	-
1	MLY	D	768	1	-	4/8/9/11	-
1	MLY	G	87	1	-	2/8/9/11	-
1	MLY	D	782	1	-	6/8/9/11	-
1	MLY	M	138	1	-	4/8/9/11	-
1	MLY	D	369	1	-	2/8/9/11	-
1	MLY	J	348	1	-	5/8/9/11	-
1	MLY	J	49	1	-	3/8/9/11	-
1	MLY	A	415	1	-	3/8/9/11	-
1	MLY	M	486	1	-	2/8/9/11	-
1	MLY	P	190	1	-	4/8/9/11	-
1	MLY	G	19	1	-	4/8/9/11	-
1	MLY	D	505	1	-	5/8/9/11	-
1	MLY	A	486	1	-	2/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	M	837	1	-	6/8/9/11	-
1	MLY	M	353	1	-	4/8/9/11	-
1	MLY	G	600	1	-	3/8/9/11	-
1	MLY	G	130	1	-	5/8/9/11	-
1	MLY	P	353	1	-	4/8/9/11	-
1	MLY	A	782	1	-	6/8/9/11	-
1	MLY	G	837	1	-	6/8/9/11	-
1	MLY	D	63	1	-	4/8/9/11	-
1	MLY	D	431	1	-	4/8/9/11	-
1	MLY	J	768	1	-	4/8/9/11	-
1	MLY	P	659	1	-	3/8/9/11	-
1	MLY	D	827	1	-	1/8/9/11	-
1	MLY	J	35	1	-	3/8/9/11	-
1	MLY	M	431	1	-	4/8/9/11	-
1	MLY	M	827	1	-	1/8/9/11	-
1	MLY	G	551	1	-	3/8/9/11	-
1	MLY	D	30	1	-	3/8/9/11	-
1	MLY	J	63	1	-	4/8/9/11	-
1	MLY	J	296	1	-	4/8/9/11	-
1	MLY	M	369	1	-	2/8/9/11	-
1	MLY	A	659	1	-	3/8/9/11	-
1	MLY	J	528	1	-	4/8/9/11	-
1	MLY	D	296	1	-	4/8/9/11	-
1	MLY	G	248	1	-	6/8/9/11	-
1	MLY	A	84	1	-	4/8/9/11	-
1	MLY	P	764	1	-	2/8/9/11	-
1	MLY	D	272	1	-	3/8/9/11	-
1	MLY	A	385	1	-	2/8/9/11	-
1	MLY	M	348	1	-	5/8/9/11	-
1	MLY	M	272	1	-	3/8/9/11	-
1	MLY	J	833	1	-	6/8/9/11	-
1	MLY	M	839	1	-	3/8/9/11	-
1	MLY	G	528	1	-	4/8/9/11	-
1	MLY	J	385	1	-	2/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	J	30	1	-	3/8/9/11	-
1	MLY	A	551	1	-	3/8/9/11	-
1	MLY	D	49	1	-	3/8/9/11	-
1	MLY	M	436	1	-	4/8/9/11	-
1	MLY	J	681	1	-	4/8/9/11	-
1	MLY	A	190	1	-	4/8/9/11	-
1	MLY	M	768	1	-	4/8/9/11	-
1	MLY	G	782	1	-	6/8/9/11	-
1	MLY	D	295	1	-	2/8/9/11	-
1	MLY	J	353	1	-	4/8/9/11	-
1	MLY	A	827	1	-	1/8/9/11	-
1	MLY	M	30	1	-	3/8/9/11	-
1	MLY	P	63	1	-	4/8/9/11	-
1	MLY	P	768	1	-	4/8/9/11	-
1	MLY	G	63	1	-	4/8/9/11	-
1	MLY	M	295	1	-	2/8/9/11	-
1	MLY	P	19	1	-	4/8/9/11	-
1	MLY	P	49	1	-	3/8/9/11	-
1	MLY	A	839	1	-	3/8/9/11	-
1	MLY	J	504	1	-	4/8/9/11	-
1	MLY	A	837	1	-	6/8/9/11	-
1	MLY	A	107	1	-	2/8/9/11	-
1	MLY	G	30	1	-	3/8/9/11	-
1	MLY	J	837	1	-	6/8/9/11	-
1	MLY	G	613	1	-	3/8/9/11	-
1	MLY	G	190	1	-	4/8/9/11	-
1	MLY	J	295	1	-	2/8/9/11	-
1	MLY	J	659	1	-	3/8/9/11	-
1	MLY	M	385	1	-	2/8/9/11	-
1	MLY	P	553	1	-	4/8/9/11	-
1	MLY	M	107	1	-	2/8/9/11	-
1	MLY	P	504	1	-	4/8/9/11	-
1	MLY	G	55	1	-	6/8/9/11	-
1	MLY	M	681	1	-	4/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	J	431	1	-	4/8/9/11	-
1	MLY	J	827	1	-	1/8/9/11	-
1	MLY	P	505	1	-	5/8/9/11	-
1	MLY	G	272	1	-	3/8/9/11	-
1	MLY	M	415	1	-	3/8/9/11	-
1	MLY	P	295	1	-	2/8/9/11	-
1	MLY	P	833	1	-	6/8/9/11	-
1	MLY	J	190	1	-	4/8/9/11	-
1	MLY	J	553	1	-	4/8/9/11	-
1	MLY	D	248	1	-	6/8/9/11	-
1	MLY	A	600	1	-	3/8/9/11	-
1	MLY	M	130	1	-	5/8/9/11	-
1	MLY	P	107	1	-	2/8/9/11	-
1	MLY	G	617	1	-	2/8/9/11	-
1	MLY	G	764	1	-	2/8/9/11	-
1	MLY	A	63	1	-	4/8/9/11	-
1	MLY	G	553	4,1	-	4/8/9/11	-
1	MLY	M	367	1	-	2/8/9/11	-
1	MLY	D	528	1	-	4/8/9/11	-
1	MLY	P	367	1	-	2/8/9/11	-
1	MLY	P	551	1	-	3/8/9/11	-
1	MLY	M	505	1	-	5/8/9/11	-
1	MLY	D	659	1	-	3/8/9/11	-
1	MLY	M	598	1	-	5/8/9/11	-
1	MLY	D	385	1	-	2/8/9/11	-
1	MLY	M	19	1	-	4/8/9/11	-
1	MLY	M	49	1	-	3/8/9/11	-
1	MLY	A	768	1	-	4/8/9/11	-
1	MLY	D	190	1	-	4/8/9/11	-
1	MLY	A	553	4,1	-	4/8/9/11	-
1	MLY	D	436	1	-	4/8/9/11	-
1	MLY	D	87	1	-	2/8/9/11	-
1	MLY	D	551	1	-	3/8/9/11	-
1	MLY	G	431	1	-	4/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	M	236	1	-	3/8/9/11	-
1	MLY	M	551	1	-	3/8/9/11	-
1	MLY	A	505	1	-	5/8/9/11	-
1	MLY	A	369	1	-	2/8/9/11	-
1	MLY	D	764	1	-	2/8/9/11	-
1	MLY	D	598	1	-	5/8/9/11	-
1	MLY	M	35	1	-	3/8/9/11	-
1	MLY	P	248	1	-	6/8/9/11	-
1	MLY	A	367	1	-	2/8/9/11	-
1	MLY	G	367	1	-	2/8/9/11	-
1	MLY	A	353	1	-	4/8/9/11	-
1	MLY	G	827	1	-	1/8/9/11	-
1	MLY	A	348	1	-	5/8/9/11	-
1	MLY	M	504	1	-	4/8/9/11	-
1	MLY	P	681	1	-	4/8/9/11	-
1	MLY	P	827	1	-	1/8/9/11	-
1	MLY	P	84	1	-	4/8/9/11	-
1	MLY	A	30	1	-	3/8/9/11	-
1	MLY	G	369	1	-	2/8/9/11	-
1	MLY	A	504	1	-	4/8/9/11	-
1	MLY	J	87	1	-	2/8/9/11	-
1	MLY	P	528	1	-	4/8/9/11	-
1	MLY	P	130	1	-	5/8/9/11	-
1	MLY	J	415	1	-	3/8/9/11	-
1	MLY	J	598	1	-	5/8/9/11	-
1	MLY	M	833	1	-	6/8/9/11	-
1	MLY	G	348	1	-	5/8/9/11	-
1	MLY	D	837	1	-	6/8/9/11	-
1	MLY	G	839	1	-	3/8/9/11	-
1	MLY	P	236	1	-	3/8/9/11	-
1	MLY	A	55	1	-	6/8/9/11	-
1	MLY	G	833	1	-	6/8/9/11	-
1	MLY	M	296	1	-	4/8/9/11	-
1	MLY	J	55	1	-	6/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	G	436	1	-	4/8/9/11	-
1	MLY	M	59	1	-	3/8/9/11	-
1	MLY	M	87	1	-	2/8/9/11	-
1	MLY	A	431	1	-	4/8/9/11	-
1	MLY	A	19	1	-	4/8/9/11	-
1	MLY	P	138	1	-	4/8/9/11	-
1	MLY	J	272	1	-	3/8/9/11	-
1	MLY	D	486	1	-	2/8/9/11	-
1	MLY	P	617	1	-	2/8/9/11	-
1	MLY	J	130	1	-	5/8/9/11	-
1	MLY	D	35	1	-	3/8/9/11	-
1	MLY	J	84	1	-	4/8/9/11	-
1	MLY	A	598	1	-	5/8/9/11	-
1	MLY	A	248	1	-	6/8/9/11	-
1	MLY	A	617	1	-	2/8/9/11	-
1	MLY	M	659	1	-	3/8/9/11	-
1	MLY	J	107	1	-	2/8/9/11	-
1	MLY	P	296	1	-	4/8/9/11	-
1	MLY	J	617	1	-	2/8/9/11	-
1	MLY	G	236	1	-	3/8/9/11	-
1	MLY	J	248	1	-	6/8/9/11	-
1	MLY	P	385	1	-	2/8/9/11	-
1	MLY	G	353	1	-	4/8/9/11	-
1	MLY	P	613	1	-	3/8/9/11	-
1	MLY	A	296	1	-	4/8/9/11	-
1	MLY	P	272	1	-	3/8/9/11	-
1	MLY	D	833	1	-	6/8/9/11	-
1	MLY	G	295	1	-	2/8/9/11	-
1	MLY	J	369	1	-	2/8/9/11	-
1	MLY	M	248	1	-	6/8/9/11	-
1	MLY	P	431	1	-	4/8/9/11	-
1	MLY	M	190	1	-	4/8/9/11	-
1	MLY	D	613	1	-	3/8/9/11	-
1	MLY	G	681	1	-	4/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	M	55	1	-	6/8/9/11	-
1	MLY	P	436	1	-	4/8/9/11	-
1	MLY	G	49	1	-	3/8/9/11	-
1	MLY	M	84	1	-	4/8/9/11	-
1	MLY	D	553	4,1	-	5/8/9/11	-
1	MLY	J	59	1	-	3/8/9/11	-
1	MLY	D	504	1	-	4/8/9/11	-
1	MLY	D	59	1	-	3/8/9/11	-
1	MLY	M	528	1	-	4/8/9/11	-
1	MLY	J	486	1	-	2/8/9/11	-
1	MLY	D	55	1	-	6/8/9/11	-
1	MLY	J	839	1	-	3/8/9/11	-
1	MLY	P	415	1	-	3/8/9/11	-
1	MLY	M	553	1	-	4/8/9/11	-
1	MLY	A	138	1	-	4/8/9/11	-
1	MLY	G	768	1	-	4/8/9/11	-
1	MLY	J	436	1	-	4/8/9/11	-
1	MLY	J	600	1	-	3/8/9/11	-
1	MLY	M	782	1	-	6/8/9/11	-
1	MLY	G	35	1	-	3/8/9/11	-
1	MLY	D	353	1	-	4/8/9/11	-
1	MLY	A	59	1	-	3/8/9/11	-
1	MLY	D	348	1	-	5/8/9/11	-
1	MLY	M	63	1	-	4/8/9/11	-
1	MLY	D	839	1	-	3/8/9/11	-

