



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 03:07 PM UTC

PDB ID : 1Y1Y / pdb_00001y1y
Title : RNA Polymerase II-TFIIS-DNA/RNA complex
Authors : Cramer, P.; Kettenberger, H.; Armache, K.-J.
Deposited on : 2004-11-19
Resolution : 4.00 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
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)	:	2.49

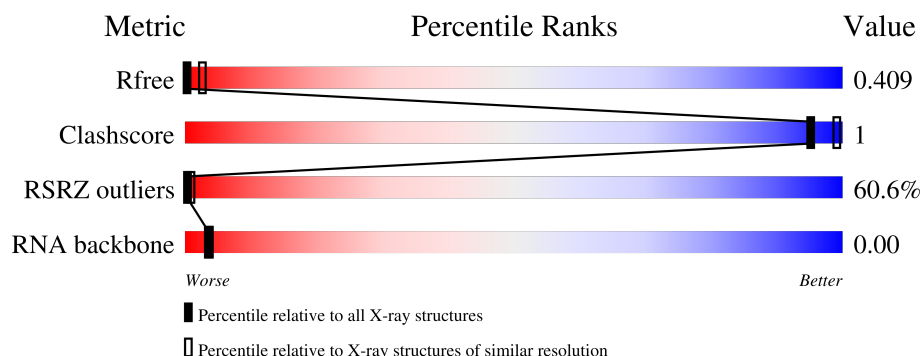
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 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}	180053	1082 (4.20-3.80)
Clashscore	190562	1129 (4.20-3.80)
RSRZ outliers	180081	1082 (4.20-3.80)
RNA backbone	3983	1017 (4.84-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	T	7	100% 100%
2	P	4	75% 100%
3	A	1733	54% 82% 18%
4	B	1224	55% 91% 9%
5	C	318	55% 84% 16%
6	D	221	44% 80% 20%

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Mol	Chain	Length	Quality of chain
7	E	215	
8	F	155	
9	G	171	
10	H	146	
11	I	122	
12	J	70	
13	K	120	
14	L	70	
15	S	179	

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 4112 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 DNA chain called 5'-D(P*TP*AP*CP*GP*CP*CP*T)-3'.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	T	7	Total P 7 7	0	0	7

- Molecule 2 is a RNA chain called 5'-R(P*AP*GP*GP*C)-3'.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	P	4	Total P 4 4	0	0	4

- Molecule 3 is a protein called DNA-directed RNA polymerase II largest subunit.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	A	1426	Total C 1426 1426	0	0	1426

- Molecule 4 is a protein called DNA-directed RNA polymerase II 140 kDa polypeptide.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	B	1112	Total C 1112 1112	8	0	1112

- Molecule 5 is a protein called DNA-directed RNA polymerase II 45 kDa polypeptide.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
5	C	266	Total C 266 266	0	0	266

- Molecule 6 is a protein called DNA-directed RNA polymerase II 32 kDa polypeptide.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
6	D	177	Total C 177 177	0	0	177

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
7	E	214	Total	C	0	0	214
			214	214			

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
8	F	84	Total	C	0	0	84
			84	84			

- Molecule 9 is a protein called DNA-directed RNA polymerase II 19 kDa polypeptide.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
9	G	171	Total	C	0	0	171
			171	171			

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
10	H	133	Total	C	0	0	133
			133	133			

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit 9.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
11	I	119	Total	C	0	0	119
			119	119			

- Molecule 12 is a protein called DNA-directed RNA polymerases I/II/III subunit 10.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
12	J	65	Total	C	0	0	65
			65	65			

- Molecule 13 is a protein called DNA-directed RNA polymerase II 13.6 kDa polypeptide.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
13	K	114	Total	C	0	0	114
			114	114			

- Molecule 14 is a protein called DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
14	L	46	Total	C	0	0	46
			46	46			

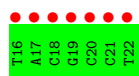
- Molecule 15 is a protein called Transcription elongation factor S-II.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
15	S	174	Total	C	0	0	174
			174	174			

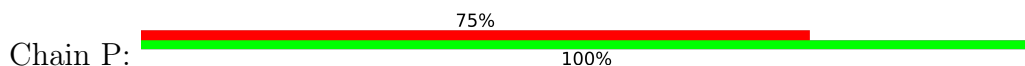
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

