



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 03:55 AM UTC

PDB ID : 6G2I / pdb_00006g2i
EMDB ID : EMD-4344
Title : Filament of acetyl-CoA carboxylase and BRCT domains of BRCA1 (ACC-BRCT) at 5.9 Å resolution
Authors : Hunkeler, M.; Hagmann, A.; Stutfeld, E.; Chami, M.; Stahlberg, H.; Maier, T.
Deposited on : 2018-03-23
Resolution : 5.90 Å(reported)

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:

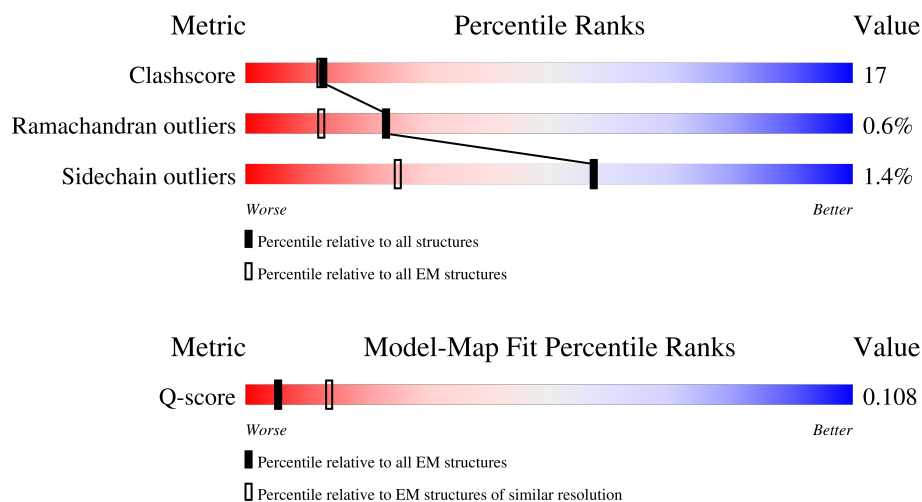
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 5.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	501 (5.40 - 6.40)

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	2346	65% 57% 29% 11%
1	B	2346	65% 56% 30% 11%
1	C	2346	45% 53% 33% 11%
1	D	2346	27% 47% 36% 5% 11%

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Mol	Chain	Length	Quality of chain
1	E	2346	
1	F	2346	
1	G	2346	
1	J	2346	
1	Q	2346	
1	R	2346	
2	H	240	
2	K	240	
2	M	240	
2	O	240	
2	S	240	
2	U	240	
2	W	240	
2	Y	240	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 288810 atoms, of which 143374 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 Acetyl-CoA carboxylase 1.

Mol	Chain	Residues	Atoms							AltConf	Trace
1	D	2080	Total	C	H	N	O	P	S	0	0
			32758	10493	16276	2855	3033	1	100		
1	E	2080	Total	C	H	N	O	P	S	0	0
			32758	10493	16276	2855	3033	1	100		
1	C	2080	Total	C	H	N	O	P	S	0	0
			32757	10493	16275	2855	3033	1	100		
1	F	2080	Total	C	H	N	O	P	S	0	0
			32757	10493	16275	2855	3033	1	100		
1	B	2080	Total	C	H	N	O	P	S	0	0
			32758	10493	16276	2855	3033	1	100		
1	A	2080	Total	C	H	N	O	P	S	0	0
			32758	10493	16276	2855	3033	1	100		
1	G	757	Total	C	H	N	O	S		0	0
			12055	3855	5997	1050	1124	29			
1	Q	757	Total	C	H	N	O	S		0	0
			12055	3855	5997	1050	1124	29			
1	J	1323	Total	C	H	N	O	P	S	0	0
			20703	6638	10279	1805	1909	1	71		
1	R	1323	Total	C	H	N	O	P	S	0	0
			20703	6638	10279	1805	1909	1	71		

- Molecule 2 is a protein called Breast cancer type 1 susceptibility protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	H	214	Total	C	H	N	O	S	0	0
			3347	1084	1648	289	312	14		
2	K	214	Total	C	H	N	O	S	0	0
			3340	1083	1644	286	313	14		
2	M	214	Total	C	H	N	O	S	0	0
			3347	1084	1648	289	312	14		
2	O	214	Total	C	H	N	O	S	0	0
			3340	1083	1644	286	313	14		
2	S	214	Total	C	H	N	O	S	0	0
			3347	1084	1648	289	312	14		

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Mol	Chain	Residues	Atoms						AltConf	Trace
2	U	214	Total	C	H	N	O	S	0	0
			3340	1083	1644	286	313	14		
2	Y	214	Total	C	H	N	O	S	0	0
			3347	1084	1648	289	312	14		
2	W	214	Total	C	H	N	O	S	0	0
			3340	1083	1644	286	313	14		

There are 208 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	1620	MET	-	initiating methionine	UNP P38398
H	1621	LYS	-	expression tag	UNP P38398
H	1622	HIS	-	expression tag	UNP P38398
H	1623	HIS	-	expression tag	UNP P38398
H	1624	HIS	-	expression tag	UNP P38398
H	1625	HIS	-	expression tag	UNP P38398
H	1626	HIS	-	expression tag	UNP P38398
H	1627	HIS	-	expression tag	UNP P38398
H	1628	PRO	-	expression tag	UNP P38398
H	1629	MET	-	expression tag	UNP P38398
H	1630	THR	-	expression tag	UNP P38398
H	1631	SER	-	expression tag	UNP P38398
H	1632	LEU	-	expression tag	UNP P38398
H	1633	TYR	-	expression tag	UNP P38398
H	1634	LYS	-	expression tag	UNP P38398
H	1635	LYS	-	expression tag	UNP P38398
H	1636	ALA	-	expression tag	UNP P38398
H	1637	GLY	-	expression tag	UNP P38398
H	1638	LEU	-	expression tag	UNP P38398
H	1639	GLU	-	expression tag	UNP P38398
H	1640	ASN	-	expression tag	UNP P38398
H	1641	LEU	-	expression tag	UNP P38398
H	1642	TYR	-	expression tag	UNP P38398
H	1643	PHE	-	expression tag	UNP P38398
H	1644	GLN	-	expression tag	UNP P38398
H	1645	GLY	-	expression tag	UNP P38398
K	1620	MET	-	initiating methionine	UNP P38398
K	1621	LYS	-	expression tag	UNP P38398
K	1622	HIS	-	expression tag	UNP P38398
K	1623	HIS	-	expression tag	UNP P38398
K	1624	HIS	-	expression tag	UNP P38398
K	1625	HIS	-	expression tag	UNP P38398

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Chain	Residue	Modelled	Actual	Comment	Reference
K	1626	HIS	-	expression tag	UNP P38398
K	1627	HIS	-	expression tag	UNP P38398
K	1628	PRO	-	expression tag	UNP P38398
K	1629	MET	-	expression tag	UNP P38398
K	1630	THR	-	expression tag	UNP P38398
K	1631	SER	-	expression tag	UNP P38398
K	1632	LEU	-	expression tag	UNP P38398
K	1633	TYR	-	expression tag	UNP P38398
K	1634	LYS	-	expression tag	UNP P38398
K	1635	LYS	-	expression tag	UNP P38398
K	1636	ALA	-	expression tag	UNP P38398
K	1637	GLY	-	expression tag	UNP P38398
K	1638	LEU	-	expression tag	UNP P38398
K	1639	GLU	-	expression tag	UNP P38398
K	1640	ASN	-	expression tag	UNP P38398
K	1641	LEU	-	expression tag	UNP P38398
K	1642	TYR	-	expression tag	UNP P38398
K	1643	PHE	-	expression tag	UNP P38398
K	1644	GLN	-	expression tag	UNP P38398
K	1645	GLY	-	expression tag	UNP P38398
M	1620	MET	-	initiating methionine	UNP P38398
M	1621	LYS	-	expression tag	UNP P38398
M	1622	HIS	-	expression tag	UNP P38398
M	1623	HIS	-	expression tag	UNP P38398
M	1624	HIS	-	expression tag	UNP P38398
M	1625	HIS	-	expression tag	UNP P38398
M	1626	HIS	-	expression tag	UNP P38398
M	1627	HIS	-	expression tag	UNP P38398
M	1628	PRO	-	expression tag	UNP P38398
M	1629	MET	-	expression tag	UNP P38398
M	1630	THR	-	expression tag	UNP P38398
M	1631	SER	-	expression tag	UNP P38398
M	1632	LEU	-	expression tag	UNP P38398
M	1633	TYR	-	expression tag	UNP P38398
M	1634	LYS	-	expression tag	UNP P38398
M	1635	LYS	-	expression tag	UNP P38398
M	1636	ALA	-	expression tag	UNP P38398
M	1637	GLY	-	expression tag	UNP P38398
M	1638	LEU	-	expression tag	UNP P38398
M	1639	GLU	-	expression tag	UNP P38398
M	1640	ASN	-	expression tag	UNP P38398
M	1641	LEU	-	expression tag	UNP P38398

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Chain	Residue	Modelled	Actual	Comment	Reference
M	1642	TYR	-	expression tag	UNP P38398
M	1643	PHE	-	expression tag	UNP P38398
M	1644	GLN	-	expression tag	UNP P38398
M	1645	GLY	-	expression tag	UNP P38398
O	1620	MET	-	initiating methionine	UNP P38398
O	1621	LYS	-	expression tag	UNP P38398
O	1622	HIS	-	expression tag	UNP P38398
O	1623	HIS	-	expression tag	UNP P38398
O	1624	HIS	-	expression tag	UNP P38398
O	1625	HIS	-	expression tag	UNP P38398
O	1626	HIS	-	expression tag	UNP P38398
O	1627	HIS	-	expression tag	UNP P38398
O	1628	PRO	-	expression tag	UNP P38398
O	1629	MET	-	expression tag	UNP P38398
O	1630	THR	-	expression tag	UNP P38398
O	1631	SER	-	expression tag	UNP P38398
O	1632	LEU	-	expression tag	UNP P38398
O	1633	TYR	-	expression tag	UNP P38398
O	1634	LYS	-	expression tag	UNP P38398
O	1635	LYS	-	expression tag	UNP P38398
O	1636	ALA	-	expression tag	UNP P38398
O	1637	GLY	-	expression tag	UNP P38398
O	1638	LEU	-	expression tag	UNP P38398
O	1639	GLU	-	expression tag	UNP P38398
O	1640	ASN	-	expression tag	UNP P38398
O	1641	LEU	-	expression tag	UNP P38398
O	1642	TYR	-	expression tag	UNP P38398
O	1643	PHE	-	expression tag	UNP P38398
O	1644	GLN	-	expression tag	UNP P38398
O	1645	GLY	-	expression tag	UNP P38398
S	1620	MET	-	initiating methionine	UNP P38398
S	1621	LYS	-	expression tag	UNP P38398
S	1622	HIS	-	expression tag	UNP P38398
S	1623	HIS	-	expression tag	UNP P38398
S	1624	HIS	-	expression tag	UNP P38398
S	1625	HIS	-	expression tag	UNP P38398
S	1626	HIS	-	expression tag	UNP P38398
S	1627	HIS	-	expression tag	UNP P38398
S	1628	PRO	-	expression tag	UNP P38398
S	1629	MET	-	expression tag	UNP P38398
S	1630	THR	-	expression tag	UNP P38398
S	1631	SER	-	expression tag	UNP P38398

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Chain	Residue	Modelled	Actual	Comment	Reference
S	1632	LEU	-	expression tag	UNP P38398
S	1633	TYR	-	expression tag	UNP P38398
S	1634	LYS	-	expression tag	UNP P38398
S	1635	LYS	-	expression tag	UNP P38398
S	1636	ALA	-	expression tag	UNP P38398
S	1637	GLY	-	expression tag	UNP P38398
S	1638	LEU	-	expression tag	UNP P38398
S	1639	GLU	-	expression tag	UNP P38398
S	1640	ASN	-	expression tag	UNP P38398
S	1641	LEU	-	expression tag	UNP P38398
S	1642	TYR	-	expression tag	UNP P38398
S	1643	PHE	-	expression tag	UNP P38398
S	1644	GLN	-	expression tag	UNP P38398
S	1645	GLY	-	expression tag	UNP P38398
U	1620	MET	-	initiating methionine	UNP P38398
U	1621	LYS	-	expression tag	UNP P38398
U	1622	HIS	-	expression tag	UNP P38398
U	1623	HIS	-	expression tag	UNP P38398
U	1624	HIS	-	expression tag	UNP P38398
U	1625	HIS	-	expression tag	UNP P38398
U	1626	HIS	-	expression tag	UNP P38398
U	1627	HIS	-	expression tag	UNP P38398
U	1628	PRO	-	expression tag	UNP P38398
U	1629	MET	-	expression tag	UNP P38398
U	1630	THR	-	expression tag	UNP P38398
U	1631	SER	-	expression tag	UNP P38398
U	1632	LEU	-	expression tag	UNP P38398
U	1633	TYR	-	expression tag	UNP P38398
U	1634	LYS	-	expression tag	UNP P38398
U	1635	LYS	-	expression tag	UNP P38398
U	1636	ALA	-	expression tag	UNP P38398
U	1637	GLY	-	expression tag	UNP P38398
U	1638	LEU	-	expression tag	UNP P38398
U	1639	GLU	-	expression tag	UNP P38398
U	1640	ASN	-	expression tag	UNP P38398
U	1641	LEU	-	expression tag	UNP P38398
U	1642	TYR	-	expression tag	UNP P38398
U	1643	PHE	-	expression tag	UNP P38398
U	1644	GLN	-	expression tag	UNP P38398
U	1645	GLY	-	expression tag	UNP P38398
Y	1620	MET	-	initiating methionine	UNP P38398
Y	1621	LYS	-	expression tag	UNP P38398

