



wwPDB X-ray Structure Validation Summary Report i

Nov 14, 2017 – 05:58 PM EST

PDB ID : 4V6B
Title : Crystal structure of human ferritin Phe167SerfsX26 mutant.
Authors : Hurley, T.D.; Vidal, R.
Deposited on : unknown
Resolution : 2.85 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the i symbol.

The following versions of software and data (see references ①) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

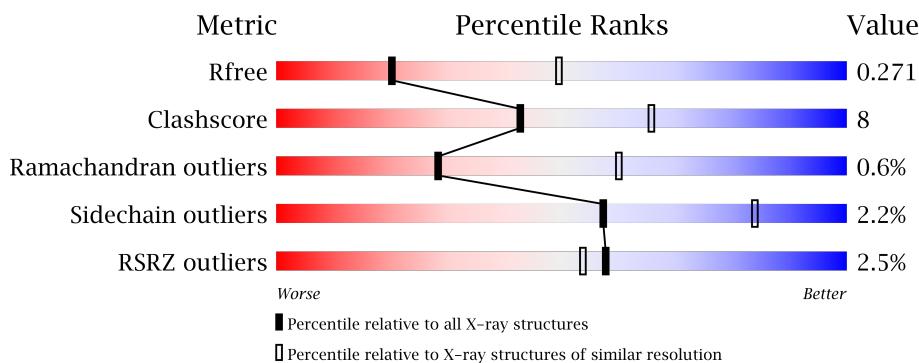
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	2469 (2.90-2.82)
Clashscore	112137	2749 (2.90-2.82)
Ramachandran outliers	110173	2687 (2.90-2.82)
Sidechain outliers	110143	2690 (2.90-2.82)
RSRZ outliers	101464	2487 (2.90-2.82)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 electron density. The numeric value is given above the bar.



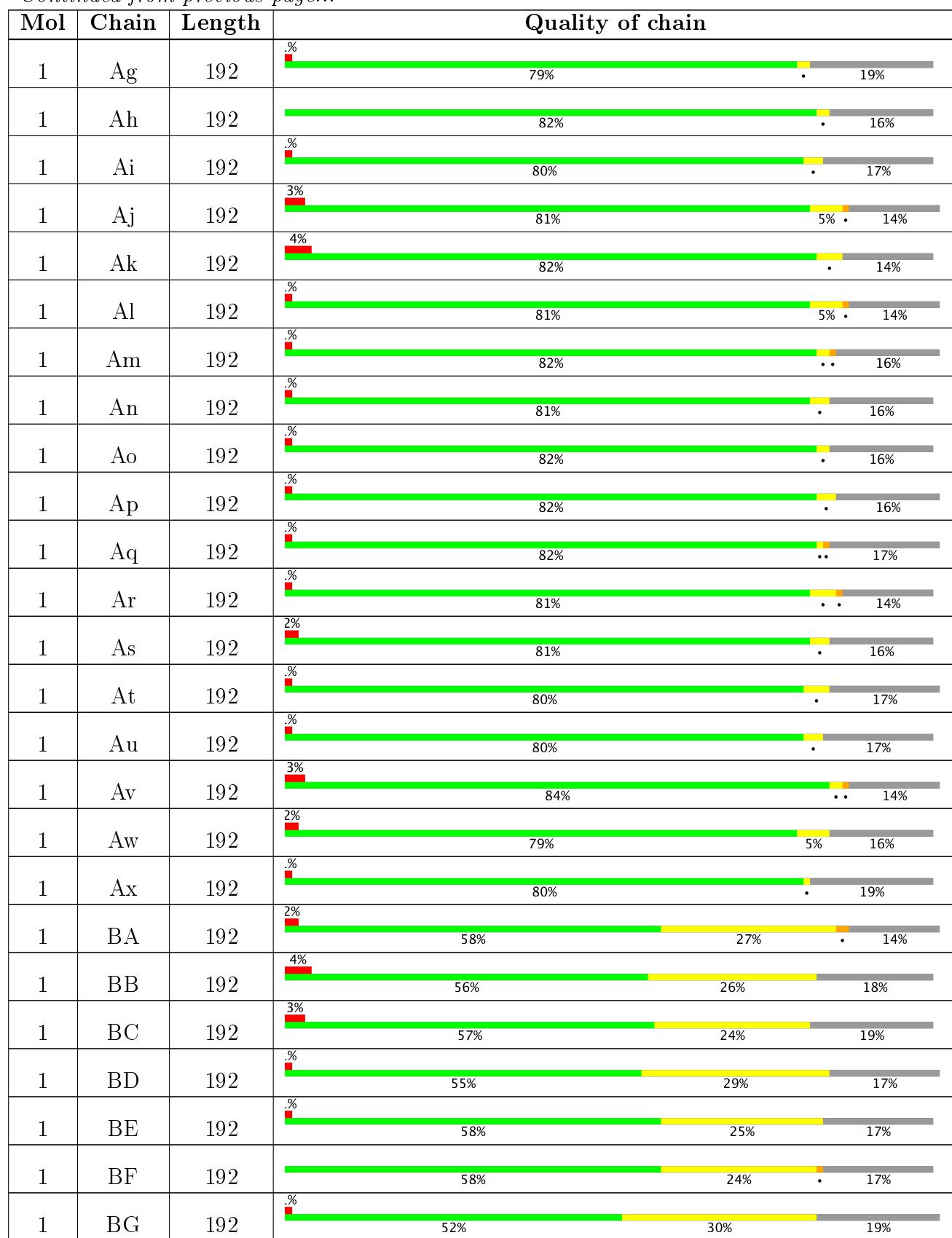
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Mol	Chain	Length	Quality of chain			
1	AF	192	.%	54%	27%	• 18%
1	AG	192	2%	58%	24%	• 17%
1	AH	192	2%	58%	25%	• 17%
1	AI	192	3%	57%	25%	• 18%
1	AJ	192	.%	55%	27%	18%
1	AK	192	.%	64%	18%	18%
1	AL	192	2%	56%	26%	• 18%
1	AM	192	.%	56%	27%	• 16%
1	AN	192	3%	55%	30%	• 14%
1	AO	192	6%	46%	38%	• 14%
1	AP	192		54%	28%	• 17%
1	AQ	192	6%	56%	28%	• 14%
1	AR	192	3%	57%	28%	15%
1	AS	192	3%	60%	23%	17%
1	AT	192	.%	47%	34%	• 18%
1	AU	192	.%	54%	29%	• 17%
1	AV	192	4%	60%	22%	• 17%
1	AW	192	.%	56%	27%	18%
1	AX	192	2%	52%	30%	• 17%
1	Aa	192	2%	82%		• 16%
1	Ab	192		80%		• 16%
1	Ac	192		82%		• 17%
1	Ad	192	2%	81%	5%	• 14%
1	Ae	192	3%	82%		• 16%
1	Af	192	.%	82%		• 16%

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Mol	Chain	Length	Quality of chain			
1	BH	192	2%	52%	28%	• 20%
1	BI	192	.%	59%	22%	19%
1	BJ	192	.%	53%	28%	• 18%
1	BK	192	4%	51%	29%	• 19%
1	BL	192		57%	24%	19%
1	BM	192	.%	64%	19%	18%
1	BN	192		58%	23%	• 17%
1	BO	192	2%	58%	24%	• 17%
1	BP	192	2%	55%	27%	• 17%
1	BQ	192	2%	64%	18%	• 17%
1	BR	192	.%	59%	24%	• 16%
1	BS	192		59%	23%	• 17%
1	BT	192	3%	55%	26%	• 18%
1	BU	192	.%	54%	29%	• 16%
1	BV	192	3%	51%	29%	• 19%
1	BW	192	2%	55%	28%	• 16%
1	BX	192	3%	48%	34%	.. 15%
1	Ba	192	2%	81%		• 18%
1	Bb	192	2%	81%		• 17%
1	Bc	192	.%	81%		• 16%
1	Bd	192	2%	82%		• 16%
1	Be	192	.%	82%		• 15%
1	Bf	192	3%	80%	6%	14%
1	Bg	192	2%	80%		• 19%
1	Bh	192	2%	81%		• 17%

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Mol	Chain	Length	Quality of chain				
1	Bi	192	.%	80%	.	18%	
1	Bj	192	2%	79%	.	20%	
1	Bk	192	.%	81%	.	17%	
1	Bl	192	.%	80%	.	17%	
1	Bm	192	2%	81%	.	17%	
1	Bn	192	2%	83%	..	14%	
1	Bo	192	2%	81%	.	19%	
1	Bp	192	4%	82%	.	16%	
1	Bq	192	2%	82%	.	17%	
1	Br	192	.%	80%	..	16%	
1	Bs	192	2%	80%	.	19%	
1	Bt	192	2%	79%	.	18%	
1	Bu	192	3%	82%	..	14%	
1	Bv	192	3%	82%	.	17%	
1	Bw	192	2%	81%	.	17%	
1	Bx	192	3%	81%	.	18%	
1	CA	192	.%	48%	34%	.	17%
1	CB	192	2%	54%	29%	.	16%
1	CC	192	.%	61%	21%	.	18%
1	CD	192	.%	62%	22%	.	16%
1	CE	192	.%	58%	24%	..	17%
1	CF	192	2%	53%	30%	.	17%
1	CG	192	.%	58%	24%	.	17%
1	CH	192	2%	52%	30%	.	17%
1	CI	192	2%	53%	30%	.	17%

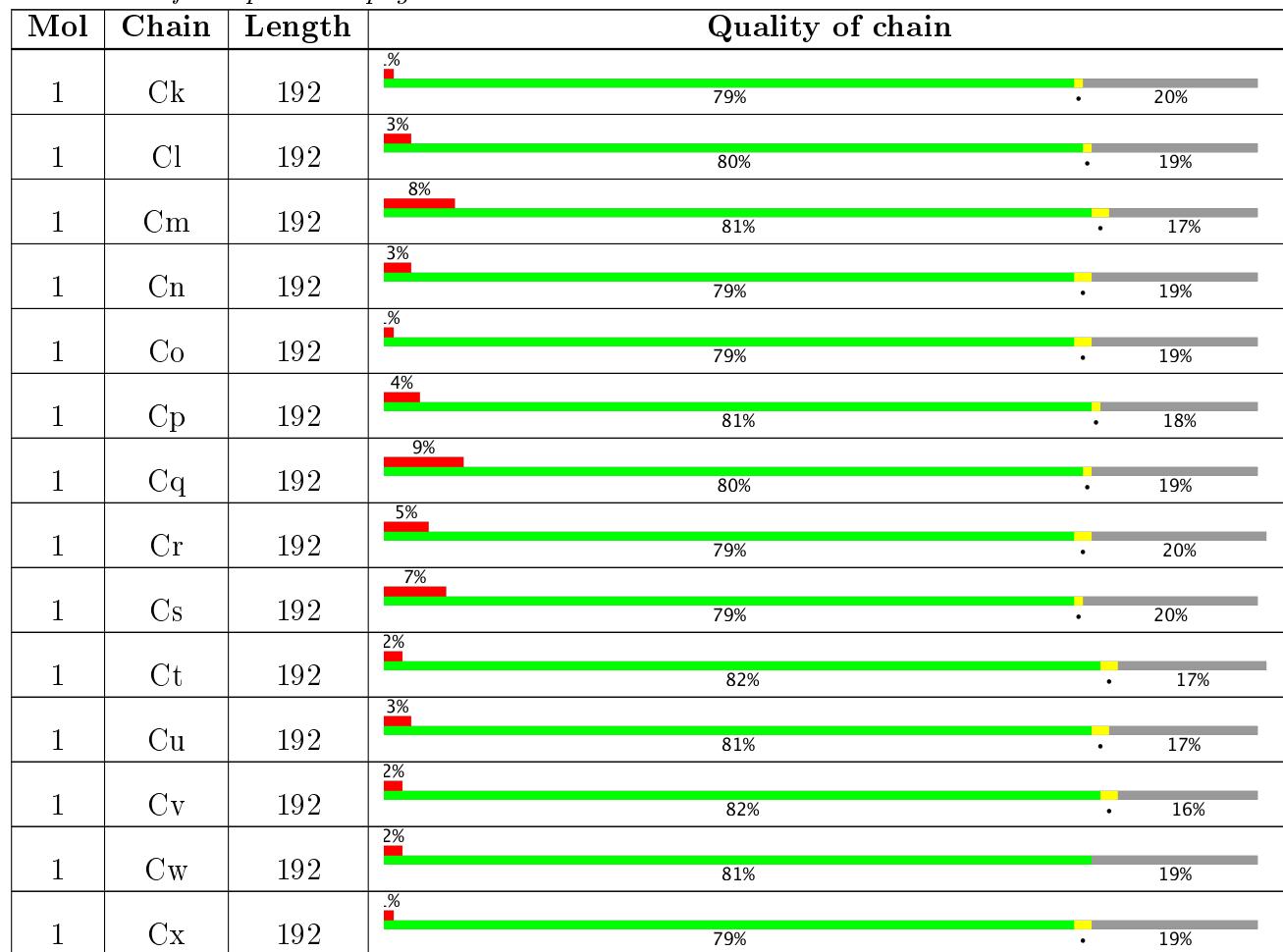
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Mol	Chain	Length	Quality of chain			
1	CJ	192	3%	49%	35%	• 14%
1	CK	192	2%	55%	28%	• 17%
1	CL	192	2%	59%	23%	• 17%
1	CM	192	2%	55%	27%	• 17%
1	CN	192	.%	56%	27%	• 16%
1	CO	192	.%	57%	26%	• 17%
1	CP	192	.%	59%	21%	• 18%
1	CQ	192	2%	57%	26%	• 16%
1	CR	192	3%	57%	28%	.. 14%
1	CS	192	2%	46%	37%	• 16%
1	CT	192	2%	54%	27%	• 18%
1	CU	192	.%	58%	24%	17%
1	CV	192	2%	56%	26%	• 18%
1	CW	192	.%	60%	20%	• 19%
1	CX	192	2%	48%	34%	• 16%
1	Ca	192	9%	79%	•	18%
1	Cb	192	2%	82%	•	17%
1	Cc	192	3%	81%	•	18%
1	Cd	192	9%	79%	•	20%
1	Ce	192	3%	79%	•	20%
1	Cf	192	9%	80%	20%	
1	Cg	192	4%	82%	•	17%
1	Ch	192	.%	81%	•	17%
1	Ci	192	8%	80%	20%	
1	Cj	192	4%	79%	•	19%

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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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CA	AB	201	-	-	-	X
2	CA	AC	201	-	-	-	X
2	CA	AF	201	-	-	-	X
2	CA	AH	201	-	-	-	X
2	CA	AM	201	-	-	-	X
2	CA	AO	201	-	-	-	X
2	CA	Aa	201	-	-	-	X
2	CA	Ac	201	-	-	-	X
2	CA	Ad	201	-	-	-	X
2	CA	Ae	201	-	-	-	X
2	CA	Ag	201	-	-	-	X
2	CA	Ah	201	-	-	-	X
2	CA	Aj	201	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CA	An	201	-	-	-	X
2	CA	BA	201	-	-	-	X
2	CA	BC	201	-	-	-	X
2	CA	BG	201	-	-	-	X
2	CA	BH	201	-	-	-	X
2	CA	BN	201	-	-	-	X
2	CA	BR	201	-	-	-	X
2	CA	Bc	201	-	-	-	X
2	CA	Bd	201	-	-	-	X
2	CA	Be	201	-	-	-	X
2	CA	Bf	201	-	-	-	X
2	CA	Bg	201	-	-	-	X
2	CA	Bu	201	-	-	-	X
2	CA	CA	201	-	-	-	X
2	CA	CB	201	-	-	-	X
2	CA	CC	201	-	-	-	X
2	CA	CE	201	-	-	-	X
2	CA	CF	201	-	-	-	X
2	CA	CO	201	-	-	-	X
2	CA	Ca	201	-	-	-	X
2	CA	Cb	201	-	-	-	X
2	CA	Ce	201	-	-	-	X
2	CA	Cl	201	-	-	-	X
2	CA	Cp	201	-	-	-	X