The worst 5 of 87 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	138	MLY	CB-CA	-3.28	1.48	1.53
1	G	138	MLY	CB-CA	-3.23	1.48	1.53
1	J	138	MLY	CB-CA	-3.21	1.48	1.53
1	A	138	MLY	CB-CA	-3.17	1.48	1.53
1	M	138	MLY	CB-CA	-3.17	1.48	1.53

There are no bond angle outliers.

There are no chirality outliers.

5 of 967 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	19	MLY	C-CA-CB-CG
1	A	49	MLY	N-CA-CB-CG
1	A	49	MLY	C-CA-CB-CG
1	A	55	MLY	N-CA-CB-CG
1	A	55	MLY	C-CA-CB-CG

There are no ring outliers.

183 monomers are involved in 776 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	107	MLY	3	0
1	G	505	MLY	1	0
1	A	528	MLY	3	0
1	A	87	MLY	3	0
1	P	782	MLY	1	0
1	P	837	MLY	1	0
1	A	272	MLY	1	0
1	M	600	MLY	1	0
1	D	415	MLY	1	0
1	P	598	MLY	1	0
1	A	49	MLY	4	0
1	A	436	MLY	2	0
1	G	84	MLY	22	0
1	P	486	MLY	3	0
1	G	59	MLY	2	0
1	P	369	MLY	1	0
1	A	764	MLY	11	0
1	A	295	MLY	6	0
1	D	600	MLY	1	0
1	J	138	MLY	1	0
1	P	55	MLY	1	0
1	J	764	MLY	5	0
1	P	348	MLY	6	0
1	P	839	MLY	12	0
1	D	617	MLY	1	0
1	M	617	MLY	1	0
1	G	415	MLY	1	0
1	M	764	MLY	8	0
1	P	600	MLY	1	0
1	G	659	MLY	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	G	138	MLY	1	0
1	G	486	MLY	3	0
1	G	598	MLY	1	0
1	J	505	MLY	9	0
1	G	107	MLY	3	0
1	P	30	MLY	1	0
1	J	782	MLY	1	0
1	P	59	MLY	2	0
1	G	296	MLY	3	0
1	P	87	MLY	3	0
1	D	138	MLY	1	0
1	D	768	MLY	1	0
1	G	87	MLY	2	0
1	D	782	MLY	67	0
1	M	138	MLY	1	0
1	D	369	MLY	1	0
1	J	348	MLY	6	0
1	J	49	MLY	2	0
1	A	415	MLY	1	0
1	M	486	MLY	3	0
1	P	190	MLY	2	0
1	A	486	MLY	3	0
1	M	837	MLY	1	0
1	G	600	MLY	1	0
1	A	782	MLY	8	0
1	G	837	MLY	1	0
1	D	63	MLY	3	0
1	J	768	MLY	8	0
1	P	659	MLY	2	0
1	D	827	MLY	3	0
1	D	30	MLY	1	0
1	J	63	MLY	3	0
1	J	296	MLY	3	0
1	A	659	MLY	2	0
1	J	528	MLY	3	0
1	D	296	MLY	2	0
1	G	248	MLY	2	0
1	P	764	MLY	6	0
1	D	272	MLY	1	0
1	M	348	MLY	5	0
1	M	272	MLY	1	0
1	M	839	MLY	12	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	G	528	MLY	2	0
1	J	30	MLY	1	0
1	A	551	MLY	2	0
1	D	49	MLY	3	0
1	M	436	MLY	2	0
1	A	190	MLY	2	0
1	M	768	MLY	9	0
1	G	782	MLY	1	0
1	D	295	MLY	6	0
1	M	30	MLY	1	0
1	P	63	MLY	3	0
1	P	768	MLY	14	0
1	G	63	MLY	3	0
1	M	295	MLY	5	0
1	P	49	MLY	3	0
1	A	839	MLY	8	0
1	A	837	MLY	3	0
1	A	107	MLY	2	0
1	G	30	MLY	1	0
1	J	837	MLY	1	0
1	G	190	MLY	2	0
1	J	295	MLY	7	0
1	J	659	MLY	2	0
1	P	553	MLY	2	0
1	M	107	MLY	3	0
1	G	55	MLY	1	0
1	P	505	MLY	21	0
1	G	272	MLY	1	0
1	M	415	MLY	1	0
1	P	295	MLY	6	0
1	J	190	MLY	2	0
1	J	553	MLY	12	0
1	D	248	MLY	2	0
1	A	600	MLY	1	0
1	P	107	MLY	3	0
1	G	617	MLY	1	0
1	G	764	MLY	19	0
1	A	63	MLY	3	0
1	G	553	MLY	27	0
1	D	528	MLY	3	0
1	M	505	MLY	28	0
1	D	659	MLY	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	M	598	MLY	1	0
1	M	49	MLY	4	0
1	A	768	MLY	12	0
1	D	190	MLY	2	0
1	A	553	MLY	17	0
1	D	436	MLY	2	0
1	D	87	MLY	2	0
1	D	551	MLY	2	0
1	A	505	MLY	26	0
1	D	764	MLY	8	0
1	D	598	MLY	1	0
1	P	248	MLY	2	0
1	G	827	MLY	1	0
1	A	348	MLY	6	0
1	A	30	MLY	1	0
1	A	504	MLY	1	0
1	J	87	MLY	3	0
1	P	528	MLY	3	0
1	J	415	MLY	1	0
1	J	598	MLY	1	0
1	G	348	MLY	6	0
1	D	837	MLY	1	0
1	G	839	MLY	4	0
1	A	55	MLY	1	0
1	M	296	MLY	3	0
1	J	55	MLY	1	0
1	G	436	MLY	2	0
1	M	59	MLY	3	0
1	M	87	MLY	2	0
1	P	138	MLY	1	0
1	J	272	MLY	1	0
1	D	486	MLY	3	0
1	P	617	MLY	1	0
1	J	84	MLY	36	0
1	A	598	MLY	1	0
1	A	248	MLY	2	0
1	A	617	MLY	1	0
1	M	659	MLY	2	0
1	J	107	MLY	2	0
1	P	296	MLY	3	0
1	J	617	MLY	1	0
1	J	248	MLY	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	296	MLY	3	0
1	P	272	MLY	1	0
1	G	295	MLY	7	0
1	J	369	MLY	1	0
1	M	248	MLY	2	0
1	M	190	MLY	2	0
1	M	55	MLY	1	0
1	P	436	MLY	3	0
1	G	49	MLY	2	0
1	D	553	MLY	18	0
1	J	59	MLY	2	0
1	D	59	MLY	3	0
1	M	528	MLY	3	0
1	J	486	MLY	3	0
1	D	55	MLY	1	0
1	J	839	MLY	13	0
1	P	415	MLY	1	0
1	M	553	MLY	3	0
1	A	138	MLY	1	0
1	G	768	MLY	9	0
1	J	436	MLY	2	0
1	J	600	MLY	1	0
1	M	782	MLY	1	0
1	A	59	MLY	3	0
1	D	348	MLY	5	0
1	M	63	MLY	4	0
1	D	839	MLY	4	0

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	P	6
1	M	5
1	D	4
1	A	4
1	J	3
1	G	3
3	C	1
3	F	1
3	I	1
3	L	1
3	O	1
3	R	1
2	B	1
2	E	1
2	H	1
2	K	1
2	N	1
2	Q	1

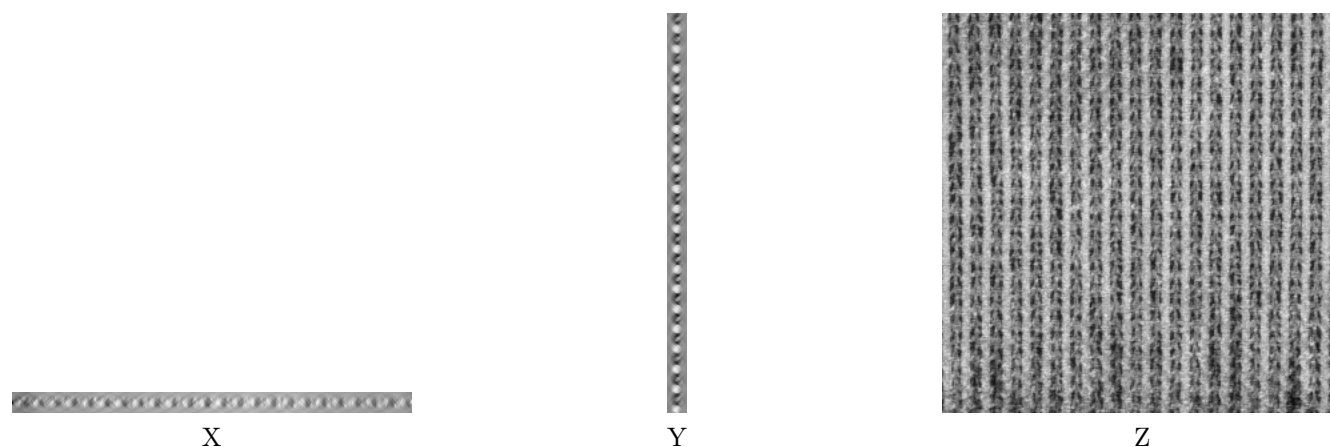
The worst 5 of 37 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	769:ALA	C	770:GLY	N	5.51
1	D	769:ALA	C	770:GLY	N	5.10
1	G	769:ALA	C	770:GLY	N	4.94
1	D	709:LYS	C	710:GLY	N	3.10
1	M	709:LYS	C	710:GLY	N	3.05