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Chain	Residue	Modelled	Actual	Comment	Reference
Y	1622	HIS	-	expression tag	UNP P38398
Y	1623	HIS	-	expression tag	UNP P38398
Y	1624	HIS	-	expression tag	UNP P38398
Y	1625	HIS	-	expression tag	UNP P38398
Y	1626	HIS	-	expression tag	UNP P38398
Y	1627	HIS	-	expression tag	UNP P38398
Y	1628	PRO	-	expression tag	UNP P38398
Y	1629	MET	-	expression tag	UNP P38398
Y	1630	THR	-	expression tag	UNP P38398
Y	1631	SER	-	expression tag	UNP P38398
Y	1632	LEU	-	expression tag	UNP P38398
Y	1633	TYR	-	expression tag	UNP P38398
Y	1634	LYS	-	expression tag	UNP P38398
Y	1635	LYS	-	expression tag	UNP P38398
Y	1636	ALA	-	expression tag	UNP P38398
Y	1637	GLY	-	expression tag	UNP P38398
Y	1638	LEU	-	expression tag	UNP P38398
Y	1639	GLU	-	expression tag	UNP P38398
Y	1640	ASN	-	expression tag	UNP P38398
Y	1641	LEU	-	expression tag	UNP P38398
Y	1642	TYR	-	expression tag	UNP P38398
Y	1643	PHE	-	expression tag	UNP P38398
Y	1644	GLN	-	expression tag	UNP P38398
Y	1645	GLY	-	expression tag	UNP P38398
W	1620	MET	-	initiating methionine	UNP P38398
W	1621	LYS	-	expression tag	UNP P38398
W	1622	HIS	-	expression tag	UNP P38398
W	1623	HIS	-	expression tag	UNP P38398
W	1624	HIS	-	expression tag	UNP P38398
W	1625	HIS	-	expression tag	UNP P38398
W	1626	HIS	-	expression tag	UNP P38398
W	1627	HIS	-	expression tag	UNP P38398
W	1628	PRO	-	expression tag	UNP P38398
W	1629	MET	-	expression tag	UNP P38398
W	1630	THR	-	expression tag	UNP P38398
W	1631	SER	-	expression tag	UNP P38398
W	1632	LEU	-	expression tag	UNP P38398
W	1633	TYR	-	expression tag	UNP P38398
W	1634	LYS	-	expression tag	UNP P38398
W	1635	LYS	-	expression tag	UNP P38398
W	1636	ALA	-	expression tag	UNP P38398
W	1637	GLY	-	expression tag	UNP P38398

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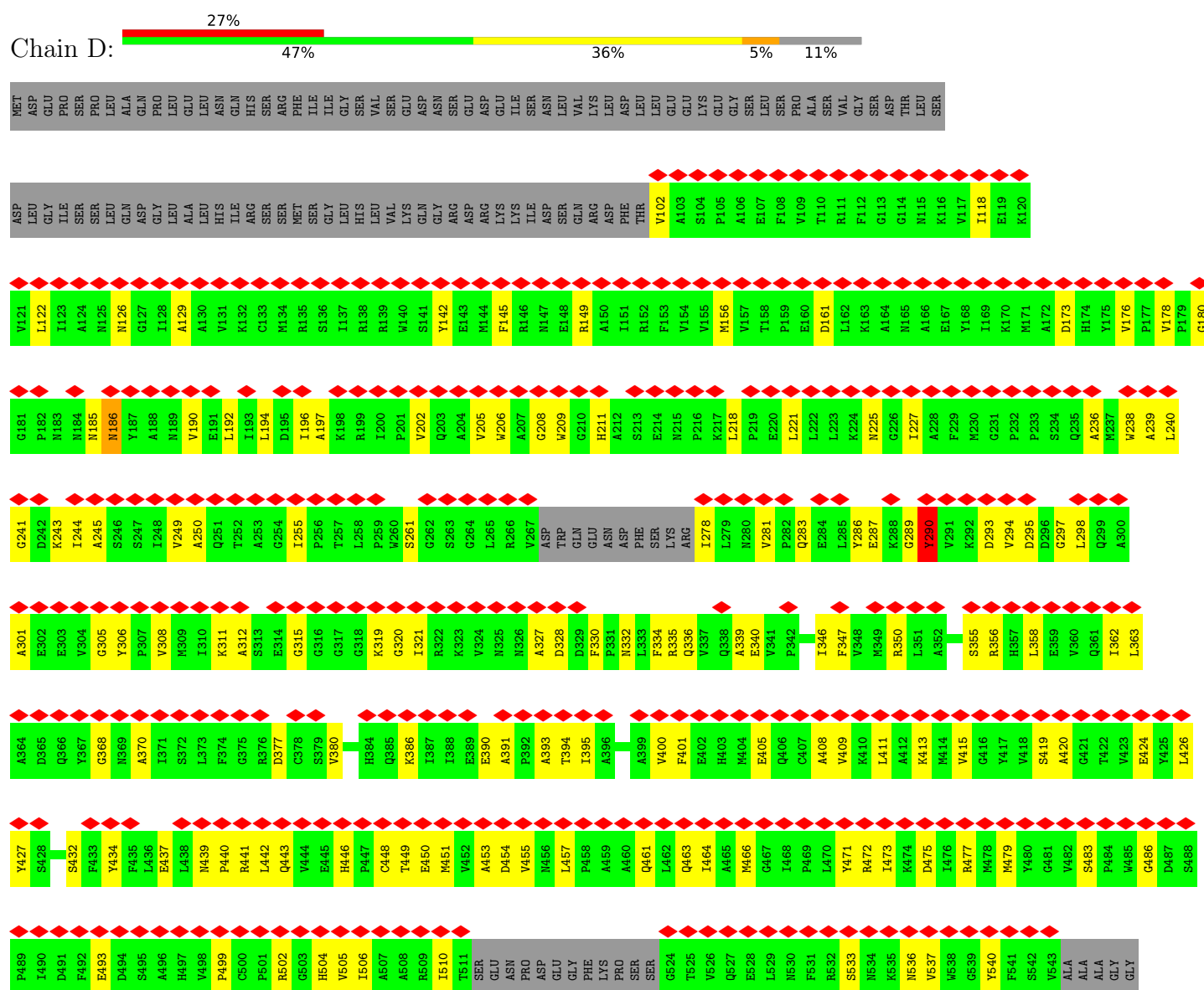
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Chain	Residue	Modelled	Actual	Comment	Reference
W	1638	LEU	-	expression tag	UNP P38398
W	1639	GLU	-	expression tag	UNP P38398
W	1640	ASN	-	expression tag	UNP P38398
W	1641	LEU	-	expression tag	UNP P38398
W	1642	TYR	-	expression tag	UNP P38398
W	1643	PHE	-	expression tag	UNP P38398
W	1644	GLN	-	expression tag	UNP P38398
W	1645	GLY	-	expression tag	UNP P38398

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.

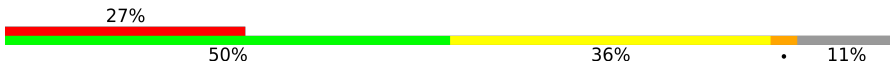
• Molecule 1: Acetyl-CoA carboxylase 1



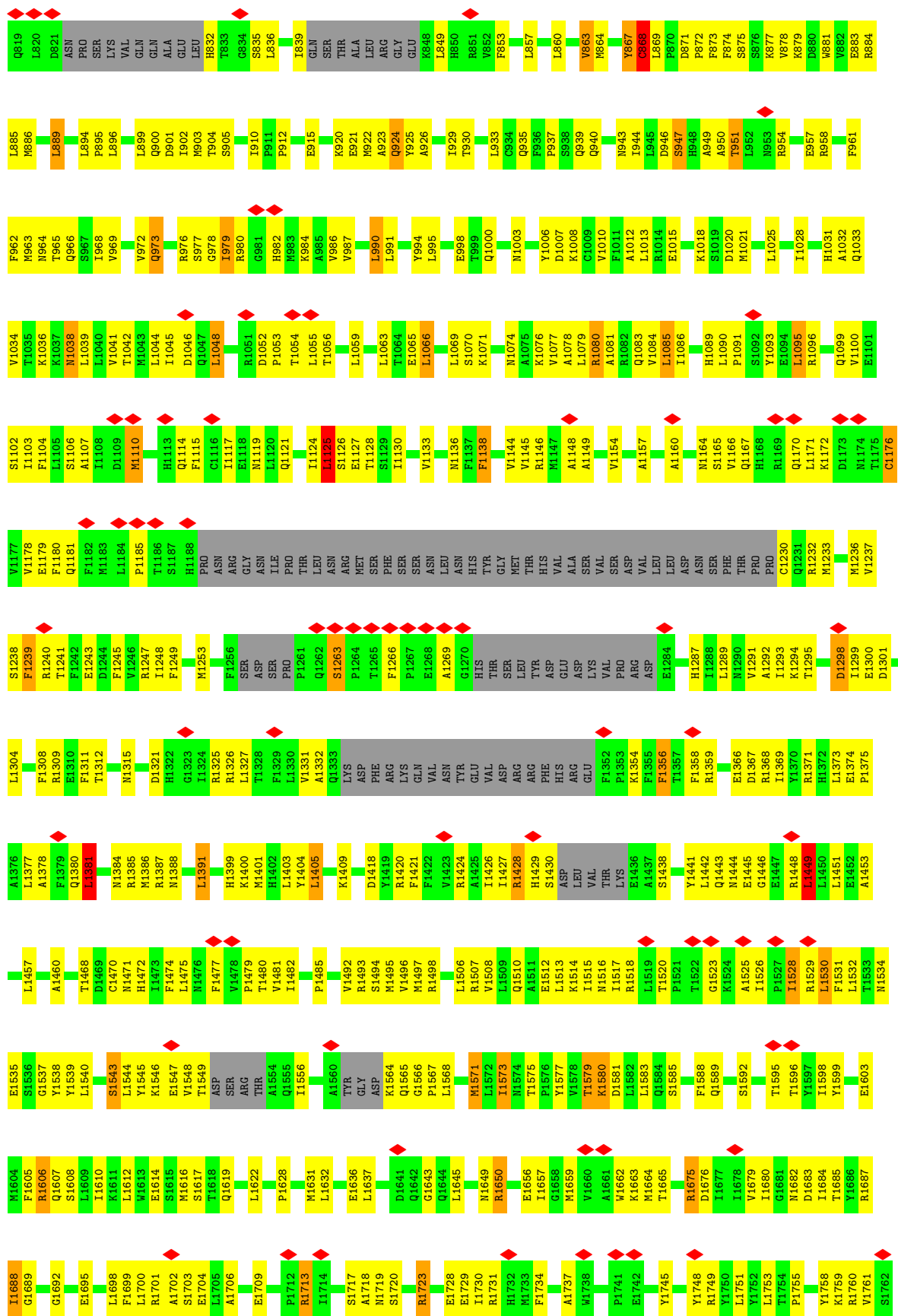


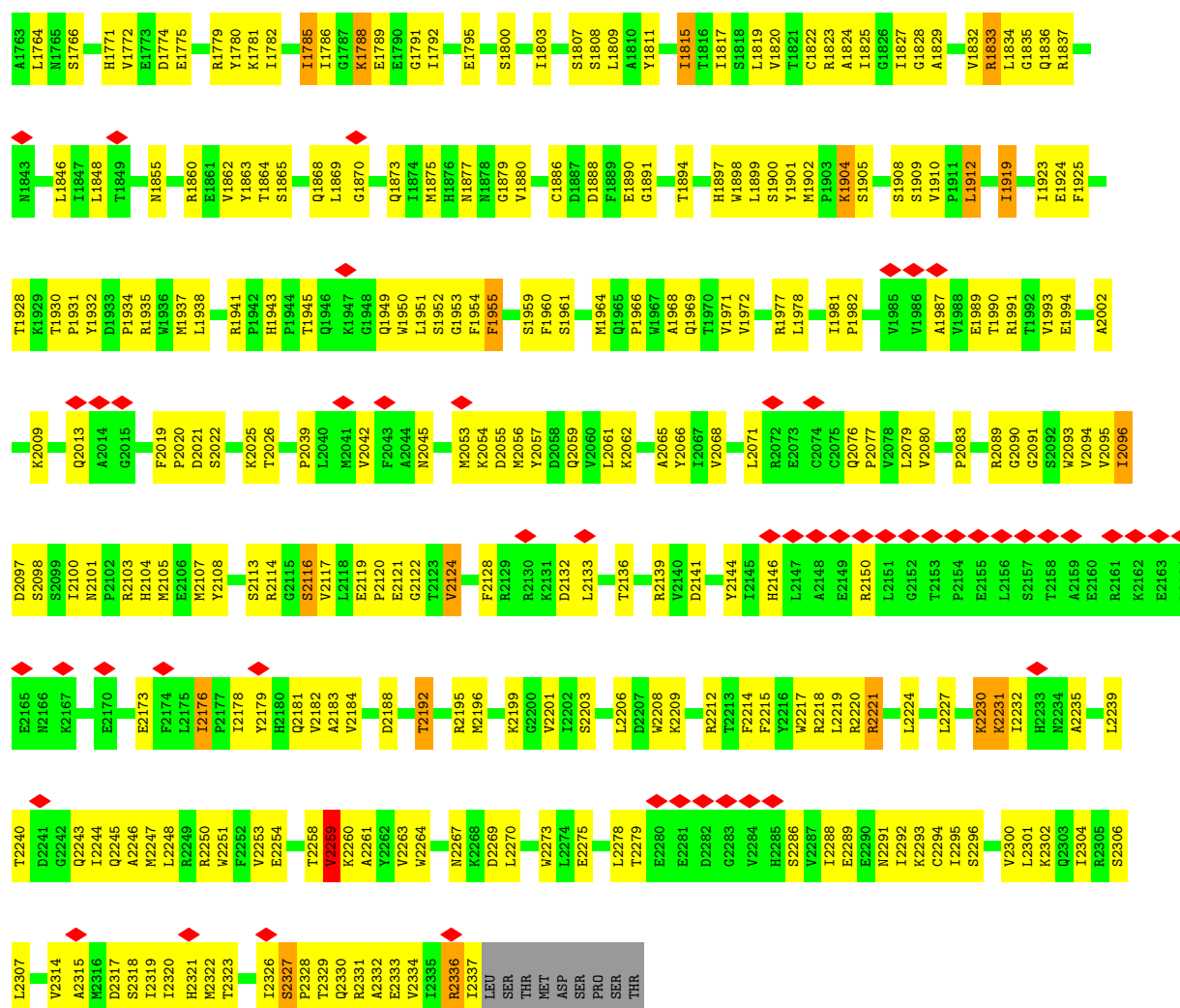


• Molecule 1: Acetyl-CoA carboxylase 1

Chain E: 

