



wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 02:44 pm BST

PDB ID : 4V9R
Title : Crystal structure of antibiotic DITYROMYCIN bound to 70S ribosome
Authors : Bulkley, D.P.; Brandi, L.; Polikanov, Y.S.; Fabbretti, A.; O'Connor, M.;
Gualerzi, C.O.; Steitz, T.A.
Deposited on : 2013-12-05
Resolution : 3.00 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

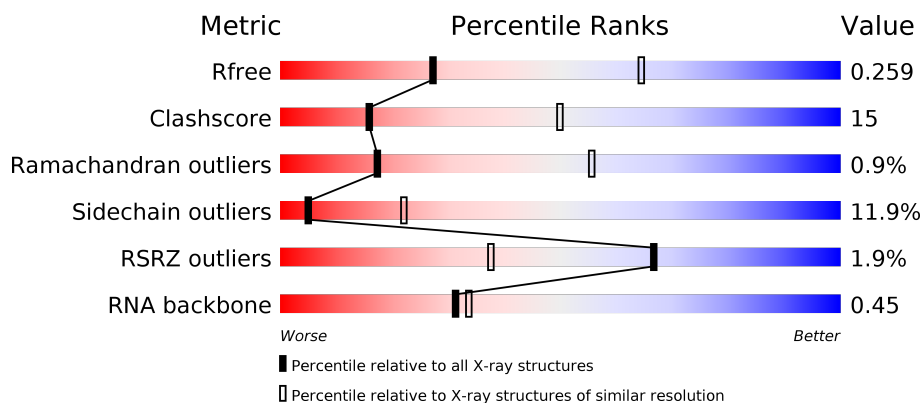
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)
RNA backbone	3102	1173 (3.30-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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	1522	 3% 29% 44% 20% 5%
1	CA	1522	 2% 32% 43% 20% 5%
2	AB	256	 2% 38% 41% 11% 10%
2	CB	256	 4% 36% 44% 10% 10%



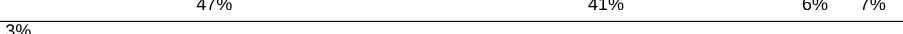


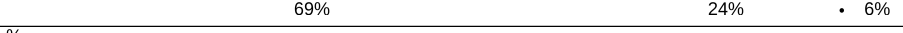

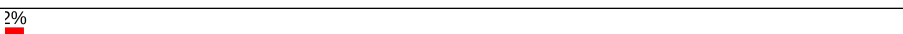
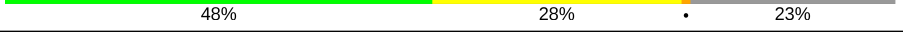
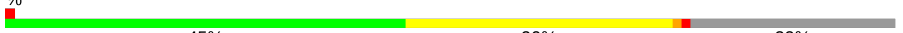



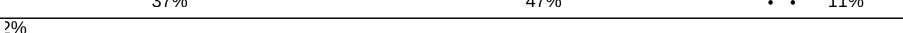
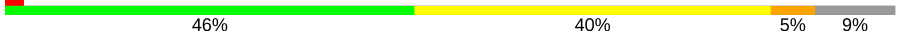

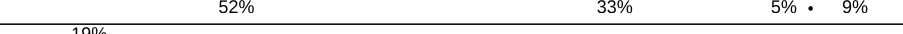




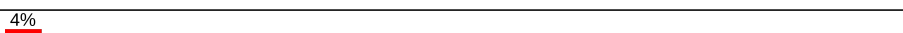



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Mol	Chain	Length	Quality of chain
3	AC	239	
3	CC	239	
4	AD	209	
4	CD	209	
5	AE	162	
5	CE	162	
6	AF	101	
6	CF	101	
7	AG	156	
7	CG	156	
8	AH	138	
8	CH	138	
9	AI	128	
9	CI	128	
10	AJ	105	
10	CJ	105	
11	AK	129	
11	CK	129	
12	AL	132	
12	CL	132	
13	AM	126	
13	CM	126	
14	AN	61	
14	CN	61	
15	AO	89	

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Mol	Chain	Length	Quality of chain
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AX	77	
23	CX	77	
24	AW	10	
24	CW	10	
25	BA	2915	
25	DA	2915	
26	BB	122	
26	DB	122	
27	BD	276	
27	DD	276	



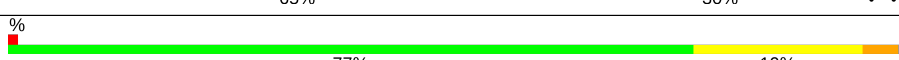
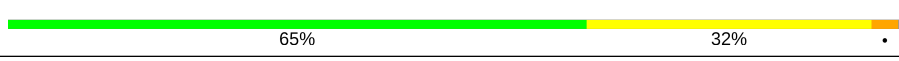
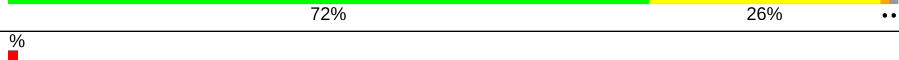
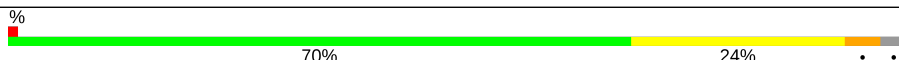

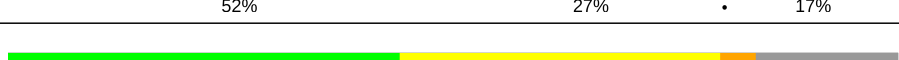

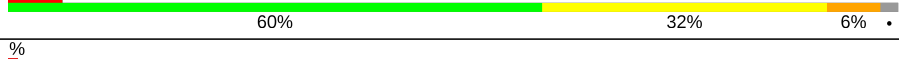


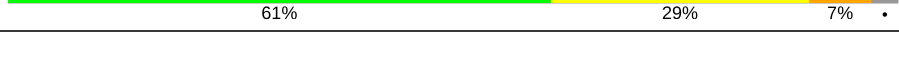

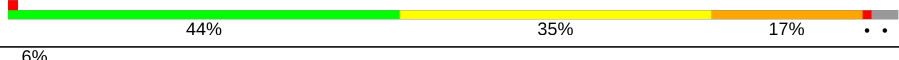
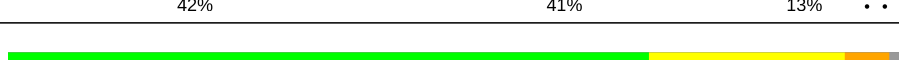





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Mol	Chain	Length	Quality of chain
28	BE	206	
28	DE	206	
29	BF	210	
29	DF	210	
30	BG	182	
30	DG	182	
31	BH	180	
31	DH	180	
32	BI	148	
32	DI	148	
33	BN	140	
33	DN	140	
34	BO	122	
34	DO	122	
35	BP	150	
35	DP	150	
36	BQ	141	
36	DQ	141	
37	BR	118	
37	DR	118	
38	BS	112	
38	DS	112	
39	BT	146	
39	DT	146	
40	BU	118	

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Mol	Chain	Length	Quality of chain
40	DU	118	
41	BV	101	
41	DV	101	
42	BW	113	
42	DW	113	
43	BX	96	
43	DX	96	
44	BY	110	
44	DY	110	
45	BZ	206	
45	DZ	206	
46	B0	85	
46	D0	85	
47	B1	98	
47	D1	98	
48	B2	72	
48	D2	72	
49	B3	60	
49	D3	60	
50	B4	71	
50	D4	71	
51	B5	60	
51	D5	60	
52	B6	54	
52	D6	54	

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Mol	Chain	Length	Quality of chain
53	B7	49	
53	D7	49	
54	B8	65	
54	D8	65	
55	B9	37	
55	D9	37	

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
56	MG	AA	3029	-	-	-	X
56	MG	AA	3030	-	-	-	X
56	MG	AA	3038	-	-	-	X
56	MG	AA	3079	-	-	-	X
56	MG	AA	3086	-	-	-	X
56	MG	AA	3147	-	-	-	X
56	MG	AA	3180	-	-	-	X
56	MG	AX	105	-	-	-	X
56	MG	BA	3139	-	-	-	X
56	MG	BA	3143	-	-	-	X
56	MG	BA	3154	-	-	-	X
56	MG	BA	3178	-	-	-	X
56	MG	BA	3230	-	-	-	X
56	MG	BA	3252	-	-	-	X
56	MG	BA	3296	-	-	-	X
56	MG	BA	3625	-	-	-	X
56	MG	BA	3740	-	-	-	X
56	MG	BD	311	-	-	-	X
56	MG	BF	306	-	-	-	X
56	MG	CA	3016	-	-	-	X
56	MG	CA	3039	-	-	-	X
56	MG	CA	3053	-	-	-	X
56	MG	CA	3054	-	-	-	X
56	MG	CA	3144	-	-	-	X
56	MG	DA	3024	-	-	-	X
56	MG	DA	3064	-	-	-	X
56	MG	DA	3113	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	DA	3356	-	-	-	X
56	MG	DA	3431	-	-	-	X
56	MG	DA	3568	-	-	-	X

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 286321 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 RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1498	Total	C	N	O	P	0	0	0
			32196	14328	5966	10404	1498			
1	CA	1503	Total	C	N	O	P	0	0	0
			32312	14381	5990	10438	1503			

- Molecule 2 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	231	Total	C	N	O	S	0	0	0
			1846	1179	331	331	5			
2	CB	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

- Molecule 3 is a protein called 30S Ribosomal Protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1552	976	302	273	1			
3	CC	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			

- Molecule 4 is a protein called 30S Ribosomal Protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0	0
			1659	1040	326	286	7			
4	CD	208	Total	C	N	O	S	0	0	0
			1674	1050	333	284	7			

- Molecule 5 is a protein called 30S Ribosomal Protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
5	CE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 6 is a protein called 30S Ribosomal Protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	100	Total	C	N	O	S	0	0	0
			806	511	143	149	3			
6	CF	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			

- Molecule 7 is a protein called 30S Ribosomal Protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	155	Total	C	N	O	S	0	0	0
			1231	766	243	216	6			
7	CG	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			

- Molecule 8 is a protein called 30S Ribosomal Protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
8	CH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			

- Molecule 9 is a protein called 30S Ribosomal Protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O		0	0	0
			983	623	193	167				
9	CI	127	Total	C	N	O		0	0	0
			978	619	190	169				

- Molecule 10 is a protein called 30S Ribosomal Protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AJ	97	Total	C	N	O		0	0	0
			709	440	138	131				

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	CJ	96	Total	C	N	O			
			714	445	138	131	0	0	0

- Molecule 11 is a protein called 30S Ribosomal Protein S11.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
11	AK	114	Total	C	N	O	S		
			829	516	155	155	3	0	0
11	CK	114	Total	C	N	O	S		
			833	519	156	155	3	0	0

- Molecule 12 is a protein called 30S Ribosomal Protein S12.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
12	AL	122	Total	C	N	O	S		
			930	585	185	159	1	0	0
12	CL	122	Total	C	N	O	S		
			930	585	185	159	1	0	0

- Molecule 13 is a protein called 30S Ribosomal Protein S13.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	AM	123	Total	C	N	O	S		
			958	592	198	166	2	0	0
13	CM	122	Total	C	N	O	S		
			950	586	197	165	2	0	0

- Molecule 14 is a protein called 30S Ribosomal Protein S14.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	AN	60	Total	C	N	O	S		
			492	312	104	72	4	0	0
14	CN	60	Total	C	N	O	S		
			492	312	104	72	4	0	0

- Molecule 15 is a protein called 30S Ribosomal Protein S15.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	AO	88	Total	C	N	O	S		
			728	456	144	126	2	0	0
15	CO	88	Total	C	N	O	S		
			728	456	144	126	2	0	0

- Molecule 16 is a protein called 30S Ribosomal Protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			
16	CP	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 17 is a protein called 30S Ribosomal Protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
17	CQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 18 is a protein called 30S Ribosomal Protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	AR	68	Total	C	N	O	0	0	0
			555	355	108	92			
18	CR	68	Total	C	N	O	0	0	0
			555	355	108	92			

- Molecule 19 is a protein called 30S Ribosomal Protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	83	Total	C	N	O	S	0	0	0
			652	417	120	113	2			
19	CS	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

- Molecule 20 is a protein called 30S Ribosomal Protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	96	Total	C	N	O	S	0	0	0
			728	446	156	124	2			
20	CT	96	Total	C	N	O	S	0	0	0
			727	446	155	124	2			

- Molecule 21 is a protein called 30S Ribosomal Protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	AU	23	Total	C	N	O	0	0	0
			199	122	48	29			
21	CU	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	7	Total	C	N	O	P	0	0	1
			114	49	22	37	6			
22	CV	6	Total	C	N	O	P	0	0	0
			113	49	22	36	6			

- Molecule 23 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AX	76	Total	C	N	O	P	0	0	0
			1623	723	294	530	76			
23	CX	76	Total	C	N	O	P	0	0	0
			1623	723	294	530	76			

- Molecule 24 is a protein called Dityromycin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
24	AW	10	Total	C	N	O	0	0	0
			93	67	10	16			
24	CW	10	Total	C	N	O	0	0	0
			93	67	10	16			

- Molecule 25 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BA	2731	Total	C	N	O	P	0	0	0
			58834	26185	11020	18899	2730			
25	DA	2714	Total	C	N	O	P	0	0	0
			58458	26018	10942	18786	2712			

- Molecule 26 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	DB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- Molecule 27 is a protein called 50S Ribosomal Protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	BD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
27	DD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

- Molecule 28 is a protein called 50S Ribosomal Protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
28	DE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 29 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	BF	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
29	DF	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 30 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	BG	181	Total	C	N	O	S	0	0	0
			1425	914	256	251	4			
30	DG	181	Total	C	N	O	S	0	0	0
			1424	911	258	251	4			

- Molecule 31 is a protein called 50S Ribosomal Protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	BH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
31	DH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 32 is a protein called 50S Ribosomal Protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BI	146	Total	C	N	O	S	0	0	0
			1085	693	189	202	1			
32	DI	146	Total	C	N	O	S	0	0	0
			1061	680	186	194	1			

- Molecule 33 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			
33	DN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 34 is a protein called 50S Ribosomal Protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
34	DO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 35 is a protein called 50S Ribosomal Protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			
35	DP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 36 is a protein called 50S Ribosomal Protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
36	DQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 37 is a protein called 50S Ribosomal Protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
37	DR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 38 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BS	110	Total	C	N	O	S	0	0	0
			877	553	175	149				
38	DS	110	Total	C	N	O	S	0	0	0
			870	549	173	148				

- Molecule 39 is a protein called 50S Ribosomal Protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BT	131	Total	C	N	O	S	0	0	0
			1091	680	225	185	1			
39	DT	131	Total	C	N	O	S	0	0	0
			1083	675	224	183	1			

- Molecule 40 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
40	DU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 41 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			
41	DV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 42 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	DW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 43 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
43	DX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 44 is a protein called 50S Ribosomal Protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	BY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			
44	DY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			

- Molecule 45 is a protein called 50S Ribosomal Protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BZ	171	Total	C	N	O	S	0	0	0
			1349	862	243	242	2			
45	DZ	174	Total	C	N	O	S	0	0	0
			1360	870	243	245	2			

- Molecule 46 is a protein called 50S Ribosomal Protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	B0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			
46	D0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			

- Molecule 47 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	B1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			
47	D1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

- Molecule 48 is a protein called 50S Ribosomal Protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	B2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
48	D2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

- Molecule 49 is a protein called 50S Ribosomal Protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	B3	59	Total	C	N	O	0	0	0
			469	298	90	81			
49	D3	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 50 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B4	69	Total	C	N	O	S	0	0	0
			551	348	99	99	5			
50	D4	69	Total	C	N	O	S	0	0	0
			531	338	97	91	5			

- Molecule 51 is a protein called 50S Ribosomal Protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			
51	D5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 52 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	B6	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
52	D6	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 53 is a protein called 50S Ribosomal Protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	B7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
53	D7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 54 is a protein called 50S Ribosomal Protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	B8	64	Total	C	N	O	S	0	0	0
			511	328	99	82	2			
54	D8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 55 is a protein called 50S Ribosomal Protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	B9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
55	D9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	BA	739	Total	Mg	0	0
			739	739		
56	AK	1	Total	Mg	0	0
			1	1		
56	DQ	4	Total	Mg	0	0
			4	4		
56	D3	1	Total	Mg	0	0
			1	1		
56	DF	5	Total	Mg	0	0
			5	5		
56	B8	2	Total	Mg	0	0
			2	2		
56	BE	9	Total	Mg	0	0
			9	9		
56	DU	2	Total	Mg	0	0
			2	2		
56	B1	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	AN	1	Total 1	Mg 1	0	0
56	BP	4	Total 4	Mg 4	0	0
56	AX	9	Total 9	Mg 9	0	0
56	CN	1	Total 1	Mg 1	0	0
56	DN	1	Total 1	Mg 1	0	0
56	AS	1	Total 1	Mg 1	0	0
56	CA	172	Total 172	Mg 172	0	0
56	B5	1	Total 1	Mg 1	0	0
56	BB	18	Total 18	Mg 18	0	0
56	D8	1	Total 1	Mg 1	0	0
56	DG	1	Total 1	Mg 1	0	0
56	CF	1	Total 1	Mg 1	0	0
56	B9	1	Total 1	Mg 1	0	0
56	BF	6	Total 6	Mg 6	0	0
56	AV	1	Total 1	Mg 1	0	0
56	BX	2	Total 2	Mg 2	0	0
56	B2	1	Total 1	Mg 1	0	0
56	AA	222	Total 222	Mg 222	0	0
56	BQ	4	Total 4	Mg 4	0	0
56	CX	3	Total 3	Mg 3	0	0
56	DV	3	Total 3	Mg 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	AM	2	Total 2	Mg 2	0	0
56	BU	9	Total 9	Mg 9	0	0
56	DR	1	Total 1	Mg 1	0	0
56	AD	1	Total 1	Mg 1	0	0
56	BN	6	Total 6	Mg 6	0	0
56	CT	1	Total 1	Mg 1	0	0
56	BG	4	Total 4	Mg 4	0	0
56	DE	6	Total 6	Mg 6	0	0
56	B3	3	Total 3	Mg 3	0	0
56	BR	3	Total 3	Mg 3	0	0
56	DA	657	Total 657	Mg 657	0	0
56	DP	2	Total 2	Mg 2	0	0
56	DW	2	Total 2	Mg 2	0	0
56	B7	4	Total 4	Mg 4	0	0
56	AL	1	Total 1	Mg 1	0	0
56	BV	3	Total 3	Mg 3	0	0
56	DO	1	Total 1	Mg 1	0	0
56	BO	1	Total 1	Mg 1	0	0
56	BZ	1	Total 1	Mg 1	0	0
56	DY	1	Total 1	Mg 1	0	0
56	D5	2	Total 2	Mg 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	BD	12	Total	Mg	0	0
			12	12		
56	B0	6	Total	Mg	0	0
			6	6		
56	CE	2	Total	Mg	0	0
			2	2		
56	BW	5	Total	Mg	0	0
			5	5		
56	DD	5	Total	Mg	0	0
			5	5		
56	AF	1	Total	Mg	0	0
			1	1		
56	DB	12	Total	Mg	0	0
			12	12		

- Molecule 57 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).

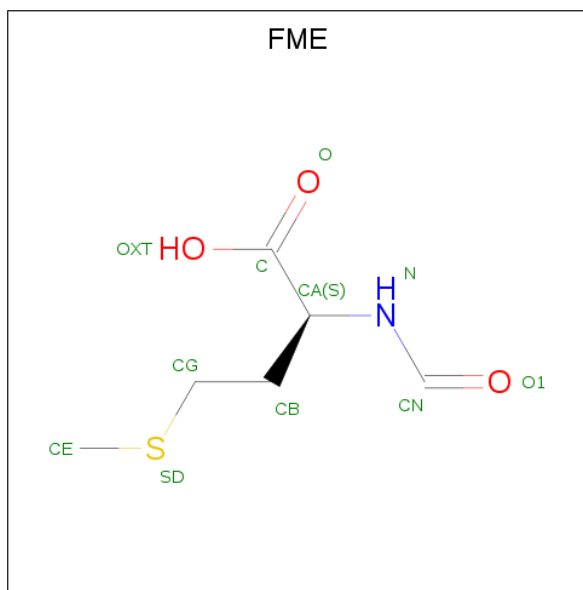


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
57	AD	1	Total	Fe	S	0	0
			8	4	4		
57	CD	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	B5	1	Total Zn 1 1	0	0
58	B4	1	Total Zn 1 1	0	0
58	CN	1	Total Zn 1 1	0	0
58	BY	1	Total Zn 1 1	0	0
58	B9	1	Total Zn 1 1	0	0
58	DY	1	Total Zn 1 1	0	0
58	D5	1	Total Zn 1 1	0	0
58	D4	1	Total Zn 1 1	0	0
58	AN	1	Total Zn 1 1	0	0
58	D6	1	Total Zn 1 1	0	0
58	D9	1	Total Zn 1 1	0	0
58	B6	1	Total Zn 1 1	0	0

- Molecule 59 is N-FORMYLMETHIONINE (three-letter code: FME) (formula: $C_6H_{11}NO_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
59	AX	1	Total	C	N	O	S	0	0
			10	6	1	2	1		
59	CX	1	Total	C	N	O	S	0	0
			10	6	1	2	1		

- Molecule 60 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	BA	1	Total	K	0	0
			1	1		
60	DA	1	Total	K	0	0
			1	1		

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	AA	147	Total	O	0	0
			147	147		
61	AD	1	Total	O	0	0
			1	1		
61	AE	2	Total	O	0	0
			2	2		
61	AJ	1	Total	O	0	0
			1	1		
61	AL	2	Total	O	0	0
			2	2		
61	AO	2	Total	O	0	0
			2	2		
61	AU	1	Total	O	0	0
			1	1		
61	AV	2	Total	O	0	0
			2	2		
61	AX	1	Total	O	0	0
			1	1		
61	BA	1086	Total	O	0	0
			1086	1086		
61	BB	26	Total	O	0	0
			26	26		
61	BD	6	Total	O	0	0
			6	6		
61	BE	13	Total	O	0	0
			13	13		
61	BF	5	Total	O	0	0
			5	5		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	BG	1	Total 1	O 1	0	0
61	BN	3	Total 3	O 3	0	0
61	BO	2	Total 2	O 2	0	0
61	BP	15	Total 15	O 15	0	0
61	BQ	3	Total 3	O 3	0	0
61	BR	1	Total 1	O 1	0	0
61	BT	2	Total 2	O 2	0	0
61	BU	5	Total 5	O 5	0	0
61	BV	2	Total 2	O 2	0	0
61	BW	4	Total 4	O 4	0	0
61	BX	4	Total 4	O 4	0	0
61	B0	4	Total 4	O 4	0	0
61	B1	2	Total 2	O 2	0	0
61	B5	2	Total 2	O 2	0	0
61	B7	1	Total 1	O 1	0	0
61	B8	7	Total 7	O 7	0	0
61	CA	186	Total 186	O 186	0	0
61	CE	2	Total 2	O 2	0	0
61	CN	1	Total 1	O 1	0	0
61	CT	1	Total 1	O 1	0	0
61	CX	2	Total 2	O 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	DA	906	Total 906	O 906	0	0
61	DB	7	Total 7	O 7	0	0
61	DD	10	Total 10	O 10	0	0
61	DE	11	Total 11	O 11	0	0
61	DF	4	Total 4	O 4	0	0
61	DO	1	Total 1	O 1	0	0
61	DP	14	Total 14	O 14	0	0
61	DQ	3	Total 3	O 3	0	0
61	DR	1	Total 1	O 1	0	0
61	DU	4	Total 4	O 4	0	0
61	DV	1	Total 1	O 1	0	0
61	DX	2	Total 2	O 2	0	0
61	DY	1	Total 1	O 1	0	0
61	D0	3	Total 3	O 3	0	0
61	D1	1	Total 1	O 1	0	0
61	D3	1	Total 1	O 1	0	0
61	D7	1	Total 1	O 1	0	0
61	D8	4	Total 4	O 4	0	0



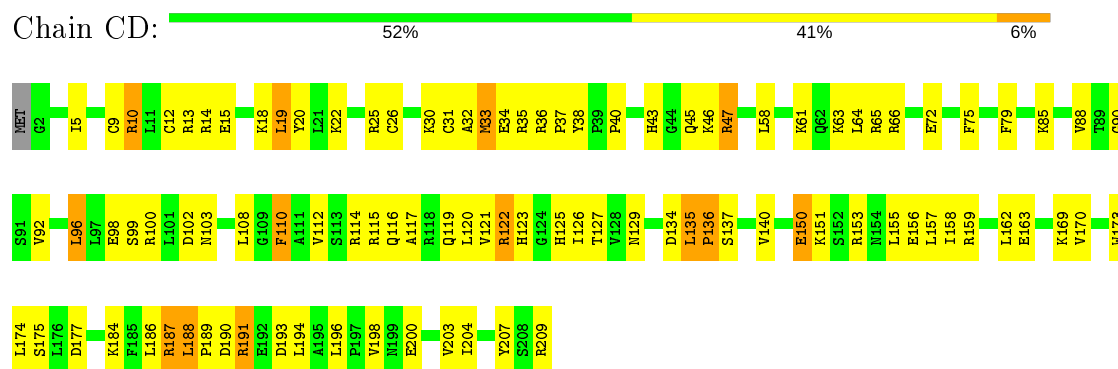
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Very often	2%
Often	32%
Sometimes	43%
Never	20%



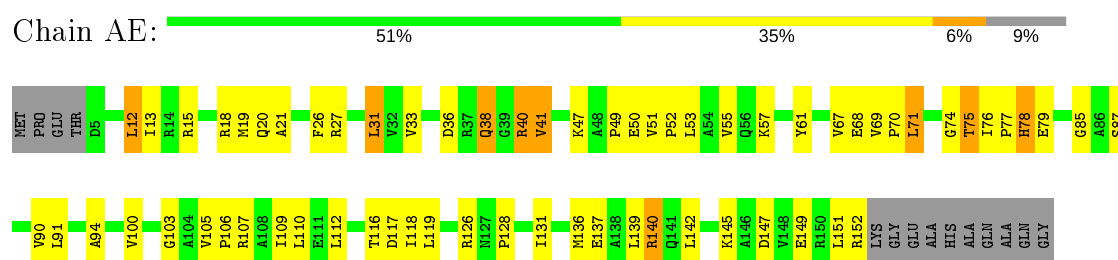




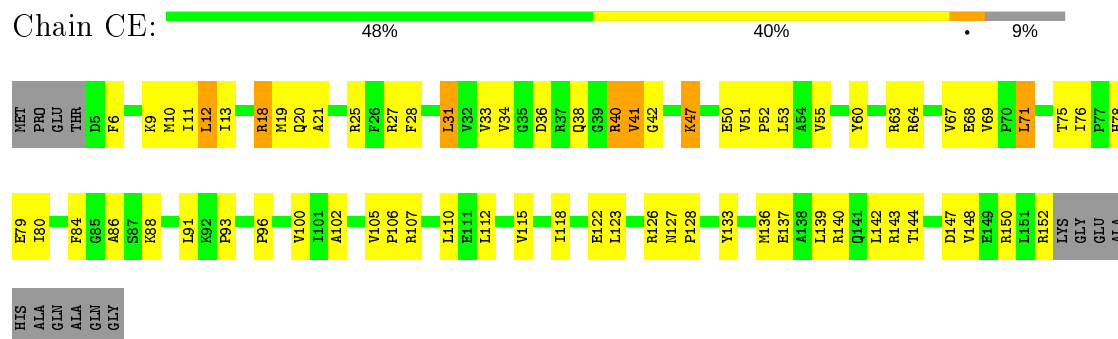
- Molecule 4: 30S Ribosomal Protein S4



- Molecule 5: 30S Ribosomal Protein S5

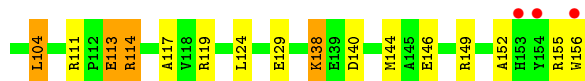


- Molecule 5: 30S Ribosomal Protein S5

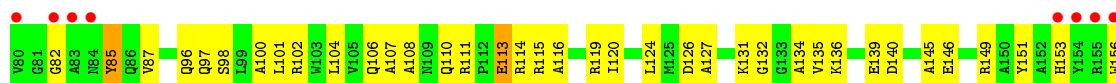




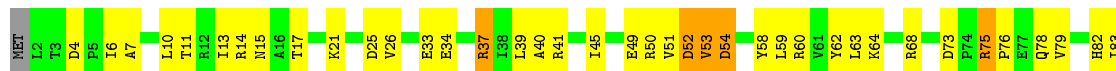
• Molecule 7: 30S Ribosomal Protein S7



• Molecule 7: 30S Ribosomal Protein S7



• Molecule 8: 30S Ribosomal Protein S8

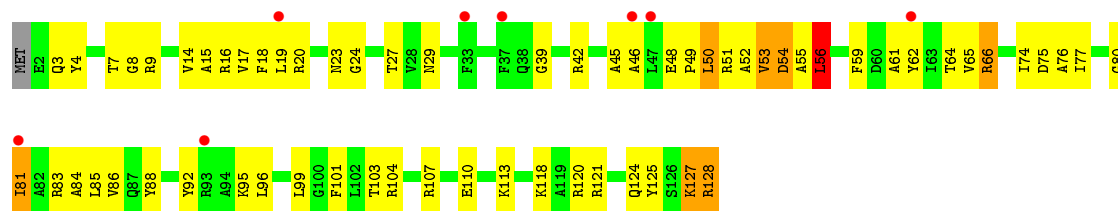


• Molecule 8: 30S Ribosomal Protein S8

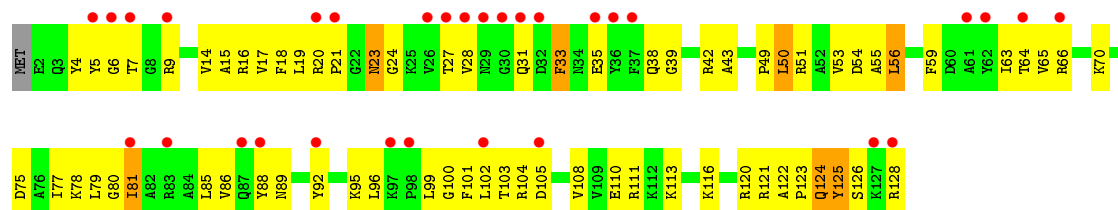


• Molecule 9: 30S Ribosomal Protein S9

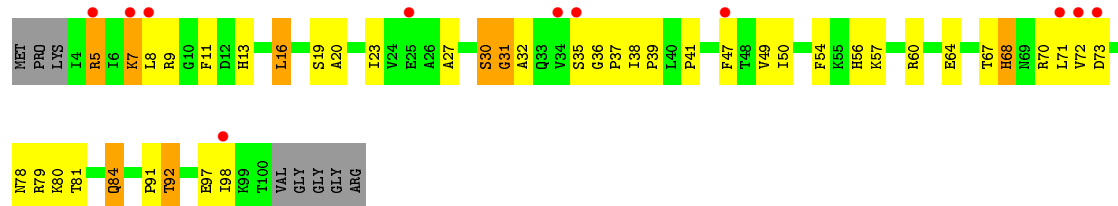




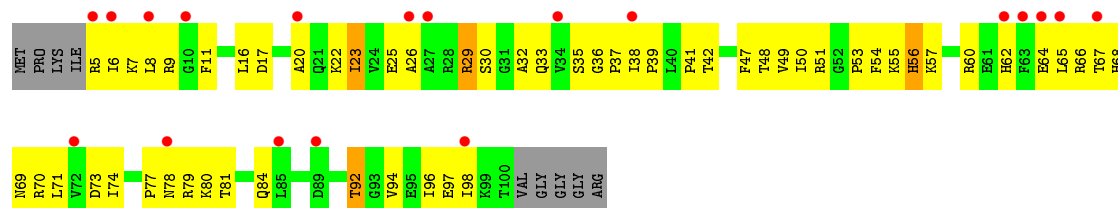
• Molecule 9: 30S Ribosomal Protein S9



• Molecule 10: 30S Ribosomal Protein S10



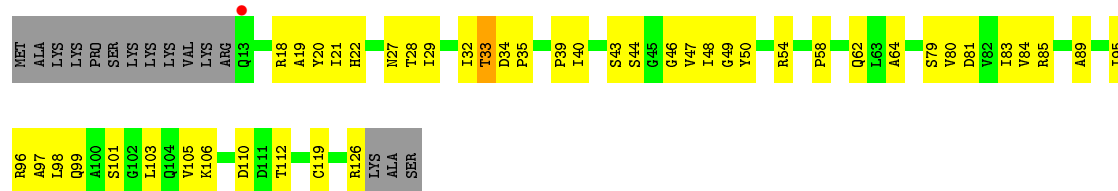
• Molecule 10: 30S Ribosomal Protein S10



• Molecule 11: 30S Ribosomal Protein S11



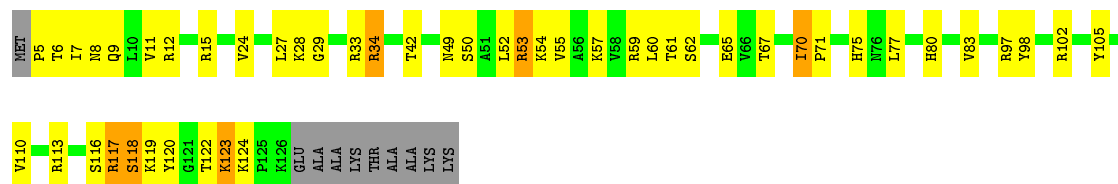
• Molecule 11: 30S Ribosomal Protein S11



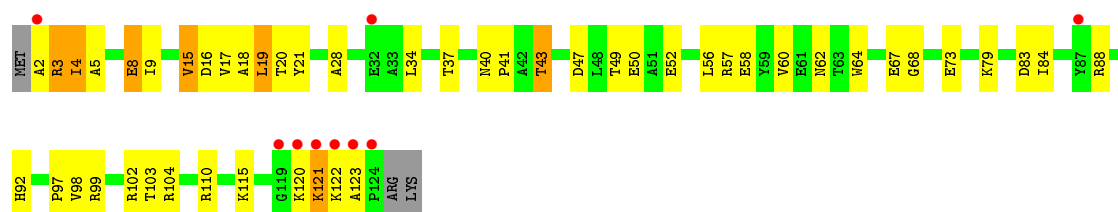
• Molecule 12: 30S Ribosomal Protein S12



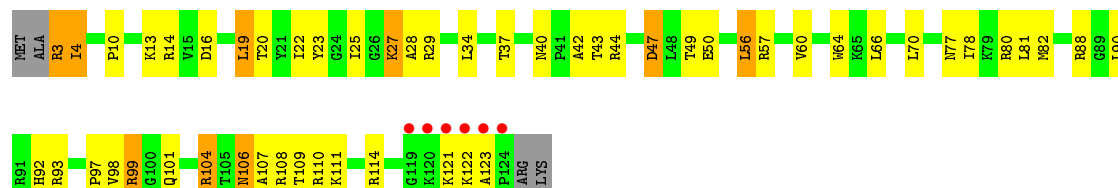
• Molecule 12: 30S Ribosomal Protein S12



• Molecule 13: 30S Ribosomal Protein S13



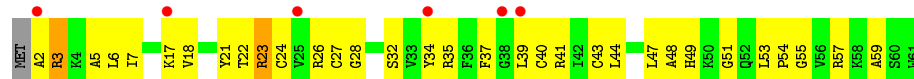
• Molecule 13: 30S Ribosomal Protein S13



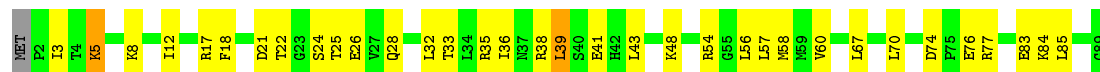
- Molecule 14: 30S Ribosomal Protein S14



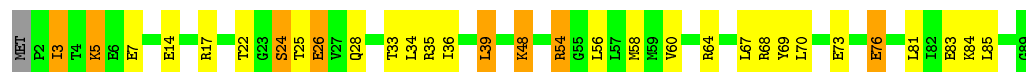
- Molecule 14: 30S Ribosomal Protein S14



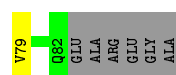
- Molecule 15: 30S Ribosomal Protein S15



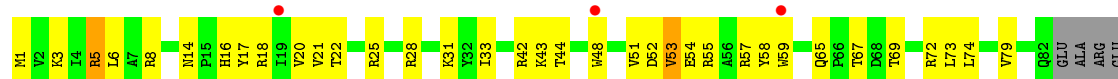
- Molecule 15: 30S Ribosomal Protein S15



