



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 07:26 AM UTC

PDB ID : 5DC3 / pdb_00005dc3
Title : Complex of yeast 80S ribosome with non-modified eIF5A
Authors : Melnikov, S.; Mailliot, J.; Shin, B.-S.; Rigger, L.; Yusupova, G.; Micura, R.;
Dever, T.E.; Yusupov, M.
Deposited on : 2015-08-23
Resolution : 3.25 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	FAILED
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.48.1

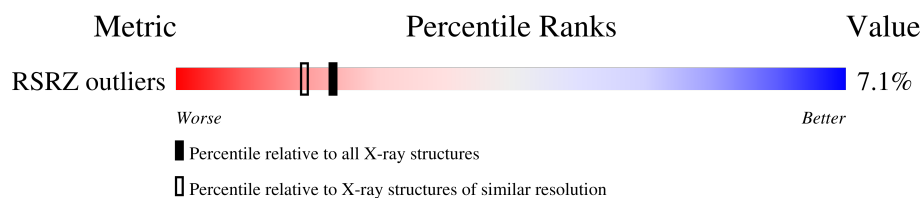
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 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))
RSRZ outliers	164620	1483 (3.30-3.22)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 404042 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	2	1781	Total	C	N	O	P	0	1	0
			37970	16975	6720	12493	1782			
1	6	1795	Total	C	N	O	P	0	1	0
			38260	17105	6763	12596	1796			

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	S0	206	Total	C	N	O	S	0	0	0
			1577	1014	278	283	2			
2	s0	206	Total	C	N	O	S	0	0	0
			1583	1017	281	283	2			

- Molecule 3 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	S1	214	Total	C	N	O	S	0	0	0
			1709	1084	310	311	4			
3	s1	216	Total	C	N	O	S	0	0	0
			1722	1091	312	315	4			

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	S2	217	Total	C	N	O	S	0	0	0
			1635	1047	289	297	2			
4	s2	217	Total	C	N	O	S	0	0	0
			1635	1047	289	297	2			

- Molecule 5 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	S3	223	Total	C	N	O	S	0	0	0
			1734	1101	313	314	6			
5	s3	223	Total	C	N	O	S	0	0	0
			1734	1101	313	314	6			

- Molecule 6 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	S4	260	Total	C	N	O	S	0	0	0
			2068	1316	389	360	3			
6	s4	260	Total	C	N	O	S	0	0	0
			2068	1316	389	360	3			

- Molecule 7 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	S5	206	Total	C	N	O	S	0	0	0
			1609	1007	300	299	3			
7	s5	206	Total	C	N	O	S	0	0	0
			1609	1007	300	299	3			

- Molecule 8 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	S6	226	Total	C	N	O	S	0	0	0
			1799	1129	346	321	3			
8	s6	218	Total	C	N	O	S	0	0	0
			1755	1102	337	313	3			

- Molecule 9 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	S7	184	Total	C	N	O	0	0	0
			1481	951	265	265			
9	s7	186	Total	C	N	O	0	0	0
			1491	957	267	267			

- Molecule 10 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	S8	188	Total	C	N	O	S	0	0	0
			1489	925	298	264	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	s8	188	Total	C	N	O	S	0	0	0
			1489	925	298	264	2			

- Molecule 11 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	S9	185	Total	C	N	O	S	0	0	0
			1494	943	289	261	1			
11	s9	185	Total	C	N	O	S	0	0	0
			1494	943	289	261	1			

- Molecule 12 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	C0	96	Total	C	N	O	S	0	0	0
			772	499	126	145	2			

- Molecule 13 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	C1	155	Total	C	N	O	S	0	0	0
			1213	774	230	206	3			
13	c1	146	Total	C	N	O	S	0	0	0
			1168	747	221	197	3			

- Molecule 14 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	C2	124	Total	C	N	O	S	0	0	0
			890	560	156	172	2			
14	c2	124	Total	C	N	O	S	0	0	0
			890	560	156	172	2			

- Molecule 15 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	C3	150	Total	C	N	O	S	0	0	0
			1192	759	224	207	2			
15	c3	150	Total	C	N	O	S	0	0	0
			1192	759	224	207	2			

- Molecule 16 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	C4	127	Total	C	N	O	S	0	0	0
			891	545	182	163	1			
16	c4	128	Total	C	N	O	S	0	0	0
			949	582	188	176	3			

- Molecule 17 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	C5	124	Total	C	N	O	S	0	0	0
			977	622	182	166	7			
17	c5	135	Total	C	N	O	S	0	0	0
			1039	658	196	178	7			

- Molecule 18 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	C6	141	Total	C	N	O		0	0	0
			1105	708	203	194				
18	c6	142	Total	C	N	O		0	0	0
			1111	711	204	196				

- Molecule 19 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	C7	120	Total	C	N	O	S	0	0	0
			926	577	177	170	2			
19	c7	117	Total	C	N	O	S	0	0	0
			906	563	174	167	2			

- Molecule 20 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	C8	145	Total	C	N	O	S	0	0	0
			1192	743	237	210	2			
20	c8	145	Total	C	N	O	S	0	0	0
			1192	743	237	210	2			

- Molecule 21 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	C9	143	Total	C	N	O	S	0	0	0
			1112	694	208	208	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	c9	143	Total	C	N	O	S	0	0	0
			1112	694	208	208	2			

- Molecule 22 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	D0	107	Total	C	N	O	S	0	0	0
			855	539	156	159	1			
22	d0	110	Total	C	N	O	S	0	0	0
			882	554	161	166	1			

- Molecule 23 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	D1	87	Total	C	N	O	S	0	0	0
			684	420	125	137	2			
23	d1	87	Total	C	N	O	S	0	0	0
			684	420	125	137	2			

- Molecule 24 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	D2	129	Total	C	N	O	S	0	0	0
			1021	650	188	180	3			
24	d2	129	Total	C	N	O	S	0	0	0
			1021	650	188	180	3			

- Molecule 25 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	D3	144	Total	C	N	O	S	0	0	0
			1121	708	220	191	2			
25	d3	144	Total	C	N	O	S	0	0	0
			1121	708	220	191	2			

- Molecule 26 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
26	D4	134	Total	C	N	O	0	0	0
			1073	676	208	189			
26	d4	134	Total	C	N	O	0	0	0
			1073	676	208	189			

- Molecule 27 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
27	D5	70	Total	C	N	O	0	0	0
			563	360	104	99			
27	d5	69	Total	C	N	O	0	0	0
			558	357	103	98			

- Molecule 28 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	D6	97	Total	C	N	O	S	0	0	0
			769	475	160	129	5			
28	d6	97	Total	C	N	O	S	0	0	0
			769	475	160	129	5			

- Molecule 29 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	D7	81	Total	C	N	O	S	0	0	0
			610	382	110	113	5			
29	d7	81	Total	C	N	O	S	0	0	0
			610	382	110	113	5			

- Molecule 30 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	D8	63	Total	C	N	O	S	0	0	0
			497	306	99	91	1			
30	d8	63	Total	C	N	O	S	0	0	0
			497	306	99	91	1			

- Molecule 31 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	D9	53	Total	C	N	O	S	0	0	0
			442	274	92	72	4			
31	d9	53	Total	C	N	O	S	0	0	0
			442	274	92	72	4			

- Molecule 32 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	E0	60	Total	C	N	O	S	0	0	0
			475	299	98	77	1			
32	e0	62	Total	C	N	O	S	0	0	0
			491	309	101	80	1			

- Molecule 33 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	E1	71	Total	C	N	O	S	0	0	0
			566	362	106	94	4			
33	e1	76	Total	C	N	O	S	0	0	0
			608	388	117	99	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E1	77	ALA	GLY	conflict	UNP P05759
e1	77	ALA	GLY	conflict	UNP P05759

- Molecule 34 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	SR	318	Total	C	N	O	S	0	0	0
			2437	1541	418	470	8			
34	sR	318	Total	C	N	O	S	0	0	0
			2442	1544	418	472	8			

- Molecule 35 is a protein called Suppressor protein STM1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	SM	159	Total	C	N	O		0	0	0
			1104	652	221	231				
35	sM	104	Total	C	N	O		0	0	0
			679	402	140	137				

- Molecule 36 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	1	3149	Total	C	N	O	P	0	0	0
			67355	30086	12142	21978	3149			
36	5	3169	Total	C	N	O	P	0	0	0
			67780	30276	12216	22120	3168			

- Molecule 37 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	3	121	Total	C	N	O	P	0	0	0
			2579	1152	461	845	121			
37	7	121	Total	C	N	O	P	0	0	0
			2579	1152	461	845	121			

- Molecule 38 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	4	158	Total	C	N	O	P	0	0	0
			3353	1500	586	1109	158			
38	8	158	Total	C	N	O	P	0	0	0
			3353	1500	586	1109	158			

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	L2	252	Total	C	N	O	S	0	0	0
			1914	1191	388	334	1			
39	l2	252	Total	C	N	O	S	0	0	0
			1912	1190	388	333	1			

- Molecule 40 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	L3	386	Total	C	N	O	S	0	0	0
			3075	1950	584	533	8			
40	l3	386	Total	C	N	O	S	0	0	0
			3075	1950	584	533	8			

- Molecule 41 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	L4	361	Total	C	N	O	S	0	0	0
			2748	1729	522	494	3			
41	l4	361	Total	C	N	O	S	0	0	0
			2748	1729	522	494	3			

- Molecule 42 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	L5	296	Total	C	N	O	S	0	0	0
			2375	1501	414	458	2			
42	l5	294	Total	C	N	O	S	0	0	0
			2359	1489	412	456	2			

- Molecule 43 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	L6	156	Total	C	N	O	S	0	0	0
			1239	800	222	216	1			
43	l6	157	Total	C	N	O	S	0	0	0
			1248	806	224	217	1			

- Molecule 44 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	L7	222	Total	C	N	O	S	0	0	0
			1784	1151	324	308	1			
44	l7	223	Total	C	N	O	S	0	0	0
			1791	1155	325	310	1			

- Molecule 45 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	L8	233	Total	C	N	O	S	0	0	0
			1804	1151	323	327	3			
45	l8	231	Total	C	N	O	S	0	0	0
			1763	1130	316	314	3			

- Molecule 46 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	L9	191	Total	C	N	O	S	0	0	0
			1518	963	274	277	4			
46	l9	191	Total	C	N	O	S	0	0	0
			1518	963	274	277	4			

- Molecule 47 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	M0	211	Total	C	N	O	S	0	0	0
			1705	1083	322	294	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	m0	213	Total	C	N	O	S	0	0	0
			1722	1094	325	297	6			

- Molecule 48 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	M1	169	Total	C	N	O	S	0	0	0
			1353	847	253	249	4			
48	m1	169	Total	C	N	O	S	0	0	0
			1353	847	253	249	4			

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	M3	193	Total	C	N	O	S	0	0	0
			1543	962	315	266				
49	m3	194	Total	C	N	O	S	0	0	0
			1548	965	316	267				

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	M4	136	Total	C	N	O	S	0	0	0
			1053	675	199	177	2			
50	m4	137	Total	C	N	O	S	0	0	0
			1059	678	200	179	2			

- Molecule 51 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	M5	203	Total	C	N	O	S	0	0	0
			1720	1077	361	281	1			
51	m5	203	Total	C	N	O	S	0	0	0
			1720	1077	361	281	1			

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	M6	197	Total	C	N	O	S	0	0	0
			1555	1003	289	262	1			
52	m6	197	Total	C	N	O	S	0	0	0
			1555	1003	289	262	1			

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
53	M7	183	Total	C	N	O	0	0	0
			1420	882	281	257			
53	m7	155	Total	C	N	O	0	0	0
			1227	764	238	225			

- Molecule 54 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	M8	185	Total	C	N	O	S	0	0	0
			1441	908	290	241	2			
54	m8	185	Total	C	N	O	S	0	0	0
			1441	908	290	241	2			

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
55	M9	188	Total	C	N	O	0	0	0
			1521	935	326	260			
55	m9	188	Total	C	N	O	0	0	0
			1521	935	326	260			

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	N0	172	Total	C	N	O	S	0	0	0
			1445	930	267	244	4			
56	n0	172	Total	C	N	O	S	0	0	0
			1445	930	267	244	4			

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	N1	159	Total	C	N	O	S	0	0	0
			1276	805	246	221	4			
57	n1	159	Total	C	N	O	S	0	0	0
			1276	805	246	221	4			

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
58	N2	100	Total	C	N	O	0	0	0
			796	516	131	149			
58	n2	98	Total	C	N	O	0	0	0
			778	505	127	146			

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
59	N3	136	Total	C	N	O	S	0	0	0
			1003	628	189	179	7			
59	n3	136	Total	C	N	O	S	0	0	0
			1003	628	189	179	7			

- Molecule 60 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
60	N4	98	Total	C	N	O	S	0	0	0
			699	443	137	118	1			
60	n4	135	Total	C	N	O	S	0	0	0
			1038	651	206	180	1			

- Molecule 61 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
61	N5	121	Total	C	N	O	S	0	0	0
			964	620	169	173	2			
61	n5	120	Total	C	N	O	S	0	0	0
			959	617	168	172	2			

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
62	N6	126	Total	C	N	O	0	0	0
			993	625	192	176			
62	n6	126	Total	C	N	O	0	0	0
			993	625	192	176			

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
63	N7	135	Total	C	N	O	0	0	0
			1092	710	202	180			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
63	n7	135	Total	C	N	O	0	0	0
			1092	710	202	180			

- Molecule 64 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
64	N8	148	Total	C	N	O	S	0	0	0
			1173	749	231	190	3			
64	n8	148	Total	C	N	O	S	0	0	0
			1173	749	231	190	3			

- Molecule 65 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
65	N9	58	Total	C	N	O	0	0	0
			462	289	100	73			
65	n9	58	Total	C	N	O	0	0	0
			462	289	100	73			

- Molecule 66 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
66	O0	97	Total	C	N	O	S	0	0	0
			743	479	124	139	1			
66	o0	100	Total	C	N	O	S	0	0	0
			767	492	128	146	1			

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
67	O1	109	Total	C	N	O	S	0	0	0
			876	556	167	152	1			
67	o1	109	Total	C	N	O	S	0	0	0
			883	559	167	156	1			

- Molecule 68 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
68	O2	127	Total	C	N	O	S	0	0	0
			1020	647	205	167	1			
68	o2	127	Total	C	N	O	S	0	0	0
			1020	647	205	167	1			

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
69	O3	106	Total	C	N	O	S	0	0	0
			850	540	165	144	1			
69	o3	106	Total	C	N	O	S	0	0	0
			850	540	165	144	1			

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
70	O4	112	Total	C	N	O	S	0	0	0
			880	545	179	152	4			
70	o4	112	Total	C	N	O	S	0	0	0
			880	545	179	152	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O4	?	-	LYS	deletion	UNP P87262
o4	?	-	LYS	deletion	UNP P87262

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
71	O5	119	Total	C	N	O	S	0	0	0
			969	615	186	167	1			
71	o5	119	Total	C	N	O	S	0	0	0
			965	612	185	167	1			

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
72	O6	99	Total	C	N	O	S	0	0	0
			771	481	156	132	2			
72	o6	99	Total	C	N	O	S	0	0	0
			770	481	156	131	2			