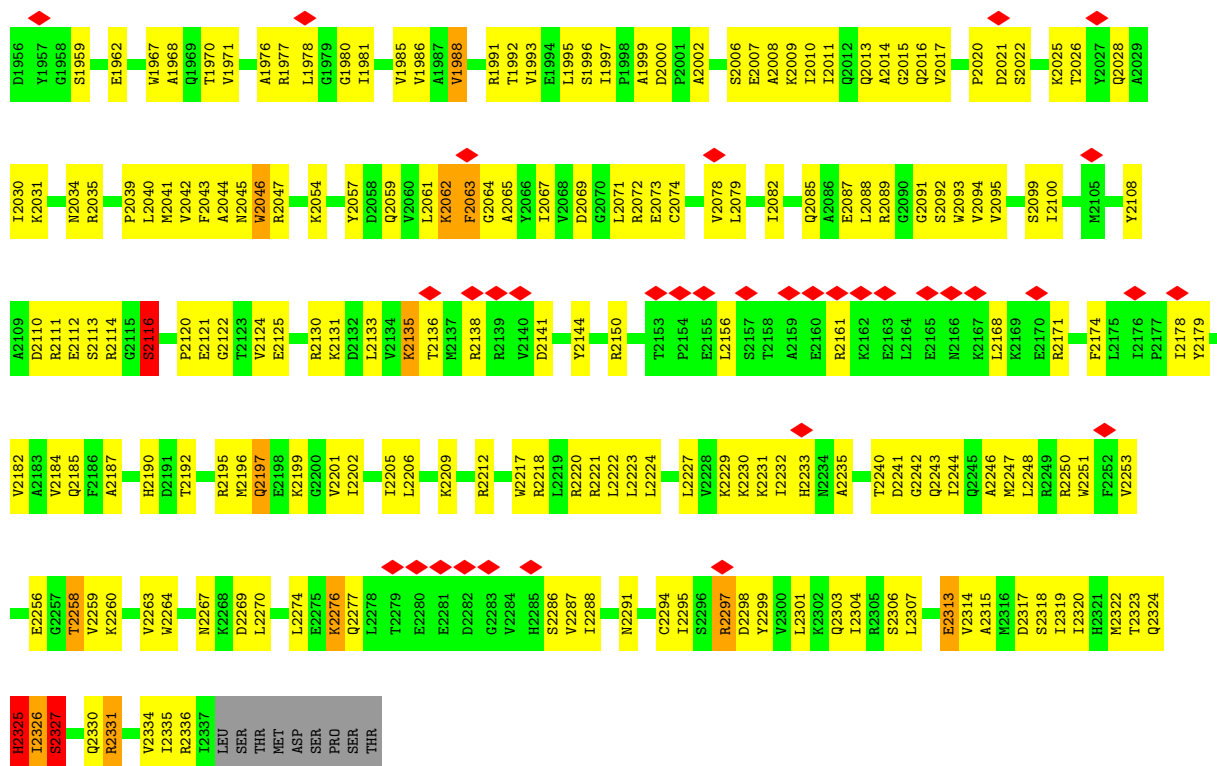
MET	ASP	LEU	GLY	PRO	SER	PRO	LEU	LEU	LEU	ASN	GLN	HIS	SER	ARG	PHE	ARG	ILE	ILE	GLY	SER	VAL	SER	SER	GLU	ASP	ASN	SER	GLY	ASP	GLU	GLU	ILE	ILE	SER	ASN	GLN	VAL	LYS	LEU	ASP	ASP	THR	LEU	LEU	SER																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										



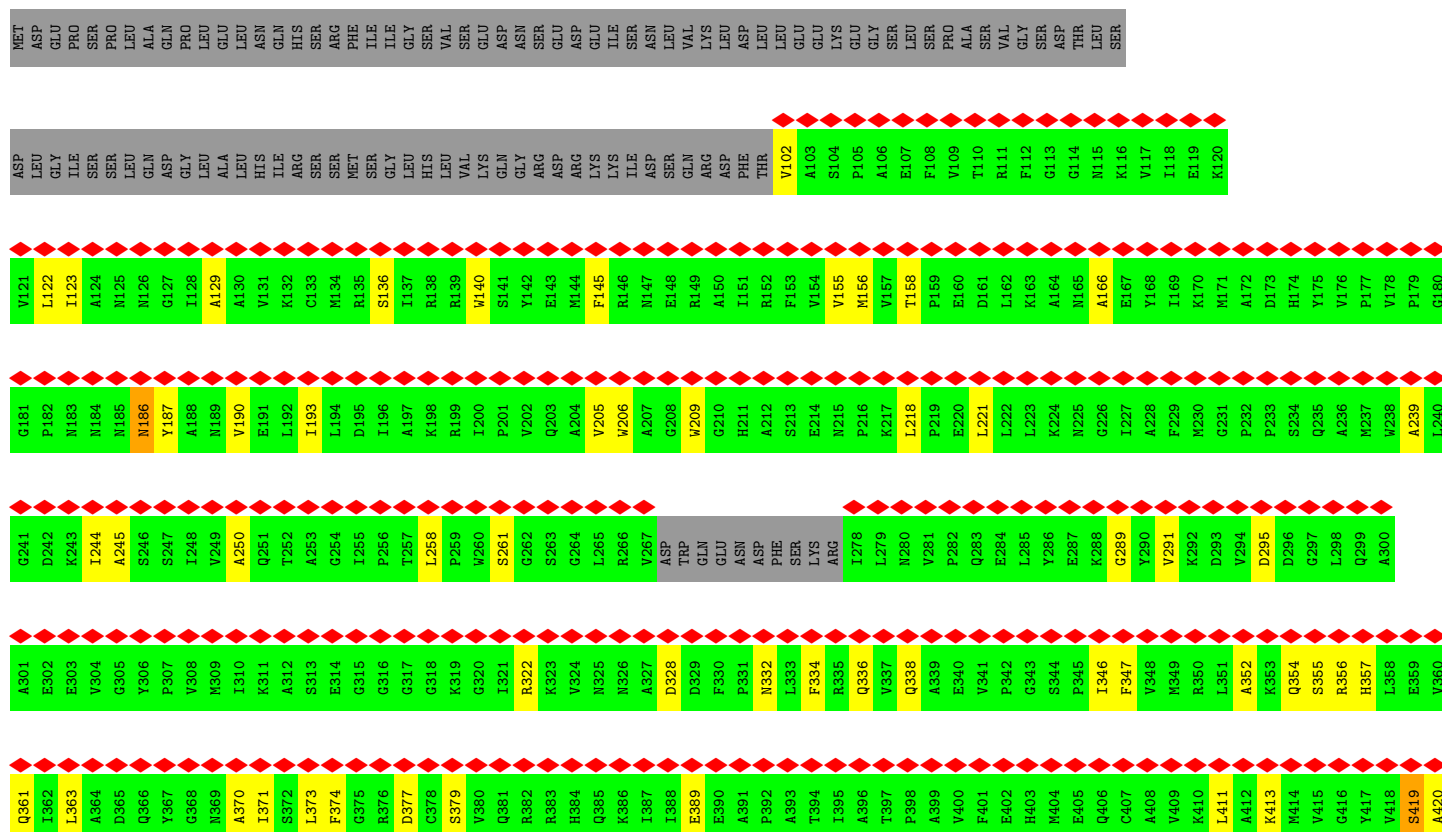


M963	N964	T965	Q966	S967	I968	V969	Q970	G908	R909	L971	V972	Q973	R974	Y975	R976	S977	G978	I979	R980	G981	H982	M983	A984	V985	V986	V987	M988	D989	L990	L991	R992	Q993	Y994	L995	R996	V997	E998	T999	Q1000	F1001	Q1002	N1003	G1004	H1005	Y1006	D1007	K1008	C1009	V1010	F1011	A1012	L1013	R1014	K955	E1015	E1016	N1017	L1018	S1019	D1020	M1021	N1022			
E781	I782	E783	V784	M785	K786	M787	V788	M789	T790	L791	T792	A793	V794	E795	S796	G797	C798	I799	H800	Y801	V802	K803	R804	P805	G806	A807	A808	L809	D810	P811	G812	C813	V814	L815	A816	K817	D818	V819	F820	S821	P822	R823	S824	V825	L826	G827	V828	L829	R830	D831	V832	L833	S834	V835	L836	P837	R838	L839	Q900						
SER	THR	ALA	LEU	ARG	GLY	GLU	R948	H949	R950	R951	V952	F953	H954	Y955	V956	L957	D958	S959	O960	V961	N962	V963	M964	N965	Q924	Y925	A926	S927	L928	I929	S930	P871	F872	F873	F874	S875	S876	K877	V878	K879	D880	Q1002	N943	I944	L945	D946	L947	M886	K887	A949	A950	V1010	L951	N952	N953	R954	S993	L994	S956	N957	R958	R959	V960	F961	F962
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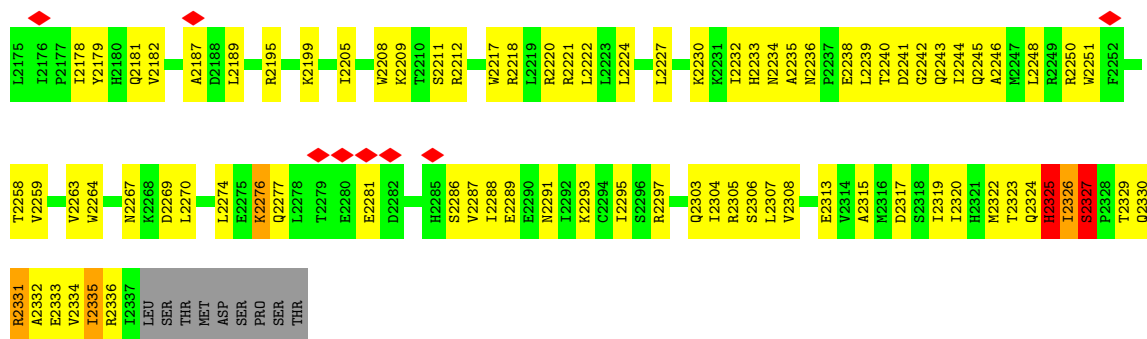


• Molecule 1: Acetyl-CoA carboxylase 1

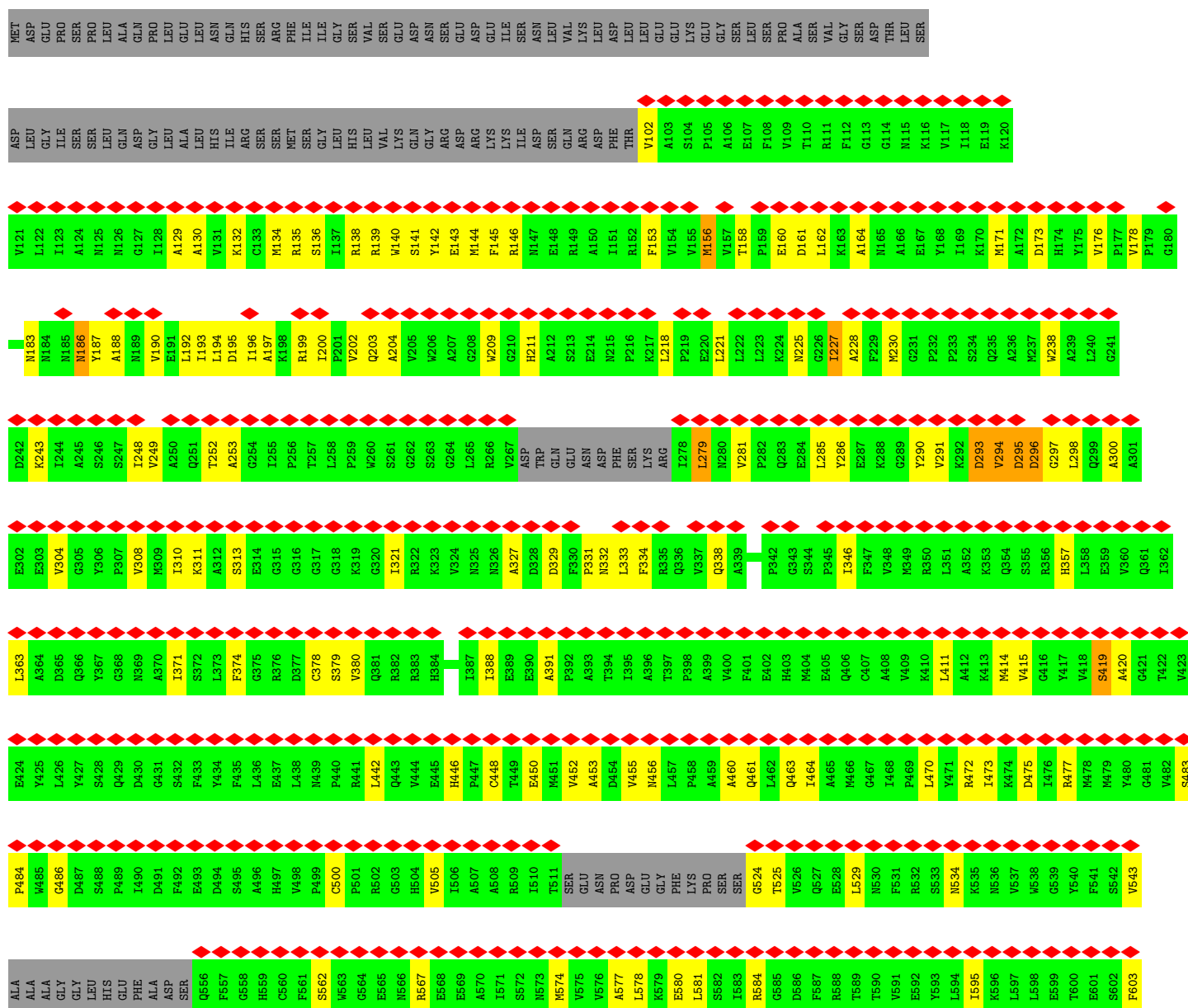


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		E2106	Q2109	T2030	D2021	Q1949	G1871	I1714	Y1715	A1554	L1403	T1328		P1267	
		E2106	Q2110	T2030	S2022	W1950	L1872	A1804		F1642	L1404	F1329		E1268	
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		E2106	Q2112	T2030	S1952	E1806	Q1873	S1807		F1558		A1332		G1270	
		E2106	Q2113	T2030								Q1333		HIS	