- Molecule 16: 30S Ribosomal Protein S16

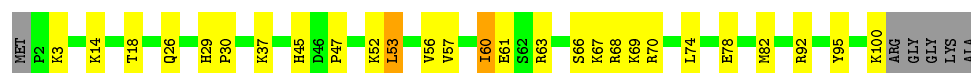


- Molecule 16: 30S Ribosomal Protein S16



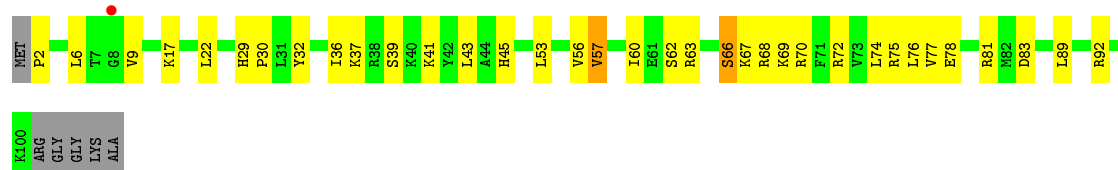
- Molecule 17: 30S Ribosomal Protein S17

Chain AQ:  69% 24% 6%



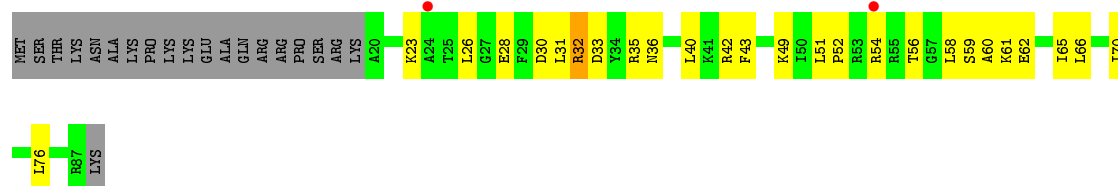
• Molecule 17: 30S Ribosomal Protein S17

Chain CQ:  61% 31% 6%



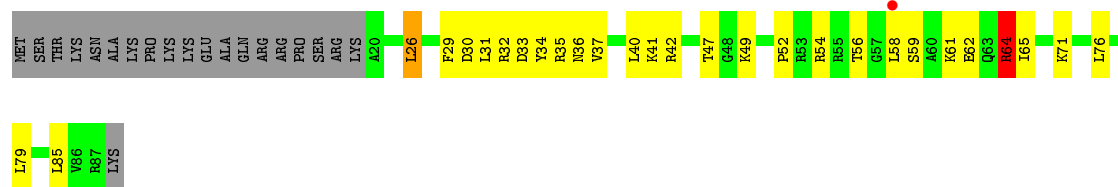
• Molecule 18: 30S Ribosomal Protein S18

Chain AR:  48% 28% 23%



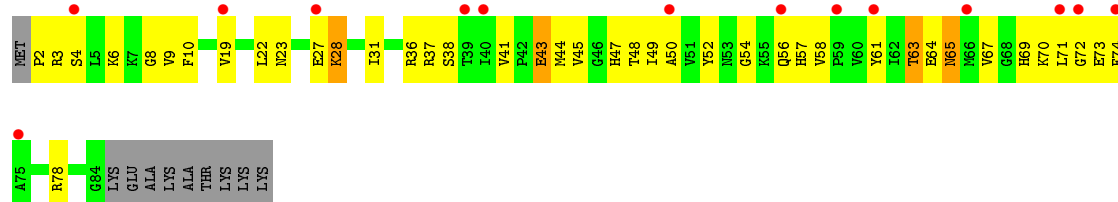
• Molecule 18: 30S Ribosomal Protein S18

Chain CR:  45% 30% 23%



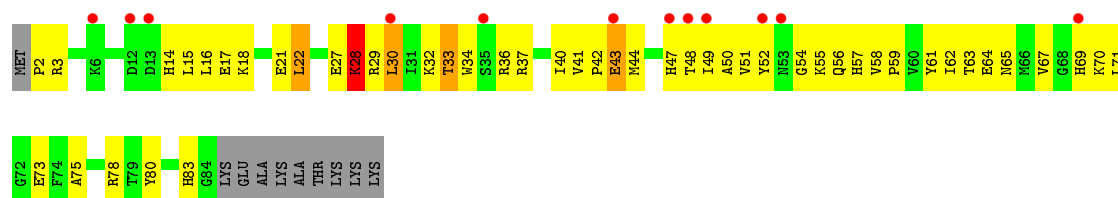
• Molecule 19: 30S Ribosomal Protein S19

Chain AS:  45% 40% 11%

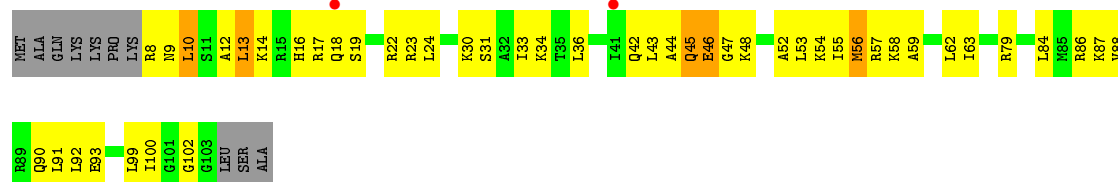


• Molecule 19: 30S Ribosomal Protein S19

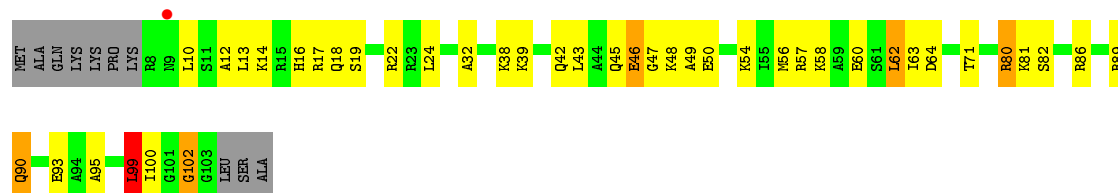
Chain CS:  37% 47% 11%



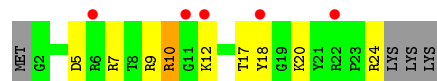
- Molecule 20: 30S Ribosomal Protein S20



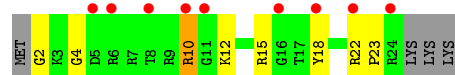
- Molecule 20: 30S Ribosomal Protein S20



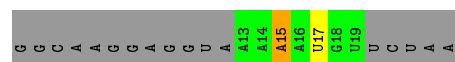
- Molecule 21: 30S Ribosomal Protein THX



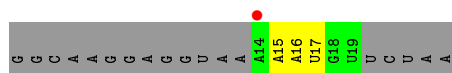
- Molecule 21: 30S Ribosomal Protein THX



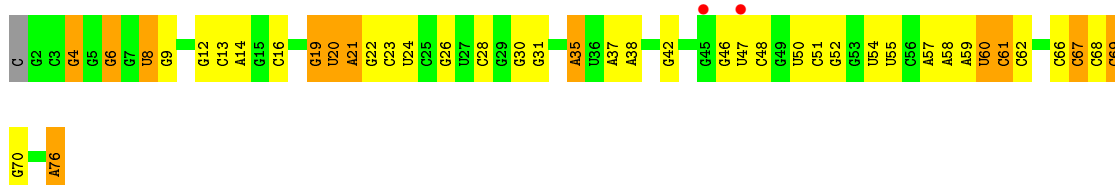
- Molecule 22: mRNA



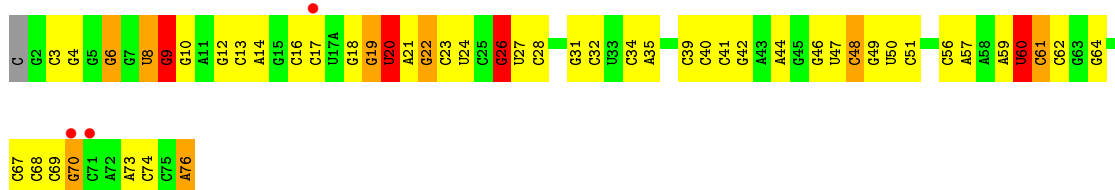
- Molecule 22: mRNA



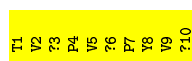
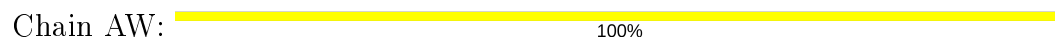
- Molecule 23: P-site tRNA



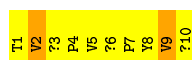
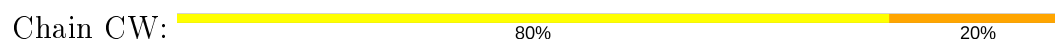
- Molecule 23: P-site tRNA



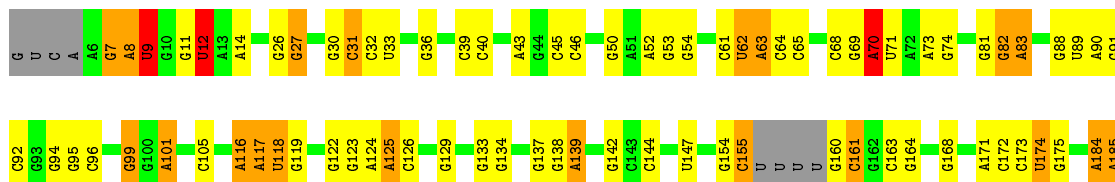
- Molecule 24: Dityromycin



- Molecule 24: Dityromycin

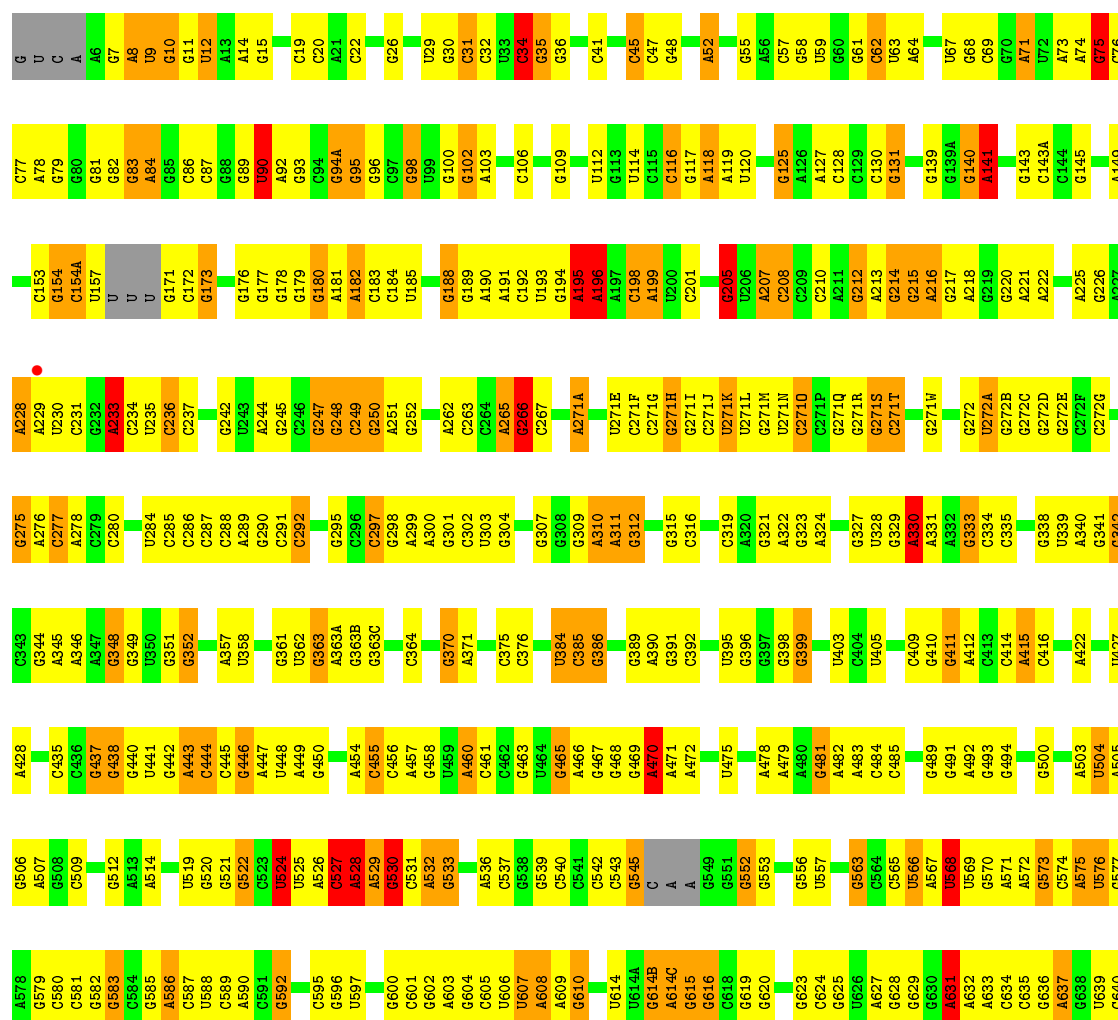


- Molecule 25: 23S Ribosomal RNA



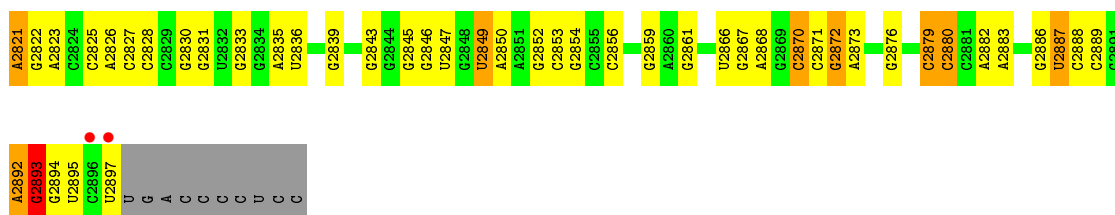






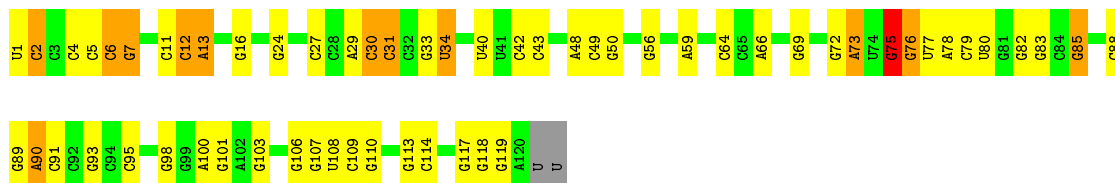
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A1614	G1539	C1468	A1393	G1319	U	G	C982	G916	G855	G776	C687	G642
C1615	U1540	A1469	U1394	U1248	G	U	A983	A917	C856	A777	C688	A643
A1616	G1541	C1320	A	C	C	C	A984	A918	C857	A778	U688	A644
C1617	A1542	U1396	U1397	G1250	G	G	C985	G919	U858	A782	C692	C845
A1644	C1543	A1471	U1398	G1251	A	A	C986	G920	G859	A783	G693	A646
G1622	A1545	C1324	C1398	G1252	C	C	C987	G921	U860	A784	G647	G647
G1630	C1546	G1327	C1399	A1253	C	C	A990	G922	A861	G785	G698	G648
C1631	A1554	C1328	C1403	A1254	A	A	C991	U923	G862	C923	G699	C650
A1631A	A1477	G1329	G1256	G1183	G	G	C994	A926	A863	A788	A704	A652B
A1632	G1478	U1405	C1404	G1186	A	A	C995	G927	G864	A789	G705	A652C
G1633	G1479	U1406	U1390	G1187	G	G	C996	G928	A866	C790	C708	G652D
A1634	C1482	C1407	U1382	C1119	G	G	A996	G932	C867	G792	U709	G652E
G1635	G1483	C1408	G1332	G1120	U	U	C997	G933	U868	A793	G710	G
G1636	A1486	C1409	C1333	C1121	U	U	C998	G934	G869	G794	G717	G
C1637	G1487	G1410	G1334	G1122	G	G	U999	G935	A870	C795	A718	C
C1638	U1488	C1411	U1335	G1123	G	G	C1000	G936	U871	C796	A719	C
U1639	U1489	A1412	A1336	G1124	C	C	C1005	U937	A872	C797	C720	C
C1640	A1490	G1413	G1337	G1125	U	U	C1006	G938	G873	G798	C726	G
G1643	C1493	G1416	G1338	G1126	U	U	C1007	G939	G874	G799	G723	C
C1644	A1494	U1417	U1339	A1129	A	A	C1008	G940	C875	A800	U724	C
G1645	A1495	G1418	U1340	U1198	G	G	C1009	G941	C876	G801	G725	G
G1646	A1496	A1419	A1269	C1200	A	A	A1010	U942	U877	A802	G726	C
G1647	U1497	U1420	C1201	G1270	A	A	A1011	U943	A878	G805	G726	G
C1648	G1498	G1421	A1204	G1271	G	G	G1012	G944	G879	C806	G730	C
G1651	U1503	G1425	U1272	U1273	C	C	C1013	A945	G880	C807	C731	C
U1503	C1504	G1426	U1274	U1275	G	G	C1014	G946	G881	U807	C732	C
A1504	G1505	A1427	A1276	A1277	G	G	C1015	G947	G882	G732	G733	C
C1505	C1506	C1428	A1278	A1279	C	C	C1016	G948	G883	G733	A734	C
A1507	G1507	G1429	G1281	G1282	A	A	C1017	G949	C884	G734	A735	C
C1508	A1508	U1430	U1281	U1282	U	U	C1018	G950	C885	A735	A736	C
C1509	C1509	U1431	G1283	G1284	C	C	C1019	G951	C886	C812	C736	C
A1509A	C1509B	C1432	A1284	A1285	U	U	C1020	G952	A887	C814	C737	C
U1509B	A1509C	U1433	G1286	G1287	U	U	A1021	G953	C888	C815	A655	C
C1510	G1511	A1434	A1288	A1289	U	U	C1022	G954	C889	C816	G738	C
U1511	U1514	G1435	U1290	U1291	U	U	G1023	G955	A890	C817	U740	C
C1516	G1515	C1436	C1364	C1365	A	A	U1024	G956	G892	G818	C657	C
G1517	C1445A	C1437	A1365	A1366	U	U	G1025	C961	C893	A819	C658	C
C1517	C1446	A1445	A1367	A1368	G	G	U1026	C962	U895	A824	C661	C
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G1526	A1449	G1450	U1371	U1372	G	G	U1028	C964	U897	U826	G663	C
G1527	A1528	G1451	U1372	U1373	U	U	A1029	C965	C898	U827	G664	C
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U1602	C1530	G1459	A1379	C1305	C	C	G1031	C967	A900	A829	G666	C
A1603	C1531	A1460	G1380	G1309	U	U	A1032	C968	C901	G830	U667	C
C1604	G1532	G1461	U1384	G1310	G	G	U1033	C969	C902	G831	G668	C
U	G1533	C1462	A1384	G1311	C	C	G1034	C970	C903	C837	G669	C
A	U	C1463	G1385	G1312	U	U	U1035	C971	C904	U905	A670	C
C1607	C1536	G1464	U1387	U1312	C	C	G1036	C972	U906	C838	A671	C
A1608	G1537	G1465	C1387	G1171	A	A	U1037	C973	G907	U839	U762	C
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				G	U	U	G1039	C975	C908	C941	A765	C
							C1040	C976	U909	U947	G765	C
							U1041	C977	A910	G848	C678	C
							G1042	C978	A911	G849	C679	C
							C1043	C979	A912	G850	G680	C
							G	C979A	U913	G852	C683	C
							A	C979B	U914	G853	A774	C

A2749	U2687	G2455	G2382	G2314	C2248	U	G	C2032	G1959	U1851	C1781	A1689
A2750	U2688	G2461	G2383	G2315	U2249	G	C	A2033	A1960	C1852	C1782	U1692
G2751	G2689	U2462	G2384	G2316	G2250	A	U	U2034	U1963	G1857	A1783	U1693
G2752	U2609	U2463	G2385	G2317	G2251	A	U	G	U1964	G1858	A1784	G1696
G2755	G2692	C2611	G2386	G2318	G2252	U	C	G2037	C1965	A1859	A1785	G1697
A2693	C2612	C2464	G2387	G2319	G2253	A	U	G2038	C1966	G1860	A1786	A1698
A2694	G2613	G2468	C2388	A2320	G2254	A	U	G2039	A1967	G1861	A1787	G1700
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C2628	C2628	C2475	G2396	G2330	U2262	G	C	G2046	G1973	C1886	U1796	U1709
A2629	A2629	A2476	G2397	G2331	U2263	G	U	G2047	C1974	G1887	C1797	C1710
G2630	G2630	C2477	U2398	G2332	U2265	C	G	G2048	G1975	A1889	U1798	C1711
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G2708	G2708	C2483	U2401	A2335	A2268	C	A	A2051	G1983	G1895	G1801	G1717
G2709	G2709	G2487	C2402	A2336	G2271	G	C	G2052	G1984	G1899	G1802	G1718
A2710	A2710	A2488	G2403	G2337	U2272	U	C	C2055	G1985	A1900	A1803	G1721
A2711	A2711	A2488	C2404	G2338	U2273	U	C	G2056	A1986	G1903	A1804	U1739
A2712	A2712	G2489	G2339	G2339	A2274	G	U	A2059	U1981	G1904	U1805	G1740
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G2718	G2718	C2496	G2411	A2346	C2282	C	C	A2071	C1999	A1915	A1816	
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G2747	G2747	G2538	A2452	A2379	U2247	C	C	G	U2033	C1963	G1854	
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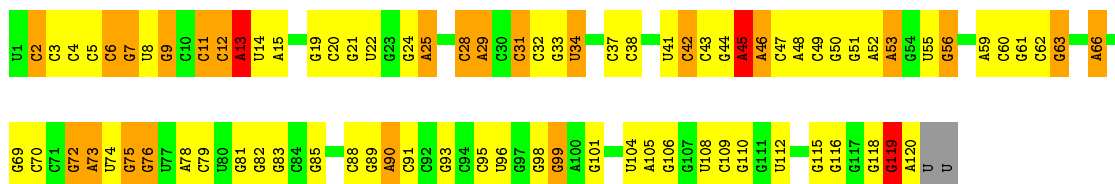
• Molecule 26: 5S Ribosomal RNA

Chain BB: 50% 38% 10% ..



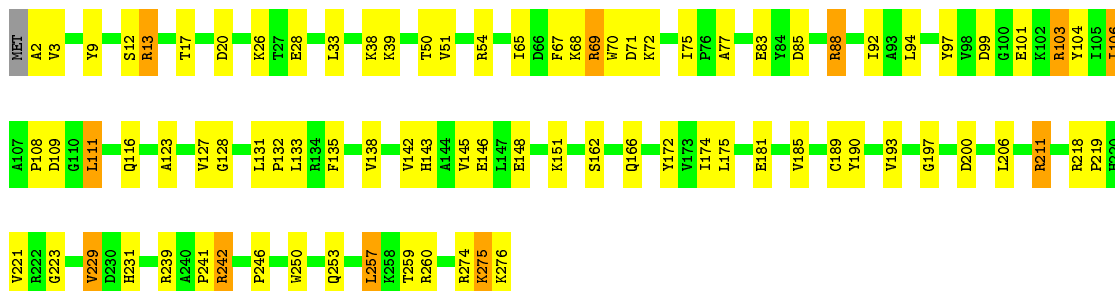
• Molecule 26: 5S Ribosomal RNA

Chain DB: 30% 47% 19% ..



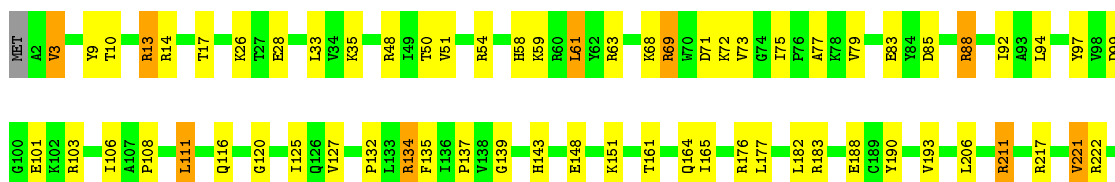
• Molecule 27: 50S Ribosomal Protein L2

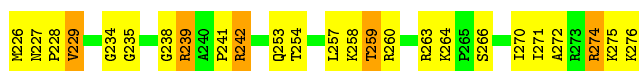
Chain BD: 69% 27% ..



• Molecule 27: 50S Ribosomal Protein L2

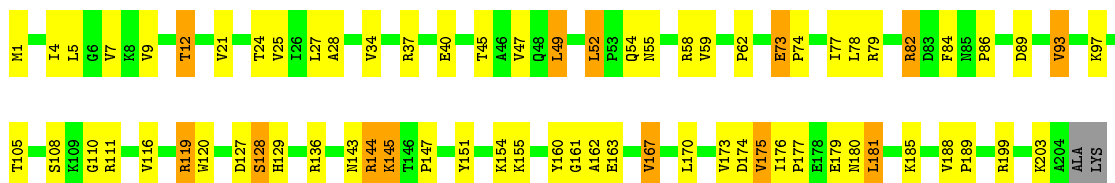
Chain DD: 67% 28% 5%





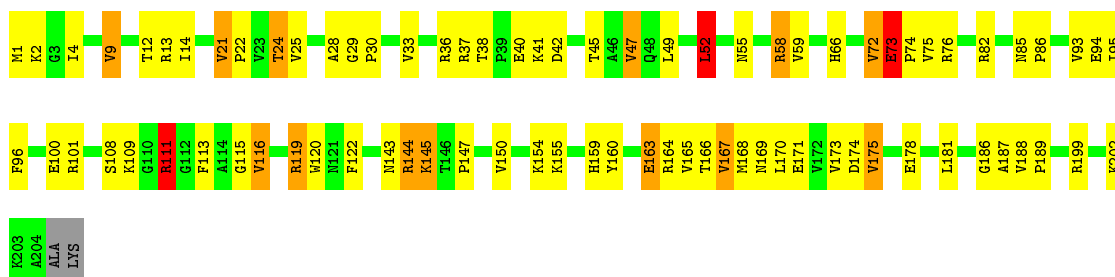
• Molecule 28: 50S Ribosomal Protein L3

Chain BE: 65% 28% 6% .



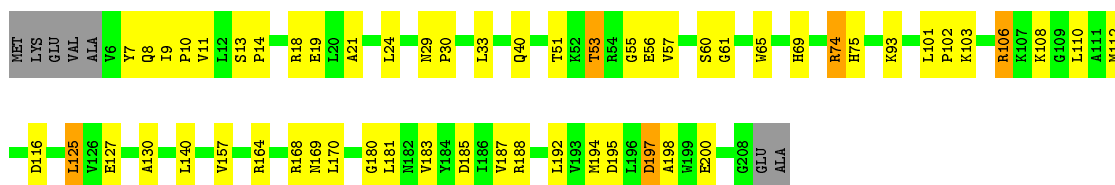
• Molecule 28: 50S Ribosomal Protein L3

Chain DE: 60% 32% 6% ..



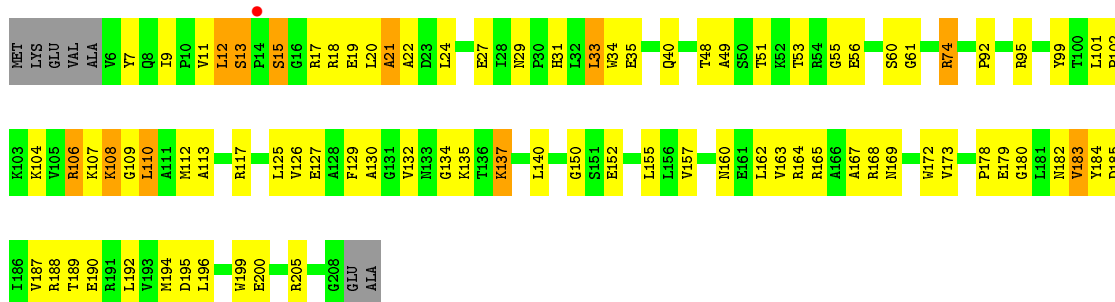
• Molecule 29: 50S Ribosomal Protein L4

Chain BF: 70% 24% . .

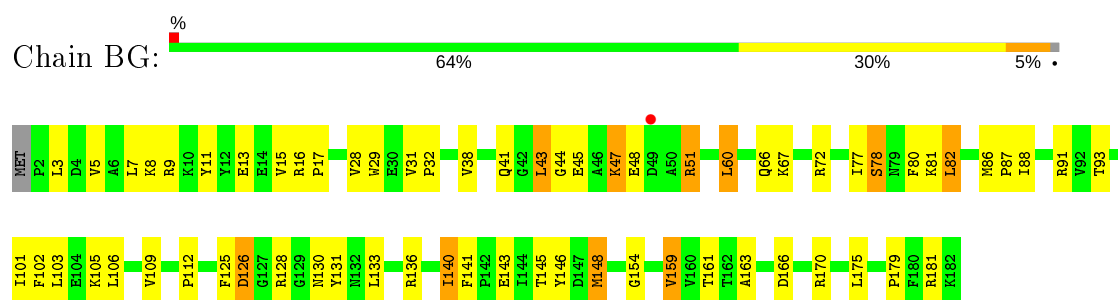


• Molecule 29: 50S Ribosomal Protein L4

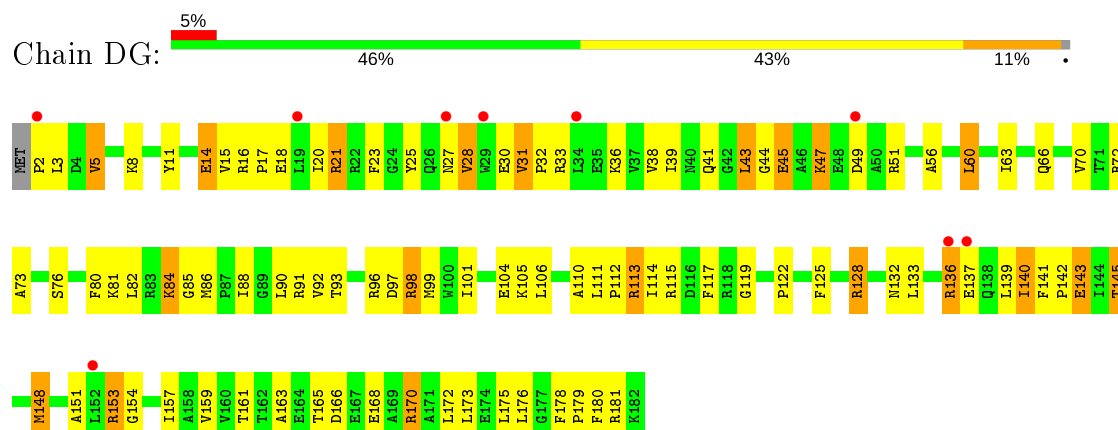
Chain DF: 56% 35% 5% .



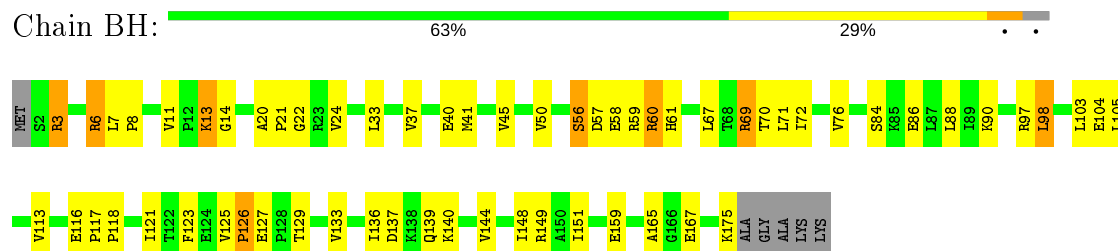
• Molecule 30: 50S Ribosomal Protein L5



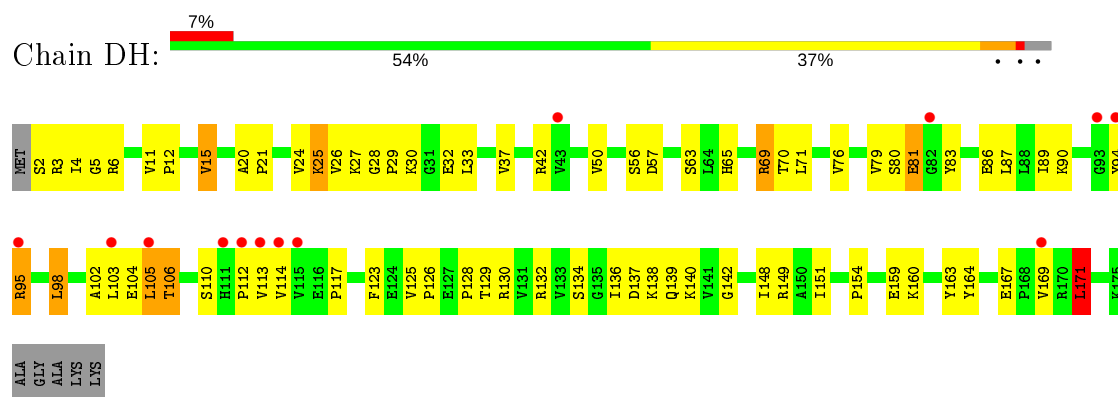
• Molecule 30: 50S Ribosomal Protein L5



• Molecule 31: 50S Ribosomal Protein L6

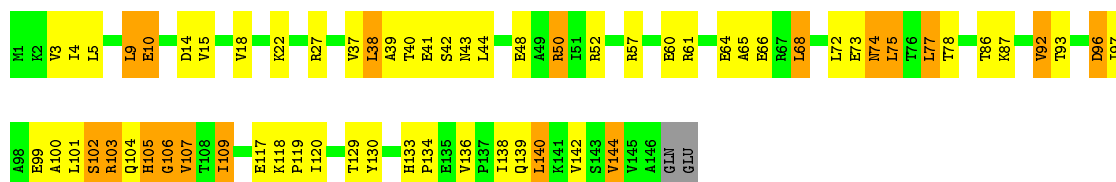


• Molecule 31: 50S Ribosomal Protein L6

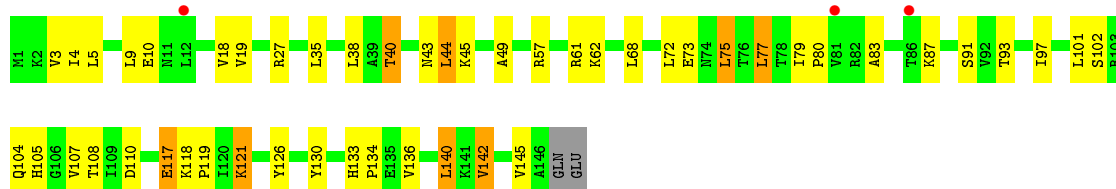


• Molecule 32: 50S Ribosomal Protein L9

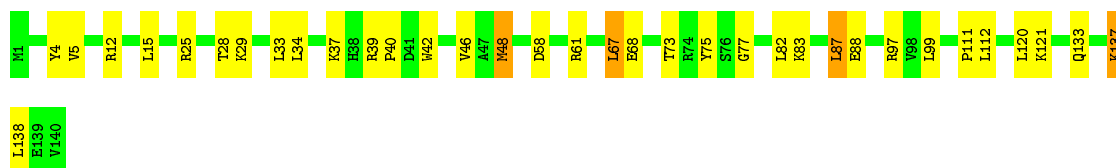
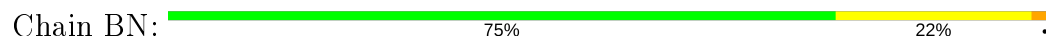




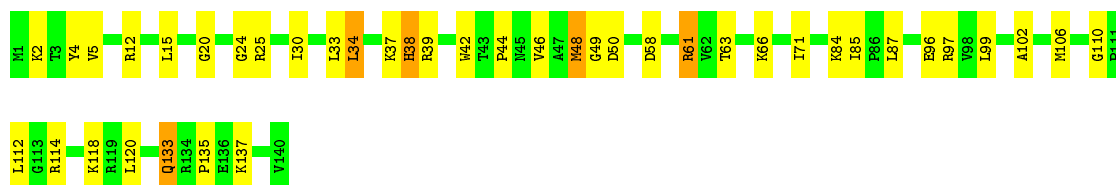
- Molecule 32: 50S Ribosomal Protein L9



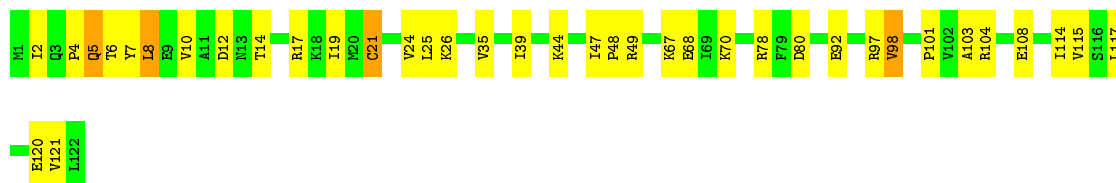
- Molecule 33: 50S Ribosomal Protein L13



