



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 16, 2023 – 09:05 PM EDT

PDB ID : 4V6B
Title : Crystal structure of human ferritin Phe167SerfsX26 mutant.
Authors : Hurley, T.D.; Vidal, R.
Deposited on : 2009-06-19
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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

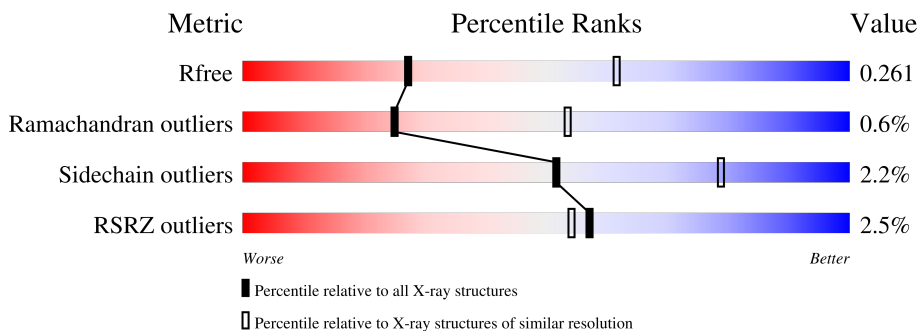
1 Overall quality at a glance

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}	130704	3168 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	192	 3% (Poor fit) 79% (Green) 18% (Grey)
1	AB	192	 4% (Poor fit) 82% (Green) 14% (Grey)
1	AC	192	 2% (Poor fit) 80% (Green) 16% (Grey)
1	AD	192	 2% (Poor fit) 82% (Green) 17% (Grey)
1	AE	192	 5% (Poor fit) 83% (Green) 14% (Grey)
1	AF	192	 % (Poor fit) 80% (Green) 18% (Grey)







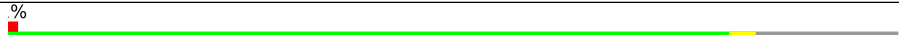
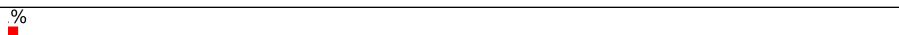
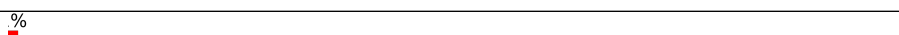
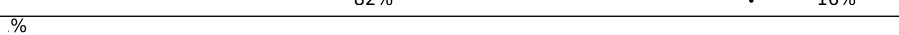
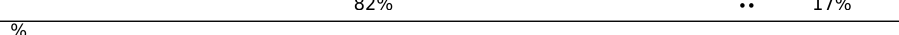
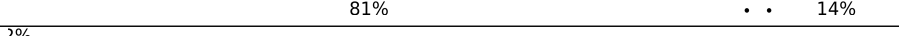













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Mol	Chain	Length	Quality of chain
1	AG	192	2% 81% 17%
1	AH	192	2% 81% 17%
1	AI	192	3% 80% 18%
1	AJ	192	% 81% 18%
1	AK	192	% 81% 18%
1	AL	192	2% 80% 18%
1	AM	192	2% 82% 16%
1	AN	192	3% 84% 14%
1	AO	192	6% 78% 8% 14%
1	AP	192	% 79% 17%
1	AQ	192	6% 83% 14%
1	AR	192	3% 83% 15%
1	AS	192	3% 81% 17%
1	AT	192	% 80% 18%
1	AU	192	% 81% 17%
1	AV	192	4% 82% 17%
1	AW	192	% 82% 18%
1	AX	192	2% 82% 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%
1	Ag	192	% 79% 19%




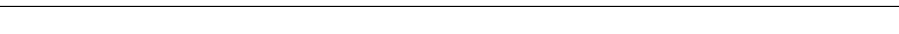
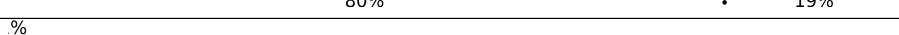
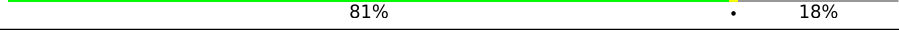



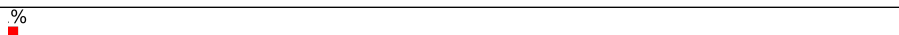
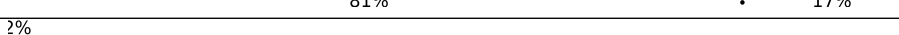




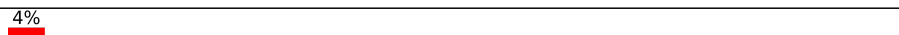






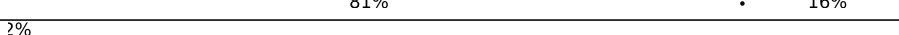


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Mol	Chain	Length	Quality of chain
1	Ah	192	 82% 16%
1	Ai	192	 80% 17%
1	Aj	192	 81% 5% 14%
1	Ak	192	 82% 14%
1	Al	192	 81% 5% 14%
1	Am	192	 82% 16%
1	An	192	 81% 16%
1	Ao	192	 82% 16%
1	Ap	192	 82% 16%
1	Aq	192	 82% 17%
1	Ar	192	 81% 14%
1	As	192	 81% 16%
1	At	192	 80% 17%
1	Au	192	 80% 17%
1	Av	192	 84% 14%
1	Aw	192	 79% 5% 16%
1	Ax	192	 80% 19%
1	BA	192	 83% 14%
1	BB	192	 80% 18%
1	BC	192	 80% 19%
1	BD	192	 83% 17%
1	BE	192	 83% 17%
1	BF	192	 80% 17%
1	BG	192	 80% 19%
1	BH	192	 78% 20%

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Mol	Chain	Length	Quality of chain
1	BI	192	 80% 19%
1	BJ	192	 80% 18%
1	BK	192	 79% 19%
1	BL	192	 80% 19%
1	BM	192	 81% 18%
1	BN	192	 81% 17%
1	BO	192	 81% 17%
1	BP	192	 81% 17%
1	BQ	192	 81% 17%
1	BR	192	 82% 16%
1	BS	192	 82% 17%
1	BT	192	 81% 18%
1	BU	192	 83% 16%
1	BV	192	 79% 19%
1	BW	192	 83% 16%
1	BX	192	 82% 15%
1	Ba	192	 81% 18%
1	Bb	192	 81% 17%
1	Bc	192	 81% 16%
1	Bd	192	 82% 16%
1	Be	192	 82% 15%
1	Bf	192	 80% 6% 14%
1	Bg	192	 80% 19%
1	Bh	192	 81% 17%
1	Bi	192	 80% 18%

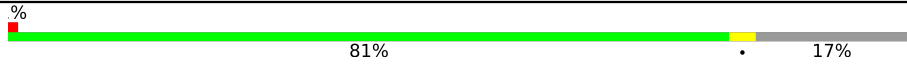

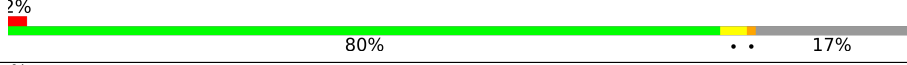

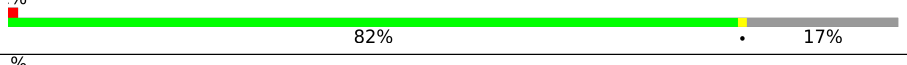
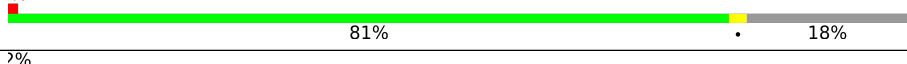
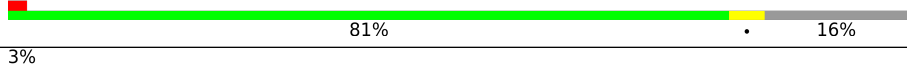

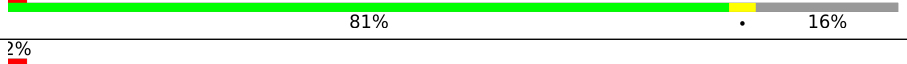


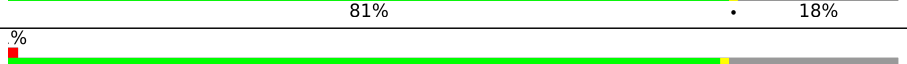
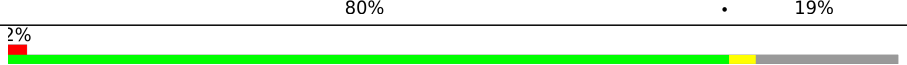
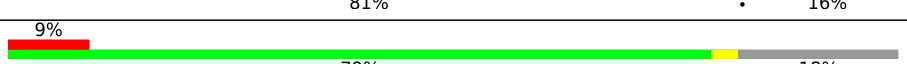

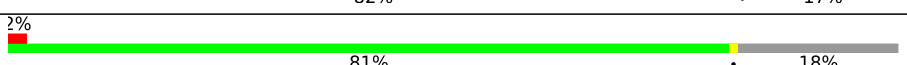
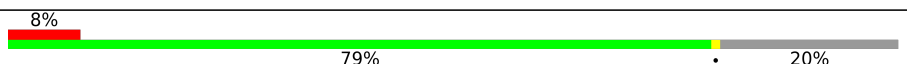
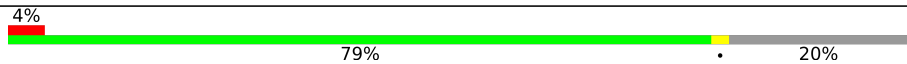
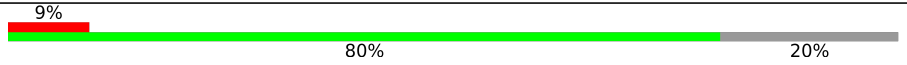


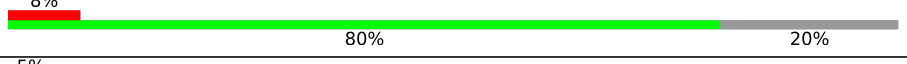
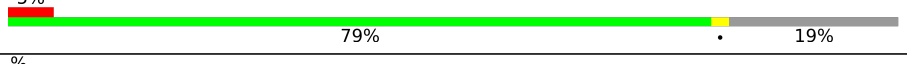


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Mol	Chain	Length	Quality of chain
1	Bj	192	79% 20%
1	Bk	192	81% 17%
1	Bl	192	80% 17%
1	Bm	192	81% 17%
1	Bn	192	83% 14%
1	Bo	192	81% 19%
1	Bp	192	82% 16%
1	Bq	192	82% 17%
1	Br	192	80% 16%
1	Bs	192	80% 19%
1	Bt	192	79% 18%
1	Bu	192	82% 14%
1	Bv	192	82% 17%
1	Bw	192	81% 17%
1	Bx	192	81% 18%
1	CA	192	81% 17%
1	CB	192	81% 16%
1	CC	192	80% 18%
1	CD	192	83% 16%
1	CE	192	82% 17%
1	CF	192	81% 17%
1	CG	192	80% 17%
1	CH	192	81% 17%
1	CI	192	80% 17%
1	CJ	192	82% 14%

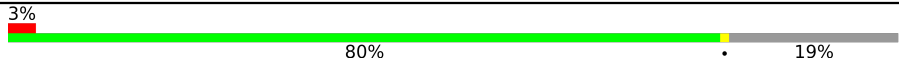
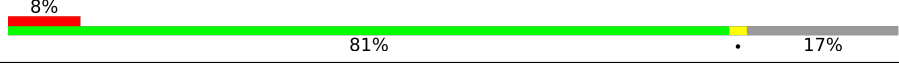
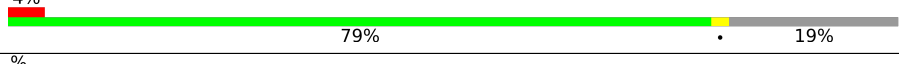


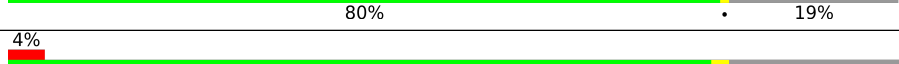
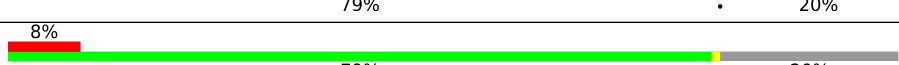
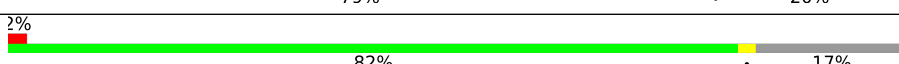
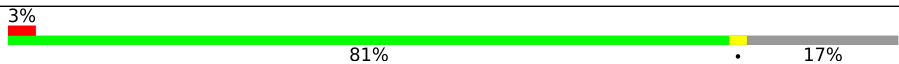


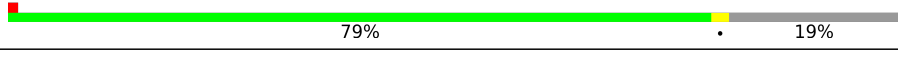

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Mol	Chain	Length	Quality of chain
1	CK	192	 81% 17%
1	CL	192	 82% 17%
1	CM	192	 80% 17%
1	CN	192	 83% 16%
1	CO	192	 82% 17%
1	CP	192	 81% 18%
1	CQ	192	 81% 16%
1	CR	192	 83% 14%
1	CS	192	 81% 16%
1	CT	192	 80% 18%
1	CU	192	 83% 17%
1	CV	192	 81% 18%
1	CW	192	 80% 19%
1	CX	192	 81% 16%
1	Ca	192	 79% 18%
1	Cb	192	 82% 17%
1	Cc	192	 81% 18%
1	Cd	192	 79% 20%
1	Ce	192	 79% 20%
1	Cf	192	 80% 20%
1	Cg	192	 82% 17%
1	Ch	192	 81% 17%
1	Ci	192	 80% 20%
1	Cj	192	 79% 19%
1	Ck	192	 79% 20%

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Mol	Chain	Length	Quality of chain
1	Cl	192	 3% 80% 19%
1	Cm	192	 8% 81% 17%
1	Cn	192	 4% 79% 19%
1	Co	192	 % 79% 19%
1	Cp	192	 4% 81% 18%
1	Cq	192	 11% 80% 19%
1	Cr	192	 4% 79% 20%
1	Cs	192	 8% 79% 20%
1	Ct	192	 2% 82% 17%
1	Cu	192	 3% 81% 17%
1	Cv	192	 2% 82% 16%
1	Cw	192	 2% 81% 19%
1	Cx	192	 % 79% 19%

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

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

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

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

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

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

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

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	CX	161	1294	814	228	246	6	0	0	0
1	Cx	156	1265	797	223	239	6	0	0	0