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
73	O7	87	Total	C	N	O	S	0	0	0
			681	414	148	114	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
73	o7	87	Total	C	N	O	S	0	0	0
			681	414	148	114	5			

- Molecule 74 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
74	O8	77	Total	C	N	O		0	0	0
			612	391	115	106				
74	o8	77	Total	C	N	O		0	0	0
			608	388	114	106				

- Molecule 75 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
75	O9	50	Total	C	N	O	S	0	0	0
			436	272	97	65	2			
75	o9	50	Total	C	N	O	S	0	0	0
			436	272	97	65	2			

- Molecule 76 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
76	Q0	52	Total	C	N	O	S	0	0	0
			417	259	86	67	5			
76	q0	52	Total	C	N	O	S	0	0	0
			417	259	86	67	5			

- Molecule 77 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
77	Q1	25	Total	C	N	O	S	0	0	0
			233	142	63	27	1			
77	q1	25	Total	C	N	O	S	0	0	0
			233	142	63	27	1			

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
78	Q2	105	Total	C	N	O	S	0	0	0
			847	534	170	138	5			
78	q2	105	Total	C	N	O	S	0	0	0
			847	534	170	138	5			

- Molecule 79 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
79	Q3	91	Total	C	N	O	S	0	0	0
			694	429	138	121	6			
79	q3	91	Total	C	N	O	S	0	0	0
			694	429	138	121	6			

- Molecule 80 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
80	c0	96	Total	C	N	O	S	0	0	0
			762	491	125	144	2			

- Molecule 81 is a protein called 60S ribosomal protein L12-A (uL11).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
81	m2	150	Total	C	N	O	S	0	0	0
			750	450	150	150				

- Molecule 82 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
82	p0	143	Total	C	N	O	S	0	0	0
			1076	686	192	195	3			

- Molecule 83 is a protein called 60S ribosomal protein P1 alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
83	p1	47	Total	C	N	O	S	0	0	0
			235	141	47	47				

- Molecule 84 is a protein called 60S ribosomal P2 beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
84	p2	46	Total	C	N	O	S	0	0	0
			230	138	46	46				

- Molecule 85 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
85	f	148	Total	C	N	O	S	0	0	0
			1116	692	188	227	9			

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
86	D6	1	Total	Zn	0	0
			1	1		
86	D7	1	Total	Zn	0	0
			1	1		
86	D9	1	Total	Zn	0	0
			1	1		
86	E1	1	Total	Zn	0	0
			1	1		
86	O7	1	Total	Zn	0	0
			1	1		
86	Q0	1	Total	Zn	0	0
			1	1		
86	Q2	1	Total	Zn	0	0
			1	1		
86	Q3	1	Total	Zn	0	0
			1	1		
86	d6	1	Total	Zn	0	0
			1	1		
86	d7	1	Total	Zn	0	0
			1	1		
86	d9	1	Total	Zn	0	0
			1	1		
86	e1	1	Total	Zn	0	0
			1	1		
86	o7	1	Total	Zn	0	0
			1	1		
86	q0	1	Total	Zn	0	0
			1	1		
86	q2	1	Total	Zn	0	0
			1	1		
86	q3	1	Total	Zn	0	0
			1	1		

MolProbity failed to run properly - this section is therefore empty.

3 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	438.23Å 289.33Å 305.47Å 90.00° 98.95° 90.00°	Depositor
Resolution (Å)	190.48 – 3.25 190.48 – 3.25	Depositor EDS
% Data completeness (in resolution range)	100.0 (190.48-3.25) 99.9 (190.48-3.25)	Depositor EDS
R_{merge}	0.41	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 3.26Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.252 , 0.301 0.258 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	86.7	Xtriage
Anisotropy	0.117	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 90.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	404042	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.52% 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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

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4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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4.3.2 Protein sidechains [i](#)

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4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 16 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	2	2
81	m2	2
80	c0	1
36	5	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	c0	84:GLU	C	87:HIS	N	7.38
1	2	1716:C	O3'	1717:G	P	5.29
1	5	2437:G	O3'	2438:A	P	3.76
1	m2	52:UNK	C	54:UNK	N	3.58
1	m2	23:UNK	C	28:UNK	N	3.14
1	2	1685:G	O3'	1686:C	P	3.04

5 Fit of model and data ⓘ

5.1 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	2	1781/1800 (98%)	0.55	91 (5%)	34 26	40, 99, 172, 210	1 (0%)
1	6	1795/1800 (99%)	0.30	39 (2%)	62 48	33, 86, 159, 201	1 (0%)
2	S0	206/251 (82%)	1.05	22 (10%)	12 12	101, 114, 125, 133	0
2	s0	206/251 (82%)	0.93	19 (9%)	16 14	83, 99, 113, 119	0
3	S1	214/254 (84%)	1.39	38 (17%)	4 4	107, 142, 167, 173	0
3	s1	216/254 (85%)	0.82	16 (7%)	22 18	84, 98, 115, 123	0
4	S2	217/253 (85%)	0.90	19 (8%)	17 16	84, 97, 111, 115	0
4	s2	217/253 (85%)	0.73	17 (7%)	20 18	68, 81, 96, 103	0
5	S3	223/239 (93%)	0.89	13 (5%)	30 24	89, 100, 122, 129	0
5	s3	223/239 (93%)	0.95	25 (11%)	11 11	84, 111, 132, 137	0
6	S4	260/260 (100%)	0.97	28 (10%)	12 11	77, 102, 110, 125	0
6	s4	260/260 (100%)	0.67	13 (5%)	35 27	60, 83, 97, 119	0
7	S5	206/224 (91%)	1.18	27 (13%)	8 8	102, 123, 131, 134	0
7	s5	206/224 (91%)	1.11	31 (15%)	6 6	87, 108, 122, 128	0
8	S6	226/236 (95%)	1.33	46 (20%)	3 3	78, 110, 127, 139	0
8	s6	218/236 (92%)	0.71	15 (6%)	24 19	60, 89, 107, 116	0
9	S7	184/189 (97%)	1.27	34 (18%)	4 4	101, 123, 139, 142	0
9	s7	186/189 (98%)	0.87	20 (10%)	12 11	77, 105, 132, 137	0
10	S8	188/200 (94%)	0.88	16 (8%)	18 16	71, 89, 123, 135	0
10	s8	188/200 (94%)	0.96	26 (13%)	8 7	56, 75, 116, 133	0
11	S9	185/196 (94%)	1.04	20 (10%)	12 11	90, 107, 133, 150	0
11	s9	185/196 (94%)	0.91	11 (5%)	29 23	72, 90, 116, 130	0
12	C0	96/105 (91%)	0.95	11 (11%)	11 10	92, 113, 133, 141	0
13	C1	155/155 (100%)	0.95	20 (12%)	9 8	73, 85, 112, 127	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	c1	146/155 (94%)	0.99	16 (10%) 12 11	59, 72, 97, 121	0
14	C2	124/142 (87%)	1.38	29 (23%) 2 2	138, 146, 152, 159	0
14	c2	124/142 (87%)	1.80	44 (35%) 1 1	169, 184, 194, 196	0
15	C3	150/150 (100%)	0.97	19 (12%) 9 9	81, 94, 113, 116	0
15	c3	150/150 (100%)	0.74	13 (8%) 17 16	67, 80, 97, 102	0
16	C4	127/136 (93%)	1.68	40 (31%) 1 1	84, 139, 155, 159	0
16	c4	128/136 (94%)	0.93	10 (7%) 20 18	66, 102, 112, 119	0
17	C5	124/141 (87%)	0.93	10 (8%) 19 17	88, 100, 112, 119	0
17	c5	135/141 (95%)	0.90	15 (11%) 12 11	78, 105, 114, 118	0
18	C6	141/142 (99%)	1.27	30 (21%) 3 2	92, 112, 117, 120	0
18	c6	142/142 (100%)	1.11	26 (18%) 4 4	80, 101, 116, 125	0
19	C7	120/136 (88%)	0.93	11 (9%) 16 14	99, 108, 126, 129	0
19	c7	117/136 (86%)	0.99	16 (13%) 8 8	87, 102, 115, 118	0
20	C8	145/145 (100%)	0.93	9 (6%) 28 22	86, 110, 131, 137	0
20	c8	145/145 (100%)	0.96	11 (7%) 21 18	88, 100, 118, 127	0
21	C9	143/143 (100%)	1.17	29 (20%) 3 3	95, 110, 121, 126	0
21	c9	143/143 (100%)	0.89	17 (11%) 10 9	84, 96, 112, 121	0
22	D0	107/120 (89%)	1.32	20 (18%) 4 4	85, 112, 128, 130	0
22	d0	110/120 (91%)	1.26	16 (14%) 7 7	84, 114, 139, 156	0
23	D1	87/87 (100%)	0.91	10 (11%) 11 10	100, 106, 118, 127	0
23	d1	87/87 (100%)	0.66	4 (4%) 38 28	80, 88, 108, 116	0
24	D2	129/129 (100%)	0.99	11 (8%) 18 16	82, 94, 103, 112	0
24	d2	129/129 (100%)	0.66	10 (7%) 20 18	65, 75, 82, 89	0
25	D3	144/144 (100%)	0.88	15 (10%) 13 12	71, 77, 86, 97	0
25	d3	144/144 (100%)	0.60	7 (4%) 36 27	58, 63, 74, 82	0
26	D4	134/134 (100%)	1.07	18 (13%) 8 8	88, 111, 122, 128	0
26	d4	134/134 (100%)	0.86	11 (8%) 19 17	68, 92, 105, 108	0
27	D5	70/107 (65%)	1.01	8 (11%) 11 10	119, 131, 137, 138	0
27	d5	69/107 (64%)	1.03	8 (11%) 11 10	97, 115, 125, 126	0
28	D6	97/97 (100%)	1.87	39 (40%) 1 1	88, 104, 150, 154	0
28	d6	97/97 (100%)	0.95	9 (9%) 16 14	71, 86, 115, 119	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
29	D7	81/81 (100%)	1.21	11 (13%) 8 8	98, 110, 134, 137	0
29	d7	81/81 (100%)	1.01	10 (12%) 9 9	80, 94, 124, 130	0
30	D8	63/66 (95%)	1.25	14 (22%) 3 2	110, 125, 137, 139	0
30	d8	63/66 (95%)	1.01	8 (12%) 9 9	103, 116, 125, 130	0
31	D9	53/55 (96%)	0.98	6 (11%) 11 10	86, 90, 106, 111	0
31	d9	53/55 (96%)	0.83	6 (11%) 11 10	81, 92, 128, 141	0
32	E0	60/62 (96%)	0.90	9 (15%) 6 6	77, 108, 128, 130	0
32	e0	62/62 (100%)	1.07	12 (19%) 4 3	66, 91, 110, 113	0
33	E1	71/76 (93%)	1.44	17 (23%) 2 2	105, 134, 149, 153	0
33	e1	76/76 (100%)	1.90	28 (36%) 1 1	112, 161, 175, 179	0
34	SR	318/318 (100%)	1.13	56 (17%) 4 4	108, 119, 131, 147	0
34	sR	318/318 (100%)	1.22	52 (16%) 5 5	110, 127, 139, 150	0
35	SM	159/273 (58%)	1.11	29 (18%) 4 4	62, 98, 144, 148	0
35	sM	104/273 (38%)	1.15	20 (19%) 4 3	56, 109, 181, 186	0
36	1	3149/3396 (92%)	0.15	65 (2%) 63 49	38, 61, 124, 213	0
36	5	3169/3396 (93%)	0.03	59 (1%) 66 52	37, 56, 124, 192	0
37	3	121/121 (100%)	0.02	0 100 100	44, 76, 91, 98	0
37	7	121/121 (100%)	-0.07	1 (0%) 82 72	41, 62, 74, 80	0
38	4	158/158 (100%)	0.08	2 (1%) 74 61	47, 64, 94, 125	0
38	8	158/158 (100%)	0.06	4 (2%) 58 44	46, 66, 95, 118	0
39	L2	252/253 (99%)	0.86	32 (12%) 9 9	46, 64, 80, 86	0
39	l2	252/253 (99%)	0.58	24 (9%) 15 14	45, 61, 75, 85	0
40	L3	386/386 (100%)	0.40	13 (3%) 48 36	44, 64, 77, 87	0
40	l3	386/386 (100%)	0.16	7 (1%) 67 53	37, 51, 64, 79	0
41	L4	361/361 (100%)	0.56	35 (9%) 15 14	42, 57, 70, 74	0
41	l4	361/361 (100%)	0.46	19 (5%) 33 25	45, 60, 74, 82	0
42	L5	296/296 (100%)	0.57	10 (3%) 48 36	60, 83, 99, 107	0
42	l5	294/296 (99%)	0.36	14 (4%) 36 27	50, 64, 89, 105	0
43	L6	156/175 (89%)	0.31	6 (3%) 44 33	52, 59, 72, 82	0
43	l6	157/175 (89%)	0.31	9 (5%) 30 24	53, 60, 78, 87	0
44	L7	222/243 (91%)	0.20	7 (3%) 50 37	42, 52, 78, 100	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	l7	223/243 (91%)	0.11	4 (1%) 67 53	42, 51, 80, 105	0
45	L8	233/255 (91%)	0.99	23 (9%) 14 13	70, 86, 109, 117	0
45	l8	231/255 (90%)	0.79	16 (6%) 24 19	73, 86, 106, 114	0
46	L9	191/191 (100%)	0.55	9 (4%) 37 28	62, 72, 83, 92	0
46	l9	191/191 (100%)	0.21	5 (2%) 57 43	47, 57, 72, 82	0
47	M0	211/220 (95%)	0.37	11 (5%) 34 26	47, 61, 88, 110	0
47	m0	213/220 (96%)	0.66	13 (6%) 28 23	45, 64, 88, 97	0
48	M1	169/173 (97%)	0.61	8 (4%) 37 28	70, 88, 99, 102	0
48	m1	169/173 (97%)	0.34	8 (4%) 37 28	54, 71, 79, 83	0
49	M3	193/198 (97%)	0.47	12 (6%) 28 22	43, 68, 93, 114	0
49	m3	194/198 (97%)	0.63	16 (8%) 19 17	44, 71, 100, 112	0
50	M4	136/137 (99%)	0.33	5 (3%) 45 34	56, 62, 74, 86	0
50	m4	137/137 (100%)	0.13	3 (2%) 62 48	51, 57, 70, 81	0
51	M5	203/203 (100%)	0.65	15 (7%) 22 18	45, 59, 70, 72	0
51	m5	203/203 (100%)	0.55	10 (4%) 36 27	46, 63, 73, 78	0
52	M6	197/198 (99%)	0.19	6 (3%) 52 39	44, 51, 67, 69	0
52	m6	197/198 (99%)	0.23	10 (5%) 34 26	37, 45, 64, 67	0
53	M7	183/183 (100%)	0.58	19 (10%) 13 12	49, 56, 93, 112	0
53	m7	155/183 (84%)	0.18	3 (1%) 66 52	42, 50, 63, 82	0
54	M8	185/185 (100%)	0.40	7 (3%) 44 33	45, 58, 71, 86	0
54	m8	185/185 (100%)	0.30	4 (2%) 62 48	44, 60, 70, 74	0
55	M9	188/188 (100%)	0.65	10 (5%) 33 25	67, 80, 140, 146	0
55	m9	188/188 (100%)	0.47	8 (4%) 40 30	53, 67, 127, 138	0
56	N0	172/172 (100%)	0.28	6 (3%) 47 35	51, 59, 70, 76	0
56	n0	172/172 (100%)	0.02	2 (1%) 76 63	45, 52, 62, 68	0
57	N1	159/159 (100%)	0.31	1 (0%) 85 77	46, 58, 95, 103	0
57	n1	159/159 (100%)	0.24	7 (4%) 39 30	43, 52, 86, 91	0
58	N2	100/120 (83%)	0.93	8 (8%) 20 17	95, 107, 121, 123	0
58	n2	98/120 (81%)	0.67	5 (5%) 34 26	78, 90, 97, 100	0
59	N3	136/136 (100%)	0.48	5 (3%) 45 34	54, 62, 72, 79	0
59	n3	136/136 (100%)	-0.01	2 (1%) 71 58	38, 47, 57, 59	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
60	N4	98/155 (63%)	1.05	17 (17%) 5 4	63, 75, 134, 138	0
60	n4	135/155 (87%)	0.84	21 (15%) 6 6	47, 94, 119, 124	0
61	N5	121/141 (85%)	0.60	7 (5%) 30 24	62, 73, 86, 99	0
61	n5	120/141 (85%)	0.55	9 (7%) 22 18	58, 72, 86, 98	0
62	N6	126/126 (100%)	0.50	5 (3%) 43 32	53, 66, 76, 81	0
62	n6	126/126 (100%)	0.57	4 (3%) 50 37	55, 68, 79, 85	0
63	N7	135/135 (100%)	0.83	9 (6%) 25 20	87, 98, 107, 111	0
63	n7	135/135 (100%)	0.68	6 (4%) 39 30	80, 92, 102, 106	0
64	N8	148/148 (100%)	0.20	1 (0%) 84 75	38, 60, 79, 86	0
64	n8	148/148 (100%)	0.22	3 (2%) 64 51	38, 61, 75, 78	0
65	N9	58/58 (100%)	0.41	2 (3%) 48 36	41, 62, 89, 95	0
65	n9	58/58 (100%)	0.58	4 (6%) 24 19	41, 60, 82, 89	0
66	O0	97/104 (93%)	0.62	6 (6%) 28 22	85, 93, 107, 109	0
66	o0	100/104 (96%)	0.45	3 (3%) 52 39	74, 83, 101, 111	0
67	O1	109/112 (97%)	0.60	3 (2%) 55 41	62, 73, 92, 98	0
67	o1	109/112 (97%)	0.18	2 (1%) 67 53	49, 60, 84, 98	0
68	O2	127/129 (98%)	0.31	5 (3%) 44 33	39, 53, 65, 71	0
68	o2	127/129 (98%)	0.55	8 (6%) 27 22	38, 56, 69, 72	0
69	O3	106/106 (100%)	0.17	1 (0%) 81 70	44, 49, 70, 78	0
69	o3	106/106 (100%)	0.09	0 100 100	42, 49, 70, 78	0
70	O4	112/119 (94%)	1.19	18 (16%) 5 5	61, 78, 107, 113	0
70	o4	112/119 (94%)	0.93	14 (12%) 9 9	54, 72, 102, 107	0
71	O5	119/119 (100%)	0.80	10 (8%) 18 16	58, 74, 82, 87	0
71	o5	119/119 (100%)	0.63	4 (3%) 48 36	62, 75, 89, 98	0
72	O6	99/99 (100%)	0.63	4 (4%) 43 32	64, 72, 94, 105	0
72	o6	99/99 (100%)	0.45	3 (3%) 52 39	66, 75, 87, 101	0
73	O7	87/87 (100%)	0.84	11 (12%) 9 9	46, 53, 71, 76	0
73	o7	87/87 (100%)	0.50	5 (5%) 30 24	43, 52, 76, 93	0
74	O8	77/77 (100%)	0.80	8 (10%) 13 12	86, 97, 109, 114	0
74	o8	77/77 (100%)	0.62	4 (5%) 34 26	80, 91, 101, 103	0
75	O9	50/50 (100%)	0.73	6 (12%) 10 9	55, 60, 64, 65	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
75	o9	50/50 (100%)	0.38	2 (4%) 43 32	52, 58, 66, 67	0
76	Q0	52/52 (100%)	0.26	0 100 100	52, 60, 76, 79	0
76	q0	52/52 (100%)	-0.01	1 (1%) 66 52	42, 47, 56, 59	0
77	Q1	25/25 (100%)	0.78	3 (12%) 10 9	62, 66, 73, 73	0
77	q1	25/25 (100%)	0.26	1 (4%) 43 32	53, 58, 59, 59	0
78	Q2	105/105 (100%)	0.12	1 (0%) 79 68	46, 58, 78, 103	0
78	q2	105/105 (100%)	0.16	1 (0%) 79 68	45, 56, 71, 94	0
79	Q3	91/91 (100%)	0.74	8 (8%) 17 16	56, 68, 82, 90	0
79	q3	91/91 (100%)	0.56	5 (5%) 32 25	47, 60, 76, 85	0
80	c0	96/105 (91%)	1.45	21 (21%) 3 2	104, 135, 149, 151	0
81	m2	0/150	-	-	-	-
82	p0	143/311 (45%)	1.23	27 (18%) 4 4	102, 125, 192, 199	0
83	p1	0/47	-	-	-	-
84	p2	0/46	-	-	-	-
85	f	148/157 (94%)	2.74	102 (68%) 0 0	35, 77, 128, 129	148 (100%)
All	All	33261/35493 (93%)	0.57	2369 (7%) 23 19	33, 76, 133, 213	150 (0%)