● Molecule 1: Acetyl-CoA carboxylase 1

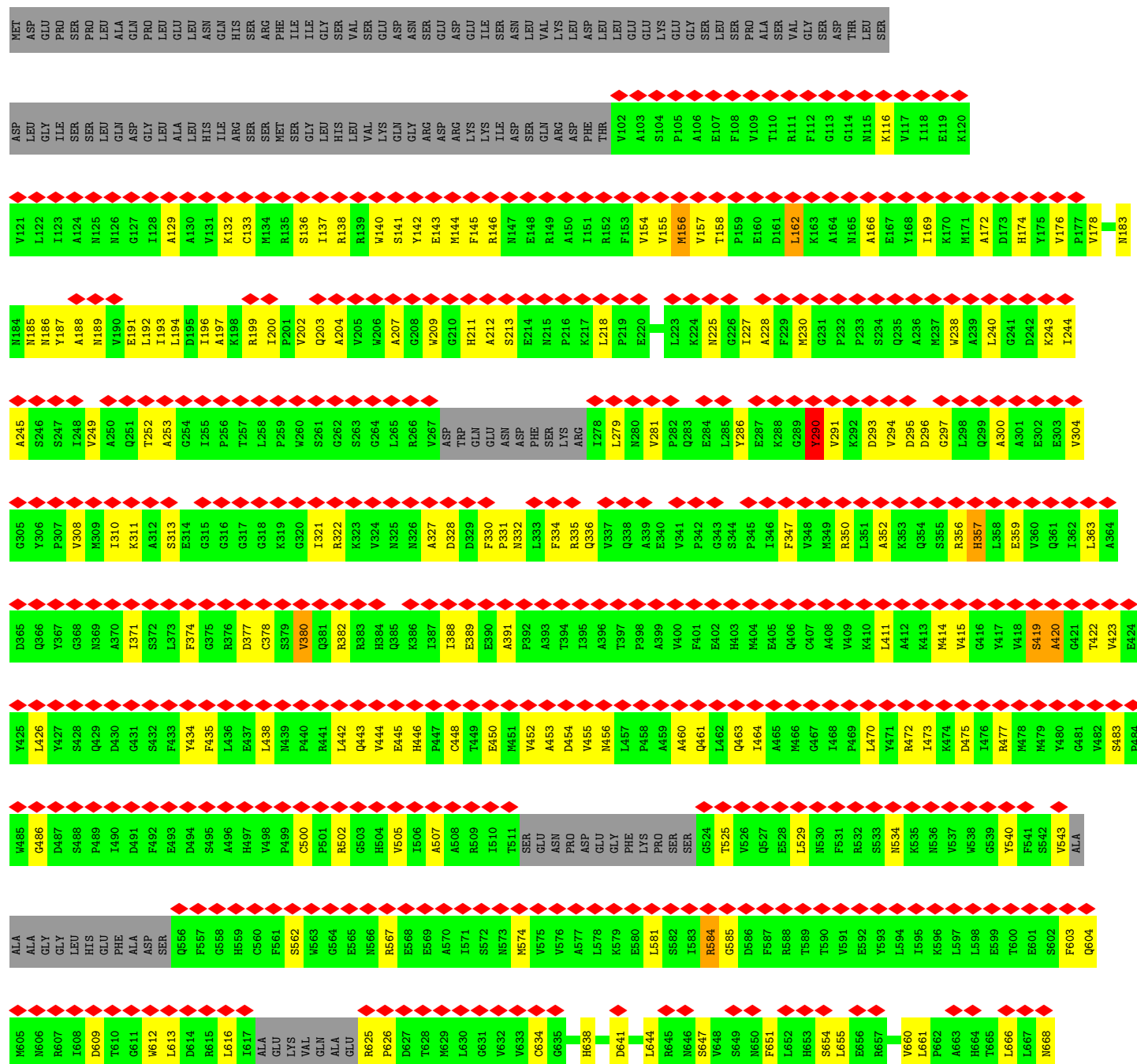


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GLY	ASN	ILE	THR	LEU	ASN	ARG	MET	SER	PHE	SER	ASN	LEU	ASN	HIS	GLY	MET	THR	HIS	VAL	ALA	SER	VAL	LEU	LEU	ASP	ASN	SER	PHE	THR	PRO	PHE	THR	M1233	G1234	G1235	M1236	V1237	S1238	F1239	R1240	T1241	F1242	E1243	D1244	F1245	V1246	R1247	L1248	F1249	D1250	E1251	V1252						
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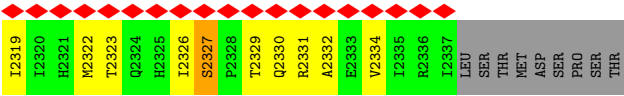


• Molecule 1: Acetyl-CoA carboxylase 1

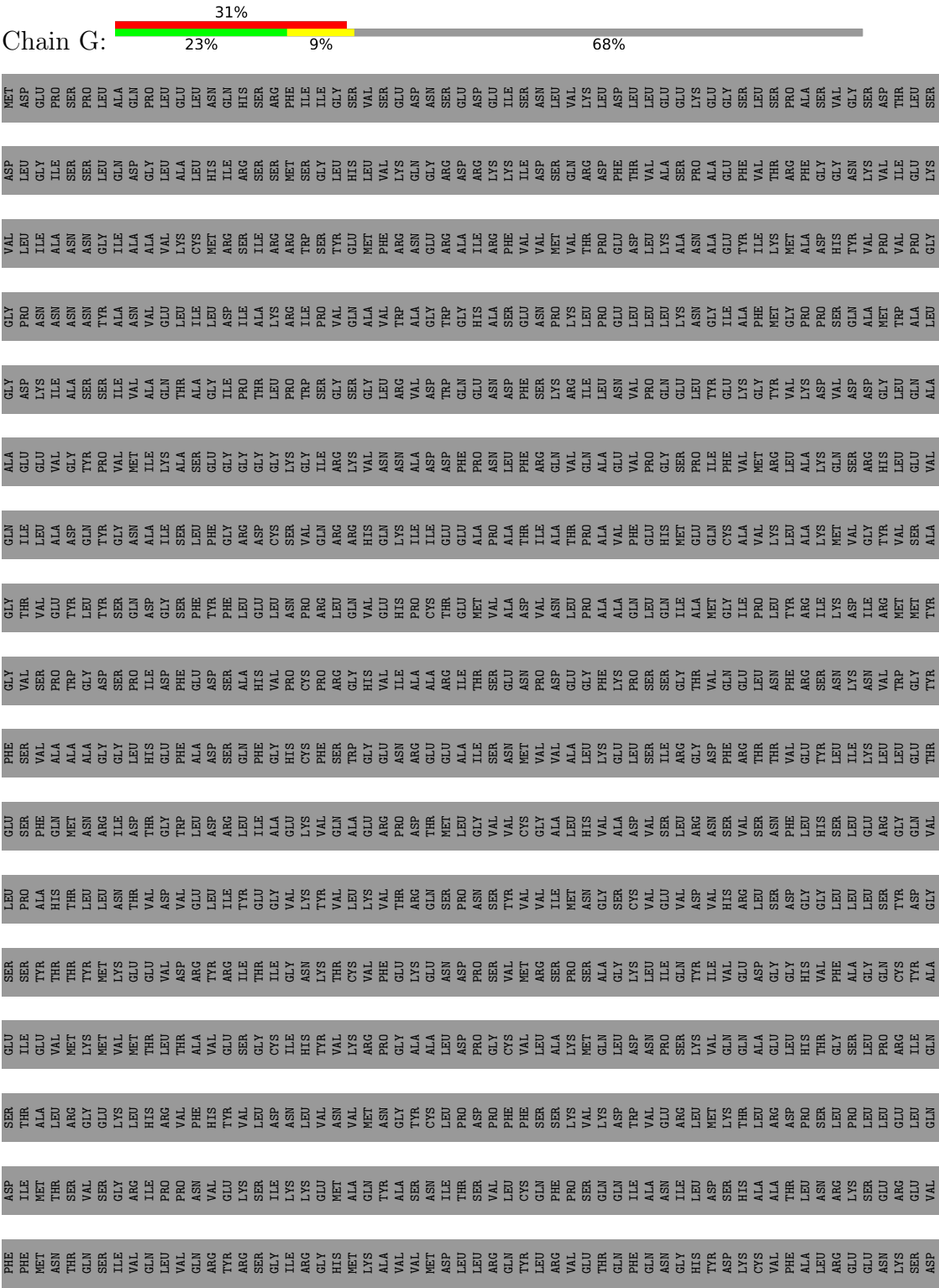


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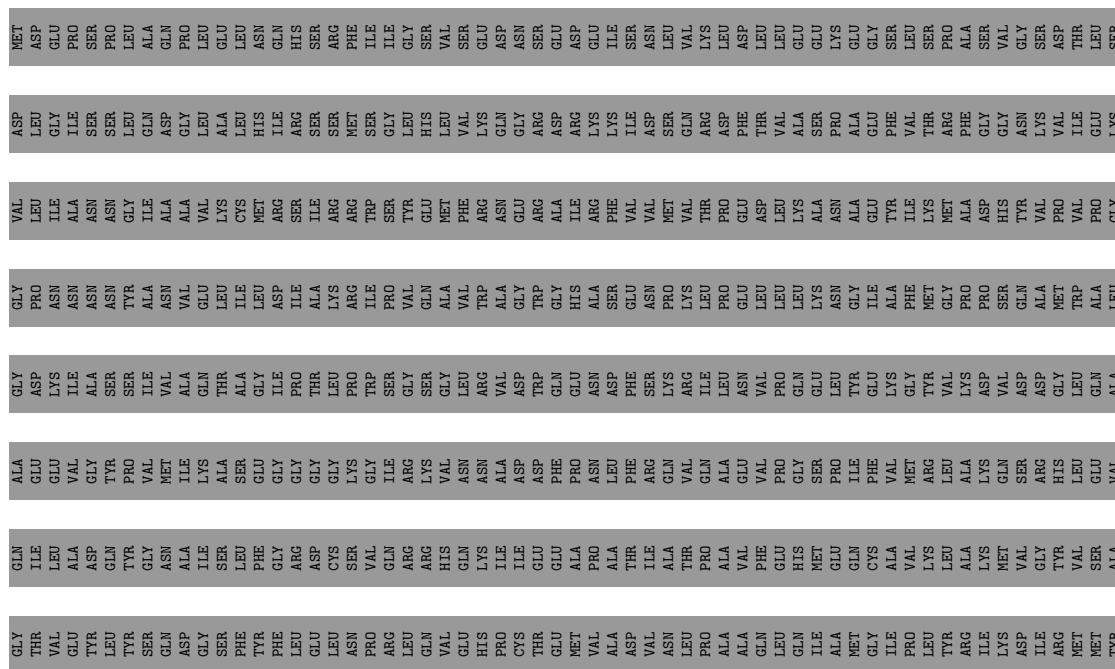
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● Molecule 1: Acetyl-CoA carboxylase 1



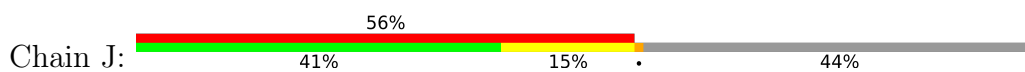






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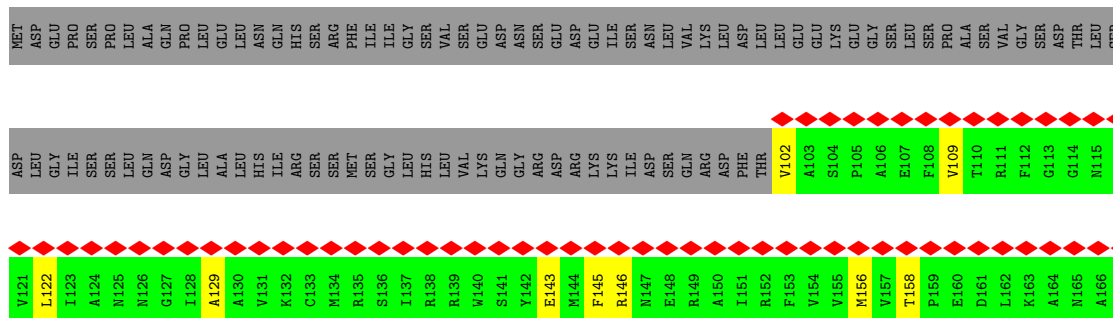
• Molecule 1: Acetyl-CoA carboxylase 1



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G181	P182	N183	N184	N185	N186	Y187	A188	A189	E191	L192	T193	L194	D195	I196	K197	A198	R199	T200	S201	V202	Q203	A204	V205	V206	A207	G208	W209	G210	H211	A212	S213	E214	N215	P216	K217	L218	P219	E220	L221	L222	L223	K224	N225	G226	I227	A228	F229	M230	G231	P232	P233	S234	Q235	A236	M237	W238	A239	L240														
G241	D242	K243	T244	A245	S246	S247	I248	V249	A250	Q251	T252	A253	G254	I255	P256	T257	L258	P259	V260	S261	G262	S263	G264	L265	R266	V267	ASP	TRP	GLN	GLY	ASN	ASP	PHE	SER	LYS	ARG	I278	L279	M280	V281	P282	Q283	E284	L285	Y286	E287	K288	G289	Y290	V291	K292	D293	V294	D295	D296	G297	L298	Q299	A300													
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F541	S542	V543	ALA	ALA	ALA	GLY	GLY	LEU	HIS	PHE	ALA	ASP	SER	O556	F557	G558	H559	C560	F561	S562	W563	G564	E565	N566	R567	E568	E569	A570	I571	S572	N573	M574	V575	V576	G577	A578	L579	R579	E580	L581	S582	I583	R584	G585	D586	F587	R588	T589	T590	S591	E592	Y593	L594	I595	K596	L597	E598	E599	T600													
E601	S602	F603	Q604	M605	M606	L607	T608	D609	T610	G611	V612	L613	D614	R615	L616	L617	ALA	GLU	LYS	VAL	GLN	ALA	GLU	R625	P626	D627	T628	M629	L630	G631	V632	V633	C634	G635	G636	A637	H638	V639	A640	D641	V642	S643	L644	R645	N646	S647	V648	S649	N650	F651	L652	H653	S654	L655	E656	R657	S658	N659	V660													
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- Molecule 1: Acetyl-CoA carboxylase 1