2 Entry composition [\(i\)](#)

There are 3 unique types of molecules in this entry. The entry contains 187090 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Ferritin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	158	Total	C	N	O	S	0	0	0
			1270	800	222	243	5			
1	Aa	161	Total	C	N	O	S	0	0	0
			1294	814	228	246	6			
1	AB	165	Total	C	N	O	S	0	0	0
			1320	832	229	253	6			
1	Ab	161	Total	C	N	O	S	0	0	0
			1287	810	225	246	6			
1	AC	161	Total	C	N	O	S	0	0	0
			1294	814	228	246	6			
1	Ac	160	Total	C	N	O	S	0	0	0
			1283	808	224	245	6			
1	AD	159	Total	C	N	O	S	0	0	0
			1275	803	223	244	5			
1	Ad	165	Total	C	N	O	S	0	0	0
			1320	832	229	253	6			
1	AE	165	Total	C	N	O	S	0	0	0
			1320	832	229	253	6			
1	Ae	162	Total	C	N	O	S	0	0	0
			1298	816	229	247	6			
1	AF	158	Total	C	N	O	S	0	0	0
			1269	800	222	241	6			
1	Af	161	Total	C	N	O	S	0	0	0
			1294	814	228	246	6			
1	AG	159	Total	C	N	O	S	0	0	0
			1275	803	223	244	5			
1	Ag	155	Total	C	N	O	S	0	0	0
			1254	791	219	238	6			
1	AH	160	Total	C	N	O	S	0	0	0
			1283	808	224	245	6			
1	Ah	161	Total	C	N	O	S	0	0	0
			1294	814	228	246	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AI	158	Total	C	N	O	S	0	0	0
			1269	800	222	241	6			
1	Ai	159	Total	C	N	O	S	0	0	0
			1278	805	223	244	6			
1	AJ	157	Total	C	N	O	S	0	0	0
			1262	795	221	240	6			
1	Aj	165	Total	C	N	O	S	0	0	0
			1320	832	229	253	6			
1	AK	157	Total	C	N	O	S	0	0	0
			1269	799	224	240	6			
1	Ak	165	Total	C	N	O	S	0	0	0
			1320	832	229	253	6			
1	AL	157	Total	C	N	O	S	0	0	0
			1261	795	221	240	5			
1	Al	165	Total	C	N	O	S	0	0	0
			1320	832	229	253	6			
1	AM	162	Total	C	N	O	S	0	0	0
			1298	816	229	247	6			
1	Am	162	Total	C	N	O	S	0	0	0
			1298	816	229	247	6			
1	AN	165	Total	C	N	O	S	0	0	0
			1320	832	229	253	6			
1	An	161	Total	C	N	O	S	0	0	0
			1287	810	225	246	6			
1	AO	165	Total	C	N	O	S	0	0	0
			1320	832	229	253	6			
1	Ao	161	Total	C	N	O	S	0	0	0
			1294	814	228	246	6			
1	AP	159	Total	C	N	O	S	0	0	0
			1278	805	223	244	6			
1	Ap	162	Total	C	N	O	S	0	0	0
			1298	816	229	247	6			
1	AQ	165	Total	C	N	O	S	0	0	0
			1319	829	232	252	6			
1	Aq	160	Total	C	N	O	S	0	0	0
			1283	808	224	245	6			
1	AR	164	Total	C	N	O	S	0	0	0
			1308	823	228	251	6			
1	Ar	165	Total	C	N	O	S	0	0	0
			1320	832	229	253	6			
1	AS	160	Total	C	N	O	S	0	0	0
			1279	805	224	245	5			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	As	161	Total	C	N	O	S		
			1294	814	228	246	6	0	0
1	AT	158	Total	C	N	O	S		
			1270	800	222	243	5	0	0
1	At	160	Total	C	N	O	S		
			1283	808	224	245	6	0	0
1	AU	160	Total	C	N	O	S		
			1283	808	224	245	6	0	0
1	Au	160	Total	C	N	O	S		
			1283	808	224	245	6	0	0
1	AV	160	Total	C	N	O	S		
			1279	805	224	245	5	0	0
1	Av	165	Total	C	N	O	S		
			1319	829	232	252	6	0	0
1	AW	158	Total	C	N	O	S		
			1270	800	222	243	5	0	0
1	Aw	161	Total	C	N	O	S		
			1287	810	225	246	6	0	0
1	AX	160	Total	C	N	O	S		
			1283	808	224	245	6	0	0
1	Ax	155	Total	C	N	O	S		
			1254	791	219	238	6	0	0
1	BA	166	Total	C	N	O	S		
			1331	838	233	254	6	0	0
1	Ba	158	Total	C	N	O	S		
			1269	800	222	241	6	0	0
1	BB	157	Total	C	N	O	S		
			1269	799	224	240	6	0	0
1	Bb	159	Total	C	N	O	S		
			1278	805	223	244	6	0	0
1	BC	155	Total	C	N	O	S		
			1250	788	219	238	5	0	0
1	Bc	161	Total	C	N	O	S		
			1294	814	228	246	6	0	0
1	BD	160	Total	C	N	O	S		
			1289	811	227	245	6	0	0
1	Bd	161	Total	C	N	O	S		
			1294	814	228	246	6	0	0
1	BE	159	Total	C	N	O	S		
			1278	805	223	244	6	0	0
1	Be	163	Total	C	N	O	S		
			1300	818	227	250	5	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BF	159	Total	C	N	O	S	0	0	0
			1275	803	223	244	5			
1	Bf	165	Total	C	N	O	S	0	0	0
			1320	832	229	253	6			
1	BG	156	Total	C	N	O	S	0	0	0
			1258	793	220	239	6			
1	Bg	156	Total	C	N	O	S	0	0	0
			1258	793	220	239	6			
1	BH	154	Total	C	N	O	S	0	0	0
			1246	786	218	237	5			
1	Bh	159	Total	C	N	O	S	0	0	0
			1278	805	223	244	6			
1	BI	155	Total	C	N	O	S	0	0	0
			1254	791	219	238	6			
1	Bi	157	Total	C	N	O	S	0	0	0
			1269	799	224	240	6			
1	BJ	157	Total	C	N	O	S	0	0	0
			1261	795	221	240	5			
1	Bj	154	Total	C	N	O	S	0	0	0
			1244	785	218	236	5			
1	BK	156	Total	C	N	O	S	0	0	0
			1258	793	220	239	6			
1	Bk	159	Total	C	N	O	S	0	0	0
			1278	805	223	244	6			
1	BL	155	Total	C	N	O	S	0	0	0
			1254	791	219	238	6			
1	Bl	159	Total	C	N	O	S	0	0	0
			1278	805	223	244	6			
1	BM	158	Total	C	N	O	S	0	0	0
			1270	800	222	243	5			
1	Bm	159	Total	C	N	O	S	0	0	0
			1275	803	223	244	5			
1	BN	159	Total	C	N	O	S	0	0	0
			1275	803	223	244	5			
1	Bn	165	Total	C	N	O	S	0	0	0
			1319	829	232	252	6			
1	BO	160	Total	C	N	O	S	0	0	0
			1283	808	224	245	6			
1	Bo	156	Total	C	N	O	S	0	0	0
			1258	793	220	239	6			
1	BP	159	Total	C	N	O	S	0	0	0
			1275	803	223	244	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Bp	162	Total	C	N	O	S	0	0	0
			1298	816	229	247	6			
1	BQ	160	Total	C	N	O	S	0	0	0
			1283	808	224	245	6			
1	Bq	160	Total	C	N	O	S	0	0	0
			1289	811	227	245	6			
1	BR	161	Total	C	N	O	S	0	0	0
			1294	814	228	246	6			
1	Br	161	Total	C	N	O	S	0	0	0
			1294	814	228	246	6			
1	BS	159	Total	C	N	O	S	0	0	0
			1280	806	226	242	6			
1	Bs	155	Total	C	N	O	S	0	0	0
			1254	791	219	238	6			
1	BT	157	Total	C	N	O	S	0	0	0
			1261	795	221	240	5			
1	Bt	158	Total	C	N	O	S	0	0	0
			1269	800	222	241	6			
1	BU	162	Total	C	N	O	S	0	0	0
			1298	816	229	247	6			
1	Bu	165	Total	C	N	O	S	0	0	0
			1320	832	229	253	6			
1	BV	156	Total	C	N	O	S	0	0	0
			1254	790	220	239	5			
1	Bv	160	Total	C	N	O	S	0	0	0
			1283	808	224	245	6			
1	BW	161	Total	C	N	O	S	0	0	0
			1287	810	225	246	6			
1	Bw	159	Total	C	N	O	S	0	0	0
			1275	803	223	244	5			
1	BX	163	Total	C	N	O	S	0	0	0
			1300	818	227	250	5			
1	Bx	157	Total	C	N	O	S	0	0	0
			1261	795	221	240	5			
1	CA	160	Total	C	N	O	S	0	0	0
			1283	808	224	245	6			
1	Ca	158	Total	C	N	O	S	0	0	0
			1269	800	222	242	5			
1	CB	161	Total	C	N	O	S	0	0	0
			1287	810	225	246	6			
1	Cb	159	Total	C	N	O	S	0	0	0
			1275	803	223	244	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	CC	157	Total	C 1261	N 795	O 221	S 240	5	0	0
1	Cc	157	Total	C 1264	N 797	O 221	S 241	5	0	0
1	CD	161	Total	C 1294	N 814	O 228	S 246	6	0	0
1	Cd	153	Total	C 1240	N 783	O 217	S 235	5	0	0
1	CE	160	Total	C 1289	N 811	O 227	S 245	6	0	0
1	Ce	154	Total	C 1246	N 786	O 218	S 237	5	0	0
1	CF	160	Total	C 1279	N 805	O 224	S 245	5	0	0
1	Cf	153	Total	C 1238	N 780	O 217	S 236	5	0	0
1	CG	160	Total	C 1289	N 811	O 227	S 245	6	0	0
1	Cg	160	Total	C 1279	N 805	O 224	S 245	5	0	0
1	CH	159	Total	C 1278	N 805	O 223	S 244	6	0	0
1	Ch	159	Total	C 1275	N 803	O 223	S 244	5	0	0
1	CI	160	Total	C 1283	N 808	O 224	S 245	6	0	0
1	Ci	153	Total	C 1240	N 783	O 217	S 235	5	0	0
1	CJ	165	Total	C 1319	N 829	O 232	S 252	6	0	0
1	Cj	156	Total	C 1265	N 797	O 223	S 239	6	0	0
1	CK	160	Total	C 1283	N 808	O 224	S 245	6	0	0
1	Ck	154	Total	C 1246	N 786	O 218	S 237	5	0	0
1	CL	159	Total	C 1278	N 805	O 223	S 244	6	0	0
1	Cl	155	Total	C 1250	N 788	O 219	S 238	5	0	0
1	CM	159	Total	C 1278	N 805	O 223	S 244	6	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Cm	159	Total	C	N	O	S	0	0	0
			1275	803	223	244	5			
1	CN	161	Total	C	N	O	S	0	0	0
			1287	810	225	246	6			
1	Cn	155	Total	C	N	O	S	0	0	0
			1254	791	219	238	6			
1	CO	159	Total	C	N	O	S	0	0	0
			1280	806	226	242	6			
1	Co	155	Total	C	N	O	S	0	0	0
			1250	788	219	238	5			
1	CP	158	Total	C	N	O	S	0	0	0
			1269	800	222	241	6			
1	Cp	158	Total	C	N	O	S	0	0	0
			1269	800	222	241	6			
1	CQ	162	Total	C	N	O	S	0	0	0
			1298	816	229	247	6			
1	Cq	155	Total	C	N	O	S	0	0	0
			1250	788	219	238	5			
1	CR	166	Total	C	N	O	S	0	0	0
			1331	838	233	254	6			
1	Cr	154	Total	C	N	O	S	0	0	0
			1246	786	218	237	5			
1	CS	161	Total	C	N	O	S	0	0	0
			1294	814	228	246	6			
1	Cs	154	Total	C	N	O	S	0	0	0
			1244	785	218	236	5			
1	CT	158	Total	C	N	O	S	0	0	0
			1269	800	222	241	6			
1	Ct	160	Total	C	N	O	S	0	0	0
			1279	805	224	245	5			
1	CU	159	Total	C	N	O	S	0	0	0
			1278	805	223	244	6			
1	Cu	159	Total	C	N	O	S	0	0	0
			1275	803	223	244	5			
1	CV	158	Total	C	N	O	S	0	0	0
			1270	800	222	243	5			
1	Cv	161	Total	C	N	O	S	0	0	0
			1287	810	225	246	6			
1	CW	155	Total	C	N	O	S	0	0	0
			1254	791	219	238	6			
1	Cw	155	Total	C	N	O	S	0	0	0
			1250	788	219	238	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	CX	161	Total	C	N	O	S	0	0	0
			1294	814	228	246	6			

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Cx	156	Total	C	N	O	S	0	0	0
			1265	797	223	239	6			

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Aa	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AB	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ab	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AC	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ac	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AD	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ad	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AE	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ae	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AF	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Af	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AG	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ag	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AH	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ah	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AI	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ai	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AJ	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Aj	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AK	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ak	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AL	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
A1	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AM	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Am	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AN	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
An	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AO	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ao	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AP	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ap	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AQ	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Aq	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3

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Chain	Residue	Modelled	Actual	Comment	Reference
AR	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ar	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AS	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
As	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AT	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
At	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AU	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Au	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AV	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Av	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AW	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Aw	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
AX	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ax	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BA	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ba	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BB	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bb	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BC	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bc	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BD	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bd	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BE	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Be	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BF	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bf	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BG	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bg	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BH	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bh	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BI	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bi	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BJ	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bj	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BK	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bk	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BL	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bl	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BM	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bm	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BN	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bn	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3

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Chain	Residue	Modelled	Actual	Comment	Reference
BO	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bo	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BP	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bp	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BQ	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bq	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BR	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Br	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BS	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bs	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BT	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bt	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BU	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bu	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BV	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bv	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BW	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bw	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
BX	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Bx	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CA	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ca	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CB	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cb	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CC	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cc	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CD	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cd	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CE	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ce	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CF	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cf	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CG	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cg	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CH	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ch	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CI	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ci	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CJ	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cj	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CK	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ck	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3

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Chain	Residue	Modelled	Actual	Comment	Reference
CL	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
C1	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CM	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cm	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CN	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cn	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CO	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Co	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CP	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cp	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CQ	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cq	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CR	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cr	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CS	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cs	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CT	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Ct	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CU	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cu	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CV	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cv	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CW	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cw	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
CX	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3
Cx	0	ARG	-	EXPRESSION TAG	UNP Q6S4P3

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	Ag	1	Total Ca 1 1	0	0
2	BA	1	Total Ca 1 1	0	0
2	CA	1	Total Ca 1 1	0	0
2	Ah	1	Total Ca 1 1	0	0
2	AB	1	Total Ca 1 1	0	0
2	Ac	1	Total Ca 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	Bd	1	Total Ca 1 1	0	0
2	CD	1	Total Ca 1 1	0	0
2	Ce	1	Total Ca 1 1	0	0
2	Cl	1	Total Ca 1 1	0	0
2	BB	1	Total Ca 1 1	0	0
2	Ba	1	Total Ca 1 1	0	0
2	Ca	1	Total Ca 1 1	0	0
2	CO	1	Total Ca 1 1	0	0
2	CF	1	Total Ca 1 1	0	0
2	Be	1	Total Ca 1 1	0	0
2	Cb	1	Total Ca 1 1	0	0
2	AA	1	Total Ca 1 1	0	0
2	An	1	Total Ca 1 1	0	0
2	CH	1	Total Ca 1 1	0	0
2	BC	1	Total Ca 1 1	0	0
2	AM	1	Total Ca 1 1	0	0
2	Bb	1	Total Ca 1 1	0	0
2	Aj	1	Total Ca 1 1	0	0
2	BN	1	Total Ca 1 1	0	0
2	Ae	1	Total Ca 1 1	0	0
2	BG	1	Total Ca 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	CC	1	Total Ca 1 1	0	0
2	Bf	1	Total Ca 1 1	0	0
2	BR	1	Total Ca 1 1	0	0
2	Aa	1	Total Ca 1 1	0	0
2	CE	1	Total Ca 1 1	0	0
2	Cn	1	Total Ca 1 1	0	0
2	Ck	1	Total Ca 1 1	0	0
2	AL	1	Total Ca 1 1	0	0
2	Bc	1	Total Ca 1 1	0	0
2	Cg	1	Total Ca 1 1	0	0
2	Bu	1	Total Ca 1 1	0	0
2	Ad	1	Total Ca 1 1	0	0
2	AH	1	Total Ca 1 1	0	0
2	Bg	1	Total Ca 1 1	0	0
2	AC	1	Total Ca 1 1	0	0
2	CB	1	Total Ca 1 1	0	0
2	Cp	1	Total Ca 1 1	0	0
2	BD	1	Total Ca 1 1	0	0
2	AO	1	Total Ca 1 1	0	0
2	AF	1	Total Ca 1 1	0	0
2	BH	1	Total Ca 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	AA	10	Total O 10 10	0	0
3	Aa	47	Total O 47 47	0	0
3	AB	14	Total O 14 14	0	0
3	Ab	30	Total O 30 30	0	0
3	AC	15	Total O 15 15	0	0
3	Ac	32	Total O 32 32	0	0
3	AD	8	Total O 8 8	0	0
3	Ad	37	Total O 37 37	0	0
3	AE	27	Total O 27 27	0	0
3	Ae	26	Total O 26 26	0	0
3	AF	16	Total O 16 16	0	0
3	Af	48	Total O 48 48	0	0
3	AG	27	Total O 27 27	0	0
3	Ag	37	Total O 37 37	0	0
3	AH	28	Total O 28 28	0	0
3	Ah	28	Total O 28 28	0	0
3	AI	6	Total O 6 6	0	0
3	Ai	40	Total O 40 40	0	0
3	AJ	9	Total O 9 9	0	0
3	Aj	28	Total O 28 28	0	0
3	AK	15	Total O 15 15	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	Ak	37	Total O 37 37	0	0
3	AL	11	Total O 11 11	0	0
3	Al	25	Total O 25 25	0	0
3	AM	26	Total O 26 26	0	0
3	Am	45	Total O 45 45	0	0
3	AN	17	Total O 17 17	0	0
3	An	41	Total O 41 41	0	0
3	AO	20	Total O 20 20	0	0
3	Ao	39	Total O 39 39	0	0
3	AP	25	Total O 25 25	0	0
3	Ap	32	Total O 32 32	0	0
3	AQ	21	Total O 21 21	0	0
3	Aq	33	Total O 33 33	0	0
3	AR	18	Total O 18 18	0	0
3	Ar	40	Total O 40 40	0	0
3	AS	20	Total O 20 20	0	0
3	As	44	Total O 44 44	0	0
3	AT	22	Total O 22 22	0	0
3	At	31	Total O 31 31	0	0
3	AU	20	Total O 20 20	0	0
3	Au	31	Total O 31 31	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	AV	17	Total O 17 17	0	0
3	Av	19	Total O 19 19	0	0
3	AW	19	Total O 19 19	0	0
3	Aw	34	Total O 34 34	0	0
3	AX	33	Total O 33 33	0	0
3	Ax	31	Total O 31 31	0	0
3	BA	15	Total O 15 15	0	0
3	Ba	10	Total O 10 10	0	0
3	BB	5	Total O 5 5	0	0
3	Bb	4	Total O 4 4	0	0
3	BC	2	Total O 2 2	0	0
3	Bc	32	Total O 32 32	0	0
3	BD	10	Total O 10 10	0	0
3	Bd	27	Total O 27 27	0	0
3	BE	15	Total O 15 15	0	0
3	Be	26	Total O 26 26	0	0
3	BF	32	Total O 32 32	0	0
3	Bf	26	Total O 26 26	0	0
3	BG	7	Total O 7 7	0	0
3	Bg	7	Total O 7 7	0	0
3	BH	11	Total O 11 11	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	Bh	19	Total O 19 19	0	0
3	BI	20	Total O 20 20	0	0
3	Bi	7	Total O 7 7	0	0
3	BJ	8	Total O 8 8	0	0
3	Bj	6	Total O 6 6	0	0
3	BK	6	Total O 6 6	0	0
3	Bk	6	Total O 6 6	0	0
3	BL	10	Total O 10 10	0	0
3	Bl	23	Total O 23 23	0	0
3	BM	25	Total O 25 25	0	0
3	Bm	25	Total O 25 25	0	0
3	BN	18	Total O 18 18	0	0
3	Bn	11	Total O 11 11	0	0
3	BO	13	Total O 13 13	0	0
3	Bo	9	Total O 9 9	0	0
3	BP	10	Total O 10 10	0	0
3	Bp	31	Total O 31 31	0	0
3	BQ	30	Total O 30 30	0	0
3	Bq	18	Total O 18 18	0	0
3	BR	21	Total O 21 21	0	0
3	Br	35	Total O 35 35	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	BS	37	Total O 37 37	0	0
3	Bs	15	Total O 15 15	0	0
3	BT	12	Total O 12 12	0	0
3	Bt	11	Total O 11 11	0	0
3	BU	5	Total O 5 5	0	0
3	Bu	28	Total O 28 28	0	0
3	BV	5	Total O 5 5	0	0
3	Bv	25	Total O 25 25	0	0
3	BW	25	Total O 25 25	0	0
3	Bw	39	Total O 39 39	0	0
3	BX	3	Total O 3 3	0	0
3	Bx	7	Total O 7 7	0	0
3	CA	29	Total O 29 29	0	0
3	Ca	11	Total O 11 11	0	0
3	CB	16	Total O 16 16	0	0
3	Cb	6	Total O 6 6	0	0
3	CC	7	Total O 7 7	0	0
3	Cc	7	Total O 7 7	0	0
3	CD	28	Total O 28 28	0	0
3	Cd	6	Total O 6 6	0	0
3	CE	15	Total O 15 15	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	Ce	6	Total O 6 6	0	0
3	CF	25	Total O 25 25	0	0
3	Cf	8	Total O 8 8	0	0
3	CG	19	Total O 19 19	0	0
3	Cg	16	Total O 16 16	0	0
3	CH	10	Total O 10 10	0	0
3	Ch	18	Total O 18 18	0	0
3	CI	30	Total O 30 30	0	0
3	Ci	9	Total O 9 9	0	0
3	CJ	18	Total O 18 18	0	0
3	Cj	9	Total O 9 9	0	0
3	CK	12	Total O 12 12	0	0
3	Ck	11	Total O 11 11	0	0
3	CL	7	Total O 7 7	0	0
3	Cl	2	Total O 2 2	0	0
3	CM	23	Total O 23 23	0	0
3	Cm	2	Total O 2 2	0	0
3	CN	25	Total O 25 25	0	0
3	Cn	4	Total O 4 4	0	0
3	CO	14	Total O 14 14	0	0
3	Co	12	Total O 12 12	0	0

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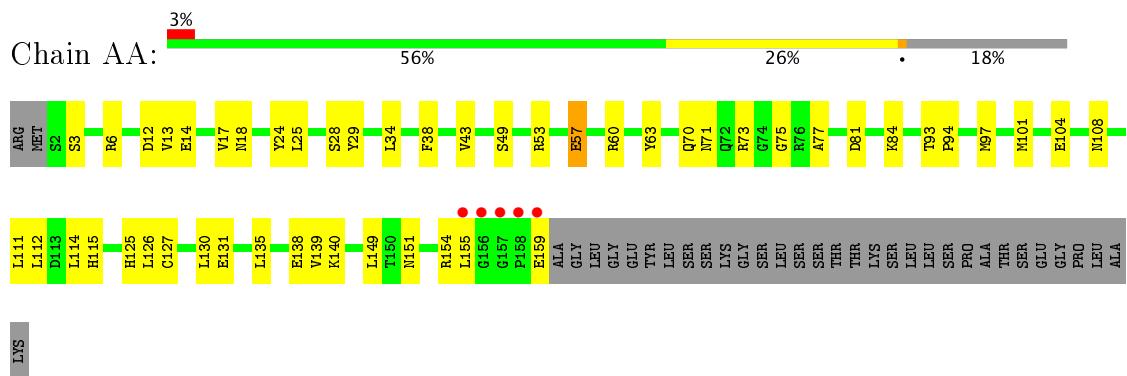
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	CP	14	Total O 14 14	0	0
3	Cp	10	Total O 10 10	0	0
3	CQ	41	Total O 41 41	0	0
3	Cq	2	Total O 2 2	0	0
3	CR	20	Total O 20 20	0	0
3	Cr	4	Total O 4 4	0	0
3	CS	28	Total O 28 28	0	0
3	CT	15	Total O 15 15	0	0
3	Ct	17	Total O 17 17	0	0
3	CU	3	Total O 3 3	0	0
3	Cu	12	Total O 12 12	0	0
3	CV	8	Total O 8 8	0	0
3	Cv	4	Total O 4 4	0	0
3	CW	15	Total O 15 15	0	0
3	Cw	10	Total O 10 10	0	0
3	CX	21	Total O 21 21	0	0
3	Cx	12	Total O 12 12	0	0

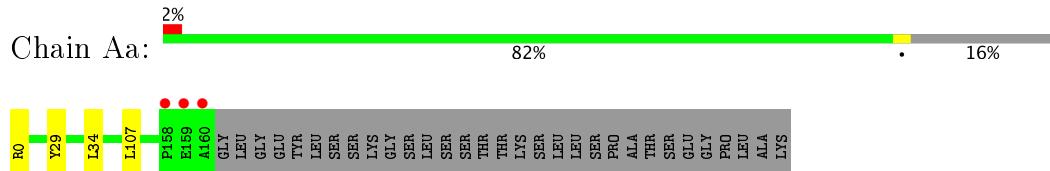
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