All (2369) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
22	d0	64	LYS	11.7
85	f	30	GLY	9.5
73	O7	88	ALA	9.3
53	M7	161	ALA	9.2
36	5	2873	U	9.1
3	S1	92	GLN	8.7
36	5	2871	G	8.4
8	S6	77	LEU	8.4
13	c1	3	THR	8.3
39	L2	201	GLY	8.1
53	M7	160	ALA	7.8
36	1	2402	A	7.7
60	N4	88	ASP	7.6
7	S5	152	GLY	7.5
21	c9	55	TYR	7.4
85	f	120	LEU	7.4
71	O5	120	ALA	7.4
8	S6	75	LEU	7.3

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Mol	Chain	Res	Type	RSRZ
36	5	2403	G	7.1
80	c0	23	ALA	7.1
1	2	1756[A]	A	7.0
3	S1	46	THR	7.0
36	1	2871	G	7.0
7	s5	37	GLN	6.9
45	l8	109	LEU	6.9
54	M8	167	SER	6.7
85	f	71	GLU	6.7
85	f	46	THR	6.7
1	2	1699	G	6.7
73	O7	2	GLY	6.6
45	L8	116	VAL	6.4
70	o4	39	ALA	6.4
60	N4	86	SER	6.3
33	e1	85	TYR	6.3
36	1	2874	G	6.3
7	S5	41	LYS	6.2
56	N0	1	MET	6.2
41	L4	69	ARG	6.2
53	M7	162	GLU	6.2
8	S6	148	SER	6.1
36	5	2402	A	6.1
8	S6	73	ILE	6.0
8	S6	74	LYS	6.0
9	S7	150	GLN	6.0
34	sR	213	SER	5.9
80	c0	22	VAL	5.8
2	s0	46	HIS	5.8
15	c3	16	ILE	5.8
7	S5	96	SER	5.7
53	M7	130	TYR	5.7
7	S5	71	ALA	5.7
9	S7	105	THR	5.7
3	s1	54	LEU	5.7
4	S2	62	PRO	5.7
7	S5	36	ALA	5.6
60	n4	95	SER	5.6
85	f	49	THR	5.6
41	l4	67	THR	5.6
4	s2	87	GLN	5.6
1	2	1708	U	5.6

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Mol	Chain	Res	Type	RSRZ
3	S1	32	ILE	5.5
5	s3	151	LYS	5.5
85	f	18	THR	5.5
16	C4	75	GLY	5.4
13	c1	2	SER	5.4
11	S9	29	LYS	5.4
33	e1	77	ALA	5.4
34	SR	284	ALA	5.3
41	l4	69	ARG	5.3
68	O2	51	SER	5.3
41	L4	67	THR	5.3
53	M7	181	ARG	5.3
16	C4	16	VAL	5.3
35	SM	85	SER	5.3
28	D6	2	PRO	5.2
75	O9	2	ALA	5.2
28	D6	92	ARG	5.2
60	N4	89	LEU	5.2
41	L4	80	GLY	5.2
85	f	42	VAL	5.2
73	o7	88	ALA	5.1
28	D6	31	PRO	5.1
49	m3	191	ALA	5.1
7	S5	151	GLY	5.1
7	S5	37	GLN	5.1
34	sR	303	ALA	5.1
26	d4	99	LYS	5.1
9	S7	109	VAL	5.1
4	s2	88	LYS	5.0
60	n4	87	LEU	5.0
41	L4	50	TYR	5.0
1	2	1695	G	5.0
34	SR	32	LEU	5.0
53	M7	184	ALA	5.0
33	e1	87	THR	5.0
70	O4	6	THR	5.0
1	2	1410	A	4.9
21	c9	18	TYR	4.9
85	f	124	LEU	4.9
39	L2	216	HIS	4.9
36	1	2401	A	4.9
45	l8	104	GLU	4.9

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Mol	Chain	Res	Type	RSRZ
41	l4	62	ALA	4.9
41	L4	63	GLU	4.9
80	c0	25	LYS	4.9
53	M7	182	ILE	4.9
41	L4	68	GLY	4.9
85	f	149	SER	4.9
4	s2	93	GLY	4.9
16	C4	15	GLY	4.9
29	d7	24	LEU	4.8
13	c1	4	GLU	4.8
80	c0	84	GLU	4.8
85	f	64	ILE	4.8
13	C1	146	ALA	4.8
3	S1	151	LYS	4.8
37	7	73	C	4.8
16	C4	133	ARG	4.8
1	2	1696	G	4.8
63	N7	26	VAL	4.8
1	2	718	U	4.8
17	c5	4	ALA	4.8
18	C6	70	THR	4.8
1	2	1694	A	4.7
36	1	2873	U	4.7
60	N4	83	THR	4.7
58	N2	89	LEU	4.7
36	1	1349	G	4.7
35	sM	119	ALA	4.7
9	S7	98	ILE	4.7
33	E1	103	LEU	4.7
18	C6	10	PHE	4.7
16	C4	39	ILE	4.7
36	1	2404	A	4.7
82	p0	93	LEU	4.7
85	f	11	ALA	4.7
8	s6	162	VAL	4.6
14	c2	105	LYS	4.6
9	S7	142	TYR	4.6
16	C4	28	VAL	4.6
40	l3	245	GLY	4.6
1	2	1707	A	4.6
28	D6	8	ASN	4.6
62	n6	126	LEU	4.6

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Mol	Chain	Res	Type	RSRZ
16	C4	74	VAL	4.6
9	s7	184	GLU	4.6
34	sR	21	THR	4.6
36	5	3276	G	4.6
3	S1	42	ASN	4.5
41	l4	79	GLY	4.5
7	s5	68	ILE	4.5
85	f	86	LYS	4.5
2	s0	162	CYS	4.5
4	s2	89	GLN	4.5
63	n7	68	ILE	4.5
28	D6	3	LYS	4.5
33	e1	81	LYS	4.5
85	f	142	MET	4.5
3	S1	53	GLY	4.5
71	o5	118	ILE	4.5
3	s1	153	HIS	4.5
4	S2	232	GLU	4.5
36	1	2403	G	4.5
60	N4	84	GLY	4.5
85	f	22	GLN	4.5
20	C8	146	ALA	4.5
3	s1	89	ASP	4.5
33	e1	88	PRO	4.5
36	5	2874	G	4.5
18	c6	2	SER	4.5
14	c2	59	LEU	4.4
85	f	85	VAL	4.4
55	M9	52	LYS	4.4
35	SM	19	VAL	4.4
51	M5	198	SER	4.4
85	f	84	VAL	4.4
25	d3	11	SER	4.4
34	SR	33	LEU	4.4
34	sR	301	LEU	4.4
47	M0	218	ALA	4.4
14	c2	75	VAL	4.4
25	D3	7	ARG	4.4
85	f	45	SER	4.4
39	L2	99	GLY	4.4
1	2	1709	C	4.4
8	S6	67	VAL	4.3

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Mol	Chain	Res	Type	RSRZ
48	m1	173	ASP	4.3
9	S7	146	GLY	4.3
17	c5	134	THR	4.3
26	D4	125	LEU	4.3
6	S4	66	MET	4.3
60	n4	68	ALA	4.3
85	f	35	LYS	4.3
8	S6	153	VAL	4.3
16	C4	13	VAL	4.3
33	E1	147	VAL	4.3
33	e1	84	VAL	4.3
33	e1	78	LYS	4.3
7	s5	82	PHE	4.3
62	N6	124	GLY	4.3
85	f	20	PRO	4.3
3	S1	91	VAL	4.3
22	D0	82	TYR	4.3
85	f	31	PHE	4.3
36	5	2404	A	4.3
18	c6	124	PRO	4.3
85	f	38	PRO	4.3
7	s5	36	ALA	4.3
9	S7	108	GLN	4.3
4	s2	105	GLY	4.3
20	c8	18	LEU	4.3
23	d1	87	ARG	4.2
36	1	2872	A	4.2
70	O4	2	ALA	4.2
14	c2	107	ASP	4.2
20	C8	76	PRO	4.2
34	SR	25	THR	4.2
48	M1	104	PHE	4.2
36	1	2954	U	4.2
2	S0	207	PRO	4.2
60	N4	90	ILE	4.2
21	C9	114	VAL	4.2
1	2	1702	A	4.2
34	sR	67	ILE	4.2
22	D0	81	THR	4.2
34	SR	161	LYS	4.2
36	5	2442	G	4.1
34	SR	44	SER	4.1

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Mol	Chain	Res	Type	RSRZ
41	L4	79	GLY	4.1
9	S7	4	PRO	4.1
57	n1	79	MET	4.1
45	L8	191	ASN	4.1
4	S2	69	ILE	4.1
33	e1	80	ARG	4.1
85	f	87	ARG	4.1
41	L4	65	TRP	4.1
33	e1	86	THR	4.1
7	S5	75	GLY	4.1
51	m5	15	GLN	4.1
1	2	1370	U	4.1
8	S6	96	SER	4.1
11	S9	5	PRO	4.1
1	2	1697	G	4.1
4	s2	90	THR	4.1
8	S6	79	LYS	4.1
33	E1	87	THR	4.1
41	L4	66	GLY	4.1
60	n4	88	ASP	4.1
39	L2	253	GLN	4.1
43	L6	130	ILE	4.1
85	f	54	HIS	4.1
6	S4	65	LEU	4.1
7	s5	42	LEU	4.1
85	f	119	GLU	4.0
32	E0	60	PRO	4.0
1	2	1698	G	4.0
10	s8	200	LYS	4.0
79	Q3	92	ALA	4.0
85	f	81	GLU	4.0
11	S9	97	LEU	4.0
20	c8	3	LEU	4.0
9	S7	123	ASP	4.0
13	c1	115	PHE	4.0
7	S5	70	VAL	4.0
18	C6	68	ARG	4.0
41	l4	71	VAL	4.0
41	l4	73	ARG	4.0
85	f	115	ALA	4.0
6	S4	54	TYR	4.0
73	O7	12	HIS	4.0