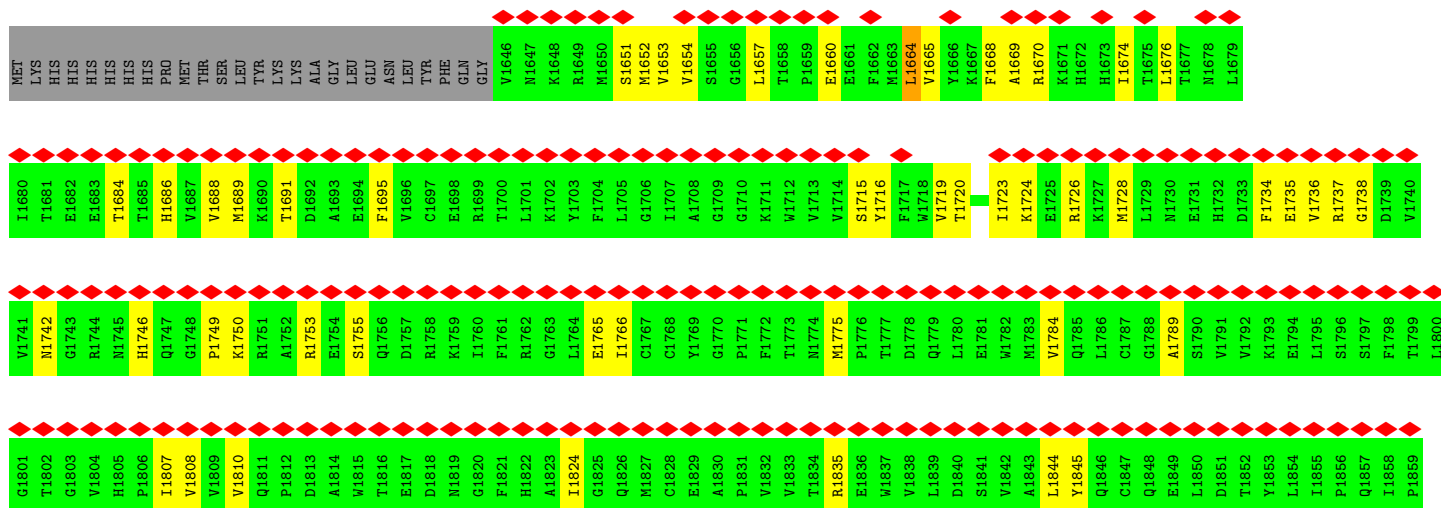
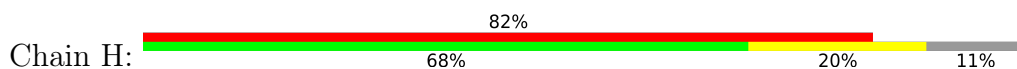


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M963	M903	ALA	E783	A663	F603	S483	V423	L363	E303	K243	N183
N964	T904	LEU	E784	H664	Q604	P484	E424	A364	V304	I244	N184
T965	S905	ARG	M785	T665	M605	V485	Y425	D365	G305	A245	N185
Q966	V906	GLY	M786	L666	N606	G486	L426	Q366	Y306	S246	N186
S967	S907	GLU	M787	L667	R607	D487	Y427	Y367	P307	S247	Y187
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V969	R909		M789	T669	D609	P489	Q429	N369	M309	V249	N189
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V972	P912		T792	V672	V612	F492	S432	S372	A312	T252	L192
Q973	M913		A793	E673	L613	E493	F433	L373	S313	A253	I193
R974	V914		V794	L674	D614	D494	Y434	G254	E194	G254	L194
Y975	E915		E795	L675	R615	S495	F435	I255	G315	I255	D195
R976	K916		S796	V676	L616	A496	L436	P256	G316	P256	I196
S977	S917		G797	E677	T617	H497	E437	D377	G317	T257	A197
G978	I918		I798	G678	ALA	V498	L438	C378	G318	L258	K198
I979	K919		T799	V679	GLU	P499	M439	S379	K319	P259	R199
R980	K920		H800	K680	LYS	C500	P440	V380	G320	W260	I200
G981	E921		Y801	V681	VAL	F501	R441	Q381	I321	S261	P201
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A985	Y925		P805	L686	P926	V505	E445	Q385	N325	L265	V205
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C987	A926		E569	G687	T628	E569	P447	I387	A327	V267	A207
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L989	L928		E688	S689	L630	A571	T449	E389	E390	TRP	W209
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D991	D930		V632	V633	V632	S572	E451	A391	P331	ASN	H211
H992	H931		V633	V634	V633	N573	M451	P392	N332	ASP	A212
L993	L932		C634	C635	C634	V575	V452	A393	L333	ASP	S213
C994	C934		G635	G636	G635	V576	A453	T394	F334	PHE	E214
Q995	Q935		A636	A637	A636	A577	D454	I395	L335	LYS	N215
F996	F936		V695	V696	V695	L578	V455	A396	Q336	ARG	N216
V997	V937		L637	L638	L637	K579	M456	T397	V337	I278	K217
E998	E938		H638	H639	H638	E580	L457	P398	Q338	L279	L218
T999	T939		V639	V640	V639	E581	P458	A399	A339	N280	P219
Q1000	Q940		A640	A641	A640	L581	A459	V400	E340	V281	E220
F1001	F941		D641	D642	D641	S582	A460	F401	V341	P282	L221
I1002	I942		V642	V643	V642	I583	Q461	E202	Q342	Q283	L222
N1003	N943		S643	S644	S643	R584	L462	H403	G343	E284	L223
G1004	G944		L644	L645	L644	G585	Q463	M404	S344	L285	L224
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Y1006	Y946		N646	N647	N646	F587	A465	Q406	I346	E287	N225
D1007	D947		S647	S648	S647	R588	M466	C407	F347	K288	G226
K1008	K948		V648	V649	V648	T589	G467	V408	G289	G289	I227
C1009	C949		S649	S650	S649	N590	I468	A408	V348	Y290	A228
V1010	V950		N650	N651	N650	V591	P469	V409	M349	V291	F229
F1011	F951		F651	F652	F651	E592	K470	K410	R350	K292	M230
A1012	A952		L652	L653	L652	S593	Y471	L411	L351	D293	G231
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R1014	R954		S654	S655	S654	I595	I473	K413	K353	D295	P233
E1015	E955		L655	L656	L655	K596	K474	M414	Q354	D296	P234
E1016	E956		E656	E657	E656	V597	I475	V415	S355	G297	Q235
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K1018	K958		S717	S718	S717	V538	I477	Y417	H357	Q299	M237
S1019	S959		V718	V719	V718	E599	R478	V418	L358	A300	W238
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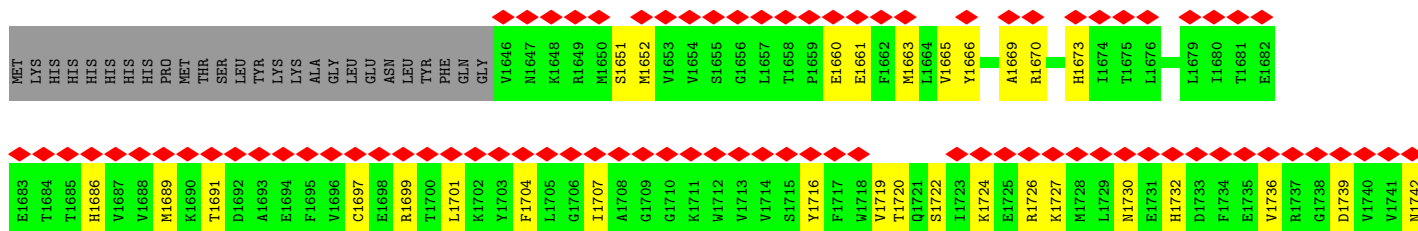
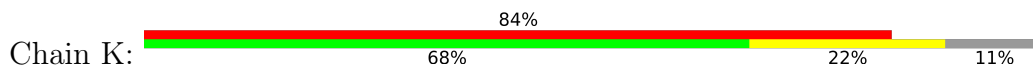


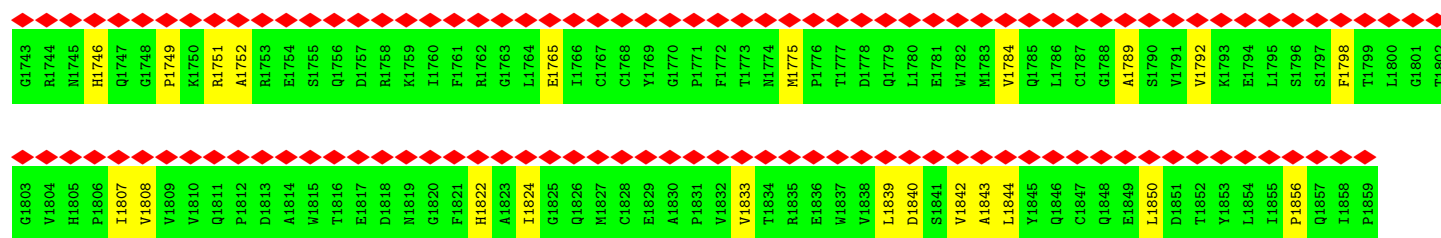
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	VAL	GLU	GLU	LEU	HIS	ASN	ALA	VAL	PHE
	HIS	GLU	GLU	GLU	MET	MET	ASN	VAL	VAL
	SER	ASP	ASN	ASN	GLU	TRP	ARG	ALA	PRO
	VAL	LEU	LYS	LYS	MET	ARG	GLY	VAL	THR
	ILE	VAL	LEU	LEU	TYR	TYR	GLY	THR	LYS
	GLU	LYS	GLY	GLY	ALA	PHE	ALA	GLU	THR
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SER	ASN	LYS	LYS	ARG	GLY	GLY	GLY	THR	ARG
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	LYS	HIS	GLU	GLU	SER	SER	MET	VAL	ASP
	CYS	ASN	PHE	PHE	ARG	LYS	LYS	GLU	PRO
	ILE	ALA	LEU	GLY	GLY	GLY	ASP	LEU	ARG
	ARG	ASN	ILE	ILE	SER	MET	MET	SER	TRP
	SER	PRO	PRO	PRO	VAL	VAL	TYR	ILE	ILE
	ASP	GLU	ILE	ILE	LEU	ASP	ASP	PRO	LEU
	TYR	LEU	THR	HIS	GLU	GLU	ALA	ALA	GLY
	VAL	ASP	GLN	GLN	GLU	PRO	VAL	GLN	ALA
THR	LEU	GLY	GLY	GLY	GLY	GLY	VAL	GLY	GLY
	GLN	GLN	ALA	ALA	THR	THR	PHE	ALA	ASN
	ILE	ILE	GLN	VAL	VAL	VAL	GLY	LYS	GLN
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	SER	ALA	PHE	PHE	ILE	ILE	TYR	SER	GLN
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	GLN	LEU	ARG	ASP	PHE	ARG	VAL	ALA	GLN
	ALA	ARG	HIS	HIS	ARG	LYS	CYS	ALA	PHE
	ASN	TRP	TRP	THR	THR	ASP	ARG	GLN	SER
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- Molecule 2: Breast cancer type 1 susceptibility protein

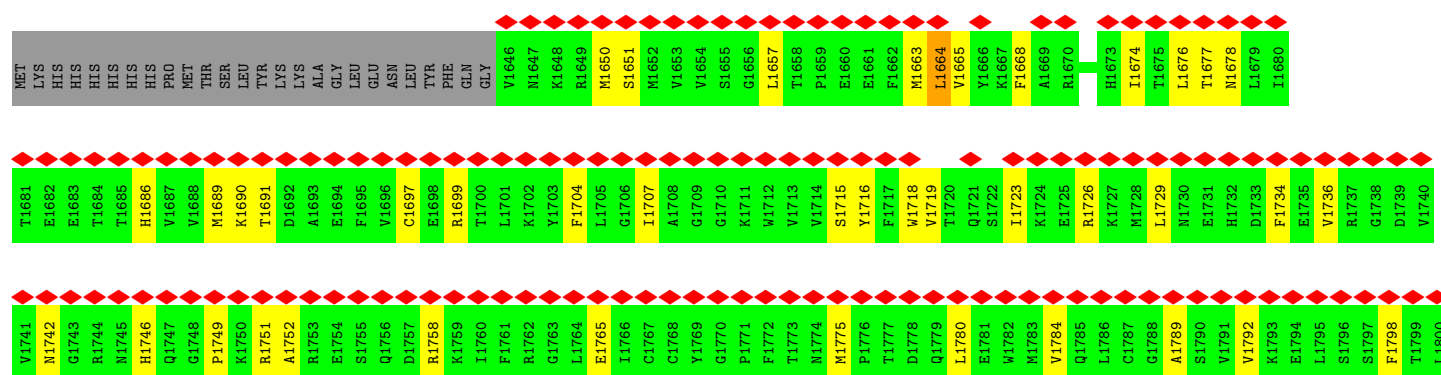
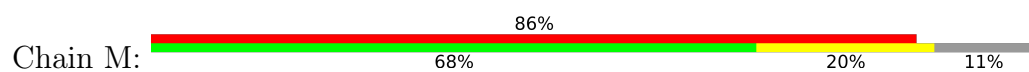