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
Al	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
Cl	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	AA	1	Total Ca 1 1	0	0
2	Aa	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
2	Ac	1	Total Ca 1 1	0	0
2	Ad	1	Total Ca 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	Ae	1	Total Ca 1 1	0	0
2	AF	1	Total Ca 1 1	0	0
2	Ag	1	Total Ca 1 1	0	0
2	AH	1	Total Ca 1 1	0	0
2	Ah	1	Total Ca 1 1	0	0
2	Aj	1	Total Ca 1 1	0	0
2	AL	1	Total Ca 1 1	0	0
2	AM	1	Total Ca 1 1	0	0
2	An	1	Total Ca 1 1	0	0
2	AO	1	Total Ca 1 1	0	0
2	BA	1	Total Ca 1 1	0	0
2	Ba	1	Total Ca 1 1	0	0
2	BB	1	Total Ca 1 1	0	0
2	Bb	1	Total Ca 1 1	0	0
2	BC	1	Total Ca 1 1	0	0
2	Bc	1	Total Ca 1 1	0	0
2	BD	1	Total Ca 1 1	0	0
2	Bd	1	Total Ca 1 1	0	0
2	Be	1	Total Ca 1 1	0	0
2	Bf	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	Bg	1	Total Ca 1 1	0	0
2	BH	1	Total Ca 1 1	0	0
2	BN	1	Total Ca 1 1	0	0
2	BR	1	Total Ca 1 1	0	0
2	Bu	1	Total Ca 1 1	0	0
2	CA	1	Total Ca 1 1	0	0
2	Ca	1	Total Ca 1 1	0	0
2	CB	1	Total Ca 1 1	0	0
2	Cb	1	Total Ca 1 1	0	0
2	CC	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	Ce	1	Total Ca 1 1	0	0
2	CF	1	Total Ca 1 1	0	0
2	Cg	1	Total Ca 1 1	0	0
2	CH	1	Total Ca 1 1	0	0
2	Ck	1	Total Ca 1 1	0	0
2	Cl	1	Total Ca 1 1	0	0
2	Cn	1	Total Ca 1 1	0	0
2	CO	1	Total Ca 1 1	0	0
2	Cp	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 37	O 37	0	0
3	AL	11	Total 11	O 11	0	0
3	Al	25	Total 25	O 25	0	0
3	AM	26	Total 26	O 26	0	0
3	Am	45	Total 45	O 45	0	0
3	AN	17	Total 17	O 17	0	0
3	An	41	Total 41	O 41	0	0
3	AO	20	Total 20	O 20	0	0
3	Ao	39	Total 39	O 39	0	0
3	AP	25	Total 25	O 25	0	0
3	Ap	32	Total 32	O 32	0	0
3	AQ	21	Total 21	O 21	0	0
3	Aq	33	Total 33	O 33	0	0
3	AR	18	Total 18	O 18	0	0
3	Ar	40	Total 40	O 40	0	0
3	AS	20	Total 20	O 20	0	0
3	As	44	Total 44	O 44	0	0
3	AT	22	Total 22	O 22	0	0
3	At	31	Total 31	O 31	0	0
3	AU	20	Total 20	O 20	0	0
3	Au	31	Total 31	O 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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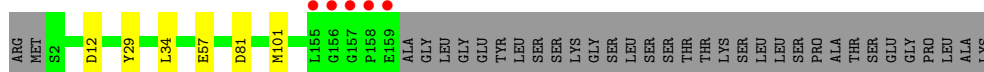
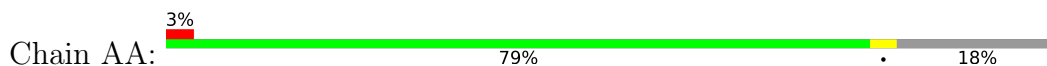
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
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3	Cp	10	Total 10	O 10	0	0
3	CQ	41	Total 41	O 41	0	0
3	Cq	2	Total 2	O 2	0	0
3	CR	20	Total 20	O 20	0	0
3	Cr	4	Total 4	O 4	0	0
3	CS	28	Total 28	O 28	0	0
3	CT	15	Total 15	O 15	0	0
3	Ct	17	Total 17	O 17	0	0
3	CU	3	Total 3	O 3	0	0
3	Cu	12	Total 12	O 12	0	0
3	CV	8	Total 8	O 8	0	0
3	Cv	4	Total 4	O 4	0	0
3	CW	15	Total 15	O 15	0	0
3	Cw	10	Total 10	O 10	0	0
3	CX	21	Total 21	O 21	0	0
3	Cx	12	Total 12	O 12	0	0

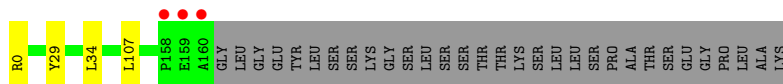
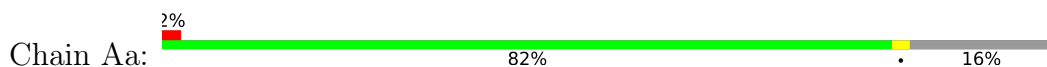
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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.

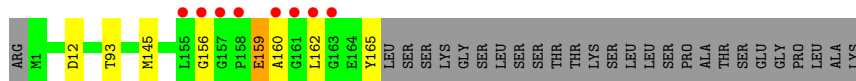
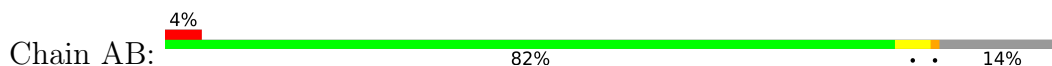
- Molecule 1: Ferritin



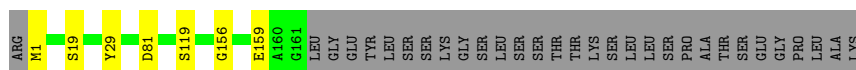
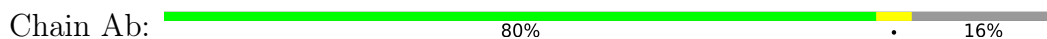
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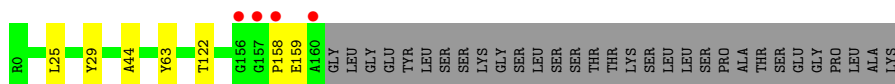
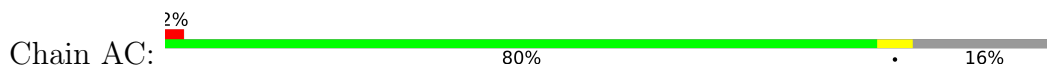
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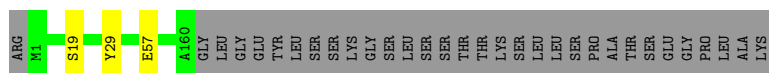
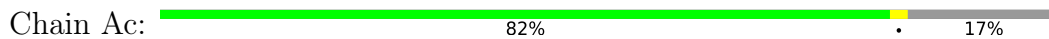
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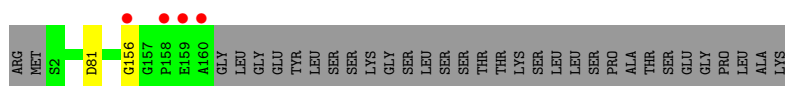
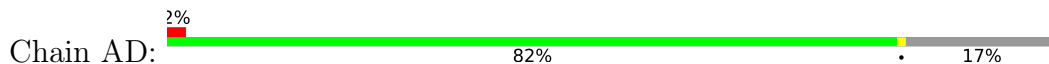
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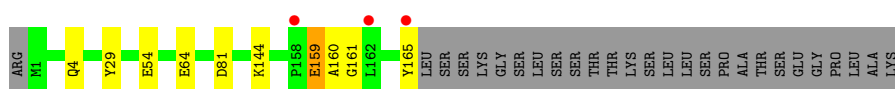
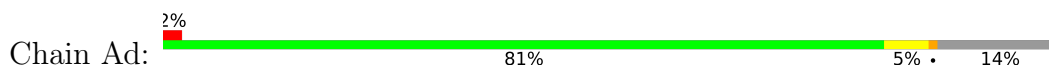
- Molecule 1: Ferritin



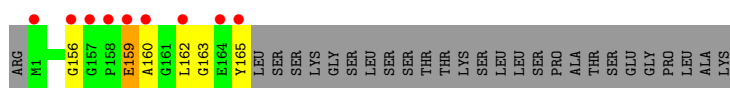
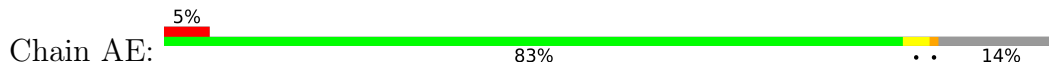
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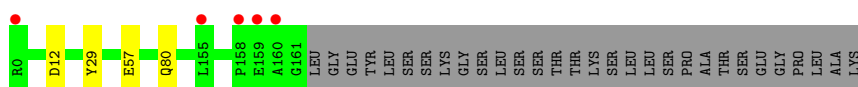
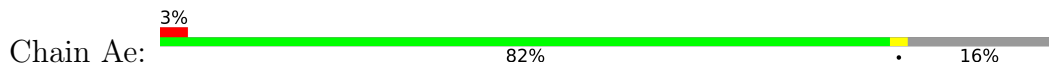
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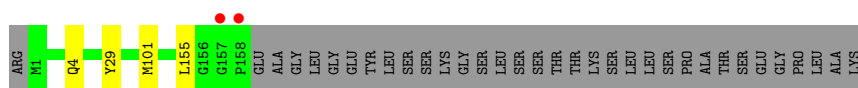
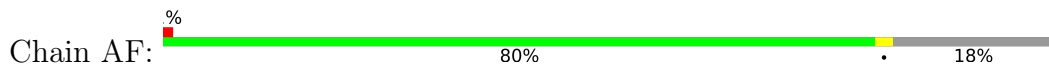
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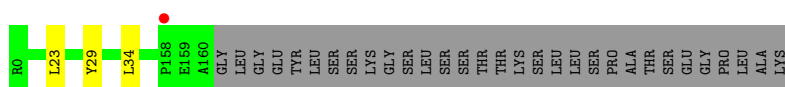
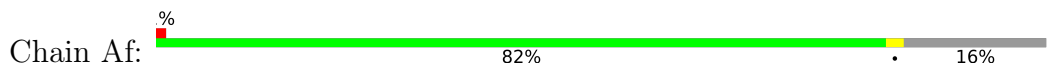
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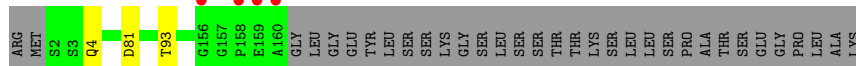
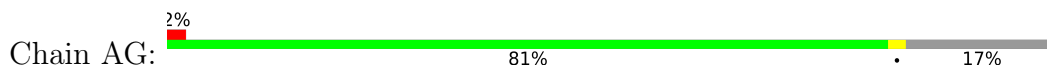
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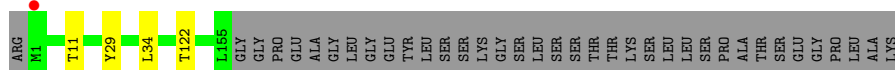
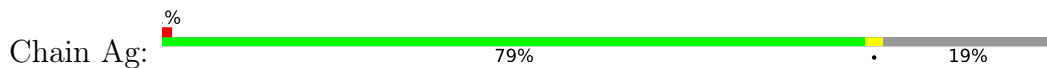
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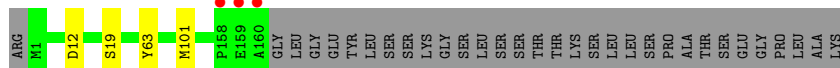
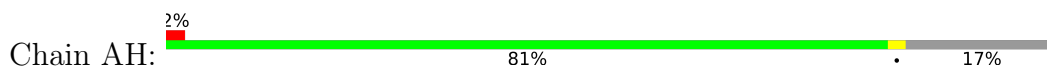
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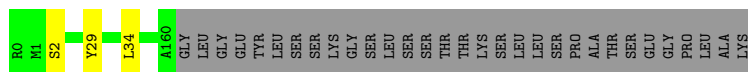
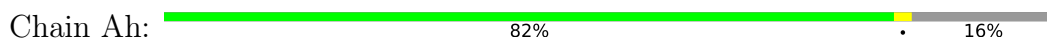
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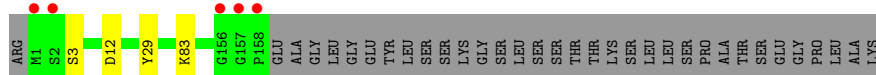
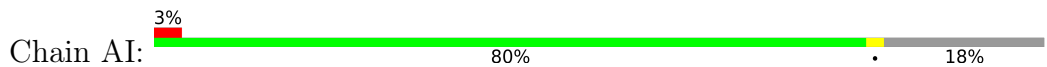
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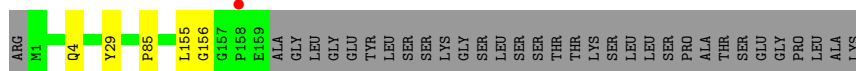
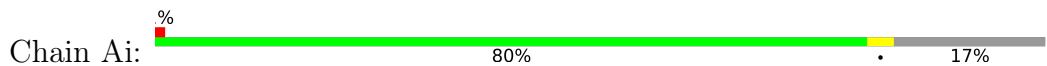
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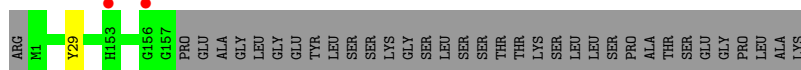
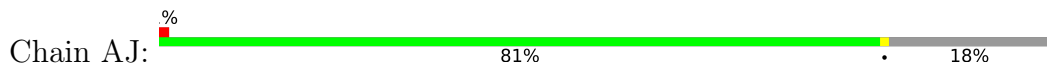
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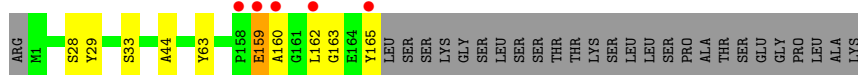
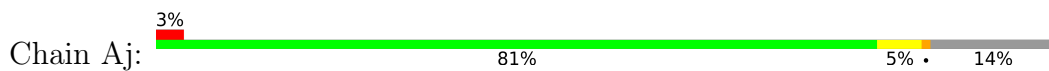
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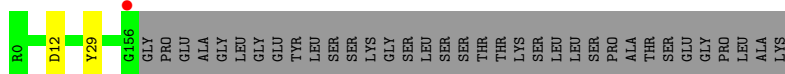
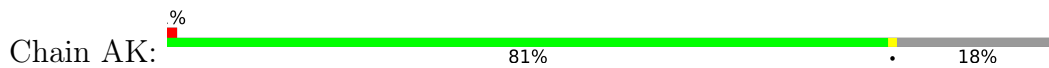
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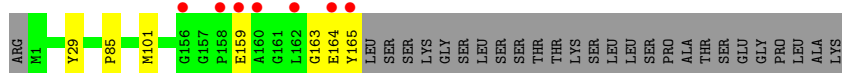
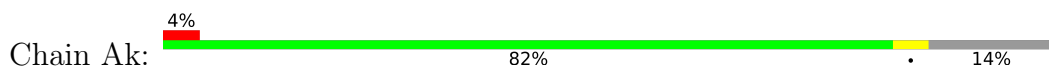
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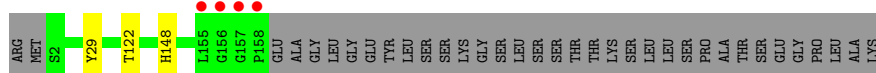
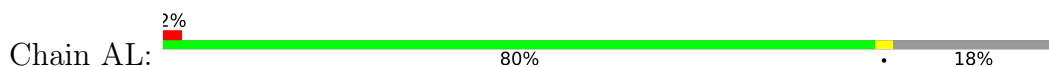
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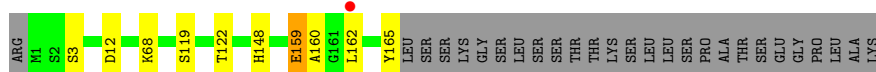
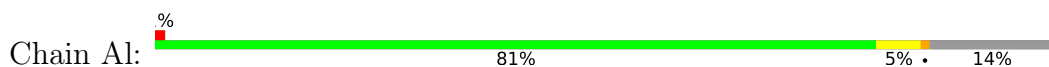
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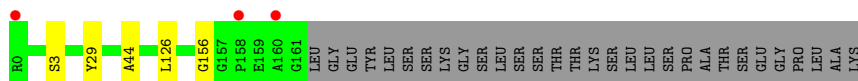
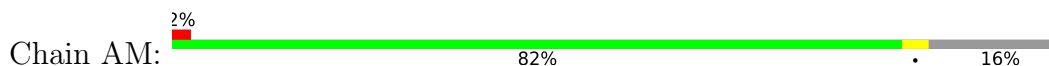
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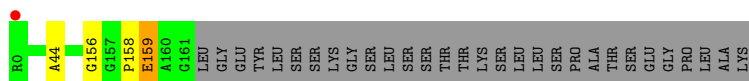
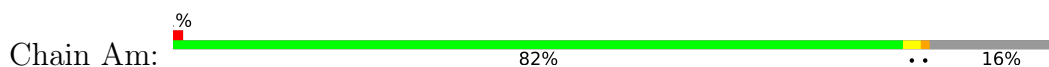
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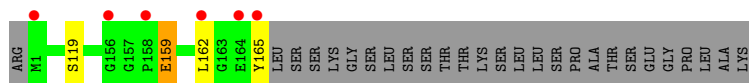
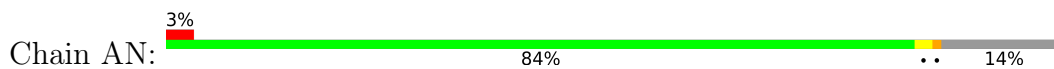
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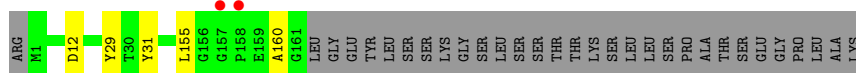
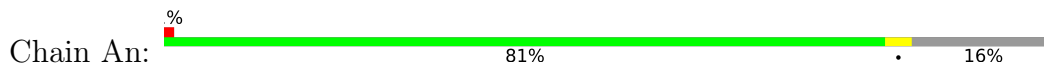
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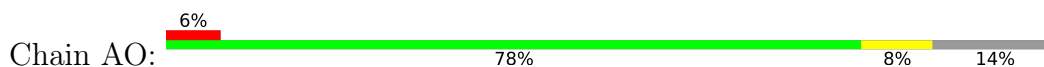
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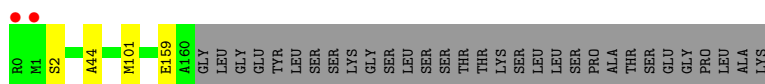
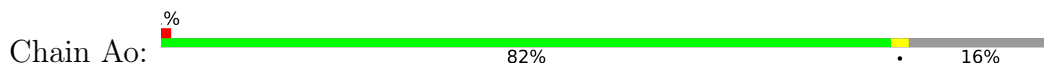
● Molecule 1: Ferritin