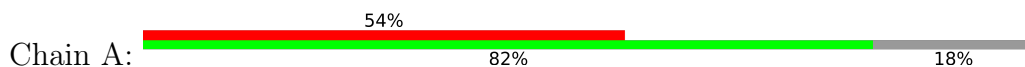
- Molecule 1: 5'-D(P*TP*AP*CP*GP*CP*CP*T)-3'



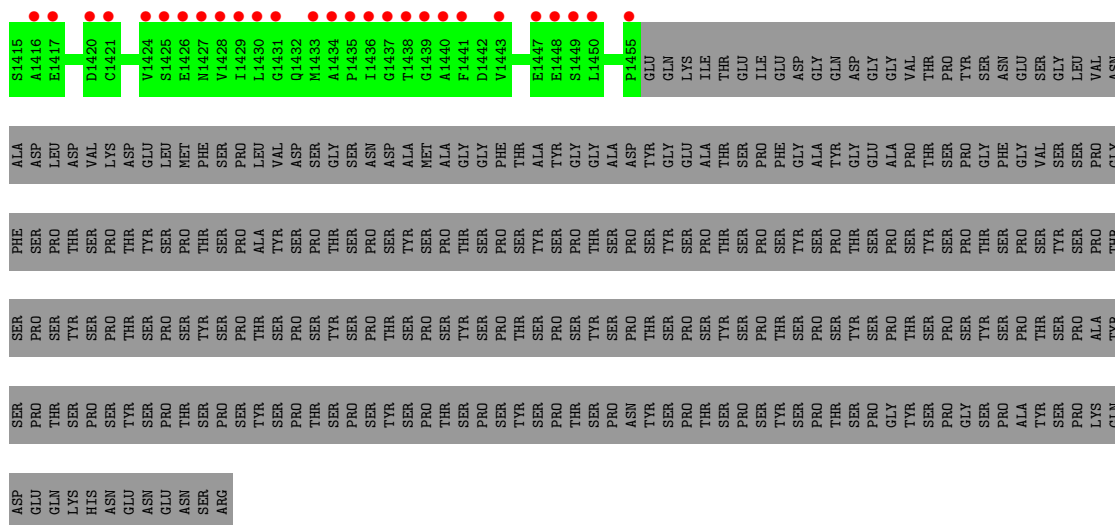
- Molecule 2: 5'-R(P*AP*GP*GP*C)-3'



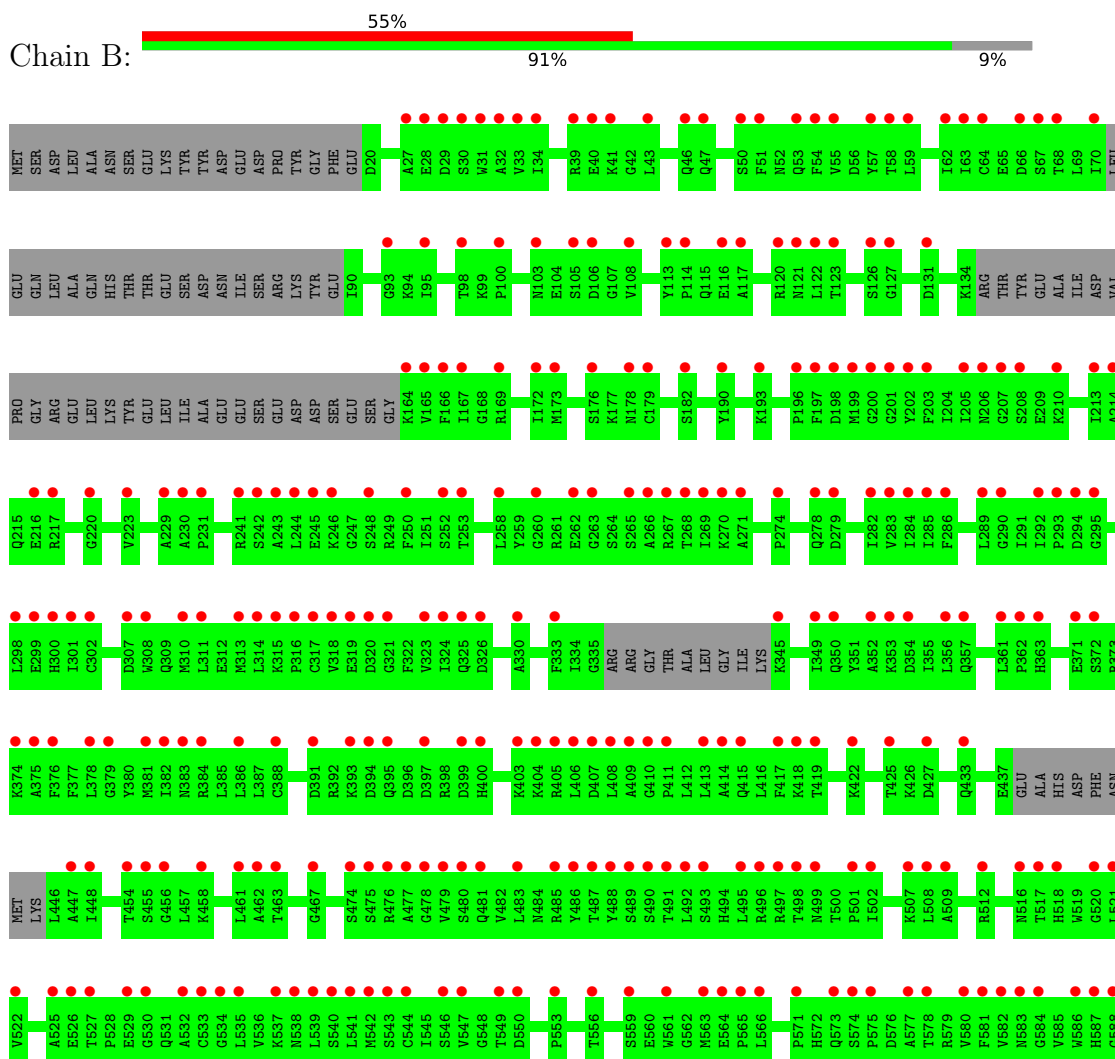
- Molecule 3: DNA-directed RNA polymerase II largest subunit