- Molecule 33: 50S Ribosomal Protein L13



- Molecule 34: 50S Ribosomal Protein L14



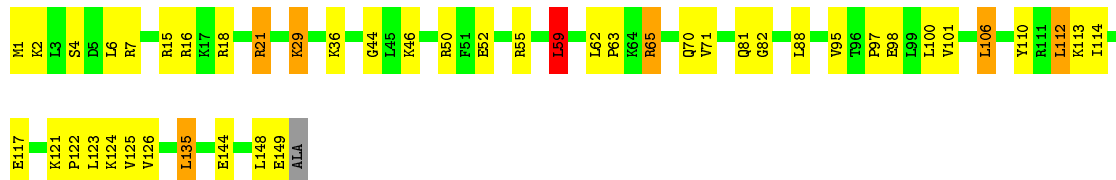
- Molecule 34: 50S Ribosomal Protein L14





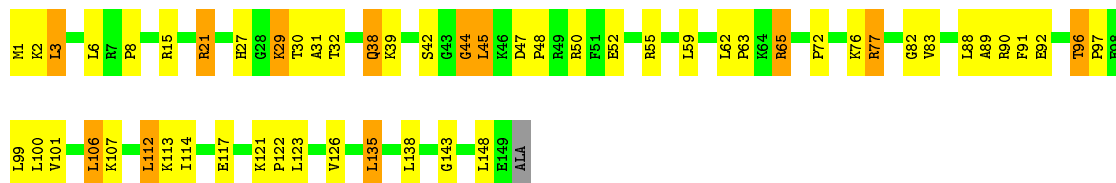
• Molecule 35: 50S Ribosomal Protein L15

Chain BP: 69% 26%



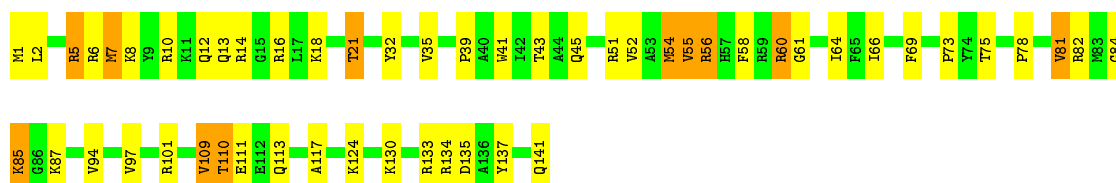
• Molecule 35: 50S Ribosomal Protein L15

Chain DP: 63% 29% 8%



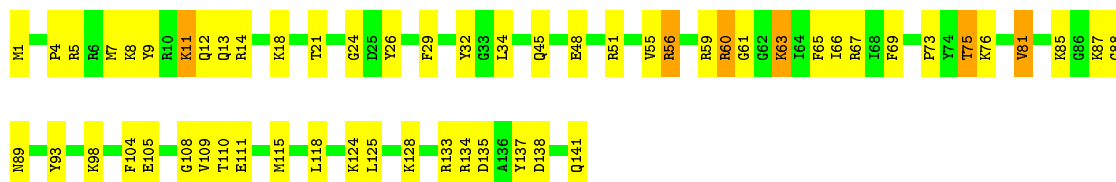
• Molecule 36: 50S Ribosomal Protein L16

Chain BQ: 62% 30% 8%



• Molecule 36: 50S Ribosomal Protein L16

Chain DQ: 60% 36%



• Molecule 37: 50S Ribosomal Protein L17

Chain BR: 68% 21% 11%



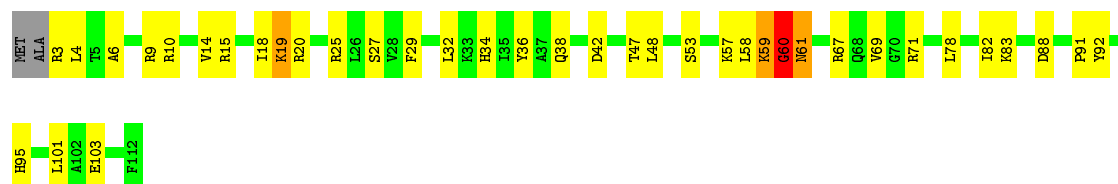
- Molecule 37: 50S Ribosomal Protein L17

Chain DR: 61% 33% 6%



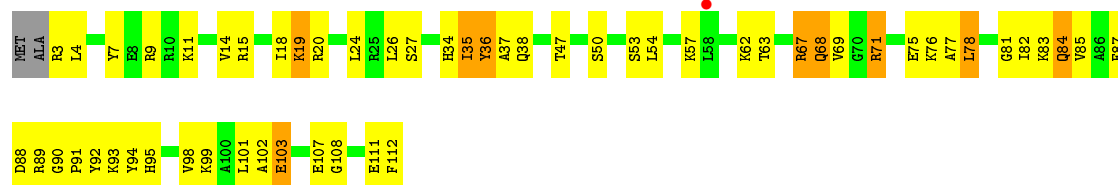
- Molecule 38: 50S Ribosomal Protein L18

Chain BS: 64% 30% 6%



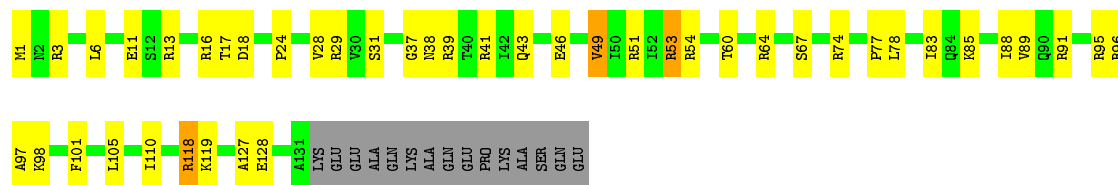
- Molecule 38: 50S Ribosomal Protein L18

Chain DS: 48% 42% 8%



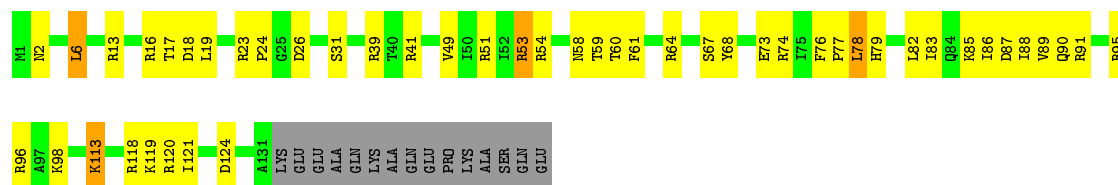
- Molecule 39: 50S Ribosomal Protein L19

Chain BT: 60% 28% 10%



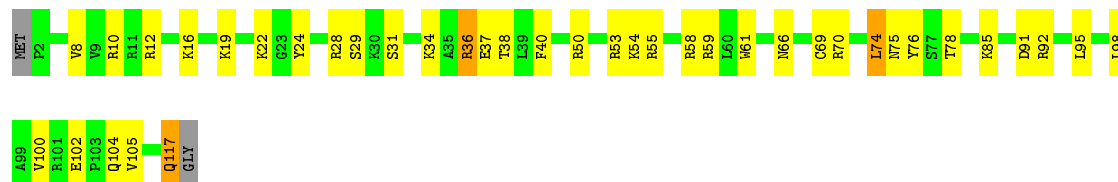
- Molecule 39: 50S Ribosomal Protein L19

Chain DT: 57% 30% 10%



- Molecule 40: 50S Ribosomal Protein L20

Chain BU: 65% 31% . .



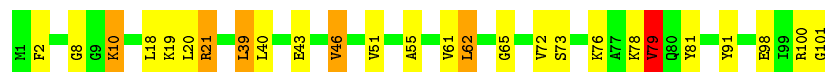
- Molecule 40: 50S Ribosomal Protein L20

Chain DU: 67% 25% 6% .



- Molecule 41: 50S Ribosomal Protein L21

Chain BV: 74% 20% 5% .



- Molecule 41: 50S Ribosomal Protein L21

Chain DV: 65% 30% . .



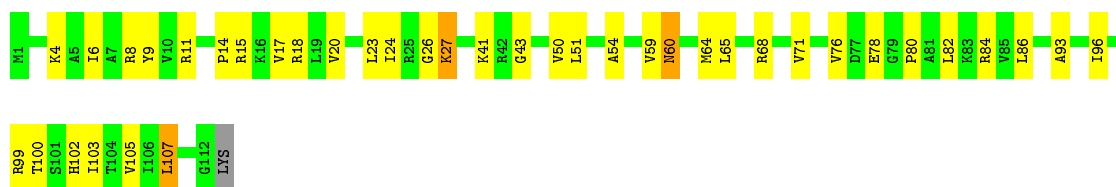
- Molecule 42: 50S Ribosomal Protein L22

Chain BW: 77% 19% . .



- Molecule 42: 50S Ribosomal Protein L22

Chain DW:  65% 32% ..




- Molecule 43: 50S Ribosomal Protein L23

Chain BX:  72% 26% ..



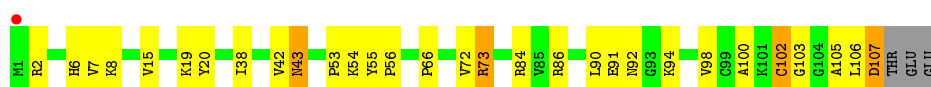
- Molecule 43: 50S Ribosomal Protein L23

Chain DX:  72% 22% ..



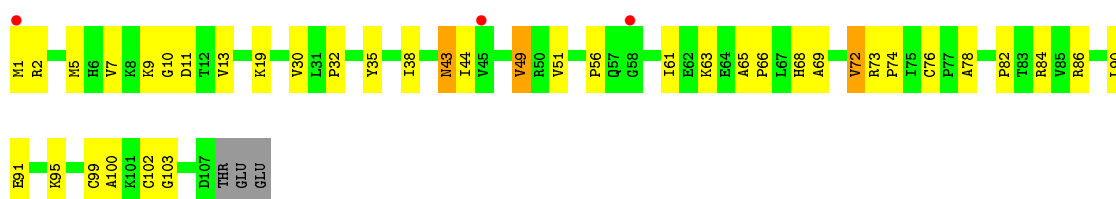
- Molecule 44: 50S Ribosomal Protein L24

Chain BY:  70% 24% ..



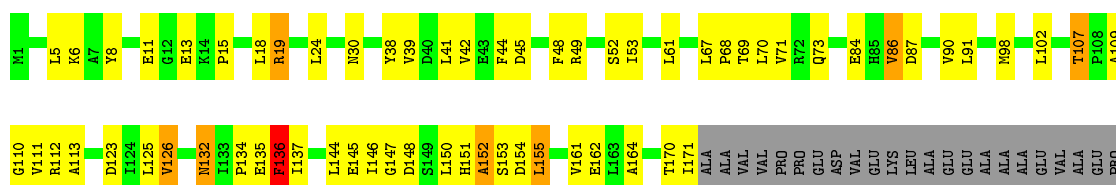
- Molecule 44: 50S Ribosomal Protein L24

Chain DY:  62% 33% ..



- Molecule 45: 50S Ribosomal Protein L25

Chain BZ:  52% 27% 17%



GLU
VAL
ILE
LYS
LYS
GLY
LYS
GLU
GLU
GLU
GLU


• Molecule 45: 50S Ribosomal Protein L25

Chain DZ:  44% 36% 16%

H1 L5 K6 A7 Y8 E11 G12 E13 K14 P15 R19 V27 M28 Y29 K30 R31 R32 L33 R34 R35 Y38 Y39 E43 F44 D45 K46 V47 F48 R49 S52 I53 H54 L61 P62 D63 Q64 Q65 S66 L67 T69 L70 W71 R72 N75 E84 R85 R86 D87 F88

F89 V90 L91 S92 D93 E94 P95 F96 E97 M98 Y99 P100 P101 T107 P108 V111 V116 L117 Q118 L119 E120 I121 R122 D123 L125 V128 S129 P130 R131 M132 I133 F136 D140 V141 S142 G143 L144 E145 I146 S153 D154 L155 K156 L157 G160 V161 E162 L163 A164 V165

• Molecule 46: 50S Ribosomal Protein L27

Chain B0:  8% 73% 19% 6%

MET A2 R3 K4 K5 G6 L7 G8 S9 T10 R11 M12 G13 R14 K19 R20 K24 R25 E27 R39 T43 M53 G54 R55 L59 E68 F69 G73 R82 P83 L84 ALA

• Molecule 46: 50S Ribosomal Protein L27

Chain D0:  6% 60% 32% 6%

MET A2 R3 K4 K5 G6 L7 G8 S9 T10 R11 M12 G13 R14 E15 Q17 S16 A18 K19 R20 V23 K24 R25 E27 G28 Q29 V31 G34 R35 L36 L37 V38 R39 Q40 R41 G42 T43 M53 G54 R55 D56 F57 T58 L59 F60 A61 E68 F69 R82 P83 L84 ALA

• Molecule 47: 50S Ribosomal Protein L28

Chain B1:  % 67% 27% 6%

MET S2 K3 R21 G22 K23 R26 G29 V30 K33 T34 T35 R40 L46 R50 V51 R52 T59 F60 A64 S65 H66 I67 Y71 E72 L73 V74 E75 R76 A77 L80 E89 I94 L95 K96 L97 L98

• Molecule 47: 50S Ribosomal Protein L28

Chain D1:  % 64% 29% 6%

MET S2 K3 V4 C5 E6 I7 S8 R11 R21 G22 K23 R26 G29 K32 T35 K39 R40 R41 V51 R52 G55 T59 F60 R61 S65 H66 Y71 R76 A77 L80 E83 G84 E89 L94 L95 K96 L97 L98

• Molecule 48: 50S Ribosomal Protein L29

Chain B2:  65% 26% 6%



• Molecule 48: 50S Ribosomal Protein L29



• Molecule 49: 50S Ribosomal Protein L30



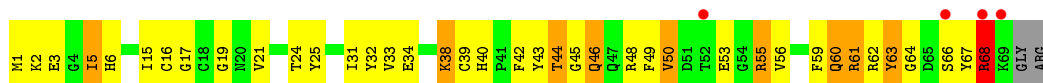
• Molecule 49: 50S Ribosomal Protein L30



• Molecule 50: 50S Ribosomal Protein L31



• Molecule 50: 50S Ribosomal Protein L31



• Molecule 51: 50S Ribosomal Protein L32



• Molecule 51: 50S Ribosomal Protein L32





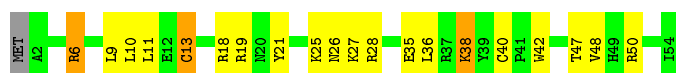
- Molecule 52: 50S Ribosomal Protein L33

Chain B6: 67% 26% 6% .



- Molecule 52: 50S Ribosomal Protein L33

Chain D6: 61% 31% 6% .



- Molecule 53: 50S Ribosomal Protein L34

Chain B7: 76% 20% . .



- Molecule 53: 50S Ribosomal Protein L34

Chain D7: 2% 67% 31% .



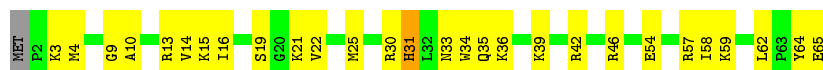
- Molecule 54: 50S Ribosomal Protein L35

Chain B8: 55% 42% . .



- Molecule 54: 50S Ribosomal Protein L35

Chain D8: 55% 42% . .

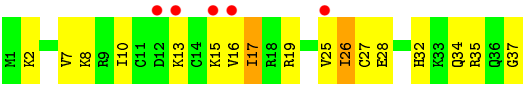


- Molecule 55: 50S Ribosomal Protein L36

Chain B9: 76% 22% .



● Molecule 55: 50S Ribosomal Protein L36



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.08Å 449.83Å 619.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.74 – 3.00 49.75 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.8 (49.74-3.00) 98.8 (49.75-3.00)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	0.24	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.203 , 0.259 0.203 , 0.259	Depositor DCC
R_{free} test set	57319 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	66.8	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 66.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	286321	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.70% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, K, 2QZ, ZN, 2QY, MVA, 004, FME, 2R3, SF4, 2R1

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	0.77	7/36038 (0.0%)	1.39	355/56244 (0.6%)
1	CA	0.76	13/36170 (0.0%)	1.43	365/56452 (0.6%)
2	AB	0.49	0/1881	0.77	0/2542
2	CB	0.56	0/1860	0.81	2/2518 (0.1%)
3	AC	0.48	0/1576	0.64	0/2130
3	CC	0.50	0/1566	0.72	2/2119 (0.1%)
4	AD	0.49	0/1689	0.76	1/2267 (0.0%)
4	CD	0.50	0/1704	0.71	0/2284
5	AE	0.47	0/1145	0.71	0/1543
5	CE	0.50	0/1149	0.76	0/1548
6	AF	0.48	0/819	0.69	0/1111
6	CF	0.53	0/829	0.76	0/1123
7	AG	0.48	0/1250	0.66	1/1679 (0.1%)
7	CG	0.50	0/1254	0.72	1/1683 (0.1%)
8	AH	0.46	0/1108	0.69	0/1494
8	CH	0.47	0/1108	0.71	0/1494
9	AI	0.47	0/1002	0.73	1/1346 (0.1%)
9	CI	0.56	0/997	0.75	2/1343 (0.1%)
10	AJ	0.47	0/722	0.67	0/982
10	CJ	0.53	0/727	0.69	0/988
11	AK	0.44	0/844	0.65	1/1145 (0.1%)
11	CK	0.46	0/848	0.67	0/1149
12	AL	0.50	0/946	0.73	0/1274
12	CL	0.52	0/946	0.74	0/1274
13	AM	0.48	0/969	0.68	0/1302
13	CM	0.48	0/961	0.66	0/1291
14	AN	0.48	0/501	0.71	0/664
14	CN	0.55	0/501	0.71	0/664
15	AO	0.49	0/739	0.76	0/985
15	CO	0.47	0/739	0.70	0/985
16	AP	0.47	0/697	0.73	0/939
16	CP	0.49	0/693	0.70	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.51	0/836	0.68	0/1117
17	CQ	0.51	0/836	0.70	0/1117
18	AR	0.48	0/560	0.73	0/746
18	CR	0.50	0/560	0.75	1/746 (0.1%)
19	AS	0.47	0/667	0.66	0/900
19	CS	0.50	0/661	0.80	1/893 (0.1%)
20	AT	0.48	0/730	0.77	0/965
20	CT	0.43	0/729	0.68	0/965
21	AU	0.47	0/203	0.62	0/266
21	CU	0.51	0/203	0.64	0/266
22	AV	0.99	0/127	1.42	2/198 (1.0%)
22	CV	0.82	0/126	1.39	1/195 (0.5%)
23	AX	0.88	8/1813 (0.4%)	1.62	47/2825 (1.7%)
23	CX	0.94	6/1813 (0.3%)	1.87	57/2825 (2.0%)
24	AW	0.46	0/20	0.84	0/23
24	CW	0.34	0/20	0.64	0/23
25	BA	1.07	33/65892 (0.1%)	1.49	877/102850 (0.9%)
25	DA	0.82	13/65466 (0.0%)	1.46	741/102184 (0.7%)
26	BB	0.83	0/2878	1.31	13/4490 (0.3%)
26	DB	0.93	2/2878 (0.1%)	1.50	45/4490 (1.0%)
27	BD	0.71	2/2186 (0.1%)	0.82	0/2944
27	DD	0.63	2/2186 (0.1%)	0.77	0/2944
28	BE	0.72	0/1592	0.77	0/2149
28	DE	0.57	0/1592	0.79	2/2149 (0.1%)
29	BF	0.73	0/1619	0.75	0/2193
29	DF	0.53	0/1615	0.80	2/2188 (0.1%)
30	BG	0.46	0/1450	0.71	0/1959
30	DG	0.54	0/1449	0.76	0/1958
31	BH	0.61	0/1356	0.72	0/1834
31	DH	0.54	0/1356	0.71	1/1834 (0.1%)
32	BI	0.51	0/1100	0.70	0/1501
32	DI	0.51	0/1076	0.74	0/1471
33	BN	0.67	0/1144	0.75	0/1543
33	DN	0.54	0/1144	0.74	0/1543
34	BO	0.66	0/943	0.78	1/1269 (0.1%)
34	DO	0.56	0/943	0.78	1/1269 (0.1%)
35	BP	0.64	0/1152	0.82	1/1533 (0.1%)
35	DP	0.55	0/1152	0.83	2/1533 (0.1%)
36	BQ	0.69	0/1143	0.81	0/1527
36	DQ	0.59	0/1143	0.77	0/1527
37	BR	0.62	0/982	0.86	0/1312
37	DR	0.51	0/982	0.70	0/1312
38	BS	0.55	0/887	0.78	1/1180 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DS	0.51	0/880	0.74	0/1172
39	BT	0.59	0/1105	0.79	0/1477
39	DT	0.53	0/1097	0.74	0/1468
40	BU	0.70	0/977	0.76	0/1301
40	DU	0.52	0/977	0.71	0/1301
41	BV	0.67	0/782	0.72	0/1049
41	DV	0.57	0/782	0.75	0/1049
42	BW	0.73	0/897	0.76	0/1205
42	DW	0.59	0/897	0.74	0/1205
43	BX	0.71	0/764	0.75	1/1025 (0.1%)
43	DX	0.56	0/764	0.80	2/1025 (0.2%)
44	BY	0.70	0/819	0.78	0/1095
44	DY	0.57	0/819	0.75	0/1095
45	BZ	0.55	0/1379	0.74	0/1873
45	DZ	0.54	0/1390	0.70	0/1890
46	B0	0.63	0/662	0.81	2/881 (0.2%)
46	D0	0.55	0/662	0.78	0/881
47	B1	0.66	0/762	0.81	3/1014 (0.3%)
47	D1	0.55	0/762	0.74	0/1014
48	B2	0.61	0/590	0.81	0/781
48	D2	0.47	0/590	0.67	0/781
49	B3	0.67	0/474	0.78	0/635
49	D3	0.50	0/469	0.70	0/630
50	B4	0.57	0/564	0.81	0/759
50	D4	0.59	0/544	0.89	1/735 (0.1%)
51	B5	0.72	0/469	0.84	1/635 (0.2%)
51	D5	0.59	0/469	0.73	1/635 (0.2%)
52	B6	0.66	0/460	0.66	0/613
52	D6	0.58	0/456	0.72	0/608
53	B7	0.74	0/426	0.82	0/561
53	D7	0.60	0/426	0.78	1/561 (0.2%)
54	B8	0.68	0/519	0.72	0/684
54	D8	0.58	0/525	0.73	0/691
55	B9	0.74	0/310	0.73	0/407
55	D9	0.61	0/310	0.80	0/407
All	All	0.81	86/305966 (0.0%)	1.30	2539/457396 (0.6%)

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
2	AB	0	3
4	CD	0	1
7	AG	0	1
9	AI	0	1
19	CS	0	1
23	CX	1	0
24	AW	0	1
24	CW	0	1
27	DD	0	1
38	BS	0	1
44	BY	0	1
45	BZ	0	1
50	B4	0	1
50	D4	0	1
All	All	1	15

The worst 5 of 86 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CA	1154	G	C6-N1	-13.21	1.30	1.39
1	CA	1119	C	N3-C4	-13.12	1.24	1.33
1	AA	343	U	C4-O4	12.79	1.33	1.23
1	CA	1154	G	N1-C2	-12.44	1.27	1.37
23	CX	76	A	N7-C5	-12.26	1.31	1.39

The worst 5 of 2539 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1119	C	N1-C2-O2	40.38	143.13	118.90
1	CA	1154	G	C5-C6-O6	34.47	149.28	128.60
23	CX	76	A	O4'-C1'-N9	33.86	135.29	108.20
1	CA	1154	G	N3-C2-N2	29.11	140.27	119.90
1	CA	1154	G	N1-C2-N2	-27.03	91.87	116.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
23	CX	76	A	C1'

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	231	GLU	Peptide

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Mol	Chain	Res	Type	Group
2	AB	8	LYS	Peptide
2	AB	9	GLU	Peptide
7	AG	79	ARG	Peptide
9	AI	52	ALA	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32196	0	16250	907	0
1	CA	32312	0	16307	1000	0
2	AB	1846	0	1867	106	0
2	CB	1825	0	1828	118	0
3	AC	1552	0	1546	51	0
3	CC	1542	0	1517	81	0
4	AD	1659	0	1676	86	0
4	CD	1674	0	1714	83	0
5	AE	1129	0	1185	44	0
5	CE	1133	0	1191	57	0
6	AF	806	0	793	34	0
6	CF	816	0	808	24	0
7	AG	1231	0	1238	33	0
7	CG	1235	0	1249	53	0
8	AH	1088	0	1126	43	0
8	CH	1088	0	1126	56	0
9	AI	983	0	986	47	0
9	CI	978	0	966	55	0
10	AJ	709	0	650	41	0
10	CJ	714	0	672	58	0
11	AK	829	0	825	17	0
11	CK	833	0	836	27	0
12	AL	930	0	980	35	0
12	CL	930	0	980	40	0
13	AM	958	0	1002	35	0
13	CM	950	0	988	50	0
14	AN	492	0	529	27	0
14	CN	492	0	529	31	0
15	AO	728	0	760	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	CO	728	0	760	26	0
16	AP	681	0	697	35	0
16	CP	677	0	686	30	0
17	AQ	823	0	891	21	0
17	CQ	823	0	891	27	0
18	AR	555	0	618	24	0
18	CR	555	0	618	19	0
19	AS	652	0	662	42	0
19	CS	646	0	644	49	0
20	AT	728	0	798	36	0
20	CT	727	0	796	26	0
21	AU	199	0	208	6	0
21	CU	199	0	208	8	0
22	AV	114	0	54	1	0
22	CV	113	0	54	1	0
23	AX	1623	0	823	23	0
23	CX	1623	0	823	22	0
24	AW	93	0	84	10	0
24	CW	93	0	84	10	0
25	BA	58834	0	29666	828	0
25	DA	58458	0	29481	1163	0
26	BB	2573	0	1306	33	0
26	DB	2573	0	1306	65	0
27	BD	2136	0	2218	62	0
27	DD	2136	0	2218	74	0
28	BE	1559	0	1618	55	0
28	DE	1559	0	1618	65	0
29	BF	1584	0	1625	38	0
29	DF	1580	0	1619	65	0
30	BG	1425	0	1443	41	0
30	DG	1424	0	1434	89	0
31	BH	1330	0	1407	37	0
31	DH	1330	0	1407	50	0
32	BI	1085	0	1114	42	0
32	DI	1061	0	1080	27	0
33	BN	1117	0	1183	18	0
33	DN	1117	0	1184	25	0
34	BO	933	0	996	26	0
34	DO	933	0	996	30	0
35	BP	1135	0	1212	42	0
35	DP	1135	0	1212	52	0
36	BQ	1122	0	1179	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	DQ	1122	0	1179	38	0
37	BR	968	0	1033	24	0
37	DR	968	0	1032	28	0
38	BS	877	0	938	30	0
38	DS	870	0	923	45	0
39	BT	1091	0	1151	36	0
39	DT	1083	0	1136	38	0
40	BU	959	0	1019	28	0
40	DU	959	0	1019	26	0
41	BV	771	0	830	15	0
41	DV	771	0	830	23	0
42	BW	886	0	940	15	0
42	DW	886	0	940	25	0
43	BX	750	0	814	19	0
43	DX	750	0	814	22	0
44	BY	806	0	881	22	0
44	DY	806	0	881	27	0
45	BZ	1349	0	1355	44	0
45	DZ	1360	0	1363	55	0
46	B0	653	0	674	19	0
46	D0	653	0	674	31	0
47	B1	755	0	826	19	0
47	D1	755	0	826	20	0
48	B2	588	0	643	13	0
48	D2	588	0	643	18	0
49	B3	469	0	518	12	0
49	D3	464	0	514	10	0
50	B4	551	0	532	38	0
50	D4	531	0	502	38	0
51	B5	455	0	465	14	0
51	D5	455	0	465	8	0
52	B6	453	0	473	10	0
52	D6	449	0	469	13	0
53	B7	418	0	467	11	0
53	D7	418	0	467	8	0
54	B8	511	0	571	31	0
54	D8	517	0	582	24	0
55	B9	307	0	335	7	0
55	D9	307	0	335	14	0
56	AA	222	0	0	0	0
56	AD	1	0	0	0	0
56	AF	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	AK	1	0	0	0	0
56	AL	1	0	0	0	0
56	AM	2	0	0	0	0
56	AN	1	0	0	0	0
56	AS	1	0	0	0	0
56	AV	1	0	0	0	0
56	AX	9	0	0	0	0
56	B0	6	0	0	0	0
56	B1	2	0	0	0	0
56	B2	1	0	0	0	0
56	B3	3	0	0	0	0
56	B5	1	0	0	0	0
56	B7	4	0	0	0	0
56	B8	2	0	0	0	0
56	B9	1	0	0	0	0
56	BA	739	0	0	0	0
56	BB	18	0	0	0	0
56	BD	12	0	0	0	0
56	BE	9	0	0	0	0
56	BF	6	0	0	0	0
56	BG	4	0	0	0	0
56	BN	6	0	0	0	0
56	BO	1	0	0	0	0
56	BP	4	0	0	0	0
56	BQ	4	0	0	0	0
56	BR	3	0	0	0	0
56	BU	9	0	0	0	0
56	BV	3	0	0	0	0
56	BW	5	0	0	0	0
56	BX	2	0	0	0	0
56	BZ	1	0	0	0	0
56	CA	172	0	0	0	0
56	CE	2	0	0	0	0
56	CF	1	0	0	0	0
56	CN	1	0	0	0	0
56	CT	1	0	0	0	0
56	CX	3	0	0	0	0
56	D3	1	0	0	0	0
56	D5	2	0	0	0	0
56	D8	1	0	0	0	0
56	DA	657	0	0	0	0
56	DB	12	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	DD	5	0	0	0	0
56	DE	6	0	0	0	0
56	DF	5	0	0	0	0
56	DG	1	0	0	0	0
56	DN	1	0	0	0	0
56	DO	1	0	0	0	0
56	DP	2	0	0	0	0
56	DQ	4	0	0	0	0
56	DR	1	0	0	0	0
56	DU	2	0	0	0	0
56	DV	3	0	0	0	0
56	DW	2	0	0	0	0
56	DY	1	0	0	0	0
57	AD	8	0	0	1	0
57	CD	8	0	0	1	0
58	AN	1	0	0	0	0
58	B4	1	0	0	0	0
58	B5	1	0	0	0	0
58	B6	1	0	0	0	0
58	B9	1	0	0	0	0
58	BY	1	0	0	0	0
58	CN	1	0	0	0	0
58	D4	1	0	0	0	0
58	D5	1	0	0	0	0
58	D6	1	0	0	0	0
58	D9	1	0	0	0	0
58	DY	1	0	0	0	0
59	AX	10	0	10	1	0
59	CX	10	0	10	2	0
60	BA	1	0	0	0	0
60	DA	1	0	0	0	0
61	AA	147	0	0	23	0
61	AD	1	0	0	0	0
61	AE	2	0	0	0	0
61	AJ	1	0	0	0	0
61	AL	2	0	0	0	0
61	AO	2	0	0	0	0
61	AU	1	0	0	1	0
61	AV	2	0	0	0	0
61	AX	1	0	0	0	0
61	B0	4	0	0	0	0
61	B1	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	B5	2	0	0	0	0
61	B7	1	0	0	1	0
61	B8	7	0	0	1	0
61	BA	1086	0	0	94	0
61	BB	26	0	0	2	0
61	BD	6	0	0	0	0
61	BE	13	0	0	3	0
61	BF	5	0	0	0	0
61	BG	1	0	0	0	0
61	BN	3	0	0	0	0
61	BO	2	0	0	0	0
61	BP	15	0	0	2	0
61	BQ	3	0	0	1	0
61	BR	1	0	0	0	0
61	BT	2	0	0	0	0
61	BU	5	0	0	0	0
61	BV	2	0	0	0	0
61	BW	4	0	0	0	0
61	BX	4	0	0	1	0
61	CA	186	0	0	24	0
61	CE	2	0	0	0	0
61	CN	1	0	0	0	0
61	CT	1	0	0	0	0
61	CX	2	0	0	0	0
61	D0	3	0	0	1	0
61	D1	1	0	0	0	0
61	D3	1	0	0	0	0
61	D7	1	0	0	0	0
61	D8	4	0	0	0	0
61	DA	906	0	0	116	0
61	DB	7	0	0	0	0
61	DD	10	0	0	0	0
61	DE	11	0	0	1	0
61	DF	4	0	0	0	0
61	DO	1	0	0	0	0
61	DP	14	0	0	2	0
61	DQ	3	0	0	1	0
61	DR	1	0	0	0	0
61	DU	4	0	0	0	0
61	DV	1	0	0	0	0
61	DX	2	0	0	1	0
61	DY	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	286321	0	191124	6684	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 15.