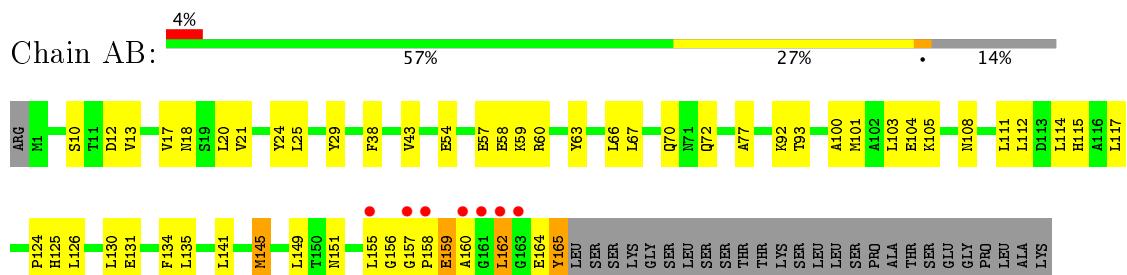
- Molecule 1: Ferritin



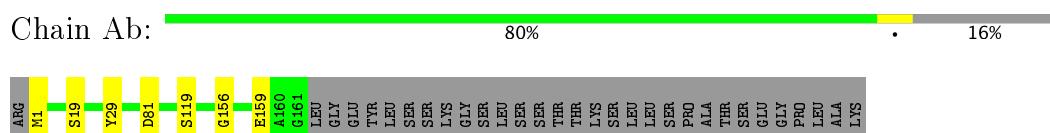
- Molecule 1: Ferritin



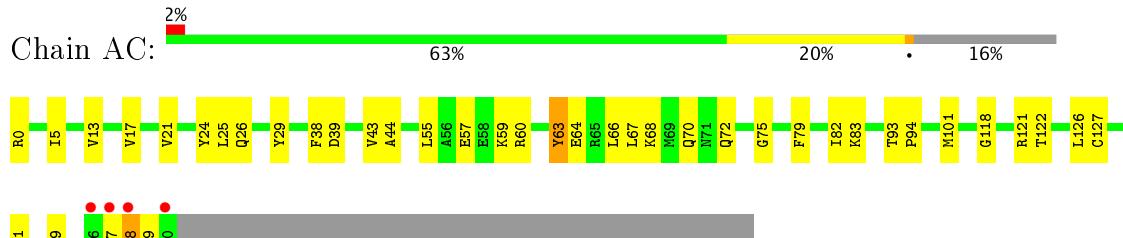
- Molecule 1: Ferritin



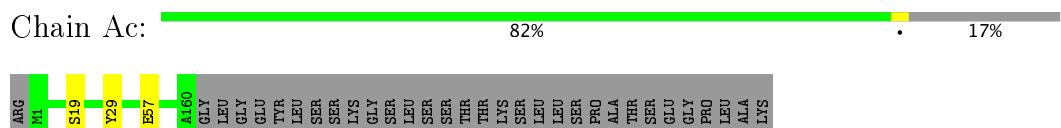
- Molecule 1: Ferritin



- Molecule 1: Ferritin



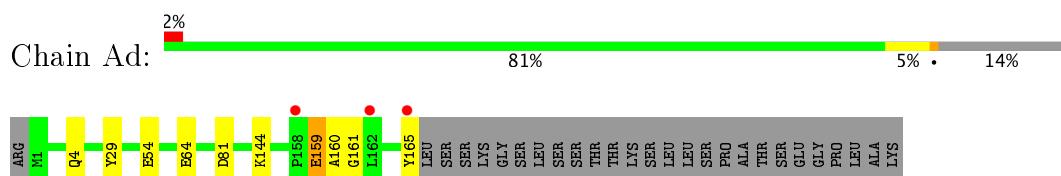
- Molecule 1: Ferritin



- Molecule 1: Ferritin



- Molecule 1: Ferritin



- Molecule 1: Ferritin

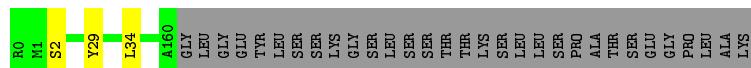


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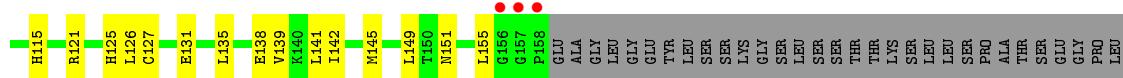
- Molecule 1: Ferritin

Chain Ah: 82% • 16%



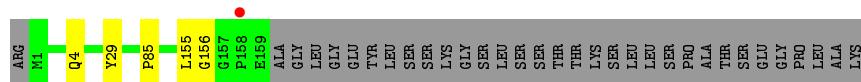
- Molecule 1: Ferritin

Chain AI: 3% 57% 25% • 18%



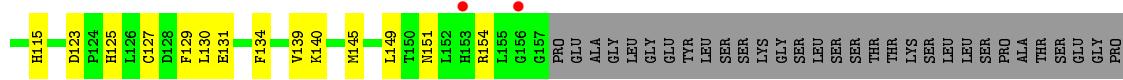
- Molecule 1: Ferritin

Chain Ai: % 80% • 17%



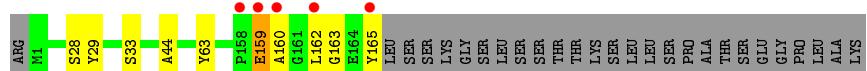
- Molecule 1: Ferritin

Chain AJ: % 55% 27% 18%

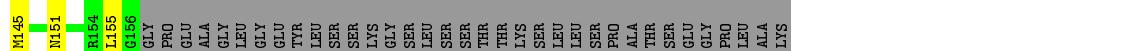


- Molecule 1: Ferritin

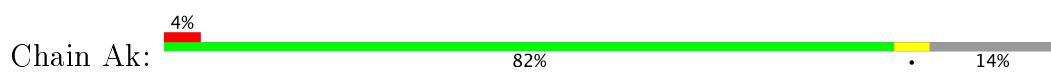
Chain Aj: 3% 81% 5% • 14%



- Molecule 1: Ferritin



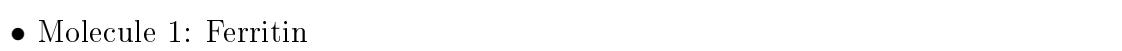
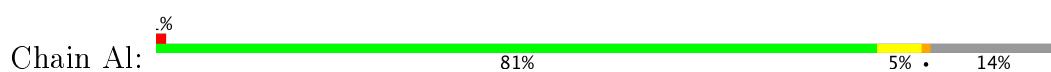
- Molecule 1: Ferritin



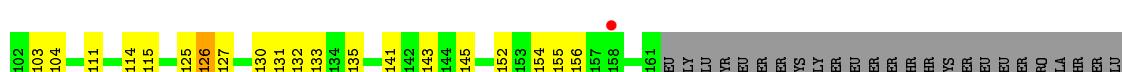
- Molecule 1: Ferritin



- Molecule 1: Ferritin

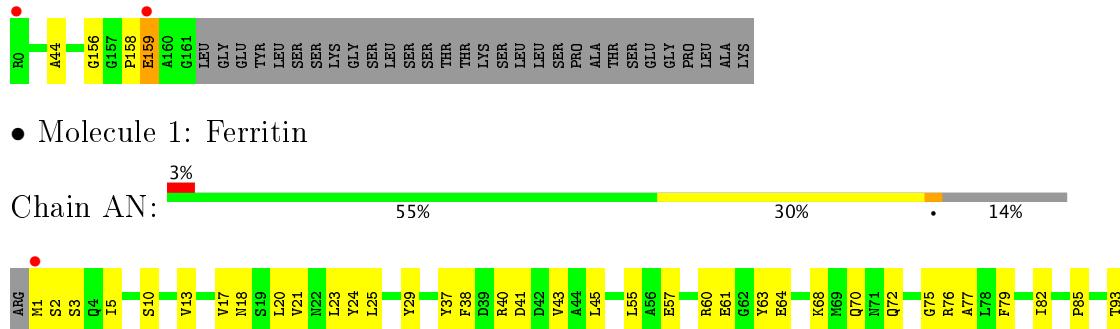
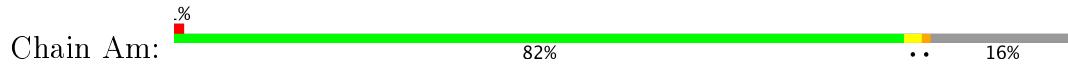


- Molecule 1: Ferritin



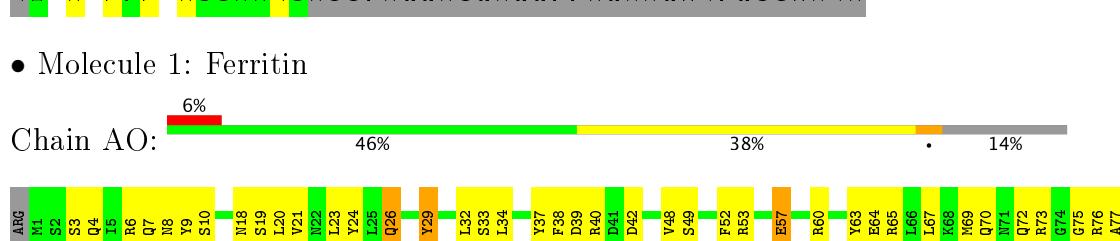
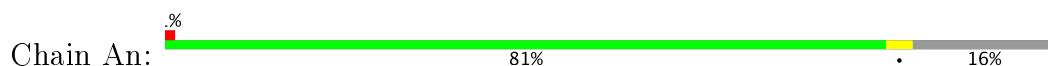
GLY
PRO
LEU
ALA
LYS

- Molecule 1: Ferritin



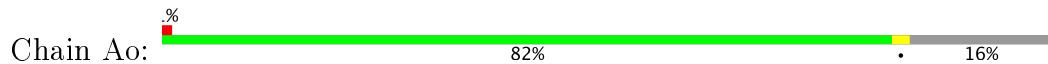
GLY
PRO
LEU
ALA
LYS

- Molecule 1: Ferritin



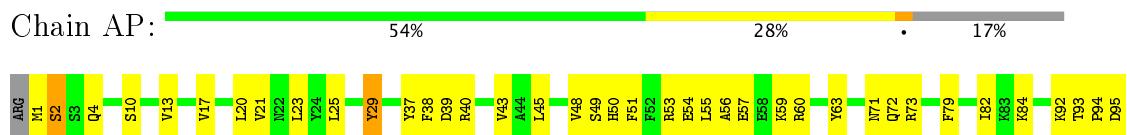
LYS
GLY
SER
LEU
SER
THR
THR
LYS
GLY
PRO
ALA
THR
SER
SER
SER
GLU
SER
THR
THR
LYS
SER
SER
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SER
SER
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GLU

- Molecule 1: Ferritin

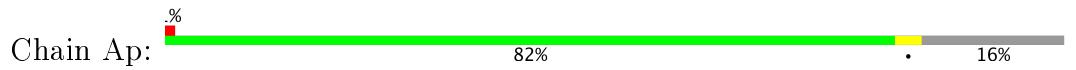


RO
M1
S2
A44
M101
E159
A160

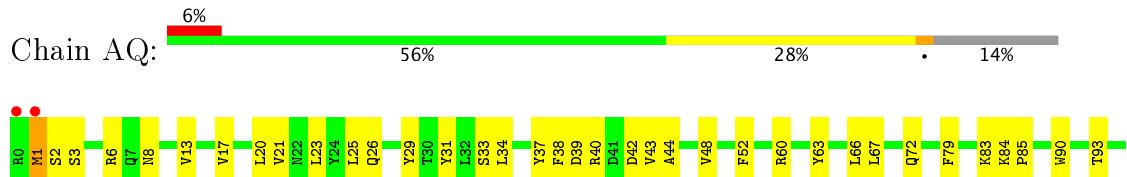
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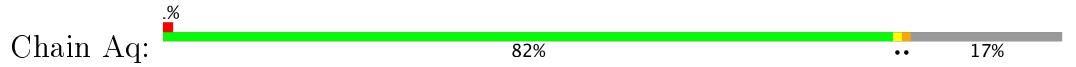
- Molecule 1: Ferritin



- Molecule 1: Ferritin



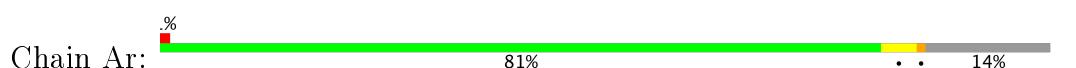
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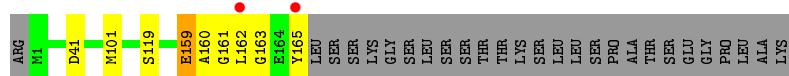


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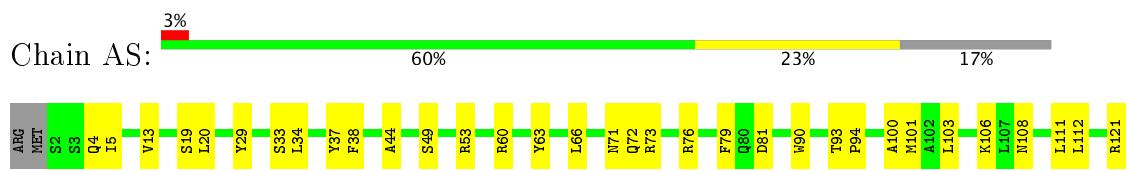


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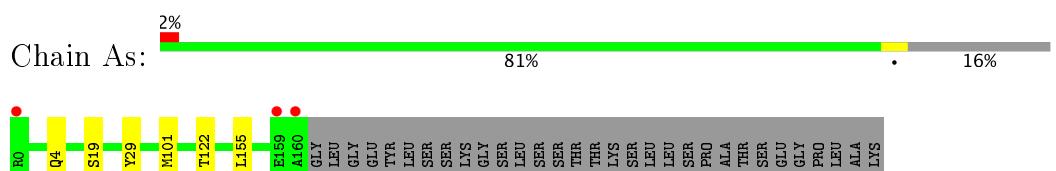




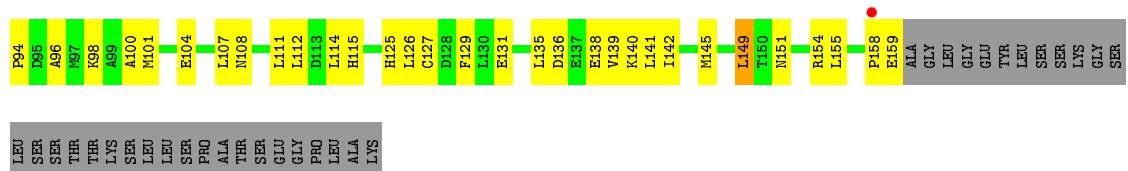
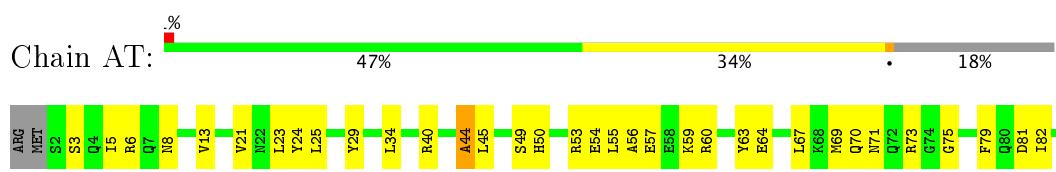
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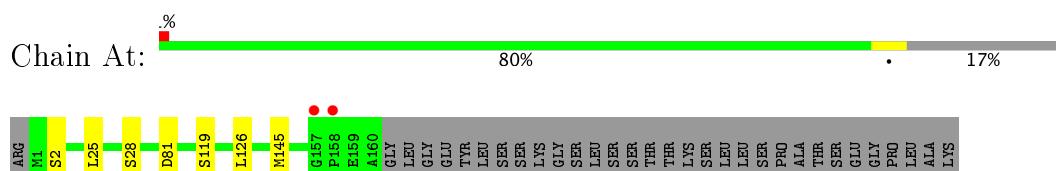
- Molecule 1: Ferritin



- Molecule 1: Ferritin

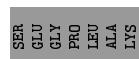


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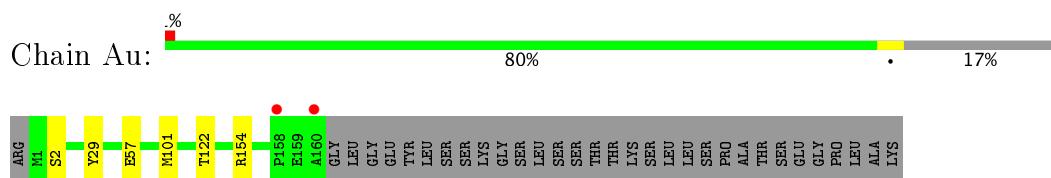


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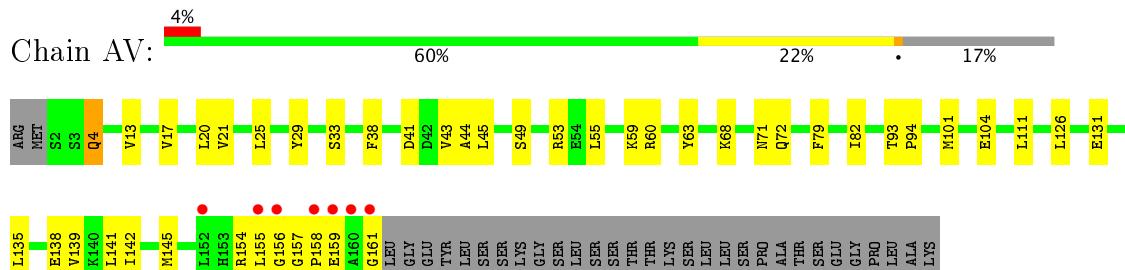




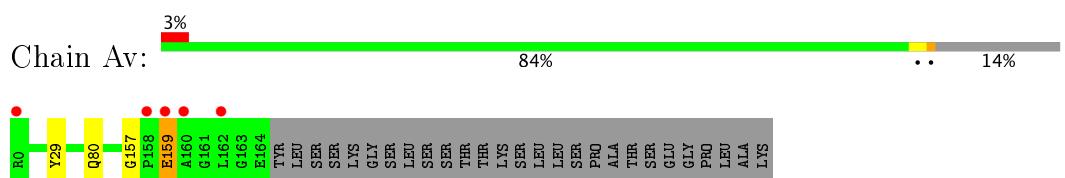
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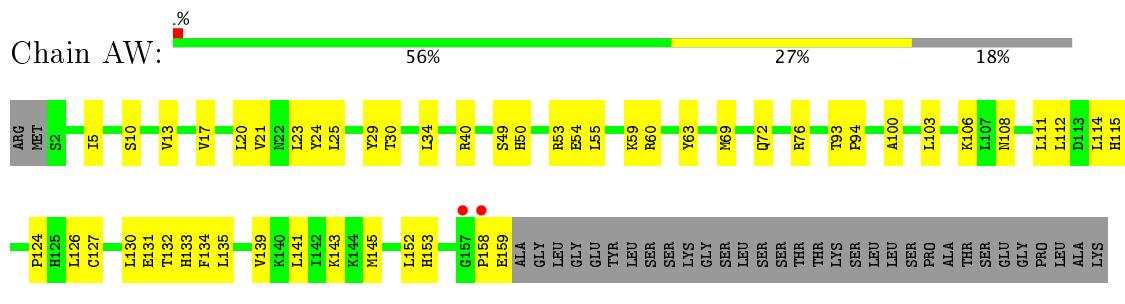
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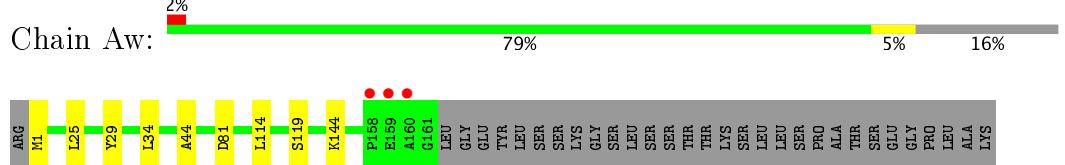
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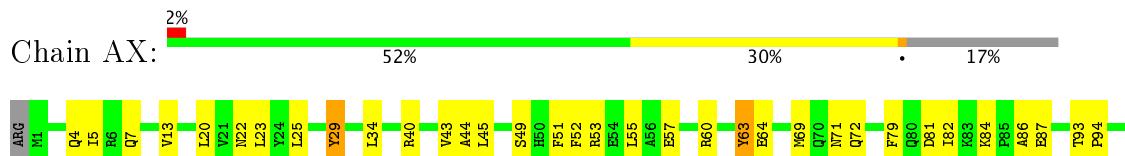
- Molecule 1: Ferritin



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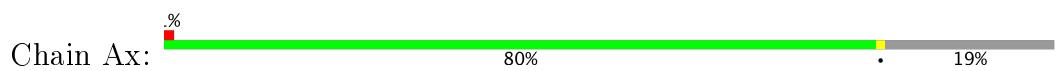


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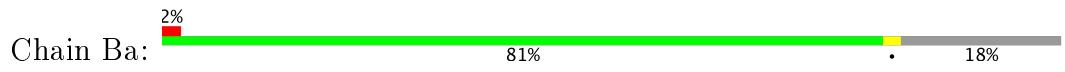
- Molecule 1: Ferritin