- Molecule 2: Breast cancer type 1 susceptibility protein

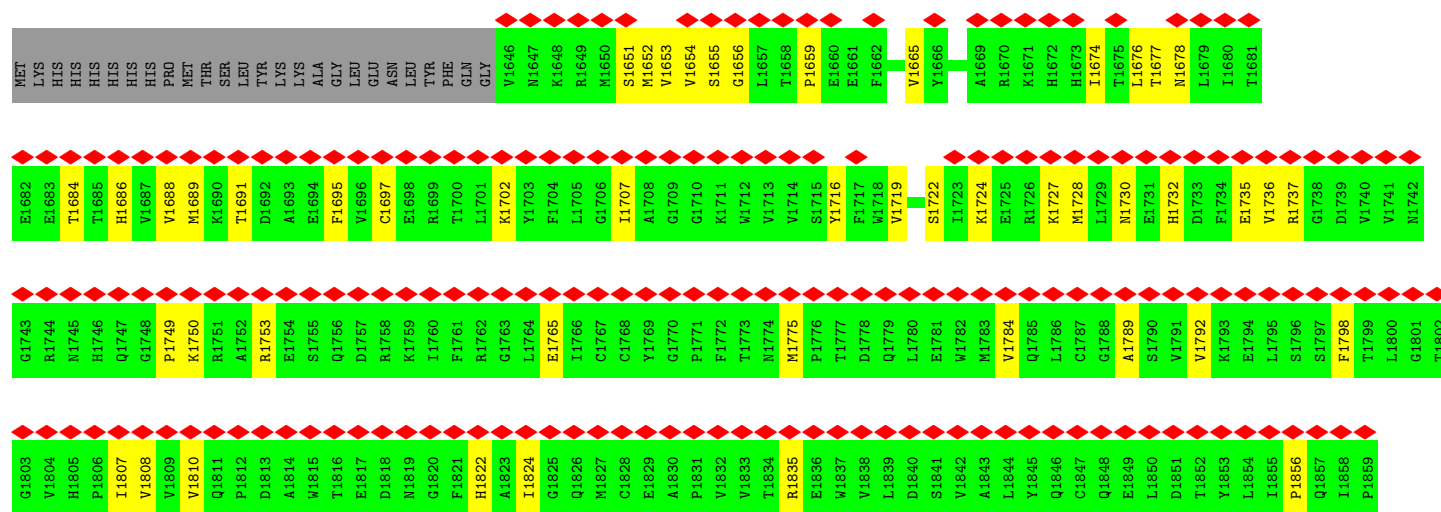
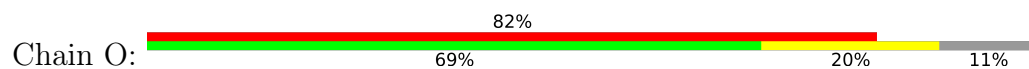




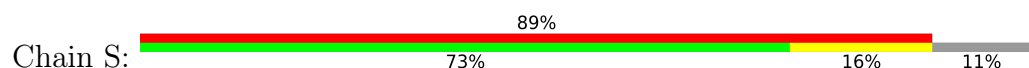
• Molecule 2: Breast cancer type 1 susceptibility protein



• Molecule 2: Breast cancer type 1 susceptibility protein



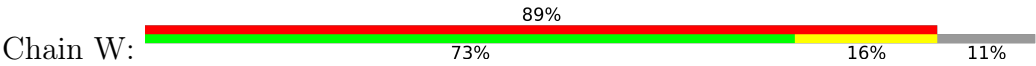
• Molecule 2: Breast cancer type 1 susceptibility protein





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● Molecule 2: Breast cancer type 1 susceptibility protein



MET	LYS	HIS	HIS	HIS	HIS	HIS	PRO	MET	THR	SER	LEU	TYR	LYS	LYS	ALA	GLY	LEU	GLU	ASN	LEU	TYR	PHE	GLN	GLY	V1646	N1647	K1648	R1649	M1650	S1651	M1652	V1653	V1654	S1655	G1656	L1657	T1658	P1659	E1660	E1661	F1662	M1663	L1664	V1665	Y1666	K1667	F1668	A1669	R1670	K1671	H1672	H1673	I1674	T1675	L1676	T1677	N1678	L1679
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V1740	V1741	N1742	G1743	R1744	N1745	H1746	Q1747	G1748	P1749	K1750	R1751	A1752	R1753	E1754	S1755	Q1756	D1757	R1758	K1759	I1760	F1761	R1762	G1763	L1764	E1765	I1766	C1767	C1768	Y1769	G1770	P1771	F1772	T1773	N1774	M1775	P1776	T1777	D1778	Q1779	L1780	E1781	W1782	M1783	V1784	Q1785	L1786	C1787	G1788	A1789	S1790	V1791	V1792	K1793	E1794	L1795	S1796	F1798	T1799
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L1800	G1801	T1802	G1803	V1804	H1805	P1806	T1807	V1808	V1809	V1810	Q1811	P1812	D1813	A1814	W1815	T1816	E1817	D1818	N1819	G1820	F1821	H1822	A1823	I1824	G1825	Q1826	M1827	C1828	E1829	A1830	P1831	V1832	V1833	T1834	R1835	E1836	W1837	V1838	L1839	D1840	S1841	V1842	A1843	L1844	Y1845	Q1846	C1847	Q1848	E1849	L1850	D1851	T1852	Y1853	L1854	I1855	P1856	Q1857	I1858	P1859
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	48483	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.081	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	397.80798, 397.80798, 397.80798	wwPDB
Map dimensions	376, 376, 376	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.058, 1.058, 1.058	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.50	0/16819	1.14	84/22785 (0.4%)
1	B	0.51	1/16819 (0.0%)	1.21	115/22785 (0.5%)
1	C	0.60	0/16819	1.17	67/22785 (0.3%)
1	D	0.70	2/16819 (0.0%)	1.40	212/22785 (0.9%)
1	E	0.69	0/16819	1.25	85/22785 (0.4%)
1	F	0.59	0/16819	1.15	55/22785 (0.2%)
1	G	0.38	0/6199	0.92	4/8406 (0.0%)
1	J	0.36	0/10619	0.95	12/14376 (0.1%)
1	Q	0.39	1/6199 (0.0%)	0.93	6/8406 (0.1%)
1	R	0.37	0/10619	0.97	22/14376 (0.2%)
2	H	0.38	0/1740	0.91	1/2364 (0.0%)
2	K	0.36	0/1737	0.83	0/2360
2	M	0.36	0/1740	0.84	0/2364
2	O	0.37	0/1737	0.87	1/2360 (0.0%)
2	S	0.31	0/1740	0.79	2/2364 (0.1%)
2	U	0.31	0/1737	0.78	0/2360
2	W	0.31	0/1737	0.79	0/2360
2	Y	0.32	0/1740	0.79	0/2364
All	All	0.54	4/148458 (0.0%)	1.13	666/201170 (0.3%)

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	0	13
1	B	0	13
1	C	0	12
1	D	1	18
1	E	0	11

Continued on next page...

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	0	12
1	J	0	11
1	R	0	11
All	All	1	101

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	1824	ALA	CA-CB	-7.23	1.43	1.53
1	D	1620	ALA	CA-CB	-7.04	1.41	1.53
1	Q	1625	PRO	CA-C	5.69	1.55	1.51
1	B	1539	TYR	CB-CG	-5.00	1.40	1.51

The worst 5 of 666 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1668	SER	CA-C-N	-17.59	97.85	119.84
1	B	1668	SER	C-N-CA	-17.59	97.85	119.84
1	D	1545	TYR	CA-C-N	11.54	140.91	122.21
1	D	1545	TYR	C-N-CA	11.54	140.91	122.21
1	D	1974	GLY	CA-C-N	10.28	138.96	122.81

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	D	1838	THR	CB

5 of 101 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	1052	ASP	Peptide
1	D	1087	ALA	Peptide
1	D	1110	MET	Peptide
1	D	924	GLN	Peptide
1	D	957	GLU	Peptide

5.2 Too-close contacts

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	16482	16276	16330	575	0
1	B	16482	16276	16330	583	0
1	C	16482	16275	16330	681	0
1	D	16482	16276	16330	814	0
1	E	16482	16276	16330	729	0
1	F	16482	16275	16330	647	0
1	G	6058	5997	6015	165	0
1	J	10424	10279	10314	229	0
1	Q	6058	5997	6015	173	0
1	R	10424	10279	10314	226	0
2	H	1699	1648	1655	33	0
2	K	1696	1644	1651	38	0
2	M	1699	1648	1655	38	0
2	O	1696	1644	1651	34	0
2	S	1699	1648	1655	23	0
2	U	1696	1644	1651	29	0
2	W	1696	1644	1651	27	0
2	Y	1699	1648	1655	20	0
All	All	145436	143374	143862	4793	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 17.

The worst 5 of 4793 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:B:2264:TRP:HA	1:B:2270:LEU:HD21	1.42	1.00
1:A:197:ALA:HB1	1:A:227:ILE:HD13	1.42	0.98
1:B:197:ALA:HB1	1:B:227:ILE:HD13	1.44	0.97
1:F:1123:LEU:HD12	1:F:1152:VAL:HG21	1.48	0.95
1:C:1123:LEU:HD12	1:C:1152:VAL:HG21	1.48	0.93

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	2047/2346 (87%)	1889 (92%)	147 (7%)	11 (0%)	24	63
1	B	2047/2346 (87%)	1888 (92%)	146 (7%)	13 (1%)	21	59
1	C	2047/2346 (87%)	1884 (92%)	150 (7%)	13 (1%)	21	59
1	D	2047/2346 (87%)	1879 (92%)	154 (8%)	14 (1%)	18	56
1	E	2047/2346 (87%)	1895 (93%)	138 (7%)	14 (1%)	18	56
1	F	2047/2346 (87%)	1884 (92%)	150 (7%)	13 (1%)	21	59
1	G	755/2346 (32%)	727 (96%)	25 (3%)	3 (0%)	30	67
1	J	1290/2346 (55%)	1157 (90%)	125 (10%)	8 (1%)	21	59
1	Q	755/2346 (32%)	727 (96%)	24 (3%)	4 (0%)	24	63
1	R	1290/2346 (55%)	1158 (90%)	124 (10%)	8 (1%)	21	59
2	H	212/240 (88%)	207 (98%)	5 (2%)	0	100	100
2	K	212/240 (88%)	206 (97%)	6 (3%)	0	100	100
2	M	212/240 (88%)	205 (97%)	7 (3%)	0	100	100
2	O	212/240 (88%)	205 (97%)	7 (3%)	0	100	100
2	S	212/240 (88%)	206 (97%)	6 (3%)	0	100	100
2	U	212/240 (88%)	205 (97%)	7 (3%)	0	100	100
2	W	212/240 (88%)	205 (97%)	7 (3%)	0	100	100
2	Y	212/240 (88%)	205 (97%)	7 (3%)	0	100	100
All	All	18068/25380 (71%)	16732 (93%)	1235 (7%)	101 (1%)	23	59

5 of 101 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	211	HIS
1	D	419	SER
1	D	868	CYS
1	D	1688	ILE
1	E	211	HIS

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	1784/2056 (87%)	1763 (99%)	21 (1%)	63	75
1	B	1784/2056 (87%)	1765 (99%)	19 (1%)	65	75
1	C	1784/2056 (87%)	1758 (98%)	26 (2%)	57	71
1	D	1784/2056 (87%)	1752 (98%)	32 (2%)	51	67
1	E	1784/2056 (87%)	1750 (98%)	34 (2%)	50	66
1	F	1784/2056 (87%)	1758 (98%)	26 (2%)	57	71
1	G	660/2056 (32%)	656 (99%)	4 (1%)	78	82
1	J	1124/2056 (55%)	1100 (98%)	24 (2%)	47	65
1	Q	660/2056 (32%)	655 (99%)	5 (1%)	73	79
1	R	1124/2056 (55%)	1098 (98%)	26 (2%)	44	64
2	H	186/214 (87%)	185 (100%)	1 (0%)	81	83
2	K	186/214 (87%)	186 (100%)	0	100	100
2	M	186/214 (87%)	185 (100%)	1 (0%)	81	83
2	O	186/214 (87%)	186 (100%)	0	100	100
2	S	186/214 (87%)	185 (100%)	1 (0%)	81	83
2	U	186/214 (87%)	186 (100%)	0	100	100
2	W	186/214 (87%)	186 (100%)	0	100	100
2	Y	186/214 (87%)	185 (100%)	1 (0%)	81	83
All	All	15760/22272 (71%)	15539 (99%)	221 (1%)	57	72

5 of 221 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	1705	LEU
1	A	734	TYR
2	S	1664	LEU
1	R	860	LEU
1	B	279	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 272 such sidechains are listed below:

Mol	Chain	Res	Type
1	R	299	GLN
1	R	1000	GLN
2	O	1732	HIS
1	C	1510	GLN
1	C	1384	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 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	SEP	B	1263	1	8,9,10	1.60	1 (12%)	7,12,14	0.86	0
1	SEP	J	1263	1	8,9,10	1.62	1 (12%)	7,12,14	1.29	1 (14%)
1	SEP	R	1263	1	8,9,10	1.63	1 (12%)	7,12,14	1.16	1 (14%)
1	SEP	E	1263	1	8,9,10	1.58	1 (12%)	7,12,14	1.17	1 (14%)
1	SEP	A	1263	1	8,9,10	1.60	1 (12%)	7,12,14	1.58	1 (14%)
1	SEP	F	1263	1	8,9,10	1.60	1 (12%)	7,12,14	0.89	0
1	SEP	D	1263	1	8,9,10	1.57	1 (12%)	7,12,14	1.06	1 (14%)
1	SEP	C	1263	1	8,9,10	1.62	1 (12%)	7,12,14	1.54	2 (28%)

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	SEP	B	1263	1	-	2/6/8/10	-
1	SEP	J	1263	1	-	2/6/8/10	-
1	SEP	R	1263	1	-	2/6/8/10	-
1	SEP	E	1263	1	-	2/6/8/10	-
1	SEP	A	1263	1	-	2/6/8/10	-
1	SEP	F	1263	1	-	2/6/8/10	-
1	SEP	D	1263	1	-	2/6/8/10	-
1	SEP	C	1263	1	-	2/6/8/10	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1263	SEP	P-O1P	3.62	1.61	1.50
1	R	1263	SEP	P-O1P	3.56	1.61	1.50
1	J	1263	SEP	P-O1P	3.55	1.61	1.50
1	B	1263	SEP	P-O1P	3.54	1.61	1.50
1	F	1263	SEP	P-O1P	3.51	1.61	1.50

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1263	SEP	OG-CB-CA	3.54	111.59	108.14
1	C	1263	SEP	OG-CB-CA	2.92	110.99	108.14
1	J	1263	SEP	OG-CB-CA	2.72	110.79	108.14
1	R	1263	SEP	OG-CB-CA	2.29	110.37	108.14
1	E	1263	SEP	OG-CB-CA	2.21	110.29	108.14

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	1263	SEP	N-CA-CB-OG
1	D	1263	SEP	C-CA-CB-OG
1	E	1263	SEP	N-CA-CB-OG
1	E	1263	SEP	C-CA-CB-OG
1	C	1263	SEP	N-CA-CB-OG

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	1263	SEP	1	0
1	F	1263	SEP	2	0
1	D	1263	SEP	1	0
1	C	1263	SEP	1	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 [i](#)

There are no chain breaks in this entry.