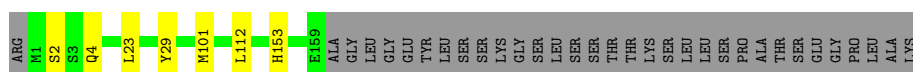
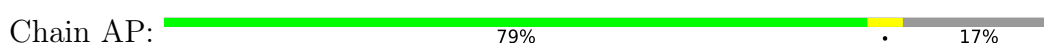
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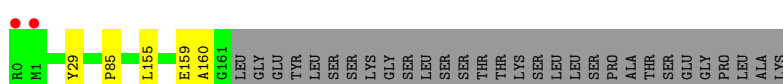
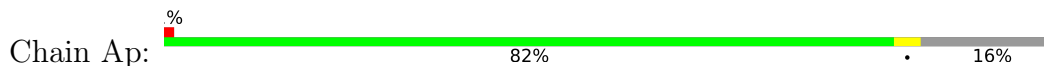
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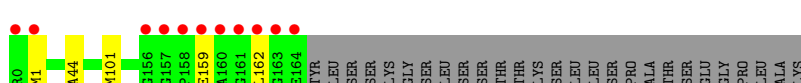
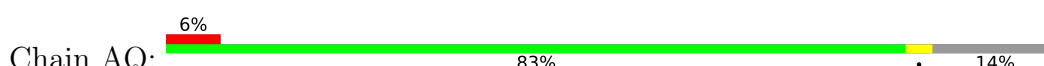
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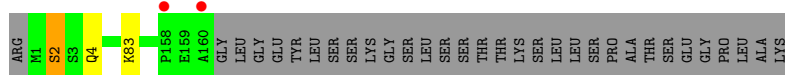
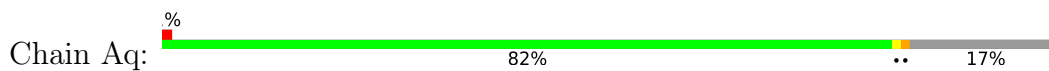
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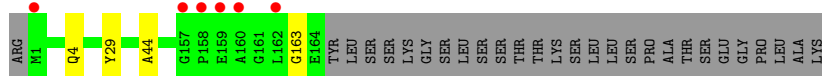
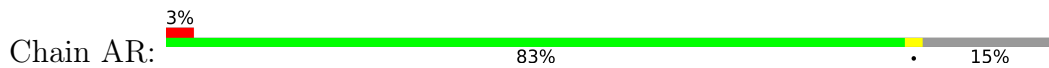
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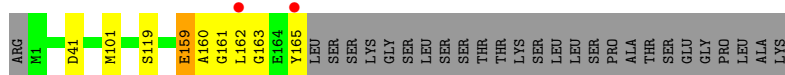
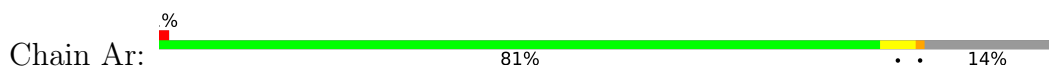
● Molecule 1: Ferritin



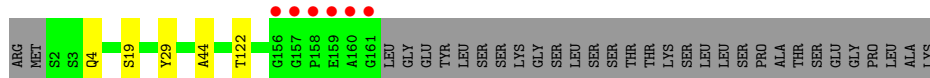
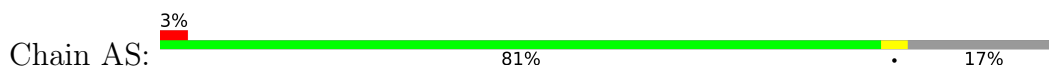
• Molecule 1: Ferritin



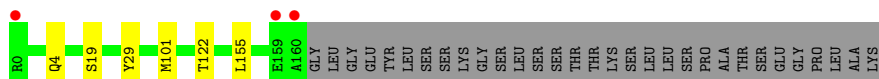
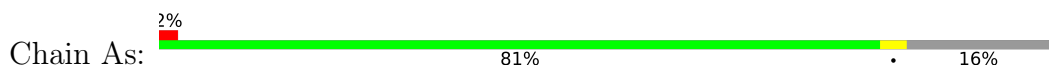
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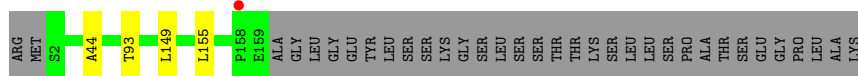
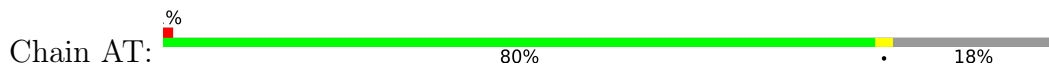
• Molecule 1: Ferritin



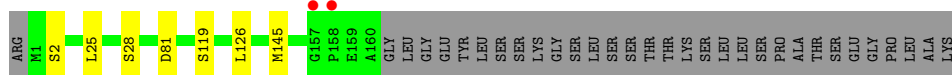
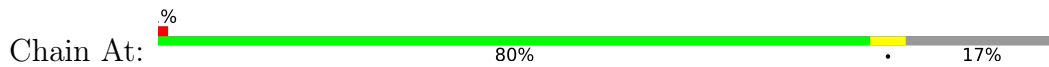
• Molecule 1: Ferritin



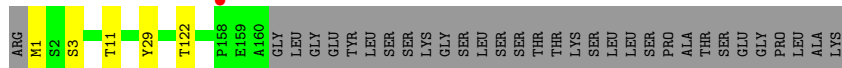
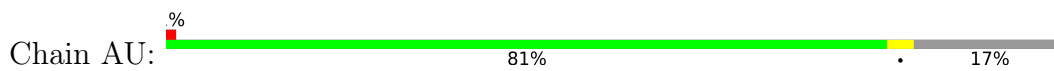
• Molecule 1: Ferritin



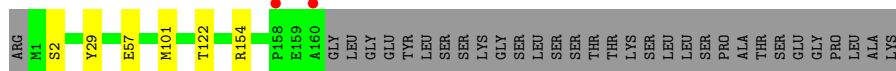
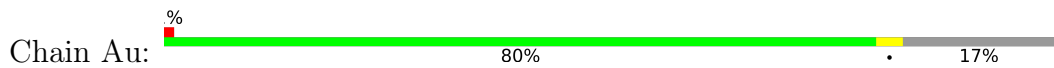
• Molecule 1: Ferritin



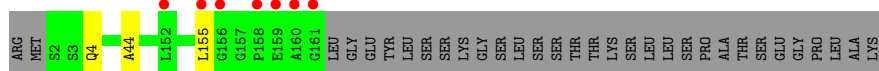
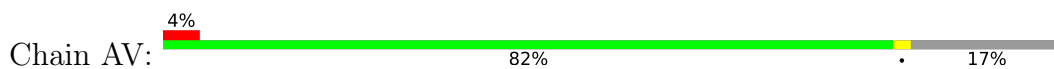
• Molecule 1: Ferritin



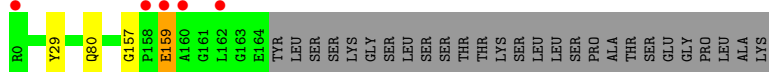
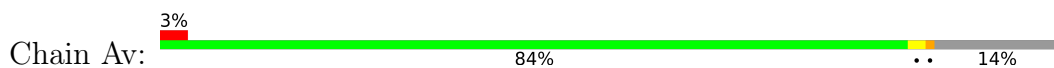
● Molecule 1: Ferritin



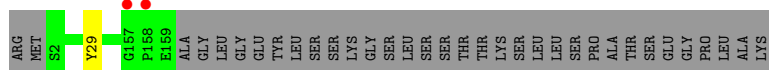
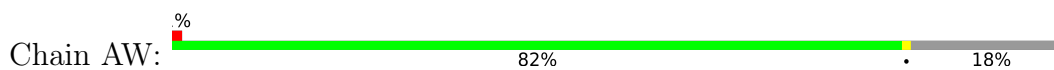
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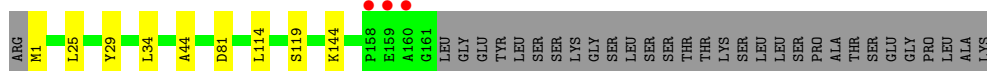
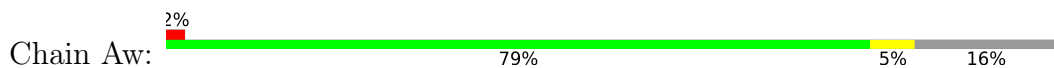
● Molecule 1: Ferritin



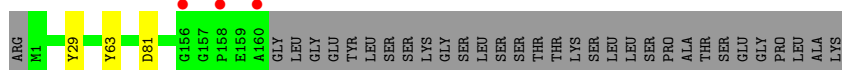
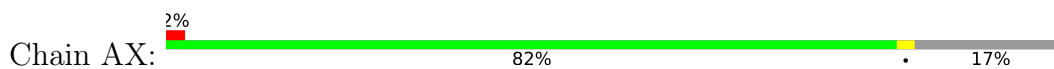
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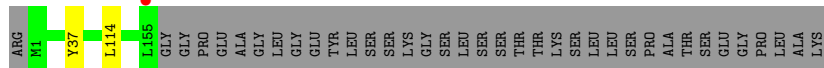
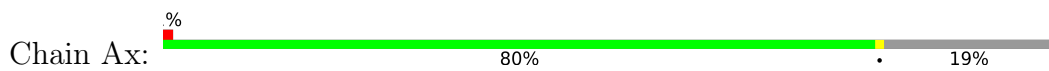
● Molecule 1: Ferritin



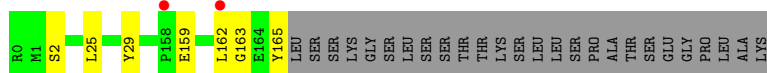
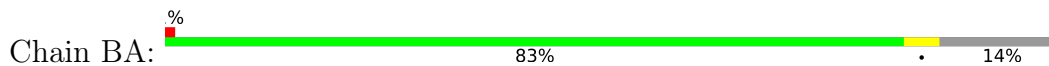
● Molecule 1: Ferritin



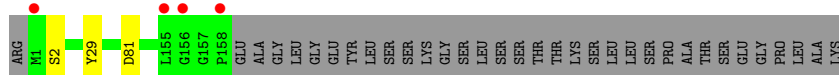
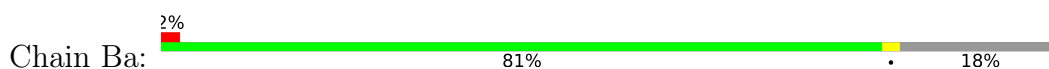
● Molecule 1: Ferritin



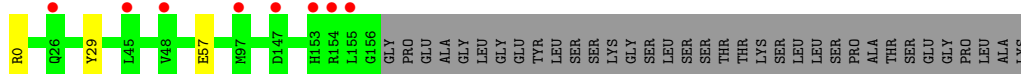
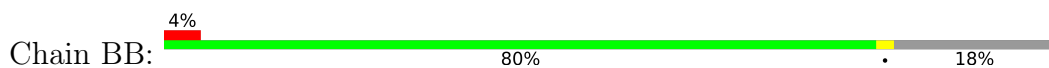
● Molecule 1: Ferritin



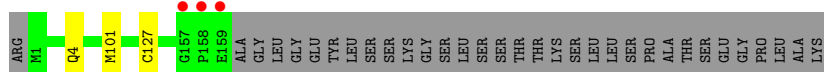
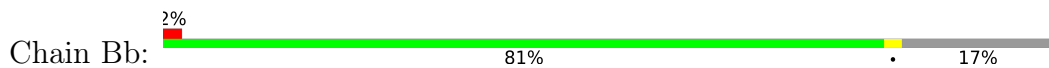
● Molecule 1: Ferritin