- Molecule 1: Ferritin



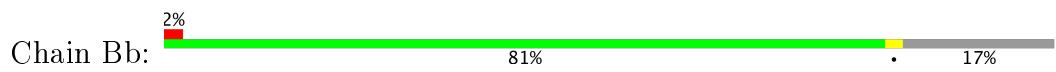
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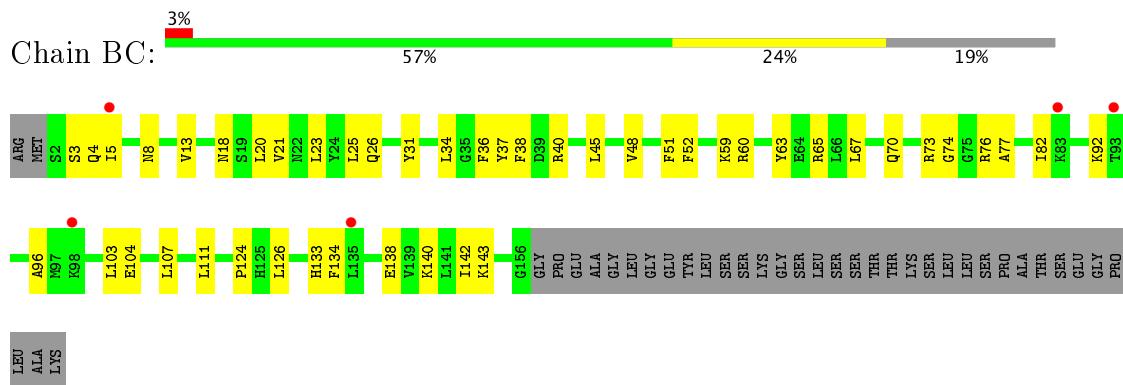
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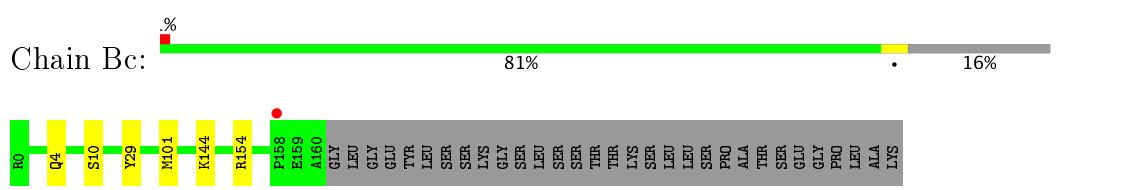
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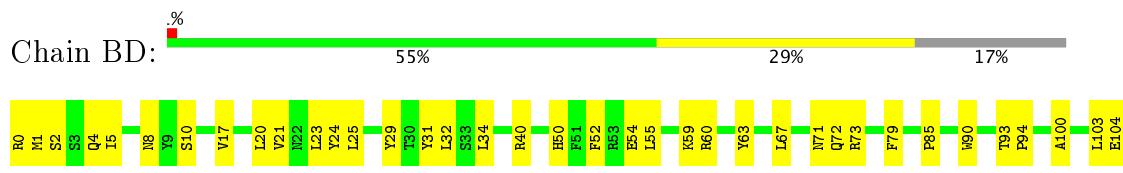
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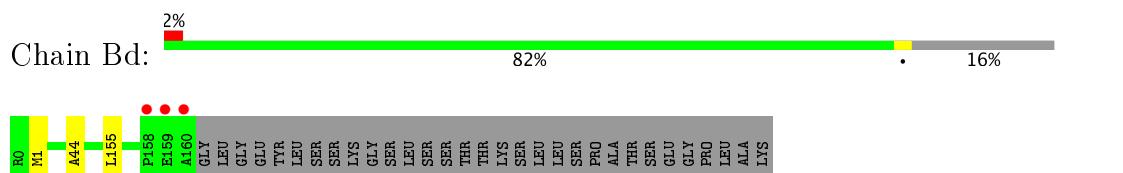
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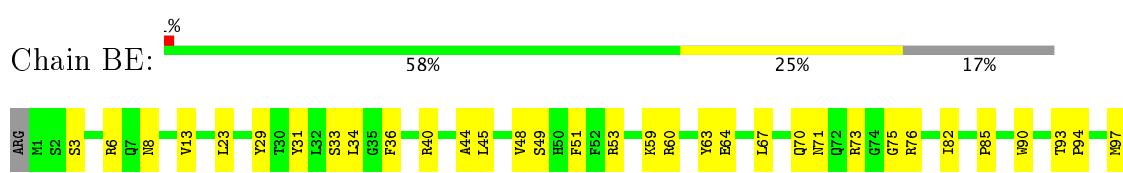
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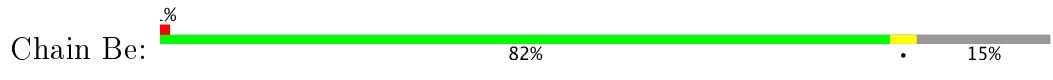
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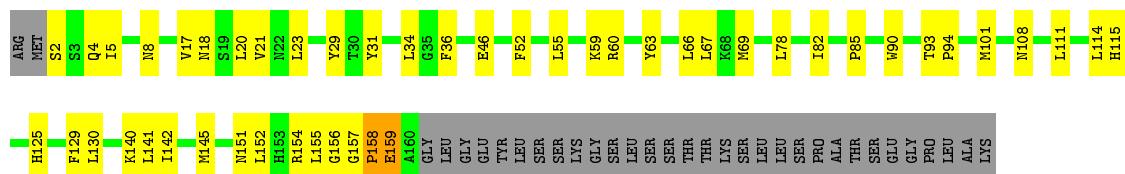
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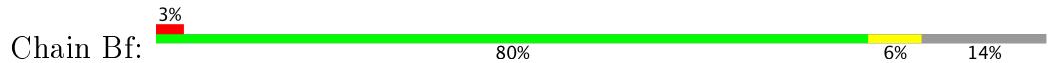
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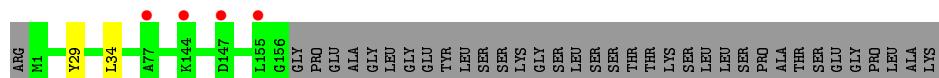
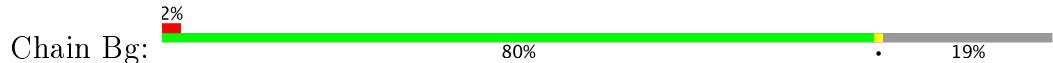
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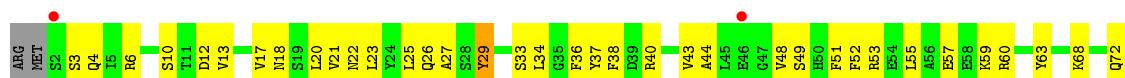
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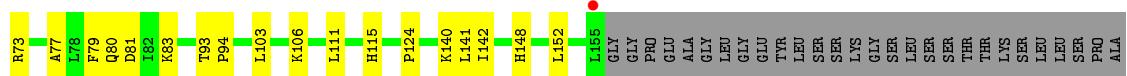


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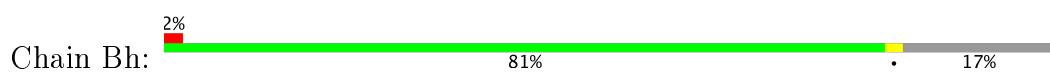


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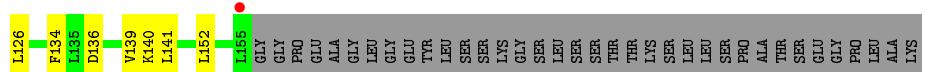




- Molecule 1: Ferritin



- Molecule 1: Ferritin



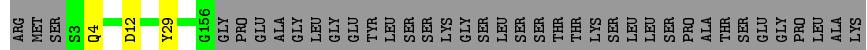
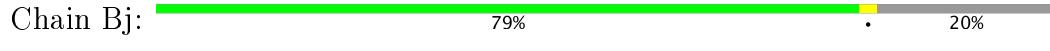
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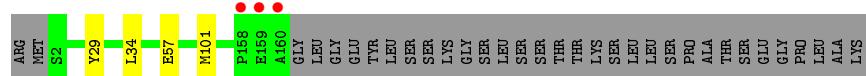
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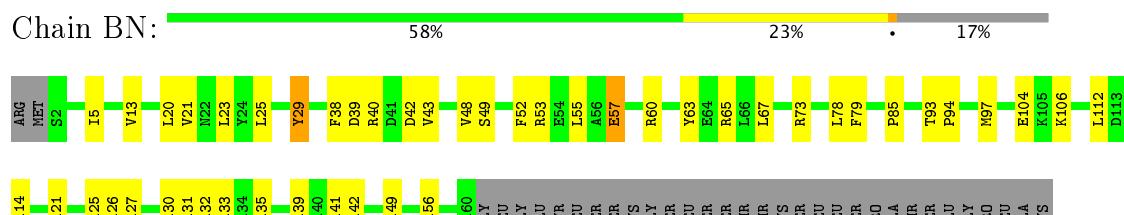
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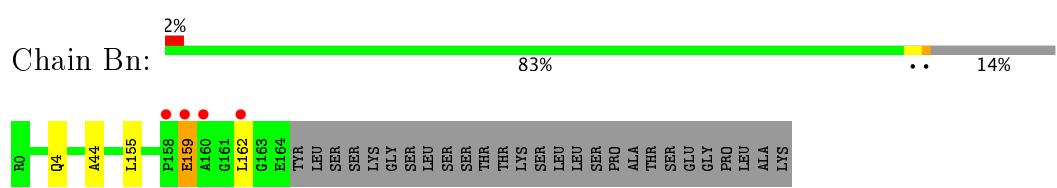
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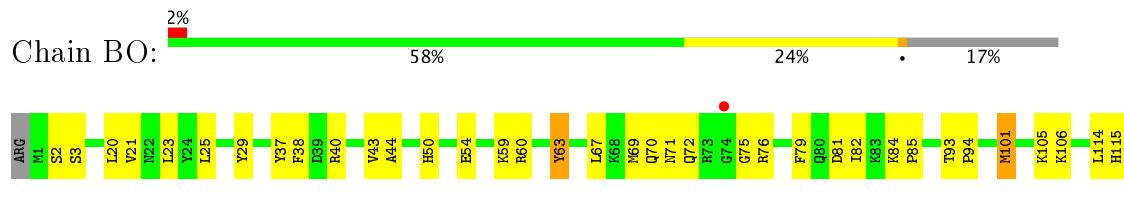
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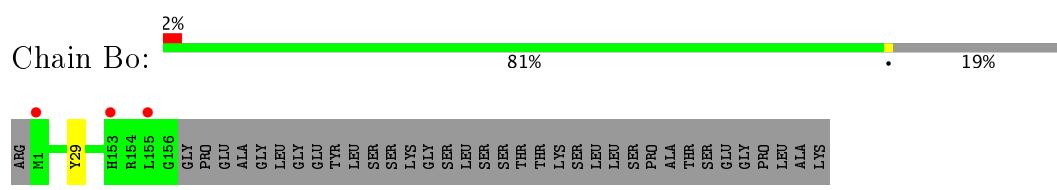
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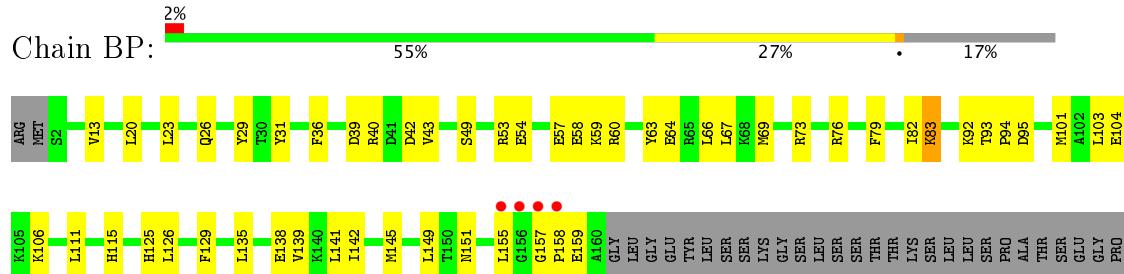
- Molecule 1: Ferritin



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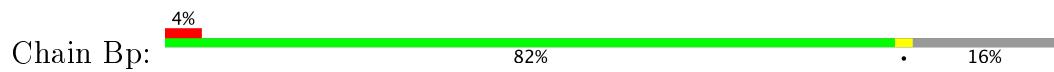


- Molecule 1: Ferritin



LEU
ALA
LYS

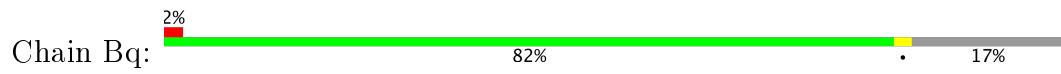
- Molecule 1: Ferritin



- Molecule 1: Ferritin



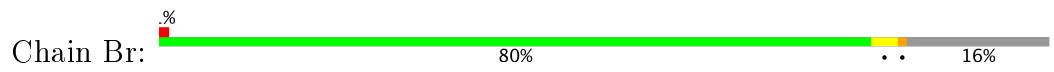
- Molecule 1: Ferritin



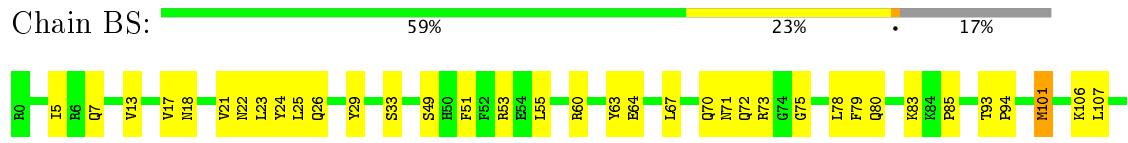
- Molecule 1: Ferritin



- Molecule 1: Ferritin

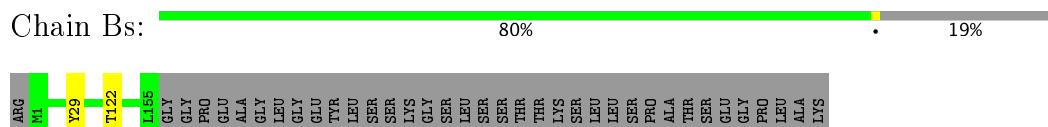


- Molecule 1: Ferritin

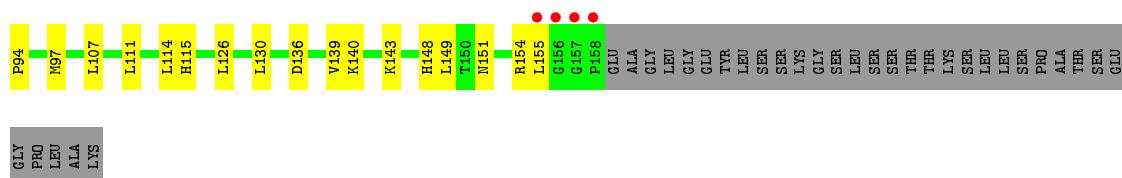




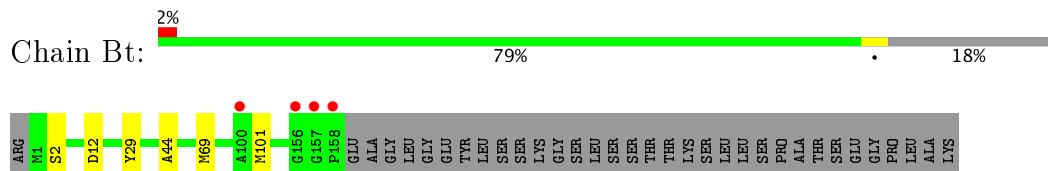
- Molecule 1: Ferritin



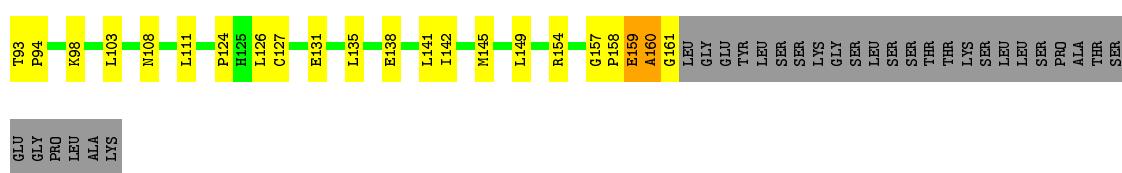
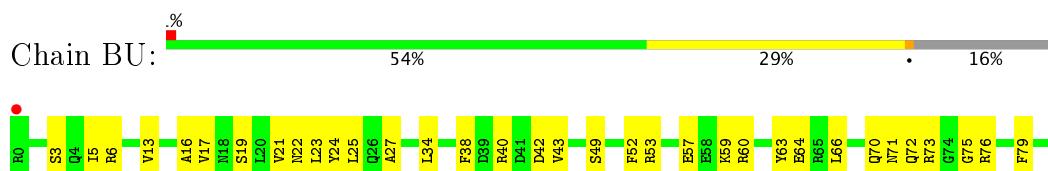
- Molecule 1: Ferritin



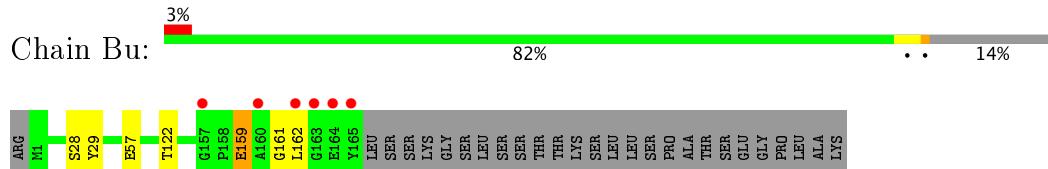
- Molecule 1: Ferritin



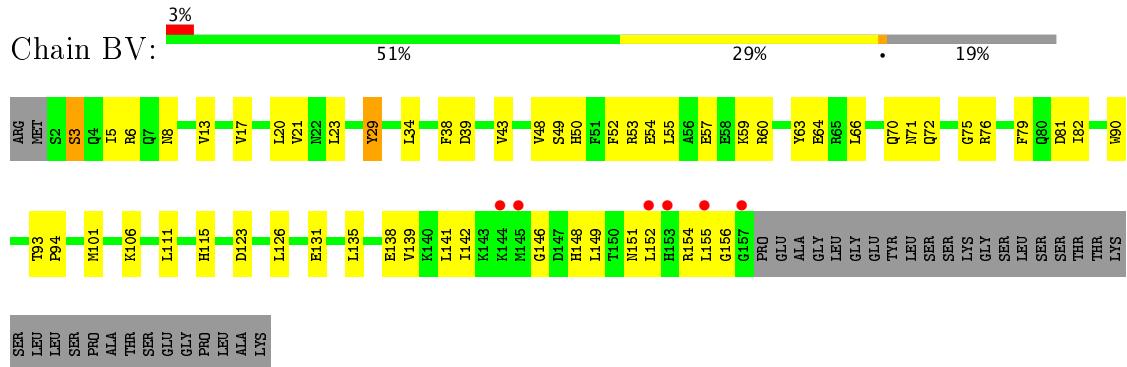
- Molecule 1: Ferritin



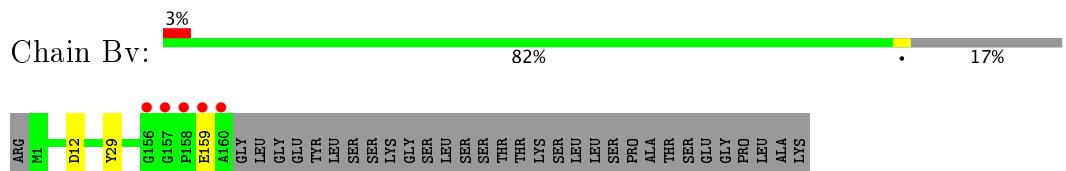
- Molecule 1: Ferritin



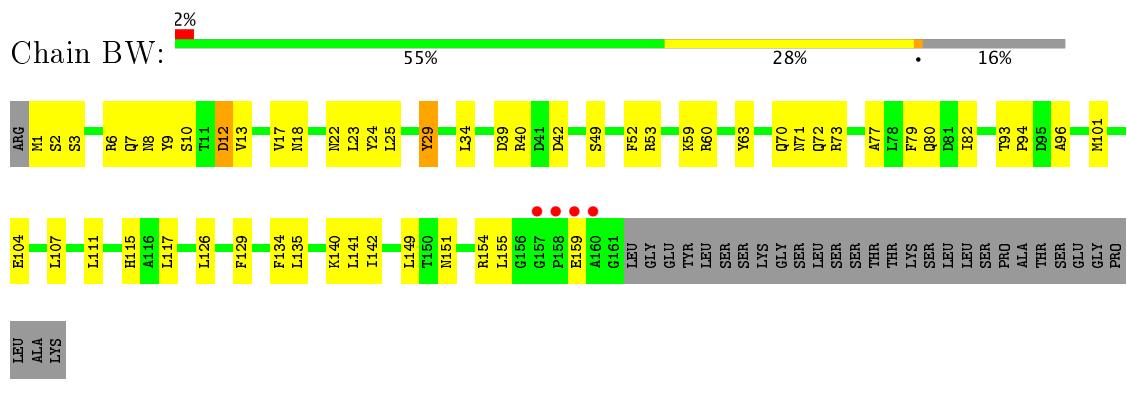
- Molecule 1: Ferritin



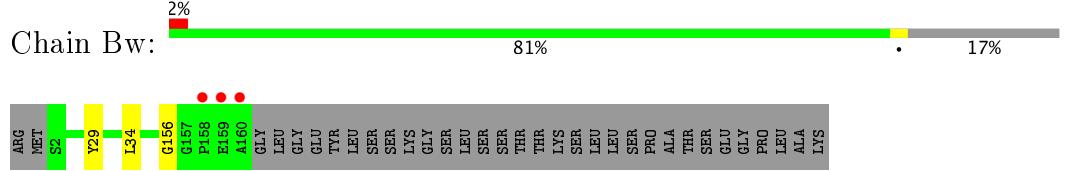
- Molecule 1: Ferritin



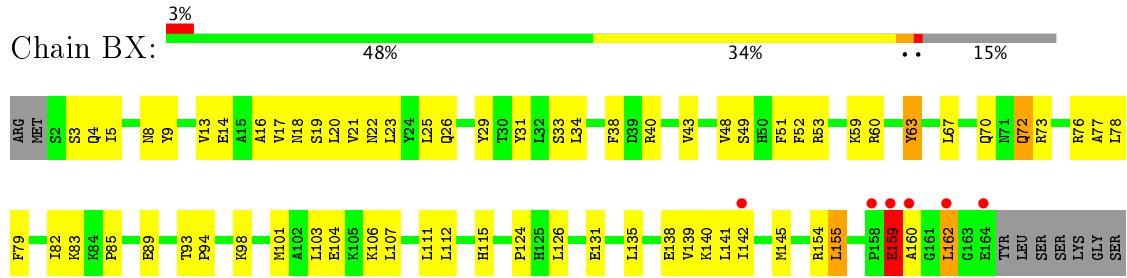
- Molecule 1: Ferritin

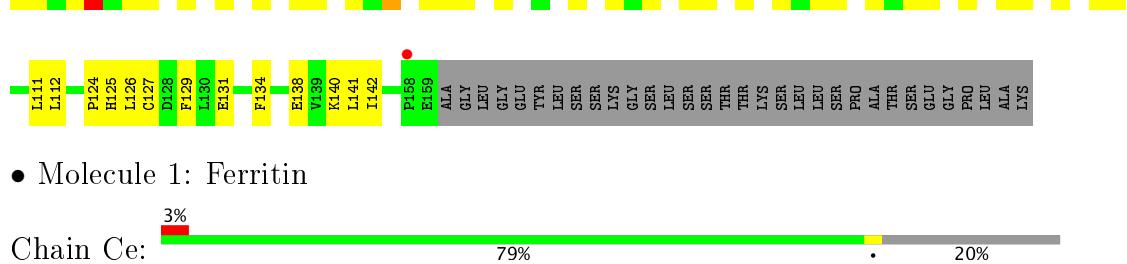
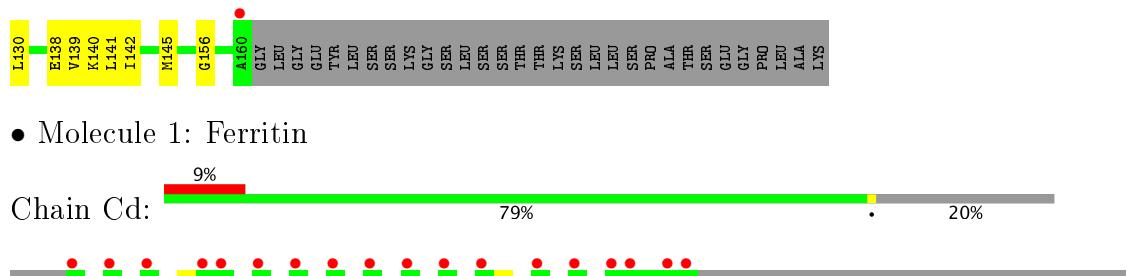
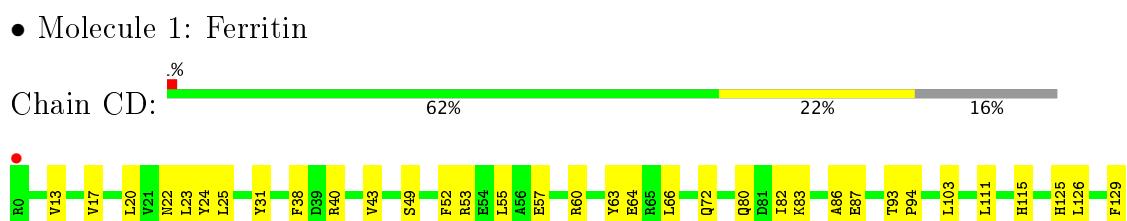
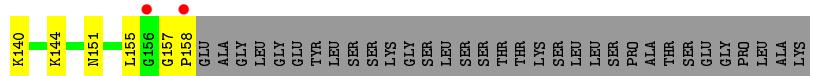
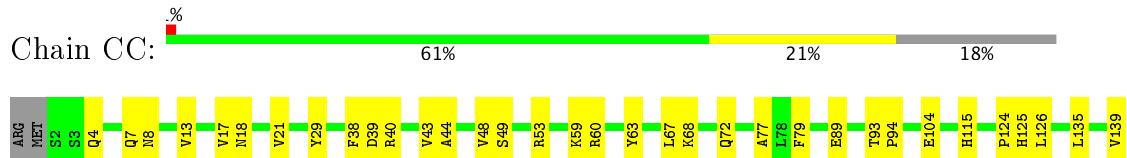