The worst 5 of 6684 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1129:C:N4	1:AA:1143:G:H1	1.46	1.12
1:CA:1002:G:H1	1:CA:1038:C:N4	1.48	1.09
1:AA:348:G:H2'	1:AA:349:A:H5'	1.30	1.06
2:AB:185:ILE:HG22	2:AB:199:TYR:HB2	1.39	1.04
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.36	1.03

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	229/256 (90%)	201 (88%)	23 (10%)	5 (2%)	6	31
2	CB	229/256 (90%)	201 (88%)	21 (9%)	7 (3%)	4	23
3	AC	204/239 (85%)	182 (89%)	20 (10%)	2 (1%)	15	53
3	CC	204/239 (85%)	181 (89%)	21 (10%)	2 (1%)	15	53
4	AD	206/209 (99%)	184 (89%)	20 (10%)	2 (1%)	15	53
4	CD	206/209 (99%)	185 (90%)	18 (9%)	3 (2%)	10	42
5	AE	146/162 (90%)	136 (93%)	8 (6%)	2 (1%)	11	43
5	CE	146/162 (90%)	134 (92%)	12 (8%)	0	100	100
6	AF	98/101 (97%)	94 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	CF	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
7	AG	153/156 (98%)	137 (90%)	15 (10%)	1 (1%)	22	60
7	CG	153/156 (98%)	139 (91%)	13 (8%)	1 (1%)	22	60
8	AH	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
8	CH	135/138 (98%)	131 (97%)	3 (2%)	1 (1%)	22	60
9	AI	125/128 (98%)	112 (90%)	10 (8%)	3 (2%)	6	29
9	CI	125/128 (98%)	115 (92%)	8 (6%)	2 (2%)	9	40
10	AJ	95/105 (90%)	84 (88%)	8 (8%)	3 (3%)	4	22
10	CJ	94/105 (90%)	84 (89%)	8 (8%)	2 (2%)	7	33
11	AK	112/129 (87%)	101 (90%)	10 (9%)	1 (1%)	17	55
11	CK	112/129 (87%)	101 (90%)	10 (9%)	1 (1%)	17	55
12	AL	120/132 (91%)	117 (98%)	3 (2%)	0	100	100
12	CL	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
13	AM	121/126 (96%)	113 (93%)	7 (6%)	1 (1%)	19	57
13	CM	120/126 (95%)	113 (94%)	6 (5%)	1 (1%)	19	57
14	AN	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
14	CN	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
15	AO	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
15	CO	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
16	AP	80/88 (91%)	74 (92%)	6 (8%)	0	100	100
16	CP	80/88 (91%)	73 (91%)	6 (8%)	1 (1%)	12	45
17	AQ	97/105 (92%)	92 (95%)	5 (5%)	0	100	100
17	CQ	97/105 (92%)	93 (96%)	4 (4%)	0	100	100
18	AR	66/88 (75%)	60 (91%)	5 (8%)	1 (2%)	10	42
18	CR	66/88 (75%)	61 (92%)	5 (8%)	0	100	100
19	AS	81/93 (87%)	76 (94%)	5 (6%)	0	100	100
19	CS	81/93 (87%)	74 (91%)	7 (9%)	0	100	100
20	AT	94/106 (89%)	84 (89%)	9 (10%)	1 (1%)	14	50
20	CT	94/106 (89%)	86 (92%)	5 (5%)	3 (3%)	4	22
21	AU	21/27 (78%)	17 (81%)	4 (19%)	0	100	100
21	CU	21/27 (78%)	18 (86%)	3 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	AW	3/10 (30%)	0	2 (67%)	1 (33%)	0	0
24	CW	3/10 (30%)	1 (33%)	1 (33%)	1 (33%)	0	0
27	BD	273/276 (99%)	260 (95%)	12 (4%)	1 (0%)	34	72
27	DD	273/276 (99%)	258 (94%)	13 (5%)	2 (1%)	22	60
28	BE	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	29	68
28	DE	202/206 (98%)	195 (96%)	4 (2%)	3 (2%)	10	42
29	BF	201/210 (96%)	195 (97%)	5 (2%)	1 (0%)	29	68
29	DF	201/210 (96%)	195 (97%)	4 (2%)	2 (1%)	15	53
30	BG	179/182 (98%)	167 (93%)	9 (5%)	3 (2%)	9	39
30	DG	179/182 (98%)	161 (90%)	14 (8%)	4 (2%)	6	31
31	BH	172/180 (96%)	165 (96%)	6 (4%)	1 (1%)	25	64
31	DH	172/180 (96%)	164 (95%)	7 (4%)	1 (1%)	25	64
32	BI	144/148 (97%)	124 (86%)	14 (10%)	6 (4%)	3	16
32	DI	144/148 (97%)	124 (86%)	17 (12%)	3 (2%)	7	33
33	BN	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
33	DN	138/140 (99%)	132 (96%)	5 (4%)	1 (1%)	22	60
34	BO	120/122 (98%)	116 (97%)	3 (2%)	1 (1%)	19	57
34	DO	120/122 (98%)	117 (98%)	2 (2%)	1 (1%)	19	57
35	BP	147/150 (98%)	138 (94%)	8 (5%)	1 (1%)	22	60
35	DP	147/150 (98%)	135 (92%)	9 (6%)	3 (2%)	7	34
36	BQ	139/141 (99%)	131 (94%)	7 (5%)	1 (1%)	22	60
36	DQ	139/141 (99%)	129 (93%)	9 (6%)	1 (1%)	22	60
37	BR	116/118 (98%)	110 (95%)	5 (4%)	1 (1%)	17	55
37	DR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
38	BS	108/112 (96%)	103 (95%)	4 (4%)	1 (1%)	17	55
38	DS	108/112 (96%)	102 (94%)	5 (5%)	1 (1%)	17	55
39	BT	129/146 (88%)	123 (95%)	6 (5%)	0	100	100
39	DT	129/146 (88%)	127 (98%)	2 (2%)	0	100	100
40	BU	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
40	DU	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
41	BV	99/101 (98%)	93 (94%)	5 (5%)	1 (1%)	15	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	DV	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	15	53
42	BW	110/113 (97%)	108 (98%)	2 (2%)	0	100	100
42	DW	110/113 (97%)	108 (98%)	2 (2%)	0	100	100
43	BX	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
43	DX	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
44	BY	105/110 (96%)	98 (93%)	7 (7%)	0	100	100
44	DY	105/110 (96%)	97 (92%)	8 (8%)	0	100	100
45	BZ	169/206 (82%)	150 (89%)	18 (11%)	1 (1%)	25	64
45	DZ	172/206 (84%)	162 (94%)	10 (6%)	0	100	100
46	B0	81/85 (95%)	76 (94%)	4 (5%)	1 (1%)	13	48
46	D0	81/85 (95%)	76 (94%)	4 (5%)	1 (1%)	13	48
47	B1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	14	50
47	D1	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	14	50
48	B2	68/72 (94%)	68 (100%)	0	0	100	100
48	D2	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
49	B3	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
49	D3	57/60 (95%)	57 (100%)	0	0	100	100
50	B4	67/71 (94%)	53 (79%)	9 (13%)	5 (8%)	1	5
50	D4	67/71 (94%)	52 (78%)	8 (12%)	7 (10%)	0	2
51	B5	57/60 (95%)	53 (93%)	4 (7%)	0	100	100
51	D5	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
52	B6	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
52	D6	51/54 (94%)	47 (92%)	4 (8%)	0	100	100
53	B7	46/49 (94%)	46 (100%)	0	0	100	100
53	D7	46/49 (94%)	44 (96%)	1 (2%)	1 (2%)	6	31
54	B8	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
54	D8	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
55	B9	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
55	D9	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
All	All	11415/12148 (94%)	10659 (93%)	648 (6%)	108 (1%)	17	55

5 of 108 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	125	PRO
3	AC	107	GLN
4	AD	166	LYS
9	AI	54	ASP
10	AJ	31	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	
2	AB	192/220 (87%)	154 (80%)	38 (20%)	1	7
2	CB	187/220 (85%)	155 (83%)	32 (17%)	2	10
3	AC	143/188 (76%)	128 (90%)	15 (10%)	7	27
3	CC	140/188 (74%)	123 (88%)	17 (12%)	5	21
4	AD	170/181 (94%)	146 (86%)	24 (14%)	3	16
4	CD	173/181 (96%)	152 (88%)	21 (12%)	5	21
5	AE	113/123 (92%)	102 (90%)	11 (10%)	8	31
5	CE	114/123 (93%)	104 (91%)	10 (9%)	10	36
6	AF	83/90 (92%)	76 (92%)	7 (8%)	11	38
6	CF	85/90 (94%)	79 (93%)	6 (7%)	14	46
7	AG	119/127 (94%)	100 (84%)	19 (16%)	2	12
7	CG	120/127 (94%)	102 (85%)	18 (15%)	3	14
8	AH	114/119 (96%)	97 (85%)	17 (15%)	3	14
8	CH	114/119 (96%)	102 (90%)	12 (10%)	7	27
9	AI	90/99 (91%)	78 (87%)	12 (13%)	4	17
9	CI	89/99 (90%)	75 (84%)	14 (16%)	2	13
10	AJ	66/92 (72%)	59 (89%)	7 (11%)	6	26
10	CJ	69/92 (75%)	65 (94%)	4 (6%)	20	55
11	AK	82/99 (83%)	75 (92%)	7 (8%)	10	38
11	CK	83/99 (84%)	77 (93%)	6 (7%)	14	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	AL	97/109 (89%)	87 (90%)	10 (10%)	7	28
12	CL	97/109 (89%)	83 (86%)	14 (14%)	3	15
13	AM	93/101 (92%)	81 (87%)	12 (13%)	4	19
13	CM	92/101 (91%)	78 (85%)	14 (15%)	3	14
14	AN	49/50 (98%)	41 (84%)	8 (16%)	2	11
14	CN	49/50 (98%)	41 (84%)	8 (16%)	2	11
15	AO	78/80 (98%)	68 (87%)	10 (13%)	4	19
15	CO	78/80 (98%)	66 (85%)	12 (15%)	2	13
16	AP	69/74 (93%)	61 (88%)	8 (12%)	5	23
16	CP	68/74 (92%)	64 (94%)	4 (6%)	19	54
17	AQ	94/97 (97%)	88 (94%)	6 (6%)	17	51
17	CQ	94/97 (97%)	86 (92%)	8 (8%)	10	38
18	AR	59/77 (77%)	56 (95%)	3 (5%)	24	60
18	CR	59/77 (77%)	53 (90%)	6 (10%)	7	28
19	AS	69/80 (86%)	63 (91%)	6 (9%)	10	37
19	CS	67/80 (84%)	59 (88%)	8 (12%)	5	22
20	AT	70/82 (85%)	60 (86%)	10 (14%)	3	15
20	CT	70/82 (85%)	61 (87%)	9 (13%)	4	19
21	AU	18/22 (82%)	15 (83%)	3 (17%)	2	11
21	CU	18/22 (82%)	16 (89%)	2 (11%)	6	25
24	AW	3/3 (100%)	2 (67%)	1 (33%)	0	1
24	CW	3/3 (100%)	2 (67%)	1 (33%)	0	1
27	BD	215/218 (99%)	193 (90%)	22 (10%)	7	28
27	DD	215/218 (99%)	195 (91%)	20 (9%)	9	33
28	BE	164/166 (99%)	140 (85%)	24 (15%)	3	15
28	DE	164/166 (99%)	140 (85%)	24 (15%)	3	15
29	BF	160/166 (96%)	145 (91%)	15 (9%)	8	32
29	DF	159/166 (96%)	142 (89%)	17 (11%)	6	26
30	BG	143/156 (92%)	124 (87%)	19 (13%)	4	17
30	DG	142/156 (91%)	117 (82%)	25 (18%)	2	10
31	BH	144/148 (97%)	128 (89%)	16 (11%)	6	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	DH	144/148 (97%)	131 (91%)	13 (9%)	9	35
32	BI	110/124 (89%)	85 (77%)	25 (23%)	1	4
32	DI	104/124 (84%)	90 (86%)	14 (14%)	4	17
33	BN	118/119 (99%)	100 (85%)	18 (15%)	2	13
33	DN	118/119 (99%)	102 (86%)	16 (14%)	3	17
34	BO	100/100 (100%)	95 (95%)	5 (5%)	24	60
34	DO	100/100 (100%)	92 (92%)	8 (8%)	12	40
35	BP	115/116 (99%)	103 (90%)	12 (10%)	7	27
35	DP	115/116 (99%)	102 (89%)	13 (11%)	6	24
36	BQ	111/111 (100%)	96 (86%)	15 (14%)	4	17
36	DQ	111/111 (100%)	97 (87%)	14 (13%)	4	20
37	BR	101/101 (100%)	83 (82%)	18 (18%)	2	9
37	DR	101/101 (100%)	84 (83%)	17 (17%)	2	11
38	BS	87/88 (99%)	78 (90%)	9 (10%)	7	28
38	DS	85/88 (97%)	73 (86%)	12 (14%)	3	16
39	BT	115/127 (91%)	103 (90%)	12 (10%)	7	27
39	DT	113/127 (89%)	103 (91%)	10 (9%)	10	36
40	BU	93/94 (99%)	85 (91%)	8 (9%)	10	37
40	DU	93/94 (99%)	79 (85%)	14 (15%)	3	14
41	BV	80/82 (98%)	68 (85%)	12 (15%)	3	14
41	DV	80/82 (98%)	70 (88%)	10 (12%)	4	20
42	BW	90/92 (98%)	83 (92%)	7 (8%)	12	42
42	DW	90/92 (98%)	82 (91%)	8 (9%)	9	35
43	BX	77/78 (99%)	74 (96%)	3 (4%)	32	69
43	DX	77/78 (99%)	73 (95%)	4 (5%)	23	59
44	BY	85/91 (93%)	76 (89%)	9 (11%)	6	26
44	DY	85/91 (93%)	77 (91%)	8 (9%)	8	32
45	BZ	145/179 (81%)	127 (88%)	18 (12%)	4	20
45	DZ	145/179 (81%)	128 (88%)	17 (12%)	5	22
46	B0	65/67 (97%)	62 (95%)	3 (5%)	27	64
46	D0	65/67 (97%)	60 (92%)	5 (8%)	13	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	B1	80/83 (96%)	70 (88%)	10 (12%)	4	20
47	D1	80/83 (96%)	69 (86%)	11 (14%)	3	17
48	B2	65/67 (97%)	56 (86%)	9 (14%)	3	17
48	D2	65/67 (97%)	57 (88%)	8 (12%)	4	21
49	B3	51/52 (98%)	44 (86%)	7 (14%)	3	17
49	D3	50/52 (96%)	42 (84%)	8 (16%)	2	12
50	B4	59/63 (94%)	47 (80%)	12 (20%)	1	6
50	D4	53/63 (84%)	44 (83%)	9 (17%)	2	10
51	B5	50/52 (96%)	45 (90%)	5 (10%)	7	29
51	D5	50/52 (96%)	45 (90%)	5 (10%)	7	29
52	B6	51/52 (98%)	47 (92%)	4 (8%)	12	42
52	D6	50/52 (96%)	43 (86%)	7 (14%)	3	16
53	B7	41/42 (98%)	39 (95%)	2 (5%)	25	61
53	D7	41/42 (98%)	38 (93%)	3 (7%)	14	44
54	B8	53/55 (96%)	50 (94%)	3 (6%)	20	56
54	D8	54/55 (98%)	52 (96%)	2 (4%)	34	70
55	B9	34/34 (100%)	33 (97%)	1 (3%)	42	76
55	D9	34/34 (100%)	31 (91%)	3 (9%)	10	36
All	All	9325/10072 (93%)	8217 (88%)	1108 (12%)	5	22

5 of 1108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	B0	10	THR
4	CD	170	VAL
44	DY	43	ASN
48	B2	30	ARG
2	CB	67	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 115 such sidechains are listed below:

Mol	Chain	Res	Type
45	BZ	32	HIS
3	CC	123	GLN
39	DT	58	ASN

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Mol	Chain	Res	Type
45	BZ	151	HIS
2	CB	224	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1495/1522 (98%)	421 (28%)	24 (1%)
1	CA	1501/1522 (98%)	421 (28%)	30 (1%)
22	AV	4/24 (16%)	1 (25%)	0
22	CV	4/24 (16%)	1 (25%)	0
23	AX	75/77 (97%)	18 (24%)	0
23	CX	75/77 (97%)	19 (25%)	0
25	BA	2722/2915 (93%)	527 (19%)	41 (1%)
25	DA	2704/2915 (92%)	526 (19%)	35 (1%)
26	BB	119/122 (97%)	21 (17%)	0
26	DB	119/122 (97%)	23 (19%)	1 (0%)
All	All	8818/9320 (94%)	1978 (22%)	131 (1%)

5 of 1978 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	7	G
1	AA	9	G
1	AA	15	G
1	AA	16	A
1	AA	22	G

5 of 131 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	BA	2459	G
1	CA	429	U
25	DA	1992	G
25	BA	2701	U
1	CA	60	A

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul

statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	2QZ	AW	1	24	7,8,9	0.42	0	8,10,12	2.37	1 (12%)
24	MVA	AW	5	24	6,7,8	0.57	0	7,8,10	1.61	1 (14%)
24	2R3	AW	8	24	12,14,15	0.78	0	16,18,20	2.05	6 (37%)
24	2R3	CW	8	24	12,14,15	0.66	0	16,18,20	2.17	5 (31%)
24	2QY	CW	10	24	12,13,14	2.26	2 (16%)	13,16,18	3.21	2 (15%)
24	MVA	CW	5	24	6,7,8	0.79	0	7,8,10	1.44	2 (28%)
24	2QZ	CW	1	24	7,8,9	0.79	0	8,10,12	3.63	3 (37%)
24	2R1	CW	6	24	10,10,11	1.77	3 (30%)	6,13,15	4.10	2 (33%)
24	MVA	CW	9	24	6,7,8	0.88	0	7,8,10	1.00	0
24	004	CW	3	24	9,10,11	1.24	1 (11%)	9,12,14	0.77	0
24	2QY	AW	10	24	12,13,14	2.14	2 (16%)	13,16,18	3.12	4 (30%)
24	2R1	AW	6	24	10,10,11	2.03	4 (40%)	6,13,15	4.80	2 (33%)
24	004	AW	3	24	9,10,11	1.09	1 (11%)	9,12,14	1.05	0
24	MVA	AW	9	24	6,7,8	0.38	0	7,8,10	0.86	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	2QZ	AW	1	24	-	3/6/10/12	-
24	MVA	AW	5	24	-	2/6/8/10	-
24	2R3	AW	8	24	-	6/11/12/14	0/1/1/1
24	2R3	CW	8	24	-	6/11/12/14	0/1/1/1
24	2QY	CW	10	24	-	1/4/8/10	0/1/1/1
24	MVA	CW	5	24	-	5/6/8/10	-
24	2QZ	CW	1	24	-	1/6/10/12	-
24	2R1	CW	6	24	-	1/2/14/16	0/1/1/1
24	MVA	CW	9	24	-	5/6/8/10	-
24	004	CW	3	24	-	0/4/6/8	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	2QY	AW	10	24	-	3/4/8/10	0/1/1/1
24	2R1	AW	6	24	-	1/2/14/16	0/1/1/1
24	004	AW	3	24	-	1/4/6/8	0/1/1/1
24	MVA	AW	9	24	-	5/6/8/10	-

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	CW	10	2QY	C-CA	7.00	1.53	1.43
24	AW	10	2QY	C-CA	6.63	1.53	1.43
24	AW	6	2R1	CA-N	3.98	1.46	1.36
24	CW	6	2R1	CA-N	3.70	1.45	1.36
24	CW	3	004	CB-CA	-3.18	1.49	1.52

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AW	6	2R1	OD2-CG2-CB	-11.05	92.15	112.24
24	CW	10	2QY	CN-N-CA	-9.39	109.17	123.45
24	AW	10	2QY	CN-N-CA	-9.29	109.33	123.45
24	CW	1	2QZ	OG1-CB-CG2	9.27	137.20	109.74
24	CW	6	2R1	OD2-CG2-CB	-9.26	95.40	112.24

There are no chirality outliers.

5 of 40 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	AW	1	2QZ	N-CA-CB-OG1
24	AW	1	2QZ	N-CA-CB-CG2
24	AW	5	MVA	CB-CA-N-CN
24	AW	8	2R3	N-CA-CB-OB
24	AW	8	2R3	N-CA-CB-CG

There are no ring outliers.

14 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	AW	1	2QZ	2	0
24	AW	5	MVA	1	0
24	AW	8	2R3	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	CW	8	2R3	2	0
24	CW	10	2QY	4	0
24	CW	5	MVA	1	0
24	CW	1	2QZ	3	0
24	CW	6	2R1	1	0
24	CW	9	MVA	3	0
24	CW	3	004	1	0
24	AW	10	2QY	3	0
24	AW	6	2R1	3	0
24	AW	3	004	1	0
24	AW	9	MVA	3	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 1991 ligands modelled in this entry, 1987 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	FME	CX	101	23	8,9,10	0.87	0	7,9,11	1.38	1 (14%)
57	SF4	CD	501	4	0,12,12	0.00	-	-		
59	FME	AX	101	23	8,9,10	1.01	1 (12%)	7,9,11	1.33	1 (14%)
57	SF4	AD	501	4	0,12,12	0.00	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	FME	CX	101	23	-	1/7/9/11	-
57	SF4	CD	501	4	-	-	0/6/5/5
59	FME	AX	101	23	-	2/7/9/11	-
57	SF4	AD	501	4	-	-	0/6/5/5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	AX	101	FME	CA-N	2.16	1.49	1.46

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AX	101	FME	CA-N-CN	-2.47	119.03	122.82
59	CX	101	FME	CA-N-CN	-2.33	119.25	122.82

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	AX	101	FME	O1-CN-N-CA
59	CX	101	FME	O1-CN-N-CA
59	AX	101	FME	CB-CG-SD-CE

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	CX	101	FME	2	0
57	CD	501	SF4	1	0
59	AX	101	FME	1	0
57	AD	501	SF4	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	1498/1522 (98%)	-0.06	45 (3%)	50	22	39, 80, 103, 118	0
1	CA	1503/1522 (98%)	-0.11	38 (2%)	57	29	41, 80, 103, 119	0
2	AB	231/256 (90%)	-0.03	6 (2%)	56	27	69, 86, 97, 105	0
2	CB	231/256 (90%)	0.20	10 (4%)	35	13	70, 88, 98, 107	0
3	AC	206/239 (86%)	0.20	8 (3%)	39	15	73, 87, 95, 104	0
3	CC	206/239 (86%)	0.34	13 (6%)	20	6	72, 89, 97, 104	0
4	AD	208/209 (99%)	-0.07	4 (1%)	66	37	61, 80, 90, 97	0
4	CD	208/209 (99%)	-0.22	0	100	100	61, 79, 89, 97	0
5	AE	148/162 (91%)	-0.34	0	100	100	51, 73, 82, 93	0
5	CE	148/162 (91%)	-0.28	0	100	100	53, 75, 84, 96	0
6	AF	100/101 (99%)	-0.29	0	100	100	63, 77, 87, 94	0
6	CF	100/101 (99%)	-0.39	0	100	100	62, 78, 87, 95	0
7	AG	155/156 (99%)	0.38	12 (7%)	13	4	74, 86, 99, 106	0
7	CG	155/156 (99%)	0.46	16 (10%)	6	2	75, 86, 99, 105	0
8	AH	137/138 (99%)	-0.11	0	100	100	60, 74, 82, 89	0
8	CH	137/138 (99%)	-0.15	0	100	100	62, 75, 83, 89	0
9	AI	127/128 (99%)	0.44	8 (6%)	20	6	73, 91, 99, 101	0
9	CI	127/128 (99%)	1.08	31 (24%)	0	0	72, 93, 100, 102	0
10	AJ	97/105 (92%)	0.72	11 (11%)	5	1	73, 91, 100, 105	0
10	CJ	96/105 (91%)	0.98	19 (19%)	1	0	77, 93, 100, 104	0
11	AK	114/129 (88%)	-0.28	0	100	100	53, 74, 87, 91	0
11	CK	114/129 (88%)	0.02	1 (0%)	84	63	55, 76, 87, 92	0
12	AL	122/132 (92%)	-0.26	0	100	100	53, 68, 80, 87	0
12	CL	122/132 (92%)	-0.22	0	100	100	53, 69, 80, 87	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	123/126 (97%)	0.35	9 (7%) 15 4	67, 85, 95, 105	0
13	CM	122/126 (96%)	0.54	6 (4%) 29 11	77, 92, 100, 109	0
14	AN	60/61 (98%)	0.11	1 (1%) 70 41	75, 87, 94, 103	0
14	CN	60/61 (98%)	0.78	6 (10%) 7 2	77, 89, 94, 100	0
15	AO	88/89 (98%)	-0.18	0 100 100	55, 72, 85, 90	0
15	CO	88/89 (98%)	-0.15	0 100 100	55, 72, 85, 91	0
16	AP	82/88 (93%)	0.47	1 (1%) 79 54	67, 78, 89, 94	0
16	CP	82/88 (93%)	0.18	3 (3%) 41 17	66, 76, 88, 94	0
17	AQ	99/105 (94%)	-0.25	0 100 100	59, 72, 83, 90	0
17	CQ	99/105 (94%)	-0.15	1 (1%) 82 59	58, 72, 83, 89	0
18	AR	68/88 (77%)	0.16	2 (2%) 51 23	65, 73, 87, 91	0
18	CR	68/88 (77%)	0.24	1 (1%) 73 46	64, 75, 87, 91	0
19	AS	83/93 (89%)	0.94	14 (16%) 1 0	77, 92, 99, 106	0
19	CS	83/93 (89%)	1.14	12 (14%) 2 1	79, 92, 101, 106	0
20	AT	96/106 (90%)	0.10	2 (2%) 63 34	62, 76, 86, 90	0
20	CT	96/106 (90%)	0.11	1 (1%) 82 59	62, 74, 86, 92	0
21	AU	23/27 (85%)	1.37	5 (21%) 0 0	73, 88, 93, 94	0
21	CU	23/27 (85%)	1.48	9 (39%) 0 0	73, 89, 92, 94	0
22	AV	7/24 (29%)	0.60	0 100 100	65, 77, 102, 104	0
22	CV	6/24 (25%)	0.79	1 (16%) 1 0	67, 78, 103, 103	0
23	AX	76/77 (98%)	0.47	2 (2%) 56 27	52, 80, 97, 105	0
23	CX	76/77 (98%)	0.35	3 (3%) 39 15	52, 82, 100, 106	0
24	AW	3/10 (30%)	-0.30	0 100 100	67, 67, 82, 98	0
24	CW	3/10 (30%)	-0.44	0 100 100	67, 67, 78, 82	0
25	BA	2731/2915 (93%)	-0.24	13 (0%) 91 75	23, 44, 85, 111	0
25	DA	2714/2915 (93%)	-0.45	18 (0%) 87 69	26, 47, 85, 118	0
26	BB	120/122 (98%)	-0.37	0 100 100	42, 68, 80, 95	0
26	DB	120/122 (98%)	-0.26	0 100 100	48, 74, 84, 97	0
27	BD	275/276 (99%)	-0.48	0 100 100	22, 42, 58, 77	0
27	DD	275/276 (99%)	-0.53	0 100 100	23, 44, 60, 79	0
28	BE	204/206 (99%)	-0.39	0 100 100	23, 45, 67, 88	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DE	204/206 (99%)	-0.47	0 100 100	24, 47, 70, 88	0
29	BF	203/210 (96%)	-0.36	0 100 100	20, 51, 77, 94	0
29	DF	203/210 (96%)	-0.50	1 (0%) 91 75	22, 54, 78, 93	0
30	BG	181/182 (99%)	-0.35	1 (0%) 89 72	59, 77, 90, 103	0
30	DG	181/182 (99%)	0.13	9 (4%) 28 10	63, 80, 92, 102	0
31	BH	174/180 (96%)	-0.37	0 100 100	50, 66, 78, 84	0
31	DH	174/180 (96%)	0.29	13 (7%) 14 4	54, 71, 82, 87	0
32	BI	146/148 (98%)	-0.36	0 100 100	45, 75, 87, 92	0
32	DI	146/148 (98%)	0.04	3 (2%) 63 34	48, 76, 86, 91	0
33	BN	140/140 (100%)	-0.43	0 100 100	32, 49, 68, 80	0
33	DN	140/140 (100%)	-0.48	0 100 100	34, 53, 72, 81	0
34	BO	122/122 (100%)	-0.50	0 100 100	25, 39, 60, 78	0
34	DO	122/122 (100%)	-0.49	0 100 100	34, 52, 68, 79	0
35	BP	149/150 (99%)	-0.35	0 100 100	26, 54, 76, 84	0
35	DP	149/150 (99%)	-0.18	0 100 100	30, 57, 79, 86	0
36	BQ	141/141 (100%)	-0.36	0 100 100	33, 51, 65, 79	0
36	DQ	141/141 (100%)	-0.46	0 100 100	35, 54, 70, 80	0
37	BR	118/118 (100%)	-0.54	0 100 100	22, 35, 51, 64	0
37	DR	118/118 (100%)	-0.42	0 100 100	36, 50, 64, 81	0
38	BS	110/112 (98%)	-0.34	0 100 100	38, 55, 69, 81	0
38	DS	110/112 (98%)	0.15	1 (0%) 84 63	66, 78, 90, 100	0
39	BT	131/146 (89%)	-0.48	0 100 100	33, 45, 75, 91	0
39	DT	131/146 (89%)	-0.53	0 100 100	44, 56, 80, 86	0
40	BU	116/118 (98%)	-0.64	0 100 100	19, 30, 50, 63	0
40	DU	116/118 (98%)	-0.36	1 (0%) 84 63	39, 61, 79, 88	0
41	BV	101/101 (100%)	-0.39	0 100 100	29, 52, 70, 77	0
41	DV	101/101 (100%)	-0.18	0 100 100	32, 58, 74, 79	0
42	BW	112/113 (99%)	-0.49	1 (0%) 84 63	27, 37, 61, 94	0
42	DW	112/113 (99%)	-0.44	0 100 100	31, 40, 63, 94	0
43	BX	95/96 (98%)	-0.41	0 100 100	32, 46, 69, 82	0
43	DX	95/96 (98%)	-0.33	1 (1%) 80 56	38, 50, 72, 83	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	BY	107/110 (97%)	-0.29	1 (0%) 84 63	44, 59, 77, 82	0
44	DY	107/110 (97%)	0.24	3 (2%) 53 25	46, 63, 80, 85	0
45	BZ	171/206 (83%)	-0.45	0 100 100	52, 71, 85, 93	0
45	DZ	174/206 (84%)	-0.17	0 100 100	56, 74, 87, 95	0
46	B0	83/85 (97%)	-0.16	7 (8%) 11 3	22, 40, 75, 104	0
46	D0	83/85 (97%)	0.19	5 (6%) 21 7	45, 66, 87, 98	0
47	B1	97/98 (98%)	-0.26	1 (1%) 82 59	25, 42, 71, 77	0
47	D1	97/98 (98%)	-0.25	1 (1%) 82 59	35, 56, 79, 85	0
48	B2	70/72 (97%)	-0.52	0 100 100	31, 48, 64, 77	0
48	D2	70/72 (97%)	-0.35	0 100 100	56, 73, 84, 86	0
49	B3	59/60 (98%)	-0.33	0 100 100	26, 38, 63, 86	0
49	D3	59/60 (98%)	0.02	2 (3%) 45 19	49, 62, 80, 93	0
50	B4	69/71 (97%)	-0.03	1 (1%) 75 49	64, 87, 101, 104	0
50	D4	69/71 (97%)	0.51	4 (5%) 23 7	85, 95, 104, 107	0
51	B5	59/60 (98%)	-0.61	0 100 100	14, 35, 55, 71	0
51	D5	59/60 (98%)	-0.55	0 100 100	29, 51, 70, 77	0
52	B6	53/54 (98%)	-0.37	0 100 100	40, 54, 68, 74	0
52	D6	53/54 (98%)	-0.39	0 100 100	42, 58, 68, 74	0
53	B7	48/49 (97%)	-0.28	0 100 100	26, 32, 67, 78	0
53	D7	48/49 (97%)	-0.18	1 (2%) 63 34	27, 34, 66, 79	0
54	B8	64/65 (98%)	-0.34	0 100 100	33, 43, 51, 57	0
54	D8	64/65 (98%)	-0.29	0 100 100	34, 46, 56, 60	0
55	B9	37/37 (100%)	0.09	0 100 100	43, 52, 68, 77	0
55	D9	37/37 (100%)	0.84	5 (13%) 3 1	48, 57, 72, 78	0
All	All	20462/21468 (95%)	-0.17	394 (1%) 66 37	14, 65, 95, 119	0

The worst 5 of 394 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	CM	124	PRO	15.8
13	CM	123	ALA	11.8
13	AM	123	ALA	8.8
13	AM	124	PRO	7.8
7	CG	78	ARG	7.3