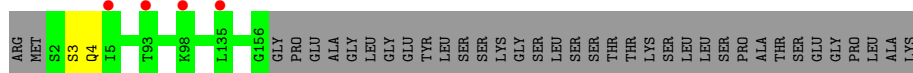
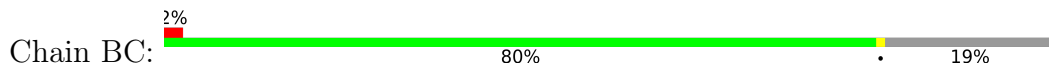
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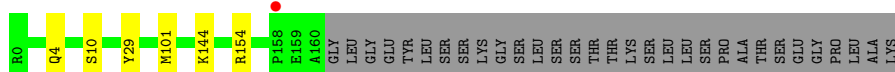
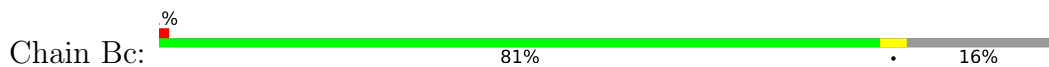
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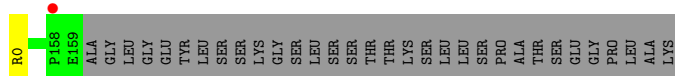
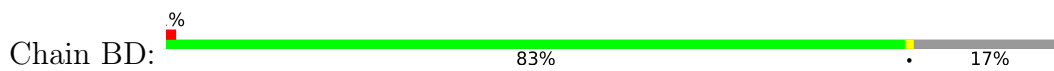
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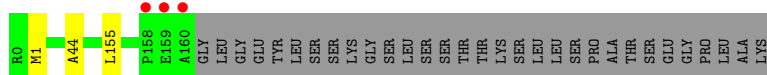
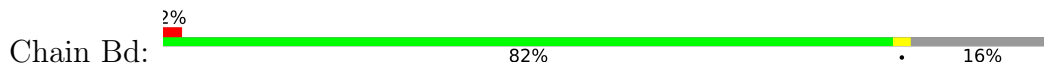
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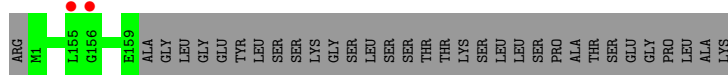
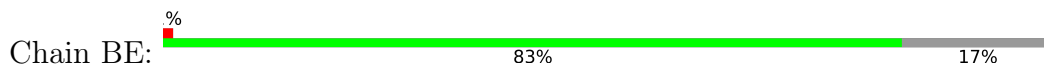
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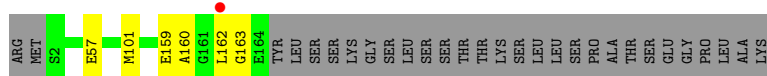
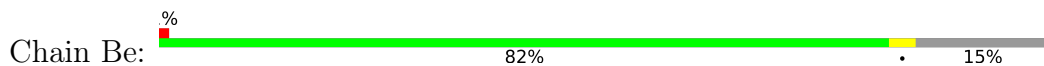
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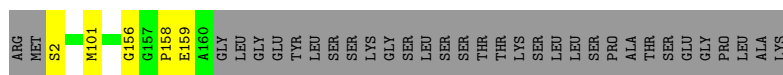
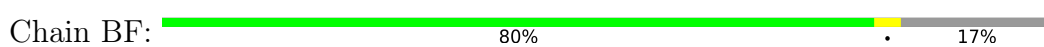
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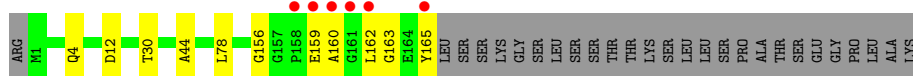
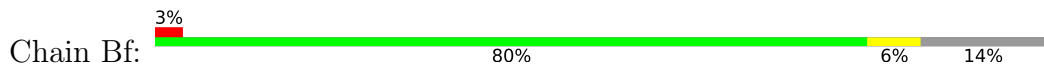
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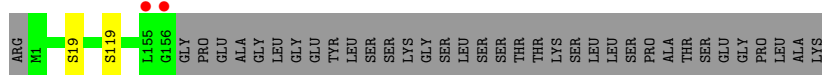
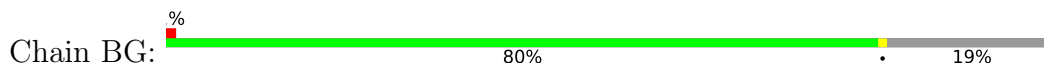
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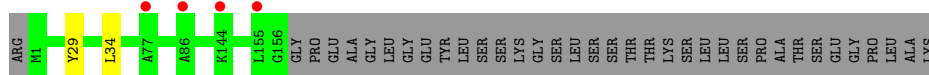
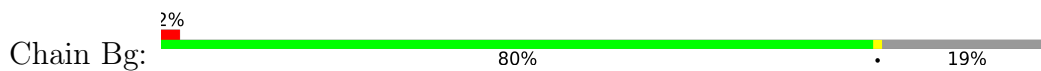
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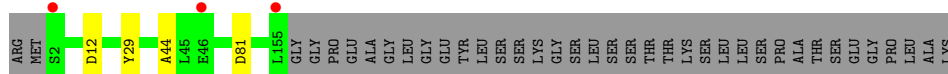
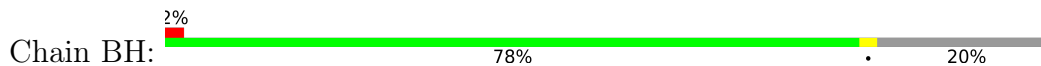
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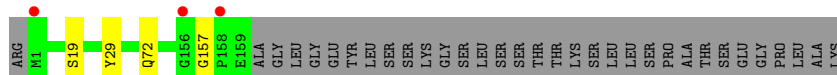
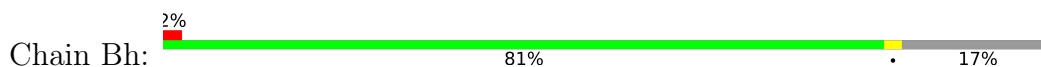
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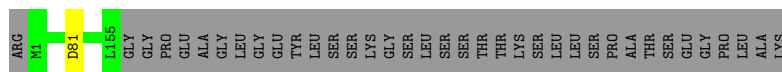
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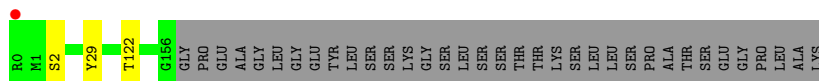
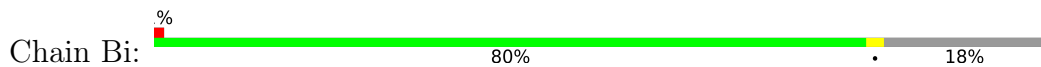
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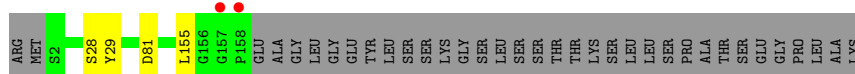
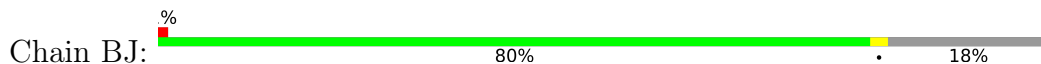
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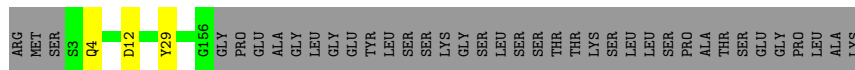
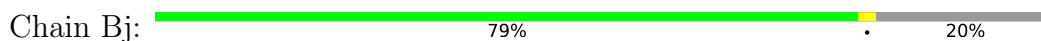
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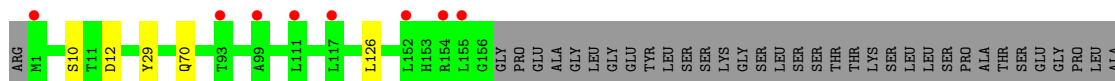
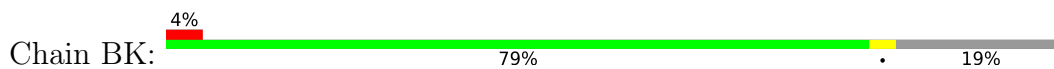
- Molecule 1: Ferritin



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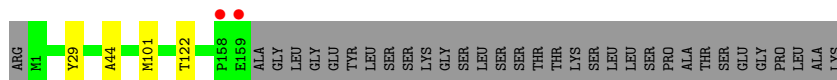
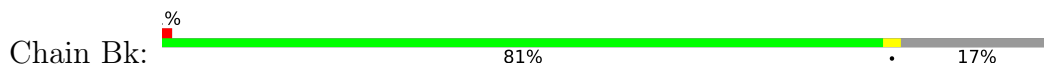


- Molecule 1: Ferritin

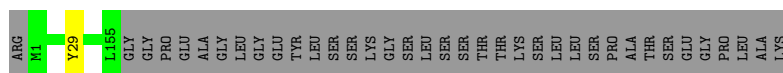
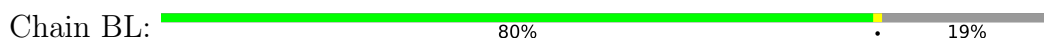


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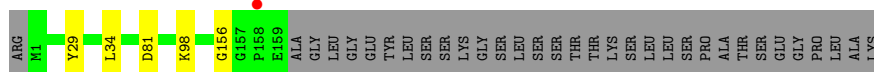
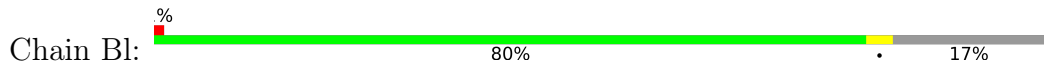
• Molecule 1: Ferritin



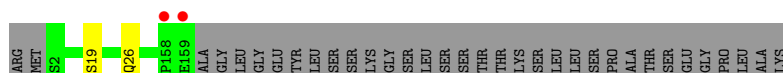
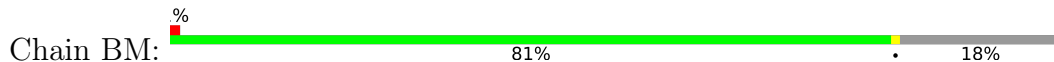
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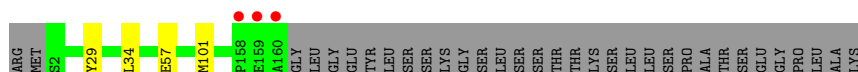
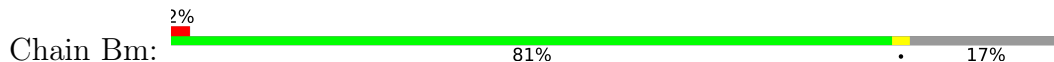
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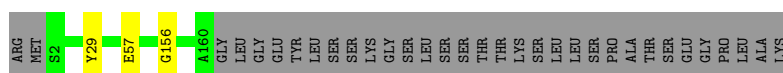
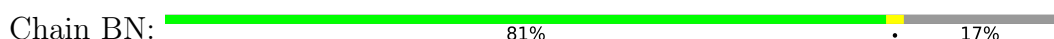
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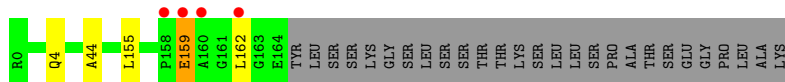
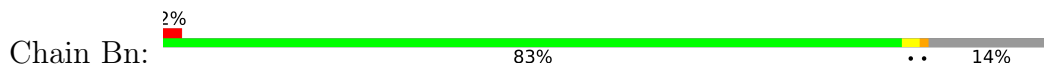
• Molecule 1: Ferritin



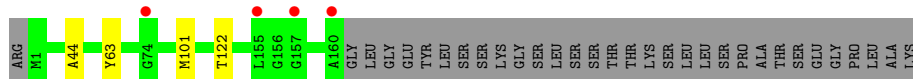
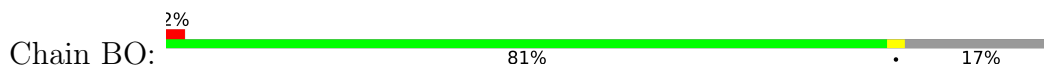
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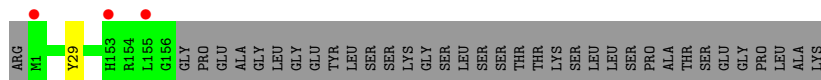
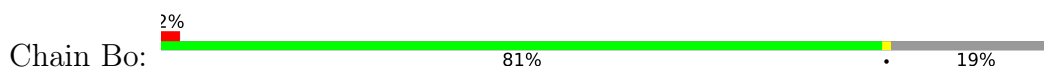
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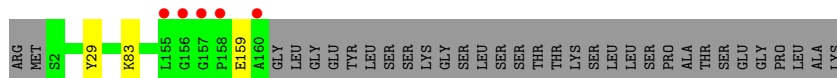
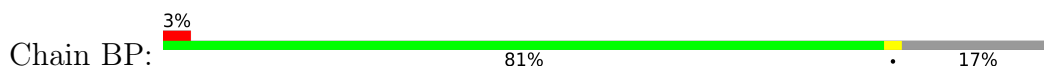
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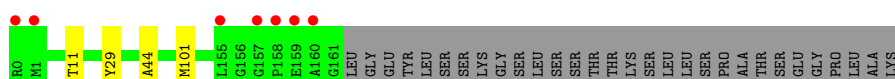
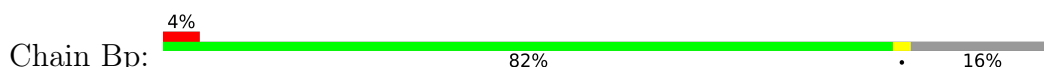
• Molecule 1: Ferritin



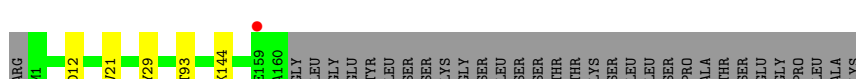
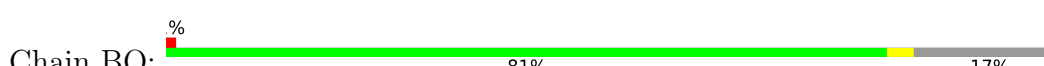
• Molecule 1: Ferritin



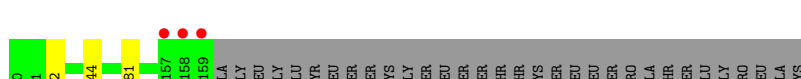
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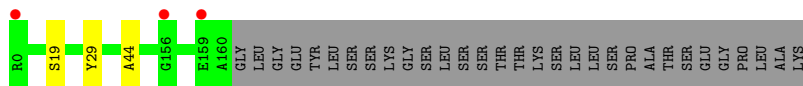
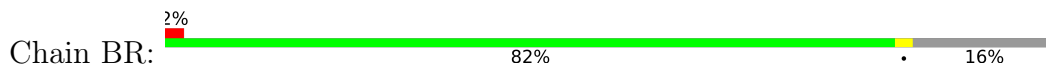
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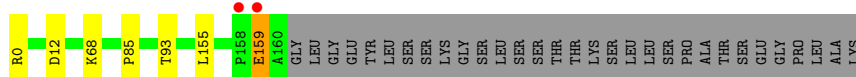
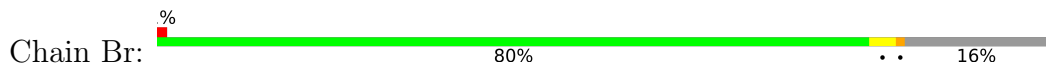
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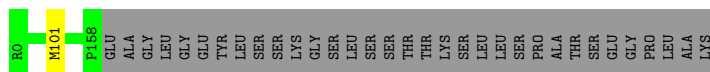
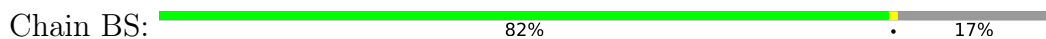
● Molecule 1: Ferritin



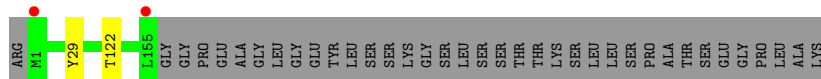
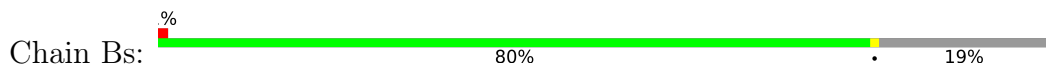
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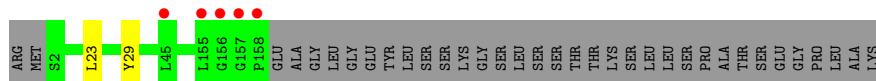
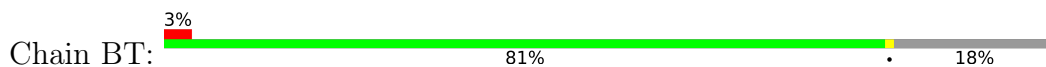
● Molecule 1: Ferritin