- Molecule 1: Ferritin



- Molecule 1: Ferritin



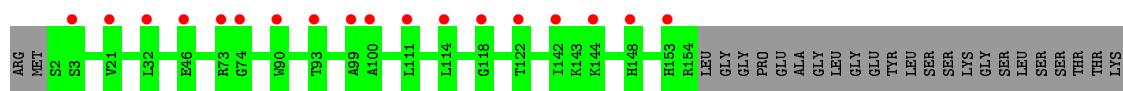




- Molecule 1: Ferritin



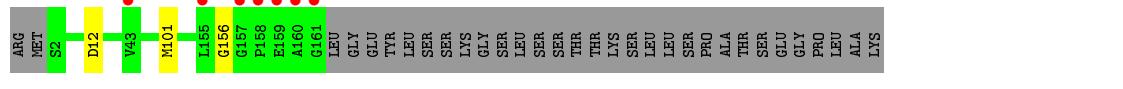
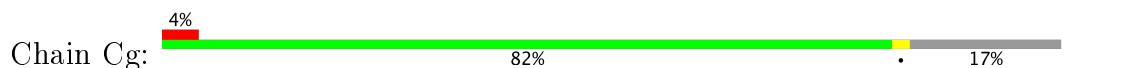
- Molecule 1: Ferritin



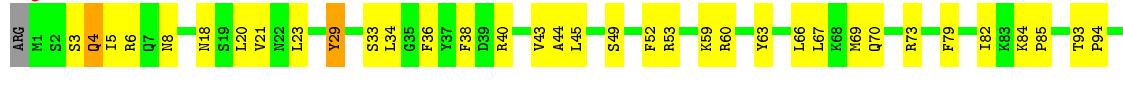
- Molecule 1: Ferritin

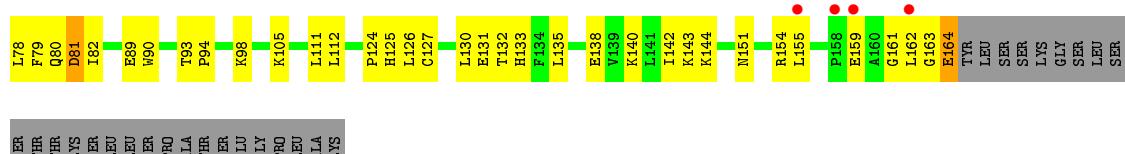
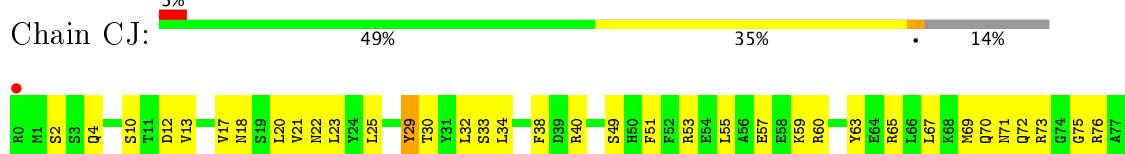
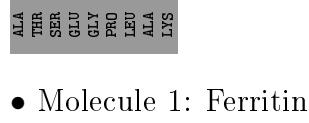
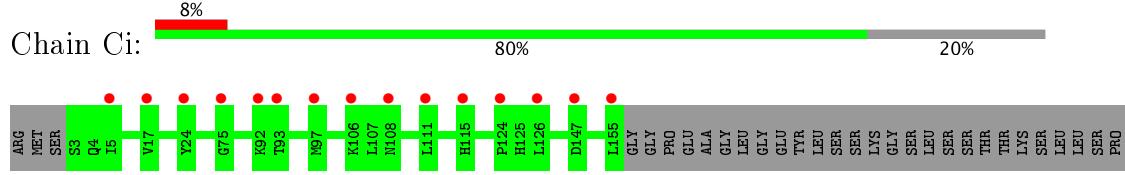
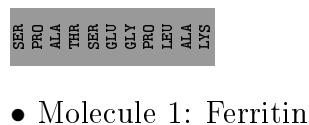
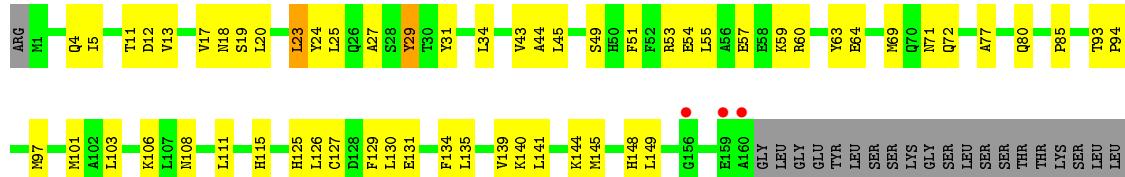
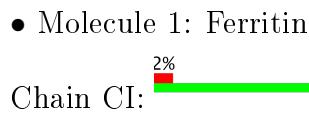
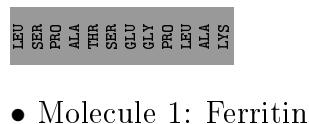
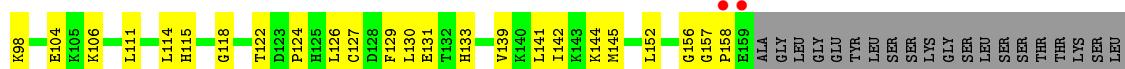


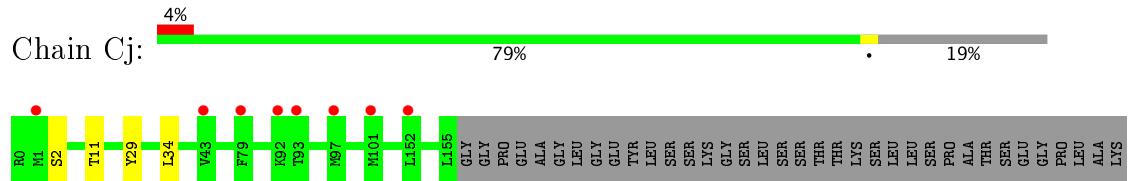
- Molecule 1: Ferritin



- Molecule 1: Ferritin





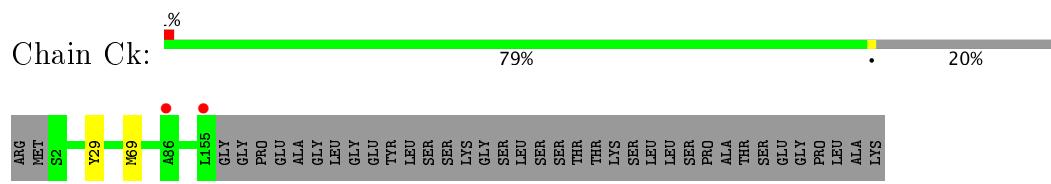


- Molecule 1: Ferritin



LYS

- Molecule 1: Ferritin



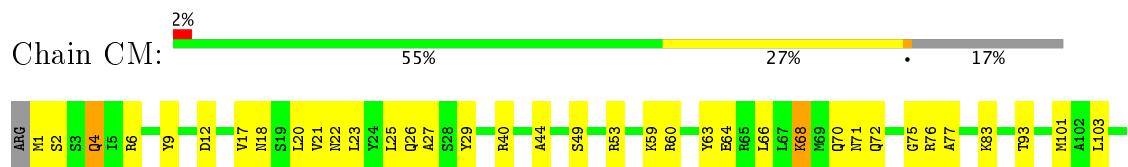
- Molecule 1: Ferritin



- Molecule 1: Ferritin

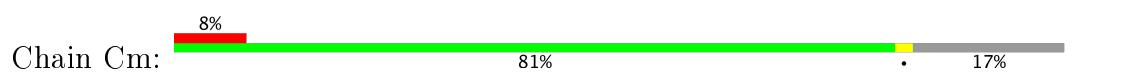


- Molecule 1: Ferritin





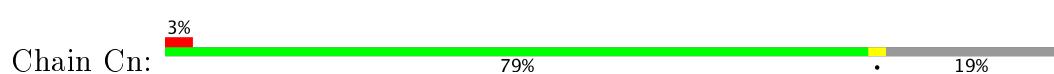
- Molecule 1: Ferritin



- Molecule 1: Ferritin



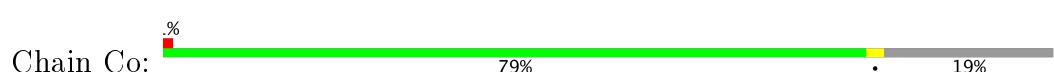
- Molecule 1: Ferritin

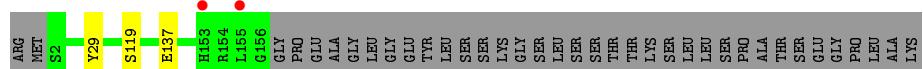


- Molecule 1: Ferritin



- Molecule 1: Ferritin

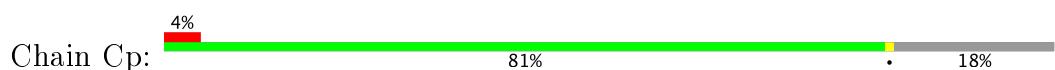




- Molecule 1: Ferritin



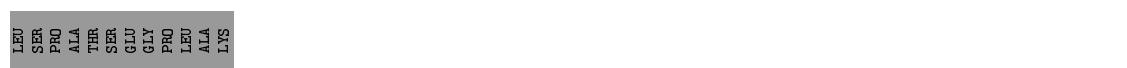
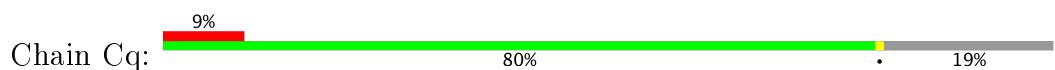
- Molecule 1: Ferritin



- Molecule 1: Ferritin

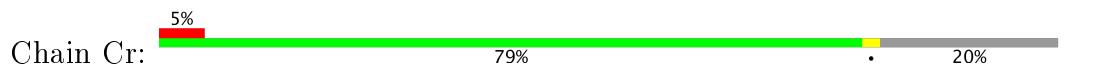


- Molecule 1: Ferritin

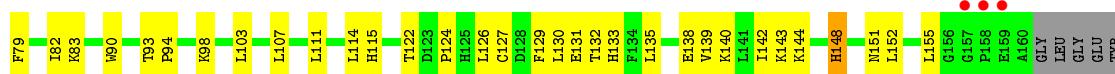
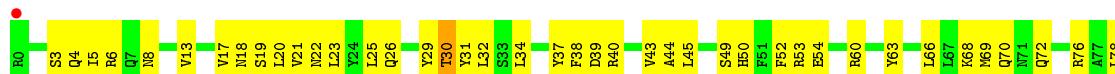




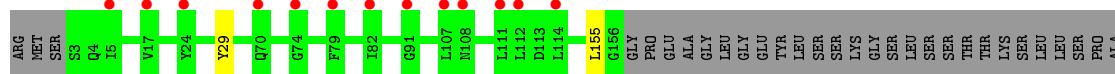
- Molecule 1: Ferritin



- Molecule 1: Ferritin



- Molecule 1: Ferritin

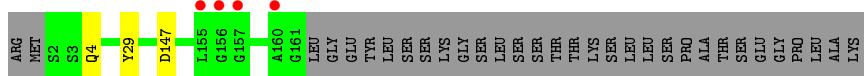


- Molecule 1: Ferritin

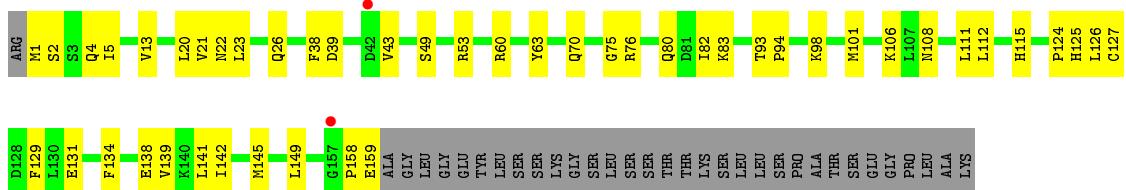


- Molecule 1: Ferritin

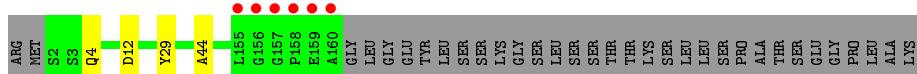
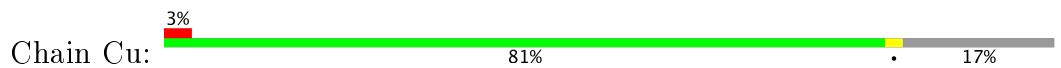




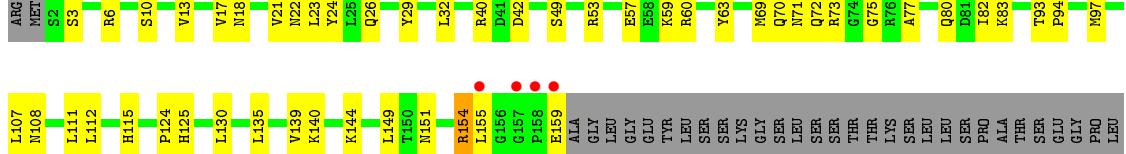
- Molecule 1: Ferritin



- Molecule 1: Ferritin

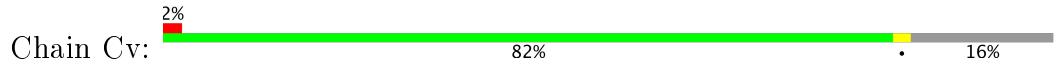


- Molecule 1: Ferritin

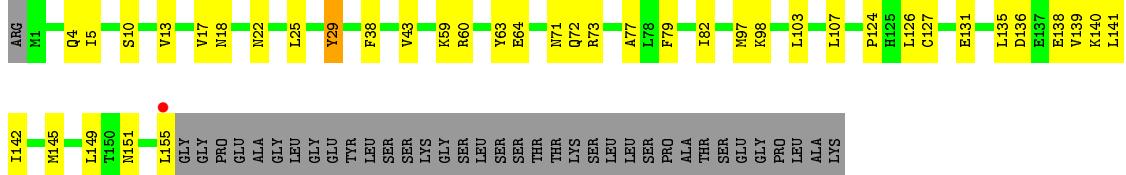


ALA
LYS

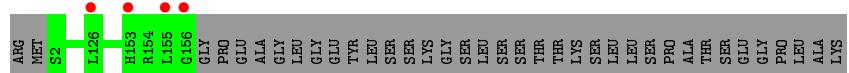
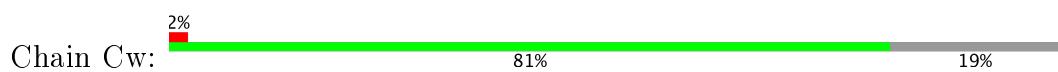
- Molecule 1: Ferritin



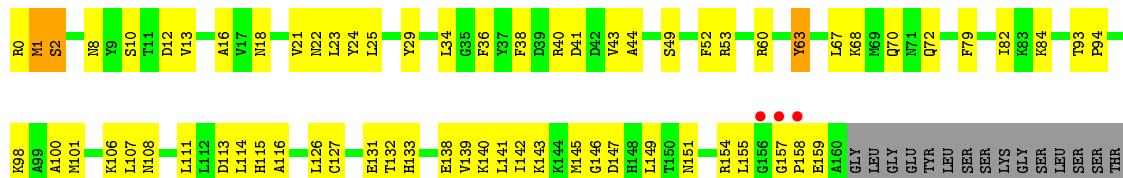
- Molecule 1: Ferritin



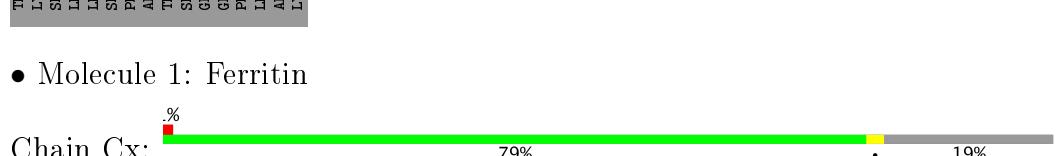
- Molecule 1: Ferritin



- Molecule 1: Ferritin



- Molecule 1: Ferritin



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	212.34 Å 236.94 Å 249.71 Å 94.69° 115.06° 114.96°	Depositor
Resolution (Å)	50.00 – 2.85 49.77 – 2.84	Depositor EDS
% Data completeness (in resolution range)	95.4 (50.00-2.85) 86.5 (49.77-2.84)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle^1$	2.80 (at 2.86 Å)	Xtriage
Refinement program	CNS	Depositor
R , R_{free}	0.249 , 0.291 0.233 , 0.271	Depositor DCC
R_{free} test set	42239 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	49.6	Xtriage
Anisotropy	0.321	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-h-k,-h-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	187090	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.71% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [\(i\)](#)

5.1 Standard geometry [\(i\)](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AA	0.37	0/1294	0.54	0/1741
1	AB	0.42	0/1345	0.63	0/1809
1	AC	0.36	0/1318	0.56	0/1772
1	AD	0.33	0/1299	0.52	0/1748
1	AE	0.47	0/1345	0.64	0/1809
1	AF	0.41	0/1293	0.56	0/1739
1	AG	0.41	0/1299	0.61	0/1748
1	AH	0.45	0/1307	0.60	0/1758
1	AI	0.35	0/1293	0.55	0/1739
1	AJ	0.38	0/1285	0.56	0/1727
1	AK	0.39	0/1292	0.56	0/1736
1	AL	0.32	0/1285	0.55	0/1729
1	AM	0.44	0/1322	0.59	0/1777
1	AN	0.43	0/1345	0.62	0/1809
1	AO	0.43	0/1345	0.63	0/1809
1	AP	0.51	0/1302	0.67	0/1751
1	AQ	0.36	0/1343	0.57	0/1805
1	AR	0.42	0/1332	0.58	0/1791
1	AS	0.35	0/1303	0.54	0/1753
1	AT	0.46	0/1294	0.62	0/1741
1	AU	0.43	0/1307	0.59	0/1758
1	AV	0.41	0/1303	0.58	0/1753
1	AW	0.37	0/1294	0.55	0/1741
1	AX	0.44	0/1307	0.61	0/1758
1	Aa	0.47	0/1318	0.65	1/1772 (0.1%)
1	Ab	0.47	0/1311	0.60	0/1763
1	Ac	0.45	0/1307	0.62	0/1758
1	Ad	0.57	0/1345	0.70	1/1809 (0.1%)
1	Ae	0.51	0/1322	0.67	0/1777
1	Af	0.47	0/1318	0.64	0/1772
1	Ag	0.52	0/1277	0.63	0/1717
1	Ah	0.51	0/1318	0.63	0/1772