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Mol	Chain	Res	Type	RSRZ
82	p0	197	PHE	4.0
40	L3	277	SER	4.0
34	sR	136	ILE	4.0
34	sR	296	ALA	4.0
39	L2	15	ILE	4.0
47	M0	219	ALA	4.0
34	sR	158	PRO	4.0
51	M5	192	LYS	3.9
85	f	132	LYS	3.9
1	2	1794	A	3.9
18	C6	119	ALA	3.9
34	sR	72	THR	3.9
49	M3	26	PHE	3.9
3	S1	55	LYS	3.9
59	N3	32	ARG	3.9
34	SR	6	VAL	3.9
49	M3	33	VAL	3.9
70	O4	23	VAL	3.9
68	o2	37	GLY	3.9
53	M7	168	LEU	3.9
22	d0	83	GLU	3.9
25	d3	21	ASN	3.9
22	d0	67	THR	3.9
14	c2	122	VAL	3.9
3	s1	117	TRP	3.9
12	C0	39	ASN	3.9
17	c5	6	ASN	3.9
79	Q3	24	ARG	3.9
13	c1	117	VAL	3.9
36	1	2397	A	3.9
1	2	716	C	3.9
1	6	659	C	3.9
85	f	126	THR	3.9
19	c7	57	LEU	3.9
10	S8	152	ILE	3.9
18	c6	3	ALA	3.9
41	L4	54	GLU	3.8
8	S6	78	THR	3.8
34	SR	20	VAL	3.8
41	L4	82	THR	3.8
51	M5	196	THR	3.8
22	D0	54	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
36	1	1570	U	3.8
18	c6	90	VAL	3.8
8	S6	71	THR	3.8
47	M0	112	GLN	3.8
85	f	121	GLY	3.8
1	6	1799	U	3.8
4	s2	85	PRO	3.8
10	s8	61	GLU	3.8
33	e1	79	LYS	3.8
18	C6	20	ALA	3.8
85	f	127	ALA	3.8
7	s5	30	PRO	3.8
28	D6	20	PRO	3.8
36	1	1103	A	3.8
17	C5	104	GLN	3.8
14	c2	31	VAL	3.8
63	n7	96	VAL	3.8
10	s8	58	LEU	3.8
22	D0	87	HIS	3.8
85	f	78	HIS	3.8
8	S6	182	GLN	3.7
45	l8	192	GLN	3.7
14	c2	103	LEU	3.7
19	c7	60	ARG	3.7
82	p0	192	ASP	3.7
8	S6	66	GLY	3.7
85	f	17	ALA	3.7
19	C7	62	GLN	3.7
3	s1	150	VAL	3.7
28	D6	44	ILE	3.7
53	M7	135	ARG	3.7
55	M9	72	GLU	3.7
85	f	39	CYS	3.7
85	f	150	PHE	3.7
14	c2	61	VAL	3.7
25	D3	9	LEU	3.7
28	D6	53	LEU	3.7
36	1	2978	U	3.7
53	M7	176	ILE	3.7
1	6	1695	G	3.7
13	c1	29	LYS	3.7
31	D9	56	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
8	S6	80	ASN	3.7
39	l2	194	ASN	3.7
56	N0	129	ILE	3.7
2	S0	99	ALA	3.7
15	C3	123	HIS	3.7
34	SR	79	TYR	3.7
9	s7	153	LEU	3.7
36	5	2401	A	3.7
34	sR	170	ILE	3.7
72	o6	58	ILE	3.7
64	n8	120	ASN	3.7
10	s8	40	ALA	3.6
70	O4	39	ALA	3.6
45	L8	202	GLU	3.6
1	2	1338	C	3.6
4	s2	84	LYS	3.6
70	O4	21	LYS	3.6
16	C4	137	LEU	3.6
60	N4	87	LEU	3.6
40	l3	244	ARG	3.6
2	S0	72	ASP	3.6
15	C3	14	SER	3.6
41	L4	81	GLY	3.6
3	S1	110	LEU	3.6
28	D6	18	VAL	3.6
1	2	1705	C	3.6
41	L4	72	ALA	3.6
3	S1	95	ASN	3.6
16	C4	18	ARG	3.6
42	l5	290	ILE	3.6
51	M5	95	GLN	3.6
51	M5	200	TRP	3.6
10	s8	179	CYS	3.6
14	c2	92	ALA	3.6
23	D1	68	SER	3.6
11	s9	149	ARG	3.6
30	D8	16	LEU	3.6
54	M8	166	LEU	3.6
58	N2	95	PHE	3.6
78	Q2	106	PHE	3.6
82	p0	70	LEU	3.6
14	C2	136	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
14	c2	71	ILE	3.6
33	E1	91	ILE	3.6
1	2	1710	U	3.6
49	m3	153	ASP	3.6
1	6	1082	C	3.6
14	c2	123	VAL	3.6
85	f	60	VAL	3.6
7	s5	44	ASN	3.6
35	sM	82	THR	3.6
36	5	2443	A	3.5
28	D6	6	ALA	3.5
32	e0	2	ALA	3.5
41	L4	73	ARG	3.5
1	2	715	U	3.5
36	1	1569	U	3.5
14	C2	83	GLU	3.5
1	2	1339	C	3.5
5	S3	176	LEU	3.5
85	f	153	ALA	3.5
73	o7	23	GLY	3.5
2	S0	158	VAL	3.5
2	s0	190	ASP	3.5
4	S2	63	VAL	3.5
46	L9	43	VAL	3.5
2	s0	173	ILE	3.5
60	N4	82	ILE	3.5
46	L9	31	ARG	3.5
8	s6	147	LEU	3.5
15	C3	53	LEU	3.5
55	M9	189	ALA	3.5
7	s5	33	VAL	3.5
34	SR	65	SER	3.5
38	8	81	U	3.5
80	c0	81	ASN	3.5
70	O4	5	VAL	3.5
75	o9	11	GLN	3.5
27	d5	50	ILE	3.5
15	C3	15	ALA	3.5
58	N2	27	VAL	3.5
72	O6	14	GLY	3.5
85	f	67	GLY	3.5
2	S0	98	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
10	s8	42	ARG	3.5
85	f	63	ASP	3.5
33	e1	117	LEU	3.4
49	M3	34	SER	3.4
39	L2	175	VAL	3.4
18	C6	118	ILE	3.4
39	L2	219	ILE	3.4
51	M5	197	LEU	3.4
85	f	134	LEU	3.4
9	s7	43	PHE	3.4
18	C6	15	SER	3.4
39	L2	195	SER	3.4
1	2	1686	C	3.4
4	s2	96	THR	3.4
70	O4	22	VAL	3.4
25	D3	2	GLY	3.4
28	D6	4	LYS	3.4
35	SM	166	LYS	3.4
20	c8	74	GLN	3.4
21	C9	36	ILE	3.4
36	1	2139	A	3.4
18	c6	44	LEU	3.4
48	M1	127	PHE	3.4
35	sM	85	SER	3.4
10	S8	179	CYS	3.4
36	5	2444	C	3.4
21	C9	67	MET	3.4
42	l5	287	ALA	3.4
73	o7	86	ALA	3.4
2	s0	189	VAL	3.4
14	c2	63	VAL	3.4
1	6	720	G	3.4
26	d4	18	LEU	3.4
22	D0	71	PRO	3.4
28	D6	58	VAL	3.4
29	d7	46	VAL	3.4
28	D6	89	ARG	3.4
8	S6	180	THR	3.4
82	p0	281	THR	3.4
41	L4	61	SER	3.4
85	f	73	LEU	3.3
85	f	65	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
15	c3	83	GLU	3.3
85	f	27	ARG	3.3
6	S4	74	GLY	3.3
66	o0	23	TYR	3.3
3	S1	140	ILE	3.3
7	s5	187	ILE	3.3
34	SR	99	THR	3.3
36	5	3275	U	3.3
3	S1	54	LEU	3.3
18	C6	117	LEU	3.3
41	L4	106	TRP	3.3
85	f	70	LEU	3.3
34	SR	62	LYS	3.3
14	c2	37	VAL	3.3
17	c5	74	ALA	3.3
34	sR	24	ALA	3.3
34	sR	104	VAL	3.3
71	o5	70	TYR	3.3
34	sR	32	LEU	3.3
66	o0	104	LEU	3.3
1	6	1491	U	3.3
25	D3	21	ASN	3.3
41	L4	114	ASN	3.3
3	S1	114	VAL	3.3
51	m5	111	ALA	3.3
36	5	2872	A	3.3
36	5	2971	A	3.3
36	5	3167	A	3.3
34	sR	115	ILE	3.3
42	L5	148	ILE	3.3
52	m6	69	GLY	3.3
9	S7	153	LEU	3.3
23	D1	69	LEU	3.3
2	s0	2	SER	3.3
14	C2	115	VAL	3.3
36	1	2205	U	3.3
24	d2	61	ILE	3.3
36	1	2808	A	3.3
48	M1	167	TYR	3.3
35	sM	167	THR	3.3
85	f	43	ASP	3.3
13	c1	139	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
26	D4	5	VAL	3.3
82	p0	187	VAL	3.3
9	S7	103	SER	3.3
51	M5	195	ASN	3.3
51	m5	76	PRO	3.3
27	d5	89	ILE	3.3
41	L4	74	ILE	3.3
22	d0	54	GLY	3.3
1	2	913	G	3.3
33	e1	96	LYS	3.2
65	n9	23	LYS	3.2
1	6	1756[A]	A	3.2
28	D6	5	ARG	3.2
22	D0	62	VAL	3.2
27	D5	36	ALA	3.2
68	o2	52	GLN	3.2
31	D9	9	SER	3.2
71	O5	118	ILE	3.2
8	S6	149	LYS	3.2
11	S9	28	LEU	3.2
35	SM	9	GLY	3.2
33	e1	150	VAL	3.2
73	O7	5	THR	3.2
39	L2	176	ASP	3.2
14	c2	133	LEU	3.2
45	L8	93	LEU	3.2
50	m4	8	LYS	3.2
80	c0	2	LEU	3.2
25	d3	18	HIS	3.2
80	c0	65	TYR	3.2
11	s9	148	VAL	3.2
41	L4	105	THR	3.2
41	L4	55	LYS	3.2
85	f	148	ILE	3.2
13	c1	5	LEU	3.2
36	5	443	G	3.2
2	s0	151	SER	3.2
28	D6	76	SER	3.2
2	S0	29	VAL	3.2
47	M0	148	VAL	3.2
28	D6	49	ALA	3.2
34	sR	25	THR	3.2

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Mol	Chain	Res	Type	RSRZ
46	L9	188	THR	3.2
74	O8	6	THR	3.2
27	D5	41	ILE	3.2
29	D7	7	LEU	3.2
26	D4	120	GLY	3.2
8	s6	88	ARG	3.2
30	d8	65	ARG	3.2
1	2	1365	C	3.2
1	2	1706	C	3.2
85	f	33	VAL	3.2
3	S1	50	LYS	3.2
34	SR	61	PHE	3.2
35	sM	35	ALA	3.2
60	N4	85	ALA	3.2
3	S1	98	THR	3.2
22	D0	86	ILE	3.2
33	E1	86	THR	3.2
34	sR	265	LEU	3.2
53	M7	136	ILE	3.2
60	N4	75	THR	3.2
13	C1	152	GLN	3.1
39	l2	72	ARG	3.1
54	M8	151	ARG	3.1
49	M3	140	SER	3.1
13	c1	142	VAL	3.1
4	S2	88	LYS	3.1
28	d6	93	LYS	3.1
15	c3	144	ALA	3.1
34	SR	78	ALA	3.1
65	N9	2	ALA	3.1
47	m0	166	ILE	3.1
85	f	138	ILE	3.1
15	C3	137	PRO	3.1
40	l3	240	ARG	3.1
10	S8	44	HIS	3.1
26	d4	135	ASP	3.1
13	c1	32	LYS	3.1
14	C2	141	SER	3.1
41	l4	89	ALA	3.1
14	C2	97	LEU	3.1
26	D4	18	LEU	3.1
8	S6	163	THR	3.1

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Mol	Chain	Res	Type	RSRZ
70	O4	64	THR	3.1
49	M3	130	GLY	3.1
85	f	98	GLY	3.1
9	s7	11	GLN	3.1
79	q3	7	LYS	3.1
17	c5	11	VAL	3.1
80	c0	21	VAL	3.1
82	p0	69	ASP	3.1
85	f	94	ASP	3.1
39	l2	16	PHE	3.1
3	s1	155	TYR	3.1
32	e0	49	LEU	3.1
33	e1	152	ALA	3.1
45	L8	114	ALA	3.1
82	p0	283	ALA	3.1
4	s2	82	ASN	3.1
15	C3	151	ASN	3.1
28	d6	11	ASN	3.1
19	c7	65	PRO	3.1
26	D4	6	THR	3.1
35	SM	97	THR	3.1
17	c5	8	LYS	3.1
26	D4	117	LYS	3.1
1	2	1337	A	3.1
45	L8	209	ALA	3.1
8	S6	226	ILE	3.1
15	c3	66	ILE	3.1
36	1	3275	U	3.1
8	s6	146	GLY	3.1
34	SR	72	THR	3.1
79	q3	3	LYS	3.1
41	L4	87	GLN	3.1
6	S4	23	LEU	3.1
7	s5	174	LEU	3.1
85	f	128	PHE	3.1
16	C4	40	ALA	3.1
28	D6	47	ALA	3.1
39	L2	241	ARG	3.1
51	m5	67	ARG	3.1
85	f	147	ALA	3.1
9	S7	91	ILE	3.1
36	5	2397	A	3.0