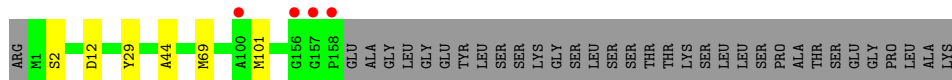
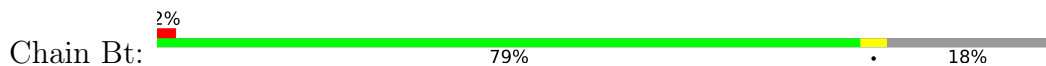
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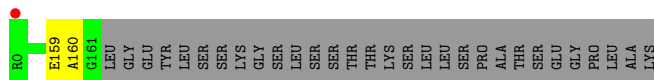
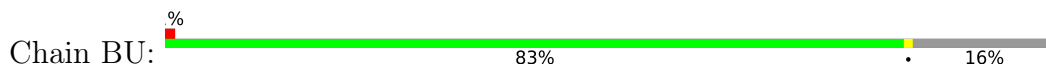
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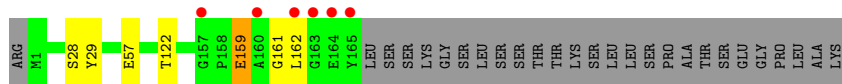
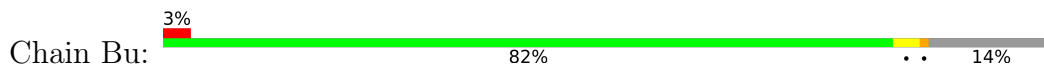
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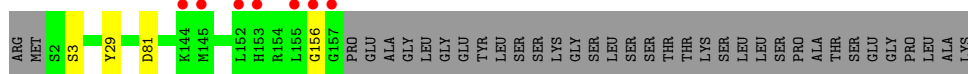
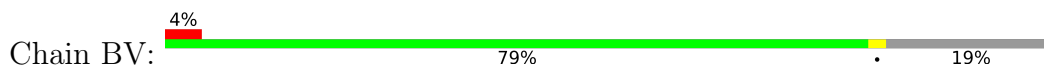
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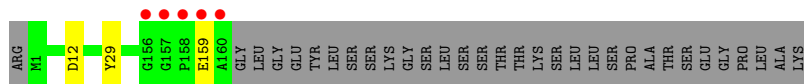
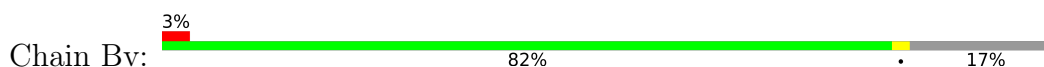
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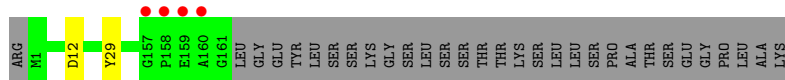
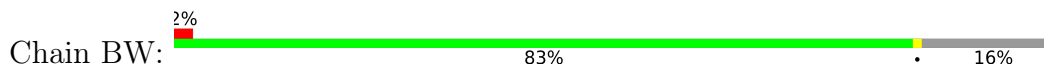
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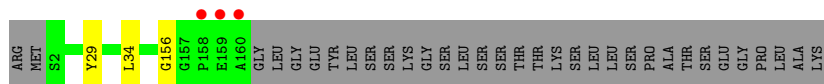
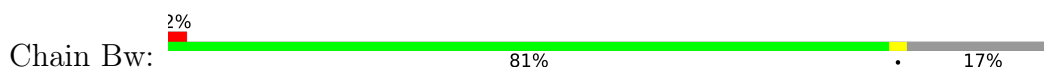
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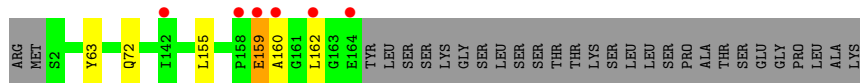
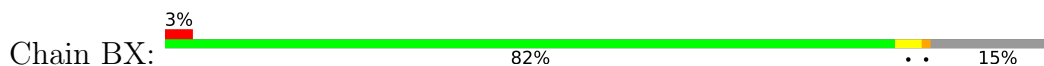
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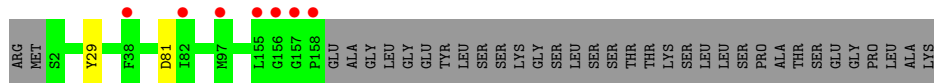
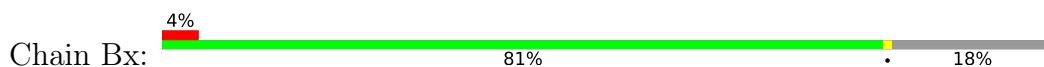
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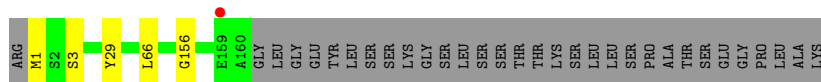
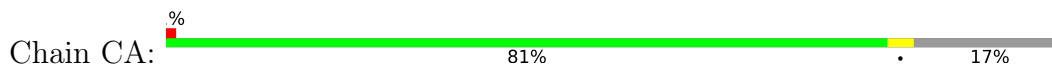
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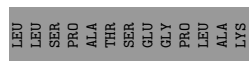
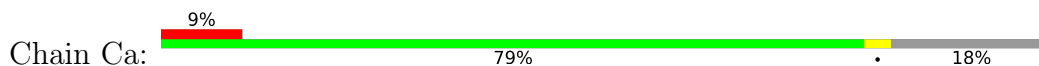
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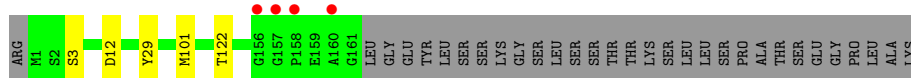
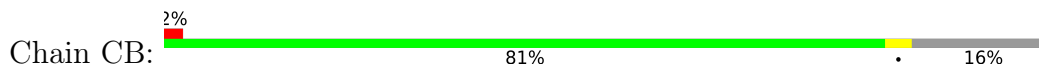
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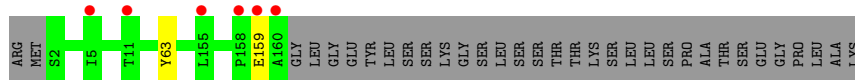
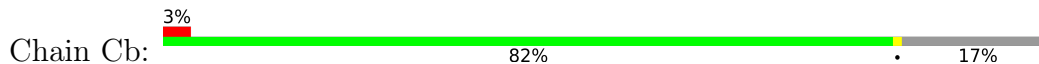
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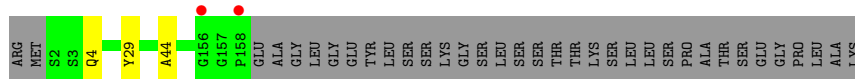
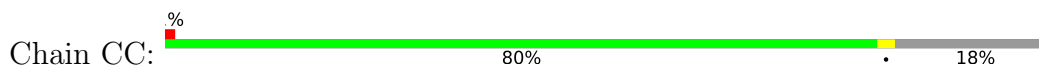
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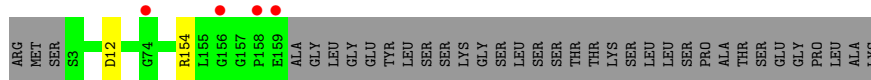
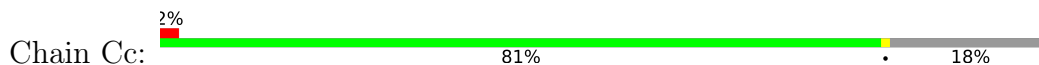
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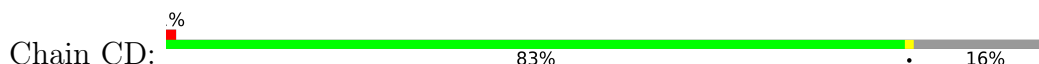
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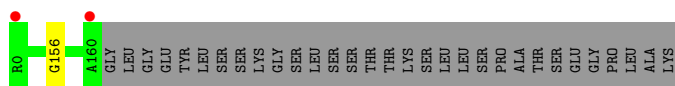


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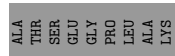
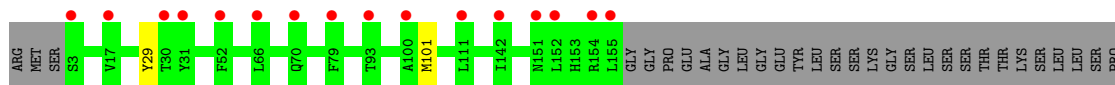
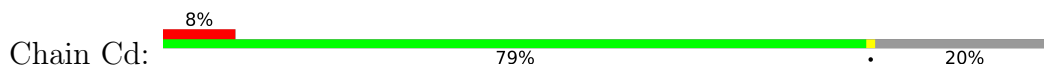


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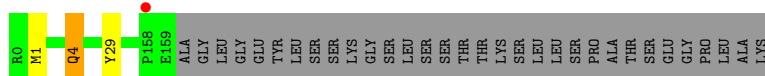
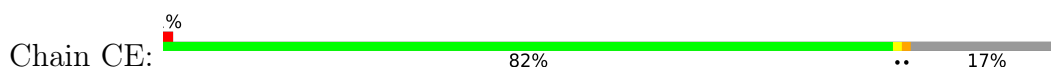




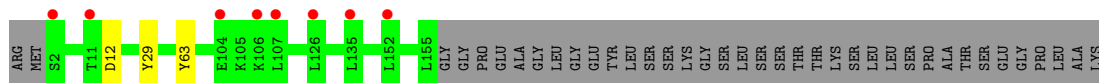
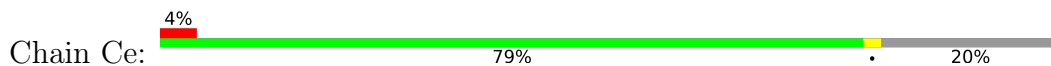
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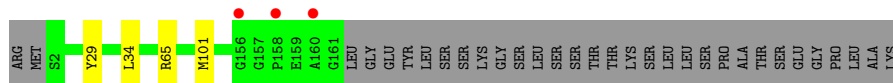
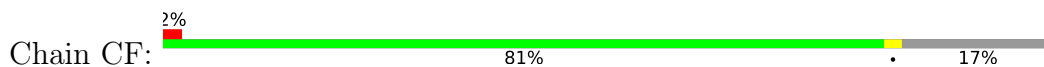
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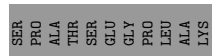
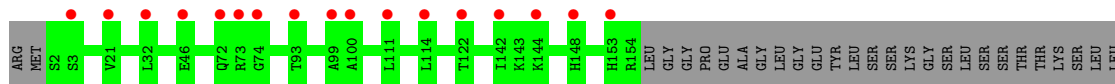
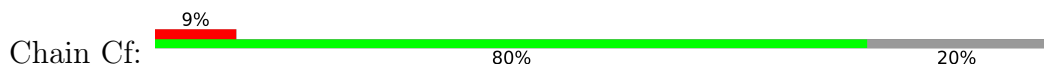
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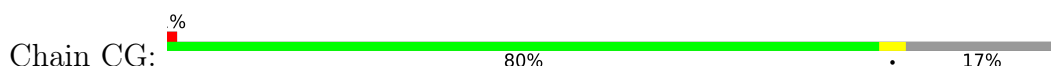
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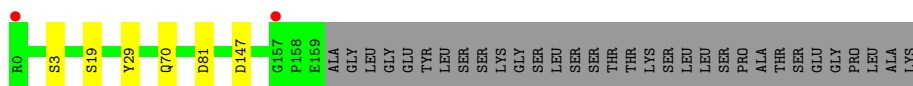


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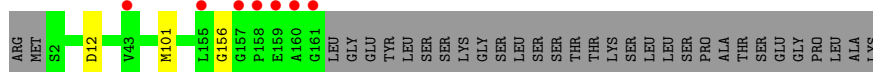
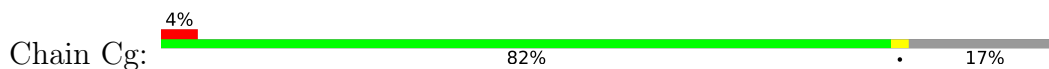


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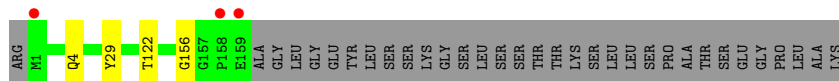
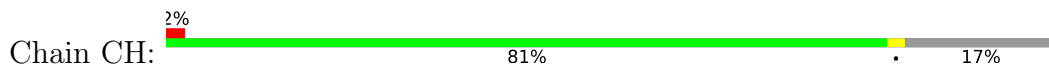




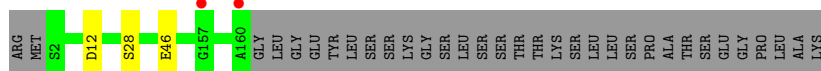
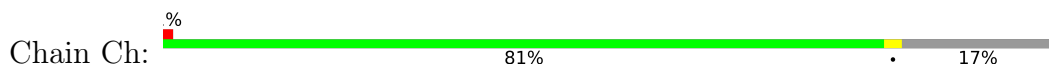
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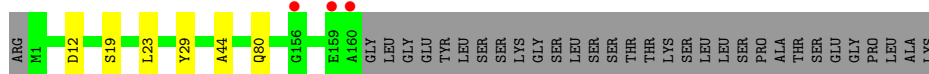
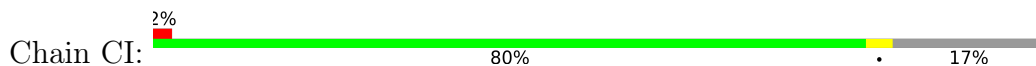
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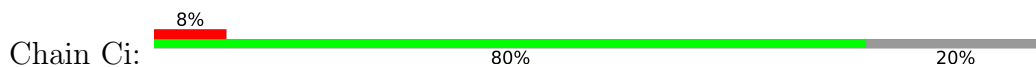
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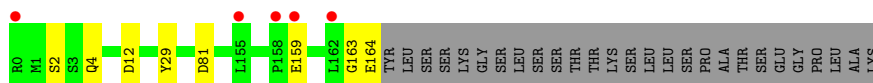
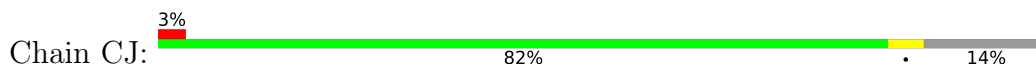
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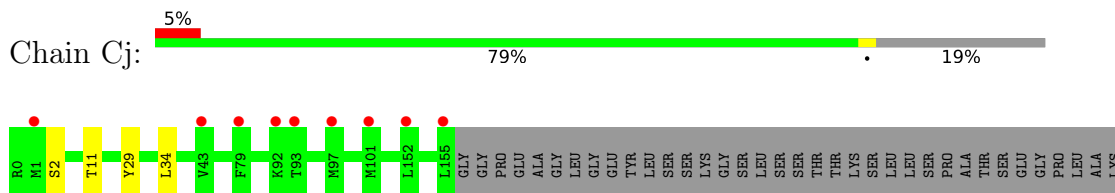
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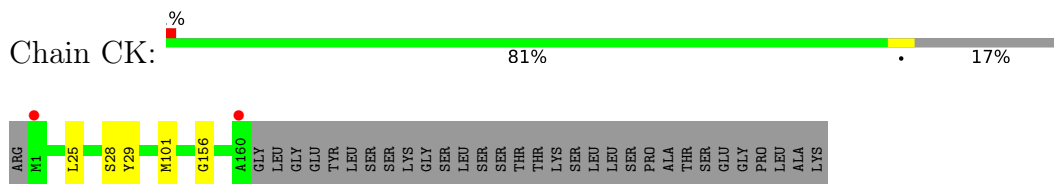
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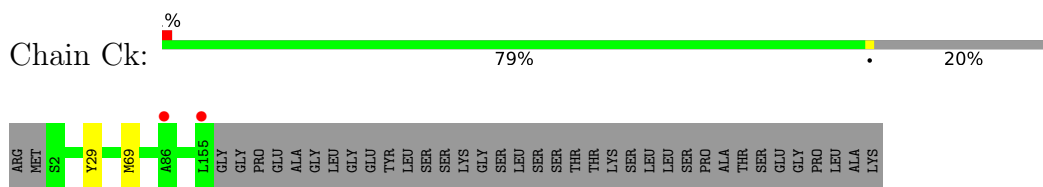
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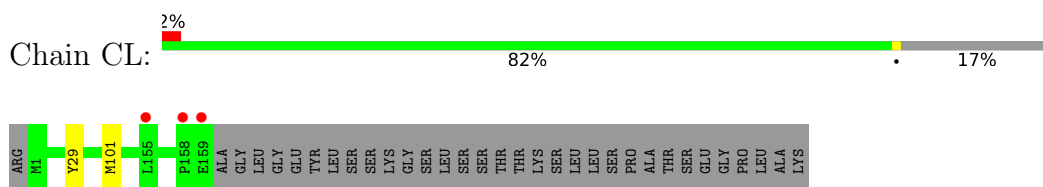
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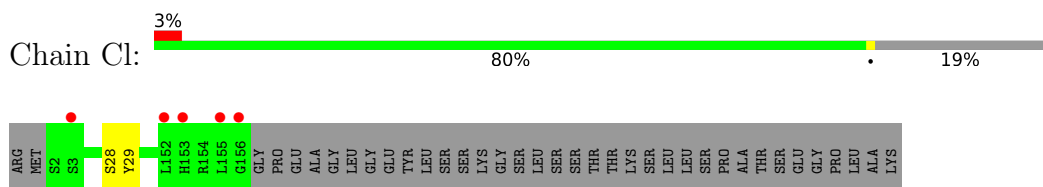
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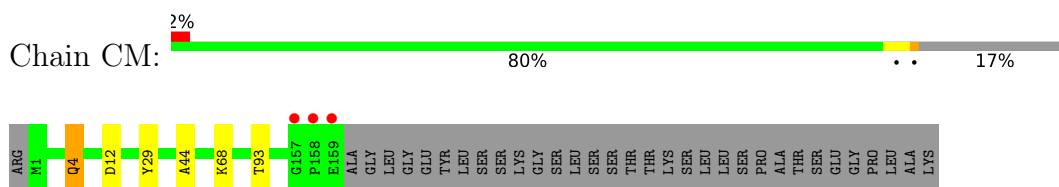
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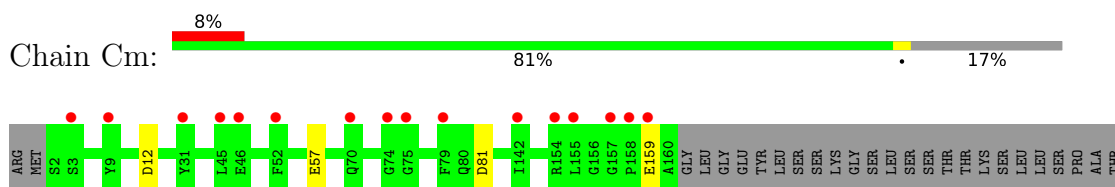
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• Molecule 1: Ferritin