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Ai	0.54	0/1302	0.69	0/1751
1	Aj	0.47	0/1345	0.66	0/1809
1	Ak	0.44	0/1345	0.62	0/1809
1	Al	0.48	0/1345	0.66	0/1809
1	Am	0.49	0/1322	0.64	0/1777
1	An	0.49	0/1311	0.63	0/1763
1	Ao	0.48	0/1318	0.64	0/1772
1	Ap	0.49	0/1322	0.65	0/1777
1	Aq	0.49	0/1307	0.65	0/1758
1	Ar	0.59	0/1345	0.69	1/1809 (0.1%)
1	As	0.47	0/1318	0.62	0/1772
1	At	0.50	0/1307	0.62	0/1758
1	Au	0.46	0/1307	0.61	0/1758
1	Av	0.45	0/1343	0.61	0/1805
1	Aw	0.57	2/1311 (0.2%)	0.69	1/1763 (0.1%)
1	Ax	0.53	0/1277	0.63	0/1717
1	BA	0.40	0/1356	0.60	0/1823
1	BB	0.37	0/1292	0.60	1/1736 (0.1%)
1	BC	0.32	0/1273	0.53	0/1712
1	BD	0.37	0/1313	0.58	0/1765
1	BE	0.38	0/1302	0.59	0/1751
1	BF	0.47	0/1299	0.62	0/1748
1	BG	0.37	0/1281	0.57	0/1722
1	BH	0.36	0/1269	0.54	0/1707
1	BI	0.38	0/1277	0.56	0/1717
1	BJ	0.37	0/1285	0.56	0/1729
1	BK	0.35	0/1281	0.52	0/1722
1	BL	0.34	0/1277	0.53	0/1717
1	BM	0.45	0/1294	0.60	0/1741
1	BN	0.42	0/1299	0.62	0/1748
1	BO	0.35	0/1307	0.54	0/1758
1	BP	0.38	0/1299	0.56	0/1748
1	BQ	0.43	0/1307	0.59	0/1758
1	BR	0.40	0/1318	0.57	0/1772
1	BS	0.45	0/1304	0.59	0/1753
1	BT	0.34	0/1285	0.57	0/1729
1	BU	0.34	0/1322	0.53	0/1777
1	BV	0.36	0/1277	0.57	0/1717
1	BW	0.36	0/1311	0.55	0/1763
1	BX	0.37	0/1324	0.59	0/1781
1	Ba	0.33	0/1293	0.53	0/1739
1	Bb	0.35	0/1302	0.52	0/1751
1	Bc	0.43	0/1318	0.60	0/1772

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Bd	0.44	0/1318	0.59	0/1772
1	Be	0.46	0/1324	0.62	0/1781
1	Bf	0.43	0/1345	0.63	0/1809
1	Bg	0.35	0/1281	0.53	0/1722
1	Bh	0.39	0/1302	0.57	0/1751
1	Bi	0.37	0/1292	0.57	0/1736
1	Bj	0.34	0/1267	0.54	0/1704
1	Bk	0.35	0/1302	0.54	0/1751
1	Bl	0.43	0/1302	0.59	0/1751
1	Bm	0.44	0/1299	0.61	0/1748
1	Bn	0.41	0/1343	0.59	0/1805
1	Bo	0.36	0/1281	0.57	0/1722
1	Bp	0.42	0/1322	0.60	0/1777
1	Bq	0.36	0/1313	0.55	0/1765
1	Br	0.55	0/1318	0.69	0/1772
1	Bs	0.37	0/1277	0.56	0/1717
1	Bt	0.34	0/1293	0.55	0/1739
1	Bu	0.48	0/1345	0.64	1/1809 (0.1%)
1	Bv	0.41	0/1307	0.56	0/1758
1	Bw	0.51	0/1299	0.67	0/1748
1	Bx	0.34	0/1285	0.55	0/1729
1	CA	0.47	0/1307	0.61	0/1758
1	CB	0.40	0/1311	0.58	0/1763
1	CC	0.33	0/1285	0.53	0/1729
1	CD	0.43	0/1318	0.60	0/1772
1	CE	0.40	0/1313	0.56	0/1765
1	CF	0.48	0/1303	0.61	0/1753
1	CG	0.42	0/1313	0.58	0/1765
1	CH	0.34	0/1302	0.53	0/1751
1	CI	0.46	0/1307	0.63	0/1758
1	CJ	0.52	1/1343 (0.1%)	0.66	0/1805
1	CK	0.36	0/1307	0.56	0/1758
1	CL	0.35	0/1302	0.54	0/1751
1	CM	0.46	0/1302	0.60	0/1751
1	CN	0.45	0/1311	0.61	0/1763
1	CO	0.36	0/1304	0.55	0/1753
1	CP	0.38	0/1293	0.55	0/1739
1	CQ	0.49	0/1322	0.61	0/1777
1	CR	0.50	0/1356	0.65	0/1823
1	CS	0.48	0/1318	0.61	0/1772
1	CT	0.41	0/1293	0.55	0/1739
1	CU	0.32	0/1302	0.52	0/1751
1	CV	0.33	0/1294	0.55	0/1741

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CW	0.37	0/1277	0.55	0/1717
1	CX	0.43	0/1318	0.62	0/1772
1	Ca	0.36	0/1293	0.59	0/1740
1	Cb	0.34	0/1299	0.54	0/1748
1	Cc	0.35	0/1288	0.55	0/1733
1	Cd	0.34	0/1263	0.54	0/1699
1	Ce	0.34	0/1269	0.53	0/1707
1	Cf	0.34	0/1261	0.51	0/1696
1	Cg	0.35	0/1303	0.53	0/1753
1	Ch	0.39	0/1299	0.58	0/1748
1	Ci	0.37	0/1263	0.54	0/1699
1	Cj	0.35	0/1288	0.57	0/1731
1	Ck	0.34	0/1269	0.54	0/1707
1	Cl	0.35	0/1273	0.56	0/1712
1	Cm	0.33	0/1299	0.53	0/1748
1	Cn	0.33	0/1277	0.52	0/1717
1	Co	0.41	0/1273	0.59	0/1712
1	Cp	0.34	0/1293	0.55	0/1739
1	Cq	0.36	0/1273	0.53	0/1712
1	Cr	0.35	0/1269	0.52	0/1707
1	Cs	0.34	0/1267	0.55	0/1704
1	Ct	0.39	0/1303	0.58	0/1753
1	Cu	0.36	0/1299	0.55	0/1748
1	Cv	0.36	0/1311	0.54	0/1763
1	Cw	0.35	0/1273	0.53	0/1712
1	Cx	0.38	0/1288	0.58	0/1731
All	All	0.41	3/187767 (0.0%)	0.59	6/252515 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AX	0	1
1	An	0	1
1	Ar	0	1
1	Ax	0	1
1	CR	0	1
1	CX	0	1
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Aw	1	MET	CG-SD	-8.22	1.59	1.81
1	Aw	1	MET	SD-CE	-5.27	1.48	1.77
1	CJ	159	GLU	CB-CG	5.21	1.62	1.52

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Aw	1	MET	CG-SD-CE	7.72	112.55	100.20
1	BB	0	ARG	N-CA-C	6.15	127.60	111.00
1	Bu	161	GLY	N-CA-C	-5.78	98.66	113.10
1	Aa	107	LEU	CA-CB-CG	5.20	127.26	115.30
1	Ad	161	GLY	N-CA-C	-5.16	100.19	113.10

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AX	63	TYR	Sidechain
1	An	31	TYR	Sidechain
1	Ar	163	GLY	Mainchain
1	Ax	37	TYR	Sidechain
1	CR	163	GLY	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	AA	1270	0	1243	31	0
1	AB	1320	0	1292	48	0
1	AC	1294	0	1273	34	0
1	AD	1275	0	1248	50	0
1	AE	1320	0	1292	70	0
1	AF	1269	0	1249	56	0
1	AG	1275	0	1248	46	0
1	AH	1283	0	1260	48	0
1	AI	1269	0	1249	39	0
1	AJ	1262	0	1242	41	0
1	AK	1269	0	1252	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AL	1261	0	1237	44	0
1	AM	1298	0	1276	57	0
1	AN	1320	0	1292	54	0
1	AO	1320	0	1292	69	0
1	AP	1278	0	1255	48	0
1	AQ	1319	0	1296	52	0
1	AR	1308	0	1283	48	0
1	AS	1279	0	1251	34	0
1	AT	1270	0	1243	65	0
1	AU	1283	0	1260	44	0
1	AV	1279	0	1251	36	0
1	AW	1270	0	1243	49	0
1	AX	1283	0	1260	56	0
1	Aa	1294	0	1273	0	0
1	Ab	1287	0	1263	0	0
1	Ac	1283	0	1260	0	0
1	Ad	1320	0	1292	0	0
1	Ae	1298	0	1276	0	0
1	Af	1294	0	1273	0	0
1	Ag	1254	0	1236	0	0
1	Ah	1294	0	1273	0	0
1	Ai	1278	0	1255	0	0
1	Aj	1320	0	1292	0	0
1	Ak	1320	0	1292	0	0
1	Al	1320	0	1292	0	0
1	Am	1298	0	1276	0	0
1	An	1287	0	1263	0	0
1	Ao	1294	0	1273	0	0
1	Ap	1298	0	1276	0	0
1	Aq	1283	0	1260	0	0
1	Ar	1320	0	1292	0	0
1	As	1294	0	1273	0	0
1	At	1283	0	1260	0	0
1	Au	1283	0	1260	0	0
1	Av	1319	0	1296	0	0
1	Aw	1287	0	1263	0	0
1	Ax	1254	0	1236	0	0
1	BA	1331	0	1305	49	0
1	BB	1269	0	1252	40	0
1	BC	1250	0	1227	48	0
1	BD	1289	0	1268	53	0
1	BE	1278	0	1255	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BF	1275	0	1248	39	0
1	BG	1258	0	1239	49	0
1	BH	1246	0	1224	47	0
1	BI	1254	0	1236	45	0
1	BJ	1261	0	1237	48	0
1	BK	1258	0	1239	47	0
1	BL	1254	0	1236	39	0
1	BM	1270	0	1243	29	0
1	BN	1275	0	1248	43	0
1	BO	1283	0	1260	46	0
1	BP	1275	0	1248	46	0
1	BQ	1283	0	1260	30	0
1	BR	1294	0	1273	41	0
1	BS	1280	0	1262	40	0
1	BT	1261	0	1237	49	0
1	BU	1298	0	1276	45	0
1	BV	1254	0	1230	49	0
1	BW	1287	0	1263	50	0
1	BX	1300	0	1271	65	0
1	Ba	1269	0	1249	0	0
1	Bb	1278	0	1255	0	0
1	Bc	1294	0	1273	0	0
1	Bd	1294	0	1273	0	0
1	Be	1300	0	1271	0	0
1	Bf	1320	0	1292	0	0
1	Bg	1258	0	1239	0	0
1	Bh	1278	0	1255	0	0
1	Bi	1269	0	1252	0	0
1	Bj	1244	0	1222	0	0
1	Bk	1278	0	1255	0	0
1	Bl	1278	0	1255	0	0
1	Bm	1275	0	1248	0	0
1	Bn	1319	0	1296	0	0
1	Bo	1258	0	1239	0	0
1	Bp	1298	0	1276	0	0
1	Bq	1289	0	1268	0	0
1	Br	1294	0	1273	0	0
1	Bs	1254	0	1236	0	0
1	Bt	1269	0	1249	0	0
1	Bu	1320	0	1292	0	0
1	Bv	1283	0	1260	0	0
1	Bw	1275	0	1248	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Bx	1261	0	1237	0	0
1	CA	1283	0	1260	57	0
1	CB	1287	0	1263	51	0
1	CC	1261	0	1237	30	0
1	CD	1294	0	1273	34	0
1	CE	1289	0	1268	36	0
1	CF	1279	0	1251	54	0
1	CG	1289	0	1268	37	0
1	CH	1278	0	1255	48	0
1	CI	1283	0	1260	46	0
1	CJ	1319	0	1296	77	0
1	CK	1283	0	1260	40	0
1	CL	1278	0	1255	41	0
1	CM	1278	0	1255	41	0
1	CN	1287	0	1263	45	0
1	CO	1280	0	1262	40	0
1	CP	1269	0	1249	32	0
1	CQ	1298	0	1276	50	0
1	CR	1331	0	1305	46	0
1	CS	1294	0	1273	65	0
1	CT	1269	0	1249	45	0
1	CU	1278	0	1255	31	0
1	CV	1270	0	1243	37	0
1	CW	1254	0	1236	34	0
1	CX	1294	0	1273	53	0
1	Ca	1269	0	1243	0	0
1	Cb	1275	0	1248	0	0
1	Cc	1264	0	1238	0	0
1	Cd	1240	0	1219	0	0
1	Ce	1246	0	1224	0	0
1	Cf	1238	0	1213	0	0
1	Cg	1279	0	1251	0	0
1	Ch	1275	0	1248	0	0
1	Ci	1240	0	1219	0	0
1	Cj	1265	0	1249	0	0
1	Ck	1246	0	1224	0	0
1	Cl	1250	0	1227	0	0
1	Cm	1275	0	1248	0	0
1	Cn	1254	0	1236	0	0
1	Co	1250	0	1227	0	0
1	Cp	1269	0	1249	0	0
1	Cq	1250	0	1227	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Cr	1246	0	1224	0	0
1	Cs	1244	0	1222	0	0
1	Ct	1279	0	1251	0	0
1	Cu	1275	0	1248	0	0
1	Cv	1287	0	1263	0	0
1	Cw	1250	0	1227	0	0
1	Cx	1265	0	1249	0	0
2	AA	1	0	0	0	0
2	AB	1	0	0	0	0
2	AC	1	0	0	0	0
2	AF	1	0	0	0	0
2	AH	1	0	0	0	0
2	AL	1	0	0	0	0
2	AM	1	0	0	0	0
2	AO	1	0	0	0	0
2	Aa	1	0	0	0	0
2	Ac	1	0	0	0	0
2	Ad	1	0	0	0	0
2	Ae	1	0	0	0	0
2	Ag	1	0	0	0	0
2	Ah	1	0	0	0	0
2	Aj	1	0	0	0	0
2	An	1	0	0	0	0
2	BA	1	0	0	0	0
2	BB	1	0	0	0	0
2	BC	1	0	0	0	0
2	BD	1	0	0	0	0
2	BG	1	0	0	0	0
2	BH	1	0	0	0	0
2	BN	1	0	0	0	0
2	BR	1	0	0	0	0
2	Ba	1	0	0	0	0
2	Bb	1	0	0	0	0
2	Bc	1	0	0	0	0
2	Bd	1	0	0	0	0
2	Be	1	0	0	0	0
2	Bf	1	0	0	0	0
2	Bg	1	0	0	0	0
2	Bu	1	0	0	0	0
2	CA	1	0	0	0	0
2	CB	1	0	0	0	0
2	CC	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	CD	1	0	0	0	0
2	CE	1	0	0	0	0
2	CF	1	0	0	0	0
2	CH	1	0	0	0	0
2	CO	1	0	0	0	0
2	Ca	1	0	0	0	0
2	Cb	1	0	0	0	0
2	Ce	1	0	0	0	0
2	Cg	1	0	0	0	0
2	Ck	1	0	0	0	0
2	Cl	1	0	0	0	0
2	Cn	1	0	0	0	0
2	Cp	1	0	0	0	0
3	AA	10	0	0	0	0
3	AB	14	0	0	0	0
3	AC	15	0	0	1	0
3	AD	8	0	0	1	0
3	AE	27	0	0	0	0
3	AF	16	0	0	0	0
3	AG	27	0	0	0	0
3	AH	28	0	0	1	0
3	AI	6	0	0	0	0
3	AJ	9	0	0	0	0
3	AK	15	0	0	0	0
3	AL	11	0	0	0	0
3	AM	26	0	0	2	0
3	AN	17	0	0	1	0
3	AO	20	0	0	2	0
3	AP	25	0	0	1	0
3	AQ	21	0	0	0	0
3	AR	18	0	0	0	0
3	AS	20	0	0	1	0
3	AT	22	0	0	2	0
3	AU	20	0	0	1	0
3	AV	17	0	0	0	0
3	AW	19	0	0	2	0
3	AX	33	0	0	1	0
3	Aa	47	0	0	0	0
3	Ab	30	0	0	0	0
3	Ac	32	0	0	0	0
3	Ad	37	0	0	0	0
3	Ae	26	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	Af	48	0	0	0	0
3	Ag	37	0	0	0	0
3	Ah	28	0	0	0	0
3	Ai	40	0	0	0	0
3	Aj	28	0	0	0	0
3	Ak	37	0	0	0	0
3	Al	25	0	0	0	0
3	Am	45	0	0	0	0
3	An	41	0	0	0	0
3	Ao	39	0	0	0	0
3	Ap	32	0	0	0	0
3	Aq	33	0	0	0	0
3	Ar	40	0	0	0	0
3	As	44	0	0	0	0
3	At	31	0	0	0	0
3	Au	31	0	0	0	0
3	Av	19	0	0	0	0
3	Aw	34	0	0	0	0
3	Ax	31	0	0	0	0
3	BA	15	0	0	0	0
3	BB	5	0	0	0	0
3	BC	2	0	0	0	0
3	BD	10	0	0	2	0
3	BE	15	0	0	0	0
3	BF	32	0	0	0	0
3	BG	7	0	0	0	0
3	BH	11	0	0	0	0
3	BI	20	0	0	0	0
3	BJ	8	0	0	2	0
3	BK	6	0	0	0	0
3	BL	10	0	0	1	0
3	BM	25	0	0	1	0
3	BN	18	0	0	0	0
3	BO	13	0	0	0	0
3	BP	10	0	0	0	0
3	BQ	30	0	0	0	0
3	BR	21	0	0	0	0
3	BS	37	0	0	0	0
3	BT	12	0	0	2	0
3	BU	5	0	0	0	0
3	BV	5	0	0	0	0
3	BW	25	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	BX	3	0	0	0	0
3	Ba	10	0	0	0	0
3	Bb	4	0	0	0	0
3	Bc	32	0	0	0	0
3	Bd	27	0	0	0	0
3	Be	26	0	0	0	0
3	Bf	26	0	0	0	0
3	Bg	7	0	0	0	0
3	Bh	19	0	0	0	0
3	Bi	7	0	0	0	0
3	Bj	6	0	0	0	0
3	Bk	6	0	0	0	0
3	Bl	23	0	0	0	0
3	Bm	25	0	0	0	0
3	Bn	11	0	0	0	0
3	Bo	9	0	0	0	0
3	Bp	31	0	0	0	0
3	Bq	18	0	0	0	0
3	Br	35	0	0	0	0
3	Bs	15	0	0	0	0
3	Bt	11	0	0	0	0
3	Bu	28	0	0	0	0
3	Bv	25	0	0	0	0
3	Bw	39	0	0	0	0
3	Bx	7	0	0	0	0
3	CA	29	0	0	0	0
3	CB	16	0	0	0	0
3	CC	7	0	0	0	0
3	CD	28	0	0	1	0
3	CE	15	0	0	0	0
3	CF	25	0	0	1	0
3	CG	19	0	0	0	0
3	CH	10	0	0	0	0
3	CI	30	0	0	1	0
3	CJ	18	0	0	2	0
3	CK	12	0	0	0	0
3	CL	7	0	0	0	0
3	CM	23	0	0	1	0
3	CN	25	0	0	0	0
3	CO	14	0	0	0	0
3	CP	14	0	0	1	0
3	CQ	41	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	CR	20	0	0	0	0
3	CS	28	0	0	0	0
3	CT	15	0	0	0	0
3	CU	3	0	0	0	0
3	CV	8	0	0	0	0
3	CW	15	0	0	0	0
3	CX	21	0	0	1	0
3	Ca	11	0	0	0	0
3	Cb	6	0	0	0	0
3	Cc	7	0	0	0	0
3	Cd	6	0	0	0	0
3	Ce	6	0	0	0	0
3	Cf	8	0	0	0	0
3	Cg	16	0	0	0	0
3	Ch	18	0	0	0	0
3	Ci	9	0	0	0	0
3	Cj	9	0	0	0	0
3	Ck	11	0	0	0	0
3	Cl	2	0	0	0	0
3	Cm	2	0	0	0	0
3	Cn	4	0	0	0	0
3	Co	12	0	0	0	0
3	Cp	10	0	0	0	0
3	Cq	2	0	0	0	0
3	Cr	4	0	0	0	0
3	Ct	17	0	0	0	0
3	Cu	12	0	0	0	0
3	Cv	4	0	0	0	0
3	Cw	10	0	0	0	0
3	Cx	12	0	0	0	0
All	All	187090	0	181001	2777	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 8.

The worst 5 of 2777 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:AJ:1:MET:HG3	1:AJ:2:SER:H	1.19	1.02
1:AM:8:ASN:HD22	1:AR:112:LEU:HD13	2.24	1.01
1:CB:8:ASN:HD22	1:CJ:112:LEU:HD13	2.31	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:23:LEU:HD11	1:AE:106:LYS:HE2	1.50	0.94
1:BI:1:MET:HG3	1:BI:2:SER:H	1.32	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 X-ray entries followed by that with respect to entries of similar resolution.