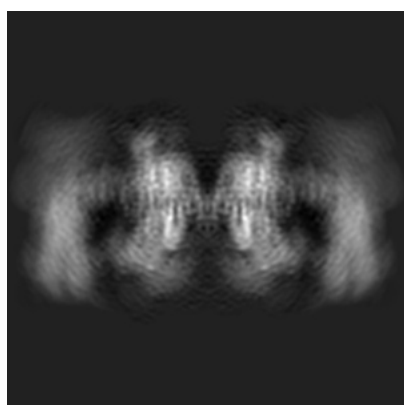
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4344. These allow visual inspection of the internal detail of the map and identification of artifacts.

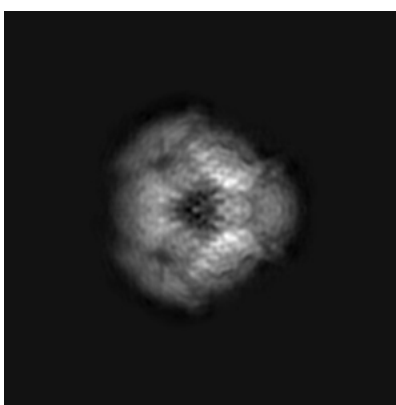
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

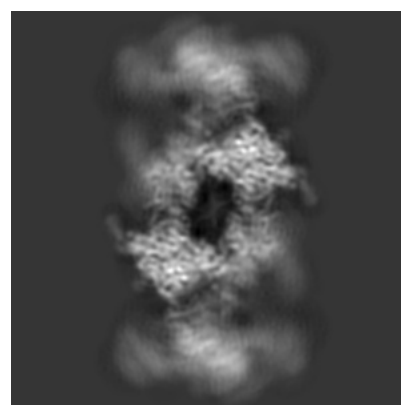
6.1.1 Primary map



X



Y

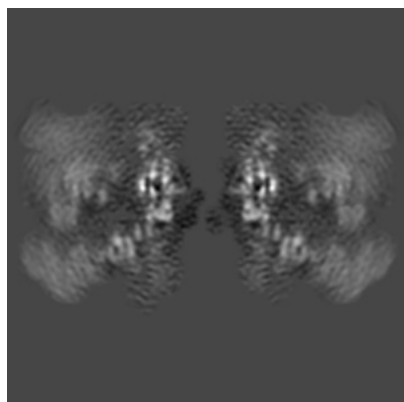


Z

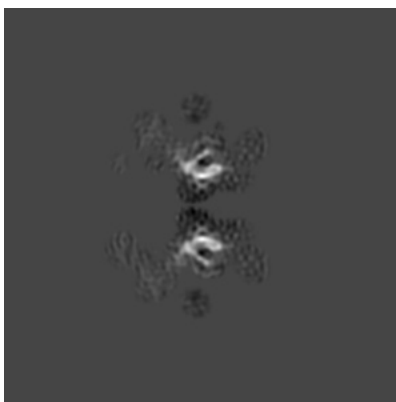
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

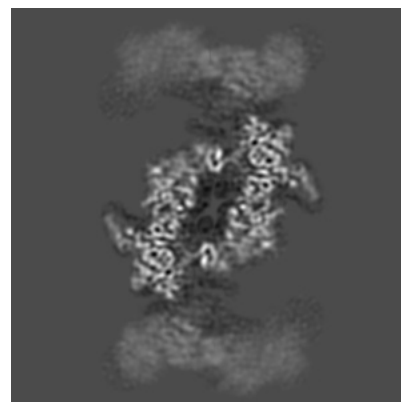
6.2.1 Primary map



X Index: 188



Y Index: 188

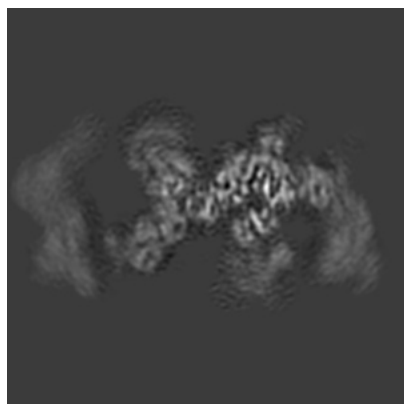


Z Index: 188

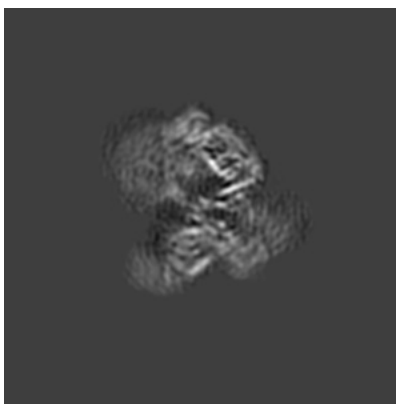
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

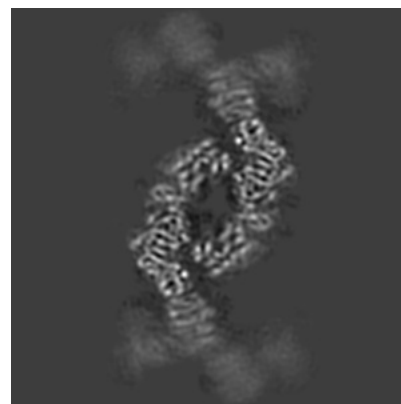
6.3.1 Primary map



X Index: 219



Y Index: 223

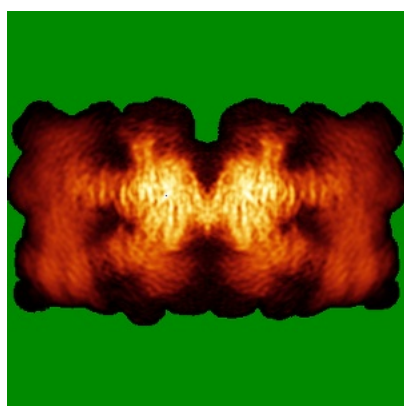


Z Index: 201

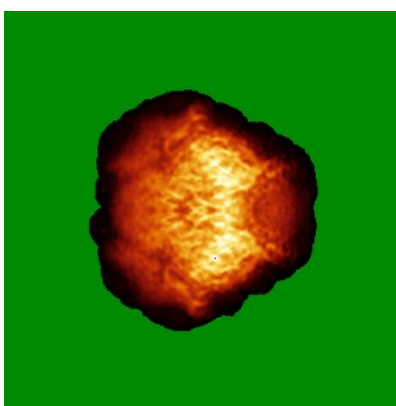
The images above show the largest variance slices of the map in three orthogonal directions.

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

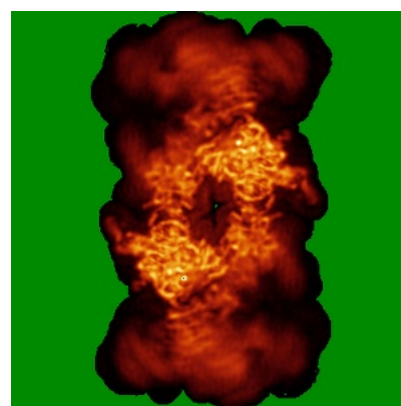
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

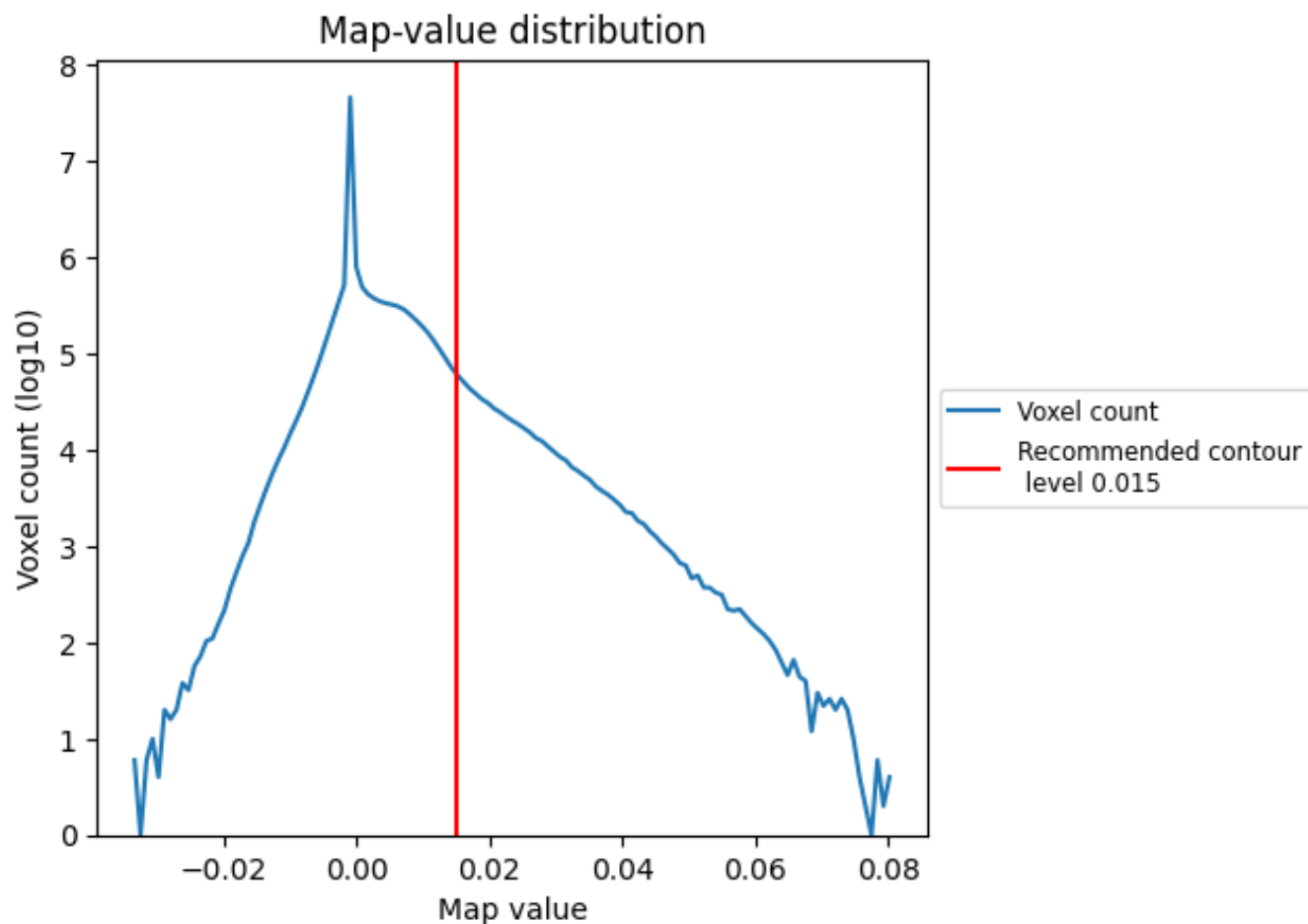
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

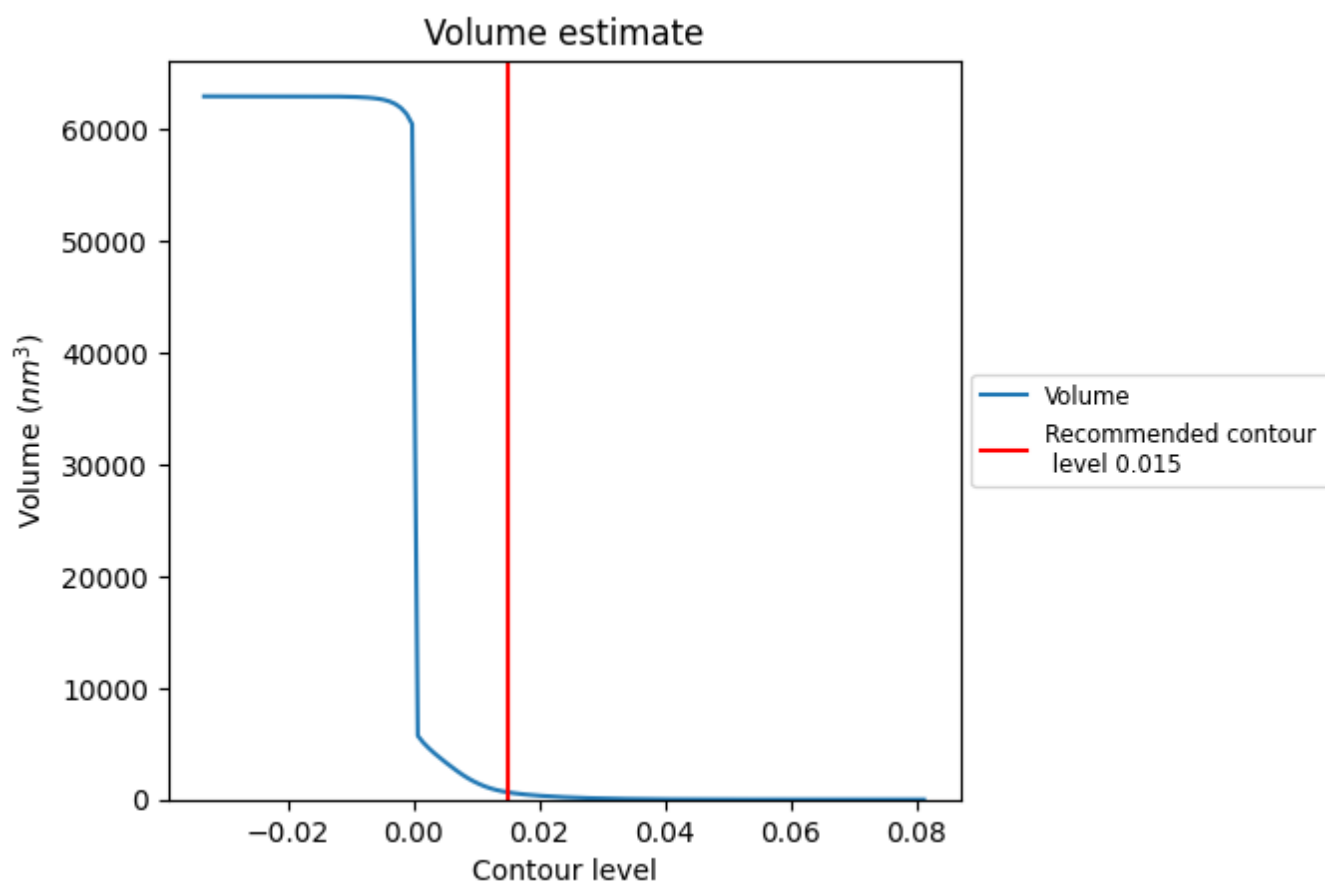
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