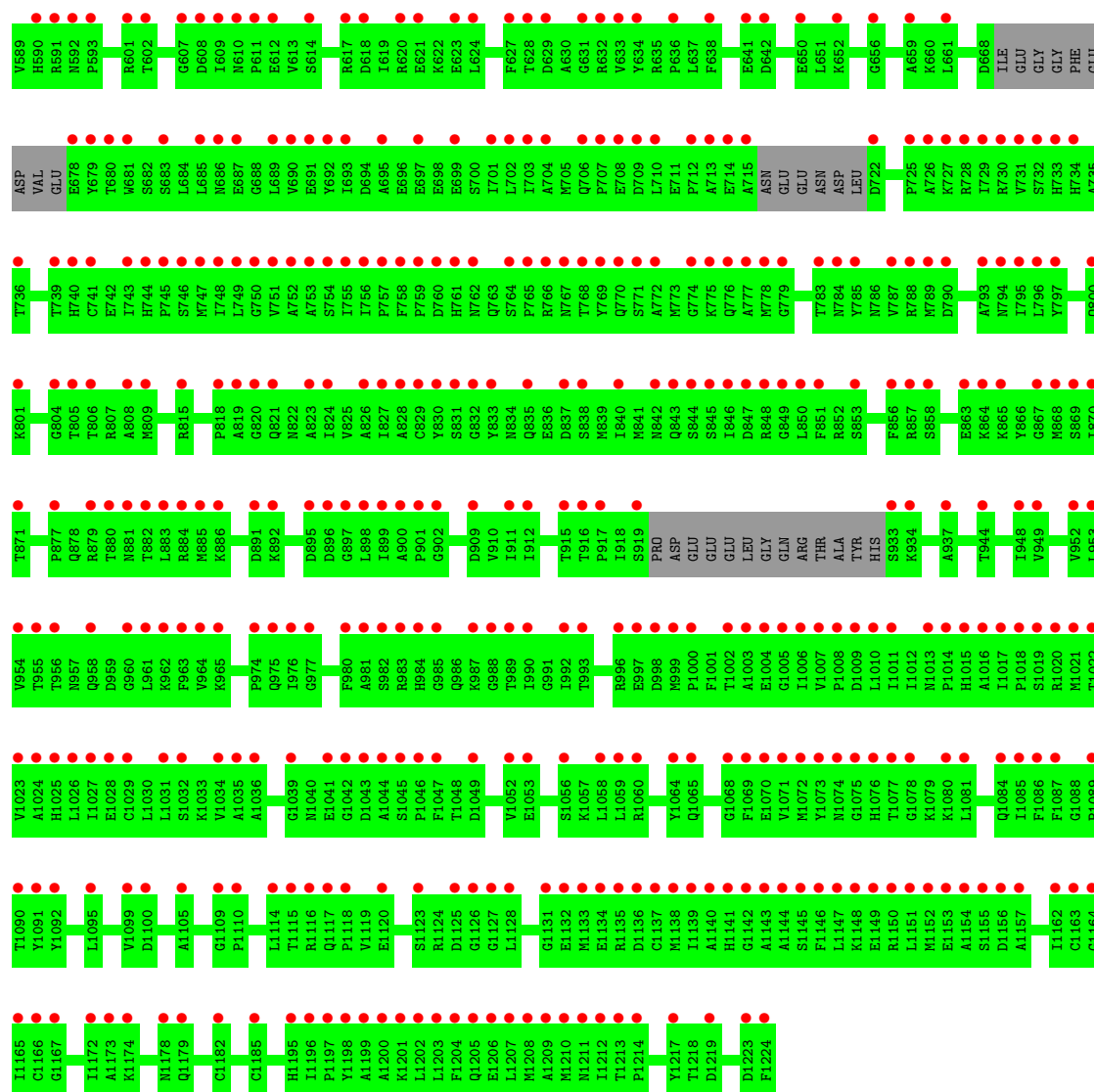




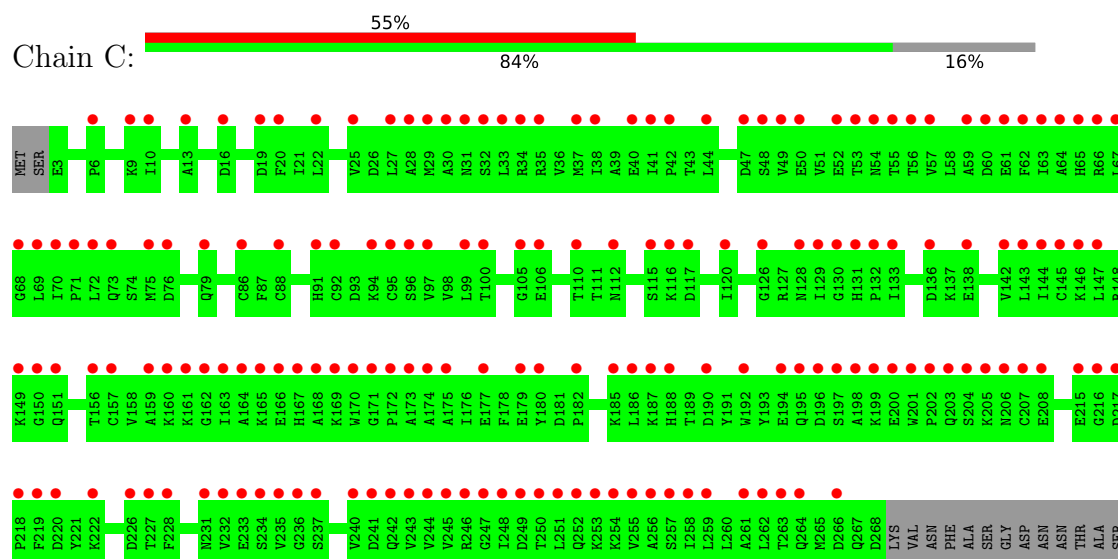


- Molecule 4: DNA-directed RNA polymerase II 140 kDa polypeptide

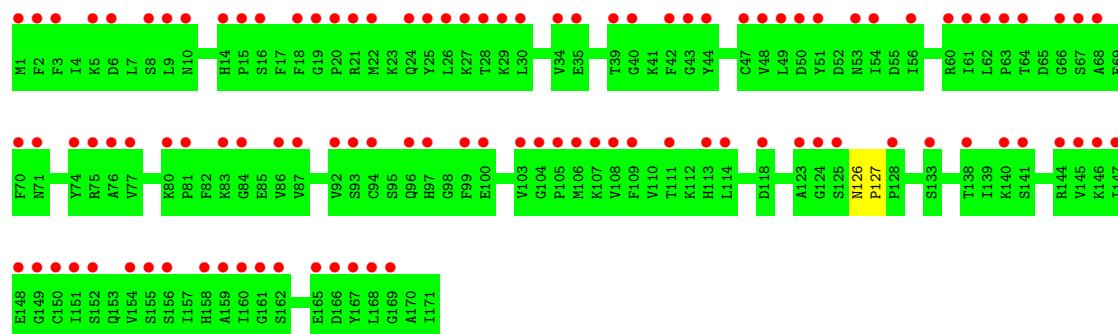




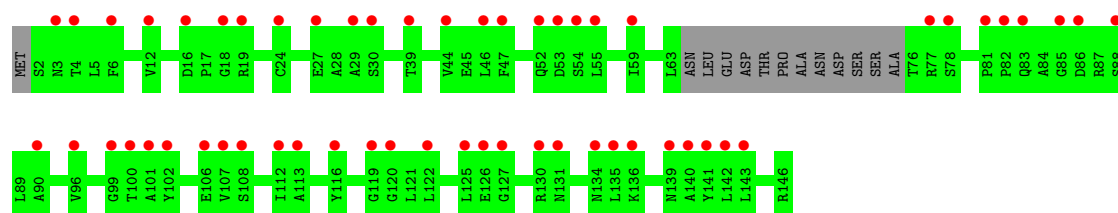