6 Tomogram visualisation [i](#)

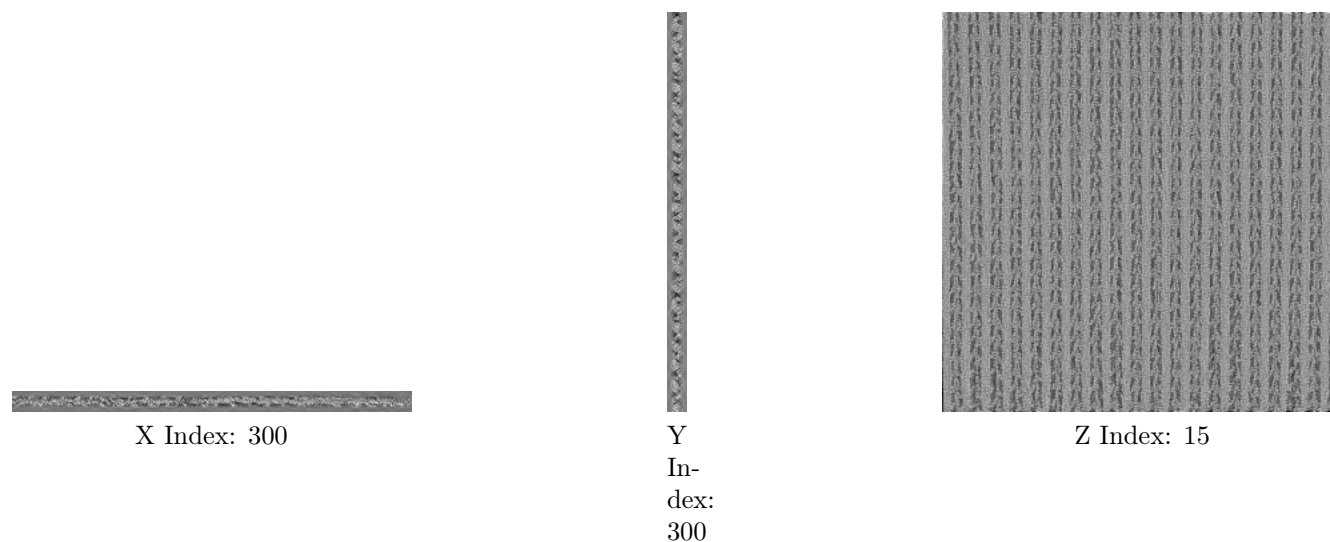
This section contains visualisations of the EMDB entry EMD-1001. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

6.1 Orthogonal projections [i](#)



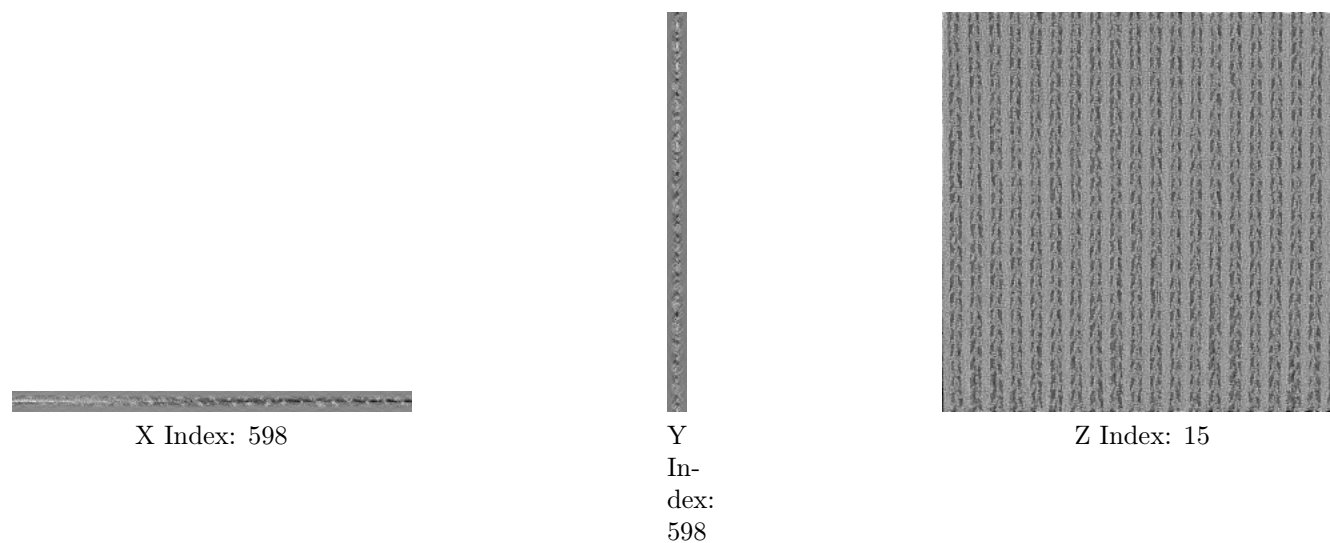
The images above show the tomogram projected in three orthogonal directions.

6.2 Central slices [i](#)



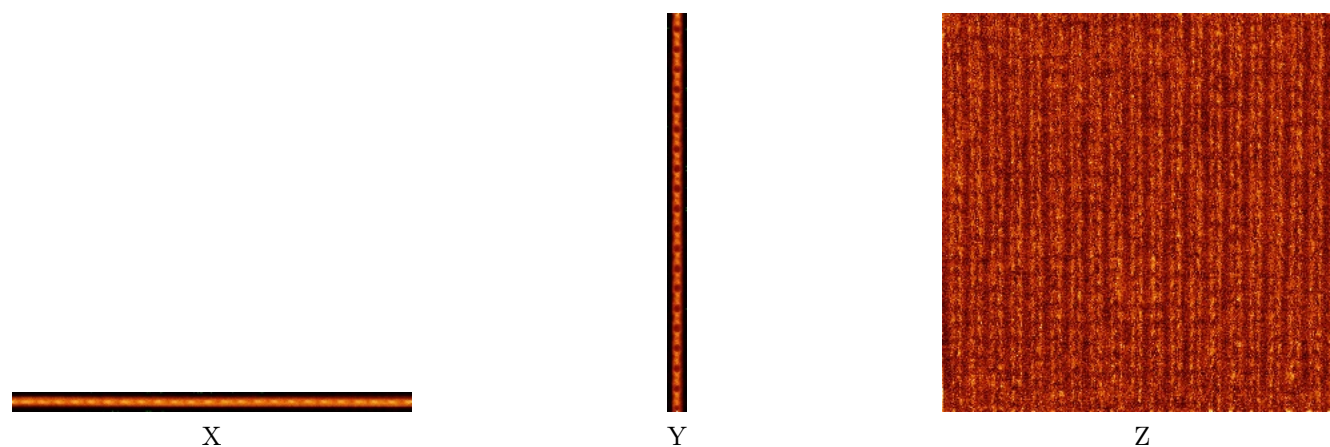
The images above show central slices of the tomogram in three orthogonal directions.

6.3 Largest variance slices [i](#)



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

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



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

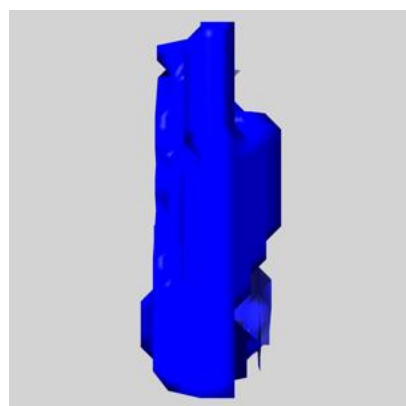
6.5 Mask visualisation [i](#)

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

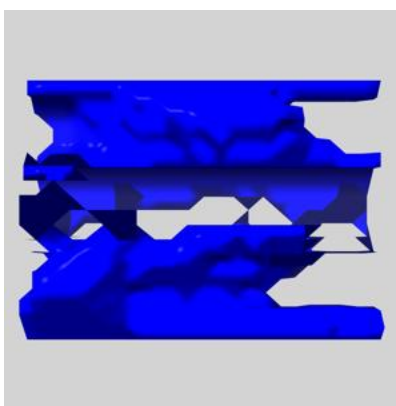
A mask typically either:

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

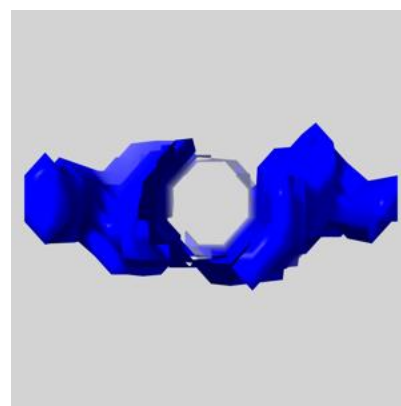
6.5.1 emd_1001_msk_25.map [i](#)



X

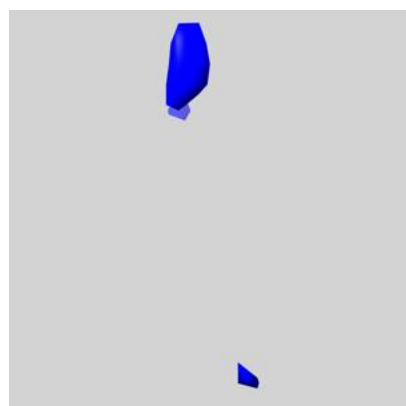


Y

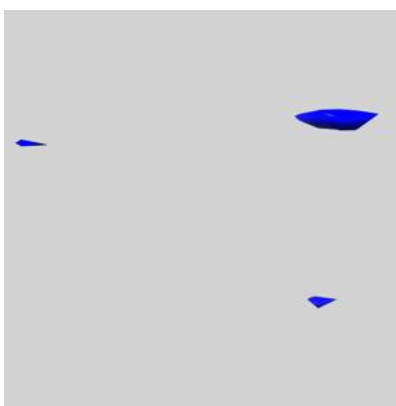


Z

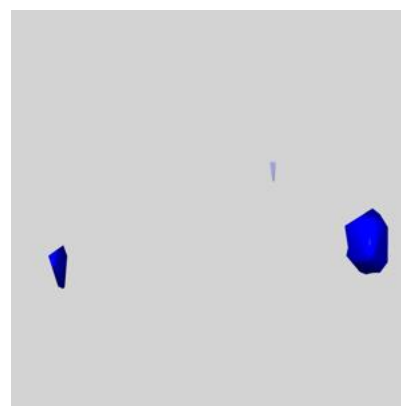
6.5.2 emd_1001_msk_24.map [i](#)