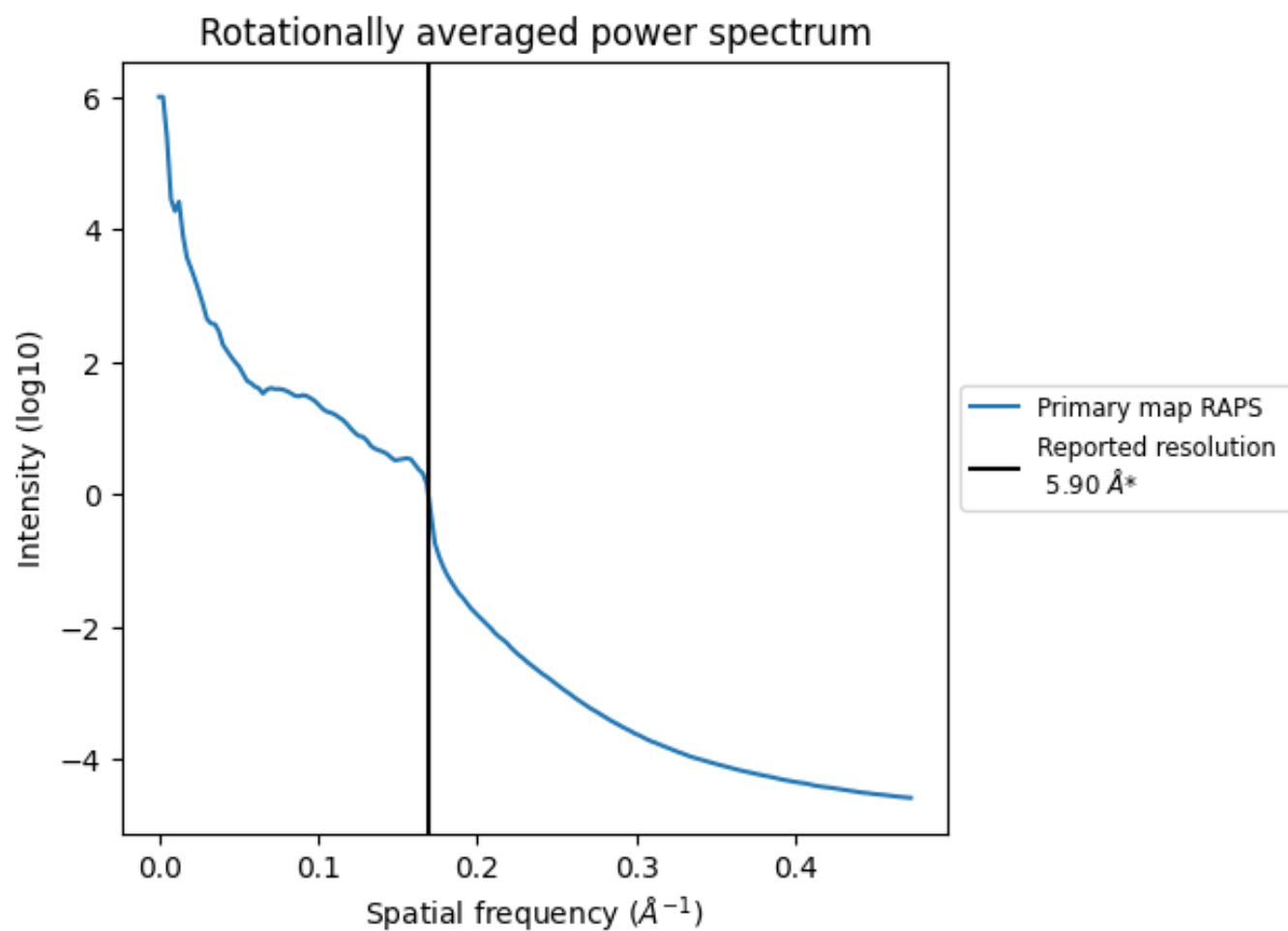
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 649 nm³; this corresponds to an approximate mass of 587 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.169 Å⁻¹

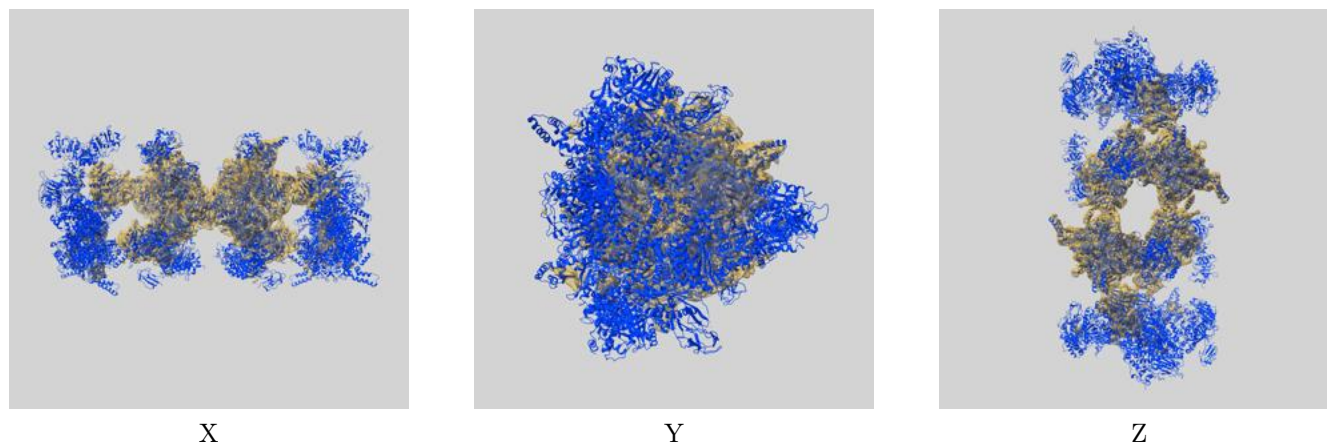
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

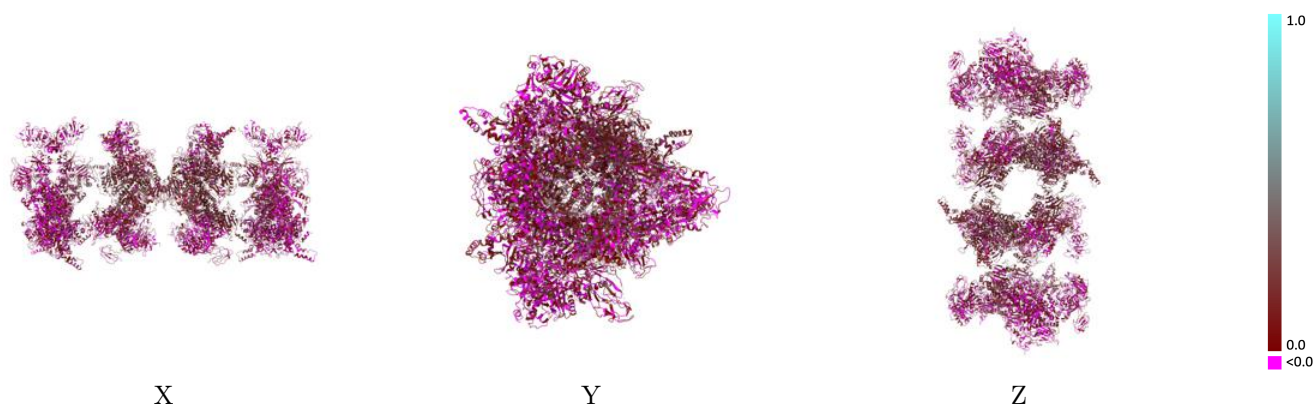
This section contains information regarding the fit between EMDB map EMD-4344 and PDB model 6G2I. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



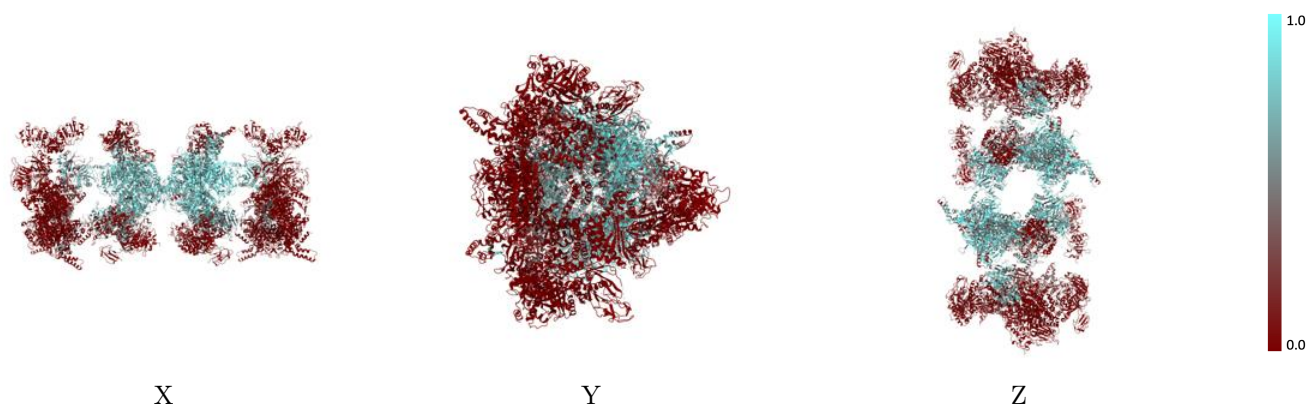
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



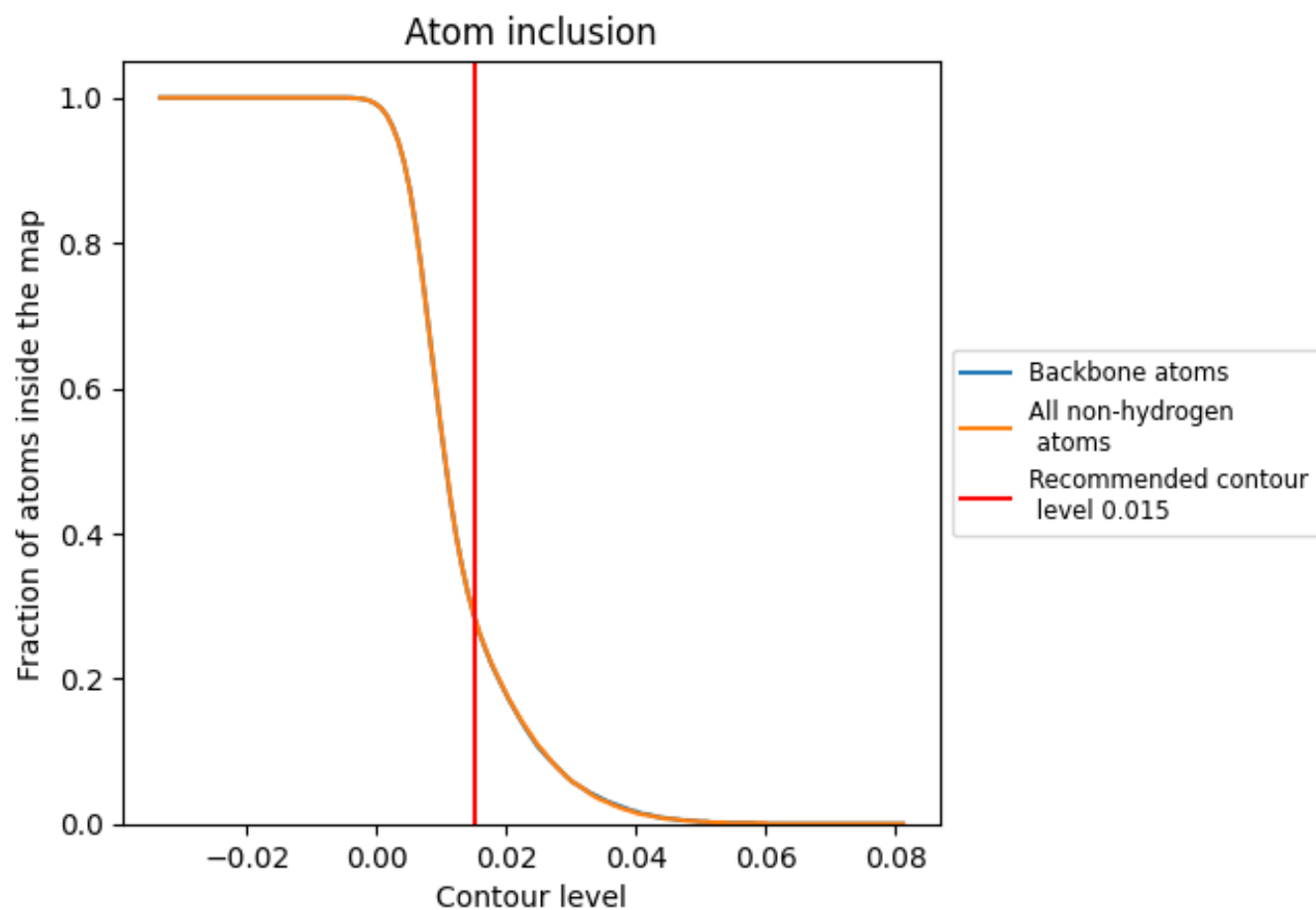
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 29% of all backbone atoms, 29% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2880	 0.1080
A	 0.2280	 0.0990
B	 0.2300	 0.1000
C	 0.4240	 0.1330
D	 0.5950	 0.1610
E	 0.5900	 0.1610
F	 0.4230	 0.1330
G	 0.0360	 0.0800
H	 0.0710	 0.0540
J	 0.0060	 0.0540
K	 0.0520	 0.0450
M	 0.0470	 0.0510
O	 0.0730	 0.0580
Q	 0.0350	 0.0770
R	 0.0060	 0.0540
S	 0.0020	 0.0510
U	 0.0020	 0.0510
W	 0.0000	 0.0370
Y	 0.0010	 0.0380