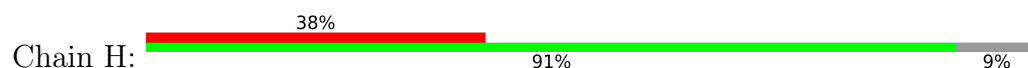
- Molecule 5: DNA-directed RNA polymerase II 45 kDa polypeptide



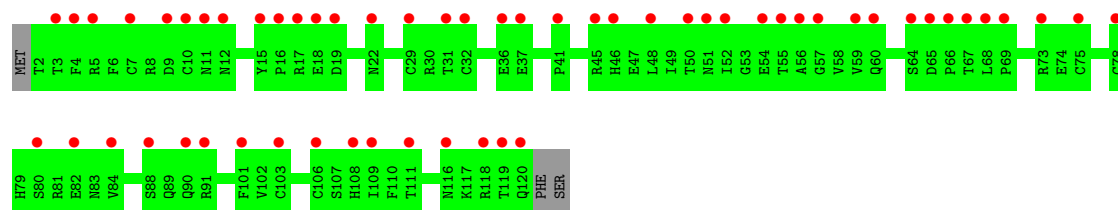
Chain G: 62% 99%



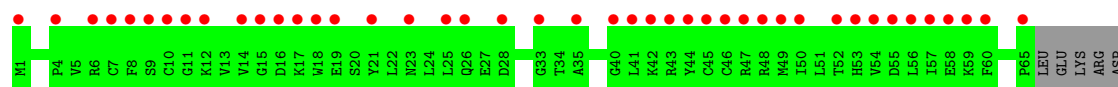
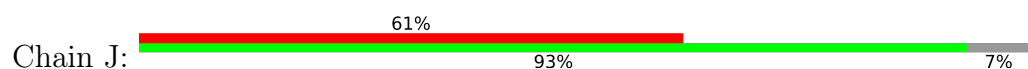