X

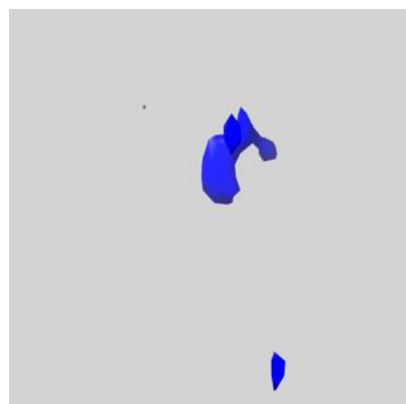


Y

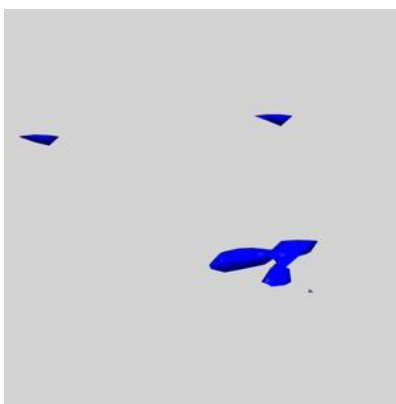


Z

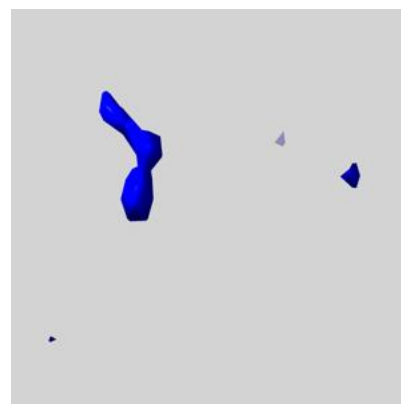
6.5.3 emd_1001_msk_23.map [i](#)



X

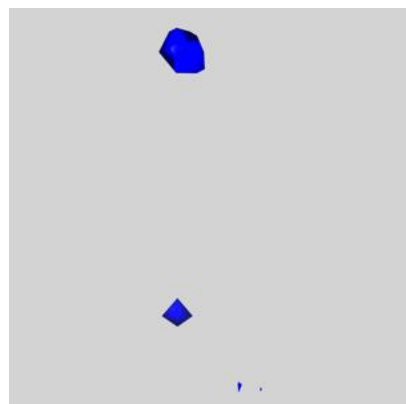


Y

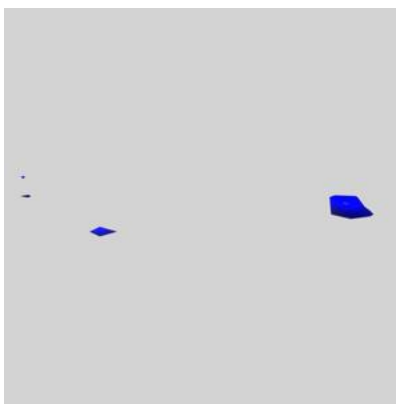


Z

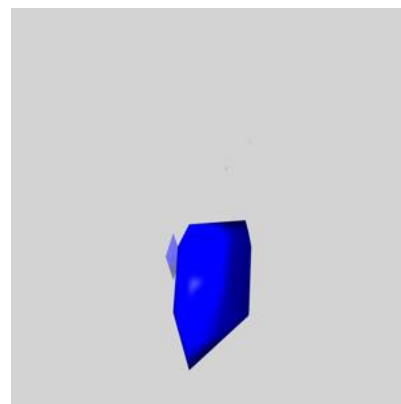
6.5.4 emd_1001_msk_22.map [i](#)



X

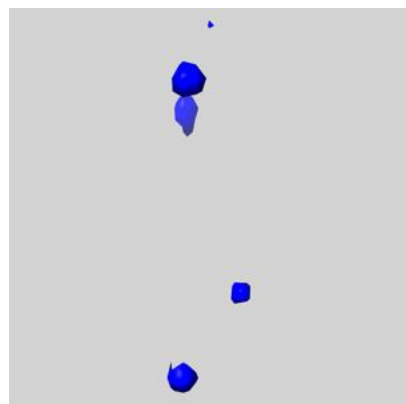


Y

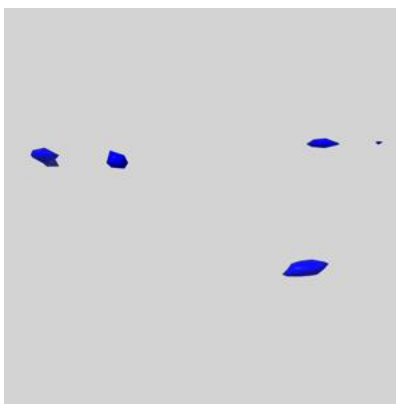


Z

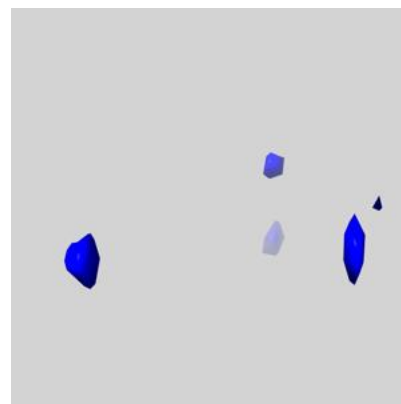
6.5.5 emd_1001_msk_21.map [i](#)



X

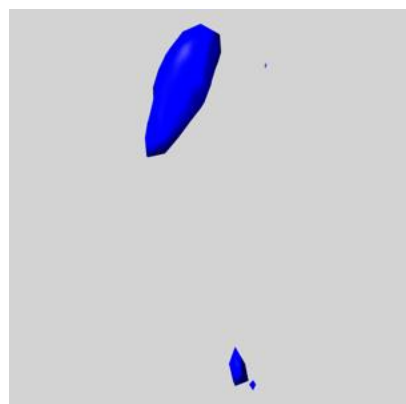


Y

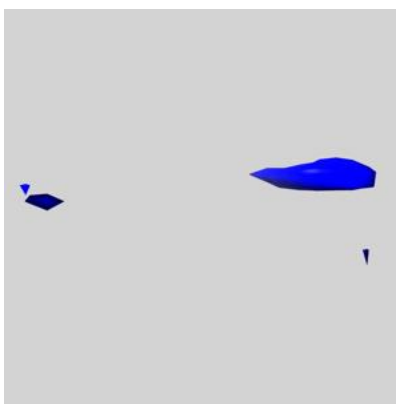


Z

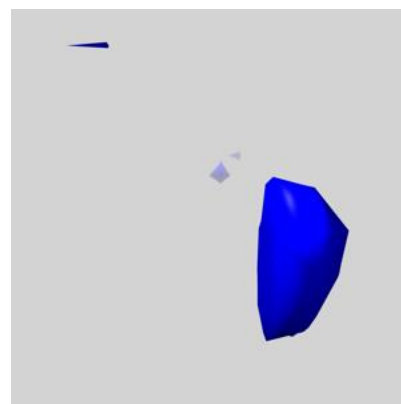
6.5.6 emd_1001_msk_20.map [i](#)



X

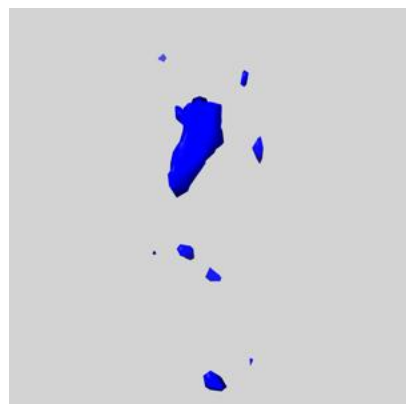


Y

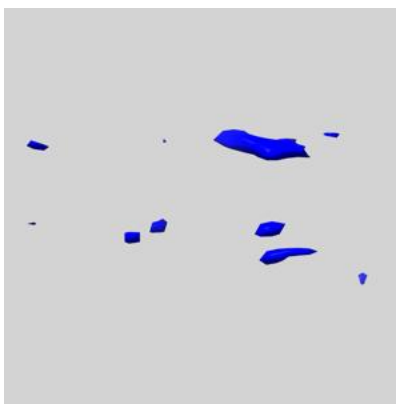


Z

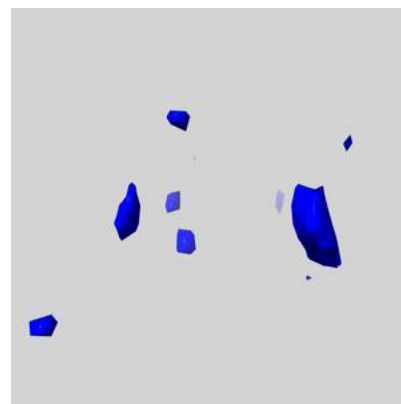
6.5.7 emd_1001_msk_19.map [i](#)



X

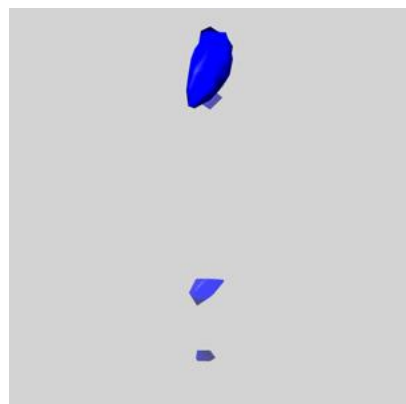


Y

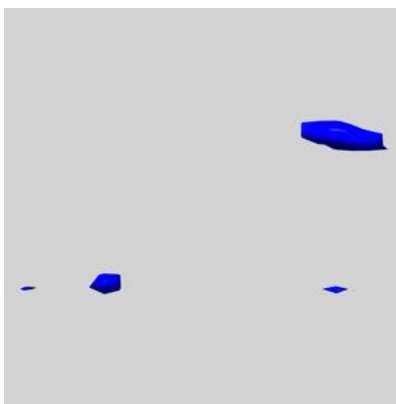


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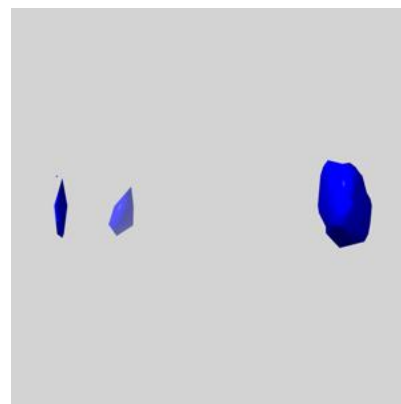
6.5.8 emd_1001_msk_18.map [i](#)