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

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
24	2R1	AW	6	10/11	0.91	0.14	66,72,84,91	0
24	2R3	AW	8	14/15	0.92	0.24	70,78,86,87	0
24	2QY	CW	10	13/14	0.92	0.16	60,72,80,86	0
24	2R1	CW	6	10/11	0.92	0.13	68,82,90,91	0
24	MVA	AW	5	8/9	0.92	0.19	69,82,86,91	0
24	004	AW	3	10/11	0.93	0.11	67,87,95,97	0
24	MVA	CW	9	8/9	0.94	0.22	70,73,84,91	0
24	2QZ	AW	1	9/10	0.95	0.23	50,71,82,83	0
24	MVA	CW	5	8/9	0.95	0.21	76,88,91,99	0
24	2R3	CW	8	14/15	0.96	0.14	62,69,77,78	0
24	2QY	AW	10	13/14	0.96	0.14	49,70,87,100	0
24	MVA	AW	9	8/9	0.96	0.28	63,74,87,88	0
24	2QZ	CW	1	9/10	0.97	0.27	63,71,80,101	0
24	004	CW	3	10/11	0.97	0.16	69,78,82,83	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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
56	MG	CA	3147	1/1	0.27	0.37	77,77,77,77	0
56	MG	AA	3086	1/1	0.28	0.72	65,65,65,65	0
56	MG	CA	3053	1/1	0.41	1.38	87,87,87,87	0
56	MG	BA	3625	1/1	0.49	0.48	80,80,80,80	0
56	MG	BA	3252	1/1	0.51	0.59	65,65,65,65	0
56	MG	BA	3296	1/1	0.52	0.67	69,69,69,69	0
56	MG	AS	3001	1/1	0.56	0.17	79,79,79,79	0
56	MG	AA	3131	1/1	0.57	0.38	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3064	1/1	0.61	0.43	55,55,55,55	0
56	MG	CA	3039	1/1	0.62	0.51	82,82,82,82	0
56	MG	CA	3065	1/1	0.63	0.33	81,81,81,81	0
56	MG	BA	3616	1/1	0.63	0.27	73,73,73,73	0
56	MG	BA	3143	1/1	0.63	0.82	41,41,41,41	0
56	MG	AA	3124	1/1	0.64	0.20	61,61,61,61	0
56	MG	BF	306	1/1	0.65	0.41	52,52,52,52	0
56	MG	DA	3568	1/1	0.65	0.43	58,58,58,58	0
56	MG	BA	3582	1/1	0.66	0.23	52,52,52,52	0
56	MG	AA	3093	1/1	0.66	0.39	90,90,90,90	0
56	MG	DA	3113	1/1	0.67	1.16	61,61,61,61	0
56	MG	DA	3314	1/1	0.67	0.19	56,56,56,56	0
56	MG	BA	3103	1/1	0.68	0.33	58,58,58,58	0
56	MG	DA	3496	1/1	0.68	0.34	76,76,76,76	0
56	MG	BA	3021	1/1	0.68	0.36	62,62,62,62	0
56	MG	AA	3002	1/1	0.68	0.20	74,74,74,74	0
56	MG	DW	202	1/1	0.69	0.39	53,53,53,53	0
56	MG	AA	3079	1/1	0.69	0.91	65,65,65,65	0
56	MG	BA	3230	1/1	0.69	1.02	70,70,70,70	0
56	MG	CA	3070	1/1	0.69	0.35	59,59,59,59	0
56	MG	CA	3016	1/1	0.70	0.43	72,72,72,72	0
56	MG	CA	3161	1/1	0.70	0.20	71,71,71,71	0
56	MG	BA	3022	1/1	0.70	0.16	66,66,66,66	0
56	MG	BA	3223	1/1	0.71	0.39	49,49,49,49	0
56	MG	AA	3001	1/1	0.71	0.26	74,74,74,74	0
56	MG	CA	3071	1/1	0.71	0.12	64,64,64,64	0
56	MG	DA	3135	1/1	0.71	0.31	58,58,58,58	0
56	MG	AA	3015	1/1	0.72	0.24	74,74,74,74	0
56	MG	DA	3356	1/1	0.72	0.45	57,57,57,57	0
56	MG	AA	3038	1/1	0.72	0.45	64,64,64,64	0
56	MG	DA	3024	1/1	0.72	0.61	59,59,59,59	0
56	MG	BA	3185	1/1	0.72	0.22	40,40,40,40	0
56	MG	DQ	3004	1/1	0.72	0.20	52,52,52,52	0
56	MG	DB	3006	1/1	0.72	0.17	54,54,54,54	0
56	MG	AA	3076	1/1	0.72	0.38	74,74,74,74	0
56	MG	DA	3122	1/1	0.73	0.14	60,60,60,60	0
56	MG	DA	3500	1/1	0.73	0.25	66,66,66,66	0
56	MG	AA	3114	1/1	0.73	0.18	73,73,73,73	0
56	MG	AA	3130	1/1	0.74	0.19	55,55,55,55	0
56	MG	DA	3008	1/1	0.74	0.27	56,56,56,56	0
56	MG	AA	3045	1/1	0.74	0.23	71,71,71,71	0
56	MG	AA	3032	1/1	0.74	0.29	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3292	1/1	0.75	0.22	59,59,59,59	0
56	MG	AA	3067	1/1	0.75	0.36	76,76,76,76	0
56	MG	DA	3096	1/1	0.75	0.34	68,68,68,68	0
56	MG	BA	3139	1/1	0.75	0.74	50,50,50,50	0
58	ZN	B4	501	1/1	0.75	0.09	152,152,152,152	0
56	MG	BA	3178	1/1	0.75	0.50	51,51,51,51	0
56	MG	AX	102	1/1	0.75	0.14	66,66,66,66	0
56	MG	CA	3018	1/1	0.75	0.30	55,55,55,55	0
56	MG	DA	3109	1/1	0.75	0.26	55,55,55,55	0
56	MG	DA	3423	1/1	0.76	0.18	29,29,29,29	0
56	MG	DA	3087	1/1	0.76	0.24	43,43,43,43	0
56	MG	DA	3131	1/1	0.76	0.23	60,60,60,60	0
56	MG	AA	3128	1/1	0.76	0.15	64,64,64,64	0
56	MG	DA	3011	1/1	0.76	0.35	42,42,42,42	0
56	MG	DA	3441	1/1	0.76	0.20	46,46,46,46	0
56	MG	AA	3089	1/1	0.76	0.33	80,80,80,80	0
56	MG	AA	3094	1/1	0.76	0.25	78,78,78,78	0
56	MG	CA	3144	1/1	0.76	0.96	84,84,84,84	0
56	MG	BA	3538	1/1	0.76	0.20	29,29,29,29	0
56	MG	DA	3456	1/1	0.76	0.20	58,58,58,58	0
56	MG	AA	3180	1/1	0.76	0.47	75,75,75,75	0
56	MG	AA	3030	1/1	0.76	0.63	66,66,66,66	0
56	MG	AA	3072	1/1	0.76	0.24	69,69,69,69	0
56	MG	CA	3033	1/1	0.76	0.18	64,64,64,64	0
56	MG	BA	3708	1/1	0.77	0.29	38,38,38,38	0
56	MG	AA	3218	1/1	0.77	0.21	73,73,73,73	0
56	MG	DA	3591	1/1	0.77	0.14	67,67,67,67	0
56	MG	BA	3239	1/1	0.77	0.21	33,33,33,33	0
56	MG	CA	3032	1/1	0.77	0.20	44,44,44,44	0
56	MG	DA	3163	1/1	0.77	0.20	52,52,52,52	0
56	MG	BA	3157	1/1	0.78	0.31	52,52,52,52	0
56	MG	BA	3126	1/1	0.78	0.34	47,47,47,47	0
56	MG	DA	3241	1/1	0.78	0.10	74,74,74,74	0
56	MG	DA	3373	1/1	0.78	0.28	52,52,52,52	0
56	MG	BB	3004	1/1	0.78	0.27	57,57,57,57	0
56	MG	CA	3074	1/1	0.78	0.24	56,56,56,56	0
56	MG	BA	3154	1/1	0.78	0.40	55,55,55,55	0
56	MG	CA	3110	1/1	0.78	0.13	93,93,93,93	0
56	MG	AA	3129	1/1	0.78	0.22	77,77,77,77	0
56	MG	CA	3034	1/1	0.78	0.28	66,66,66,66	0
56	MG	AX	105	1/1	0.78	0.47	72,72,72,72	0
56	MG	DA	3464	1/1	0.78	0.20	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BD	311	1/1	0.78	0.84	53,53,53,53	0
56	MG	BA	3740	1/1	0.78	1.13	57,57,57,57	0
56	MG	CA	3114	1/1	0.78	0.19	67,67,67,67	0
56	MG	DA	3263	1/1	0.79	0.14	48,48,48,48	0
56	MG	BA	3409	1/1	0.79	0.17	40,40,40,40	0
56	MG	DA	3549	1/1	0.79	0.37	73,73,73,73	0
56	MG	CA	3127	1/1	0.79	0.20	72,72,72,72	0
56	MG	BZ	3001	1/1	0.79	0.19	47,47,47,47	0
56	MG	BQ	3002	1/1	0.79	0.23	51,51,51,51	0
56	MG	BA	3098	1/1	0.79	0.25	42,42,42,42	0
56	MG	DA	3155	1/1	0.79	0.28	50,50,50,50	0
56	MG	CA	3056	1/1	0.79	0.18	63,63,63,63	0
56	MG	AX	108	1/1	0.79	0.14	66,66,66,66	0
56	MG	CA	3139	1/1	0.79	0.24	76,76,76,76	0
56	MG	CA	3054	1/1	0.79	0.41	74,74,74,74	0
56	MG	BA	3137	1/1	0.79	0.20	59,59,59,59	0
56	MG	DA	3170	1/1	0.79	0.24	45,45,45,45	0
56	MG	DA	3431	1/1	0.79	0.40	56,56,56,56	0
56	MG	DA	3295	1/1	0.79	0.23	31,31,31,31	0
56	MG	AA	3009	1/1	0.79	0.22	71,71,71,71	0
56	MG	AA	3065	1/1	0.79	0.25	50,50,50,50	0
56	MG	BB	3005	1/1	0.79	0.19	62,62,62,62	0
56	MG	AA	3029	1/1	0.79	1.02	60,60,60,60	0
56	MG	AA	3147	1/1	0.79	0.41	51,51,51,51	0
56	MG	BA	3697	1/1	0.79	0.19	63,63,63,63	0
56	MG	DA	3212	1/1	0.79	0.07	48,48,48,48	0
56	MG	AA	3025	1/1	0.79	0.13	78,78,78,78	0
56	MG	BA	3018	1/1	0.80	0.27	54,54,54,54	0
56	MG	CA	3063	1/1	0.80	0.12	57,57,57,57	0
59	FME	CX	101	10/11	0.80	0.43	59,80,100,106	0
56	MG	BA	3259	1/1	0.80	0.22	59,59,59,59	0
56	MG	CA	3041	1/1	0.80	0.39	71,71,71,71	0
56	MG	BA	3661	1/1	0.80	0.27	69,69,69,69	0
56	MG	BG	3002	1/1	0.80	0.11	51,51,51,51	0
56	MG	DA	3141	1/1	0.80	0.19	63,63,63,63	0
56	MG	AA	3148	1/1	0.80	0.24	72,72,72,72	0
56	MG	AA	3120	1/1	0.80	0.44	53,53,53,53	0
56	MG	CA	3027	1/1	0.80	0.27	64,64,64,64	0
56	MG	BA	3283	1/1	0.80	0.18	61,61,61,61	0
56	MG	DA	3491	1/1	0.80	0.27	55,55,55,55	0
56	MG	CA	3042	1/1	0.80	0.28	69,69,69,69	0
56	MG	AA	3115	1/1	0.80	0.19	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3004	1/1	0.80	0.22	45,45,45,45	0
56	MG	CX	103	1/1	0.80	0.23	57,57,57,57	0
56	MG	BA	3530	1/1	0.80	0.23	72,72,72,72	0
56	MG	DA	3531	1/1	0.81	0.12	44,44,44,44	0
56	MG	DB	3003	1/1	0.81	0.20	70,70,70,70	0
56	MG	AA	3022	1/1	0.81	0.24	56,56,56,56	0
56	MG	BA	3358	1/1	0.81	0.15	78,78,78,78	0
56	MG	CA	3167	1/1	0.81	0.08	68,68,68,68	0
56	MG	BA	3257	1/1	0.81	0.25	56,56,56,56	0
56	MG	DA	3346	1/1	0.81	0.20	64,64,64,64	0
56	MG	BA	3291	1/1	0.81	0.15	44,44,44,44	0
56	MG	DA	3557	1/1	0.81	0.26	74,74,74,74	0
56	MG	BA	3694	1/1	0.81	0.27	48,48,48,48	0
56	MG	BA	3606	1/1	0.81	0.10	44,44,44,44	0
56	MG	BA	3405	1/1	0.81	0.25	57,57,57,57	0
56	MG	BB	3017	1/1	0.81	0.20	80,80,80,80	0
56	MG	BA	3188	1/1	0.81	0.29	49,49,49,49	0
56	MG	BA	3155	1/1	0.81	0.46	56,56,56,56	0
56	MG	BA	3313	1/1	0.81	0.12	56,56,56,56	0
56	MG	DA	3053	1/1	0.81	0.19	47,47,47,47	0
56	MG	BA	3674	1/1	0.82	0.30	67,67,67,67	0
56	MG	AA	3135	1/1	0.82	0.31	49,49,49,49	0
56	MG	BA	3307	1/1	0.82	0.16	35,35,35,35	0
56	MG	DA	3596	1/1	0.82	0.13	68,68,68,68	0
56	MG	DA	3642	1/1	0.82	0.18	67,67,67,67	0
56	MG	AA	3084	1/1	0.82	0.32	71,71,71,71	0
56	MG	BA	3485	1/1	0.82	0.19	67,67,67,67	0
56	MG	BA	3601	1/1	0.82	0.19	61,61,61,61	0
56	MG	DD	302	1/1	0.82	0.61	48,48,48,48	0
56	MG	BA	3107	1/1	0.82	0.15	60,60,60,60	0
56	MG	AA	3140	1/1	0.82	0.12	65,65,65,65	0
56	MG	DA	3153	1/1	0.82	0.32	51,51,51,51	0
56	MG	BA	3248	1/1	0.82	0.37	68,68,68,68	0
56	MG	DA	3232	1/1	0.82	0.12	39,39,39,39	0
56	MG	DA	3214	1/1	0.82	0.09	48,48,48,48	0
56	MG	DA	3203	1/1	0.82	0.14	48,48,48,48	0
56	MG	AA	3077	1/1	0.82	0.39	67,67,67,67	0
56	MG	AA	3222	1/1	0.82	0.14	64,64,64,64	0
56	MG	DA	3012	1/1	0.82	0.39	52,52,52,52	0
56	MG	CA	3152	1/1	0.82	0.32	45,45,45,45	0
56	MG	BA	3302	1/1	0.83	0.26	48,48,48,48	0
56	MG	BA	3006	1/1	0.83	0.27	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3073	1/1	0.83	0.51	74,74,74,74	0
56	MG	DA	3098	1/1	0.83	1.02	45,45,45,45	0
56	MG	CA	3162	1/1	0.83	0.25	60,60,60,60	0
56	MG	DA	3227	1/1	0.83	0.17	40,40,40,40	0
56	MG	CA	3024	1/1	0.83	0.34	57,57,57,57	0
56	MG	DA	3603	1/1	0.83	0.23	66,66,66,66	0
56	MG	DA	3171	1/1	0.83	0.89	58,58,58,58	0
56	MG	CA	3172	1/1	0.83	0.22	65,65,65,65	0
56	MG	DA	3296	1/1	0.83	0.46	65,65,65,65	0
58	ZN	D4	501	1/1	0.83	0.08	155,155,155,155	0
56	MG	BA	3163	1/1	0.83	0.37	50,50,50,50	0
56	MG	DA	3068	1/1	0.83	0.22	52,52,52,52	0
56	MG	AA	3051	1/1	0.83	0.16	56,56,56,56	0
56	MG	DA	3100	1/1	0.83	0.63	55,55,55,55	0
56	MG	DA	3089	1/1	0.83	0.27	51,51,51,51	0
56	MG	DU	3001	1/1	0.83	0.90	61,61,61,61	0
56	MG	BA	3349	1/1	0.84	0.17	31,31,31,31	0
56	MG	DA	3222	1/1	0.84	0.22	45,45,45,45	0
56	MG	DF	304	1/1	0.84	0.51	39,39,39,39	0
56	MG	BA	3517	1/1	0.84	0.12	52,52,52,52	0
56	MG	BA	3255	1/1	0.84	0.21	53,53,53,53	0
56	MG	DA	3157	1/1	0.84	0.49	56,56,56,56	0
56	MG	CA	3150	1/1	0.84	0.18	63,63,63,63	0
56	MG	DA	3220	1/1	0.84	0.36	61,61,61,61	0
56	MG	DA	3125	1/1	0.84	0.48	55,55,55,55	0
56	MG	BA	3067	1/1	0.84	0.46	55,55,55,55	0
56	MG	AA	3069	1/1	0.84	0.09	77,77,77,77	0
56	MG	DD	304	1/1	0.84	0.53	40,40,40,40	0
56	MG	CA	3091	1/1	0.84	0.15	95,95,95,95	0
56	MG	DA	3468	1/1	0.84	0.28	47,47,47,47	0
56	MG	CA	3103	1/1	0.84	0.50	101,101,101,101	0
56	MG	AA	3027	1/1	0.84	0.27	67,67,67,67	0
56	MG	BN	3003	1/1	0.84	0.42	67,67,67,67	0
56	MG	AA	3028	1/1	0.84	0.47	72,72,72,72	0
56	MG	DA	3103	1/1	0.84	0.36	52,52,52,52	0
56	MG	DG	3001	1/1	0.84	0.11	68,68,68,68	0
56	MG	AA	3127	1/1	0.84	0.21	50,50,50,50	0
56	MG	AA	3090	1/1	0.84	0.18	64,64,64,64	0
56	MG	BA	3249	1/1	0.84	0.39	46,46,46,46	0
56	MG	DA	3005	1/1	0.84	0.40	50,50,50,50	0
56	MG	DA	3344	1/1	0.84	0.12	48,48,48,48	0
56	MG	CA	3048	1/1	0.85	0.24	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3092	1/1	0.85	0.26	28,28,28,28	0
56	MG	DA	3041	1/1	0.85	0.41	54,54,54,54	0
56	MG	BA	3074	1/1	0.85	0.17	38,38,38,38	0
56	MG	DA	3077	1/1	0.85	0.32	48,48,48,48	0
56	MG	AX	104	1/1	0.85	0.25	62,62,62,62	0
56	MG	BA	3299	1/1	0.85	0.32	56,56,56,56	0
56	MG	AA	3126	1/1	0.85	0.17	54,54,54,54	0
56	MG	BA	3596	1/1	0.85	0.25	79,79,79,79	0
56	MG	DA	3627	1/1	0.85	0.24	52,52,52,52	0
56	MG	CA	3119	1/1	0.85	0.48	73,73,73,73	0
56	MG	CA	3062	1/1	0.85	0.34	67,67,67,67	0
56	MG	DA	3164	1/1	0.85	0.16	40,40,40,40	0
56	MG	DA	3225	1/1	0.85	0.12	64,64,64,64	0
56	MG	CA	3057	1/1	0.85	0.22	40,40,40,40	0
56	MG	CA	3160	1/1	0.85	0.14	49,49,49,49	0
56	MG	BA	3060	1/1	0.85	0.59	64,64,64,64	0
56	MG	BA	3397	1/1	0.85	0.07	44,44,44,44	0
56	MG	AA	3088	1/1	0.85	0.34	53,53,53,53	0
56	MG	DA	3448	1/1	0.85	0.33	67,67,67,67	0
56	MG	AA	3189	1/1	0.85	0.15	74,74,74,74	0
56	MG	DA	3190	1/1	0.85	0.10	54,54,54,54	0
56	MG	AA	3050	1/1	0.85	0.31	50,50,50,50	0
56	MG	DA	3057	1/1	0.85	0.25	57,57,57,57	0
56	MG	BA	3156	1/1	0.85	0.42	61,61,61,61	0
56	MG	BA	3204	1/1	0.85	0.20	48,48,48,48	0
56	MG	CA	3134	1/1	0.85	0.23	92,92,92,92	0
56	MG	DA	3361	1/1	0.85	0.13	58,58,58,58	0
56	MG	BA	3634	1/1	0.85	0.11	77,77,77,77	0
56	MG	BA	3068	1/1	0.85	0.45	43,43,43,43	0
56	MG	CA	3157	1/1	0.85	0.18	56,56,56,56	0
56	MG	CA	3067	1/1	0.85	0.27	66,66,66,66	0
56	MG	DA	3554	1/1	0.85	0.27	62,62,62,62	0
56	MG	BA	3121	1/1	0.85	0.26	50,50,50,50	0
56	MG	BA	3110	1/1	0.85	0.24	43,43,43,43	0
56	MG	BA	3331	1/1	0.86	0.17	61,61,61,61	0
56	MG	BA	3514	1/1	0.86	0.21	49,49,49,49	0
56	MG	AA	3071	1/1	0.86	0.23	60,60,60,60	0
56	MG	BA	3571	1/1	0.86	0.20	48,48,48,48	0
56	MG	DA	3645	1/1	0.86	0.41	57,57,57,57	0
56	MG	DA	3371	1/1	0.86	0.24	37,37,37,37	0
59	FME	AX	101	10/11	0.86	0.45	55,74,92,107	0
56	MG	DA	3066	1/1	0.86	0.31	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3158	1/1	0.86	0.44	43,43,43,43	0
56	MG	BA	3733	1/1	0.86	0.42	40,40,40,40	0
56	MG	BA	3228	1/1	0.86	0.35	23,23,23,23	0
56	MG	AA	3209	1/1	0.86	0.38	66,66,66,66	0
56	MG	DA	3188	1/1	0.86	0.51	52,52,52,52	0
56	MG	BR	203	1/1	0.86	0.51	48,48,48,48	0
56	MG	CA	3030	1/1	0.86	0.36	74,74,74,74	0
56	MG	BW	3001	1/1	0.86	0.29	55,55,55,55	0
56	MG	DA	3001	1/1	0.86	0.26	76,76,76,76	0
56	MG	BA	3238	1/1	0.86	0.17	48,48,48,48	0
56	MG	BA	3071	1/1	0.86	0.22	55,55,55,55	0
56	MG	DA	3221	1/1	0.86	0.27	56,56,56,56	0
56	MG	B9	502	1/1	0.86	0.26	49,49,49,49	0
56	MG	AA	3023	1/1	0.86	0.12	56,56,56,56	0
56	MG	BA	3217	1/1	0.86	0.33	59,59,59,59	0
56	MG	BA	3300	1/1	0.86	0.29	48,48,48,48	0
56	MG	BA	3085	1/1	0.86	0.38	35,35,35,35	0
56	MG	CA	3036	1/1	0.86	0.23	56,56,56,56	0
56	MG	AA	3121	1/1	0.86	0.46	52,52,52,52	0
56	MG	DA	3036	1/1	0.86	0.27	35,35,35,35	0
56	MG	DA	3110	1/1	0.86	0.17	46,46,46,46	0
56	MG	BA	3250	1/1	0.86	0.28	61,61,61,61	0
56	MG	BA	3207	1/1	0.86	0.37	44,44,44,44	0
56	MG	BA	3641	1/1	0.86	0.14	33,33,33,33	0
56	MG	DA	3003	1/1	0.86	0.18	43,43,43,43	0
56	MG	BA	3028	1/1	0.86	0.31	59,59,59,59	0
56	MG	BA	3082	1/1	0.86	0.16	54,54,54,54	0
56	MG	BA	3717	1/1	0.86	0.11	51,51,51,51	0
56	MG	BB	3003	1/1	0.86	0.23	40,40,40,40	0
56	MG	BA	3203	1/1	0.86	0.22	45,45,45,45	0
56	MG	CA	3055	1/1	0.86	0.25	61,61,61,61	0
56	MG	AA	3064	1/1	0.86	0.27	65,65,65,65	0
56	MG	AA	3042	1/1	0.86	0.28	50,50,50,50	0
56	MG	BA	3029	1/1	0.86	0.66	53,53,53,53	0
56	MG	CA	3122	1/1	0.86	0.20	70,70,70,70	0
56	MG	DA	3621	1/1	0.86	0.17	46,46,46,46	0
56	MG	BA	3722	1/1	0.86	0.27	49,49,49,49	0
56	MG	CA	3028	1/1	0.86	0.56	62,62,62,62	0
56	MG	AA	3026	1/1	0.86	0.18	52,52,52,52	0
56	MG	AA	3117	1/1	0.86	0.15	64,64,64,64	0
56	MG	BA	3636	1/1	0.86	0.13	54,54,54,54	0
56	MG	BA	3251	1/1	0.86	0.27	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	AA	3033	1/1	0.86	0.45	68,68,68,68	0
56	MG	BA	3506	1/1	0.86	0.25	33,33,33,33	0
56	MG	AA	3133	1/1	0.86	0.69	71,71,71,71	0
56	MG	BA	3084	1/1	0.86	0.50	47,47,47,47	0
56	MG	AA	3203	1/1	0.86	0.15	76,76,76,76	0
56	MG	AA	3142	1/1	0.87	0.37	60,60,60,60	0
56	MG	DA	3626	1/1	0.87	0.17	63,63,63,63	0
56	MG	DA	3165	1/1	0.87	0.32	48,48,48,48	0
56	MG	AA	3020	1/1	0.87	0.18	80,80,80,80	0
56	MG	CA	3019	1/1	0.87	0.15	62,62,62,62	0
56	MG	DA	3074	1/1	0.87	0.31	60,60,60,60	0
56	MG	DA	3035	1/1	0.87	0.71	58,58,58,58	0
56	MG	DA	3208	1/1	0.87	0.19	46,46,46,46	0
56	MG	BA	3133	1/1	0.87	0.60	53,53,53,53	0
56	MG	BA	3070	1/1	0.87	0.24	46,46,46,46	0
56	MG	DA	3528	1/1	0.87	0.15	33,33,33,33	0
56	MG	BA	3484	1/1	0.87	0.16	40,40,40,40	0
56	MG	CA	3029	1/1	0.87	0.17	54,54,54,54	0
56	MG	DA	3458	1/1	0.87	0.22	47,47,47,47	0
56	MG	AA	3063	1/1	0.87	0.14	57,57,57,57	0
56	MG	DA	3457	1/1	0.87	0.15	44,44,44,44	0
56	MG	DA	3079	1/1	0.87	0.28	44,44,44,44	0
56	MG	DA	3015	1/1	0.87	0.33	54,54,54,54	0
56	MG	DA	3213	1/1	0.87	0.08	48,48,48,48	0
56	MG	DA	3424	1/1	0.87	0.19	58,58,58,58	0
56	MG	CA	3084	1/1	0.87	0.18	80,80,80,80	0
56	MG	AA	3039	1/1	0.87	0.20	62,62,62,62	0
56	MG	DU	3002	1/1	0.87	0.58	52,52,52,52	0
56	MG	BA	3192	1/1	0.87	0.36	48,48,48,48	0
56	MG	DA	3338	1/1	0.87	0.16	58,58,58,58	0
56	MG	CA	3007	1/1	0.87	0.41	63,63,63,63	0
56	MG	DA	3115	1/1	0.87	0.08	64,64,64,64	0
56	MG	DA	3119	1/1	0.87	0.15	44,44,44,44	0
56	MG	BA	3224	1/1	0.87	0.40	48,48,48,48	0
56	MG	BA	3099	1/1	0.87	0.31	55,55,55,55	0
56	MG	BA	3240	1/1	0.87	0.26	54,54,54,54	0
56	MG	BA	3081	1/1	0.87	0.29	44,44,44,44	0
56	MG	DA	3112	1/1	0.87	0.31	49,49,49,49	0
56	MG	BA	3293	1/1	0.87	0.28	69,69,69,69	0
56	MG	BA	3109	1/1	0.88	0.28	62,62,62,62	0
56	MG	BA	3039	1/1	0.88	0.29	44,44,44,44	0
56	MG	AA	3125	1/1	0.88	0.14	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3261	1/1	0.88	0.28	45,45,45,45	0
56	MG	DA	3062	1/1	0.88	0.39	58,58,58,58	0
56	MG	DB	3002	1/1	0.88	0.20	72,72,72,72	0
56	MG	AA	3003	1/1	0.88	0.25	70,70,70,70	0
56	MG	DA	3243	1/1	0.88	0.41	49,49,49,49	0
56	MG	DA	3455	1/1	0.88	0.21	53,53,53,53	0
56	MG	AA	3143	1/1	0.88	0.20	67,67,67,67	0
56	MG	BA	3704	1/1	0.88	0.34	58,58,58,58	0
56	MG	DA	3287	1/1	0.88	0.06	53,53,53,53	0
56	MG	BA	3105	1/1	0.88	0.19	54,54,54,54	0
56	MG	DA	3006	1/1	0.88	0.08	41,41,41,41	0
56	MG	BA	3649	1/1	0.88	0.25	43,43,43,43	0
56	MG	AA	3037	1/1	0.88	0.28	53,53,53,53	0
56	MG	BA	3713	1/1	0.88	0.22	49,49,49,49	0
56	MG	DA	3117	1/1	0.88	0.17	46,46,46,46	0
56	MG	DB	3008	1/1	0.88	0.12	36,36,36,36	0
56	MG	BA	3675	1/1	0.88	0.26	68,68,68,68	0
56	MG	DA	3086	1/1	0.88	0.30	43,43,43,43	0
56	MG	AN	101	1/1	0.88	0.17	64,64,64,64	0
56	MG	BA	3172	1/1	0.88	0.12	54,54,54,54	0
56	MG	BA	3094	1/1	0.88	0.47	62,62,62,62	0
56	MG	CA	3021	1/1	0.88	0.25	54,54,54,54	0
56	MG	DA	3205	1/1	0.88	0.26	41,41,41,41	0
56	MG	DA	3608	1/1	0.88	0.29	63,63,63,63	0
56	MG	DA	3049	1/1	0.88	0.18	56,56,56,56	0
56	MG	BA	3135	1/1	0.88	0.26	57,57,57,57	0
56	MG	CA	3142	1/1	0.88	0.20	80,80,80,80	0
56	MG	BA	3242	1/1	0.88	0.18	45,45,45,45	0
56	MG	BA	3076	1/1	0.88	0.22	40,40,40,40	0
56	MG	DA	3460	1/1	0.88	0.10	47,47,47,47	0
56	MG	AA	3164	1/1	0.88	0.23	61,61,61,61	0
56	MG	CA	3043	1/1	0.88	0.34	62,62,62,62	0
56	MG	DA	3462	1/1	0.88	0.22	71,71,71,71	0
60	K	DA	3234	1/1	0.88	0.27	102,102,102,102	0
56	MG	DA	3465	1/1	0.88	0.17	41,41,41,41	0
56	MG	DA	3180	1/1	0.88	0.20	47,47,47,47	0
56	MG	DA	3029	1/1	0.88	0.12	62,62,62,62	0
56	MG	BA	3007	1/1	0.88	0.25	55,55,55,55	0
56	MG	BA	3563	1/1	0.88	0.39	66,66,66,66	0
56	MG	BA	3640	1/1	0.88	0.21	31,31,31,31	0
56	MG	BA	3626	1/1	0.88	0.13	50,50,50,50	0
56	MG	DA	3187	1/1	0.88	0.67	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3647	1/1	0.88	0.56	45,45,45,45	0
56	MG	DA	3186	1/1	0.88	0.29	38,38,38,38	0
56	MG	BA	3122	1/1	0.88	0.65	68,68,68,68	0
56	MG	BA	3687	1/1	0.88	0.14	59,59,59,59	0
56	MG	BA	3707	1/1	0.88	0.17	57,57,57,57	0
56	MG	BA	3429	1/1	0.89	0.16	55,55,55,55	0
56	MG	DA	3144	1/1	0.89	0.34	37,37,37,37	0
56	MG	DA	3318	1/1	0.89	0.19	47,47,47,47	0
56	MG	BA	3567	1/1	0.89	0.10	54,54,54,54	0
56	MG	BA	3225	1/1	0.89	0.40	42,42,42,42	0
56	MG	BA	3599	1/1	0.89	0.10	56,56,56,56	0
56	MG	DA	3099	1/1	0.89	0.34	39,39,39,39	0
56	MG	BA	3064	1/1	0.89	0.38	49,49,49,49	0
56	MG	DA	3175	1/1	0.89	0.30	52,52,52,52	0
56	MG	BA	3161	1/1	0.89	0.13	50,50,50,50	0
56	MG	BA	3680	1/1	0.89	0.24	62,62,62,62	0
56	MG	AV	101	1/1	0.89	0.24	51,51,51,51	0
56	MG	DA	3354	1/1	0.89	0.18	39,39,39,39	0
56	MG	DA	3282	1/1	0.89	0.31	58,58,58,58	0
56	MG	AA	3017	1/1	0.89	0.29	57,57,57,57	0
56	MG	DA	3143	1/1	0.89	0.20	53,53,53,53	0
56	MG	DA	3613	1/1	0.89	0.31	64,64,64,64	0
56	MG	DA	3038	1/1	0.89	0.33	37,37,37,37	0
56	MG	DB	3005	1/1	0.89	0.25	41,41,41,41	0
56	MG	BA	3561	1/1	0.89	0.25	39,39,39,39	0
56	MG	AA	3102	1/1	0.89	0.05	68,68,68,68	0
56	MG	BA	3167	1/1	0.89	0.46	50,50,50,50	0
56	MG	AA	3075	1/1	0.89	0.11	50,50,50,50	0
56	MG	DA	3081	1/1	0.89	0.23	56,56,56,56	0
56	MG	BA	3289	1/1	0.89	0.13	53,53,53,53	0
56	MG	BW	3002	1/1	0.89	0.18	34,34,34,34	0
56	MG	CA	3171	1/1	0.89	0.15	61,61,61,61	0
56	MG	DA	3618	1/1	0.89	0.25	61,61,61,61	0
56	MG	BA	3444	1/1	0.89	0.27	29,29,29,29	0
56	MG	BA	3058	1/1	0.89	0.39	41,41,41,41	0
56	MG	D3	101	1/1	0.89	0.55	54,54,54,54	0
56	MG	AX	107	1/1	0.89	0.44	82,82,82,82	0
56	MG	BA	3166	1/1	0.89	0.20	41,41,41,41	0
56	MG	BA	3246	1/1	0.89	0.33	38,38,38,38	0
56	MG	AF	3001	1/1	0.89	0.16	62,62,62,62	0
56	MG	DA	3108	1/1	0.89	0.41	50,50,50,50	0
56	MG	DA	3289	1/1	0.89	0.17	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3121	1/1	0.89	0.26	46,46,46,46	0
56	MG	BA	3435	1/1	0.89	0.21	59,59,59,59	0
56	MG	DA	3434	1/1	0.89	0.19	51,51,51,51	0
56	MG	DA	3278	1/1	0.89	0.08	39,39,39,39	0
56	MG	CA	3135	1/1	0.89	0.37	61,61,61,61	0
56	MG	CA	3117	1/1	0.89	0.15	58,58,58,58	0
56	MG	BA	3604	1/1	0.89	0.38	64,64,64,64	0
56	MG	CA	3163	1/1	0.89	0.24	60,60,60,60	0
56	MG	BA	3247	1/1	0.89	0.21	58,58,58,58	0
56	MG	BA	3164	1/1	0.89	0.49	57,57,57,57	0
56	MG	DA	3606	1/1	0.89	0.18	58,58,58,58	0
56	MG	DA	3067	1/1	0.89	0.29	35,35,35,35	0
56	MG	CA	3156	1/1	0.89	0.26	80,80,80,80	0
56	MG	AX	103	1/1	0.89	0.10	57,57,57,57	0
56	MG	CA	3061	1/1	0.89	0.48	68,68,68,68	0
56	MG	DA	3102	1/1	0.89	0.27	49,49,49,49	0
56	MG	CA	3035	1/1	0.89	0.26	49,49,49,49	0
56	MG	BA	3629	1/1	0.89	0.14	51,51,51,51	0
56	MG	DA	3392	1/1	0.89	0.14	60,60,60,60	0
56	MG	BA	3524	1/1	0.89	0.13	50,50,50,50	0
56	MG	DA	3160	1/1	0.89	0.24	47,47,47,47	0
56	MG	AA	3082	1/1	0.89	0.16	52,52,52,52	0
56	MG	DA	3447	1/1	0.90	0.18	56,56,56,56	0
56	MG	BN	3005	1/1	0.90	1.02	63,63,63,63	0
56	MG	BA	3048	1/1	0.90	0.35	33,33,33,33	0
56	MG	DA	3532	1/1	0.90	0.10	60,60,60,60	0
56	MG	DA	3139	1/1	0.90	0.22	47,47,47,47	0
56	MG	CA	3006	1/1	0.90	0.09	72,72,72,72	0
56	MG	DE	301	1/1	0.90	0.83	51,51,51,51	0
56	MG	DA	3106	1/1	0.90	0.40	45,45,45,45	0
56	MG	AA	3119	1/1	0.90	0.31	42,42,42,42	0
56	MG	DA	3584	1/1	0.90	0.15	47,47,47,47	0
56	MG	CA	3106	1/1	0.90	0.39	72,72,72,72	0
56	MG	DA	3061	1/1	0.90	0.27	47,47,47,47	0
56	MG	DA	3517	1/1	0.90	0.28	47,47,47,47	0
56	MG	BA	3334	1/1	0.90	0.14	41,41,41,41	0
56	MG	DA	3137	1/1	0.90	0.31	62,62,62,62	0
56	MG	BA	3180	1/1	0.90	0.33	48,48,48,48	0
56	MG	DA	3409	1/1	0.90	0.10	54,54,54,54	0
56	MG	BA	3738	1/1	0.90	0.22	58,58,58,58	0
56	MG	CN	502	1/1	0.90	0.31	70,70,70,70	0
56	MG	BA	3648	1/1	0.90	0.16	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	B7	104	1/1	0.90	0.22	55,55,55,55	0
56	MG	DA	3219	1/1	0.90	0.36	49,49,49,49	0
56	MG	DA	3472	1/1	0.90	0.18	38,38,38,38	0
56	MG	DA	3078	1/1	0.90	0.15	49,49,49,49	0
56	MG	BA	3723	1/1	0.90	0.17	25,25,25,25	0
56	MG	AA	3105	1/1	0.90	0.30	54,54,54,54	0
56	MG	DA	3189	1/1	0.90	0.21	55,55,55,55	0
56	MG	AA	3049	1/1	0.90	0.39	46,46,46,46	0
56	MG	DA	3116	1/1	0.90	0.39	43,43,43,43	0
56	MG	BP	203	1/1	0.90	0.62	39,39,39,39	0
56	MG	BA	3023	1/1	0.90	0.43	34,34,34,34	0
56	MG	BA	3086	1/1	0.90	0.32	50,50,50,50	0
56	MG	CA	3145	1/1	0.90	0.11	67,67,67,67	0