- Molecule 10: DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide



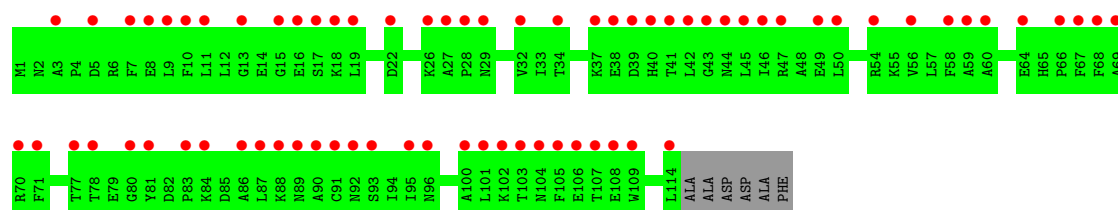
- Molecule 11: DNA-directed RNA polymerase II subunit 9



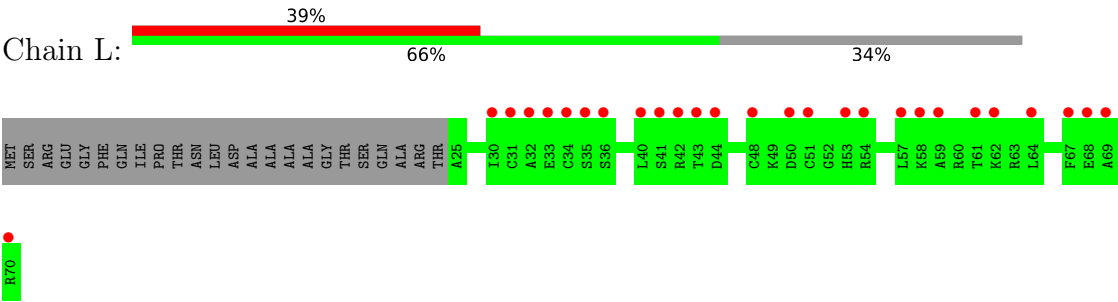
- Molecule 12: DNA-directed RNA polymerases I/II/III subunit 10