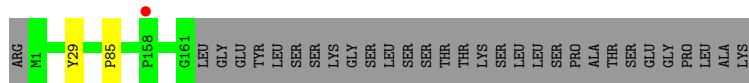
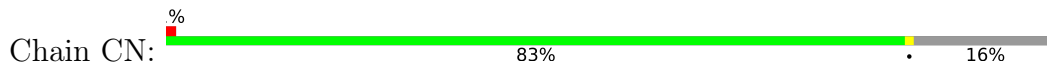


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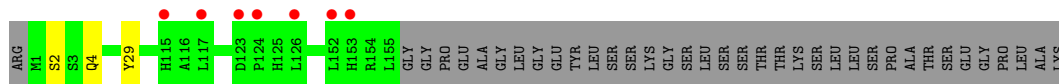
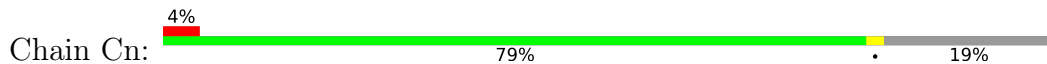


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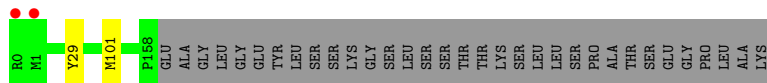
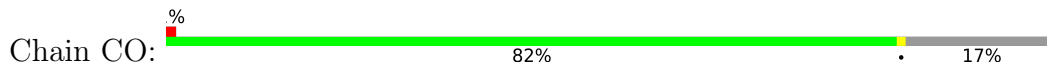
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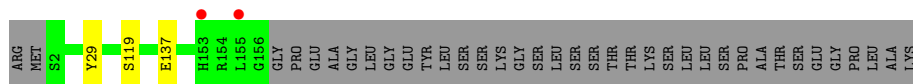
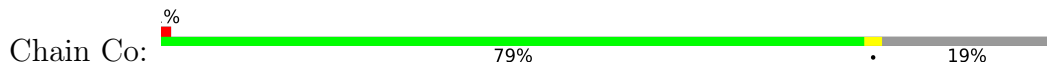
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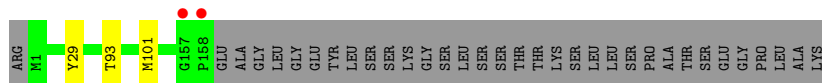
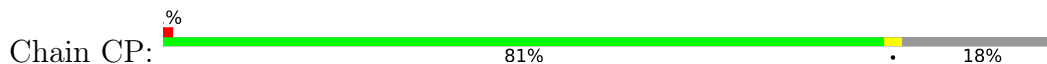
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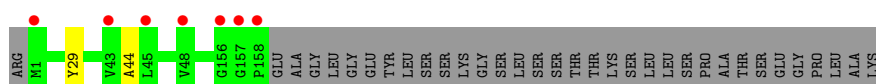
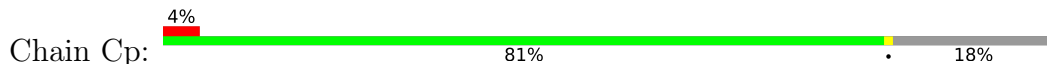
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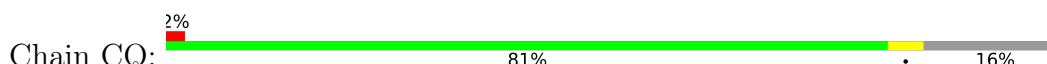
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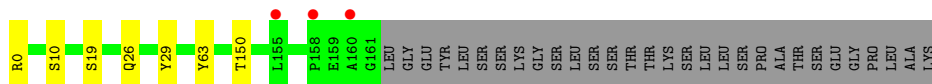


● Molecule 1: Ferritin

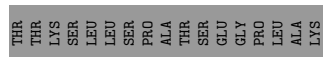
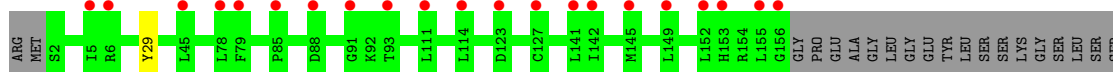
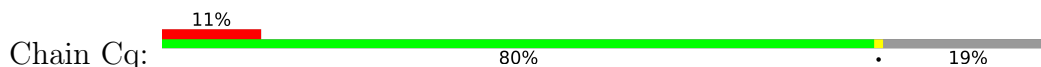


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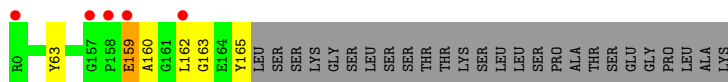
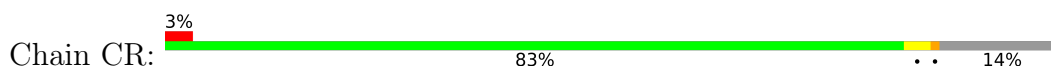




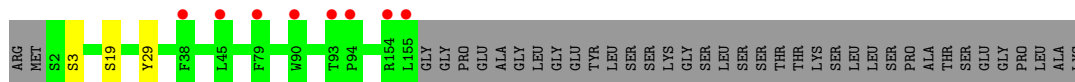
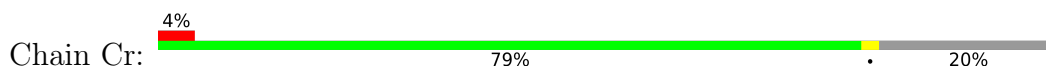
● Molecule 1: Ferritin



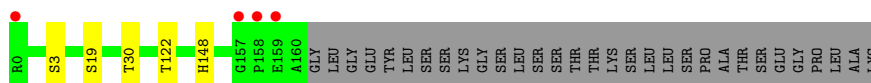
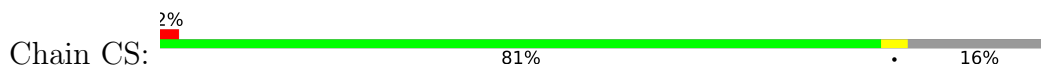
● Molecule 1: Ferritin



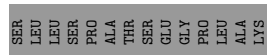
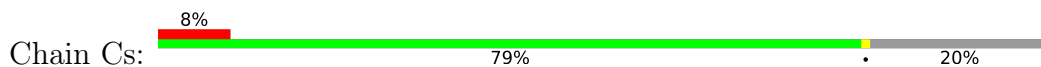
● Molecule 1: Ferritin



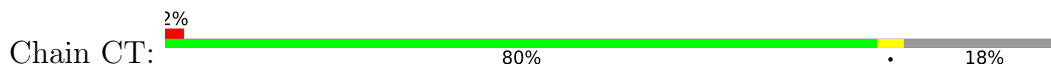
● Molecule 1: Ferritin

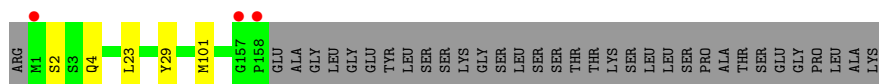


● Molecule 1: Ferritin

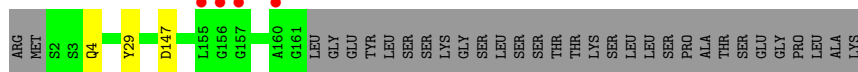
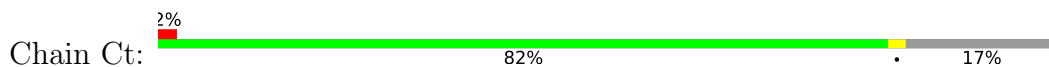


● Molecule 1: Ferritin

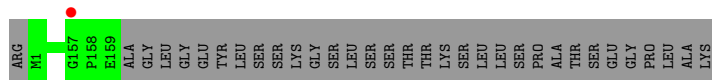
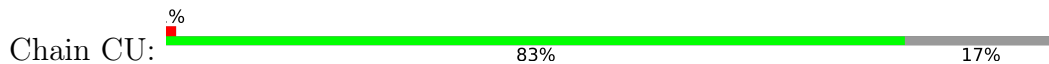




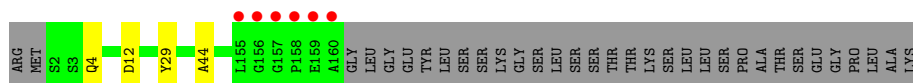
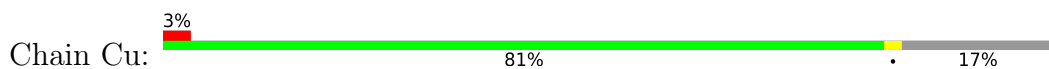
● Molecule 1: Ferritin



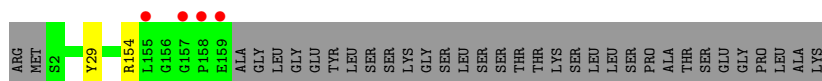
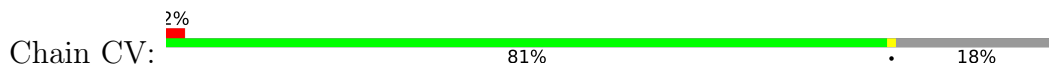
● Molecule 1: Ferritin



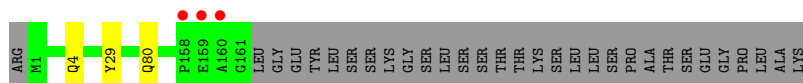
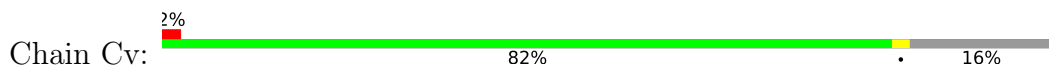
● Molecule 1: Ferritin



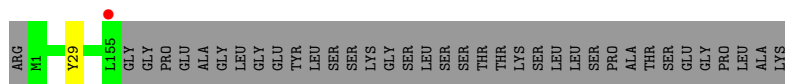
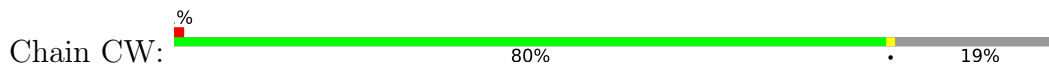
● Molecule 1: Ferritin



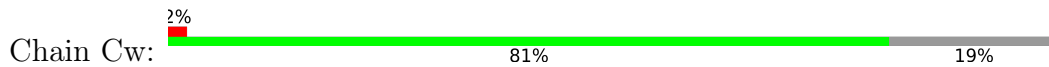
● Molecule 1: Ferritin

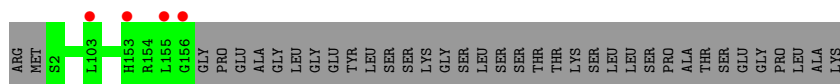


● Molecule 1: Ferritin

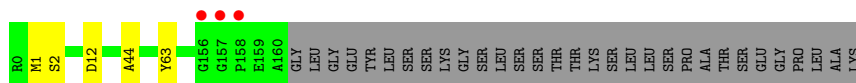
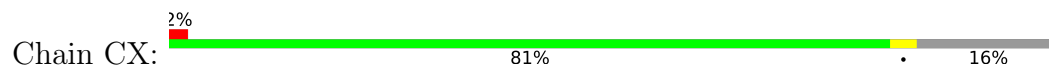


● Molecule 1: Ferritin

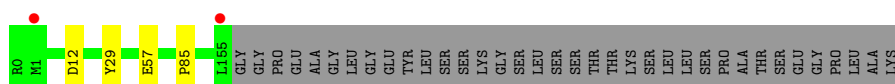
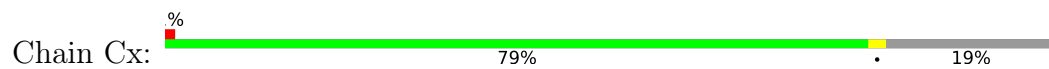




- Molecule 1: Ferritin



- Molecule 1: Ferritin



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	212.34Å 236.94Å 249.71Å 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) 94.7 (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 2.86Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.249 , 0.291 0.224 , 0.261	Depositor DCC
R_{free} test set	42321 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	49.6	Xtrriage
Anisotropy	0.321	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 49.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.000 for h,-h-k,-h-l	Xtrriage
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

Xtrriage'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](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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%)	5	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AC	159/192 (83%)	146 (92%)	10 (6%)	3 (2%)	8	24
1	AD	157/192 (82%)	151 (96%)	5 (3%)	1 (1%)	25	53
1	AE	163/192 (85%)	147 (90%)	11 (7%)	5 (3%)	4	14
1	AF	156/192 (81%)	151 (97%)	4 (3%)	1 (1%)	25	53
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%)	25	53
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%)	12	33
1	AN	163/192 (85%)	154 (94%)	7 (4%)	2 (1%)	13	35
1	AO	163/192 (85%)	148 (91%)	11 (7%)	4 (2%)	5	18
1	AP	157/192 (82%)	152 (97%)	5 (3%)	0	100	100
1	AQ	163/192 (85%)	150 (92%)	10 (6%)	3 (2%)	8	25
1	AR	162/192 (84%)	152 (94%)	8 (5%)	2 (1%)	13	35
1	AS	158/192 (82%)	149 (94%)	8 (5%)	1 (1%)	25	53
1	AT	156/192 (81%)	144 (92%)	10 (6%)	2 (1%)	12	33
1	AU	158/192 (82%)	152 (96%)	5 (3%)	1 (1%)	25	53
1	AV	158/192 (82%)	148 (94%)	8 (5%)	2 (1%)	12	33
1	AW	156/192 (81%)	150 (96%)	6 (4%)	0	100	100
1	AX	158/192 (82%)	149 (94%)	8 (5%)	1 (1%)	25	53
1	Aa	159/192 (83%)	153 (96%)	6 (4%)	0	100	100
1	Ab	159/192 (83%)	151 (95%)	6 (4%)	2 (1%)	12	33
1	Ac	158/192 (82%)	155 (98%)	3 (2%)	0	100	100
1	Ad	163/192 (85%)	152 (93%)	8 (5%)	3 (2%)	8	25
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%)	12	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Aj	163/192 (85%)	147 (90%)	11 (7%)	5 (3%)	4	14
1	Ak	163/192 (85%)	153 (94%)	8 (5%)	2 (1%)	13	35
1	Al	163/192 (85%)	149 (91%)	10 (6%)	4 (2%)	5	18
1	Am	160/192 (83%)	149 (93%)	7 (4%)	4 (2%)	5	18
1	An	159/192 (83%)	149 (94%)	8 (5%)	2 (1%)	12	33
1	Ao	159/192 (83%)	150 (94%)	7 (4%)	2 (1%)	12	33
1	Ap	160/192 (83%)	150 (94%)	7 (4%)	3 (2%)	8	24
1	Aq	158/192 (82%)	146 (92%)	11 (7%)	1 (1%)	25	53
1	Ar	163/192 (85%)	152 (93%)	8 (5%)	3 (2%)	8	25
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%)	25	53
1	Av	163/192 (85%)	148 (91%)	13 (8%)	2 (1%)	13	35
1	Aw	159/192 (83%)	149 (94%)	9 (6%)	1 (1%)	25	53
1	Ax	153/192 (80%)	150 (98%)	3 (2%)	0	100	100
1	BA	164/192 (85%)	150 (92%)	12 (7%)	2 (1%)	13	35
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%)	8	24
1	BG	154/192 (80%)	145 (94%)	9 (6%)	0	100	100
1	BH	152/192 (79%)	146 (96%)	5 (3%)	1 (1%)	22	50
1	BI	153/192 (80%)	150 (98%)	3 (2%)	0	100	100
1	BJ	155/192 (81%)	147 (95%)	7 (4%)	1 (1%)	25	53
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%)	25	53
1	BO	158/192 (82%)	146 (92%)	11 (7%)	1 (1%)	25	53
1	BP	157/192 (82%)	150 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BQ	158/192 (82%)	152 (96%)	6 (4%)	0	100	100
1	BR	159/192 (83%)	150 (94%)	8 (5%)	1 (1%)	25	53
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%)	25	53
1	BV	154/192 (80%)	149 (97%)	3 (2%)	2 (1%)	12	33
1	BW	159/192 (83%)	154 (97%)	5 (3%)	0	100	100
1	BX	161/192 (84%)	150 (93%)	7 (4%)	4 (2%)	5	18
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%)	8	24
1	Be	161/192 (84%)	146 (91%)	12 (8%)	3 (2%)	8	24
1	Bf	163/192 (85%)	147 (90%)	11 (7%)	5 (3%)	4	14
1	Bg	154/192 (80%)	150 (97%)	4 (3%)	0	100	100
1	Bh	157/192 (82%)	151 (96%)	5 (3%)	1 (1%)	25	53
1	Bi	155/192 (81%)	148 (96%)	6 (4%)	1 (1%)	25	53
1	Bj	152/192 (79%)	147 (97%)	5 (3%)	0	100	100
1	Bk	157/192 (82%)	148 (94%)	8 (5%)	1 (1%)	25	53
1	Bl	157/192 (82%)	150 (96%)	6 (4%)	1 (1%)	25	53
1	Bm	157/192 (82%)	151 (96%)	6 (4%)	0	100	100
1	Bn	163/192 (85%)	153 (94%)	7 (4%)	3 (2%)	8	25
1	Bo	154/192 (80%)	149 (97%)	5 (3%)	0	100	100
1	Bp	160/192 (83%)	148 (92%)	11 (7%)	1 (1%)	25	53
1	Bq	158/192 (82%)	150 (95%)	6 (4%)	2 (1%)	12	33
1	Br	159/192 (83%)	148 (93%)	9 (6%)	2 (1%)	12	33
1	Bs	153/192 (80%)	148 (97%)	5 (3%)	0	100	100
1	Bt	156/192 (81%)	147 (94%)	7 (4%)	2 (1%)	12	33
1	Bu	163/192 (85%)	152 (93%)	9 (6%)	2 (1%)	13	35
1	Bv	158/192 (82%)	149 (94%)	8 (5%)	1 (1%)	25	53
1	Bw	157/192 (82%)	150 (96%)	6 (4%)	1 (1%)	25	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Bx	155/192 (81%)	147 (95%)	8 (5%)	0	100	100
1	CA	158/192 (82%)	153 (97%)	4 (2%)	1 (1%)	25	53
1	CB	159/192 (83%)	154 (97%)	5 (3%)	0	100	100
1	CC	155/192 (81%)	149 (96%)	5 (3%)	1 (1%)	25	53
1	CD	159/192 (83%)	152 (96%)	6 (4%)	1 (1%)	25	53
1	CE	158/192 (82%)	149 (94%)	7 (4%)	2 (1%)	12	33
1	CF	158/192 (82%)	150 (95%)	8 (5%)	0	100	100
1	CG	158/192 (82%)	153 (97%)	4 (2%)	1 (1%)	25	53
1	CH	157/192 (82%)	146 (93%)	10 (6%)	1 (1%)	25	53
1	CI	158/192 (82%)	147 (93%)	10 (6%)	1 (1%)	25	53
1	CJ	163/192 (85%)	153 (94%)	8 (5%)	2 (1%)	13	35
1	CK	158/192 (82%)	152 (96%)	5 (3%)	1 (1%)	25	53
1	CL	157/192 (82%)	150 (96%)	7 (4%)	0	100	100
1	CM	157/192 (82%)	148 (94%)	7 (4%)	2 (1%)	12	33
1	CN	159/192 (83%)	152 (96%)	7 (4%)	0	100	100
1	CO	157/192 (82%)	146 (93%)	11 (7%)	0	100	100
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%)	8	25
1	CS	159/192 (83%)	150 (94%)	9 (6%)	0	100	100
1	CT	156/192 (81%)	147 (94%)	8 (5%)	1 (1%)	25	53
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%)	12	33
1	Ca	156/192 (81%)	148 (95%)	5 (3%)	3 (2%)	8	24
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Cg	158/192 (82%)	150 (95%)	7 (4%)	1 (1%)	25	53
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%)	25	53
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%)	25	53
1	Cq	153/192 (80%)	146 (95%)	7 (5%)	0	100	100
1	Cr	152/192 (79%)	147 (97%)	4 (3%)	1 (1%)	22	50
1	Cs	152/192 (79%)	147 (97%)	4 (3%)	1 (1%)	22	50
1	Ct	158/192 (82%)	154 (98%)	4 (2%)	0	100	100
1	Cu	157/192 (82%)	149 (95%)	7 (4%)	1 (1%)	25	53
1	Cv	159/192 (83%)	151 (95%)	8 (5%)	0	100	100
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%)	25	53