56	MG	DA	3060	1/1	0.90	0.34	51,51,51,51	0
56	MG	B7	101	1/1	0.90	0.19	45,45,45,45	0
56	MG	CA	3131	1/1	0.90	0.14	48,48,48,48	0
56	MG	DA	3298	1/1	0.90	0.26	45,45,45,45	0
56	MG	AA	3098	1/1	0.90	0.43	76,76,76,76	0
56	MG	CA	3124	1/1	0.90	0.17	64,64,64,64	0
56	MG	BA	3244	1/1	0.90	0.19	46,46,46,46	0
56	MG	AA	3068	1/1	0.90	0.11	67,67,67,67	0
56	MG	DA	3529	1/1	0.90	0.48	72,72,72,72	0
56	MG	BA	3602	1/1	0.90	0.16	44,44,44,44	0
56	MG	AA	3139	1/1	0.90	0.20	58,58,58,58	0
56	MG	BA	3739	1/1	0.90	0.38	50,50,50,50	0
56	MG	BA	3066	1/1	0.90	0.24	49,49,49,49	0
56	MG	DA	3353	1/1	0.90	0.17	54,54,54,54	0
56	MG	DA	3090	1/1	0.90	0.27	59,59,59,59	0
56	MG	BB	3014	1/1	0.90	0.09	68,68,68,68	0
56	MG	CA	3025	1/1	0.90	0.12	102,102,102,102	0
56	MG	CA	3009	1/1	0.90	0.13	55,55,55,55	0
56	MG	DA	3396	1/1	0.90	0.14	37,37,37,37	0
56	MG	BA	3123	1/1	0.90	0.27	47,47,47,47	0
56	MG	BA	3460	1/1	0.90	0.18	66,66,66,66	0
56	MG	AA	3073	1/1	0.90	0.11	63,63,63,63	0
56	MG	BA	3654	1/1	0.90	0.15	49,49,49,49	0
56	MG	BA	3190	1/1	0.90	0.25	42,42,42,42	0
56	MG	BA	3182	1/1	0.90	0.36	43,43,43,43	0
56	MG	AD	502	1/1	0.90	0.63	56,56,56,56	0
56	MG	AA	3087	1/1	0.90	0.21	87,87,87,87	0
56	MG	DB	3010	1/1	0.90	0.19	66,66,66,66	0
56	MG	CA	3101	1/1	0.90	0.11	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	AA	3052	1/1	0.90	0.24	58,58,58,58	0
56	MG	DA	3418	1/1	0.90	0.22	57,57,57,57	0
56	MG	BA	3716	1/1	0.90	0.24	77,77,77,77	0
56	MG	CA	3126	1/1	0.90	0.25	56,56,56,56	0
56	MG	DA	3391	1/1	0.90	0.14	54,54,54,54	0
56	MG	DA	3428	1/1	0.90	0.28	30,30,30,30	0
56	MG	DA	3042	1/1	0.90	0.35	38,38,38,38	0
56	MG	BA	3089	1/1	0.90	0.23	50,50,50,50	0
56	MG	BA	3146	1/1	0.90	0.39	56,56,56,56	0
56	MG	DA	3283	1/1	0.90	0.19	47,47,47,47	0
56	MG	DA	3256	1/1	0.90	0.12	41,41,41,41	0
56	MG	AA	3092	1/1	0.90	0.50	59,59,59,59	0
56	MG	BA	3688	1/1	0.90	0.05	58,58,58,58	0
56	MG	DA	3630	1/1	0.90	0.09	67,67,67,67	0
56	MG	DA	3521	1/1	0.90	0.19	46,46,46,46	0
56	MG	DA	3017	1/1	0.90	0.25	51,51,51,51	0
56	MG	DA	3485	1/1	0.90	0.20	44,44,44,44	0
56	MG	BW	3005	1/1	0.90	0.44	38,38,38,38	0
56	MG	BA	3265	1/1	0.90	0.23	39,39,39,39	0
56	MG	BA	3269	1/1	0.90	0.11	32,32,32,32	0
56	MG	AA	3136	1/1	0.90	0.11	68,68,68,68	0
56	MG	DA	3436	1/1	0.91	0.32	61,61,61,61	0
56	MG	DA	3071	1/1	0.91	0.52	46,46,46,46	0
56	MG	BA	3581	1/1	0.91	0.32	54,54,54,54	0
56	MG	BA	3134	1/1	0.91	0.14	34,34,34,34	0
56	MG	BA	3281	1/1	0.91	0.23	45,45,45,45	0
56	MG	BA	3676	1/1	0.91	0.17	63,63,63,63	0
56	MG	CE	3001	1/1	0.91	0.20	66,66,66,66	0
56	MG	DA	3623	1/1	0.91	0.12	63,63,63,63	0
56	MG	BA	3264	1/1	0.91	0.18	29,29,29,29	0
56	MG	BA	3346	1/1	0.91	0.17	33,33,33,33	0
56	MG	BA	3191	1/1	0.91	0.20	56,56,56,56	0
56	MG	DA	3475	1/1	0.91	0.12	35,35,35,35	0
56	MG	BA	3020	1/1	0.91	0.29	43,43,43,43	0
56	MG	BA	3477	1/1	0.91	0.16	52,52,52,52	0
56	MG	DA	3172	1/1	0.91	0.33	46,46,46,46	0
56	MG	AA	3173	1/1	0.91	0.15	37,37,37,37	0
56	MG	BA	3431	1/1	0.91	0.25	54,54,54,54	0
56	MG	AA	3167	1/1	0.91	0.18	78,78,78,78	0
56	MG	DA	3530	1/1	0.91	0.16	57,57,57,57	0
56	MG	BA	3059	1/1	0.91	0.37	35,35,35,35	0
56	MG	BD	304	1/1	0.91	0.44	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3284	1/1	0.91	0.72	76,76,76,76	0
56	MG	DA	3210	1/1	0.91	0.28	46,46,46,46	0
56	MG	BA	3138	1/1	0.91	0.17	54,54,54,54	0
56	MG	BU	205	1/1	0.91	0.36	39,39,39,39	0
56	MG	DA	3654	1/1	0.91	0.29	50,50,50,50	0
56	MG	BA	3088	1/1	0.91	0.25	55,55,55,55	0
56	MG	BA	3184	1/1	0.91	0.81	51,51,51,51	0
56	MG	DA	3537	1/1	0.91	0.16	74,74,74,74	0
56	MG	AA	3204	1/1	0.91	0.17	70,70,70,70	0
56	MG	DA	3374	1/1	0.91	0.14	40,40,40,40	0
56	MG	DA	3202	1/1	0.91	0.21	39,39,39,39	0
56	MG	DA	3091	1/1	0.91	0.50	50,50,50,50	0
56	MG	DA	3040	1/1	0.91	0.21	45,45,45,45	0
56	MG	BA	3097	1/1	0.91	0.16	30,30,30,30	0
56	MG	BA	3499	1/1	0.91	0.18	50,50,50,50	0
56	MG	AA	3219	1/1	0.91	0.18	54,54,54,54	0
56	MG	DA	3395	1/1	0.91	0.14	40,40,40,40	0
56	MG	AA	3080	1/1	0.91	0.23	58,58,58,58	0
56	MG	BA	3667	1/1	0.91	0.22	72,72,72,72	0
56	MG	BW	3003	1/1	0.91	0.26	39,39,39,39	0
56	MG	BA	3241	1/1	0.91	0.41	41,41,41,41	0
56	MG	BA	3686	1/1	0.91	0.29	65,65,65,65	0
56	MG	DA	3637	1/1	0.91	0.20	59,59,59,59	0
56	MG	CA	3159	1/1	0.91	0.74	76,76,76,76	0
56	MG	AA	3182	1/1	0.91	0.13	48,48,48,48	0
56	MG	DA	3483	1/1	0.91	0.14	55,55,55,55	0
56	MG	DA	3276	1/1	0.91	0.11	26,26,26,26	0
56	MG	AA	3134	1/1	0.91	0.37	70,70,70,70	0
56	MG	BA	3632	1/1	0.91	0.15	55,55,55,55	0
56	MG	BA	3279	1/1	0.91	0.16	60,60,60,60	0
56	MG	DA	3402	1/1	0.91	0.17	33,33,33,33	0
56	MG	BA	3046	1/1	0.91	0.41	52,52,52,52	0
56	MG	DA	3328	1/1	0.91	0.28	33,33,33,33	0
56	MG	BA	3647	1/1	0.91	0.26	40,40,40,40	0
56	MG	BA	3053	1/1	0.91	0.19	52,52,52,52	0
56	MG	BA	3702	1/1	0.91	0.24	56,56,56,56	0
56	MG	BA	3271	1/1	0.91	0.32	40,40,40,40	0
56	MG	DA	3254	1/1	0.91	0.14	52,52,52,52	0
56	MG	DA	3195	1/1	0.91	0.20	51,51,51,51	0
56	MG	DA	3560	1/1	0.91	0.07	57,57,57,57	0
56	MG	DA	3454	1/1	0.91	0.11	52,52,52,52	0
56	MG	BA	3118	1/1	0.91	0.26	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3467	1/1	0.91	0.15	44,44,44,44	0
56	MG	DA	3540	1/1	0.91	0.13	76,76,76,76	0
56	MG	DW	201	1/1	0.91	0.33	45,45,45,45	0
56	MG	DA	3240	1/1	0.91	0.17	58,58,58,58	0
56	MG	BA	3550	1/1	0.91	0.19	32,32,32,32	0
56	MG	BA	3432	1/1	0.91	0.14	27,27,27,27	0
56	MG	BX	102	1/1	0.91	0.23	60,60,60,60	0
56	MG	BQ	3004	1/1	0.91	0.33	41,41,41,41	0
56	MG	BA	3119	1/1	0.91	0.11	56,56,56,56	0
56	MG	DA	3138	1/1	0.91	0.41	53,53,53,53	0
56	MG	BN	3002	1/1	0.91	0.20	52,52,52,52	0
56	MG	DA	3565	1/1	0.91	0.22	48,48,48,48	0
56	MG	DA	3617	1/1	0.91	0.07	51,51,51,51	0
56	MG	DA	3655	1/1	0.91	0.17	62,62,62,62	0
56	MG	AA	3081	1/1	0.91	0.38	46,46,46,46	0
56	MG	DA	3249	1/1	0.91	0.20	25,25,25,25	0
56	MG	DA	3598	1/1	0.91	0.17	45,45,45,45	0
56	MG	CA	3064	1/1	0.91	0.14	74,74,74,74	0
56	MG	AA	3096	1/1	0.91	0.27	52,52,52,52	0
56	MG	AA	3197	1/1	0.91	0.19	64,64,64,64	0
56	MG	DA	3043	1/1	0.91	0.54	56,56,56,56	0
56	MG	BA	3213	1/1	0.91	0.14	63,63,63,63	0
56	MG	DA	3154	1/1	0.91	0.49	45,45,45,45	0
56	MG	BA	3153	1/1	0.91	0.32	47,47,47,47	0
56	MG	DA	3405	1/1	0.91	0.33	53,53,53,53	0
56	MG	BA	3372	1/1	0.91	0.17	42,42,42,42	0
56	MG	DA	3073	1/1	0.91	0.16	50,50,50,50	0
56	MG	BU	204	1/1	0.91	0.33	49,49,49,49	0
56	MG	BA	3635	1/1	0.91	0.20	52,52,52,52	0
56	MG	BF	302	1/1	0.91	0.26	49,49,49,49	0
56	MG	CA	3146	1/1	0.91	0.18	61,61,61,61	0
56	MG	CA	3015	1/1	0.91	0.33	53,53,53,53	0
60	K	BA	3304	1/1	0.91	0.32	93,93,93,93	0
56	MG	BA	3267	1/1	0.91	0.18	56,56,56,56	0
56	MG	DA	3299	1/1	0.91	0.12	35,35,35,35	0
56	MG	DA	3009	1/1	0.91	0.11	33,33,33,33	0
56	MG	DA	3201	1/1	0.92	0.24	43,43,43,43	0
56	MG	BA	3465	1/1	0.92	0.09	51,51,51,51	0
56	MG	DA	3025	1/1	0.92	0.49	38,38,38,38	0
56	MG	DA	3084	1/1	0.92	0.18	55,55,55,55	0
56	MG	AA	3109	1/1	0.92	0.21	59,59,59,59	0
56	MG	DA	3364	1/1	0.92	0.17	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3267	1/1	0.92	0.28	40,40,40,40	0
56	MG	DA	3629	1/1	0.92	0.14	30,30,30,30	0
56	MG	AA	3199	1/1	0.92	0.15	62,62,62,62	0
56	MG	DA	3027	1/1	0.92	0.63	49,49,49,49	0
56	MG	DA	3124	1/1	0.92	0.13	66,66,66,66	0
56	MG	DE	305	1/1	0.92	0.45	68,68,68,68	0
56	MG	DA	3072	1/1	0.92	0.14	40,40,40,40	0
56	MG	BA	3473	1/1	0.92	0.15	55,55,55,55	0
56	MG	BA	3196	1/1	0.92	0.19	45,45,45,45	0
56	MG	CA	3058	1/1	0.92	0.20	36,36,36,36	0
56	MG	DA	3575	1/1	0.92	0.11	51,51,51,51	0
56	MG	BA	3518	1/1	0.92	0.10	52,52,52,52	0
56	MG	D5	102	1/1	0.92	0.59	44,44,44,44	0
56	MG	CA	3082	1/1	0.92	0.12	46,46,46,46	0
56	MG	DA	3262	1/1	0.92	0.22	60,60,60,60	0
56	MG	CA	3002	1/1	0.92	0.07	74,74,74,74	0
56	MG	BA	3338	1/1	0.92	0.21	62,62,62,62	0
56	MG	DA	3502	1/1	0.92	0.18	48,48,48,48	0
56	MG	DV	202	1/1	0.92	0.61	45,45,45,45	0
56	MG	BP	201	1/1	0.92	0.57	37,37,37,37	0
56	MG	BA	3187	1/1	0.92	0.23	53,53,53,53	0
56	MG	BA	3075	1/1	0.92	0.24	36,36,36,36	0
56	MG	DA	3016	1/1	0.92	0.22	33,33,33,33	0
56	MG	BA	3001	1/1	0.92	0.33	52,52,52,52	0
56	MG	DA	3523	1/1	0.92	0.12	47,47,47,47	0
56	MG	DA	3097	1/1	0.92	0.17	58,58,58,58	0
56	MG	DA	3151	1/1	0.92	0.33	48,48,48,48	0
56	MG	DA	3542	1/1	0.92	0.23	44,44,44,44	0
56	MG	BA	3031	1/1	0.92	0.61	44,44,44,44	0
56	MG	BA	3212	1/1	0.92	0.16	47,47,47,47	0
56	MG	BA	3568	1/1	0.92	0.22	68,68,68,68	0
56	MG	CA	3008	1/1	0.92	1.01	59,59,59,59	0
56	MG	BB	3011	1/1	0.92	0.16	45,45,45,45	0
56	MG	BA	3714	1/1	0.92	0.15	72,72,72,72	0
56	MG	BA	3718	1/1	0.92	0.16	52,52,52,52	0
56	MG	DA	3646	1/1	0.92	0.20	42,42,42,42	0
56	MG	BB	3009	1/1	0.92	0.12	49,49,49,49	0
56	MG	DA	3351	1/1	0.92	0.24	58,58,58,58	0
56	MG	BA	3415	1/1	0.92	0.14	28,28,28,28	0
56	MG	BA	3423	1/1	0.92	0.35	45,45,45,45	0
56	MG	CA	3031	1/1	0.92	0.31	55,55,55,55	0
56	MG	BA	3033	1/1	0.92	0.50	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CT	3001	1/1	0.92	0.21	57,57,57,57	0
56	MG	AA	3058	1/1	0.92	0.36	59,59,59,59	0
56	MG	BA	3709	1/1	0.92	0.16	77,77,77,77	0
56	MG	DA	3018	1/1	0.92	0.28	41,41,41,41	0
56	MG	BA	3254	1/1	0.92	0.30	40,40,40,40	0
56	MG	BA	3408	1/1	0.92	0.13	28,28,28,28	0
56	MG	B0	106	1/1	0.92	0.08	43,43,43,43	0
56	MG	AA	3099	1/1	0.92	0.51	49,49,49,49	0
56	MG	DA	3567	1/1	0.92	0.10	68,68,68,68	0
56	MG	AA	3194	1/1	0.92	0.18	50,50,50,50	0
56	MG	BA	3260	1/1	0.92	0.12	47,47,47,47	0
56	MG	BA	3416	1/1	0.92	0.17	25,25,25,25	0
56	MG	AA	3041	1/1	0.92	0.14	41,41,41,41	0
56	MG	BB	3008	1/1	0.92	0.21	49,49,49,49	0
56	MG	DA	3146	1/1	0.92	0.20	34,34,34,34	0
56	MG	BD	301	1/1	0.92	0.41	35,35,35,35	0
56	MG	AA	3215	1/1	0.92	0.94	77,77,77,77	0
56	MG	BA	3027	1/1	0.92	0.19	53,53,53,53	0
56	MG	BA	3044	1/1	0.92	0.37	32,32,32,32	0
56	MG	BA	3354	1/1	0.92	0.29	45,45,45,45	0
56	MG	BA	3317	1/1	0.92	0.24	40,40,40,40	0
56	MG	DA	3589	1/1	0.92	0.11	65,65,65,65	0
56	MG	BA	3211	1/1	0.92	0.08	43,43,43,43	0
56	MG	AA	3162	1/1	0.92	0.14	79,79,79,79	0
56	MG	BB	3006	1/1	0.92	0.29	34,34,34,34	0
56	MG	BA	3090	1/1	0.92	0.24	42,42,42,42	0
56	MG	CA	3012	1/1	0.92	0.13	50,50,50,50	0
56	MG	BA	3481	1/1	0.92	0.20	41,41,41,41	0
56	MG	BA	3324	1/1	0.92	0.30	54,54,54,54	0
56	MG	DA	3181	1/1	0.92	0.33	55,55,55,55	0
56	MG	DA	3306	1/1	0.92	0.16	51,51,51,51	0
56	MG	BA	3689	1/1	0.92	0.18	25,25,25,25	0
56	MG	DA	3444	1/1	0.92	0.27	43,43,43,43	0
56	MG	BA	3294	1/1	0.92	0.16	59,59,59,59	0
56	MG	DA	3593	1/1	0.92	0.24	62,62,62,62	0
56	MG	AA	3106	1/1	0.92	0.27	68,68,68,68	0
56	MG	DA	3473	1/1	0.92	0.17	50,50,50,50	0
56	MG	CA	3014	1/1	0.92	0.17	56,56,56,56	0
56	MG	CA	3141	1/1	0.92	0.31	85,85,85,85	0
56	MG	BA	3174	1/1	0.92	0.21	52,52,52,52	0
56	MG	AA	3044	1/1	0.92	0.13	60,60,60,60	0
56	MG	DA	3614	1/1	0.92	0.12	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3026	1/1	0.92	0.15	36,36,36,36	0
56	MG	DA	3561	1/1	0.92	0.14	40,40,40,40	0
56	MG	DA	3636	1/1	0.92	0.11	64,64,64,64	0
56	MG	BA	3278	1/1	0.92	0.19	53,53,53,53	0
56	MG	BA	3216	1/1	0.92	0.28	46,46,46,46	0
56	MG	BA	3266	1/1	0.92	0.19	47,47,47,47	0
56	MG	AA	3097	1/1	0.92	0.41	53,53,53,53	0
56	MG	BA	3644	1/1	0.92	0.10	38,38,38,38	0
56	MG	BA	3008	1/1	0.92	0.14	30,30,30,30	0
56	MG	DA	3013	1/1	0.92	0.10	38,38,38,38	0
56	MG	BA	3141	1/1	0.92	0.55	43,43,43,43	0
56	MG	BA	3612	1/1	0.92	0.17	41,41,41,41	0
56	MG	BA	3392	1/1	0.92	0.13	53,53,53,53	0
56	MG	BA	3253	1/1	0.92	0.28	63,63,63,63	0
56	MG	BA	3016	1/1	0.92	0.52	50,50,50,50	0
56	MG	CA	3037	1/1	0.92	0.23	45,45,45,45	0
56	MG	AA	3014	1/1	0.92	0.13	24,24,24,24	0
56	MG	BA	3646	1/1	0.92	0.24	39,39,39,39	0
56	MG	CA	3138	1/1	0.92	0.12	59,59,59,59	0
56	MG	DA	3507	1/1	0.92	0.20	53,53,53,53	0
56	MG	DA	3586	1/1	0.92	0.12	57,57,57,57	0
56	MG	CA	3164	1/1	0.92	0.35	43,43,43,43	0
56	MG	AA	3057	1/1	0.92	0.16	45,45,45,45	0
56	MG	CA	3107	1/1	0.92	0.08	71,71,71,71	0
56	MG	BA	3447	1/1	0.92	0.12	76,76,76,76	0
56	MG	DA	3509	1/1	0.92	0.09	57,57,57,57	0
56	MG	BA	3385	1/1	0.92	0.06	56,56,56,56	0
56	MG	DA	3023	1/1	0.92	0.40	64,64,64,64	0
56	MG	DQ	3001	1/1	0.92	0.26	40,40,40,40	0
56	MG	AA	3012	1/1	0.92	0.16	58,58,58,58	0
56	MG	DA	3111	1/1	0.92	0.20	67,67,67,67	0
56	MG	DA	3585	1/1	0.92	0.26	62,62,62,62	0
56	MG	BA	3662	1/1	0.92	0.15	46,46,46,46	0
56	MG	DA	3493	1/1	0.92	0.25	38,38,38,38	0
56	MG	DA	3602	1/1	0.92	0.17	63,63,63,63	0
56	MG	DA	3407	1/1	0.93	0.14	35,35,35,35	0
56	MG	BA	3504	1/1	0.93	0.18	54,54,54,54	0
56	MG	BA	3692	1/1	0.93	0.20	36,36,36,36	0
56	MG	BA	3117	1/1	0.93	0.27	37,37,37,37	0
56	MG	BA	3147	1/1	0.93	0.60	42,42,42,42	0
56	MG	BA	3696	1/1	0.93	0.27	36,36,36,36	0
56	MG	BU	207	1/1	0.93	0.35	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3076	1/1	0.93	0.28	48,48,48,48	0
56	MG	BA	3113	1/1	0.93	0.20	48,48,48,48	0
56	MG	BA	3611	1/1	0.93	0.11	61,61,61,61	0
56	MG	BA	3357	1/1	0.93	0.17	45,45,45,45	0
56	MG	AA	3062	1/1	0.93	0.15	30,30,30,30	0
56	MG	DA	3426	1/1	0.93	0.14	41,41,41,41	0
56	MG	DA	3185	1/1	0.93	0.33	42,42,42,42	0
56	MG	AA	3110	1/1	0.93	0.13	41,41,41,41	0
56	MG	DA	3255	1/1	0.93	0.15	46,46,46,46	0
56	MG	DA	3484	1/1	0.93	0.05	47,47,47,47	0
56	MG	DA	3566	1/1	0.93	0.12	55,55,55,55	0
56	MG	BA	3189	1/1	0.93	0.17	39,39,39,39	0
56	MG	CA	3066	1/1	0.93	0.08	47,47,47,47	0
56	MG	AA	3048	1/1	0.93	0.10	52,52,52,52	0
56	MG	DA	3065	1/1	0.93	0.19	40,40,40,40	0
56	MG	AA	3214	1/1	0.93	0.31	42,42,42,42	0
56	MG	BA	3055	1/1	0.93	0.31	44,44,44,44	0
56	MG	CA	3089	1/1	0.93	0.17	54,54,54,54	0
56	MG	CA	3125	1/1	0.93	0.20	64,64,64,64	0
56	MG	BA	3472	1/1	0.93	0.12	53,53,53,53	0
56	MG	DB	3012	1/1	0.93	0.19	50,50,50,50	0
56	MG	DA	3055	1/1	0.93	0.20	55,55,55,55	0
56	MG	BA	3175	1/1	0.93	0.50	40,40,40,40	0
56	MG	AA	3116	1/1	0.93	0.41	62,62,62,62	0
56	MG	CA	3026	1/1	0.93	0.18	52,52,52,52	0
56	MG	AA	3100	1/1	0.93	0.59	43,43,43,43	0
56	MG	DA	3274	1/1	0.93	0.40	49,49,49,49	0
56	MG	BA	3509	1/1	0.93	0.21	29,29,29,29	0
56	MG	DA	3123	1/1	0.93	0.17	61,61,61,61	0
56	MG	CA	3129	1/1	0.93	0.23	54,54,54,54	0
56	MG	BA	3725	1/1	0.93	0.11	29,29,29,29	0
56	MG	BA	3256	1/1	0.93	0.12	60,60,60,60	0
56	MG	BE	302	1/1	0.93	0.17	29,29,29,29	0
56	MG	BF	304	1/1	0.93	0.48	30,30,30,30	0
56	MG	AA	3123	1/1	0.93	0.38	38,38,38,38	0
56	MG	CA	3078	1/1	0.93	0.25	51,51,51,51	0
56	MG	DQ	3003	1/1	0.93	0.21	58,58,58,58	0
56	MG	BA	3245	1/1	0.93	0.23	45,45,45,45	0
56	MG	DA	3050	1/1	0.93	0.48	30,30,30,30	0
56	MG	CA	3023	1/1	0.93	0.20	37,37,37,37	0
56	MG	DA	3411	1/1	0.93	0.23	33,33,33,33	0
56	MG	BA	3572	1/1	0.93	0.19	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DE	302	1/1	0.93	0.33	46,46,46,46	0
56	MG	DA	3168	1/1	0.93	0.67	46,46,46,46	0
56	MG	DA	3288	1/1	0.93	0.22	68,68,68,68	0
56	MG	BA	3455	1/1	0.93	0.38	47,47,47,47	0
56	MG	DA	3092	1/1	0.93	0.30	48,48,48,48	0
56	MG	DA	3231	1/1	0.93	0.11	45,45,45,45	0
56	MG	AA	3085	1/1	0.93	0.43	57,57,57,57	0
56	MG	BA	3505	1/1	0.93	0.26	45,45,45,45	0
56	MG	AA	3113	1/1	0.93	0.11	56,56,56,56	0
56	MG	DA	3167	1/1	0.93	0.25	46,46,46,46	0
56	MG	DA	3054	1/1	0.93	0.09	34,34,34,34	0
56	MG	BA	3262	1/1	0.93	0.31	44,44,44,44	0
56	MG	BA	3038	1/1	0.93	0.12	51,51,51,51	0
56	MG	BA	3100	1/1	0.93	0.21	42,42,42,42	0
56	MG	DA	3469	1/1	0.93	0.15	52,52,52,52	0
56	MG	CA	3017	1/1	0.93	0.17	54,54,54,54	0
56	MG	DA	3345	1/1	0.93	0.13	16,16,16,16	0
56	MG	DA	3427	1/1	0.93	0.14	29,29,29,29	0
56	MG	AA	3053	1/1	0.93	0.40	56,56,56,56	0
56	MG	AA	3056	1/1	0.93	0.23	61,61,61,61	0
56	MG	BA	3705	1/1	0.93	0.22	64,64,64,64	0
56	MG	BA	3621	1/1	0.93	0.22	57,57,57,57	0
56	MG	DA	3385	1/1	0.93	0.32	58,58,58,58	0
56	MG	BA	3631	1/1	0.93	0.16	41,41,41,41	0
56	MG	BA	3061	1/1	0.93	0.35	44,44,44,44	0
56	MG	DA	3599	1/1	0.93	0.25	69,69,69,69	0
56	MG	BF	305	1/1	0.93	0.31	38,38,38,38	0
56	MG	DA	3261	1/1	0.93	0.24	44,44,44,44	0
56	MG	AA	3035	1/1	0.93	0.27	59,59,59,59	0
56	MG	DA	3056	1/1	0.93	0.38	37,37,37,37	0
56	MG	BA	3005	1/1	0.93	0.17	43,43,43,43	0
56	MG	DA	3230	1/1	0.93	0.18	61,61,61,61	0
56	MG	DA	3104	1/1	0.93	0.17	46,46,46,46	0
56	MG	BA	3171	1/1	0.93	0.40	42,42,42,42	0
56	MG	BA	3729	1/1	0.93	0.14	54,54,54,54	0
56	MG	CA	3153	1/1	0.93	0.10	85,85,85,85	0
56	MG	B0	101	1/1	0.93	0.26	57,57,57,57	0
56	MG	AA	3112	1/1	0.93	0.09	53,53,53,53	0
56	MG	AA	3059	1/1	0.93	0.70	49,49,49,49	0
56	MG	AA	3055	1/1	0.93	0.28	56,56,56,56	0
56	MG	AA	3031	1/1	0.93	0.22	41,41,41,41	0
56	MG	DD	301	1/1	0.93	0.24	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3367	1/1	0.93	0.19	29,29,29,29	0
56	MG	BA	3258	1/1	0.93	0.17	35,35,35,35	0
56	MG	DA	3425	1/1	0.93	0.19	51,51,51,51	0
56	MG	AA	3138	1/1	0.93	0.39	38,38,38,38	0
56	MG	BA	3549	1/1	0.93	0.30	49,49,49,49	0
56	MG	BV	3003	1/1	0.93	0.26	27,27,27,27	0
56	MG	BA	3073	1/1	0.93	0.20	43,43,43,43	0
56	MG	BA	3693	1/1	0.93	0.27	57,57,57,57	0
56	MG	DA	3524	1/1	0.93	0.24	51,51,51,51	0
56	MG	AM	3002	1/1	0.93	0.58	60,60,60,60	0
56	MG	DA	3325	1/1	0.93	0.24	31,31,31,31	0
56	MG	DA	3033	1/1	0.93	0.22	41,41,41,41	0
56	MG	BG	3004	1/1	0.93	0.06	53,53,53,53	0
56	MG	BG	3003	1/1	0.93	0.21	53,53,53,53	0
56	MG	DA	3330	1/1	0.93	0.13	30,30,30,30	0
56	MG	DB	3001	1/1	0.93	0.19	80,80,80,80	0
56	MG	DA	3516	1/1	0.93	0.20	54,54,54,54	0
56	MG	AA	3006	1/1	0.93	0.09	84,84,84,84	0
56	MG	B2	101	1/1	0.93	0.28	34,34,34,34	0
58	ZN	DY	501	1/1	0.93	0.04	90,90,90,90	0
56	MG	DA	3644	1/1	0.93	0.63	50,50,50,50	0
56	MG	BA	3011	1/1	0.93	0.17	39,39,39,39	0
56	MG	BA	3454	1/1	0.93	0.24	20,20,20,20	0
56	MG	BA	3669	1/1	0.93	0.21	61,61,61,61	0
56	MG	BA	3144	1/1	0.93	0.13	52,52,52,52	0
56	MG	DA	3130	1/1	0.93	0.09	34,34,34,34	0
56	MG	BA	3101	1/1	0.93	0.42	47,47,47,47	0
56	MG	DA	3536	1/1	0.93	0.15	57,57,57,57	0
56	MG	DA	3390	1/1	0.93	0.20	58,58,58,58	0
56	MG	DA	3197	1/1	0.93	0.34	43,43,43,43	0
56	MG	DA	3037	1/1	0.93	0.37	37,37,37,37	0
56	MG	DF	302	1/1	0.93	0.20	47,47,47,47	0
56	MG	BA	3732	1/1	0.93	0.48	56,56,56,56	0
56	MG	BA	3051	1/1	0.93	0.30	34,34,34,34	0
56	MG	DA	3574	1/1	0.93	0.20	22,22,22,22	0
56	MG	BA	3301	1/1	0.93	0.53	44,44,44,44	0
56	MG	BD	312	1/1	0.93	0.97	72,72,72,72	0
56	MG	B0	104	1/1	0.93	0.32	55,55,55,55	0
56	MG	DA	3534	1/1	0.93	0.14	62,62,62,62	0
56	MG	BA	3179	1/1	0.93	0.32	53,53,53,53	0
56	MG	BN	3001	1/1	0.93	0.34	65,65,65,65	0
56	MG	CA	3046	1/1	0.94	0.25	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3056	1/1	0.94	0.25	39,39,39,39	0
56	MG	DA	3340	1/1	0.94	0.12	29,29,29,29	0
56	MG	DA	3051	1/1	0.94	0.14	39,39,39,39	0
56	MG	DA	3612	1/1	0.94	0.32	46,46,46,46	0
56	MG	BA	3433	1/1	0.94	0.29	46,46,46,46	0
56	MG	BA	3093	1/1	0.94	0.46	52,52,52,52	0
56	MG	CA	3004	1/1	0.94	0.34	88,88,88,88	0
56	MG	BA	3672	1/1	0.94	0.25	63,63,63,63	0
56	MG	AA	3190	1/1	0.94	0.31	61,61,61,61	0
56	MG	BA	3594	1/1	0.94	0.28	55,55,55,55	0
56	MG	DA	3478	1/1	0.94	0.10	58,58,58,58	0
56	MG	DN	5001	1/1	0.94	0.12	71,71,71,71	0
56	MG	CA	3128	1/1	0.94	0.28	55,55,55,55	0
56	MG	DA	3417	1/1	0.94	0.19	54,54,54,54	0
56	MG	BA	3375	1/1	0.94	0.17	44,44,44,44	0
56	MG	BA	3539	1/1	0.94	0.21	23,23,23,23	0
56	MG	DA	3070	1/1	0.94	0.43	51,51,51,51	0
56	MG	DA	3620	1/1	0.94	0.20	66,66,66,66	0
56	MG	BA	3605	1/1	0.94	0.10	35,35,35,35	0
56	MG	BU	208	1/1	0.94	0.18	42,42,42,42	0
56	MG	BA	3326	1/1	0.94	0.24	15,15,15,15	0
56	MG	DV	203	1/1	0.94	0.31	41,41,41,41	0
56	MG	DA	3639	1/1	0.94	0.14	55,55,55,55	0
56	MG	AA	3179	1/1	0.94	0.24	34,34,34,34	0
56	MG	BA	3614	1/1	0.94	0.20	48,48,48,48	0
56	MG	DA	3322	1/1	0.94	0.06	41,41,41,41	0
56	MG	BE	306	1/1	0.94	0.45	38,38,38,38	0
56	MG	DA	3134	1/1	0.94	0.22	37,37,37,37	0
56	MG	DA	3570	1/1	0.94	0.12	67,67,67,67	0
56	MG	BA	3310	1/1	0.94	0.12	59,59,59,59	0
56	MG	BA	3720	1/1	0.94	0.17	51,51,51,51	0
56	MG	DA	3132	1/1	0.94	0.64	47,47,47,47	0
56	MG	BA	3585	1/1	0.94	0.22	25,25,25,25	0
56	MG	BA	3384	1/1	0.94	0.28	47,47,47,47	0
56	MG	BD	309	1/1	0.94	0.18	43,43,43,43	0
56	MG	BA	3620	1/1	0.94	0.29	57,57,57,57	0
56	MG	DA	3556	1/1	0.94	0.10	35,35,35,35	0
56	MG	BA	3168	1/1	0.94	0.45	52,52,52,52	0
56	MG	BA	3183	1/1	0.94	0.25	40,40,40,40	0
56	MG	DA	3452	1/1	0.94	0.19	64,64,64,64	0
56	MG	AA	3166	1/1	0.94	0.21	55,55,55,55	0
56	MG	DA	3236	1/1	0.94	0.16	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3211	1/1	0.94	0.20	46,46,46,46	0
56	MG	CA	3010	1/1	0.94	0.15	34,34,34,34	0
56	MG	BA	3270	1/1	0.94	0.30	29,29,29,29	0
56	MG	B0	103	1/1	0.94	0.17	46,46,46,46	0
56	MG	DA	3192	1/1	0.94	0.47	48,48,48,48	0
56	MG	AA	3060	1/1	0.94	0.38	52,52,52,52	0
56	MG	AA	3201	1/1	0.94	0.12	76,76,76,76	0
56	MG	BP	202	1/1	0.94	0.41	47,47,47,47	0
56	MG	BA	3235	1/1	0.94	0.38	44,44,44,44	0
56	MG	AA	3005	1/1	0.94	0.28	66,66,66,66	0
56	MG	BA	3037	1/1	0.94	0.56	39,39,39,39	0
56	MG	BA	3226	1/1	0.94	0.31	31,31,31,31	0
56	MG	CA	3005	1/1	0.94	0.38	37,37,37,37	0
56	MG	BA	3390	1/1	0.94	0.08	40,40,40,40	0
56	MG	BA	3590	1/1	0.94	0.17	23,23,23,23	0
56	MG	BA	3104	1/1	0.94	0.39	34,34,34,34	0
56	MG	DB	3009	1/1	0.94	0.38	41,41,41,41	0
56	MG	DB	3011	1/1	0.94	0.33	49,49,49,49	0
56	MG	BA	3142	1/1	0.94	0.23	57,57,57,57	0
56	MG	DP	202	1/1	0.94	0.22	54,54,54,54	0
56	MG	DA	3147	1/1	0.94	0.20	46,46,46,46	0
56	MG	DA	3406	1/1	0.94	0.07	48,48,48,48	0
56	MG	AM	3001	1/1	0.94	0.08	76,76,76,76	0
56	MG	BA	3578	1/1	0.94	0.19	47,47,47,47	0
56	MG	DA	3403	1/1	0.94	0.21	42,42,42,42	0
56	MG	CA	3123	1/1	0.94	0.12	75,75,75,75	0
56	MG	BA	3017	1/1	0.94	0.32	38,38,38,38	0
56	MG	BA	3047	1/1	0.94	0.35	30,30,30,30	0
56	MG	BA	3710	1/1	0.94	0.06	57,57,57,57	0
56	MG	CA	3013	1/1	0.94	0.09	46,46,46,46	0
56	MG	DA	3173	1/1	0.94	0.29	50,50,50,50	0
56	MG	DA	3587	1/1	0.94	0.22	57,57,57,57	0
56	MG	DA	3010	1/1	0.94	0.25	42,42,42,42	0
56	MG	DA	3601	1/1	0.94	0.23	50,50,50,50	0
56	MG	BA	3588	1/1	0.94	0.20	41,41,41,41	0
56	MG	BA	3615	1/1	0.94	0.23	55,55,55,55	0
56	MG	AA	3004	1/1	0.94	0.16	50,50,50,50	0
56	MG	DA	3384	1/1	0.94	0.13	24,24,24,24	0
56	MG	BA	3012	1/1	0.94	0.11	34,34,34,34	0
56	MG	AA	3054	1/1	0.94	0.19	46,46,46,46	0
56	MG	AA	3198	1/1	0.94	0.16	73,73,73,73	0
56	MG	BA	3726	1/1	0.94	0.32	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3468	1/1	0.94	0.18	45,45,45,45	0
56	MG	BA	3132	1/1	0.94	0.21	28,28,28,28	0
56	MG	DA	3539	1/1	0.94	0.20	35,35,35,35	0
56	MG	AA	3118	1/1	0.94	0.42	39,39,39,39	0
56	MG	BA	3025	1/1	0.94	0.20	48,48,48,48	0
56	MG	BA	3486	1/1	0.94	0.27	55,55,55,55	0
56	MG	CA	3068	1/1	0.94	0.11	47,47,47,47	0
56	MG	AA	3078	1/1	0.94	0.32	55,55,55,55	0
56	MG	AA	3146	1/1	0.94	0.20	55,55,55,55	0
56	MG	D5	101	1/1	0.94	0.63	44,44,44,44	0
56	MG	DA	3333	1/1	0.94	0.14	61,61,61,61	0
56	MG	DE	306	1/1	0.94	0.13	44,44,44,44	0