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Mol	Chain	Res	Type	RSRZ
51	M5	191	TRP	3.0
85	f	16	SER	3.0
5	s3	185	LYS	3.0
14	c2	102	GLY	3.0
16	c4	92	LYS	3.0
18	C6	12	LYS	3.0
55	m9	83	GLY	3.0
39	L2	252	THR	3.0
3	S1	20	VAL	3.0
34	SR	7	LEU	3.0
74	O8	43	PHE	3.0
85	f	37	ARG	3.0
2	s0	170	ILE	3.0
23	D1	34	ILE	3.0
49	m3	88	ALA	3.0
34	sR	250	TYR	3.0
7	S5	91	GLU	3.0
10	s8	30	GLY	3.0
28	D6	9	GLY	3.0
33	E1	104	SER	3.0
14	c2	111	ASN	3.0
51	m5	90	ASN	3.0
1	2	713	A	3.0
18	C6	9	THR	3.0
14	C2	61	VAL	3.0
61	n5	114	VAL	3.0
5	S3	21	LEU	3.0
14	c2	32	LEU	3.0
15	C3	124	ARG	3.0
30	D8	66	LEU	3.0
70	o4	33	GLN	3.0
31	D9	55	PHE	3.0
4	s2	92	ALA	3.0
10	s8	198	ALA	3.0
36	5	3277	U	3.0
39	l2	15	ILE	3.0
59	N3	25	CYS	3.0
82	p0	107	ALA	3.0
6	S4	143	ASP	3.0
10	s8	176	SER	3.0
28	d6	58	VAL	3.0
41	L4	52	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
4	S2	240	LEU	3.0
34	sR	314	GLN	3.0
36	1	1581	C	3.0
15	C3	57	ALA	3.0
34	SR	43	ILE	3.0
58	n2	46	ALA	3.0
60	n4	122	ALA	3.0
16	C4	71	CYS	3.0
1	2	1380	U	3.0
13	C1	56	LYS	3.0
7	s5	39	GLU	3.0
15	C3	119	GLU	3.0
8	S6	99	GLY	3.0
85	f	116	PRO	3.0
11	S9	96	VAL	3.0
21	C9	6	VAL	3.0
2	s0	146	LEU	3.0
72	O6	27	SER	3.0
85	f	92	LEU	3.0
19	c7	104	ASN	3.0
4	S2	242	ILE	3.0
7	S5	130	ILE	3.0
43	l6	130	ILE	3.0
56	N0	2	ALA	3.0
34	SR	216	LYS	3.0
36	1	1866	C	3.0
36	5	3166	C	3.0
15	c3	40	TYR	3.0
39	L2	189	TYR	3.0
1	6	794	U	3.0
5	S3	210	GLU	3.0
8	s6	161	GLU	3.0
17	C5	71	GLU	3.0
32	E0	6	GLY	3.0
36	5	2979	U	3.0
36	5	2980	U	3.0
47	m0	204	GLY	3.0
8	S6	97	VAL	3.0
8	s6	160	ARG	3.0
9	S7	144	VAL	3.0
18	c6	68	ARG	3.0
35	SM	170	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
42	L5	277	LEU	3.0
14	C2	26	ASP	3.0
35	SM	11	ASP	3.0
16	C4	26	THR	3.0
29	d7	47	PHE	3.0
59	N3	2	SER	3.0
6	S4	110	ALA	3.0
7	s5	29	ILE	3.0
19	c7	97	ASN	3.0
52	M6	42	ASN	3.0
63	N7	2	ALA	3.0
66	O0	95	ALA	3.0
80	c0	28	ASN	3.0
85	f	62	ILE	3.0
26	d4	128	LYS	2.9
41	L4	46	LYS	2.9
67	O1	27	LYS	2.9
32	E0	54	ARG	2.9
79	Q3	36	ARG	2.9
82	p0	47	GLY	2.9
7	S5	24	VAL	2.9
46	L9	191	LEU	2.9
63	N7	90	GLU	2.9
1	2	719	U	2.9
9	s7	70	PHE	2.9
13	C1	156	PHE	2.9
50	M4	115	PHE	2.9
8	s6	170	THR	2.9
85	f	34	ILE	2.9
60	n4	72	SER	2.9
9	S7	104	ARG	2.9
41	l4	93	MET	2.9
70	o4	58	ARG	2.9
8	s6	169	TYR	2.9
13	C1	147	GLY	2.9
2	S0	126	PRO	2.9
12	C0	42	VAL	2.9
16	C4	120	PRO	2.9
55	M9	51	VAL	2.9
9	s7	127	GLU	2.9
41	l4	94	CYS	2.9
45	L8	107	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
50	M4	116	GLU	2.9
52	M6	40	GLU	2.9
16	C4	82	LYS	2.9
18	c6	46	PHE	2.9
58	N2	28	PHE	2.9
6	s4	165	ALA	2.9
34	SR	36	ALA	2.9
1	6	864	U	2.9
14	c2	39	ASP	2.9
35	SM	95	SER	2.9
36	1	2953	U	2.9
10	s8	59	ARG	2.9
18	C6	21	HIS	2.9
8	S6	63	MET	2.9
19	c7	118	PRO	2.9
27	d5	59	TYR	2.9
28	d6	65	PRO	2.9
30	D8	41	VAL	2.9
60	N4	76	VAL	2.9
61	n5	24	LEU	2.9
67	o1	4	LEU	2.9
70	o4	38	LEU	2.9
39	L2	198	LYS	2.9
50	m4	92	GLU	2.9
9	s7	8	ILE	2.9
29	d7	32	PHE	2.9
34	sR	122	ILE	2.9
21	C9	83	ALA	2.9
42	l5	267	ALA	2.9
45	L8	131	ALA	2.9
34	SR	96	THR	2.9
17	c5	137	ARG	2.9
1	2	717	C	2.9
14	C2	103	LEU	2.9
34	sR	33	LEU	2.9
55	M9	184	LEU	2.9
6	S4	139	VAL	2.9
18	C6	22	VAL	2.9
70	O4	35	VAL	2.9
12	C0	4	PRO	2.9
29	D7	38	PRO	2.9
14	c2	126	TRP	2.9

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Mol	Chain	Res	Type	RSRZ
31	d9	7	TRP	2.9
39	l2	251	LYS	2.9
8	S6	175	ILE	2.9
63	N7	124	ALA	2.9
10	S8	8	ARG	2.9
15	c3	56	ASP	2.9
62	n6	7	ASP	2.9
33	E1	100	LEU	2.9
6	S4	167	GLY	2.9
17	C5	105	VAL	2.9
26	D4	122	GLY	2.9
32	e0	51	ASN	2.9
60	n4	27	LYS	2.9
85	f	143	GLY	2.9
1	2	1704	U	2.9
1	6	1340	U	2.9
36	5	1534	A	2.9
85	f	99	PHE	2.9
16	C4	116	GLU	2.8
15	c3	7	ALA	2.8
17	c5	7	ALA	2.8
47	m0	68	ALA	2.8
75	O9	21	ARG	2.8
53	M7	169	THR	2.8
58	N2	55	THR	2.8
14	c2	78	LEU	2.8
45	l8	238	LEU	2.8
21	C9	129	GLN	2.8
48	m1	39	GLN	2.8
31	D9	6	VAL	2.8
35	SM	64	LYS	2.8
41	L4	71	VAL	2.8
32	e0	59	GLY	2.8
43	l6	66	SER	2.8
45	l8	122	LYS	2.8
63	N7	96	VAL	2.8
63	N7	113	VAL	2.8
15	c3	8	GLY	2.8
35	sM	40	PRO	2.8
74	O8	57	ASN	2.8
14	C2	89	ILE	2.8
18	c6	43	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
58	n2	11	ILE	2.8
71	O5	75	TYR	2.8
27	d5	39	ALA	2.8
34	sR	27	ALA	2.8
36	1	3175	U	2.8
1	6	1700	C	2.8
36	1	2821	C	2.8
36	5	2492	C	2.8
2	S0	162	CYS	2.8
16	C4	89	THR	2.8
16	C4	91	THR	2.8
35	SM	87	THR	2.8
33	e1	102	VAL	2.8
45	l8	77	GLN	2.8
7	S5	72	HIS	2.8
14	C2	82	PRO	2.8
28	D6	88	SER	2.8
46	L9	13	PRO	2.8
49	m3	4	SER	2.8
60	N4	72	SER	2.8
5	s3	217	ILE	2.8
7	S5	69	PHE	2.8
7	s5	40	ILE	2.8
18	C6	32	ASN	2.8
18	c6	49	TYR	2.8
23	D1	53	TYR	2.8
61	n5	141	TYR	2.8
8	S6	225	GLU	2.8
3	S1	61	LEU	2.8
5	S3	69	LEU	2.8
10	S8	58	LEU	2.8
21	C9	132	LEU	2.8
45	L8	152	LEU	2.8
63	N7	42	LEU	2.8
1	2	538	A	2.8
7	s5	70	VAL	2.8
16	C4	67	VAL	2.8
21	C9	37	VAL	2.8
35	sM	174	VAL	2.8
47	M0	149	VAL	2.8
53	M7	165	VAL	2.8
55	M9	177	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
22	d0	12	GLN	2.8
9	s7	2	SER	2.8
14	c2	64	SER	2.8
12	C0	96	ASN	2.8
34	sR	257	ALA	2.8
45	L8	130	TYR	2.8
49	M3	37	ASN	2.8
52	M6	191	ALA	2.8
14	c2	132	GLU	2.8
85	f	117	GLU	2.8
9	S7	126	LEU	2.8
16	c4	129	LYS	2.8
51	M5	204	LYS	2.8
9	s7	20	VAL	2.8
23	D1	52	THR	2.8
54	M8	2	GLY	2.8
2	S0	170	ILE	2.8
19	c7	28	PHE	2.8
34	SR	131	ILE	2.8
85	f	83	PRO	2.8
2	s0	101	ARG	2.8
9	S7	141	ARG	2.8
60	n4	94	ARG	2.8
65	N9	14	ARG	2.8
7	S5	78	ALA	2.8
19	C7	126	ALA	2.8
20	c8	98	TYR	2.8
32	E0	61	SER	2.8
70	o4	2	ALA	2.8
4	S2	41	LEU	2.8
53	M7	163	LYS	2.8
19	C7	99	VAL	2.8
1	2	714	G	2.8
1	2	1584	G	2.8
39	L2	53	GLY	2.8
43	l6	67	GLY	2.8
4	s2	91	ARG	2.7
6	S4	145	ARG	2.7
14	c2	106	ILE	2.8
16	C4	14	PHE	2.8
16	C4	135	ARG	2.7
24	D2	34	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
30	D8	53	ILE	2.8
42	l5	55	PHE	2.8
42	l5	247	ILE	2.8
85	f	139	ILE	2.8
36	1	2979	U	2.7
4	s2	118	ALA	2.7
10	S8	150	ALA	2.7
2	s0	150	ASP	2.7
11	s9	145	SER	2.7
14	c2	65	SER	2.7
28	D6	33	ASP	2.7
1	6	1707	A	2.7
29	D7	3	LEU	2.7
36	1	926	A	2.7
42	L5	146	LEU	2.7
55	M9	44	LEU	2.7
1	2	1700	C	2.7
14	C2	135	MET	2.7
28	D6	90	GLU	2.7
21	c9	4	VAL	2.7
35	SM	106	VAL	2.7
82	p0	188	VAL	2.7
24	d2	53	ILE	2.7
27	d5	41	ILE	2.7
5	S3	153	ALA	2.7
34	SR	162	ALA	2.7
52	m6	61	ALA	2.7
74	o8	34	ALA	2.7
85	f	141	ALA	2.7
58	n2	70	LYS	2.7
70	o4	37	LYS	2.7
1	2	320	U	2.7
5	s3	109	LEU	2.7
18	c6	38	LEU	2.7
36	1	2955	U	2.7
34	sR	26	SER	2.7
46	L9	190	ASP	2.7
24	D2	111	MET	2.7
2	S0	189	VAL	2.7
8	S6	179	VAL	2.7
14	c2	120	VAL	2.7
19	c7	66	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
26	D4	129	VAL	2.7
35	SM	167	GLU	2.7
54	m8	148	GLU	2.7
1	2	1693	A	2.7
36	1	2208	A	2.7
1	2	1482	C	2.7
14	c2	72	ILE	2.7
21	c9	111	ILE	2.7
36	1	1762	C	2.7
39	l2	2	GLY	2.7
52	M6	80	PHE	2.7
85	f	41	ILE	2.7
18	C6	35	PRO	2.7
7	s5	158	GLN	2.7
13	C1	46	LYS	2.7
17	c5	131	ALA	2.7
18	c6	132	LYS	2.7
27	D5	97	LYS	2.7
33	E1	145	HIS	2.7
39	l2	60	LYS	2.7
45	l8	120	LYS	2.7
79	q3	2	ALA	2.7
33	E1	117	LEU	2.7
34	sR	23	LEU	2.7
61	N5	40	LEU	2.7
1	6	1708	U	2.7
42	L5	6	ASP	2.7
9	S7	147	ASN	2.7
14	c2	76	GLU	2.7
25	D3	27	ASN	2.7
25	d3	10	ASN	2.7
26	D4	31	ASN	2.7
35	sM	129	GLU	2.7
36	5	2503	G	2.7
3	S1	93	GLY	2.7
24	d2	60	LYS	2.7
49	M3	127	PRO	2.7
60	n4	117	LYS	2.7
85	f	66	THR	2.7
36	5	2494	A	2.7
1	2	1796	C	2.7
14	C2	32	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
14	c2	62	LEU	2.7
47	m0	220	GLN	2.7
79	q3	55	TRP	2.7
22	D0	117	VAL	2.7
26	D4	100	VAL	2.7
79	Q3	71	VAL	2.7
30	D8	49	ARG	2.7
3	S1	89	ASP	2.7
19	c7	96	SER	2.7
35	SM	137	GLU	2.7
62	N6	11	ASP	2.7
41	l4	66	GLY	2.7
85	f	14	GLY	2.7
41	l4	104	LYS	2.7
71	O5	32	LYS	2.7
16	C4	96	PRO	2.7
32	E0	48	THR	2.7
41	L4	103	THR	2.7
21	C9	50	ALA	2.7
60	n4	125	ALA	2.7
82	p0	25	LEU	2.7
82	p0	106	ALA	2.7
52	m6	122	GLN	2.7
1	6	678	A	2.7
36	5	1103	A	2.7
1	2	1342	C	2.7
43	l6	129	GLU	2.6
8	s6	79	LYS	2.6
14	C2	117	GLY	2.6
18	C6	132	LYS	2.6
24	d2	9	ASP	2.6
26	d4	72	PHE	2.6
28	D6	93	LYS	2.6
40	L3	245	GLY	2.6
45	L8	119	GLY	2.6
85	f	15	SER	2.6
85	f	108	ASP	2.6
25	D3	22	ASN	2.6
44	L7	209	ASN	2.6
2	S0	97	PRO	2.6
3	S1	188	LEU	2.6
5	s3	176	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
34	sR	2	ALA	2.6
34	sR	81	LEU	2.6
36	1	1564	U	2.6
36	5	2978	U	2.6
45	l8	113	ALA	2.6
68	o2	128	LEU	2.6
1	2	1795	U	2.6
25	D3	48	HIS	2.6
3	S1	229	MET	2.6
85	f	125	GLN	2.6
9	S7	20	VAL	2.6
27	D5	40	VAL	2.6
28	D6	86	VAL	2.6
34	sR	157	VAL	2.6
1	2	1351	G	2.6
1	2	1521	G	2.6
14	c2	136	ILE	2.6
70	O4	54	ILE	2.6
72	O6	7	ILE	2.6
4	S2	208	GLU	2.6
23	D1	10	GLU	2.6
39	l2	248	GLY	2.6
41	L4	100	PHE	2.6
41	l4	63	GLU	2.6
46	L9	85	GLY	2.6
36	5	2495	C	2.6
45	L8	158	ASP	2.6
3	S1	217	LEU	2.6
4	S2	207	LEU	2.6
14	c2	36	LEU	2.6
46	l9	191	LEU	2.6
4	S2	214	ALA	2.6
24	D2	10	ALA	2.6
67	O1	101	ALA	2.6
68	o2	127	ALA	2.6
34	SR	306	THR	2.6
10	s8	103	GLN	2.6
12	C0	93	GLN	2.6
21	C9	7	ARG	2.6
50	M4	126	GLN	2.6
75	O9	46	ARG	2.6
36	1	1782	U	2.6