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%)	27	57
1	AB	138/161 (86%)	133 (96%)	5 (4%)	35	66
1	AC	136/161 (84%)	132 (97%)	4 (3%)	42	72
1	AD	134/161 (83%)	133 (99%)	1 (1%)	84	94
1	AE	138/161 (86%)	136 (99%)	2 (1%)	67	86
1	AF	134/161 (83%)	131 (98%)	3 (2%)	52	79
1	AG	134/161 (83%)	131 (98%)	3 (2%)	52	79
1	AH	135/161 (84%)	131 (97%)	4 (3%)	41	72
1	AI	134/161 (83%)	131 (98%)	3 (2%)	52	79
1	AJ	133/161 (83%)	132 (99%)	1 (1%)	81	93
1	AK	134/161 (83%)	132 (98%)	2 (2%)	65	86
1	AL	133/161 (83%)	130 (98%)	3 (2%)	50	78
1	AM	136/161 (84%)	133 (98%)	3 (2%)	52	79
1	AN	138/161 (86%)	135 (98%)	3 (2%)	52	79
1	AO	138/161 (86%)	127 (92%)	11 (8%)	12	31
1	AP	135/161 (84%)	128 (95%)	7 (5%)	23	51
1	AQ	138/161 (86%)	136 (99%)	2 (1%)	67	86
1	AR	137/161 (85%)	135 (98%)	2 (2%)	65	86
1	AS	134/161 (83%)	130 (97%)	4 (3%)	41	72
1	AT	134/161 (83%)	132 (98%)	2 (2%)	65	86
1	AU	135/161 (84%)	131 (97%)	4 (3%)	41	72
1	AV	134/161 (83%)	133 (99%)	1 (1%)	84	94
1	AW	134/161 (83%)	133 (99%)	1 (1%)	84	94
1	AX	135/161 (84%)	134 (99%)	1 (1%)	84	94
1	Aa	136/161 (84%)	133 (98%)	3 (2%)	52	79
1	Ab	135/161 (84%)	130 (96%)	5 (4%)	34	65
1	Ac	135/161 (84%)	132 (98%)	3 (2%)	52	79
1	Ad	138/161 (86%)	131 (95%)	7 (5%)	24	52
1	Ae	136/161 (84%)	132 (97%)	4 (3%)	42	72
1	Af	136/161 (84%)	133 (98%)	3 (2%)	52	79
1	Ag	133/161 (83%)	129 (97%)	4 (3%)	41	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Ah	136/161 (84%)	133 (98%)	3 (2%)	52	79
1	Ai	135/161 (84%)	132 (98%)	3 (2%)	52	79
1	Aj	138/161 (86%)	132 (96%)	6 (4%)	29	59
1	Ak	138/161 (86%)	133 (96%)	5 (4%)	35	66
1	Al	138/161 (86%)	131 (95%)	7 (5%)	24	52
1	Am	136/161 (84%)	135 (99%)	1 (1%)	84	94
1	An	135/161 (84%)	133 (98%)	2 (2%)	65	86
1	Ao	136/161 (84%)	134 (98%)	2 (2%)	65	86
1	Ap	136/161 (84%)	134 (98%)	2 (2%)	65	86
1	Aq	135/161 (84%)	132 (98%)	3 (2%)	52	79
1	Ar	138/161 (86%)	133 (96%)	5 (4%)	35	66
1	As	136/161 (84%)	130 (96%)	6 (4%)	28	58
1	At	135/161 (84%)	128 (95%)	7 (5%)	23	51
1	Au	135/161 (84%)	130 (96%)	5 (4%)	34	65
1	Av	138/161 (86%)	135 (98%)	3 (2%)	52	79
1	Aw	135/161 (84%)	128 (95%)	7 (5%)	23	51
1	Ax	133/161 (83%)	132 (99%)	1 (1%)	81	93
1	BA	139/161 (86%)	134 (96%)	5 (4%)	35	66
1	BB	134/161 (83%)	132 (98%)	2 (2%)	65	86
1	BC	132/161 (82%)	130 (98%)	2 (2%)	65	86
1	BD	136/161 (84%)	135 (99%)	1 (1%)	84	94
1	BE	135/161 (84%)	135 (100%)	0	100	100
1	BF	134/161 (83%)	132 (98%)	2 (2%)	65	86
1	BG	133/161 (83%)	131 (98%)	2 (2%)	65	86
1	BH	132/161 (82%)	129 (98%)	3 (2%)	50	78
1	BI	133/161 (83%)	132 (99%)	1 (1%)	81	93
1	BJ	133/161 (83%)	130 (98%)	3 (2%)	50	78
1	BK	133/161 (83%)	128 (96%)	5 (4%)	33	64
1	BL	133/161 (83%)	132 (99%)	1 (1%)	81	93
1	BM	134/161 (83%)	132 (98%)	2 (2%)	65	86
1	BN	134/161 (83%)	132 (98%)	2 (2%)	65	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BO	135/161 (84%)	132 (98%)	3 (2%)	52	79
1	BP	134/161 (83%)	131 (98%)	3 (2%)	52	79
1	BQ	135/161 (84%)	130 (96%)	5 (4%)	34	65
1	BR	136/161 (84%)	134 (98%)	2 (2%)	65	86
1	BS	135/161 (84%)	134 (99%)	1 (1%)	84	94
1	BT	133/161 (83%)	131 (98%)	2 (2%)	65	86
1	BU	136/161 (84%)	135 (99%)	1 (1%)	84	94
1	BV	132/161 (82%)	130 (98%)	2 (2%)	65	86
1	BW	135/161 (84%)	133 (98%)	2 (2%)	65	86
1	BX	136/161 (84%)	133 (98%)	3 (2%)	52	79
1	Ba	134/161 (83%)	131 (98%)	3 (2%)	52	79
1	Bb	135/161 (84%)	132 (98%)	3 (2%)	52	79
1	Bc	136/161 (84%)	130 (96%)	6 (4%)	28	58
1	Bd	136/161 (84%)	136 (100%)	0	100	100
1	Be	136/161 (84%)	133 (98%)	3 (2%)	52	79
1	Bf	138/161 (86%)	132 (96%)	6 (4%)	29	59
1	Bg	133/161 (83%)	131 (98%)	2 (2%)	65	86
1	Bh	135/161 (84%)	132 (98%)	3 (2%)	52	79
1	Bi	134/161 (83%)	132 (98%)	2 (2%)	65	86
1	Bj	131/161 (81%)	128 (98%)	3 (2%)	50	78
1	Bk	135/161 (84%)	132 (98%)	3 (2%)	52	79
1	Bl	135/161 (84%)	131 (97%)	4 (3%)	41	72
1	Bm	134/161 (83%)	130 (97%)	4 (3%)	41	72
1	Bn	138/161 (86%)	135 (98%)	3 (2%)	52	79
1	Bo	133/161 (83%)	132 (99%)	1 (1%)	81	93
1	Bp	136/161 (84%)	133 (98%)	3 (2%)	52	79
1	Bq	136/161 (84%)	135 (99%)	1 (1%)	84	94
1	Br	136/161 (84%)	130 (96%)	6 (4%)	28	58
1	Bs	133/161 (83%)	131 (98%)	2 (2%)	65	86
1	Bt	134/161 (83%)	130 (97%)	4 (3%)	41	72
1	Bu	138/161 (86%)	133 (96%)	5 (4%)	35	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Bv	135/161 (84%)	133 (98%)	2 (2%)	65	86
1	Bw	134/161 (83%)	132 (98%)	2 (2%)	65	86
1	Bx	133/161 (83%)	131 (98%)	2 (2%)	65	86
1	CA	135/161 (84%)	131 (97%)	4 (3%)	41	72
1	CB	135/161 (84%)	130 (96%)	5 (4%)	34	65
1	CC	133/161 (83%)	131 (98%)	2 (2%)	65	86
1	CD	136/161 (84%)	136 (100%)	0	100	100
1	CE	136/161 (84%)	134 (98%)	2 (2%)	65	86
1	CF	134/161 (83%)	130 (97%)	4 (3%)	41	72
1	CG	136/161 (84%)	131 (96%)	5 (4%)	34	65
1	CH	135/161 (84%)	132 (98%)	3 (2%)	52	79
1	CI	135/161 (84%)	130 (96%)	5 (4%)	34	65
1	CJ	138/161 (86%)	133 (96%)	5 (4%)	35	66
1	CK	135/161 (84%)	131 (97%)	4 (3%)	41	72
1	CL	135/161 (84%)	133 (98%)	2 (2%)	65	86
1	CM	135/161 (84%)	130 (96%)	5 (4%)	34	65
1	CN	135/161 (84%)	133 (98%)	2 (2%)	65	86
1	CO	135/161 (84%)	133 (98%)	2 (2%)	65	86
1	CP	134/161 (83%)	131 (98%)	3 (2%)	52	79
1	CQ	136/161 (84%)	129 (95%)	7 (5%)	24	52
1	CR	139/161 (86%)	136 (98%)	3 (2%)	52	79
1	CS	136/161 (84%)	131 (96%)	5 (4%)	34	65
1	CT	134/161 (83%)	130 (97%)	4 (3%)	41	72
1	CU	135/161 (84%)	135 (100%)	0	100	100
1	CV	134/161 (83%)	132 (98%)	2 (2%)	65	86
1	CW	133/161 (83%)	132 (99%)	1 (1%)	81	93
1	CX	136/161 (84%)	134 (98%)	2 (2%)	65	86
1	Ca	133/161 (83%)	130 (98%)	3 (2%)	50	78
1	Cb	134/161 (83%)	132 (98%)	2 (2%)	65	86
1	Cc	133/161 (83%)	131 (98%)	2 (2%)	65	86
1	Cd	131/161 (81%)	129 (98%)	2 (2%)	65	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Ce	132/161 (82%)	129 (98%)	3 (2%)	50	78
1	Cf	131/161 (81%)	131 (100%)	0	100	100
1	Cg	134/161 (83%)	132 (98%)	2 (2%)	65	86
1	Ch	134/161 (83%)	131 (98%)	3 (2%)	52	79
1	Ci	131/161 (81%)	131 (100%)	0	100	100
1	Cj	134/161 (83%)	131 (98%)	3 (2%)	52	79
1	Ck	132/161 (82%)	130 (98%)	2 (2%)	65	86
1	Cl	132/161 (82%)	130 (98%)	2 (2%)	65	86
1	Cm	134/161 (83%)	130 (97%)	4 (3%)	41	72
1	Cn	133/161 (83%)	130 (98%)	3 (2%)	50	78
1	Co	132/161 (82%)	129 (98%)	3 (2%)	50	78
1	Cp	134/161 (83%)	133 (99%)	1 (1%)	84	94
1	Cq	132/161 (82%)	131 (99%)	1 (1%)	81	93
1	Cr	132/161 (82%)	130 (98%)	2 (2%)	65	86
1	Cs	131/161 (81%)	130 (99%)	1 (1%)	81	93
1	Ct	134/161 (83%)	131 (98%)	3 (2%)	52	79
1	Cu	134/161 (83%)	131 (98%)	3 (2%)	52	79
1	Cv	135/161 (84%)	132 (98%)	3 (2%)	52	79
1	Cw	132/161 (82%)	132 (100%)	0	100	100
1	Cx	134/161 (83%)	130 (97%)	4 (3%)	41	72
All	All	19400/23184 (84%)	18968 (98%)	432 (2%)	52	79