56	MG	BU	206	1/1	0.94	0.27	41,41,41,41	0
56	MG	AA	3217	1/1	0.94	0.42	64,64,64,64	0
56	MG	DA	3440	1/1	0.94	0.07	48,48,48,48	0
56	MG	BA	3425	1/1	0.94	0.22	42,42,42,42	0
56	MG	BA	3597	1/1	0.94	0.29	46,46,46,46	0
56	MG	B8	5002	1/1	0.94	0.23	48,48,48,48	0
56	MG	DA	3595	1/1	0.94	0.22	53,53,53,53	0
56	MG	DA	3619	1/1	0.94	0.13	67,67,67,67	0
56	MG	CA	3115	1/1	0.94	0.08	81,81,81,81	0
56	MG	DA	3246	1/1	0.94	0.16	55,55,55,55	0
56	MG	DA	3235	1/1	0.94	0.41	46,46,46,46	0
56	MG	AA	3175	1/1	0.94	0.14	70,70,70,70	0
56	MG	CF	3001	1/1	0.94	0.19	56,56,56,56	0
56	MG	CA	3116	1/1	0.94	0.15	76,76,76,76	0
56	MG	DA	3658	1/1	0.94	0.30	50,50,50,50	0
56	MG	DA	3244	1/1	0.94	0.19	23,23,23,23	0
56	MG	BD	305	1/1	0.94	0.25	41,41,41,41	0
56	MG	BA	3610	1/1	0.94	1.00	49,49,49,49	0
56	MG	DA	3386	1/1	0.94	0.17	18,18,18,18	0
56	MG	CA	3038	1/1	0.94	0.26	54,54,54,54	0
56	MG	DA	3470	1/1	0.94	0.17	45,45,45,45	0
56	MG	BA	3215	1/1	0.94	0.09	32,32,32,32	0
56	MG	BA	3298	1/1	0.94	0.38	45,45,45,45	0
56	MG	BA	3540	1/1	0.94	0.33	29,29,29,29	0
56	MG	BA	3043	1/1	0.94	0.38	33,33,33,33	0
56	MG	DA	3520	1/1	0.94	0.11	38,38,38,38	0
56	MG	DA	3148	1/1	0.94	0.13	41,41,41,41	0
56	MG	CA	3121	1/1	0.94	0.45	59,59,59,59	0
56	MG	DA	3268	1/1	0.94	0.18	42,42,42,42	0
56	MG	DA	3494	1/1	0.94	0.12	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3368	1/1	0.94	0.14	22,22,22,22	0
56	MG	DA	3245	1/1	0.94	0.25	43,43,43,43	0
56	MG	CA	3003	1/1	0.94	0.13	69,69,69,69	0
56	MG	DA	3397	1/1	0.94	0.19	40,40,40,40	0
56	MG	DA	3499	1/1	0.94	0.22	44,44,44,44	0
56	MG	BA	3087	1/1	0.94	0.33	48,48,48,48	0
56	MG	BA	3456	1/1	0.94	0.20	24,24,24,24	0
56	MG	DA	3237	1/1	0.94	0.34	37,37,37,37	0
56	MG	BA	3593	1/1	0.94	0.13	51,51,51,51	0
56	MG	BA	3660	1/1	0.94	0.15	58,58,58,58	0
56	MG	BA	3054	1/1	0.94	0.19	39,39,39,39	0
56	MG	DA	3319	1/1	0.94	0.13	31,31,31,31	0
56	MG	BA	3583	1/1	0.94	0.18	57,57,57,57	0
56	MG	DA	3377	1/1	0.94	0.19	32,32,32,32	0
56	MG	BA	3650	1/1	0.94	0.13	44,44,44,44	0
56	MG	BA	3151	1/1	0.94	0.21	40,40,40,40	0
56	MG	BA	3232	1/1	0.94	0.19	32,32,32,32	0
56	MG	AA	3137	1/1	0.94	0.14	40,40,40,40	0
56	MG	CX	104	1/1	0.94	0.11	52,52,52,52	0
56	MG	AA	3213	1/1	0.94	0.12	74,74,74,74	0
56	MG	DA	3404	1/1	0.94	0.17	57,57,57,57	0
56	MG	DA	3184	1/1	0.94	0.17	54,54,54,54	0
56	MG	DA	3506	1/1	0.94	0.09	61,61,61,61	0
56	MG	AA	3007	1/1	0.94	0.17	68,68,68,68	0
56	MG	CA	3047	1/1	0.94	0.18	56,56,56,56	0
56	MG	BA	3737	1/1	0.94	0.22	39,39,39,39	0
56	MG	AA	3043	1/1	0.94	0.32	63,63,63,63	0
56	MG	DA	3292	1/1	0.94	0.18	34,34,34,34	0
56	MG	BA	3580	1/1	0.94	0.17	58,58,58,58	0
56	MG	DA	3150	1/1	0.94	0.09	57,57,57,57	0
56	MG	BA	3359	1/1	0.94	0.15	63,63,63,63	0
56	MG	DA	3628	1/1	0.94	0.15	38,38,38,38	0
56	MG	CA	3079	1/1	0.94	0.10	37,37,37,37	0
56	MG	DA	3270	1/1	0.94	0.28	55,55,55,55	0
56	MG	BA	3569	1/1	0.94	0.08	55,55,55,55	0
56	MG	BA	3208	1/1	0.94	0.13	50,50,50,50	0
56	MG	DA	3022	1/1	0.94	0.18	41,41,41,41	0
56	MG	BA	3042	1/1	0.94	0.14	50,50,50,50	0
56	MG	BA	3128	1/1	0.94	0.16	28,28,28,28	0
56	MG	DA	3226	1/1	0.94	0.18	47,47,47,47	0
56	MG	BA	3627	1/1	0.94	0.29	50,50,50,50	0
56	MG	DA	3059	1/1	0.94	0.05	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3173	1/1	0.94	0.23	41,41,41,41	0
56	MG	DA	3641	1/1	0.94	0.21	47,47,47,47	0
56	MG	AA	3074	1/1	0.94	0.30	40,40,40,40	0
56	MG	BE	304	1/1	0.94	0.49	45,45,45,45	0
56	MG	DA	3380	1/1	0.94	0.09	40,40,40,40	0
56	MG	BA	3015	1/1	0.94	0.28	30,30,30,30	0
56	MG	DA	3583	1/1	0.94	0.24	35,35,35,35	0
56	MG	DA	3019	1/1	0.94	0.21	32,32,32,32	0
56	MG	BA	3186	1/1	0.94	0.17	50,50,50,50	0
56	MG	BA	3181	1/1	0.94	0.13	37,37,37,37	0
56	MG	AA	3132	1/1	0.94	0.21	59,59,59,59	0
56	MG	AA	3207	1/1	0.94	0.19	51,51,51,51	0
56	MG	BA	3446	1/1	0.94	0.21	25,25,25,25	0
56	MG	BA	3202	1/1	0.94	0.47	29,29,29,29	0
56	MG	BA	3643	1/1	0.94	0.20	59,59,59,59	0
56	MG	BA	3453	1/1	0.94	0.31	54,54,54,54	0
56	MG	AA	3211	1/1	0.94	0.11	58,58,58,58	0
56	MG	DB	3004	1/1	0.94	0.11	56,56,56,56	0
56	MG	DA	3075	1/1	0.94	0.21	45,45,45,45	0
56	MG	BA	3052	1/1	0.94	0.26	29,29,29,29	0
56	MG	AA	3178	1/1	0.94	0.17	63,63,63,63	0
56	MG	DA	3161	1/1	0.95	0.19	51,51,51,51	0
56	MG	DA	3290	1/1	0.95	0.20	59,59,59,59	0
56	MG	AK	3001	1/1	0.95	0.13	48,48,48,48	0
56	MG	BA	3290	1/1	0.95	0.15	35,35,35,35	0
56	MG	DA	3379	1/1	0.95	0.13	63,63,63,63	0
56	MG	DA	3635	1/1	0.95	0.12	39,39,39,39	0
56	MG	BA	3341	1/1	0.95	0.17	31,31,31,31	0
56	MG	BR	202	1/1	0.95	0.25	25,25,25,25	0
56	MG	DA	3105	1/1	0.95	0.16	56,56,56,56	0
56	MG	BA	3519	1/1	0.95	0.07	57,57,57,57	0
56	MG	BA	3404	1/1	0.95	0.10	42,42,42,42	0
56	MG	CA	3090	1/1	0.95	0.15	63,63,63,63	0
56	MG	DA	3194	1/1	0.95	0.60	65,65,65,65	0
56	MG	DA	3281	1/1	0.95	0.14	33,33,33,33	0
56	MG	BA	3613	1/1	0.95	0.18	47,47,47,47	0
56	MG	BA	3371	1/1	0.95	0.17	38,38,38,38	0
56	MG	DA	3259	1/1	0.95	0.22	45,45,45,45	0
56	MG	BA	3402	1/1	0.95	0.22	23,23,23,23	0
56	MG	AA	3200	1/1	0.95	0.30	79,79,79,79	0
56	MG	DA	3640	1/1	0.95	0.19	53,53,53,53	0
56	MG	DA	3513	1/1	0.95	0.18	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3656	1/1	0.95	0.27	70,70,70,70	0
56	MG	BA	3547	1/1	0.95	0.19	30,30,30,30	0
56	MG	BA	3377	1/1	0.95	0.14	27,27,27,27	0
56	MG	DA	3039	1/1	0.95	0.60	46,46,46,46	0
56	MG	BA	3442	1/1	0.95	0.18	33,33,33,33	0
56	MG	DA	3525	1/1	0.95	0.10	56,56,56,56	0
56	MG	CA	3136	1/1	0.95	0.23	70,70,70,70	0
56	MG	BV	3001	1/1	0.95	0.26	42,42,42,42	0
56	MG	DA	3643	1/1	0.95	0.27	18,18,18,18	0
56	MG	BB	3007	1/1	0.95	0.15	49,49,49,49	0
56	MG	BA	3332	1/1	0.95	0.13	52,52,52,52	0
56	MG	BA	3565	1/1	0.95	0.13	75,75,75,75	0
56	MG	BA	3106	1/1	0.95	0.32	52,52,52,52	0
56	MG	BA	3471	1/1	0.95	0.11	28,28,28,28	0
56	MG	BA	3719	1/1	0.95	0.07	63,63,63,63	0
56	MG	DA	3443	1/1	0.95	0.23	30,30,30,30	0
56	MG	DA	3352	1/1	0.95	0.26	24,24,24,24	0
56	MG	DA	3578	1/1	0.95	0.15	68,68,68,68	0
56	MG	BA	3721	1/1	0.95	0.34	56,56,56,56	0
56	MG	AA	3187	1/1	0.95	0.06	72,72,72,72	0
56	MG	AA	3163	1/1	0.95	0.24	23,23,23,23	0
56	MG	B3	3403	1/1	0.95	0.39	37,37,37,37	0
56	MG	B8	5001	1/1	0.95	0.16	62,62,62,62	0
56	MG	AA	3181	1/1	0.95	0.19	46,46,46,46	0
56	MG	BA	3712	1/1	0.95	0.24	47,47,47,47	0
56	MG	BA	3131	1/1	0.95	0.13	31,31,31,31	0
56	MG	AA	3170	1/1	0.95	0.16	83,83,83,83	0
56	MG	DA	3651	1/1	0.95	0.14	48,48,48,48	0
56	MG	CA	3111	1/1	0.95	0.10	69,69,69,69	0
56	MG	DA	3128	1/1	0.95	0.33	54,54,54,54	0
56	MG	AA	3171	1/1	0.95	0.29	77,77,77,77	0
56	MG	BA	3558	1/1	0.95	0.19	47,47,47,47	0
56	MG	DO	5001	1/1	0.95	0.10	33,33,33,33	0
56	MG	BA	3219	1/1	0.95	0.36	36,36,36,36	0
56	MG	BA	3009	1/1	0.95	0.24	36,36,36,36	0
56	MG	BA	3108	1/1	0.95	0.17	32,32,32,32	0
56	MG	CA	3102	1/1	0.95	0.06	55,55,55,55	0
56	MG	BA	3624	1/1	0.95	0.17	73,73,73,73	0
56	MG	BA	3288	1/1	0.95	0.10	45,45,45,45	0
56	MG	DA	3590	1/1	0.95	0.18	39,39,39,39	0
56	MG	BA	3573	1/1	0.95	0.14	53,53,53,53	0
56	MG	CA	3051	1/1	0.95	0.16	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3094	1/1	0.95	0.25	26,26,26,26	0
56	MG	CA	3154	1/1	0.95	0.16	54,54,54,54	0
56	MG	DA	3432	1/1	0.95	0.22	37,37,37,37	0
56	MG	DA	3363	1/1	0.95	0.20	56,56,56,56	0
56	MG	AA	3185	1/1	0.95	0.28	47,47,47,47	0
56	MG	DA	3166	1/1	0.95	0.08	37,37,37,37	0
56	MG	DA	3501	1/1	0.95	0.11	67,67,67,67	0
56	MG	DA	3439	1/1	0.95	0.23	45,45,45,45	0
56	MG	BA	3466	1/1	0.95	0.12	53,53,53,53	0
56	MG	DF	301	1/1	0.95	0.38	40,40,40,40	0
56	MG	DA	3199	1/1	0.95	0.15	46,46,46,46	0
56	MG	AA	3107	1/1	0.95	0.31	44,44,44,44	0
56	MG	DA	3266	1/1	0.95	0.19	32,32,32,32	0
56	MG	BA	3475	1/1	0.95	0.07	42,42,42,42	0
56	MG	DA	3264	1/1	0.95	0.20	38,38,38,38	0
56	MG	BA	3062	1/1	0.95	0.44	46,46,46,46	0
56	MG	BA	3532	1/1	0.95	0.21	42,42,42,42	0
56	MG	DA	3285	1/1	0.95	0.12	41,41,41,41	0
56	MG	BA	3699	1/1	0.95	0.15	23,23,23,23	0
56	MG	BA	3199	1/1	0.95	0.31	31,31,31,31	0
56	MG	AA	3177	1/1	0.95	0.13	58,58,58,58	0
56	MG	BW	3004	1/1	0.95	0.61	46,46,46,46	0
56	MG	BA	3328	1/1	0.95	0.19	41,41,41,41	0
56	MG	BA	3096	1/1	0.95	0.22	35,35,35,35	0
56	MG	DA	3588	1/1	0.95	0.13	47,47,47,47	0
56	MG	BA	3234	1/1	0.95	0.36	48,48,48,48	0
56	MG	AA	3016	1/1	0.95	0.10	70,70,70,70	0
56	MG	BA	3366	1/1	0.95	0.14	30,30,30,30	0
56	MG	AA	3019	1/1	0.95	0.42	64,64,64,64	0
56	MG	BA	3312	1/1	0.95	0.11	43,43,43,43	0
56	MG	BA	3236	1/1	0.95	0.33	37,37,37,37	0
56	MG	BA	3679	1/1	0.95	0.12	39,39,39,39	0
56	MG	BA	3690	1/1	0.95	0.23	55,55,55,55	0
56	MG	DA	3504	1/1	0.95	0.15	46,46,46,46	0
56	MG	AA	3061	1/1	0.95	0.09	57,57,57,57	0
56	MG	DA	3552	1/1	0.95	0.13	42,42,42,42	0
56	MG	AA	3070	1/1	0.95	0.19	68,68,68,68	0
56	MG	DA	3611	1/1	0.95	0.16	51,51,51,51	0
56	MG	BA	3533	1/1	0.95	0.29	30,30,30,30	0
56	MG	CA	3059	1/1	0.95	0.18	51,51,51,51	0
56	MG	BA	3194	1/1	0.95	0.52	43,43,43,43	0
56	MG	BA	3677	1/1	0.95	0.22	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3237	1/1	0.95	0.16	43,43,43,43	0
56	MG	DA	3142	1/1	0.95	0.23	33,33,33,33	0
56	MG	BA	3734	1/1	0.95	0.33	42,42,42,42	0
56	MG	BA	3668	1/1	0.95	0.21	42,42,42,42	0
56	MG	BA	3169	1/1	0.95	0.23	39,39,39,39	0
56	MG	DA	3030	1/1	0.95	0.26	49,49,49,49	0
56	MG	DA	3200	1/1	0.95	0.93	48,48,48,48	0
56	MG	DA	3398	1/1	0.95	0.10	50,50,50,50	0
56	MG	DA	3547	1/1	0.95	0.12	47,47,47,47	0
56	MG	DA	3415	1/1	0.95	0.10	22,22,22,22	0
56	MG	BA	3069	1/1	0.95	0.10	33,33,33,33	0
56	MG	AA	3011	1/1	0.95	0.64	44,44,44,44	0
56	MG	DA	3140	1/1	0.95	0.31	55,55,55,55	0
56	MG	DA	3107	1/1	0.95	0.13	50,50,50,50	0
56	MG	AA	3160	1/1	0.95	0.29	52,52,52,52	0
56	MG	BA	3277	1/1	0.95	0.45	45,45,45,45	0
56	MG	BA	3618	1/1	0.95	0.23	37,37,37,37	0
56	MG	DA	3467	1/1	0.95	0.37	48,48,48,48	0
56	MG	DA	3127	1/1	0.95	0.16	44,44,44,44	0
56	MG	DV	201	1/1	0.95	0.30	56,56,56,56	0
56	MG	CA	3060	1/1	0.95	0.35	59,59,59,59	0
56	MG	DA	3076	1/1	0.95	0.46	38,38,38,38	0
56	MG	DA	3437	1/1	0.95	0.21	46,46,46,46	0
56	MG	BA	3510	1/1	0.95	0.16	66,66,66,66	0
56	MG	DA	3178	1/1	0.95	0.20	43,43,43,43	0
56	MG	DA	3269	1/1	0.95	0.14	47,47,47,47	0
56	MG	BA	3507	1/1	0.95	0.21	37,37,37,37	0
56	MG	BA	3545	1/1	0.95	0.19	20,20,20,20	0
56	MG	BA	3333	1/1	0.95	0.15	27,27,27,27	0
56	MG	BA	3428	1/1	0.95	0.42	36,36,36,36	0
56	MG	BA	3112	1/1	0.95	0.11	46,46,46,46	0
56	MG	DA	3569	1/1	0.95	0.07	54,54,54,54	0
56	MG	BB	3015	1/1	0.95	0.09	35,35,35,35	0
56	MG	DA	3445	1/1	0.95	0.44	60,60,60,60	0
56	MG	BD	302	1/1	0.95	0.60	44,44,44,44	0
56	MG	BA	3010	1/1	0.95	0.09	35,35,35,35	0
56	MG	BA	3492	1/1	0.95	0.18	48,48,48,48	0
56	MG	DA	3093	1/1	0.95	0.12	51,51,51,51	0
56	MG	DA	3572	1/1	0.95	0.10	39,39,39,39	0
56	MG	BA	3177	1/1	0.95	0.57	35,35,35,35	0
56	MG	BA	3391	1/1	0.95	0.20	39,39,39,39	0
56	MG	DA	3394	1/1	0.95	0.07	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3252	1/1	0.95	0.23	36,36,36,36	0
56	MG	BA	3386	1/1	0.95	0.13	29,29,29,29	0
56	MG	BA	3449	1/1	0.95	0.10	59,59,59,59	0
56	MG	DA	3209	1/1	0.95	0.10	44,44,44,44	0
56	MG	BE	305	1/1	0.95	0.68	44,44,44,44	0
56	MG	BU	201	1/1	0.95	0.64	33,33,33,33	0
56	MG	AA	3184	1/1	0.95	0.14	81,81,81,81	0
56	MG	BE	307	1/1	0.95	0.29	51,51,51,51	0
56	MG	CA	3108	1/1	0.95	0.17	45,45,45,45	0
56	MG	AA	3206	1/1	0.95	0.12	79,79,79,79	0
56	MG	DA	3449	1/1	0.95	0.29	46,46,46,46	0
56	MG	BA	3684	1/1	0.95	0.16	44,44,44,44	0
56	MG	BA	3350	1/1	0.95	0.27	36,36,36,36	0
56	MG	DA	3543	1/1	0.95	0.20	52,52,52,52	0
56	MG	DA	3541	1/1	0.95	0.16	55,55,55,55	0
56	MG	BA	3388	1/1	0.95	0.26	30,30,30,30	0
56	MG	DD	305	1/1	0.95	0.14	73,73,73,73	0
56	MG	BA	3536	1/1	0.95	0.17	37,37,37,37	0
56	MG	DA	3177	1/1	0.95	0.21	30,30,30,30	0
56	MG	BA	3034	1/1	0.95	0.15	37,37,37,37	0
56	MG	DD	303	1/1	0.95	0.62	48,48,48,48	0
56	MG	BA	3711	1/1	0.95	0.46	64,64,64,64	0
56	MG	AA	3176	1/1	0.95	0.11	60,60,60,60	0
56	MG	DA	3002	1/1	0.95	0.23	47,47,47,47	0
56	MG	BA	3361	1/1	0.95	0.12	39,39,39,39	0
56	MG	AX	106	1/1	0.95	0.09	64,64,64,64	0
56	MG	BB	3002	1/1	0.95	0.19	49,49,49,49	0
56	MG	BA	3150	1/1	0.95	0.32	42,42,42,42	0
56	MG	DA	3316	1/1	0.95	0.27	47,47,47,47	0
58	ZN	CN	501	1/1	0.95	0.11	104,104,104,104	0
56	MG	CA	3170	1/1	0.95	0.38	44,44,44,44	0
56	MG	AL	3001	1/1	0.95	0.15	50,50,50,50	0
56	MG	BA	3323	1/1	0.95	0.17	25,25,25,25	0
56	MG	BP	204	1/1	0.95	0.08	53,53,53,53	0
56	MG	AA	3101	1/1	0.95	0.12	61,61,61,61	0
56	MG	AA	3216	1/1	0.95	0.30	60,60,60,60	0
56	MG	BA	3019	1/1	0.95	0.10	42,42,42,42	0
56	MG	CA	3105	1/1	0.95	0.07	59,59,59,59	0
56	MG	BA	3542	1/1	0.95	0.19	37,37,37,37	0
56	MG	DA	3482	1/1	0.95	0.18	45,45,45,45	0
56	MG	DA	3533	1/1	0.95	0.14	59,59,59,59	0
56	MG	BA	3502	1/1	0.95	0.21	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3193	1/1	0.95	0.20	42,42,42,42	0
56	MG	DA	3514	1/1	0.95	0.20	60,60,60,60	0
56	MG	BA	3399	1/1	0.95	0.25	22,22,22,22	0
56	MG	DA	3492	1/1	0.95	0.09	44,44,44,44	0
56	MG	CA	3100	1/1	0.95	0.18	72,72,72,72	0
56	MG	BA	3078	1/1	0.95	0.33	44,44,44,44	0
56	MG	BA	3193	1/1	0.95	0.48	53,53,53,53	0
56	MG	DA	3607	1/1	0.95	0.17	68,68,68,68	0
56	MG	CA	3087	1/1	0.95	0.14	40,40,40,40	0
56	MG	BA	3657	1/1	0.95	0.19	29,29,29,29	0
56	MG	BA	3376	1/1	0.95	0.32	35,35,35,35	0
56	MG	BA	3353	1/1	0.95	0.25	31,31,31,31	0
56	MG	BA	3595	1/1	0.95	0.15	37,37,37,37	0
56	MG	BA	3564	1/1	0.95	0.17	26,26,26,26	0
56	MG	DA	3162	1/1	0.95	0.06	69,69,69,69	0
56	MG	B3	3402	1/1	0.95	0.08	49,49,49,49	0
56	MG	DA	3548	1/1	0.95	0.16	60,60,60,60	0
56	MG	DA	3284	1/1	0.95	0.17	45,45,45,45	0
56	MG	BA	3063	1/1	0.95	0.14	34,34,34,34	0
56	MG	DA	3348	1/1	0.95	0.10	39,39,39,39	0
56	MG	BA	3280	1/1	0.95	0.33	44,44,44,44	0
56	MG	AA	3205	1/1	0.95	0.20	66,66,66,66	0
56	MG	BA	3221	1/1	0.95	0.63	55,55,55,55	0
56	MG	DA	3381	1/1	0.95	0.24	68,68,68,68	0
56	MG	AA	3047	1/1	0.95	0.47	59,59,59,59	0
56	MG	BA	3297	1/1	0.95	0.39	43,43,43,43	0
56	MG	CA	3001	1/1	0.95	0.20	48,48,48,48	0
56	MG	DA	3206	1/1	0.95	0.42	36,36,36,36	0
56	MG	BA	3024	1/1	0.96	0.13	31,31,31,31	0
56	MG	DA	3334	1/1	0.96	0.16	37,37,37,37	0
56	MG	DA	3133	1/1	0.96	0.12	31,31,31,31	0
56	MG	DA	3032	1/1	0.96	0.10	36,36,36,36	0
56	MG	BA	3214	1/1	0.96	0.22	37,37,37,37	0
56	MG	BA	3458	1/1	0.96	0.21	46,46,46,46	0
56	MG	DA	3597	1/1	0.96	0.14	66,66,66,66	0
56	MG	DA	3489	1/1	0.96	0.08	36,36,36,36	0
56	MG	BA	3470	1/1	0.96	0.05	44,44,44,44	0
56	MG	BA	3233	1/1	0.96	0.19	49,49,49,49	0
56	MG	BA	3663	1/1	0.96	0.21	73,73,73,73	0
56	MG	BA	3195	1/1	0.96	0.12	37,37,37,37	0
56	MG	CA	3022	1/1	0.96	0.05	67,67,67,67	0
56	MG	DA	3250	1/1	0.96	0.09	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3529	1/1	0.96	0.22	22,22,22,22	0
56	MG	DA	3576	1/1	0.96	0.18	57,57,57,57	0
56	MG	BA	3555	1/1	0.96	0.25	31,31,31,31	0
56	MG	AA	3036	1/1	0.96	0.22	69,69,69,69	0
56	MG	BN	3006	1/1	0.96	0.06	33,33,33,33	0
56	MG	DA	3120	1/1	0.96	0.62	50,50,50,50	0
56	MG	BA	3548	1/1	0.96	0.28	40,40,40,40	0
56	MG	BA	3586	1/1	0.96	0.25	26,26,26,26	0
56	MG	BA	3306	1/1	0.96	0.16	19,19,19,19	0
56	MG	BA	3451	1/1	0.96	0.10	31,31,31,31	0
56	MG	CA	3093	1/1	0.96	0.09	65,65,65,65	0
56	MG	CE	3002	1/1	0.96	0.07	69,69,69,69	0
56	MG	BA	3724	1/1	0.96	0.21	22,22,22,22	0
56	MG	DA	3198	1/1	0.96	0.31	34,34,34,34	0
56	MG	BA	3347	1/1	0.96	0.14	44,44,44,44	0
56	MG	DA	3277	1/1	0.96	0.07	46,46,46,46	0
56	MG	AA	3083	1/1	0.96	0.09	56,56,56,56	0
56	MG	BA	3608	1/1	0.96	0.15	51,51,51,51	0
56	MG	BA	3498	1/1	0.96	0.29	81,81,81,81	0
56	MG	B1	3001	1/1	0.96	0.79	63,63,63,63	0
56	MG	DA	3563	1/1	0.96	0.15	49,49,49,49	0
56	MG	BA	3552	1/1	0.96	0.28	30,30,30,30	0
56	MG	DA	3239	1/1	0.96	0.11	54,54,54,54	0
56	MG	AA	3174	1/1	0.96	0.18	49,49,49,49	0
56	MG	BA	3515	1/1	0.96	0.24	46,46,46,46	0
56	MG	DA	3248	1/1	0.96	0.20	30,30,30,30	0
56	MG	BA	3303	1/1	0.96	0.21	11,11,11,11	0
56	MG	BA	3438	1/1	0.96	0.21	30,30,30,30	0
56	MG	BU	209	1/1	0.96	0.96	36,36,36,36	0
56	MG	DA	3474	1/1	0.96	0.09	49,49,49,49	0
56	MG	BA	3512	1/1	0.96	0.18	42,42,42,42	0
56	MG	BU	202	1/1	0.96	0.71	41,41,41,41	0
56	MG	DA	3297	1/1	0.96	0.16	36,36,36,36	0
56	MG	CA	3086	1/1	0.96	0.13	70,70,70,70	0
56	MG	CA	3118	1/1	0.96	0.08	39,39,39,39	0
56	MG	CA	3143	1/1	0.96	0.06	91,91,91,91	0
56	MG	DA	3604	1/1	0.96	0.08	50,50,50,50	0
56	MG	DA	3515	1/1	0.96	0.07	57,57,57,57	0
56	MG	AA	3145	1/1	0.96	0.24	63,63,63,63	0
56	MG	AA	3195	1/1	0.96	0.21	58,58,58,58	0
56	MG	CA	3049	1/1	0.96	0.14	51,51,51,51	0
56	MG	DA	3114	1/1	0.96	0.19	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BE	308	1/1	0.96	0.26	27,27,27,27	0
56	MG	BA	3715	1/1	0.96	0.34	44,44,44,44	0
56	MG	CA	3083	1/1	0.96	0.10	30,30,30,30	0
56	MG	B0	102	1/1	0.96	0.18	50,50,50,50	0
56	MG	BA	3479	1/1	0.96	0.15	44,44,44,44	0
56	MG	BA	3609	1/1	0.96	0.26	29,29,29,29	0
56	MG	BA	3464	1/1	0.96	0.18	40,40,40,40	0
56	MG	DA	3215	1/1	0.96	0.30	43,43,43,43	0
56	MG	AA	3144	1/1	0.96	0.09	56,56,56,56	0
56	MG	BA	3274	1/1	0.96	0.14	54,54,54,54	0
56	MG	BA	3592	1/1	0.96	0.16	43,43,43,43	0
56	MG	BA	3114	1/1	0.96	0.25	46,46,46,46	0
56	MG	DA	3399	1/1	0.96	0.21	39,39,39,39	0
56	MG	DA	3335	1/1	0.96	0.21	36,36,36,36	0
56	MG	DA	3302	1/1	0.96	0.27	42,42,42,42	0
56	MG	DA	3329	1/1	0.96	0.13	40,40,40,40	0
56	MG	CA	3140	1/1	0.96	0.14	75,75,75,75	0
56	MG	BA	3513	1/1	0.96	0.31	51,51,51,51	0
56	MG	BA	3273	1/1	0.96	0.61	35,35,35,35	0
56	MG	DA	3343	1/1	0.96	0.12	37,37,37,37	0
56	MG	DA	3300	1/1	0.96	0.16	47,47,47,47	0
56	MG	DA	3007	1/1	0.96	0.26	43,43,43,43	0
56	MG	AA	3066	1/1	0.96	0.20	41,41,41,41	0
56	MG	BA	3116	1/1	0.96	0.25	30,30,30,30	0
56	MG	DA	3310	1/1	0.96	0.27	30,30,30,30	0
56	MG	DA	3550	1/1	0.96	0.10	54,54,54,54	0
56	MG	DA	3004	1/1	0.96	0.16	24,24,24,24	0
56	MG	BA	3658	1/1	0.96	0.25	62,62,62,62	0
56	MG	BA	3622	1/1	0.96	0.26	32,32,32,32	0
56	MG	DA	3538	1/1	0.96	0.19	37,37,37,37	0
56	MG	BA	3413	1/1	0.96	0.08	19,19,19,19	0
56	MG	CA	3040	1/1	0.96	0.36	47,47,47,47	0
56	MG	DA	3280	1/1	0.96	0.25	46,46,46,46	0
56	MG	BA	3111	1/1	0.96	0.17	43,43,43,43	0
56	MG	BA	3231	1/1	0.96	0.26	50,50,50,50	0
56	MG	DA	3476	1/1	0.96	0.13	35,35,35,35	0
56	MG	BA	3427	1/1	0.96	0.19	20,20,20,20	0
56	MG	DA	3126	1/1	0.96	0.12	61,61,61,61	0
56	MG	BA	3314	1/1	0.96	0.14	22,22,22,22	0
56	MG	AA	3151	1/1	0.96	0.07	49,49,49,49	0
56	MG	BD	310	1/1	0.96	0.33	48,48,48,48	0
56	MG	BA	3398	1/1	0.96	0.13	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3735	1/1	0.96	0.28	47,47,47,47	0
56	MG	BA	3050	1/1	0.96	0.17	33,33,33,33	0
56	MG	AA	3191	1/1	0.96	0.11	56,56,56,56	0
56	MG	BA	3148	1/1	0.96	0.60	49,49,49,49	0
56	MG	DA	3442	1/1	0.96	0.30	58,58,58,58	0
56	MG	DA	3228	1/1	0.96	0.19	49,49,49,49	0
56	MG	BA	3083	1/1	0.96	0.10	33,33,33,33	0
56	MG	BA	3681	1/1	0.96	0.15	54,54,54,54	0
56	MG	DA	3034	1/1	0.96	0.19	40,40,40,40	0
56	MG	BA	3700	1/1	0.96	0.25	26,26,26,26	0
56	MG	CA	3072	1/1	0.96	0.23	57,57,57,57	0
56	MG	AA	3034	1/1	0.96	0.20	46,46,46,46	0
56	MG	AA	3172	1/1	0.96	0.07	36,36,36,36	0
56	MG	DA	3028	1/1	0.96	0.07	34,34,34,34	0
56	MG	DA	3657	1/1	0.96	0.35	55,55,55,55	0
56	MG	DR	5001	1/1	0.96	0.19	39,39,39,39	0
56	MG	BA	3623	1/1	0.96	0.15	43,43,43,43	0
56	MG	AA	3111	1/1	0.96	0.16	70,70,70,70	0
56	MG	DA	3438	1/1	0.96	0.30	50,50,50,50	0
56	MG	CA	3148	1/1	0.96	0.17	65,65,65,65	0
56	MG	CA	3113	1/1	0.96	0.26	84,84,84,84	0
56	MG	DA	3577	1/1	0.96	0.19	44,44,44,44	0
56	MG	DA	3605	1/1	0.96	0.07	58,58,58,58	0
56	MG	DA	3503	1/1	0.96	0.09	41,41,41,41	0
56	MG	BA	3671	1/1	0.96	0.10	44,44,44,44	0
56	MG	BA	3487	1/1	0.96	0.20	47,47,47,47	0
56	MG	DA	3571	1/1	0.96	0.09	57,57,57,57	0
56	MG	BA	3576	1/1	0.96	0.10	45,45,45,45	0
56	MG	BA	3420	1/1	0.96	0.18	13,13,13,13	0
56	MG	DE	303	1/1	0.96	0.15	36,36,36,36	0
56	MG	BB	3018	1/1	0.96	0.27	54,54,54,54	0
56	MG	CA	3085	1/1	0.96	0.27	58,58,58,58	0
56	MG	BA	3364	1/1	0.96	0.21	30,30,30,30	0
56	MG	DA	3553	1/1	0.96	0.18	58,58,58,58	0
56	MG	AA	3095	1/1	0.96	0.19	54,54,54,54	0
56	MG	BA	3162	1/1	0.96	0.28	43,43,43,43	0
56	MG	DA	3014	1/1	0.96	0.26	38,38,38,38	0
56	MG	BA	3165	1/1	0.96	0.47	44,44,44,44	0
56	MG	BQ	3001	1/1	0.96	0.32	38,38,38,38	0
56	MG	BA	3406	1/1	0.96	0.22	54,54,54,54	0
56	MG	BA	3127	1/1	0.96	0.36	42,42,42,42	0
56	MG	DA	3433	1/1	0.96	0.23	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3319	1/1	0.96	0.14	34,34,34,34	0
56	MG	DA	3610	1/1	0.96	0.11	49,49,49,49	0
56	MG	DA	3562	1/1	0.96	0.21	41,41,41,41	0
56	MG	DA	3527	1/1	0.96	0.11	58,58,58,58	0
56	MG	CA	3109	1/1	0.96	0.10	79,79,79,79	0
56	MG	CX	102	1/1	0.96	0.07	60,60,60,60	0
56	MG	CA	3044	1/1	0.96	0.12	52,52,52,52	0
56	MG	DA	3088	1/1	0.96	0.16	47,47,47,47	0
56	MG	BA	3459	1/1	0.96	0.13	51,51,51,51	0
56	MG	CA	3020	1/1	0.96	0.22	45,45,45,45	0
56	MG	BD	303	1/1	0.96	0.25	35,35,35,35	0
56	MG	DY	502	1/1	0.96	0.07	66,66,66,66	0
56	MG	BA	3526	1/1	0.96	0.09	49,49,49,49	0
56	MG	CA	3169	1/1	0.96	0.19	52,52,52,52	0
56	MG	BA	3434	1/1	0.96	0.31	22,22,22,22	0
56	MG	BA	3728	1/1	0.96	0.24	56,56,56,56	0
56	MG	AA	3021	1/1	0.96	0.16	76,76,76,76	0
56	MG	BA	3630	1/1	0.96	0.13	48,48,48,48	0
56	MG	DA	3376	1/1	0.96	0.16	42,42,42,42	0
56	MG	DA	3624	1/1	0.96	0.11	54,54,54,54	0
56	MG	AA	3221	1/1	0.96	0.12	52,52,52,52	0
56	MG	BA	3136	1/1	0.96	0.19	47,47,47,47	0
56	MG	BA	3013	1/1	0.96	0.45	36,36,36,36	0
56	MG	BA	3335	1/1	0.96	0.15	51,51,51,51	0
56	MG	DA	3095	1/1	0.96	0.24	53,53,53,53	0
56	MG	BA	3400	1/1	0.96	0.18	29,29,29,29	0
56	MG	AA	3202	1/1	0.96	0.22	72,72,72,72	0
56	MG	BA	3461	1/1	0.96	0.14	33,33,33,33	0
56	MG	BA	3685	1/1	0.96	0.26	58,58,58,58	0
56	MG	BA	3344	1/1	0.96	0.15	65,65,65,65	0
56	MG	DA	3435	1/1	0.96	0.16	56,56,56,56	0
56	MG	DA	3471	1/1	0.96	0.13	32,32,32,32	0
56	MG	BA	3439	1/1	0.96	0.09	35,35,35,35	0
56	MG	BA	3365	1/1	0.96	0.06	63,63,63,63	0
56	MG	BA	3525	1/1	0.96	0.16	31,31,31,31	0
56	MG	BU	203	1/1	0.96	0.26	26,26,26,26	0
56	MG	AA	3108	1/1	0.96	0.31	72,72,72,72	0
56	MG	DB	3007	1/1	0.96	0.29	45,45,45,45	0
56	MG	DA	3323	1/1	0.96	0.19	60,60,60,60	0
56	MG	BA	3566	1/1	0.96	0.22	43,43,43,43	0
56	MG	AX	109	1/1	0.96	0.10	56,56,56,56	0
56	MG	DA	3021	1/1	0.96	0.09	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3036	1/1	0.96	0.17	25,25,25,25	0
56	MG	DA	3305	1/1	0.96	0.20	33,33,33,33	0
56	MG	AA	3122	1/1	0.96	0.42	40,40,40,40	0
56	MG	DA	3594	1/1	0.96	0.31	63,63,63,63	0
56	MG	BA	3342	1/1	0.96	0.24	46,46,46,46	0
56	MG	DA	3058	1/1	0.96	0.16	56,56,56,56	0
56	MG	DA	3303	1/1	0.96	0.17	37,37,37,37	0
56	MG	AA	3196	1/1	0.96	0.28	78,78,78,78	0
56	MG	DQ	3002	1/1	0.96	0.34	51,51,51,51	0
56	MG	BA	3395	1/1	0.96	0.41	56,56,56,56	0
56	MG	DA	3044	1/1	0.96	0.22	45,45,45,45	0