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Mol	Chain	Res	Type	RSRZ
85	f	136	VAL	2.6
2	S0	174	TRP	2.6
34	SR	150	TRP	2.6
51	M5	189	LYS	2.6
6	s4	244	ILE	2.6
24	D2	27	ILE	2.6
8	S6	144	PHE	2.6
17	c5	138	PHE	2.6
25	d3	2	GLY	2.6
45	L8	118	GLU	2.6
60	n4	66	GLU	2.6
20	C8	15	LEU	2.6
74	O8	51	LEU	2.6
1	2	506	A	2.6
1	6	538	A	2.6
10	S8	115	ALA	2.6
11	s9	152	SER	2.6
21	C9	8	ASP	2.6
28	D6	56	ALA	2.6
39	L2	185	ALA	2.6
85	f	61	ALA	2.6
1	2	1777	G	2.6
1	2	696	C	2.6
10	s8	8	ARG	2.6
39	l2	252	THR	2.6
34	SR	94	VAL	2.6
13	C1	148	LYS	2.6
51	m5	72	LYS	2.6
16	C4	112	ILE	2.6
3	S1	223	PHE	2.6
9	s7	24	PHE	2.6
5	s3	218	LEU	2.6
14	c2	28	LEU	2.6
15	c3	53	LEU	2.6
34	SR	210	LEU	2.6
60	n4	96	LEU	2.6
5	s3	153	ALA	2.6
13	c1	144	ALA	2.6
72	O6	22	PRO	2.6
80	c0	83	PRO	2.6
85	f	146	ALA	2.6
7	S5	76	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
28	D6	85	ARG	2.6
56	n0	18	SER	2.6
5	s3	85	VAL	2.6
15	C3	5	HIS	2.6
19	C7	123	ASN	2.6
30	D8	55	VAL	2.6
35	SM	17	VAL	2.6
51	m5	34	ASN	2.6
52	m6	184	THR	2.6
59	N3	115	THR	2.6
82	p0	105	VAL	2.6
33	e1	89	LYS	2.6
66	O0	40	LYS	2.6
77	Q1	25	LYS	2.6
32	e0	63	GLN	2.6
39	l2	253	GLN	2.6
1	2	1711	C	2.6
14	C2	72	ILE	2.6
36	1	2150	G	2.6
16	C4	27	PHE	2.6
33	E1	105	TYR	2.6
10	s8	71	GLY	2.6
18	c6	52	LEU	2.6
21	c9	87	GLY	2.6
26	d4	28	LEU	2.6
41	l4	88	GLY	2.6
80	c0	40	LEU	2.6
4	S2	231	ALA	2.6
16	C4	21	ALA	2.6
40	L3	217	ALA	2.6
40	l3	19	ARG	2.6
61	N5	23	ALA	2.6
5	S3	186	VAL	2.6
5	s3	137	VAL	2.6
6	S4	196	VAL	2.6
15	C3	12	SER	2.6
18	c6	55	VAL	2.6
18	c6	136	SER	2.6
26	D4	25	VAL	2.6
7	s5	60	ASP	2.6
27	d5	97	LYS	2.6
44	L7	26	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
63	N7	14	VAL	2.6
73	o7	87	SER	2.6
18	C6	17	THR	2.6
18	C6	74	HIS	2.6
23	d1	75	ASN	2.6
29	D7	61	THR	2.6
85	f	122	ASP	2.6
9	S7	125	ILE	2.5
16	C4	115	ILE	2.5
35	sM	120	GLN	2.5
48	m1	120	ILE	2.5
6	S4	261	LEU	2.5
6	s4	261	LEU	2.5
8	S6	169	TYR	2.5
13	c1	90	TYR	2.5
38	8	80	A	2.5
46	l9	186	PHE	2.5
15	c3	125	LEU	2.5
18	c6	57	LEU	2.5
42	L5	51	LEU	2.5
85	f	90	TYR	2.5
1	2	1096	C	2.5
1	2	1703	C	2.5
5	S3	149	ALA	2.5
15	c3	15	ALA	2.5
41	L4	70	ALA	2.5
51	m5	147	ARG	2.5
53	M7	158	ALA	2.5
8	S6	222	GLU	2.5
40	L3	94	GLU	2.5
49	m3	192	GLU	2.5
1	2	1340	U	2.5
8	s6	131	LYS	2.5
22	D0	31	VAL	2.5
36	1	1095	U	2.5
36	5	3155	U	2.5
85	f	113	VAL	2.5
19	c7	25	THR	2.5
28	D6	57	SER	2.5
68	O2	26	HIS	2.5
75	O9	47	THR	2.5
13	C1	150	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
53	m7	137	ASN	2.5
8	S6	65	GLN	2.5
8	s6	144	PHE	2.5
30	d8	9	LEU	2.5
63	n7	130	PHE	2.5
74	O8	78	LEU	2.5
48	M1	83	GLY	2.5
70	o4	16	ARG	2.5
8	S6	138	ALA	2.5
26	d4	80	ALA	2.5
45	L8	117	ALA	2.5
49	M3	132	ALA	2.5
55	m9	189	ALA	2.5
72	o6	96	ALA	2.5
82	p0	284	ALA	2.5
1	2	173	A	2.5
1	6	1800	A	2.5
36	1	884	A	2.5
3	S1	90	GLU	2.5
7	S5	213	LYS	2.5
28	D6	28	LYS	2.5
34	SR	40	LYS	2.5
22	d0	97	VAL	2.5
85	f	57	VAL	2.5
9	S7	8	ILE	2.5
39	l2	19	HIS	2.5
43	l6	149	ILE	2.5
1	6	1199	G	2.5
1	6	1717	G	2.5
73	O7	87	SER	2.5
85	f	47	SER	2.5
45	L8	91	PHE	2.5
66	o0	12	GLN	2.5
10	s8	177	GLY	2.5
25	D3	29	TYR	2.5
39	l2	13	GLY	2.5
45	l8	44	ARG	2.5
71	O5	3	GLY	2.5
2	s0	145	ALA	2.5
11	s9	183	ALA	2.5
18	c6	24	ALA	2.5
20	c8	27	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
62	N6	116	LYS	2.5
14	C2	30	VAL	2.5
14	c2	91	VAL	2.5
21	C9	118	PRO	2.5
30	d8	44	VAL	2.5
41	l4	147	GLU	2.5
60	n4	126	GLU	2.5
71	O5	64	GLU	2.5
36	5	440	A	2.5
3	S1	101	HIS	2.5
22	D0	91	ILE	2.5
28	D6	83	ILE	2.5
33	e1	145	HIS	2.5
34	SR	66	HIS	2.5
7	s5	43	PHE	2.5
11	S9	61	THR	2.5
19	c7	46	LEU	2.5
40	l3	242	THR	2.5
47	m0	167	LEU	2.5
1	2	870	C	2.5
1	6	1634	C	2.5
14	C2	107	ASP	2.5
18	C6	123	ARG	2.5
34	SR	108	SER	2.5
36	1	2405	C	2.5
36	5	1582	C	2.5
36	1	1568	U	2.5
39	l2	208	ASP	2.5
65	n9	18	ARG	2.5
1	2	144	U	2.5
7	S5	61	TYR	2.5
10	S8	106	ALA	2.5
17	C5	52	LYS	2.5
18	C6	14	LYS	2.5
43	L6	147	ALA	2.5
80	c0	38	LYS	2.5
21	C9	115	GLU	2.5
40	L3	7	GLU	2.5
46	L9	14	GLU	2.5
7	S5	29	ILE	2.5
8	S6	101	ILE	2.5
15	C3	34	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
16	C4	76	ILE	2.5
22	d0	19	ILE	2.5
25	D3	18	HIS	2.5
33	e1	103	LEU	2.5
34	sR	34	LEU	2.5
14	c2	34	THR	2.5
1	2	1701	A	2.5
36	5	1350	A	2.5
36	5	2441	A	2.5
11	s9	48	GLN	2.5
18	C6	13	LYS	2.5
21	c9	85	SER	2.5
34	sR	268	GLN	2.5
41	L4	88	GLY	2.5
44	l7	242	SER	2.5
45	L8	52	TRP	2.5
5	S3	114	ALA	2.5
34	SR	305	TYR	2.5
34	sR	36	ALA	2.5
1	2	1379	C	2.5
36	1	2314	U	2.5
36	5	1356	U	2.5
13	C1	7	VAL	2.5
44	l7	102	VAL	2.5
35	sM	166	GLU	2.5
28	D6	41	ILE	2.4
54	M8	93	ILE	2.4
57	n1	76	ILE	2.4
9	s7	126	LEU	2.4
11	S9	36	LEU	2.4
11	S9	105	LEU	2.4
70	o4	57	LEU	2.4
74	O8	31	LEU	2.4
1	2	1002	G	2.4
2	s0	165	ARG	2.4
36	1	2400	G	2.4
31	d9	27	HIS	2.4
41	L4	58	HIS	2.4
16	C4	70	LYS	2.4
30	D8	45	LYS	2.4
60	N4	70	LYS	2.4
85	f	40	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
25	D3	4	GLY	2.4
39	L2	196	TRP	2.4
4	S2	155	ALA	2.4
13	C1	145	ALA	2.4
17	C5	92	SER	2.4
18	C6	6	SER	2.4
44	L7	211	SER	2.4
49	m3	132	ALA	2.4
50	M4	5	SER	2.4
11	S9	38	ASN	2.4
23	d1	36	VAL	2.4
25	D3	10	ASN	2.4
45	l8	124	ASP	2.4
34	SR	110	VAL	2.4
34	sR	290	VAL	2.4
35	SM	10	ASN	2.4
35	SM	18	VAL	2.4
62	n6	8	VAL	2.4
36	1	3351	U	2.4
38	8	22	U	2.4
1	2	1078	C	2.4
5	S3	217	ILE	2.4
6	S4	38	LEU	2.4
8	S6	68	LEU	2.4
8	s6	76	LEU	2.4
9	s7	134	GLU	2.4
35	SM	58	GLU	2.4
43	L6	129	GLU	2.4
46	L9	189	GLU	2.4
49	M3	164	GLU	2.4
57	n1	160	ILE	2.4
15	C3	121	ARG	2.4
15	C3	125	LEU	2.4
22	d0	50	LEU	2.4
47	m0	103	LEU	2.4
54	m8	180	ARG	2.4
26	d4	85	PHE	2.4
63	n7	92	PHE	2.4
82	p0	73	PHE	2.4
21	C9	110	LYS	2.4
34	SR	46	LYS	2.4
41	L4	104	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
43	L6	175	LYS	2.4
80	c0	12	HIS	2.4
10	s8	95	THR	2.4
34	sR	168	THR	2.4
41	l4	103	THR	2.4
60	n4	83	THR	2.4
27	D5	73	GLY	2.4
5	s3	219	ALA	2.4
29	D7	51	GLN	2.4
33	E1	152	ALA	2.4
35	SM	168	ALA	2.4
45	l8	123	GLN	2.4
55	m9	40	ALA	2.4
55	m9	183	ALA	2.4
68	O2	127	ALA	2.4
11	s9	13	SER	2.4
26	d4	69	SER	2.4
28	D6	54	SER	2.4
36	5	1576	G	2.4
36	5	2418	G	2.4
48	m1	54	VAL	2.4
56	N0	79	VAL	2.4
7	S5	104	ASN	2.4
8	S6	135	PRO	2.4
17	c5	103	ASN	2.4
18	c6	51	PRO	2.4
39	l2	141	PRO	2.4
85	f	88	ASN	2.4
40	L3	251	CYS	2.4
3	S1	181	LEU	2.4
5	s3	184	ILE	2.4
6	s4	246	LEU	2.4
8	S6	158	ILE	2.4
14	c2	97	LEU	2.4
19	c7	95	ARG	2.4
55	m9	185	LEU	2.4
57	N1	85	LEU	2.4
70	o4	41	ARG	2.4
1	2	1151	A	2.4
1	6	1701	A	2.4
36	1	1588	A	2.4
33	e1	83	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
36	1	1567	U	2.4
36	5	1567	U	2.4
1	2	1082	C	2.4
1	6	658	C	2.4
36	5	2812	C	2.4
38	4	28	C	2.4
10	s8	122	GLY	2.4
45	l8	110	THR	2.4
55	m9	84	THR	2.4
60	n4	75	THR	2.4
2	S0	5	ALA	2.4
18	c6	119	ALA	2.4
39	L2	204	MET	2.4
40	L3	250	ALA	2.4
53	m7	132	ALA	2.4
2	S0	86	VAL	2.4
6	S4	111	VAL	2.4
14	C2	116	VAL	2.4
47	M0	220	GLN	2.4
60	n4	67	VAL	2.4
13	c1	97	TYR	2.4
53	m7	130	TYR	2.4
2	s0	152	PRO	2.4
8	s6	130	PRO	2.4
75	O9	6	SER	2.4
85	f	36	SER	2.4
85	f	101	SER	2.4
6	S4	162	ILE	2.4
18	C6	65	ILE	2.4
18	c6	54	LEU	2.4
22	d0	22	ILE	2.4
23	D1	75	ASN	2.4
29	d7	21	LEU	2.4
10	s8	75	LYS	2.4
22	D0	53	LYS	2.4
35	SM	153	LYS	2.4
68	o2	16	LYS	2.4
70	O4	67	LYS	2.4
21	c9	21	PHE	2.4
35	sM	163	GLU	2.4
57	n1	86	GLU	2.4
58	n2	15	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
62	N6	88	GLU	2.4
1	2	1681	A	2.4
1	6	1424	A	2.4
36	1	1800	A	2.4
1	2	626	U	2.4
3	s1	60	ALA	2.4
20	c8	146	ALA	2.4
32	E0	56	MET	2.4
38	4	158	U	2.4
85	f	77	THR	2.4
4	s2	86	VAL	2.4
31	d9	6	VAL	2.4
34	sR	113	VAL	2.4
63	n7	75	VAL	2.4
1	2	1332	C	2.4
1	2	1355	C	2.4
16	C4	136	ARG	2.4
28	D6	62	TYR	2.4
36	1	47	C	2.4
36	1	818	C	2.4
39	L2	242	ARG	2.4
44	L7	141	TYR	2.4
9	S7	100	PRO	2.4
11	S9	2	PRO	2.4
3	S1	130	SER	2.4
5	s3	86	LEU	2.4
17	C5	65	LEU	2.4
20	c8	10	SER	2.4
21	C9	41	SER	2.4
21	C9	117	SER	2.4
25	D3	133	LEU	2.4
33	e1	100	LEU	2.4
34	SR	115	ILE	2.4
35	SM	171	PRO	2.4
35	sM	39	PRO	2.4
82	p0	78	PRO	2.4
3	s1	116	LYS	2.4
8	S6	93	LYS	2.4
7	S5	79	ASN	2.4
34	sR	297	ASP	2.4
52	m6	182	ASN	2.4
85	f	79	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
39	l2	186	PHE	2.4
52	m6	64	PHE	2.4
3	S1	196	GLU	2.4
24	D2	18	GLU	2.4
67	o1	82	GLU	2.4
85	f	58	HIS	2.4
14	C2	104	GLY	2.4
6	s4	84	ALA	2.4
7	S5	74	ALA	2.4
16	C4	64	ALA	2.4
34	SR	83	ALA	2.4
78	q2	33	ALA	2.4
3	s1	91	VAL	2.4
5	s3	91	VAL	2.4
29	d7	54	VAL	2.4
34	SR	8	VAL	2.4
51	M5	60	VAL	2.4
53	M7	157	VAL	2.4
1	2	730	G	2.4
1	2	1692	G	2.4
1	6	1694	A	2.4
10	s8	195	ARG	2.4
14	c2	108	ARG	2.4
35	SM	89	ARG	2.4
36	5	169	U	2.4
9	S7	99	LEU	2.3
18	C6	87	LYS	2.3
22	D0	99	ILE	2.3
33	E1	106	TYR	2.3
43	L6	11	PRO	2.3
43	l6	146	ILE	2.3
47	m0	27	PRO	2.3
85	f	93	LEU	2.3
65	n9	22	LYS	2.3
14	c2	119	SER	2.3
28	D6	29	SER	2.3
44	l7	211	SER	2.3
5	s3	224	ASP	2.3
32	E0	46	ASN	2.3
36	1	1857	C	2.3
36	5	3278	C	2.3
7	s5	31	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
11	S9	4	ALA	2.3
15	C3	2	GLY	2.3
45	l8	246	MET	2.3
47	m0	188	GLY	2.3
59	n3	3	GLY	2.3
16	C4	48	VAL	2.3
34	SR	290	VAL	2.3
34	sR	94	VAL	2.3
48	M1	18	VAL	2.3
66	O0	80	ALA	2.3
71	O5	2	ALA	2.3
71	o5	120	ALA	2.3
6	S4	159	THR	2.3
13	c1	116	ARG	2.3
20	c8	20	THR	2.3
22	d0	27	THR	2.3
34	SR	85	TRP	2.3
5	s3	202	LEU	2.3
6	S4	44	LEU	2.3
9	s7	154	LEU	2.3
21	c9	22	LEU	2.3
34	sR	62	LYS	2.3
39	L2	179	LEU	2.3
9	S7	181	ILE	2.3
80	c0	95	GLN	2.3
17	C5	125	PRO	2.3
33	e1	105	TYR	2.3
46	l9	3	TYR	2.3
49	M3	133	PRO	2.3
1	2	742	U	2.3
1	6	679	U	2.3
3	s1	30	PHE	2.3
1	6	1696	G	2.3
36	1	1486	G	2.3
13	c1	28	SER	2.3
16	c4	55	SER	2.3
17	c5	136	SER	2.3
19	C7	125	SER	2.3
73	O7	7	SER	2.3
85	f	12	ASP	2.3
35	sM	159	GLU	2.3
5	s3	150	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	2	1399	C	2.3
1	2	1481	C	2.3
6	S4	26	CYS	2.3
7	s5	153	GLY	2.3
18	C6	134	ALA	2.3
29	D7	13	ALA	2.3
40	L3	336	VAL	2.3
42	l5	125	VAL	2.3
45	L8	141	ALA	2.3
45	L8	256	ALA	2.3
56	N0	88	HIS	2.3
60	n4	121	ALA	2.3
7	s5	92	ARG	2.3
60	N4	93	ARG	2.3
4	s2	117	THR	2.3
16	c4	91	THR	2.3
21	c9	28	LEU	2.3
22	D0	60	THR	2.3
27	D5	50	ILE	2.3
39	l2	5	ILE	2.3
2	s0	207	PRO	2.3
39	l2	103	PRO	2.3
21	C9	91	TYR	2.3
63	n7	49	TYR	2.3
10	S8	160	PHE	2.3
68	o2	17	PHE	2.3
11	S9	184	SER	2.3
15	C3	147	SER	2.3
36	5	1764	U	2.3
41	L4	64	SER	2.3
82	p0	282	SER	2.3
6	s4	39	ARG	2.3
22	D0	74	GLU	2.3
18	C6	7	VAL	2.3
23	D1	62	ARG	2.3
23	d1	35	ASN	2.3
32	e0	32	GLY	2.3
34	sR	162	ALA	2.3
39	L2	30	ARG	2.3
39	L2	220	GLY	2.3
39	l2	227	ARG	2.3
51	M5	182	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
7	s5	133	VAL	2.3
7	s5	154	ALA	2.3
51	M5	2	GLY	2.3
53	M7	183	ALA	2.3
85	f	131	GLY	2.3
1	2	1690	G	2.3
1	6	660	G	2.3
6	S4	22	LYS	2.3
10	s8	142	LYS	2.3
22	D0	61	LYS	2.3
28	D6	19	LYS	2.3
36	1	870	G	2.3
36	1	2185	G	2.3
77	q1	25	LYS	2.3
3	S1	47	LEU	2.3
8	S6	147	LEU	2.3
13	C1	91	LEU	2.3
80	c0	82	LEU	2.3
2	S0	133	ILE	2.3
35	sM	165	ILE	2.3
45	L8	36	ILE	2.3
45	L8	237	ILE	2.3
76	q0	77	ILE	2.3
34	sR	88	THR	2.3
36	1	2507	C	2.3
15	c3	62	GLN	2.3
71	O5	39	PRO	2.3
4	S2	66	PHE	2.3
9	S7	183	PHE	2.3
21	c9	91	TYR	2.3
31	D9	52	PHE	2.3
49	m3	183	ARG	2.3
72	o6	62	ARG	2.3
5	s3	135	GLU	2.3
9	s7	12	ALA	2.3
14	C2	21	GLU	2.3
14	c2	121	VAL	2.3
22	d0	100	VAL	2.3
27	D5	62	VAL	2.3
29	d7	60	SER	2.3
50	m4	9	ALA	2.3
56	N0	85	SER	2.3