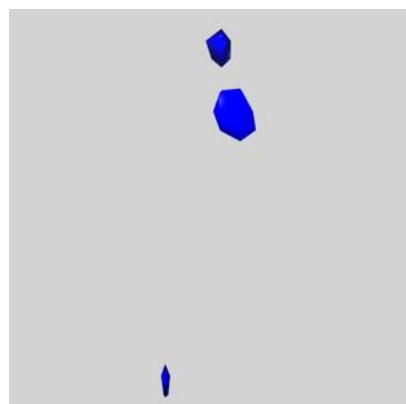
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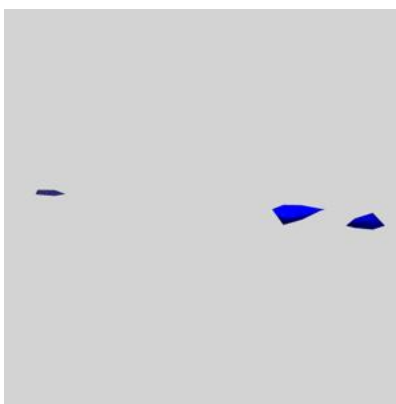
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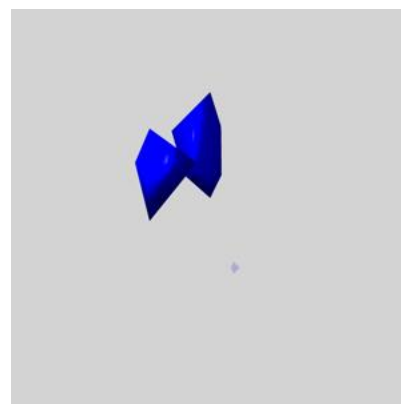
Z

6.5.9 emd_1001_msk_17.map [i](#)

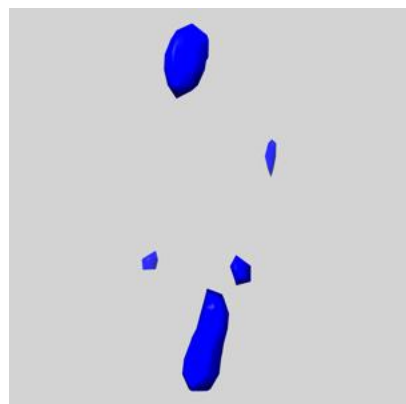
X



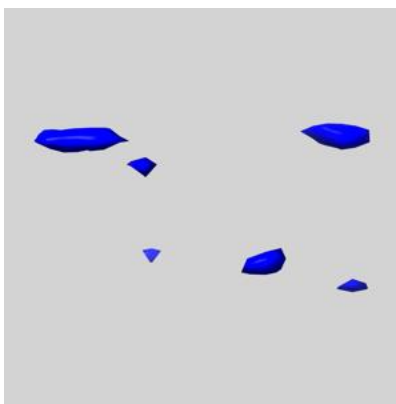
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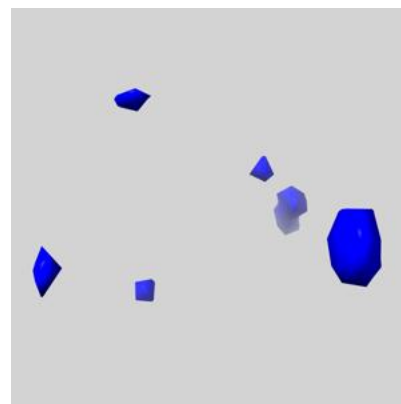
Z

6.5.10 emd_1001_msk_16.map [i](#)

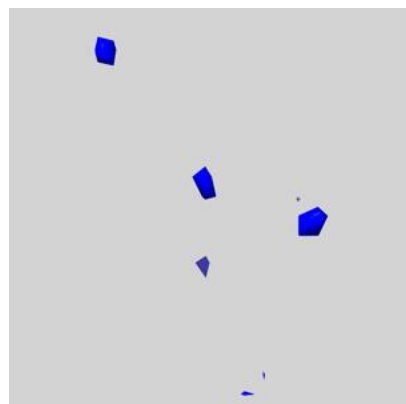
X



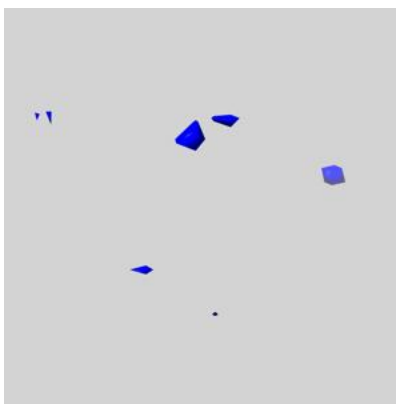
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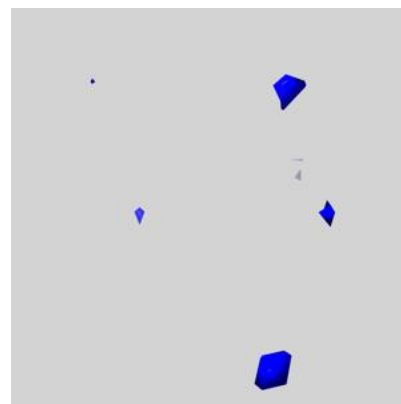
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6.5.11 emd_1001_msk_15.map [i](#)

X

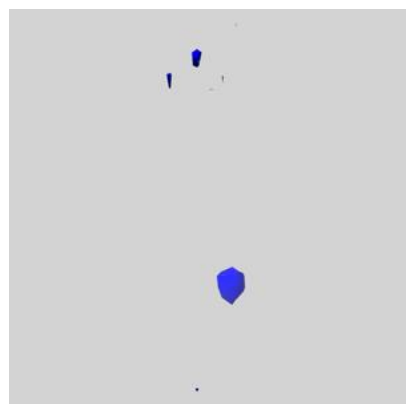


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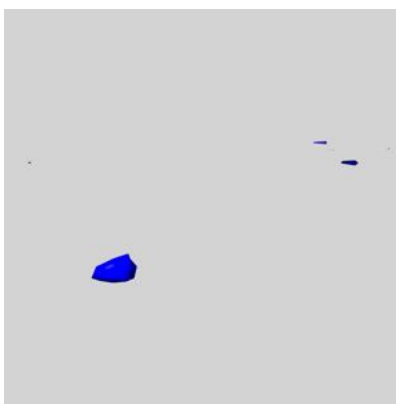


Z

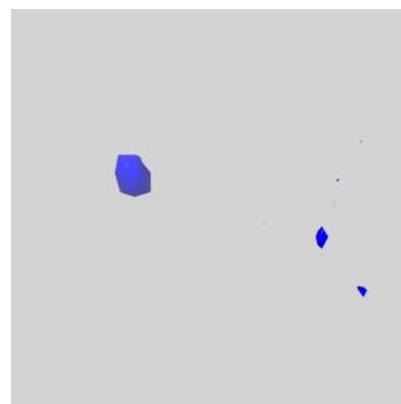
6.5.12 emd_1001_msk_14.map [i](#)



X

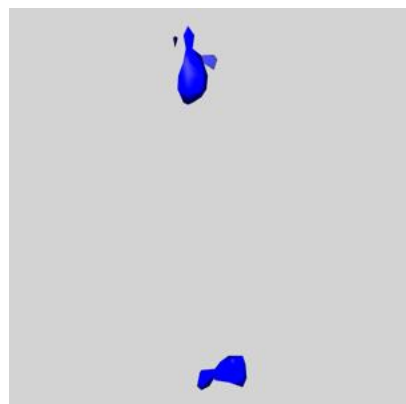


Y

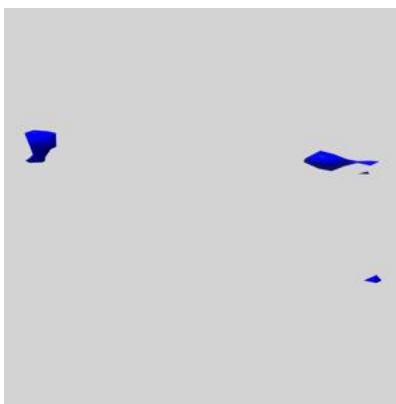


Z

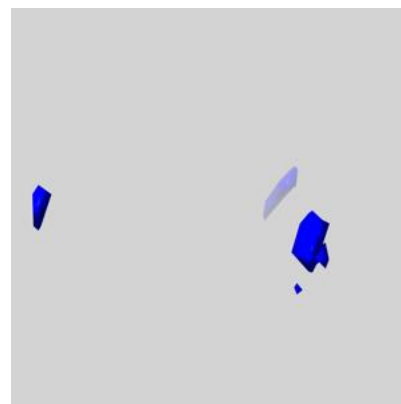
6.5.13 emd_1001_msk_13.map [i](#)



X

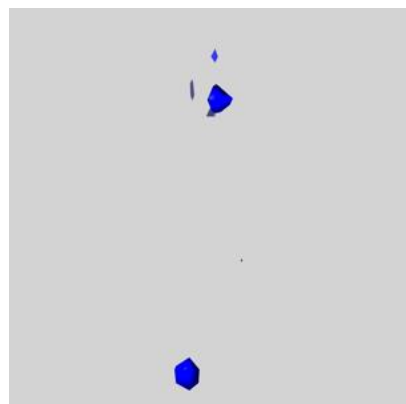


Y

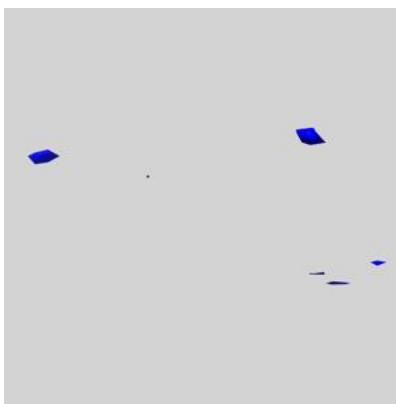


Z

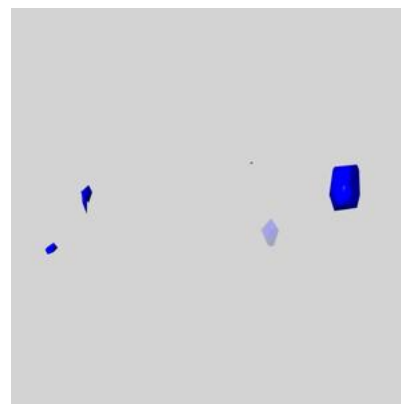
6.5.14 emd_1001_msk_12.map [i](#)