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	AA	156/192 (81%)	151 (97%)	5 (3%)	0	100 100
1	AB	163/192 (85%)	149 (91%)	10 (6%)	4 (2%)	6 22
1	AC	159/192 (83%)	146 (92%)	10 (6%)	3 (2%)	9 29
1	AD	157/192 (82%)	151 (96%)	5 (3%)	1 (1%)	28 60
1	AE	163/192 (85%)	147 (90%)	11 (7%)	5 (3%)	5 17
1	AF	156/192 (81%)	151 (97%)	4 (3%)	1 (1%)	28 60
1	AG	157/192 (82%)	150 (96%)	7 (4%)	0	100 100
1	AH	158/192 (82%)	148 (94%)	10 (6%)	0	100 100
1	AI	156/192 (81%)	147 (94%)	8 (5%)	1 (1%)	28 60
1	AJ	155/192 (81%)	149 (96%)	6 (4%)	0	100 100
1	AK	155/192 (81%)	152 (98%)	3 (2%)	0	100 100
1	AL	155/192 (81%)	147 (95%)	8 (5%)	0	100 100
1	AM	160/192 (83%)	151 (94%)	7 (4%)	2 (1%)	14 39
1	AN	163/192 (85%)	154 (94%)	7 (4%)	2 (1%)	15 42
1	AO	163/192 (85%)	148 (91%)	11 (7%)	4 (2%)	6 22
1	AP	157/192 (82%)	152 (97%)	5 (3%)	0	100 100
1	AQ	163/192 (85%)	150 (92%)	10 (6%)	3 (2%)	10 31
1	AR	162/192 (84%)	152 (94%)	8 (5%)	2 (1%)	15 42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	AS	158/192 (82%)	149 (94%)	8 (5%)	1 (1%)	28 60
1	AT	156/192 (81%)	144 (92%)	10 (6%)	2 (1%)	14 39
1	AU	158/192 (82%)	152 (96%)	5 (3%)	1 (1%)	28 60
1	AV	158/192 (82%)	148 (94%)	8 (5%)	2 (1%)	14 39
1	AW	156/192 (81%)	150 (96%)	6 (4%)	0	100 100
1	AX	158/192 (82%)	149 (94%)	8 (5%)	1 (1%)	28 60
1	Aa	159/192 (83%)	153 (96%)	6 (4%)	0	100 100
1	Ab	159/192 (83%)	151 (95%)	6 (4%)	2 (1%)	14 39
1	Ac	158/192 (82%)	155 (98%)	3 (2%)	0	100 100
1	Ad	163/192 (85%)	152 (93%)	8 (5%)	3 (2%)	10 31
1	Ae	160/192 (83%)	157 (98%)	3 (2%)	0	100 100
1	Af	159/192 (83%)	152 (96%)	7 (4%)	0	100 100
1	Ag	153/192 (80%)	148 (97%)	5 (3%)	0	100 100
1	Ah	159/192 (83%)	153 (96%)	6 (4%)	0	100 100
1	Ai	157/192 (82%)	150 (96%)	5 (3%)	2 (1%)	14 39
1	Aj	163/192 (85%)	147 (90%)	11 (7%)	5 (3%)	5 17
1	Ak	163/192 (85%)	153 (94%)	8 (5%)	2 (1%)	15 42
1	Al	163/192 (85%)	149 (91%)	10 (6%)	4 (2%)	6 22
1	Am	160/192 (83%)	149 (93%)	7 (4%)	4 (2%)	6 22
1	An	159/192 (83%)	149 (94%)	8 (5%)	2 (1%)	14 39
1	Ao	159/192 (83%)	150 (94%)	7 (4%)	2 (1%)	14 39
1	Ap	160/192 (83%)	150 (94%)	7 (4%)	3 (2%)	9 29
1	Aq	158/192 (82%)	146 (92%)	11 (7%)	1 (1%)	28 60
1	Ar	163/192 (85%)	152 (93%)	8 (5%)	3 (2%)	10 31
1	As	159/192 (83%)	153 (96%)	6 (4%)	0	100 100
1	At	158/192 (82%)	151 (96%)	7 (4%)	0	100 100
1	Au	158/192 (82%)	153 (97%)	4 (2%)	1 (1%)	28 60
1	Av	163/192 (85%)	148 (91%)	13 (8%)	2 (1%)	15 42
1	Aw	159/192 (83%)	149 (94%)	9 (6%)	1 (1%)	28 60
1	Ax	153/192 (80%)	150 (98%)	3 (2%)	0	100 100
1	BA	164/192 (85%)	150 (92%)	12 (7%)	2 (1%)	15 42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	BB	155/192 (81%)	146 (94%)	9 (6%)	0	100 100
1	BC	153/192 (80%)	148 (97%)	5 (3%)	0	100 100
1	BD	158/192 (82%)	151 (96%)	7 (4%)	0	100 100
1	BE	157/192 (82%)	150 (96%)	7 (4%)	0	100 100
1	BF	157/192 (82%)	147 (94%)	7 (4%)	3 (2%)	9 29
1	BG	154/192 (80%)	145 (94%)	9 (6%)	0	100 100
1	BH	152/192 (79%)	146 (96%)	5 (3%)	1 (1%)	25 56
1	BI	153/192 (80%)	150 (98%)	3 (2%)	0	100 100
1	BJ	155/192 (81%)	147 (95%)	7 (4%)	1 (1%)	28 60
1	BK	154/192 (80%)	147 (96%)	7 (4%)	0	100 100
1	BL	153/192 (80%)	149 (97%)	4 (3%)	0	100 100
1	BM	156/192 (81%)	151 (97%)	5 (3%)	0	100 100
1	BN	157/192 (82%)	150 (96%)	6 (4%)	1 (1%)	28 60
1	BO	158/192 (82%)	146 (92%)	11 (7%)	1 (1%)	28 60
1	BP	157/192 (82%)	150 (96%)	7 (4%)	0	100 100
1	BQ	158/192 (82%)	152 (96%)	6 (4%)	0	100 100
1	BR	159/192 (83%)	150 (94%)	8 (5%)	1 (1%)	28 60
1	BS	157/192 (82%)	152 (97%)	5 (3%)	0	100 100
1	BT	155/192 (81%)	150 (97%)	5 (3%)	0	100 100
1	BU	160/192 (83%)	152 (95%)	7 (4%)	1 (1%)	28 60
1	BV	154/192 (80%)	149 (97%)	3 (2%)	2 (1%)	14 39
1	BW	159/192 (83%)	154 (97%)	5 (3%)	0	100 100
1	BX	161/192 (84%)	150 (93%)	7 (4%)	4 (2%)	6 22
1	Ba	156/192 (81%)	149 (96%)	7 (4%)	0	100 100
1	Bb	157/192 (82%)	148 (94%)	9 (6%)	0	100 100
1	Bc	159/192 (83%)	147 (92%)	12 (8%)	0	100 100
1	Bd	159/192 (83%)	152 (96%)	4 (2%)	3 (2%)	9 29
1	Be	161/192 (84%)	146 (91%)	12 (8%)	3 (2%)	9 29
1	Bf	163/192 (85%)	147 (90%)	11 (7%)	5 (3%)	5 17
1	Bg	154/192 (80%)	150 (97%)	4 (3%)	0	100 100
1	Bh	157/192 (82%)	151 (96%)	5 (3%)	1 (1%)	28 60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	Bi	155/192 (81%)	148 (96%)	6 (4%)	1 (1%)	28 60
1	Bj	152/192 (79%)	147 (97%)	5 (3%)	0	100 100
1	Bk	157/192 (82%)	148 (94%)	8 (5%)	1 (1%)	28 60
1	Bl	157/192 (82%)	150 (96%)	6 (4%)	1 (1%)	28 60
1	Bm	157/192 (82%)	151 (96%)	6 (4%)	0	100 100
1	Bn	163/192 (85%)	153 (94%)	7 (4%)	3 (2%)	10 31
1	Bo	154/192 (80%)	149 (97%)	5 (3%)	0	100 100
1	Bp	160/192 (83%)	148 (92%)	11 (7%)	1 (1%)	28 60
1	Bq	158/192 (82%)	150 (95%)	6 (4%)	2 (1%)	14 39
1	Br	159/192 (83%)	148 (93%)	9 (6%)	2 (1%)	14 39
1	Bs	153/192 (80%)	148 (97%)	5 (3%)	0	100 100
1	Bt	156/192 (81%)	147 (94%)	7 (4%)	2 (1%)	14 39
1	Bu	163/192 (85%)	152 (93%)	9 (6%)	2 (1%)	15 42
1	Bv	158/192 (82%)	149 (94%)	8 (5%)	1 (1%)	28 60
1	Bw	157/192 (82%)	150 (96%)	6 (4%)	1 (1%)	28 60
1	Bx	155/192 (81%)	147 (95%)	8 (5%)	0	100 100
1	CA	158/192 (82%)	153 (97%)	4 (2%)	1 (1%)	28 60
1	CB	159/192 (83%)	154 (97%)	5 (3%)	0	100 100
1	CC	155/192 (81%)	149 (96%)	5 (3%)	1 (1%)	28 60
1	CD	159/192 (83%)	152 (96%)	6 (4%)	1 (1%)	28 60
1	CE	158/192 (82%)	149 (94%)	7 (4%)	2 (1%)	14 39
1	CF	158/192 (82%)	150 (95%)	8 (5%)	0	100 100
1	CG	158/192 (82%)	153 (97%)	4 (2%)	1 (1%)	28 60
1	CH	157/192 (82%)	146 (93%)	10 (6%)	1 (1%)	28 60
1	CI	158/192 (82%)	147 (93%)	10 (6%)	1 (1%)	28 60
1	CJ	163/192 (85%)	153 (94%)	8 (5%)	2 (1%)	15 42
1	CK	158/192 (82%)	152 (96%)	5 (3%)	1 (1%)	28 60
1	CL	157/192 (82%)	150 (96%)	7 (4%)	0	100 100
1	CM	157/192 (82%)	148 (94%)	7 (4%)	2 (1%)	14 39
1	CN	159/192 (83%)	152 (96%)	7 (4%)	0	100 100
1	CO	157/192 (82%)	146 (93%)	11 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	CP	156/192 (81%)	152 (97%)	4 (3%)	0	100 100
1	CQ	160/192 (83%)	150 (94%)	10 (6%)	0	100 100
1	CR	164/192 (85%)	150 (92%)	11 (7%)	3 (2%)	10 31
1	CS	159/192 (83%)	150 (94%)	9 (6%)	0	100 100
1	CT	156/192 (81%)	147 (94%)	8 (5%)	1 (1%)	28 60
1	CU	157/192 (82%)	152 (97%)	5 (3%)	0	100 100
1	CV	156/192 (81%)	149 (96%)	7 (4%)	0	100 100
1	CW	153/192 (80%)	151 (99%)	2 (1%)	0	100 100
1	CX	159/192 (83%)	147 (92%)	10 (6%)	2 (1%)	14 39
1	Ca	156/192 (81%)	148 (95%)	5 (3%)	3 (2%)	9 29
1	Cb	157/192 (82%)	148 (94%)	9 (6%)	0	100 100
1	Cc	155/192 (81%)	148 (96%)	7 (4%)	0	100 100
1	Cd	151/192 (79%)	146 (97%)	5 (3%)	0	100 100
1	Ce	152/192 (79%)	148 (97%)	4 (3%)	0	100 100
1	Cf	151/192 (79%)	146 (97%)	5 (3%)	0	100 100
1	Cg	158/192 (82%)	150 (95%)	7 (4%)	1 (1%)	28 60
1	Ch	157/192 (82%)	149 (95%)	8 (5%)	0	100 100
1	Ci	151/192 (79%)	147 (97%)	4 (3%)	0	100 100
1	Cj	154/192 (80%)	146 (95%)	7 (4%)	1 (1%)	28 60
1	Ck	152/192 (79%)	147 (97%)	5 (3%)	0	100 100
1	Cl	153/192 (80%)	150 (98%)	3 (2%)	0	100 100
1	Cm	157/192 (82%)	148 (94%)	9 (6%)	0	100 100
1	Cn	153/192 (80%)	149 (97%)	4 (3%)	0	100 100
1	Co	153/192 (80%)	151 (99%)	2 (1%)	0	100 100
1	Cp	156/192 (81%)	149 (96%)	6 (4%)	1 (1%)	28 60
1	Cq	153/192 (80%)	146 (95%)	7 (5%)	0	100 100
1	Cr	152/192 (79%)	147 (97%)	4 (3%)	1 (1%)	25 56
1	Cs	152/192 (79%)	147 (97%)	4 (3%)	1 (1%)	25 56
1	Ct	158/192 (82%)	154 (98%)	4 (2%)	0	100 100
1	Cu	157/192 (82%)	149 (95%)	7 (4%)	1 (1%)	28 60
1	Cv	159/192 (83%)	151 (95%)	8 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	Cw	153/192 (80%)	149 (97%)	4 (3%)	0	100 100
1	Cx	154/192 (80%)	151 (98%)	3 (2%)	0	100 100
All	All	22658/27648 (82%)	21530 (95%)	982 (4%)	146 (1%)	28 60

5 of 146 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AE	162	LEU
1	AO	4	GLN
1	Aq	2	SER
1	Au	2	SER
1	Bi	2	SER

5.3.2 Protein sidechains [\(i\)](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	AA	134/161 (83%)	128 (96%)	6 (4%)	32 63
1	AB	138/161 (86%)	133 (96%)	5 (4%)	40 72
1	AC	136/161 (84%)	132 (97%)	4 (3%)	48 78
1	AD	134/161 (83%)	133 (99%)	1 (1%)	87 95
1	AE	138/161 (86%)	136 (99%)	2 (1%)	71 90
1	AF	134/161 (83%)	131 (98%)	3 (2%)	57 84
1	AG	134/161 (83%)	131 (98%)	3 (2%)	57 84
1	AH	135/161 (84%)	131 (97%)	4 (3%)	46 77
1	AI	134/161 (83%)	131 (98%)	3 (2%)	57 84
1	AJ	133/161 (83%)	132 (99%)	1 (1%)	85 95
1	AK	134/161 (83%)	132 (98%)	2 (2%)	70 89
1	AL	133/161 (83%)	130 (98%)	3 (2%)	56 83
1	AM	136/161 (84%)	133 (98%)	3 (2%)	57 84
1	AN	138/161 (86%)	135 (98%)	3 (2%)	57 84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	AO	138/161 (86%)	127 (92%)	11 (8%)	14 35
1	AP	135/161 (84%)	128 (95%)	7 (5%)	27 57
1	AQ	138/161 (86%)	136 (99%)	2 (1%)	71 90
1	AR	137/161 (85%)	135 (98%)	2 (2%)	70 89
1	AS	134/161 (83%)	130 (97%)	4 (3%)	46 77
1	AT	134/161 (83%)	132 (98%)	2 (2%)	70 89
1	AU	135/161 (84%)	131 (97%)	4 (3%)	46 77
1	AV	134/161 (83%)	133 (99%)	1 (1%)	87 95
1	AW	134/161 (83%)	133 (99%)	1 (1%)	87 95
1	AX	135/161 (84%)	134 (99%)	1 (1%)	87 95
1	Aa	136/161 (84%)	133 (98%)	3 (2%)	57 84
1	Ab	135/161 (84%)	130 (96%)	5 (4%)	39 71
1	Ac	135/161 (84%)	132 (98%)	3 (2%)	57 84
1	Ad	138/161 (86%)	131 (95%)	7 (5%)	28 58
1	Ae	136/161 (84%)	132 (97%)	4 (3%)	48 78
1	Af	136/161 (84%)	133 (98%)	3 (2%)	57 84
1	Ag	133/161 (83%)	129 (97%)	4 (3%)	46 77
1	Ah	136/161 (84%)	133 (98%)	3 (2%)	57 84
1	Ai	135/161 (84%)	132 (98%)	3 (2%)	57 84
1	Aj	138/161 (86%)	132 (96%)	6 (4%)	33 65
1	Ak	138/161 (86%)	133 (96%)	5 (4%)	40 72
1	Al	138/161 (86%)	131 (95%)	7 (5%)	28 58
1	Am	136/161 (84%)	135 (99%)	1 (1%)	87 95
1	An	135/161 (84%)	133 (98%)	2 (2%)	70 89
1	Ao	136/161 (84%)	134 (98%)	2 (2%)	70 89
1	Ap	136/161 (84%)	134 (98%)	2 (2%)	70 89
1	Aq	135/161 (84%)	132 (98%)	3 (2%)	57 84
1	Ar	138/161 (86%)	133 (96%)	5 (4%)	40 72
1	As	136/161 (84%)	130 (96%)	6 (4%)	33 64
1	At	135/161 (84%)	128 (95%)	7 (5%)	27 57
1	Au	135/161 (84%)	130 (96%)	5 (4%)	39 71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	Av	138/161 (86%)	135 (98%)	3 (2%)	57 84
1	Aw	135/161 (84%)	128 (95%)	7 (5%)	27 57
1	Ax	133/161 (83%)	132 (99%)	1 (1%)	85 95
1	BA	139/161 (86%)	134 (96%)	5 (4%)	40 72
1	BB	134/161 (83%)	132 (98%)	2 (2%)	70 89
1	BC	132/161 (82%)	130 (98%)	2 (2%)	70 89
1	BD	136/161 (84%)	135 (99%)	1 (1%)	87 95
1	BE	135/161 (84%)	135 (100%)	0	100 100
1	BF	134/161 (83%)	132 (98%)	2 (2%)	70 89
1	BG	133/161 (83%)	131 (98%)	2 (2%)	70 89
1	BH	132/161 (82%)	129 (98%)	3 (2%)	56 83
1	BI	133/161 (83%)	132 (99%)	1 (1%)	85 95
1	BJ	133/161 (83%)	130 (98%)	3 (2%)	56 83
1	BK	133/161 (83%)	128 (96%)	5 (4%)	38 70
1	BL	133/161 (83%)	132 (99%)	1 (1%)	85 95
1	BM	134/161 (83%)	132 (98%)	2 (2%)	70 89
1	BN	134/161 (83%)	132 (98%)	2 (2%)	70 89
1	BO	135/161 (84%)	132 (98%)	3 (2%)	57 84
1	BP	134/161 (83%)	131 (98%)	3 (2%)	57 84
1	BQ	135/161 (84%)	130 (96%)	5 (4%)	39 71
1	BR	136/161 (84%)	134 (98%)	2 (2%)	70 89
1	BS	135/161 (84%)	134 (99%)	1 (1%)	87 95
1	BT	133/161 (83%)	131 (98%)	2 (2%)	70 89
1	BU	136/161 (84%)	135 (99%)	1 (1%)	87 95
1	BV	132/161 (82%)	130 (98%)	2 (2%)	70 89
1	BW	135/161 (84%)	133 (98%)	2 (2%)	70 89
1	BX	136/161 (84%)	133 (98%)	3 (2%)	57 84
1	Ba	134/161 (83%)	131 (98%)	3 (2%)	57 84
1	Bb	135/161 (84%)	132 (98%)	3 (2%)	57 84
1	Bc	136/161 (84%)	130 (96%)	6 (4%)	33 64
1	Bd	136/161 (84%)	136 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	Be	136/161 (84%)	133 (98%)	3 (2%)	57 84
1	Bf	138/161 (86%)	132 (96%)	6 (4%)	33 65
1	Bg	133/161 (83%)	131 (98%)	2 (2%)	70 89
1	Bh	135/161 (84%)	132 (98%)	3 (2%)	57 84
1	Bi	134/161 (83%)	132 (98%)	2 (2%)	70 89
1	Bj	131/161 (81%)	128 (98%)	3 (2%)	56 83
1	Bk	135/161 (84%)	132 (98%)	3 (2%)	57 84
1	Bl	135/161 (84%)	131 (97%)	4 (3%)	46 77
1	Bm	134/161 (83%)	130 (97%)	4 (3%)	46 77
1	Bn	138/161 (86%)	135 (98%)	3 (2%)	57 84
1	Bo	133/161 (83%)	132 (99%)	1 (1%)	85 95
1	Bp	136/161 (84%)	133 (98%)	3 (2%)	57 84
1	Bq	136/161 (84%)	135 (99%)	1 (1%)	87 95
1	Br	136/161 (84%)	130 (96%)	6 (4%)	33 64
1	Bs	133/161 (83%)	131 (98%)	2 (2%)	70 89
1	Bt	134/161 (83%)	130 (97%)	4 (3%)	46 77
1	Bu	138/161 (86%)	133 (96%)	5 (4%)	40 72
1	Bv	135/161 (84%)	133 (98%)	2 (2%)	70 89
1	Bw	134/161 (83%)	132 (98%)	2 (2%)	70 89
1	Bx	133/161 (83%)	131 (98%)	2 (2%)	70 89
1	CA	135/161 (84%)	131 (97%)	4 (3%)	46 77
1	CB	135/161 (84%)	130 (96%)	5 (4%)	39 71
1	CC	133/161 (83%)	131 (98%)	2 (2%)	70 89
1	CD	136/161 (84%)	136 (100%)	0	100 100
1	CE	136/161 (84%)	134 (98%)	2 (2%)	70 89
1	CF	134/161 (83%)	130 (97%)	4 (3%)	46 77
1	CG	136/161 (84%)	131 (96%)	5 (4%)	39 71
1	CH	135/161 (84%)	132 (98%)	3 (2%)	57 84
1	CI	135/161 (84%)	130 (96%)	5 (4%)	39 71
1	CJ	138/161 (86%)	133 (96%)	5 (4%)	40 72
1	CK	135/161 (84%)	131 (97%)	4 (3%)	46 77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	CL	135/161 (84%)	133 (98%)	2 (2%)	70 89
1	CM	135/161 (84%)	130 (96%)	5 (4%)	39 71
1	CN	135/161 (84%)	133 (98%)	2 (2%)	70 89
1	CO	135/161 (84%)	133 (98%)	2 (2%)	70 89
1	CP	134/161 (83%)	131 (98%)	3 (2%)	57 84
1	CQ	136/161 (84%)	129 (95%)	7 (5%)	28 58
1	CR	139/161 (86%)	136 (98%)	3 (2%)	57 84
1	CS	136/161 (84%)	131 (96%)	5 (4%)	39 71
1	CT	134/161 (83%)	130 (97%)	4 (3%)	46 77
1	CU	135/161 (84%)	135 (100%)	0	100 100
1	CV	134/161 (83%)	132 (98%)	2 (2%)	70 89
1	CW	133/161 (83%)	132 (99%)	1 (1%)	85 95
1	CX	136/161 (84%)	134 (98%)	2 (2%)	70 89
1	Ca	133/161 (83%)	130 (98%)	3 (2%)	56 83
1	Cb	134/161 (83%)	132 (98%)	2 (2%)	70 89
1	Cc	133/161 (83%)	131 (98%)	2 (2%)	70 89
1	Cd	131/161 (81%)	129 (98%)	2 (2%)	70 89
1	Ce	132/161 (82%)	129 (98%)	3 (2%)	56 83
1	Cf	131/161 (81%)	131 (100%)	0	100 100
1	Cg	134/161 (83%)	132 (98%)	2 (2%)	70 89
1	Ch	134/161 (83%)	131 (98%)	3 (2%)	57 84
1	Ci	131/161 (81%)	131 (100%)	0	100 100
1	Cj	134/161 (83%)	131 (98%)	3 (2%)	57 84
1	Ck	132/161 (82%)	130 (98%)	2 (2%)	70 89
1	Cl	132/161 (82%)	130 (98%)	2 (2%)	70 89
1	Cm	134/161 (83%)	130 (97%)	4 (3%)	46 77
1	Cn	133/161 (83%)	130 (98%)	3 (2%)	56 83
1	Co	132/161 (82%)	129 (98%)	3 (2%)	56 83
1	Cp	134/161 (83%)	133 (99%)	1 (1%)	87 95
1	Cq	132/161 (82%)	131 (99%)	1 (1%)	85 95
1	Cr	132/161 (82%)	130 (98%)	2 (2%)	70 89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	Cs	131/161 (81%)	130 (99%)	1 (1%)	85 95
1	Ct	134/161 (83%)	131 (98%)	3 (2%)	57 84
1	Cu	134/161 (83%)	131 (98%)	3 (2%)	57 84
1	Cv	135/161 (84%)	132 (98%)	3 (2%)	57 84
1	Cw	132/161 (82%)	132 (100%)	0	100 100
1	Cx	134/161 (83%)	130 (97%)	4 (3%)	46 77
All	All	19400/23184 (84%)	18968 (98%)	432 (2%)	57 84