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Mol	Chain	Res	Type	RSRZ
71	O5	19	SER	2.3
32	e0	29	LYS	2.3
33	e1	82	LYS	2.3
40	L3	200	GLU	2.3
55	m9	186	LYS	2.3
57	n1	104	GLU	2.3
74	o8	2	ALA	2.3
82	p0	184	GLY	2.3
6	S4	104	ASP	2.3
39	L2	215	ASN	2.3
28	D6	17	HIS	2.3
36	1	3079	U	2.3
18	c6	118	ILE	2.3
22	D0	19	ILE	2.3
36	1	1605	A	2.3
36	5	2445	A	2.3
61	N5	63	ILE	2.3
6	S4	80	THR	2.3
9	S7	133	THR	2.3
41	l4	75	PRO	2.3
42	l5	275	THR	2.3
54	m8	6	THR	2.3
13	C1	127	GLN	2.3
1	2	1150	G	2.3
33	E1	85	TYR	2.3
21	C9	57	ARG	2.3
33	E1	150	VAL	2.3
70	o4	36	LYS	2.3
85	f	114	LYS	2.3
6	s4	14	ALA	2.3
13	C1	154	ALA	2.3
39	l2	213	GLY	2.3
42	l5	295	GLY	2.3
45	L8	154	ALA	2.3
47	M0	114	GLY	2.3
47	m0	219	ALA	2.3
56	n0	2	ALA	2.3
69	O3	2	ALA	2.3
8	s6	35	GLU	2.3
9	S7	93	LEU	2.3
14	c2	21	GLU	2.3
26	d4	125	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
34	sR	210	LEU	2.3
40	L3	47	LEU	2.3
42	L5	131	LEU	2.3
7	S5	40	ILE	2.2
49	m3	6	ASN	2.2
85	f	95	ILE	2.2
1	2	174	U	2.2
2	S0	203	PHE	2.2
6	s4	95	THR	2.2
10	S8	168	CYS	2.2
21	C9	46	PRO	2.2
35	sM	54	PRO	2.2
39	L2	31	THR	2.2
42	L5	3	PHE	2.2
58	N2	100	THR	2.2
70	O4	71	THR	2.2
1	2	793	A	2.2
15	C3	128	TYR	2.2
36	1	2398	A	2.2
36	1	2813	A	2.2
79	Q3	32	GLN	2.2
16	c4	90	ARG	2.2
29	d7	17	ARG	2.2
10	S8	200	LYS	2.2
11	s9	37	LYS	2.2
9	s7	136	VAL	2.2
16	c4	13	VAL	2.2
26	D4	24	VAL	2.2
27	d5	62	VAL	2.2
29	D7	4	VAL	2.2
30	D8	28	VAL	2.2
3	s1	207	LEU	2.2
7	S5	150	GLY	2.2
7	s5	155	ALA	2.2
12	C0	30	ALA	2.2
14	c2	27	ALA	2.2
29	D7	53	ALA	2.2
30	d8	24	GLY	2.2
34	SR	279	ALA	2.2
35	SM	15	ALA	2.2
41	L4	57	GLY	2.2
42	L5	292	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
49	m3	90	ALA	2.2
52	m6	196	ALA	2.2
61	N5	82	LEU	2.2
75	O9	3	ALA	2.2
1	2	540	G	2.2
1	2	1518	C	2.2
1	2	1537	C	2.2
1	6	1720	G	2.2
36	5	1507	G	2.2
47	M0	212	GLU	2.2
3	S1	169	SER	2.2
3	s1	84	ILE	2.2
5	s3	208	ILE	2.2
16	C4	83	ILE	2.2
18	C6	43	ILE	2.2
20	C8	81	ILE	2.2
34	SR	136	ILE	2.2
39	L2	218	HIS	2.2
40	L3	243	HIS	2.2
73	O7	48	ASN	2.2
25	D3	24	TRP	2.2
51	m5	200	TRP	2.2
3	s1	142	PHE	2.2
5	s3	43	PRO	2.2
8	S6	104	PRO	2.2
20	c8	76	PRO	2.2
24	d2	29	PRO	2.2
34	sR	30	PRO	2.2
48	m1	45	PRO	2.2
19	C7	30	THR	2.2
1	2	134	U	2.2
7	s5	66	GLN	2.2
14	C2	108	ARG	2.2
14	c2	33	ARG	2.2
23	D1	58	TYR	2.2
32	e0	17	GLN	2.2
70	O4	4	ARG	2.2
4	S2	157	LYS	2.2
25	D3	123	LYS	2.2
33	e1	143	LYS	2.2
49	m3	131	LYS	2.2
53	M7	159	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
73	O7	3	LYS	2.2
80	c0	54	TYR	2.2
6	S4	102	VAL	2.2
14	C2	31	VAL	2.2
34	SR	113	VAL	2.2
2	s0	99	ALA	2.2
8	S6	221	ALA	2.2
9	S7	12	ALA	2.2
21	C9	108	LEU	2.2
25	d3	15	LEU	2.2
49	m3	51	LEU	2.2
16	C4	95	GLY	2.2
30	D8	24	GLY	2.2
22	D0	108	ILE	2.2
24	D2	53	ILE	2.2
40	l3	188	ILE	2.2
17	C5	69	GLU	2.2
44	L7	131	GLU	2.2
60	N4	66	GLU	2.2
85	f	152	GLU	2.2
33	e1	93	HIS	2.2
30	D8	37	SER	2.2
39	L2	223	SER	2.2
82	p0	24	SER	2.2
1	2	1077	C	2.2
4	S2	144	TRP	2.2
31	d9	55	PHE	2.2
32	E0	27	PRO	2.2
34	SR	198	ASN	2.2
34	sR	241	PHE	2.2
35	SM	52	PRO	2.2
35	sM	130	ASP	2.2
64	n8	46	ASP	2.2
67	O1	112	ASP	2.2
9	S7	139	ARG	2.2
26	D4	20	ARG	2.2
40	L3	369	ARG	2.2
1	2	676	G	2.2
2	s0	134	LYS	2.2
3	s1	143	THR	2.2
7	s5	94	THR	2.2
14	C2	130	THR	2.2

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Mol	Chain	Res	Type	RSRZ
16	C4	119	THR	2.2
22	d0	78	THR	2.2
30	D8	36	THR	2.2
35	sM	83	LYS	2.2
36	1	2534	G	2.2
60	n4	124	LYS	2.2
80	c0	64	TYR	2.2
26	D4	12	VAL	2.2
29	D7	2	VAL	2.2
39	l2	107	VAL	2.2
6	s4	207	LEU	2.2
19	c7	100	LEU	2.2
35	SM	117	LEU	2.2
18	c6	91	ALA	2.2
35	sM	134	ALA	2.2
36	5	250	U	2.2
73	O7	86	ALA	2.2
82	p0	280	ALA	2.2
85	f	154	ALA	2.2
4	S2	178	ILE	2.2
11	S9	129	ILE	2.2
21	C9	124	ILE	2.2
24	d2	27	ILE	2.2
46	l9	187	ILE	2.2
34	SR	160	GLU	2.2
36	5	1566	A	2.2
52	M6	100	GLU	2.2
32	e0	5	HIS	2.2
9	S7	115	SER	2.2
15	C3	25	TRP	2.2
22	d0	76	SER	2.2
33	e1	122	SER	2.2
34	SR	26	SER	2.2
19	C7	65	PRO	2.2
35	SM	38	PRO	2.2
34	sR	17	ASN	2.2
45	l8	43	LYS	2.2
48	M1	8	PRO	2.2
51	M5	193	ARG	2.2
20	C8	44	ASN	2.2
22	D0	64	LYS	2.2
24	D2	60	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
77	Q1	14	LYS	2.2
43	l6	142	ASP	2.2
59	N3	9	THR	2.2
1	6	1709	C	2.2
2	S0	18	LEU	2.2
4	S2	102	VAL	2.2
7	S5	174	LEU	2.2
8	S6	69	LEU	2.2
8	S6	190	GLN	2.2
8	s6	182	GLN	2.2
14	c2	45	LEU	2.2
21	C9	71	VAL	2.2
28	D6	50	VAL	2.2
38	8	83	C	2.2
49	m3	154	VAL	2.2
57	n1	27	LEU	2.2
61	N5	124	VAL	2.2
34	sR	227	ALA	2.2
43	l6	17	ALA	2.2
50	M4	9	ALA	2.2
68	O2	29	ALA	2.2
85	f	25	ALA	2.2
12	C0	89	GLY	2.2
34	SR	55	GLY	2.2
1	2	1367	G	2.2
36	5	170	G	2.2
36	5	251	G	2.2
1	2	965	U	2.2
1	2	1657	U	2.2
1	6	833	U	2.2
36	1	1436	U	2.2
36	5	1568	U	2.2
3	S1	41	ARG	2.2
7	s5	144	GLU	2.2
10	S8	109	PHE	2.2
11	S9	104	PHE	2.2
20	c8	132	ARG	2.2
43	L6	134	ARG	2.2
20	C8	48	LYS	2.2
22	D0	77	LYS	2.2
35	sM	170	LYS	2.2
70	O4	7	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
2	S0	42	PRO	2.2
2	s0	194	PRO	2.2
12	C0	88	PRO	2.2
17	C5	53	PRO	2.2
33	E1	88	PRO	2.2
60	N4	98	PRO	2.2
36	5	3279	A	2.2
85	f	44	MET	2.2
2	S0	17	LEU	2.2
3	S1	96	LEU	2.2
5	S3	222	VAL	2.2
9	s7	81	LEU	2.2
16	C4	32	ASP	2.2
19	c7	4	VAL	2.2
20	C8	22	VAL	2.2
24	D2	11	LEU	2.2
26	D4	27	VAL	2.2
27	d5	51	LEU	2.2
32	e0	62	VAL	2.2
34	sR	266	ASP	2.2
48	M1	160	VAL	2.2
74	o8	55	VAL	2.2
85	f	82	VAL	2.2
3	S1	156	ALA	2.1
14	C2	69	ALA	2.1
18	c6	83	GLN	2.2
34	sR	232	TYR	2.2
39	L2	229	ALA	2.1
39	L2	250	GLN	2.2
44	L7	49	ALA	2.1
79	Q3	25	GLN	2.2
82	p0	276	ALA	2.1
16	C4	131	GLY	2.1
2	s0	98	ILE	2.1
70	O4	81	CYS	2.1
80	c0	43	ILE	2.1
1	2	321	C	2.1
8	S6	142	ARG	2.1
32	e0	55	ARG	2.1
39	L2	247	ARG	2.1
52	m6	78	ARG	2.1
9	S7	151	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
13	C1	32	LYS	2.1
34	SR	263	PHE	2.1
39	l2	143	GLU	2.1
42	l5	263	GLU	2.1
49	m3	189	GLU	2.1
80	c0	33	GLU	2.1
1	2	1398	U	2.1
1	6	935	U	2.1
1	2	1364	G	2.1
14	c2	100	TRP	2.1
25	d3	6	PRO	2.1
36	5	240	U	2.1
36	5	1554	U	2.1
36	1	3276	G	2.1
41	l4	65	TRP	2.1
10	S8	69	SER	2.1
11	s9	80	LEU	2.1
16	c4	48	VAL	2.1
19	C7	110	VAL	2.1
20	C8	5	VAL	2.1
24	D2	76	SER	2.1
34	SR	89	LEU	2.1
34	SR	243	LEU	2.1
45	l8	121	SER	2.1
47	M0	167	LEU	2.1
79	Q3	21	SER	2.1
85	f	102	LEU	2.1
10	s8	36	THR	2.1
16	C4	77	THR	2.1
41	L4	60	THR	2.1
42	L5	68	THR	2.1
51	M5	190	THR	2.1
55	M9	29	THR	2.1
77	Q1	10	THR	2.1
3	S1	22	ASP	2.1
6	S4	79	ASP	2.1
6	s4	13	ALA	2.1
8	S6	100	ALA	2.1
10	S8	148	ALA	2.1
11	S9	25	ASP	2.1
12	C0	13	GLN	2.1
12	C0	41	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
17	c5	133	ALA	2.1
18	C6	120	ASP	2.1
47	m0	195	ALA	2.1
5	s3	115	ILE	2.1
7	s5	150	GLY	2.1
9	S7	135	ILE	2.1
54	M8	156	GLY	2.1
63	N7	25	ILE	2.1
3	s1	152	ARG	2.1
10	s8	31	ARG	2.1
55	M9	74	ARG	2.1
13	c1	141	LYS	2.1
21	C9	92	LYS	2.1
25	D3	3	LYS	2.1
58	N2	107	PHE	2.1
6	s4	69	HIS	2.1
21	C9	144	GLU	2.1
29	D7	19	HIS	2.1
65	n9	7	HIS	2.1
36	1	1923	C	2.1
49	m3	133	PRO	2.1
14	C2	28	LEU	2.1
34	sR	121	MET	2.1
5	S3	181	VAL	2.1
33	E1	102	VAL	2.1
52	M6	3	VAL	2.1
61	n5	83	VAL	2.1
62	n6	58	VAL	2.1
82	p0	50	VAL	2.1
36	1	1764	U	2.1
4	s2	181	SER	2.1
30	d8	21	SER	2.1
34	sR	120	SER	2.1
41	L4	53	SER	2.1
85	f	123	SER	2.1
5	S3	171	ALA	2.1
16	C4	17	ALA	2.1
16	C4	85	ALA	2.1
19	C7	25	THR	2.1
21	C9	139	THR	2.1
21	c9	50	ALA	2.1
39	L2	224	THR	2.1