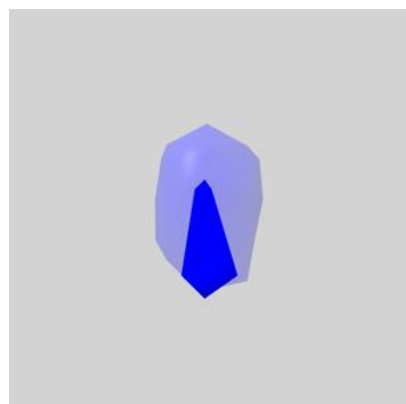
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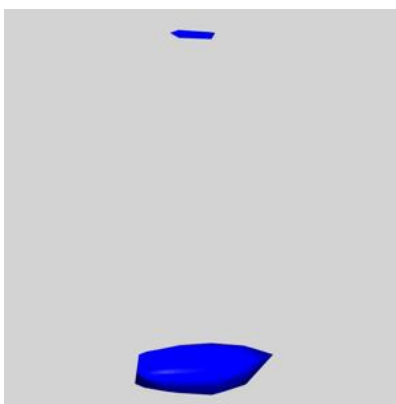
Y



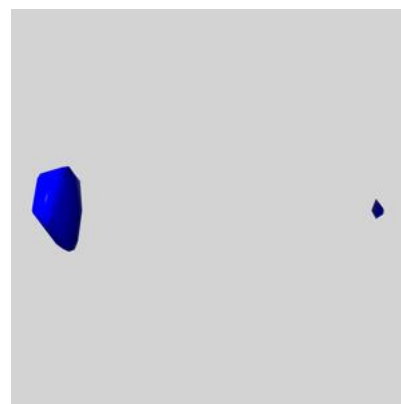
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6.5.15 emd_1001_msk_11.map [i](#)

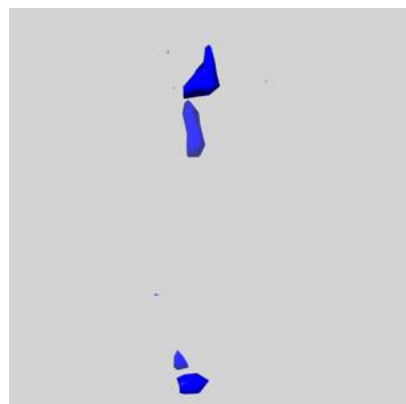
X



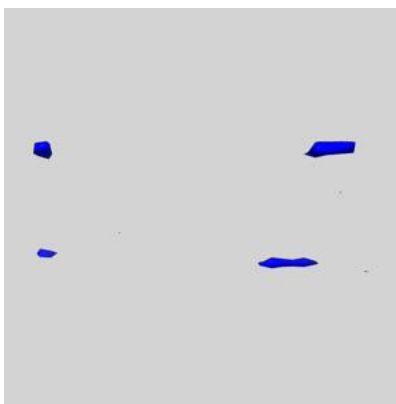
Y



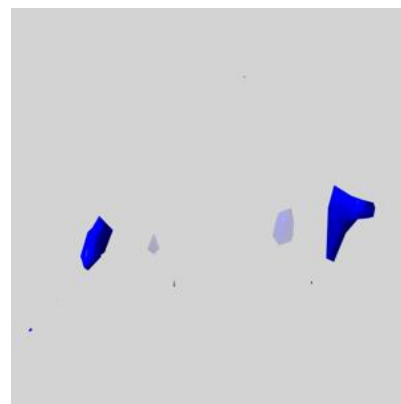
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6.5.16 emd_1001_msk_10.map [i](#)

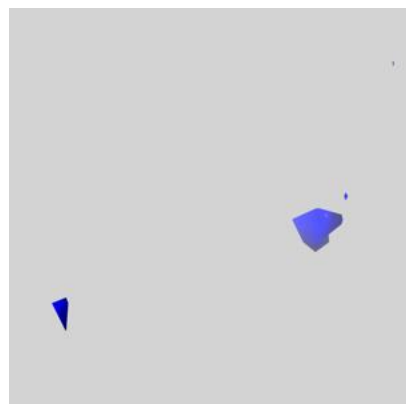
X



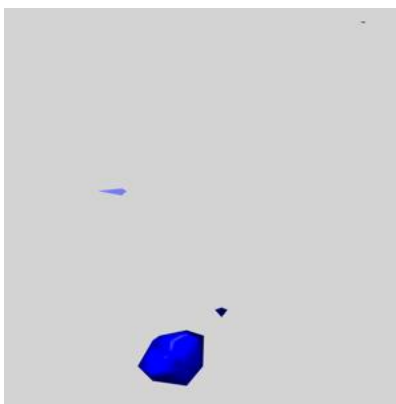
Y



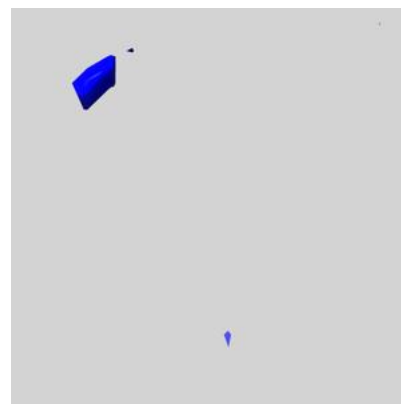
Z

6.5.17 emd_1001_msk_9.map [i](#)

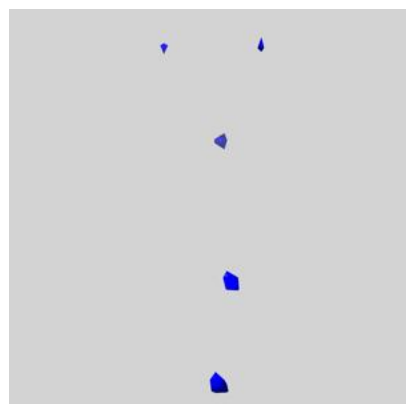
X



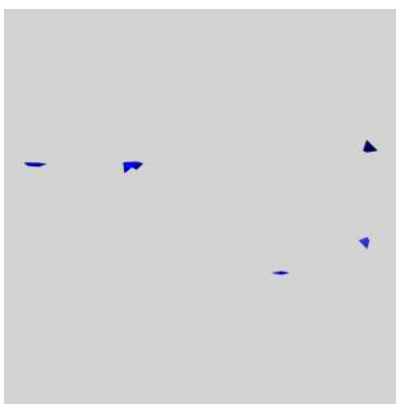
Y



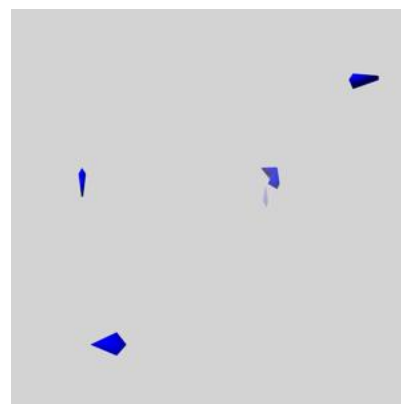
Z

6.5.18 emd_1001_msk_8.map [i](#)

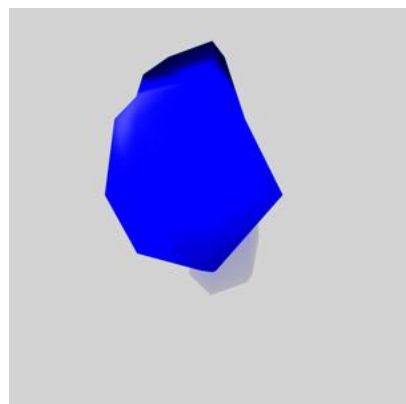
X



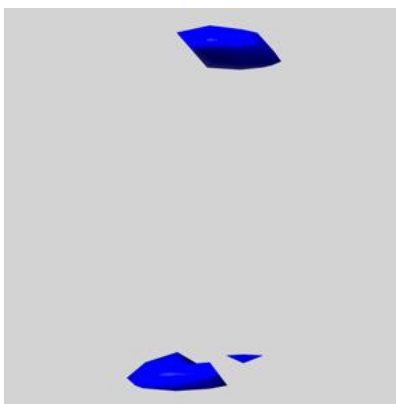
Y



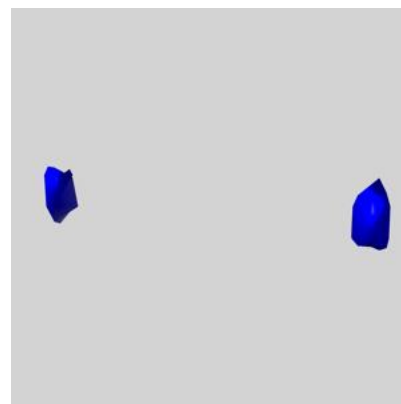
Z

6.5.19 emd_1001_msk_7.map [i](#)

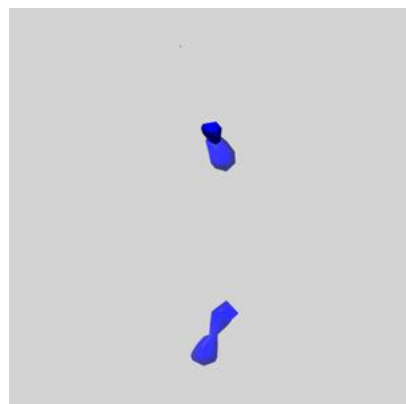
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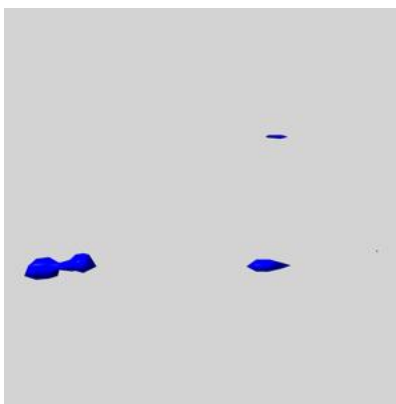
Y



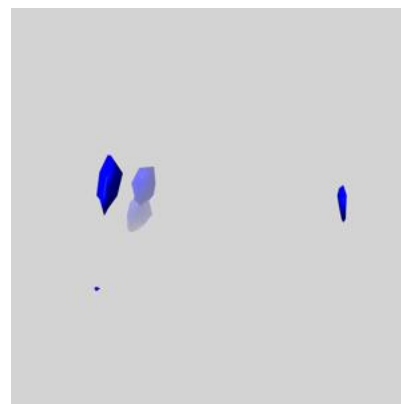
Z

6.5.20 emd_1001_msk_6.map [i](#)