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

Mol	Chain	Res	Type
1	BK	126	LEU
1	Bu	29	TYR
1	CR	63	TYR
1	Bl	81	ASP
1	Bp	101	MET

Sometimes 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	50	HIS
1	CQ	72	GLN
1	BW	71	ASN
1	CP	108	ASN
1	Ct	4	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 monosaccharides 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%) 47 42	31, 61, 82, 117	0
1	AB	165/192 (85%)	-0.24	8 (4%) 30 26	26, 54, 95, 109	0
1	AC	161/192 (83%)	-0.32	4 (2%) 57 54	38, 58, 77, 111	0
1	AD	159/192 (82%)	-0.24	4 (2%) 57 54	51, 68, 82, 118	0
1	AE	165/192 (85%)	-0.40	9 (5%) 25 20	12, 34, 96, 112	0
1	AF	158/192 (82%)	-0.49	2 (1%) 77 76	19, 47, 66, 104	0
1	AG	159/192 (82%)	-0.45	4 (2%) 57 54	31, 47, 63, 123	0
1	AH	160/192 (83%)	-0.25	3 (1%) 66 64	21, 42, 69, 112	0
1	AI	158/192 (82%)	-0.21	5 (3%) 47 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	1 (0%) 89 89	33, 59, 75, 101	0
1	AL	157/192 (81%)	-0.18	4 (2%) 57 54	52, 68, 82, 120	0
1	AM	162/192 (84%)	-0.47	3 (1%) 66 64	17, 39, 69, 112	0
1	AN	165/192 (85%)	-0.33	6 (3%) 42 37	31, 48, 89, 107	0
1	AO	165/192 (85%)	-0.21	11 (6%) 17 13	17, 46, 87, 110	0
1	AP	159/192 (82%)	-0.54	0 100 100	7, 30, 51, 102	0
1	AQ	165/192 (85%)	-0.15	11 (6%) 17 13	33, 62, 90, 110	0
1	AR	164/192 (85%)	-0.35	6 (3%) 41 36	20, 46, 89, 111	0
1	AS	160/192 (83%)	-0.21	6 (3%) 40 35	32, 56, 87, 117	0
1	AT	158/192 (82%)	-0.51	1 (0%) 89 89	15, 43, 62, 110	0
1	AU	160/192 (83%)	-0.49	1 (0%) 89 89	24, 42, 68, 107	0
1	AV	160/192 (83%)	-0.20	7 (4%) 34 29	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%)	-0.35	3 (1%) 66 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%)	-0.51	3 (1%) 66 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%)	-0.56	0 100 100	15, 35, 66, 103	0
1	Ad	165/192 (85%)	-0.58	3 (1%) 68 66	7, 26, 87, 107	0
1	Ae	162/192 (84%)	-0.33	5 (3%) 49 44	8, 29, 65, 113	0
1	Af	161/192 (83%)	-0.45	1 (0%) 89 89	10, 28, 56, 106	0
1	Ag	155/192 (80%)	-0.65	1 (0%) 89 89	8, 28, 45, 70	0
1	Ah	161/192 (83%)	-0.42	0 100 100	12, 32, 55, 109	0
1	Ai	159/192 (82%)	-0.54	1 (0%) 89 89	8, 23, 46, 96	0
1	Aj	165/192 (85%)	-0.20	5 (3%) 50 45	12, 31, 85, 109	0
1	Ak	165/192 (85%)	-0.34	7 (4%) 36 31	18, 37, 86, 107	0
1	Al	165/192 (85%)	-0.39	1 (0%) 89 89	8, 33, 81, 108	0
1	Am	162/192 (84%)	-0.49	1 (0%) 89 89	11, 31, 57, 102	0
1	An	161/192 (83%)	-0.58	2 (1%) 79 78	13, 28, 56, 96	0
1	Ao	161/192 (83%)	-0.50	2 (1%) 79 78	11, 32, 54, 105	0
1	Ap	162/192 (84%)	-0.58	2 (1%) 79 78	11, 30, 63, 101	0
1	Aq	160/192 (83%)	-0.51	2 (1%) 77 76	9, 30, 58, 110	0
1	Ar	165/192 (85%)	-0.49	2 (1%) 79 78	9, 28, 81, 105	0
1	As	161/192 (83%)	-0.51	3 (1%) 66 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%) 50 45	16, 39, 85, 110	0
1	Aw	161/192 (83%)	-0.47	3 (1%) 66 64	8, 31, 58, 109	0
1	Ax	155/192 (80%)	-0.71	1 (0%) 89 89	11, 31, 45, 76	0
1	BA	166/192 (86%)	-0.25	2 (1%) 79 78	30, 51, 87, 108	0
1	BB	157/192 (81%)	0.47	8 (5%) 28 23	68, 86, 98, 109	0
1	BC	155/192 (80%)	0.24	4 (2%) 56 52	64, 84, 94, 103	0
1	BD	160/192 (83%)	-0.30	1 (0%) 89 89	22, 52, 76, 105	0
1	BE	159/192 (82%)	-0.38	2 (1%) 77 76	26, 46, 72, 111	0
1	BF	159/192 (82%)	-0.63	0 100 100	13, 32, 53, 102	0
1	BG	156/192 (81%)	-0.22	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%) 66 64	40, 70, 86, 99	0
1	BI	155/192 (80%)	-0.36	0 100 100	19, 52, 73, 97	0
1	BJ	157/192 (81%)	-0.06	2 (1%) 77 76	50, 69, 91, 111	0
1	BK	156/192 (81%)	0.49	8 (5%) 28 23	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%)	-0.33	2 (1%) 77 76	9, 33, 54, 102	0
1	BN	159/192 (82%)	-0.36	0 100 100	20, 41, 63, 114	0
1	BO	160/192 (83%)	-0.11	4 (2%) 57 54	37, 62, 86, 114	0
1	BP	159/192 (82%)	-0.26	5 (3%) 49 44	29, 55, 83, 114	0
1	BQ	160/192 (83%)	-0.49	1 (0%) 89 89	17, 37, 63, 114	0
1	BR	161/192 (83%)	-0.44	3 (1%) 66 64	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%)	0.20	5 (3%) 47 42	58, 74, 92, 118	0
1	BU	162/192 (84%)	0.05	1 (0%) 89 89	55, 78, 91, 115	0
1	BV	156/192 (81%)	0.27	7 (4%) 33 28	69, 87, 96, 111	0
1	BW	161/192 (83%)	-0.15	4 (2%) 57 54	38, 60, 81, 117	0
1	BX	163/192 (84%)	0.31	6 (3%) 41 36	61, 78, 91, 110	0
1	Ba	158/192 (82%)	-0.11	4 (2%) 57 54	52, 71, 88, 111	0
1	Bb	159/192 (82%)	-0.01	3 (1%) 66 64	49, 72, 90, 118	0
1	Bc	161/192 (83%)	-0.41	1 (0%) 89 89	15, 38, 69, 109	0
1	Bd	161/192 (83%)	-0.47	3 (1%) 66 64	21, 40, 64, 114	0
1	Be	163/192 (84%)	-0.47	1 (0%) 89 89	13, 36, 77, 107	0
1	Bf	165/192 (85%)	-0.31	6 (3%) 42 37	14, 44, 85, 110	0
1	Bg	156/192 (81%)	0.11	4 (2%) 56 52	54, 76, 89, 108	0
1	Bh	159/192 (82%)	-0.45	3 (1%) 66 64	30, 48, 72, 108	0
1	Bi	157/192 (81%)	-0.22	1 (0%) 89 89	32, 58, 70, 94	0
1	Bj	154/192 (80%)	0.09	0 100 100	55, 76, 85, 96	0
1	Bk	159/192 (82%)	-0.20	2 (1%) 77 76	37, 57, 80, 114	0
1	Bl	159/192 (82%)	-0.53	1 (0%) 89 89	12, 38, 61, 109	0
1	Bm	159/192 (82%)	-0.52	3 (1%) 66 64	18, 36, 59, 113	0
1	Bn	165/192 (85%)	-0.09	4 (2%) 59 56	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%) 66 64	44, 65, 84, 96	0
1	Bp	162/192 (84%)	-0.39	7 (4%) 35 30	17, 41, 79, 116	0
1	Bq	160/192 (83%)	-0.11	3 (1%) 66 64	26, 55, 76, 111	0
1	Br	161/192 (83%)	-0.58	2 (1%) 79 78	8, 28, 57, 105	0
1	Bs	155/192 (80%)	-0.24	2 (1%) 77 76	37, 57, 80, 97	0
1	Bt	158/192 (82%)	0.14	4 (2%) 57 54	61, 79, 93, 110	0
1	Bu	165/192 (85%)	-0.40	6 (3%) 42 37	14, 36, 83, 106	0
1	Bv	160/192 (83%)	-0.43	5 (3%) 49 44	23, 45, 72, 120	0
1	Bw	159/192 (82%)	-0.40	3 (1%) 66 64	11, 29, 55, 112	0
1	Bx	157/192 (81%)	0.23	7 (4%) 33 28	62, 83, 95, 113	0
1	CA	160/192 (83%)	-0.51	1 (0%) 89 89	12, 36, 61, 111	0
1	CB	161/192 (83%)	-0.25	4 (2%) 57 54	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%)	-0.49	2 (1%) 79 78	13, 39, 68, 107	0
1	CE	160/192 (83%)	-0.27	1 (0%) 89 89	29, 52, 80, 112	0
1	CF	160/192 (83%)	-0.48	3 (1%) 66 64	11, 35, 53, 101	0
1	CG	160/192 (83%)	-0.41	2 (1%) 77 76	21, 45, 72, 112	0
1	CH	159/192 (82%)	-0.13	3 (1%) 66 64	33, 62, 79, 119	0
1	CI	160/192 (83%)	-0.21	3 (1%) 66 64	15, 35, 74, 107	0
1	CJ	165/192 (85%)	-0.38	5 (3%) 50 45	24, 44, 85, 105	0
1	CK	160/192 (83%)	-0.28	2 (1%) 77 76	22, 60, 77, 115	0
1	CL	159/192 (82%)	-0.35	3 (1%) 66 64	38, 57, 73, 121	0
1	CM	159/192 (82%)	-0.46	3 (1%) 66 64	16, 42, 63, 112	0
1	CN	161/192 (83%)	-0.51	1 (0%) 89 89	16, 40, 77, 110	0
1	CO	159/192 (82%)	-0.37	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%)	-0.48	3 (1%) 66 64	9, 31, 61, 104	0
1	CR	166/192 (86%)	-0.40	5 (3%) 50 45	24, 42, 82, 107	0
1	CS	161/192 (83%)	-0.34	4 (2%) 57 54	10, 35, 65, 114	0
1	CT	158/192 (82%)	-0.40	3 (1%) 66 64	26, 50, 66, 106	0
1	CU	159/192 (82%)	-0.23	1 (0%) 89 89	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%)	-0.21	4 (2%) 57 54	55, 68, 84, 120	0
1	CW	155/192 (80%)	-0.49	1 (0%) 89 89	27, 47, 69, 87	0
1	CX	161/192 (83%)	-0.47	3 (1%) 66 64	20, 48, 70, 107	0
1	Ca	158/192 (82%)	0.62	18 (11%) 5 3	58, 89, 103, 121	0
1	Cb	159/192 (82%)	0.02	6 (3%) 40 35	37, 69, 87, 109	0
1	Cc	157/192 (81%)	-0.12	4 (2%) 57 54	40, 69, 86, 118	0
1	Cd	153/192 (79%)	0.65	16 (10%) 6 4	76, 91, 104, 109	0
1	Ce	154/192 (80%)	0.26	8 (5%) 27 22	59, 81, 92, 95	0
1	Cf	153/192 (79%)	0.84	17 (11%) 5 3	83, 97, 107, 110	0
1	Cg	160/192 (83%)	0.02	7 (4%) 34 29	48, 68, 93, 126	0
1	Ch	159/192 (82%)	-0.43	2 (1%) 77 76	23, 49, 66, 114	0
1	Ci	153/192 (79%)	0.62	15 (9%) 7 5	69, 89, 104, 111	0
1	Cj	156/192 (81%)	0.31	9 (5%) 23 18	61, 81, 100, 112	0
1	Ck	154/192 (80%)	-0.08	2 (1%) 77 76	45, 74, 92, 104	0
1	Cl	155/192 (80%)	0.18	5 (3%) 47 42	56, 85, 97, 113	0
1	Cm	159/192 (82%)	0.42	16 (10%) 7 5	71, 88, 100, 113	0
1	Cn	155/192 (80%)	0.22	7 (4%) 33 28	65, 86, 101, 104	0
1	Co	155/192 (80%)	-0.34	2 (1%) 77 76	26, 52, 71, 100	0
1	Cp	158/192 (82%)	-0.08	7 (4%) 34 29	46, 67, 89, 109	0
1	Cq	155/192 (80%)	0.75	21 (13%) 3 2	83, 96, 106, 112	0
1	Cr	154/192 (80%)	0.20	8 (5%) 27 22	78, 91, 103, 111	0
1	Cs	154/192 (80%)	0.57	16 (10%) 6 4	83, 98, 106, 107	0
1	Ct	160/192 (83%)	-0.38	4 (2%) 57 54	34, 51, 79, 115	0
1	Cu	159/192 (82%)	-0.23	6 (3%) 40 35	44, 62, 81, 119	0
1	Cv	161/192 (83%)	-0.13	3 (1%) 66 64	39, 59, 81, 119	0
1	Cw	155/192 (80%)	0.19	4 (2%) 56 52	71, 89, 98, 107	0
1	Cx	156/192 (81%)	-0.21	2 (1%) 77 76	39, 59, 78, 99	0
All	All	22946/27648 (82%)	-0.23	578 (2%) 57 54	7, 52, 95, 126	0

The worst 5 of 578 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Ci	155	LEU	6.3

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Mol	Chain	Res	Type	RSRZ
1	Bn	159	GLU	6.2
1	Ar	162	LEU	6.1
1	Av	159	GLU	5.6
1	Av	162	LEU	5.6

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 monosaccharides 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. 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	B-factors(Å ²)	Q<0.9
2	CA	BN	201	1/1	0.55	0.35	73,73,73,73	0
2	CA	An	201	1/1	0.58	0.30	61,61,61,61	0
2	CA	Cl	201	1/1	0.59	0.45	85,85,85,85	1
2	CA	Cn	201	1/1	0.65	0.17	108,108,108,108	0
2	CA	BB	201	1/1	0.71	0.12	86,86,86,86	0
2	CA	AC	201	1/1	0.72	0.32	86,86,86,86	0
2	CA	BG	201	1/1	0.73	0.27	94,94,94,94	0
2	CA	Bb	201	1/1	0.76	0.26	98,98,98,98	0
2	CA	BR	201	1/1	0.76	0.31	72,72,72,72	0
2	CA	Cg	201	1/1	0.78	0.18	85,85,85,85	0
2	CA	Ag	201	1/1	0.79	0.25	55,55,55,55	0
2	CA	Ac	201	1/1	0.79	0.27	70,70,70,70	0
2	CA	Bd	201	1/1	0.79	0.27	61,61,61,61	0
2	CA	CE	201	1/1	0.80	0.31	83,83,83,83	0
2	CA	BA	201	1/1	0.83	0.24	78,78,78,78	0
2	CA	CA	201	1/1	0.83	0.32	67,67,67,67	0
2	CA	AB	201	1/1	0.84	0.21	75,75,75,75	0
2	CA	Aa	201	1/1	0.84	0.24	58,58,58,58	0
2	CA	BC	201	1/1	0.84	0.45	73,73,73,73	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CA	BD	201	1/1	0.85	0.19	81,81,81,81	0
2	CA	Ba	201	1/1	0.85	0.18	80,80,80,80	0
2	CA	Ck	201	1/1	0.85	0.18	78,78,78,78	0
2	CA	AF	201	1/1	0.85	0.25	68,68,68,68	0
2	CA	CC	201	1/1	0.85	0.20	96,96,96,96	0
2	CA	AA	201	1/1	0.86	0.18	106,106,106,106	0
2	CA	CO	201	1/1	0.86	0.21	68,68,68,68	0
2	CA	AL	201	1/1	0.87	0.17	84,84,84,84	0
2	CA	Bc	201	1/1	0.88	0.31	73,73,73,73	0
2	CA	Be	201	1/1	0.88	0.31	66,66,66,66	0
2	CA	Ce	201	1/1	0.88	0.27	106,106,106,106	0
2	CA	AO	201	1/1	0.88	0.24	67,67,67,67	0
2	CA	Bg	201	1/1	0.90	0.24	88,88,88,88	0
2	CA	Aj	201	1/1	0.90	0.29	56,56,56,56	0
2	CA	Ae	201	1/1	0.90	0.26	70,70,70,70	0
2	CA	AM	201	1/1	0.90	0.24	68,68,68,68	0
2	CA	Cb	201	1/1	0.91	0.26	80,80,80,80	0
2	CA	AH	201	1/1	0.91	0.28	62,62,62,62	0
2	CA	Ad	201	1/1	0.91	0.23	54,54,54,54	0
2	CA	CB	201	1/1	0.92	0.24	60,60,60,60	0
2	CA	Bf	201	1/1	0.92	0.27	68,68,68,68	0
2	CA	CF	201	1/1	0.93	0.33	63,63,63,63	0
2	CA	BH	201	1/1	0.95	0.26	96,96,96,96	0
2	CA	CH	201	1/1	0.96	0.15	69,69,69,69	0
2	CA	Cp	201	1/1	0.96	0.25	69,69,69,69	0
2	CA	Ca	201	1/1	0.97	0.42	87,87,87,87	1
2	CA	CD	201	1/1	0.97	0.17	68,68,68,68	0
2	CA	Bu	201	1/1	0.97	0.27	61,61,61,61	0
2	CA	Ah	201	1/1	0.97	0.28	56,56,56,56	0

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

There are no such residues in this entry.