5 of 432 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Bc	154	ARG
1	BM	26	GLN
1	CR	63	TYR
1	BF	101	MET
1	Bi	29	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 253 such sidechains are listed below:

Mol	Chain	Res	Type
1	BM	8	ASN
1	Bv	72	GLN
1	Cs	72	GLN
1	Bo	50	HIS
1	Bs	26	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry [\(i\)](#)

Of 48 ligands modelled in this entry, 48 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

6 Fit of model and data [\(i\)](#)

6.1 Protein, DNA and RNA chains [\(i\)](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	AA	158/192 (82%)	-0.35	5 (3%)	48 42	31, 61, 82, 117	0
1	AB	165/192 (85%)	-0.22	7 (4%)	37 31	26, 54, 95, 109	0
1	AC	161/192 (83%)	-0.32	4 (2%)	58 54	38, 58, 77, 111	0
1	AD	159/192 (82%)	-0.26	4 (2%)	58 54	51, 68, 82, 118	0
1	AE	165/192 (85%)	-0.40	8 (4%)	31 27	12, 34, 96, 112	0
1	AF	158/192 (82%)	-0.48	2 (1%)	77 76	19, 47, 66, 104	0
1	AG	159/192 (82%)	-0.46	4 (2%)	58 54	31, 47, 63, 123	0
1	AH	160/192 (83%)	-0.23	3 (1%)	67 64	21, 42, 69, 112	0
1	AI	158/192 (82%)	-0.20	5 (3%)	48 42	54, 70, 84, 114	0
1	AJ	157/192 (81%)	-0.28	2 (1%)	77 76	25, 60, 79, 99	0
1	AK	157/192 (81%)	-0.35	2 (1%)	77 76	33, 59, 75, 101	0
1	AL	157/192 (81%)	-0.19	4 (2%)	58 54	52, 68, 82, 120	0
1	AM	162/192 (84%)	-0.46	2 (1%)	79 77	17, 39, 69, 112	0
1	AN	165/192 (85%)	-0.32	6 (3%)	43 37	31, 48, 89, 107	0
1	AO	165/192 (85%)	-0.22	11 (6%)	19 14	17, 46, 87, 110	0
1	AP	159/192 (82%)	-0.53	0	100 100	7, 30, 51, 102	0
1	AQ	165/192 (85%)	-0.14	11 (6%)	19 14	33, 62, 90, 110	0
1	AR	164/192 (85%)	-0.34	6 (3%)	42 36	20, 46, 89, 111	0
1	AS	160/192 (83%)	-0.20	6 (3%)	41 35	32, 56, 87, 117	0
1	AT	158/192 (82%)	-0.50	1 (0%)	89 88	15, 43, 62, 110	0
1	AU	160/192 (83%)	-0.48	1 (0%)	89 88	24, 42, 68, 107	0
1	AV	160/192 (83%)	-0.21	7 (4%)	35 30	30, 49, 82, 115	0
1	AW	158/192 (82%)	-0.33	2 (1%)	77 76	26, 56, 76, 113	0
1	AX	160/192 (83%)	-0.33	3 (1%)	67 64	23, 45, 78, 118	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	Aa	161/192 (83%)	-0.50	3 (1%)	67	64	12, 30, 54, 109	0
1	Ab	161/192 (83%)	-0.58	0	100	100	13, 35, 65, 110	0
1	Ac	160/192 (83%)	-0.55	0	100	100	15, 35, 66, 103	0
1	Ad	165/192 (85%)	-0.56	3 (1%)	69	66	7, 26, 87, 107	0
1	Ae	162/192 (84%)	-0.30	5 (3%)	49	43	8, 29, 65, 113	0
1	Af	161/192 (83%)	-0.44	1 (0%)	89	88	10, 28, 56, 106	0
1	Ag	155/192 (80%)	-0.63	1 (0%)	89	88	8, 28, 45, 70	0
1	Ah	161/192 (83%)	-0.41	0	100	100	12, 32, 55, 109	0
1	Ai	159/192 (82%)	-0.53	1 (0%)	89	88	8, 23, 46, 96	0
1	Aj	165/192 (85%)	-0.18	5 (3%)	51	45	12, 31, 85, 109	0
1	Ak	165/192 (85%)	-0.33	7 (4%)	37	31	18, 37, 86, 107	0
1	Al	165/192 (85%)	-0.36	1 (0%)	89	88	8, 33, 81, 108	0
1	Am	162/192 (84%)	-0.46	2 (1%)	79	77	11, 31, 57, 102	0
1	An	161/192 (83%)	-0.57	2 (1%)	79	77	13, 28, 56, 96	0
1	Ao	161/192 (83%)	-0.47	2 (1%)	79	77	11, 32, 54, 105	0
1	Ap	162/192 (84%)	-0.58	2 (1%)	79	77	11, 30, 63, 101	0
1	Aq	160/192 (83%)	-0.50	2 (1%)	77	76	9, 30, 58, 110	0
1	Ar	165/192 (85%)	-0.47	2 (1%)	79	77	9, 28, 81, 105	0
1	As	161/192 (83%)	-0.49	3 (1%)	67	64	9, 32, 60, 109	0
1	At	160/192 (83%)	-0.60	2 (1%)	77	76	9, 31, 67, 107	0
1	Au	160/192 (83%)	-0.30	2 (1%)	77	76	19, 40, 66, 104	0
1	Av	165/192 (85%)	-0.31	5 (3%)	51	45	16, 39, 85, 110	0
1	Aw	161/192 (83%)	-0.45	3 (1%)	67	64	8, 31, 58, 109	0
1	Ax	155/192 (80%)	-0.70	1 (0%)	89	88	11, 31, 45, 76	0
1	BA	166/192 (86%)	-0.24	3 (1%)	69	66	30, 51, 87, 108	0
1	BB	157/192 (81%)	0.44	8 (5%)	29	24	68, 86, 98, 109	0
1	BC	155/192 (80%)	0.22	5 (3%)	48	42	64, 84, 94, 103	0
1	BD	160/192 (83%)	-0.30	2 (1%)	77	76	22, 52, 76, 105	0
1	BE	159/192 (82%)	-0.39	2 (1%)	77	76	26, 46, 72, 111	0
1	BF	159/192 (82%)	-0.61	0	100	100	13, 32, 53, 102	0
1	BG	156/192 (81%)	-0.21	2 (1%)	77	76	31, 58, 70, 94	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	BH	154/192 (80%)	0.05	3 (1%)	67	64	40, 70, 86, 99	0
1	BI	155/192 (80%)	-0.36	1 (0%)	89	88	19, 52, 73, 97	0
1	BJ	157/192 (81%)	-0.07	2 (1%)	77	76	50, 69, 91, 111	0
1	BK	156/192 (81%)	0.45	8 (5%)	29	24	71, 87, 98, 105	0
1	BL	155/192 (80%)	0.04	0	100	100	57, 74, 89, 92	0
1	BM	158/192 (82%)	-0.32	2 (1%)	77	76	9, 33, 54, 102	0
1	BN	159/192 (82%)	-0.33	0	100	100	20, 41, 63, 114	0
1	BO	160/192 (83%)	-0.11	4 (2%)	58	54	37, 62, 86, 114	0
1	BP	159/192 (82%)	-0.25	4 (2%)	58	54	29, 55, 83, 114	0
1	BQ	160/192 (83%)	-0.46	3 (1%)	67	64	17, 37, 63, 114	0
1	BR	161/192 (83%)	-0.43	2 (1%)	79	77	18, 42, 68, 103	0
1	BS	159/192 (82%)	-0.41	0	100	100	18, 34, 54, 98	0
1	BT	157/192 (81%)	0.19	5 (3%)	48	42	58, 74, 92, 118	0
1	BU	162/192 (84%)	0.06	1 (0%)	89	88	55, 78, 91, 115	0
1	BV	156/192 (81%)	0.24	6 (3%)	41	35	69, 87, 96, 111	0
1	BW	161/192 (83%)	-0.15	4 (2%)	58	54	38, 60, 81, 117	0
1	BX	163/192 (84%)	0.30	6 (3%)	42	36	61, 78, 91, 110	0
1	Ba	158/192 (82%)	-0.12	4 (2%)	58	54	52, 71, 88, 111	0
1	Bb	159/192 (82%)	-0.03	3 (1%)	67	64	49, 72, 90, 118	0
1	Bc	161/192 (83%)	-0.42	1 (0%)	89	88	15, 38, 69, 109	0
1	Bd	161/192 (83%)	-0.45	3 (1%)	67	64	21, 40, 64, 114	0
1	Be	163/192 (84%)	-0.45	1 (0%)	89	88	13, 36, 77, 107	0
1	Bf	165/192 (85%)	-0.29	5 (3%)	51	45	14, 44, 85, 110	0
1	Bg	156/192 (81%)	0.09	4 (2%)	56	52	54, 76, 89, 108	0
1	Bh	159/192 (82%)	-0.44	3 (1%)	67	64	30, 48, 72, 108	0
1	Bi	157/192 (81%)	-0.21	1 (0%)	89	88	32, 58, 70, 94	0
1	Bj	154/192 (80%)	0.06	0	100	100	55, 76, 85, 96	0
1	Bk	159/192 (82%)	-0.20	1 (0%)	89	88	37, 57, 80, 114	0
1	Bl	159/192 (82%)	-0.52	1 (0%)	89	88	12, 38, 61, 109	0
1	Bm	159/192 (82%)	-0.51	3 (1%)	67	64	18, 36, 59, 113	0
1	Bn	165/192 (85%)	-0.09	4 (2%)	59	55	33, 61, 89, 111	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	Bo	156/192 (81%)	-0.19	3 (1%)	67	64	44, 65, 84, 96	0
1	Bp	162/192 (84%)	-0.38	7 (4%)	36	31	17, 41, 79, 116	0
1	Bq	160/192 (83%)	-0.12	3 (1%)	67	64	26, 55, 76, 111	0
1	Br	161/192 (83%)	-0.58	2 (1%)	79	77	8, 28, 57, 105	0
1	Bs	155/192 (80%)	-0.24	0	100	100	37, 57, 80, 97	0
1	Bt	158/192 (82%)	0.14	4 (2%)	58	54	61, 79, 93, 110	0
1	Bu	165/192 (85%)	-0.40	6 (3%)	43	37	14, 36, 83, 106	0
1	Bv	160/192 (83%)	-0.42	5 (3%)	49	43	23, 45, 72, 120	0
1	Bw	159/192 (82%)	-0.39	3 (1%)	67	64	11, 29, 55, 112	0
1	Bx	157/192 (81%)	0.21	6 (3%)	41	35	62, 83, 95, 113	0
1	CA	160/192 (83%)	-0.48	1 (0%)	89	88	12, 36, 61, 111	0
1	CB	161/192 (83%)	-0.25	3 (1%)	67	64	19, 52, 79, 108	0
1	CC	157/192 (81%)	-0.24	2 (1%)	77	76	45, 65, 78, 109	0
1	CD	161/192 (83%)	-0.48	2 (1%)	79	77	13, 39, 68, 107	0
1	CE	160/192 (83%)	-0.27	2 (1%)	77	76	29, 52, 80, 112	0
1	CF	160/192 (83%)	-0.47	3 (1%)	67	64	11, 35, 53, 101	0
1	CG	160/192 (83%)	-0.39	2 (1%)	77	76	21, 45, 72, 112	0
1	CH	159/192 (82%)	-0.11	3 (1%)	67	64	33, 62, 79, 119	0
1	CI	160/192 (83%)	-0.22	3 (1%)	67	64	15, 35, 74, 107	0
1	CJ	165/192 (85%)	-0.36	5 (3%)	51	45	24, 44, 85, 105	0
1	CK	160/192 (83%)	-0.29	3 (1%)	67	64	22, 60, 77, 115	0
1	CL	159/192 (82%)	-0.34	3 (1%)	67	64	38, 57, 73, 121	0
1	CM	159/192 (82%)	-0.44	3 (1%)	67	64	16, 42, 63, 112	0
1	CN	161/192 (83%)	-0.50	1 (0%)	89	88	16, 40, 77, 110	0
1	CO	159/192 (82%)	-0.36	2 (1%)	77	76	38, 58, 74, 99	0
1	CP	158/192 (82%)	-0.38	2 (1%)	77	76	25, 57, 76, 110	0
1	CQ	162/192 (84%)	-0.46	3 (1%)	67	64	9, 31, 61, 104	0
1	CR	166/192 (86%)	-0.39	5 (3%)	51	45	24, 42, 82, 107	0
1	CS	161/192 (83%)	-0.32	4 (2%)	58	54	10, 35, 65, 114	0
1	CT	158/192 (82%)	-0.40	3 (1%)	67	64	26, 50, 66, 106	0
1	CU	159/192 (82%)	-0.23	2 (1%)	77	76	51, 67, 82, 120	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	CV	158/192 (82%)	-0.23	4 (2%)	58	54	55, 68, 84, 120
1	CW	155/192 (80%)	-0.49	1 (0%)	89	88	27, 47, 69, 87
1	CX	161/192 (83%)	-0.47	3 (1%)	67	64	20, 48, 70, 107
1	Ca	158/192 (82%)	0.59	18 (11%)	6	4	58, 89, 103, 121
1	Cb	159/192 (82%)	0.01	4 (2%)	58	54	37, 69, 87, 109
1	Cc	157/192 (81%)	-0.11	5 (3%)	48	42	40, 69, 86, 118
1	Cd	153/192 (79%)	0.63	18 (11%)	5	3	76, 91, 104, 109
1	Ce	154/192 (80%)	0.24	6 (3%)	40	34	59, 81, 92, 95
1	Cf	153/192 (79%)	0.84	18 (11%)	5	3	83, 97, 107, 110
1	Cg	160/192 (83%)	0.03	7 (4%)	35	30	48, 68, 93, 126
1	Ch	159/192 (82%)	-0.42	2 (1%)	77	76	23, 49, 66, 114
1	Ci	153/192 (79%)	0.62	15 (9%)	8	5	69, 89, 104, 111
1	Cj	156/192 (81%)	0.29	8 (5%)	29	24	61, 81, 100, 112
1	Ck	154/192 (80%)	-0.08	2 (1%)	77	76	45, 74, 92, 104
1	Cl	155/192 (80%)	0.17	5 (3%)	48	42	56, 85, 97, 113
1	Cm	159/192 (82%)	0.41	16 (10%)	8	5	71, 88, 100, 113
1	Cn	155/192 (80%)	0.20	6 (3%)	40	34	65, 86, 101, 104
1	Co	155/192 (80%)	-0.34	2 (1%)	77	76	26, 52, 71, 100
1	Cp	158/192 (82%)	-0.07	7 (4%)	35	30	46, 67, 89, 109
1	Cq	155/192 (80%)	0.71	18 (11%)	5	3	83, 96, 106, 112
1	Cr	154/192 (80%)	0.19	9 (5%)	24	19	78, 91, 103, 111
1	Cs	154/192 (80%)	0.55	13 (8%)	12	8	83, 98, 106, 107
1	Ct	160/192 (83%)	-0.37	4 (2%)	58	54	34, 51, 79, 115
1	Cu	159/192 (82%)	-0.23	6 (3%)	41	35	44, 62, 81, 119
1	Cv	161/192 (83%)	-0.13	3 (1%)	67	64	39, 59, 81, 119
1	Cw	155/192 (80%)	0.18	4 (2%)	56	52	71, 89, 98, 107
1	Cx	156/192 (81%)	-0.20	2 (1%)	77	76	39, 59, 78, 99
All	All	22946/27648 (82%)	-0.23	570 (2%)	58	54	7, 52, 95, 126
							0

The worst 5 of 570 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Ci	155	LEU	6.5

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Mol	Chain	Res	Type	RSRZ
1	Ar	162	LEU	6.0
1	Bn	159	GLU	5.8
1	Av	162	LEU	5.8
1	Av	159	GLU	5.7

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

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

6.3 Carbohydrates [\(i\)](#)

There are no carbohydrates in this entry.

6.4 Ligands [\(i\)](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	CA	Bd	201	1/1	0.84	0.28	26.73	61,61,61,61	0
2	CA	CF	201	1/1	0.91	0.33	9.67	63,63,63,63	0
2	CA	CA	201	1/1	0.84	0.34	9.36	67,67,67,67	0
2	CA	An	201	1/1	0.59	0.32	8.96	61,61,61,61	0
2	CA	BN	201	1/1	0.63	0.36	8.76	73,73,73,73	0
2	CA	Ac	201	1/1	0.82	0.28	8.47	70,70,70,70	0
2	CA	Bu	201	1/1	0.97	0.28	7.50	61,61,61,61	0
2	CA	Be	201	1/1	0.93	0.33	6.33	66,66,66,66	0
2	CA	AC	201	1/1	0.86	0.32	6.31	86,86,86,86	0
2	CA	BH	201	1/1	0.95	0.26	6.20	96,96,96,96	0
2	CA	BR	201	1/1	0.84	0.32	5.82	72,72,72,72	0
2	CA	Ah	201	1/1	0.96	0.28	5.62	56,56,56,56	0
2	CA	Cl	201	1/1	0.69	0.44	5.59	85,85,85,85	1
2	CA	Bf	201	1/1	0.95	0.26	5.55	68,68,68,68	0
2	CA	Cb	201	1/1	0.90	0.27	5.36	80,80,80,80	0
2	CA	Ca	201	1/1	0.97	0.42	5.13	87,87,87,87	1
2	CA	Ce	201	1/1	0.90	0.27	5.11	106,106,106,106	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	CA	Ae	201	1/1	0.94	0.24	5.09	70,70,70,70	0
2	CA	BC	201	1/1	0.95	0.45	4.98	73,73,73,73	1
2	CA	BA	201	1/1	0.85	0.24	4.78	78,78,78,78	0
2	CA	AO	201	1/1	0.92	0.25	4.74	67,67,67,67	0
2	CA	CE	201	1/1	0.87	0.30	4.74	83,83,83,83	0
2	CA	Bc	201	1/1	0.92	0.30	4.32	73,73,73,73	0
2	CA	AM	201	1/1	0.91	0.24	4.31	68,68,68,68	0
2	CA	Aa	201	1/1	0.83	0.24	3.74	58,58,58,58	0
2	CA	AH	201	1/1	0.94	0.27	3.62	62,62,62,62	0
2	CA	Ad	201	1/1	0.93	0.24	3.52	54,54,54,54	0
2	CA	AF	201	1/1	0.86	0.24	3.46	68,68,68,68	0
2	CA	Ag	201	1/1	0.80	0.25	3.44	55,55,55,55	0
2	CA	BG	201	1/1	0.69	0.28	3.34	94,94,94,94	0
2	CA	Aj	201	1/1	0.94	0.28	3.30	56,56,56,56	0
2	CA	Bg	201	1/1	0.90	0.23	3.26	88,88,88,88	0
2	CA	CB	201	1/1	0.95	0.23	3.23	60,60,60,60	0
2	CA	Cp	201	1/1	0.94	0.25	2.97	69,69,69,69	0
2	CA	CC	201	1/1	0.91	0.24	2.82	96,96,96,96	0
2	CA	CO	201	1/1	0.90	0.21	2.46	68,68,68,68	0
2	CA	AB	201	1/1	0.81	0.22	2.43	75,75,75,75	0
2	CA	Bb	201	1/1	0.70	0.23	1.74	98,98,98,98	0
2	CA	CD	201	1/1	0.98	0.18	1.42	68,68,68,68	0
2	CA	Ba	201	1/1	0.83	0.19	1.16	80,80,80,80	0
2	CA	Cg	201	1/1	0.75	0.17	0.82	85,85,85,85	0
2	CA	Ck	201	1/1	0.87	0.18	0.68	78,78,78,78	0
2	CA	AL	201	1/1	0.91	0.18	0.62	84,84,84,84	0
2	CA	AA	201	1/1	0.89	0.18	0.46	106,106,106,106	0
2	CA	BD	201	1/1	0.85	0.20	0.22	81,81,81,81	0
2	CA	CH	201	1/1	0.96	0.15	-0.19	69,69,69,69	0
2	CA	Cn	201	1/1	0.70	0.15	-0.59	108,108,108,108	0
2	CA	BB	201	1/1	0.69	0.13	-2.48	86,86,86,86	0

6.5 Other polymers (i)

There are no such residues in this entry.