X

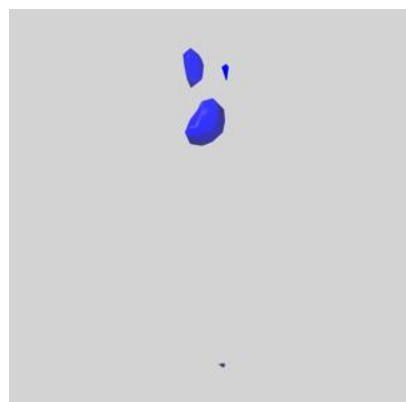


Y

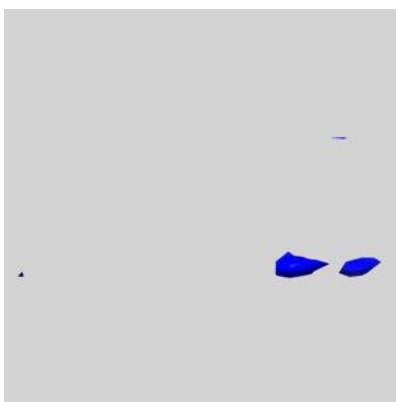


Z

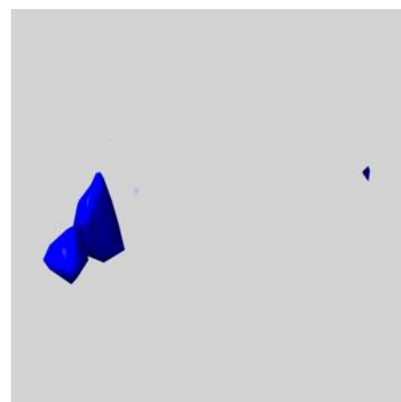
6.5.21 emd_1001_msk_5.map [i](#)



X

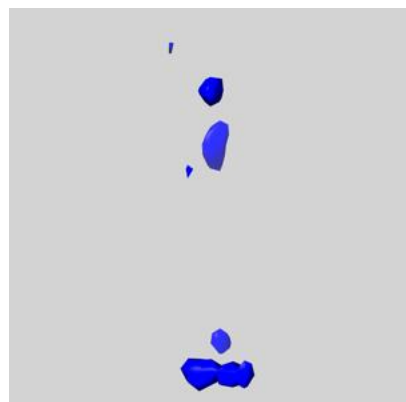


Y

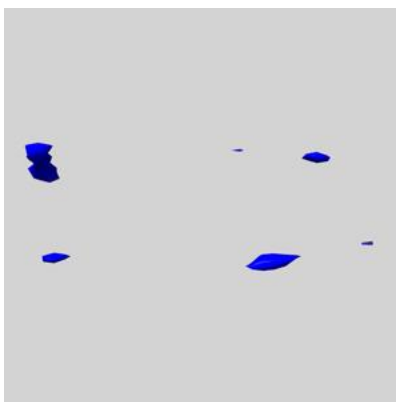


Z

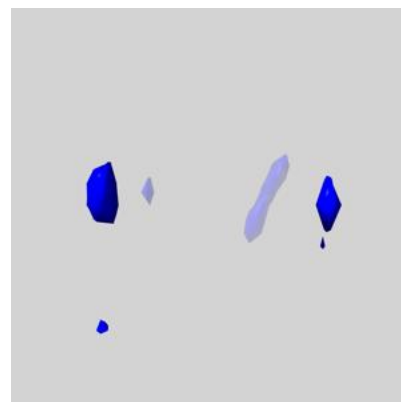
6.5.22 emd_1001_msk_4.map [i](#)



X

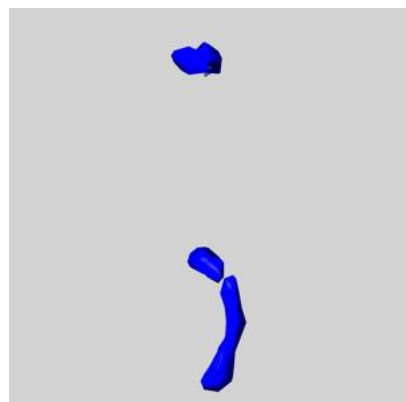


Y

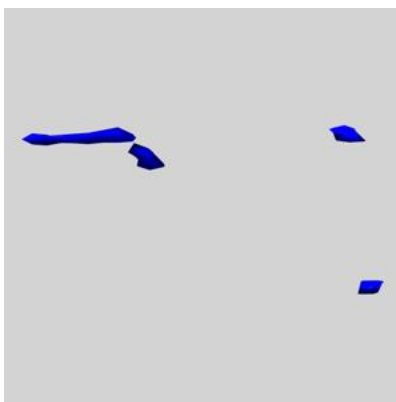


Z

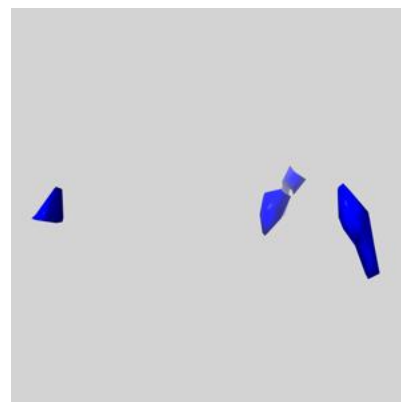
6.5.23 emd_1001_msk_3.map [i](#)



X

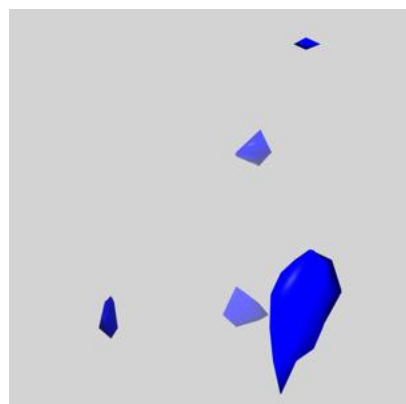


Y

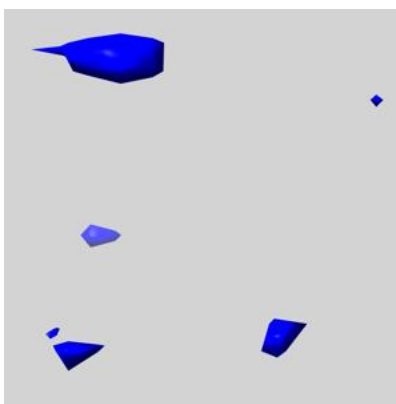


Z

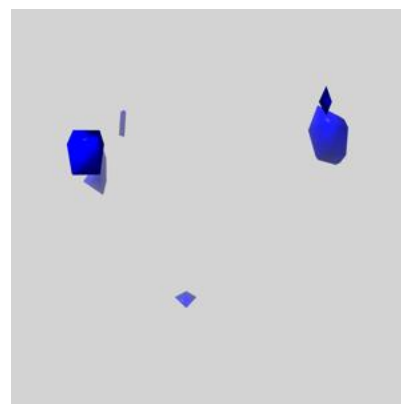
6.5.24 emd_1001_msk_2.map [i](#)



X

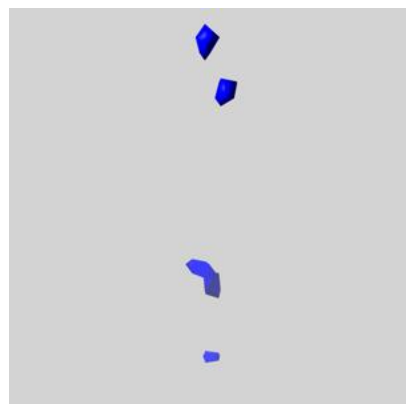


Y

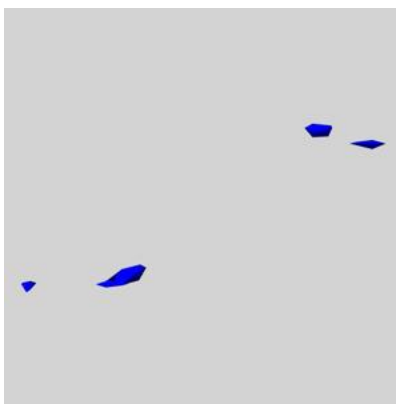


Z

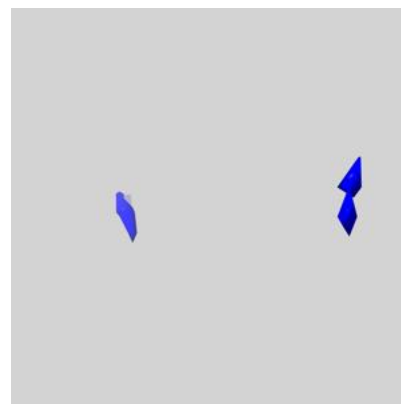
6.5.25 emd_1001_msk_1.map [i](#)



X

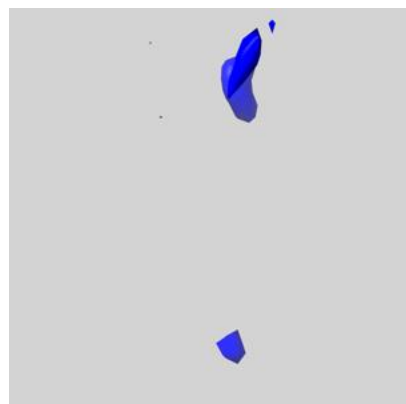


Y

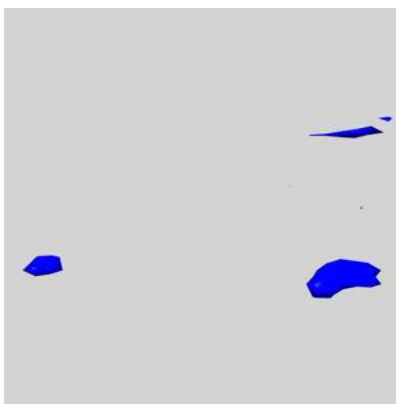


Z

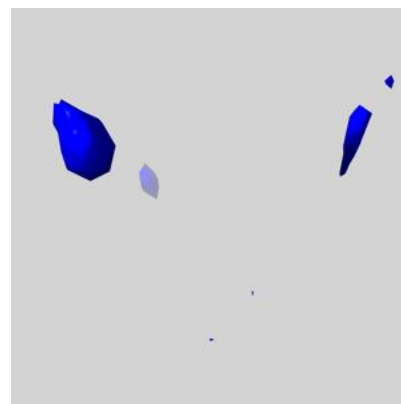
6.5.26 emd_1001_msk_26.map [i](#)