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Mol	Chain	Res	Type	RSRZ
49	m3	87	ALA	2.1
79	q3	11	THR	2.1
20	c8	75	ASN	2.1
26	D4	94	TYR	2.1
28	D6	11	ASN	2.1
5	s3	179	GLN	2.1
7	S5	187	ILE	2.1
28	D6	52	ASP	2.1
36	1	2165	G	2.1
85	f	72	ASP	2.1
3	S1	213	ARG	2.1
6	S4	49	ARG	2.1
9	S7	111	LYS	2.1
64	n8	27	LYS	2.1
1	6	1719	A	2.1
12	C0	59	PHE	2.1
34	SR	278	PHE	2.1
34	sR	61	PHE	2.1
36	5	1571	A	2.1
36	5	2183	A	2.1
14	C2	126	TRP	2.1
24	D2	65	LEU	2.1
24	d2	26	LEU	2.1
26	D4	28	LEU	2.1
28	d6	2	PRO	2.1
42	l5	124	GLU	2.1
45	l8	112	GLU	2.1
33	e1	139	LEU	2.1
34	sR	202	LEU	2.1
34	sR	206	PRO	2.1
61	N5	101	GLU	2.1
5	s3	136	VAL	2.1
18	c6	69	VAL	2.1
22	d0	116	VAL	2.1
23	D1	32	VAL	2.1
33	E1	114	VAL	2.1
47	m0	149	VAL	2.1
1	2	172	C	2.1
1	6	393	C	2.1
1	6	717	C	2.1
7	s5	183	ALA	2.1
14	c2	128	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
34	SR	257	ALA	2.1
39	L2	182	ALA	2.1
49	M3	142	ALA	2.1
61	n5	23	ALA	2.1
75	o9	39	ALA	2.1
82	p0	294	ALA	2.1
2	S0	153	SER	2.1
10	S8	62	THR	2.1
13	C1	3	THR	2.1
13	C1	44	THR	2.1
18	c6	79	TYR	2.1
19	c7	41	ILE	2.1
30	D8	40	ILE	2.1
32	E0	41	THR	2.1
33	e1	125	THR	2.1
39	l2	225	ILE	2.1
45	L8	110	THR	2.1
55	M9	143	ILE	2.1
66	O0	48	THR	2.1
70	O4	66	SER	2.1
1	2	711	U	2.1
1	2	1738	U	2.1
1	6	710	U	2.1
4	s2	97	ARG	2.1
6	S4	127	LYS	2.1
6	s4	245	LYS	2.1
7	s5	77	TYR	2.1
13	C1	73	GLY	2.1
28	d6	14	GLY	2.1
21	c9	127	ASN	2.1
29	d7	18	LYS	2.1
30	d8	45	LYS	2.1
31	d9	17	GLY	2.1
35	SM	27	LYS	2.1
35	SM	169	TYR	2.1
36	1	3287	U	2.1
39	L2	183	GLY	2.1
39	l2	164	GLY	2.1
74	o8	33	LYS	2.1
80	c0	39	ASN	2.1
80	c0	98	ASN	2.1
4	S2	57	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
10	s8	109	PHE	2.1
13	C1	153	PHE	2.1
1	2	195	G	2.1
1	2	1416	G	2.1
3	S1	103	MET	2.1
3	s1	110	LEU	2.1
28	D6	64	LEU	2.1
36	5	1268	G	2.1
36	5	1655	G	2.1
36	5	3348	G	2.1
49	M3	172	LEU	2.1
61	n5	113	LEU	2.1
66	O0	16	LEU	2.1
70	O4	30	LEU	2.1
1	2	733	A	2.1
8	S6	91	GLU	2.1
11	S9	186	GLU	2.1
18	C6	40	GLU	2.1
22	D0	118	VAL	2.1
30	D8	44	VAL	2.1
30	D8	60	GLU	2.1
36	1	2207	A	2.1
52	m6	40	GLU	2.1
82	p0	17	GLU	2.1
3	S1	227	ALA	2.1
14	C2	112	ALA	2.1
21	c9	19	ALA	2.1
35	SM	141	ALA	2.1
42	l5	284	ALA	2.1
42	l5	291	ALA	2.1
82	p0	275	ALA	2.1
10	s8	169	ILE	2.1
14	C2	71	ILE	2.1
22	d0	20	ILE	2.1
24	d2	86	ILE	2.1
43	l6	70	LYS	2.1
48	m1	174	LYS	2.1
55	m9	151	ARG	2.1
60	n4	97	LYS	2.1
71	o5	103	LYS	2.1
85	f	48	LYS	2.1
7	s5	75	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
7	s5	152	GLY	2.1
10	s8	39	GLY	2.1
26	d4	76	TYR	2.1
28	d6	73	TYR	2.1
29	D7	45	THR	2.1
33	e1	115	THR	2.1
47	m0	181	TYR	2.1
68	O2	22	SER	2.1
44	L7	25	GLN	2.1
48	M1	6	GLN	2.1
53	M7	179	GLN	2.1
1	6	662	U	2.1
1	6	1362	U	2.1
3	S1	24	PHE	2.1
16	c4	53	ASP	2.1
36	1	2875	U	2.1
48	m1	111	ASP	2.1
85	f	129	ASP	2.1
7	S5	108	LEU	2.1
8	S6	216	LEU	2.1
14	C2	78	LEU	2.1
79	Q3	22	LEU	2.1
9	s7	4	PRO	2.1
9	s7	100	PRO	2.1
11	S9	136	VAL	2.1
15	C3	33	VAL	2.1
21	C9	104	VAL	2.1
28	d6	60	PRO	2.1
29	d7	66	PRO	2.1
30	d8	48	VAL	2.1
32	e0	14	VAL	2.1
34	SR	56	VAL	2.1
58	n2	66	VAL	2.1
73	O7	6	PRO	2.1
85	f	52	HIS	2.1
19	C7	35	CYS	2.1
21	C9	126	GLU	2.1
24	d2	51	GLU	2.1
60	n4	99	GLU	2.1
6	S4	6	LYS	2.0
11	S9	174	ARG	2.0
6	s4	162	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
13	C1	151	LYS	2.0
16	C4	68	ALA	2.0
17	c5	9	LYS	2.0
34	SR	102	ARG	2.0
39	L2	225	ILE	2.0
61	n5	142	ILE	2.0
66	O0	45	ALA	2.0
70	o4	50	ALA	2.0
73	o7	10	LYS	2.0
85	f	151	LYS	2.0
1	6	1337	A	2.0
1	6	729	G	2.0
5	s3	95	GLY	2.0
64	N8	108	GLY	2.0
35	sM	65	THR	2.0
58	N2	33	TYR	2.0
70	o4	62	TYR	2.0
18	c6	60	PHE	2.0
40	L3	298	PHE	2.0
52	m6	71	PHE	2.0
34	sR	248	ASN	2.0
8	S6	76	LEU	2.0
10	s8	121	LEU	2.0
11	S9	60	LEU	2.0
14	C2	41	LEU	2.0
21	C9	28	LEU	2.0
34	SR	42	LEU	2.0
41	l4	11	LEU	2.0
48	m1	12	LEU	2.0
34	SR	121	MET	2.0
9	S7	132	PRO	2.0
18	C6	78	VAL	2.0
24	d2	62	VAL	2.0
26	D4	30	PRO	2.0
47	m0	79	VAL	2.0
61	N5	26	VAL	2.0
27	D5	82	HIS	2.0
36	5	2098	C	2.0
68	o2	13	HIS	2.0
2	S0	135	GLU	2.0
10	s8	199	LYS	2.0
13	C1	136	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
21	c9	103	LYS	2.0
30	d8	61	ARG	2.0
31	d9	4	GLU	2.0
40	l3	262	TRP	2.0
42	l5	257	GLU	2.0
44	l7	98	LYS	2.0
61	n5	25	LYS	2.0
70	O4	16	ARG	2.0
85	f	56	LYS	2.0
6	S4	33	ALA	2.0
9	s7	49	ILE	2.0
31	D9	50	ILE	2.0
42	L5	291	ALA	2.0
42	l5	78	ALA	2.0
45	L8	218	ILE	2.0
74	O8	5	ILE	2.0
6	S4	203	GLY	2.0
8	S6	55	GLY	2.0
10	S8	118	GLY	2.0
15	c3	59	GLY	2.0
70	o4	78	GLY	2.0
8	S6	170	THR	2.0
11	s9	8	TYR	2.0
22	d0	29	THR	2.0
61	n5	123	TYR	2.0
9	S7	24	PHE	2.0
11	s9	110	GLN	2.0
21	c9	14	PHE	2.0
21	c9	54	PHE	2.0
41	L4	90	PHE	2.0
16	c4	22	SER	2.0
34	SR	81	LEU	2.0
34	sR	82	SER	2.0
36	1	48	A	2.0
36	5	2256	A	2.0
54	m8	7	SER	2.0
28	d6	8	ASN	2.0
59	n3	28	ASN	2.0
1	6	540	G	2.0
5	s3	138	VAL	2.0
5	s3	222	VAL	2.0
17	C5	126	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
18	c6	19	VAL	2.0
21	C9	35	ASP	2.0
21	c9	9	VAL	2.0
24	D2	25	VAL	2.0
34	SR	217	ASP	2.0
36	1	363	G	2.0
46	l9	12	VAL	2.0
16	c4	57	PRO	2.0
5	S3	200	LYS	2.0
11	S9	10	LYS	2.0
18	C6	26	LYS	2.0
19	c7	3	ARG	2.0
20	C8	139	LYS	2.0
28	D6	80	HIS	2.0
60	n4	43	ARG	2.0
68	o2	54	LYS	2.0
70	o4	19	LYS	2.0
71	O5	105	ARG	2.0
1	2	909	U	2.0
2	S0	20	ALA	2.0
9	s7	185	ILE	2.0
14	c2	69	ALA	2.0
34	SR	123	ILE	2.0
35	SM	66	ALA	2.0
36	5	2875	U	2.0
39	l2	129	ALA	2.0
41	l4	72	ALA	2.0
47	M0	33	ILE	2.0
47	M0	186	GLU	2.0
49	m3	38	ALA	2.0
51	m5	39	ALA	2.0
57	n1	121	ALA	2.0
74	O8	18	ALA	2.0
17	c5	129	GLY	2.0
19	C7	2	GLY	2.0
36	1	877	C	2.0
54	M8	183	GLY	2.0
60	N4	62	GLY	2.0
62	N6	92	GLY	2.0
73	O7	4	GLY	2.0
82	p0	3	GLY	2.0

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

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

5.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
86	ZN	d7	101	1/1	0.77	0.21	134,134,134,134	0
86	ZN	D7	101	1/1	0.91	0.14	140,140,140,140	0
86	ZN	e1	501	1/1	0.93	0.12	165,165,165,165	0
86	ZN	E1	501	1/1	0.95	0.08	133,133,133,133	0
86	ZN	Q2	501	1/1	0.96	0.14	78,78,78,78	0
86	ZN	D6	500	1/1	0.97	0.09	99,99,99,99	0
86	ZN	q2	501	1/1	0.97	0.12	74,74,74,74	0
86	ZN	d6	500	1/1	0.98	0.05	82,82,82,82	0
86	ZN	D9	101	1/1	0.98	0.03	89,89,89,89	0
86	ZN	d9	101	1/1	0.99	0.03	93,93,93,93	0
86	ZN	Q0	500	1/1	0.99	0.04	57,57,57,57	0
86	ZN	q0	500	1/1	0.99	0.03	48,48,48,48	0
86	ZN	Q3	501	1/1	0.99	0.03	74,74,74,74	0
86	ZN	q3	501	1/1	0.99	0.06	64,64,64,64	0
86	ZN	o7	501	1/1	1.00	0.02	53,53,53,53	0
86	ZN	O7	100	1/1	1.00	0.01	53,53,53,53	0

5.5 Other polymers [i](#)

There are no such residues in this entry.