56	MG	DA	3308	1/1	0.96	0.09	32,32,32,32	0
56	MG	BA	3373	1/1	0.96	0.08	48,48,48,48	0
56	MG	DA	3451	1/1	0.96	0.06	68,68,68,68	0
56	MG	BA	3638	1/1	0.96	0.09	73,73,73,73	0
56	MG	BA	3295	1/1	0.96	0.14	30,30,30,30	0
56	MG	DA	3367	1/1	0.97	0.07	55,55,55,55	0
56	MG	DA	3535	1/1	0.97	0.14	58,58,58,58	0
56	MG	BA	3002	1/1	0.97	0.14	38,38,38,38	0
56	MG	BA	3308	1/1	0.97	0.18	33,33,33,33	0
56	MG	BA	3229	1/1	0.97	0.35	50,50,50,50	0
56	MG	DA	3342	1/1	0.97	0.18	31,31,31,31	0
56	MG	AA	3152	1/1	0.97	0.12	29,29,29,29	0
56	MG	BA	3145	1/1	0.97	0.30	40,40,40,40	0
56	MG	DA	3459	1/1	0.97	0.12	43,43,43,43	0
56	MG	DA	3656	1/1	0.97	0.07	62,62,62,62	0
56	MG	BA	3065	1/1	0.97	0.30	31,31,31,31	0
56	MG	AA	3018	1/1	0.97	0.22	51,51,51,51	0
56	MG	DA	3631	1/1	0.97	0.19	49,49,49,49	0
56	MG	CA	3069	1/1	0.97	0.21	63,63,63,63	0
56	MG	BA	3543	1/1	0.97	0.22	24,24,24,24	0
56	MG	BA	3551	1/1	0.97	0.17	31,31,31,31	0
56	MG	CA	3092	1/1	0.97	0.08	56,56,56,56	0
56	MG	DA	3592	1/1	0.97	0.15	49,49,49,49	0
56	MG	DA	3466	1/1	0.97	0.09	43,43,43,43	0
56	MG	DA	3421	1/1	0.97	0.16	43,43,43,43	0
56	MG	BA	3653	1/1	0.97	0.15	46,46,46,46	0
56	MG	BA	3095	1/1	0.97	0.70	55,55,55,55	0
56	MG	DA	3419	1/1	0.97	0.11	53,53,53,53	0
56	MG	DA	3375	1/1	0.97	0.08	40,40,40,40	0
56	MG	BA	3305	1/1	0.97	0.13	48,48,48,48	0
56	MG	AA	3193	1/1	0.97	0.13	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3325	1/1	0.97	0.20	39,39,39,39	0
56	MG	DA	3358	1/1	0.97	0.16	38,38,38,38	0
56	MG	DA	3393	1/1	0.97	0.26	35,35,35,35	0
56	MG	BA	3503	1/1	0.97	0.14	56,56,56,56	0
56	MG	CA	3080	1/1	0.97	0.13	51,51,51,51	0
56	MG	BA	3651	1/1	0.97	0.34	52,52,52,52	0
56	MG	DA	3047	1/1	0.97	0.09	36,36,36,36	0
56	MG	BA	3032	1/1	0.97	0.30	36,36,36,36	0
56	MG	CA	3104	1/1	0.97	0.14	60,60,60,60	0
56	MG	DA	3331	1/1	0.97	0.17	27,27,27,27	0
56	MG	AA	3150	1/1	0.97	0.27	67,67,67,67	0
56	MG	DA	3481	1/1	0.97	0.08	59,59,59,59	0
56	MG	DF	303	1/1	0.97	0.28	42,42,42,42	0
56	MG	BO	201	1/1	0.97	0.10	63,63,63,63	0
56	MG	BA	3560	1/1	0.97	0.27	24,24,24,24	0
56	MG	BA	3619	1/1	0.97	0.15	42,42,42,42	0
56	MG	BA	3476	1/1	0.97	0.09	47,47,47,47	0
56	MG	DA	3634	1/1	0.97	0.20	33,33,33,33	0
56	MG	BA	3655	1/1	0.97	0.12	44,44,44,44	0
56	MG	AA	3141	1/1	0.97	0.23	51,51,51,51	0
56	MG	DA	3224	1/1	0.97	0.10	53,53,53,53	0
56	MG	BA	3422	1/1	0.97	0.14	23,23,23,23	0
56	MG	BA	3731	1/1	0.97	0.39	52,52,52,52	0
56	MG	BA	3557	1/1	0.97	0.28	35,35,35,35	0
56	MG	BA	3401	1/1	0.97	0.14	49,49,49,49	0
56	MG	BA	3511	1/1	0.97	0.13	40,40,40,40	0
56	MG	BA	3041	1/1	0.97	0.42	45,45,45,45	0
56	MG	BA	3706	1/1	0.97	0.14	38,38,38,38	0
56	MG	DA	3152	1/1	0.97	0.26	43,43,43,43	0
56	MG	BA	3220	1/1	0.97	0.27	27,27,27,27	0
56	MG	DA	3632	1/1	0.97	0.18	60,60,60,60	0
56	MG	DA	3615	1/1	0.97	0.08	57,57,57,57	0
56	MG	DA	3389	1/1	0.97	0.23	32,32,32,32	0
56	MG	DA	3370	1/1	0.97	0.23	40,40,40,40	0
56	MG	BA	3352	1/1	0.97	0.16	58,58,58,58	0
56	MG	DA	3251	1/1	0.97	0.29	50,50,50,50	0
56	MG	DA	3362	1/1	0.97	0.36	42,42,42,42	0
56	MG	BR	201	1/1	0.97	0.38	44,44,44,44	0
56	MG	BA	3263	1/1	0.97	0.58	35,35,35,35	0
56	MG	BA	3282	1/1	0.97	0.15	34,34,34,34	0
56	MG	DA	3512	1/1	0.97	0.07	37,37,37,37	0
56	MG	BD	307	1/1	0.97	0.26	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	CA	3130	1/1	0.97	0.10	59,59,59,59	0
56	MG	DA	3414	1/1	0.97	0.18	59,59,59,59	0
56	MG	BA	3698	1/1	0.97	0.38	58,58,58,58	0
56	MG	CA	3155	1/1	0.97	0.18	71,71,71,71	0
56	MG	BA	3462	1/1	0.97	0.23	30,30,30,30	0
56	MG	BA	3600	1/1	0.97	0.33	54,54,54,54	0
56	MG	B1	3002	1/1	0.97	0.14	29,29,29,29	0
56	MG	BA	3546	1/1	0.97	0.26	46,46,46,46	0
56	MG	CA	3097	1/1	0.97	0.16	60,60,60,60	0
56	MG	BA	3520	1/1	0.97	0.08	69,69,69,69	0
56	MG	DA	3332	1/1	0.97	0.12	29,29,29,29	0
56	MG	DA	3336	1/1	0.97	0.16	36,36,36,36	0
56	MG	CA	3120	1/1	0.97	0.21	59,59,59,59	0
56	MG	DA	3341	1/1	0.97	0.07	40,40,40,40	0
56	MG	AA	3212	1/1	0.97	0.15	36,36,36,36	0
56	MG	D8	5001	1/1	0.97	0.23	53,53,53,53	0
56	MG	BA	3701	1/1	0.97	0.15	69,69,69,69	0
56	MG	BA	3343	1/1	0.97	0.19	37,37,37,37	0
56	MG	BA	3340	1/1	0.97	0.19	57,57,57,57	0
56	MG	DA	3326	1/1	0.97	0.08	61,61,61,61	0
56	MG	B7	103	1/1	0.97	0.40	46,46,46,46	0
56	MG	DA	3497	1/1	0.97	0.06	37,37,37,37	0
56	MG	DA	3063	1/1	0.97	0.10	55,55,55,55	0
56	MG	BA	3527	1/1	0.97	0.22	45,45,45,45	0
56	MG	BA	3633	1/1	0.97	0.32	54,54,54,54	0
56	MG	CA	3112	1/1	0.97	0.26	69,69,69,69	0
56	MG	AA	3008	1/1	0.97	0.27	61,61,61,61	0
56	MG	DA	3069	1/1	0.97	0.20	49,49,49,49	0
56	MG	BA	3508	1/1	0.97	0.17	46,46,46,46	0
56	MG	DA	3488	1/1	0.97	0.19	48,48,48,48	0
56	MG	DA	3118	1/1	0.97	0.09	44,44,44,44	0
56	MG	AA	3149	1/1	0.97	0.07	49,49,49,49	0
56	MG	AA	3165	1/1	0.97	0.13	24,24,24,24	0
56	MG	DA	3046	1/1	0.97	0.09	48,48,48,48	0
56	MG	AA	3158	1/1	0.97	0.17	47,47,47,47	0
56	MG	BA	3457	1/1	0.97	0.11	25,25,25,25	0
56	MG	BA	3489	1/1	0.97	0.12	50,50,50,50	0
56	MG	DA	3229	1/1	0.97	0.14	44,44,44,44	0
56	MG	BA	3736	1/1	0.97	0.14	40,40,40,40	0
56	MG	BA	3727	1/1	0.97	0.18	27,27,27,27	0
56	MG	BA	3227	1/1	0.97	0.16	67,67,67,67	0
56	MG	DA	3258	1/1	0.97	0.28	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3372	1/1	0.97	0.10	37,37,37,37	0
56	MG	DA	3313	1/1	0.97	0.18	30,30,30,30	0
56	MG	CA	3098	1/1	0.97	0.17	37,37,37,37	0
56	MG	DA	3600	1/1	0.97	0.17	73,73,73,73	0
56	MG	BA	3072	1/1	0.97	0.69	45,45,45,45	0
56	MG	AA	3208	1/1	0.97	0.34	38,38,38,38	0
56	MG	DA	3218	1/1	0.97	0.11	31,31,31,31	0
56	MG	BA	3516	1/1	0.97	0.20	64,64,64,64	0
56	MG	BE	309	1/1	0.97	0.14	37,37,37,37	0
56	MG	BA	3205	1/1	0.97	0.29	38,38,38,38	0
56	MG	DA	3271	1/1	0.97	0.08	45,45,45,45	0
56	MG	CA	3166	1/1	0.97	0.08	71,71,71,71	0
56	MG	AA	3155	1/1	0.97	0.19	54,54,54,54	0
56	MG	AA	3188	1/1	0.97	0.25	52,52,52,52	0
56	MG	BA	3336	1/1	0.97	0.18	46,46,46,46	0
56	MG	DA	3648	1/1	0.97	0.23	43,43,43,43	0
56	MG	DA	3580	1/1	0.97	0.17	35,35,35,35	0
56	MG	CA	3081	1/1	0.97	0.09	72,72,72,72	0
56	MG	BA	3040	1/1	0.97	0.23	40,40,40,40	0
56	MG	DA	3294	1/1	0.97	0.20	30,30,30,30	0
56	MG	BA	3091	1/1	0.97	0.34	55,55,55,55	0
56	MG	BA	3535	1/1	0.97	0.18	42,42,42,42	0
56	MG	DA	3551	1/1	0.97	0.10	43,43,43,43	0
56	MG	CA	3158	1/1	0.97	0.10	64,64,64,64	0
56	MG	DA	3558	1/1	0.97	0.17	77,77,77,77	0
56	MG	BA	3330	1/1	0.97	0.09	35,35,35,35	0
56	MG	DA	3309	1/1	0.97	0.17	25,25,25,25	0
56	MG	BA	3321	1/1	0.97	0.20	47,47,47,47	0
56	MG	DA	3446	1/1	0.97	0.16	46,46,46,46	0
56	MG	CA	3052	1/1	0.97	0.15	47,47,47,47	0
56	MG	DA	3337	1/1	0.97	0.15	50,50,50,50	0
56	MG	BA	3316	1/1	0.97	0.14	51,51,51,51	0
56	MG	BA	3598	1/1	0.97	0.23	32,32,32,32	0
56	MG	CA	3011	1/1	0.97	0.26	27,27,27,27	0
56	MG	BA	3389	1/1	0.97	0.14	52,52,52,52	0
56	MG	DE	304	1/1	0.97	0.18	30,30,30,30	0
56	MG	DA	3286	1/1	0.97	0.22	26,26,26,26	0
56	MG	DA	3145	1/1	0.97	0.42	52,52,52,52	0
56	MG	CA	3096	1/1	0.97	0.10	54,54,54,54	0
56	MG	DA	3410	1/1	0.97	0.09	40,40,40,40	0
56	MG	BA	3115	1/1	0.97	0.17	28,28,28,28	0
56	MG	BA	3544	1/1	0.97	0.22	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3416	1/1	0.97	0.36	34,34,34,34	0
56	MG	BA	3329	1/1	0.97	0.08	49,49,49,49	0
56	MG	BA	3369	1/1	0.97	0.12	49,49,49,49	0
56	MG	BA	3493	1/1	0.97	0.13	51,51,51,51	0
56	MG	BA	3678	1/1	0.97	0.10	47,47,47,47	0
56	MG	DA	3477	1/1	0.97	0.53	35,35,35,35	0
56	MG	BA	3642	1/1	0.97	0.16	52,52,52,52	0
56	MG	DA	3317	1/1	0.97	0.19	34,34,34,34	0
56	MG	CA	3165	1/1	0.97	0.15	47,47,47,47	0
58	ZN	AN	102	1/1	0.97	0.11	88,88,88,88	0
56	MG	BA	3360	1/1	0.97	0.18	39,39,39,39	0
56	MG	BA	3152	1/1	0.97	0.08	52,52,52,52	0
56	MG	BA	3149	1/1	0.97	0.04	58,58,58,58	0
56	MG	BA	3574	1/1	0.97	0.08	52,52,52,52	0
56	MG	BA	3440	1/1	0.97	0.10	40,40,40,40	0
56	MG	BA	3666	1/1	0.97	0.34	54,54,54,54	0
56	MG	DA	3048	1/1	0.97	0.36	29,29,29,29	0
56	MG	DA	3216	1/1	0.97	0.18	47,47,47,47	0
56	MG	BA	3272	1/1	0.97	0.07	49,49,49,49	0
56	MG	BA	3396	1/1	0.97	0.20	41,41,41,41	0
56	MG	DA	3129	1/1	0.97	0.38	45,45,45,45	0
56	MG	DA	3242	1/1	0.97	0.23	31,31,31,31	0
56	MG	BA	3102	1/1	0.97	0.08	45,45,45,45	0
56	MG	BA	3579	1/1	0.97	0.30	21,21,21,21	0
56	MG	DP	201	1/1	0.97	0.31	52,52,52,52	0
56	MG	DA	3498	1/1	0.97	0.12	75,75,75,75	0
56	MG	AA	3154	1/1	0.97	0.08	60,60,60,60	0
56	MG	BA	3276	1/1	0.97	0.27	9,9,9,9	0
56	MG	BA	3287	1/1	0.97	0.14	11,11,11,11	0
56	MG	CA	3050	1/1	0.97	0.18	54,54,54,54	0
56	MG	CA	3088	1/1	0.97	0.19	49,49,49,49	0
56	MG	BA	3478	1/1	0.97	0.21	36,36,36,36	0
56	MG	DA	3156	1/1	0.97	0.64	38,38,38,38	0
56	MG	BA	3363	1/1	0.97	0.17	29,29,29,29	0
56	MG	DA	3238	1/1	0.97	0.13	37,37,37,37	0
56	MG	BA	3200	1/1	0.97	0.28	32,32,32,32	0
56	MG	BA	3209	1/1	0.97	0.43	39,39,39,39	0
56	MG	BA	3243	1/1	0.97	0.09	43,43,43,43	0
56	MG	BA	3554	1/1	0.97	0.21	25,25,25,25	0
56	MG	BF	301	1/1	0.97	0.56	46,46,46,46	0
56	MG	DA	3429	1/1	0.97	0.09	30,30,30,30	0
56	MG	BA	3370	1/1	0.97	0.07	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3469	1/1	0.97	0.13	60,60,60,60	0
56	MG	BA	3382	1/1	0.97	0.20	21,21,21,21	0
56	MG	BA	3387	1/1	0.97	0.26	49,49,49,49	0
56	MG	DA	3169	1/1	0.97	0.25	58,58,58,58	0
56	MG	BA	3379	1/1	0.97	0.08	43,43,43,43	0
56	MG	BA	3521	1/1	0.97	0.12	38,38,38,38	0
56	MG	AA	3040	1/1	0.97	0.07	46,46,46,46	0
56	MG	BA	3474	1/1	0.97	0.27	43,43,43,43	0
56	MG	DA	3413	1/1	0.97	0.18	44,44,44,44	0
56	MG	DA	3136	1/1	0.97	0.08	39,39,39,39	0
56	MG	BA	3730	1/1	0.97	0.19	43,43,43,43	0
56	MG	DA	3324	1/1	0.97	0.17	24,24,24,24	0
56	MG	BA	3197	1/1	0.97	0.44	39,39,39,39	0
56	MG	DA	3368	1/1	0.97	0.17	34,34,34,34	0
56	MG	BA	3120	1/1	0.97	0.26	56,56,56,56	0
56	MG	BA	3322	1/1	0.97	0.14	46,46,46,46	0
56	MG	BA	3584	1/1	0.97	0.10	43,43,43,43	0
56	MG	DA	3653	1/1	0.97	0.12	52,52,52,52	0
56	MG	BA	3383	1/1	0.97	0.14	51,51,51,51	0
56	MG	BA	3049	1/1	0.97	0.17	17,17,17,17	0
56	MG	BA	3318	1/1	0.97	0.13	30,30,30,30	0
56	MG	DA	3207	1/1	0.97	0.11	41,41,41,41	0
56	MG	BA	3424	1/1	0.97	0.17	44,44,44,44	0
56	MG	DA	3519	1/1	0.97	0.10	39,39,39,39	0
56	MG	BA	3426	1/1	0.97	0.08	34,34,34,34	0
56	MG	BA	3537	1/1	0.97	0.16	45,45,45,45	0
56	MG	BA	3222	1/1	0.97	0.52	56,56,56,56	0
56	MG	DA	3031	1/1	0.97	0.18	60,60,60,60	0
56	MG	DA	3339	1/1	0.97	0.29	35,35,35,35	0
56	MG	DA	3366	1/1	0.97	0.09	43,43,43,43	0
56	MG	AA	3010	1/1	0.97	0.15	71,71,71,71	0
56	MG	DA	3369	1/1	0.98	0.05	53,53,53,53	0
56	MG	BV	3002	1/1	0.98	0.55	42,42,42,42	0
56	MG	BA	3320	1/1	0.98	0.21	41,41,41,41	0
56	MG	DA	3505	1/1	0.98	0.14	24,24,24,24	0
56	MG	BA	3351	1/1	0.98	0.25	21,21,21,21	0
58	ZN	D9	501	1/1	0.98	0.05	63,63,63,63	0
56	MG	BA	3490	1/1	0.98	0.11	40,40,40,40	0
56	MG	BN	3004	1/1	0.98	0.47	69,69,69,69	0
56	MG	BB	3013	1/1	0.98	0.17	31,31,31,31	0
56	MG	BA	3327	1/1	0.98	0.16	21,21,21,21	0
56	MG	BA	3652	1/1	0.98	0.22	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3393	1/1	0.98	0.23	27,27,27,27	0
56	MG	BA	3080	1/1	0.98	0.09	12,12,12,12	0
56	MG	BA	3488	1/1	0.98	0.29	43,43,43,43	0
56	MG	DA	3461	1/1	0.98	0.08	40,40,40,40	0
56	MG	DA	3544	1/1	0.98	0.36	42,42,42,42	0
56	MG	BA	3309	1/1	0.98	0.13	43,43,43,43	0
58	ZN	D6	501	1/1	0.98	0.11	65,65,65,65	0
56	MG	DA	3579	1/1	0.98	0.21	38,38,38,38	0
56	MG	BA	3437	1/1	0.98	0.12	37,37,37,37	0
56	MG	BA	3014	1/1	0.98	0.37	48,48,48,48	0
56	MG	DA	3052	1/1	0.98	0.10	20,20,20,20	0
56	MG	BA	3637	1/1	0.98	0.79	52,52,52,52	0
56	MG	CA	3137	1/1	0.98	0.12	59,59,59,59	0
56	MG	CA	3133	1/1	0.98	0.20	45,45,45,45	0
56	MG	DA	3378	1/1	0.98	0.09	38,38,38,38	0
56	MG	BA	3603	1/1	0.98	0.29	40,40,40,40	0
56	MG	DA	3388	1/1	0.98	0.11	25,25,25,25	0
56	MG	DA	3559	1/1	0.98	0.12	47,47,47,47	0
56	MG	BA	3130	1/1	0.98	0.40	51,51,51,51	0
56	MG	DA	3420	1/1	0.98	0.06	43,43,43,43	0
56	MG	AA	3192	1/1	0.98	0.08	73,73,73,73	0
56	MG	BA	3124	1/1	0.98	0.20	46,46,46,46	0
56	MG	BA	3482	1/1	0.98	0.09	59,59,59,59	0
56	MG	CA	3132	1/1	0.98	0.08	66,66,66,66	0
56	MG	DA	3085	1/1	0.98	0.09	35,35,35,35	0
56	MG	BA	3673	1/1	0.98	0.16	60,60,60,60	0
56	MG	AA	3220	1/1	0.98	0.09	42,42,42,42	0
56	MG	DA	3359	1/1	0.98	0.21	21,21,21,21	0
56	MG	BA	3703	1/1	0.98	0.14	44,44,44,44	0
56	MG	DA	3450	1/1	0.98	0.18	47,47,47,47	0
56	MG	BA	3589	1/1	0.98	0.23	34,34,34,34	0
56	MG	DA	3347	1/1	0.98	0.20	39,39,39,39	0
56	MG	BA	3315	1/1	0.98	0.31	43,43,43,43	0
56	MG	B7	102	1/1	0.98	0.28	29,29,29,29	0
56	MG	BA	3628	1/1	0.98	0.10	39,39,39,39	0
56	MG	DA	3265	1/1	0.98	0.29	44,44,44,44	0
56	MG	BA	3534	1/1	0.98	0.22	36,36,36,36	0
56	MG	BD	306	1/1	0.98	0.47	47,47,47,47	0
56	MG	DA	3149	1/1	0.98	0.07	47,47,47,47	0
56	MG	BA	3497	1/1	0.98	0.42	28,28,28,28	0
56	MG	BA	3436	1/1	0.98	0.29	35,35,35,35	0
56	MG	DA	3633	1/1	0.98	0.26	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3645	1/1	0.98	0.16	63,63,63,63	0
56	MG	BE	301	1/1	0.98	0.22	28,28,28,28	0
56	MG	CA	3077	1/1	0.98	0.27	51,51,51,51	0
56	MG	DA	3217	1/1	0.98	0.27	33,33,33,33	0
56	MG	DA	3020	1/1	0.98	0.32	45,45,45,45	0
56	MG	BQ	3003	1/1	0.98	0.19	15,15,15,15	0
56	MG	DA	3582	1/1	0.98	0.36	44,44,44,44	0
56	MG	DA	3555	1/1	0.98	0.14	43,43,43,43	0
56	MG	DA	3311	1/1	0.98	0.32	33,33,33,33	0
56	MG	CA	3095	1/1	0.98	0.15	35,35,35,35	0
56	MG	CA	3149	1/1	0.98	0.18	81,81,81,81	0
56	MG	DA	3649	1/1	0.98	0.08	39,39,39,39	0
56	MG	CA	3094	1/1	0.98	0.22	37,37,37,37	0
56	MG	CA	3151	1/1	0.98	0.14	80,80,80,80	0
56	MG	BA	3463	1/1	0.98	0.10	32,32,32,32	0
56	MG	BA	3176	1/1	0.98	0.21	50,50,50,50	0
56	MG	DA	3257	1/1	0.98	0.20	25,25,25,25	0
56	MG	DA	3312	1/1	0.98	0.23	24,24,24,24	0
56	MG	BA	3639	1/1	0.98	0.10	35,35,35,35	0
56	MG	AA	3156	1/1	0.98	0.13	31,31,31,31	0
56	MG	BA	3286	1/1	0.98	0.23	42,42,42,42	0
56	MG	AA	3157	1/1	0.98	0.06	26,26,26,26	0
56	MG	DA	3430	1/1	0.98	0.18	75,75,75,75	0
56	MG	CA	3099	1/1	0.98	0.39	64,64,64,64	0
56	MG	DA	3183	1/1	0.98	0.14	42,42,42,42	0
56	MG	DA	3408	1/1	0.98	0.18	35,35,35,35	0
56	MG	BA	3682	1/1	0.98	0.35	50,50,50,50	0
56	MG	DA	3453	1/1	0.98	0.10	44,44,44,44	0
56	MG	DA	3479	1/1	0.98	0.14	35,35,35,35	0
56	MG	DA	3490	1/1	0.98	0.14	46,46,46,46	0
56	MG	DA	3638	1/1	0.98	0.10	53,53,53,53	0
56	MG	BA	3443	1/1	0.98	0.34	34,34,34,34	0
56	MG	AA	3091	1/1	0.98	0.26	75,75,75,75	0
56	MG	DA	3080	1/1	0.98	0.11	43,43,43,43	0
56	MG	AA	3168	1/1	0.98	0.27	80,80,80,80	0
56	MG	DA	3564	1/1	0.98	0.11	29,29,29,29	0
56	MG	DA	3650	1/1	0.98	0.05	35,35,35,35	0
56	MG	DA	3174	1/1	0.98	0.44	26,26,26,26	0
56	MG	AA	3161	1/1	0.98	0.08	61,61,61,61	0
56	MG	B0	105	1/1	0.98	0.27	44,44,44,44	0
56	MG	DA	3315	1/1	0.98	0.12	39,39,39,39	0
56	MG	AX	110	1/1	0.98	0.17	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	AA	3104	1/1	0.98	0.16	35,35,35,35	0
56	MG	BA	3030	1/1	0.98	0.33	26,26,26,26	0
56	MG	BA	3198	1/1	0.98	0.35	29,29,29,29	0
56	MG	BA	3452	1/1	0.98	0.11	16,16,16,16	0
56	MG	BB	3001	1/1	0.98	0.15	56,56,56,56	0
56	MG	DA	3204	1/1	0.98	0.36	44,44,44,44	0
56	MG	DA	3526	1/1	0.98	0.12	49,49,49,49	0
56	MG	DA	3365	1/1	0.98	0.06	52,52,52,52	0
56	MG	DA	3357	1/1	0.98	0.12	50,50,50,50	0
56	MG	B5	502	1/1	0.98	0.10	56,56,56,56	0
56	MG	DA	3545	1/1	0.98	0.28	35,35,35,35	0
56	MG	BA	3591	1/1	0.98	0.22	38,38,38,38	0
56	MG	BA	3659	1/1	0.98	0.10	42,42,42,42	0
56	MG	DA	3101	1/1	0.98	0.28	59,59,59,59	0
56	MG	BB	3016	1/1	0.98	0.15	24,24,24,24	0
56	MG	BA	3695	1/1	0.98	0.25	34,34,34,34	0
56	MG	BA	3450	1/1	0.98	0.14	40,40,40,40	0
56	MG	BF	303	1/1	0.98	0.12	42,42,42,42	0
56	MG	AA	3183	1/1	0.98	0.11	56,56,56,56	0
56	MG	DF	305	1/1	0.98	0.43	55,55,55,55	0
56	MG	BA	3125	1/1	0.98	0.30	26,26,26,26	0
56	MG	DA	3196	1/1	0.98	0.09	54,54,54,54	0
56	MG	CA	3045	1/1	0.98	0.09	60,60,60,60	0
56	MG	DA	3486	1/1	0.98	0.08	52,52,52,52	0
56	MG	DA	3622	1/1	0.98	0.17	40,40,40,40	0
56	MG	BA	3587	1/1	0.98	0.22	23,23,23,23	0
56	MG	BA	3003	1/1	0.98	0.08	24,24,24,24	0
56	MG	DA	3387	1/1	0.98	0.15	50,50,50,50	0
56	MG	DA	3522	1/1	0.98	0.23	46,46,46,46	0
56	MG	BA	3559	1/1	0.98	0.40	29,29,29,29	0
56	MG	BD	308	1/1	0.98	0.34	21,21,21,21	0
56	MG	BA	3495	1/1	0.98	0.27	27,27,27,27	0
56	MG	DA	3401	1/1	0.98	0.13	41,41,41,41	0
56	MG	BA	3374	1/1	0.98	0.28	26,26,26,26	0
56	MG	DA	3307	1/1	0.98	0.12	40,40,40,40	0
56	MG	BA	3268	1/1	0.98	0.19	29,29,29,29	0
56	MG	BA	3553	1/1	0.98	0.17	46,46,46,46	0
56	MG	DA	3400	1/1	0.98	0.18	42,42,42,42	0
56	MG	BA	3170	1/1	0.98	0.48	34,34,34,34	0
56	MG	DA	3350	1/1	0.98	0.24	21,21,21,21	0
56	MG	DA	3511	1/1	0.98	0.10	47,47,47,47	0
56	MG	BA	3403	1/1	0.98	0.20	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3491	1/1	0.98	0.23	38,38,38,38	0
56	MG	DA	3487	1/1	0.98	0.09	44,44,44,44	0
56	MG	BA	3410	1/1	0.98	0.18	21,21,21,21	0
56	MG	BA	3311	1/1	0.98	0.27	52,52,52,52	0
56	MG	AA	3186	1/1	0.98	0.14	51,51,51,51	0
56	MG	DA	3463	1/1	0.98	0.06	32,32,32,32	0
56	MG	DA	3412	1/1	0.98	0.16	34,34,34,34	0
56	MG	BA	3057	1/1	0.98	0.40	36,36,36,36	0
56	MG	DA	3082	1/1	0.98	0.08	7,7,7,7	0
56	MG	BA	3664	1/1	0.98	0.12	63,63,63,63	0
56	MG	BE	303	1/1	0.98	0.10	39,39,39,39	0
56	MG	BA	3160	1/1	0.98	0.17	24,24,24,24	0
56	MG	AA	3153	1/1	0.98	0.10	46,46,46,46	0
56	MG	DA	3275	1/1	0.98	0.26	34,34,34,34	0
56	MG	B3	3401	1/1	0.98	0.18	24,24,24,24	0
56	MG	BA	3129	1/1	0.98	0.67	44,44,44,44	0
56	MG	CA	3075	1/1	0.98	0.35	76,76,76,76	0
56	MG	AA	3210	1/1	0.98	0.07	48,48,48,48	0
56	MG	BA	3607	1/1	0.98	0.20	74,74,74,74	0
56	MG	DA	3510	1/1	0.98	0.13	67,67,67,67	0
56	MG	DA	3279	1/1	0.98	0.29	32,32,32,32	0
56	MG	BA	3411	1/1	0.98	0.19	21,21,21,21	0
58	ZN	BY	501	1/1	0.98	0.09	67,67,67,67	0
56	MG	BA	3394	1/1	0.98	0.21	45,45,45,45	0
56	MG	BA	3035	1/1	0.98	0.15	32,32,32,32	0
56	MG	BA	3201	1/1	0.98	0.27	36,36,36,36	0
56	MG	BA	3380	1/1	0.98	0.10	32,32,32,32	0
56	MG	BA	3577	1/1	0.98	0.15	63,63,63,63	0
56	MG	BA	3356	1/1	0.98	0.13	33,33,33,33	0
56	MG	DA	3518	1/1	0.98	0.10	40,40,40,40	0
56	MG	BA	3556	1/1	0.98	0.18	25,25,25,25	0
56	MG	BA	3421	1/1	0.98	0.15	28,28,28,28	0
56	MG	BA	3348	1/1	0.98	0.10	29,29,29,29	0
56	MG	BA	3522	1/1	0.98	0.13	42,42,42,42	0
56	MG	BA	3355	1/1	0.98	0.09	39,39,39,39	0
56	MG	DA	3508	1/1	0.98	0.06	30,30,30,30	0
56	MG	BA	3206	1/1	0.98	0.28	32,32,32,32	0
56	MG	BA	3562	1/1	0.98	0.14	42,42,42,42	0
56	MG	BA	3531	1/1	0.98	0.18	28,28,28,28	0
56	MG	DA	3480	1/1	0.98	0.17	42,42,42,42	0
58	ZN	D5	103	1/1	0.98	0.07	61,61,61,61	0
56	MG	BA	3501	1/1	0.98	0.18	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3083	1/1	0.98	0.18	44,44,44,44	0
56	MG	DA	3495	1/1	0.98	0.07	53,53,53,53	0
56	MG	DA	3233	1/1	0.98	0.34	58,58,58,58	0
56	MG	DA	3301	1/1	0.98	0.28	30,30,30,30	0
56	MG	BA	3210	1/1	0.98	0.30	39,39,39,39	0
56	MG	AA	3159	1/1	0.98	0.32	57,57,57,57	0
56	MG	BA	3445	1/1	0.98	0.17	16,16,16,16	0
56	MG	DA	3253	1/1	0.98	0.13	35,35,35,35	0
56	MG	DA	3304	1/1	0.98	0.20	44,44,44,44	0
56	MG	DA	3273	1/1	0.98	0.23	32,32,32,32	0
56	MG	DA	3045	1/1	0.98	0.25	49,49,49,49	0
56	MG	DA	3247	1/1	0.98	0.32	34,34,34,34	0
56	MG	DA	3609	1/1	0.98	0.23	49,49,49,49	0
56	MG	BA	3494	1/1	0.98	0.27	28,28,28,28	0
56	MG	DA	3223	1/1	0.98	0.09	41,41,41,41	0
56	MG	BA	3339	1/1	0.98	0.14	47,47,47,47	0
56	MG	BG	3001	1/1	0.98	0.09	65,65,65,65	0
56	MG	DA	3546	1/1	0.98	0.22	38,38,38,38	0
56	MG	BA	3378	1/1	0.98	0.18	24,24,24,24	0
56	MG	BA	3079	1/1	0.98	0.33	50,50,50,50	0
56	MG	DA	3320	1/1	0.98	0.21	50,50,50,50	0
56	MG	AA	3046	1/1	0.98	0.15	60,60,60,60	0
56	MG	BA	3500	1/1	0.98	0.13	43,43,43,43	0
56	MG	DA	3321	1/1	0.98	0.12	31,31,31,31	0
56	MG	BA	3570	1/1	0.98	0.20	33,33,33,33	0
56	MG	DA	3349	1/1	0.98	0.09	27,27,27,27	0
56	MG	DA	3179	1/1	0.99	0.41	36,36,36,36	0
56	MG	BA	3496	1/1	0.99	0.45	21,21,21,21	0
56	MG	DA	3176	1/1	0.99	0.09	52,52,52,52	0
56	MG	DA	3182	1/1	0.99	0.20	29,29,29,29	0
57	SF4	CD	501	8/8	0.99	0.11	63,76,87,96	0
56	MG	BA	3523	1/1	0.99	0.16	32,32,32,32	0
56	MG	BA	3407	1/1	0.99	0.22	35,35,35,35	0
56	MG	BA	3575	1/1	0.99	0.13	26,26,26,26	0
56	MG	DA	3293	1/1	0.99	0.10	34,34,34,34	0
56	MG	BA	3670	1/1	0.99	0.10	55,55,55,55	0
56	MG	BA	3337	1/1	0.99	0.10	48,48,48,48	0
56	MG	BA	3480	1/1	0.99	0.12	22,22,22,22	0
56	MG	DA	3327	1/1	0.99	0.12	45,45,45,45	0
56	MG	DA	3581	1/1	0.99	0.24	41,41,41,41	0
56	MG	BA	3045	1/1	0.99	0.16	27,27,27,27	0
56	MG	DA	3260	1/1	0.99	0.07	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	DA	3026	1/1	0.99	0.22	36,36,36,36	0
56	MG	BA	3683	1/1	0.99	0.29	37,37,37,37	0
56	MG	BA	3691	1/1	0.99	0.10	40,40,40,40	0
56	MG	BA	3345	1/1	0.99	0.05	37,37,37,37	0
56	MG	DA	3625	1/1	0.99	0.16	48,48,48,48	0
56	MG	DA	3616	1/1	0.99	0.18	41,41,41,41	0
56	MG	BA	3541	1/1	0.99	0.14	37,37,37,37	0
56	MG	BA	3414	1/1	0.99	0.22	51,51,51,51	0
56	MG	BA	3483	1/1	0.99	0.21	18,18,18,18	0
56	MG	BX	101	1/1	0.99	0.09	38,38,38,38	0
58	ZN	B6	501	1/1	0.99	0.12	51,51,51,51	0
56	MG	DA	3355	1/1	0.99	0.38	39,39,39,39	0
56	MG	BA	3430	1/1	0.99	0.12	47,47,47,47	0
56	MG	BA	3077	1/1	0.99	0.18	20,20,20,20	0
56	MG	DA	3158	1/1	0.99	0.40	47,47,47,47	0
56	MG	BA	3418	1/1	0.99	0.26	20,20,20,20	0
56	MG	DA	3159	1/1	0.99	0.13	50,50,50,50	0
56	MG	BA	3381	1/1	0.99	0.07	25,25,25,25	0
56	MG	BA	3448	1/1	0.99	0.22	23,23,23,23	0
58	ZN	B5	501	1/1	0.99	0.10	49,49,49,49	0
56	MG	BA	3528	1/1	0.99	0.22	44,44,44,44	0
56	MG	AA	3103	1/1	0.99	0.12	43,43,43,43	0
57	SF4	AD	501	8/8	0.99	0.13	62,75,82,88	0
56	MG	BA	3441	1/1	0.99	0.23	29,29,29,29	0
56	MG	BA	3617	1/1	0.99	0.35	30,30,30,30	0
56	MG	AA	3169	1/1	0.99	0.26	62,62,62,62	0
56	MG	BA	3665	1/1	0.99	0.18	39,39,39,39	0
56	MG	DA	3360	1/1	0.99	0.10	36,36,36,36	0
56	MG	BA	3218	1/1	0.99	0.12	58,58,58,58	0
56	MG	BA	3275	1/1	0.99	0.18	28,28,28,28	0
56	MG	AA	3024	1/1	0.99	0.11	49,49,49,49	0
56	MG	BA	3159	1/1	0.99	0.29	47,47,47,47	0
56	MG	DA	3382	1/1	0.99	0.06	44,44,44,44	0
56	MG	BA	3285	1/1	0.99	0.17	44,44,44,44	0
56	MG	BA	3140	1/1	0.99	0.31	50,50,50,50	0
56	MG	DA	3272	1/1	0.99	0.14	36,36,36,36	0
56	MG	CA	3168	1/1	0.99	0.46	79,79,79,79	0
56	MG	DA	3573	1/1	0.99	0.17	32,32,32,32	0
56	MG	DA	3383	1/1	0.99	0.18	27,27,27,27	0
56	MG	DA	3652	1/1	0.99	0.26	26,26,26,26	0
56	MG	BA	3419	1/1	0.99	0.31	36,36,36,36	0
56	MG	BA	3412	1/1	0.99	0.27	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
56	MG	BA	3417	1/1	0.99	0.19	21,21,21,21	0
56	MG	AA	3013	1/1	0.99	0.25	75,75,75,75	0
56	MG	DA	3291	1/1	0.99	0.18	42,42,42,42	0
56	MG	DA	3422	1/1	0.99	0.23	45,45,45,45	0
56	MG	BA	3362	1/1	1.00	0.17	23,23,23,23	0
58	ZN	B9	501	1/1	1.00	0.12	49,49,49,49	0
56	MG	BB	3010	1/1	1.00	0.20	44,44,44,44	0
56	MG	BB	3012	1/1	1.00	0.16	42,42,42,42	0
56	MG	DA	3191	1/1	1.00	0.16	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.