X



Y

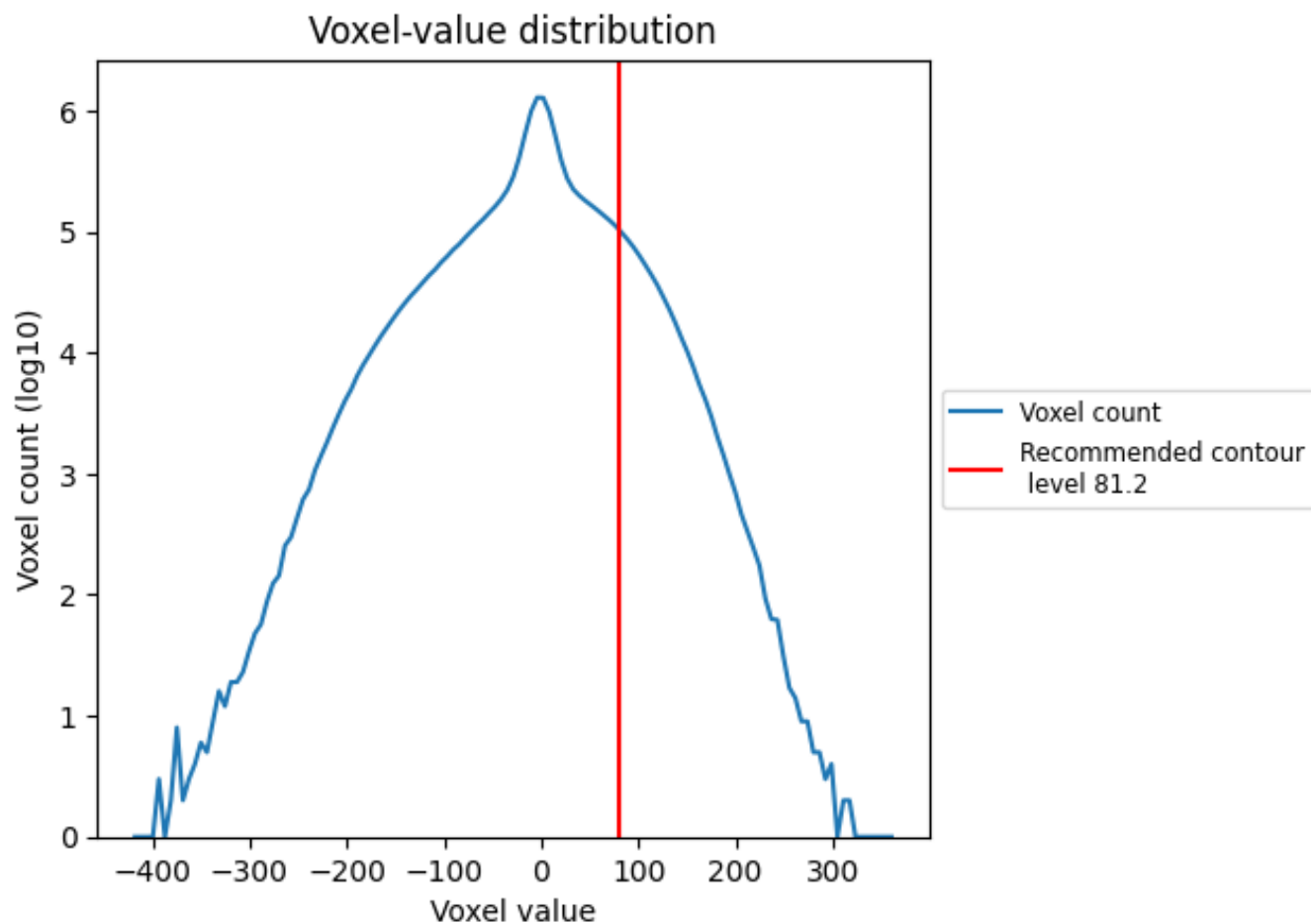


Z

7 Tomogram analysis [i](#)

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

7.1 Voxel-value distribution [i](#)



The voxel-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic.

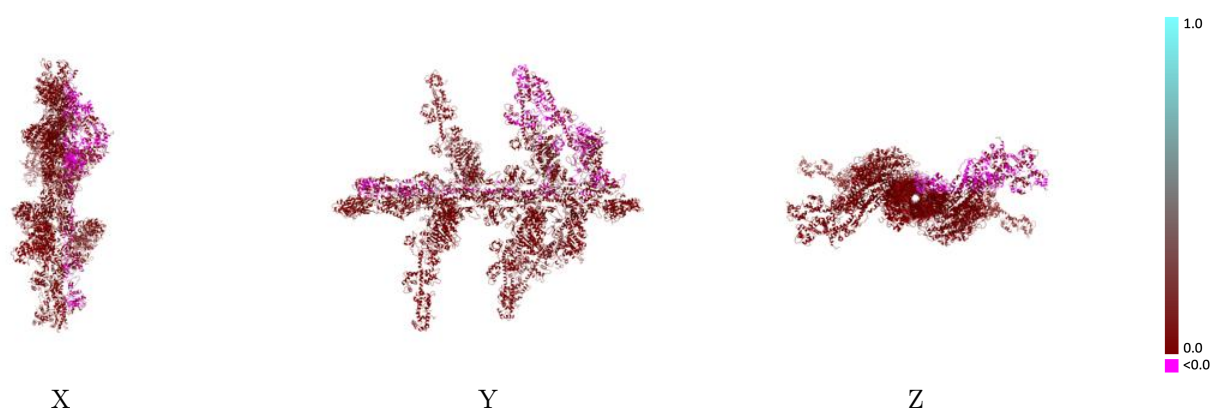
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1001 and PDB model 1MVW. Per-residue inclusion information can be found in section 3 on page 7.

8.1 Map-model overlay [i](#)

This section was not generated.

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

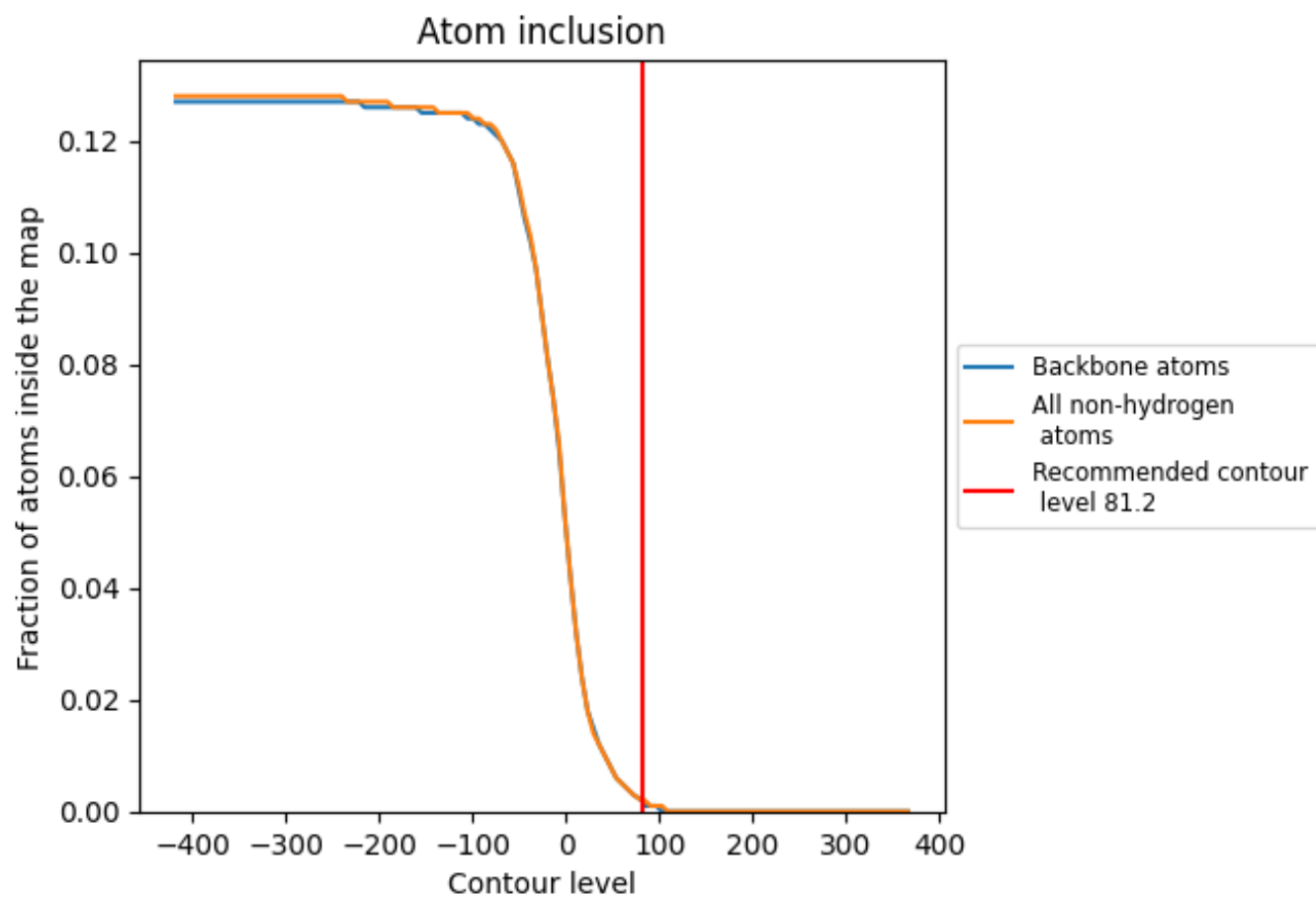


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.



































































8.4 Atom inclusion [i](#)



At the recommended contour level, 0% of all backbone atoms, 0% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (81.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.0020	 -0.0010
1	 0.0000	 0.0040
2	 0.0000	 0.0000
3	 0.0000	 -0.0070
4	 0.0000	 0.0000
5	 0.0000	 -0.0080
6	 0.0000	 0.0000
7	 0.0000	 0.0000
8	 0.0000	 -0.0010
9	 0.0000	 -0.0030
A	 0.0000	 -0.0100
B	 0.0000	 -0.0040
C	 0.0000	 0.0220
D	 0.0000	 0.0000
E	 0.0000	 0.0000
F	 0.0000	 0.0000
G	 0.0000	 0.0040
H	 0.0000	 0.0010
I	 0.0580	 0.0020
J	 0.0000	 0.0000
K	 0.0000	 0.0000
L	 0.0000	 0.0000
M	 0.0000	 0.0000
N	 0.0000	 0.0000
O	 0.0000	 0.0000
P	 0.0000	 -0.0000
Q	 0.0000	 0.0000
R	 0.0000	 0.0000
V	 0.0000	 0.0010
W	 0.0000	 -0.0000
X	 0.0000	 0.0000
Y	 0.0370	 0.0030
Z	 0.0000	 0.0000