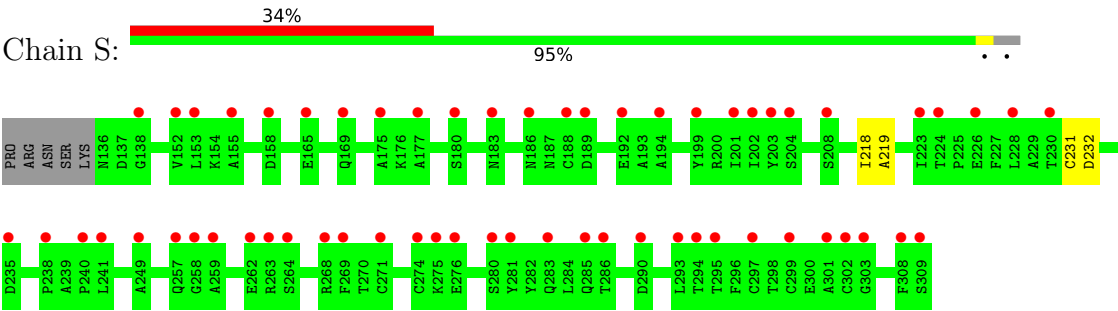
- Molecule 13: DNA-directed RNA polymerase II 13.6 kDa polypeptide



- Molecule 14: DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide



- Molecule 15: Transcription elongation factor S-II



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	220.20Å 395.70Å 282.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 4.00 50.00 – 4.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-4.00) 98.6 (50.00-4.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.11 (at 4.00Å)	Xtriage
Refinement program	unknown	Depositor
R, R_{free}	0.281 , (Not available) 0.413 , 0.409	Depositor DCC
R_{free} test set	2038 reflections (1.97%)	wwPDB-VP
Wilson B-factor (Å ²)	106.8	Xtriage
Anisotropy	0.380	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	9.76 , 298.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.004 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.015 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.68	EDS
Total number of atoms	4112	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.11% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	T	7	0	0	0	0
2	P	4	0	0	0	0
3	A	1426	0	0	1	0
4	B	1112	0	0	0	0
5	C	266	0	0	0	0
6	D	177	0	0	0	0
7	E	214	0	0	1	0
8	F	84	0	0	0	0
9	G	171	0	0	1	0
10	H	133	0	0	0	0
11	I	119	0	0	0	0
12	J	65	0	0	0	0
13	K	114	0	0	0	0
14	L	46	0	0	0	0
15	S	174	0	0	2	0
All	All	4112	0	0	5	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 1.

All (5) 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)
15:S:218:ILE:CA	15:S:219:ALA:CA	2.73	0.66
9:G:126:ASN:CA	9:G:127:PRO:CA	2.78	0.62
3:A:447:GLN:CA	3:A:448:PRO:CA	2.83	0.56
15:S:231:CYS:CA	15:S:232:ASP:CA	2.86	0.53
7:E:128:PRO:CA	7:E:129:PRO:CA	2.90	0.49

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	P	0/4	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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	T	7/7 (100%)	5.60	7 (100%) 0 0	68, 74, 104, 109	0
2	P	4/4 (100%)	3.74	3 (75%) 0 0	82, 86, 92, 95	0
3	A	1426/1733 (82%)	3.54	941 (65%) 0 1	19, 69, 145, 200	0
4	B	1104/1224 (90%)	3.28	670 (60%) 0 1	22, 82, 164, 198	0
5	C	266/318 (83%)	3.55	174 (65%) 0 1	38, 77, 136, 162	0
6	D	177/221 (80%)	2.56	97 (54%) 0 1	41, 93, 159, 174	0
7	E	214/215 (99%)	3.34	129 (60%) 0 1	39, 110, 172, 189	0
8	F	84/155 (54%)	2.77	46 (54%) 0 1	19, 53, 95, 117	0
9	G	171/171 (100%)	2.98	106 (61%) 0 1	43, 72, 110, 129	0
10	H	133/146 (91%)	2.49	56 (42%) 0 1	81, 132, 175, 192	0
11	I	119/122 (97%)	2.32	57 (47%) 0 1	64, 125, 171, 216	0
12	J	65/70 (92%)	3.78	43 (66%) 0 1	48, 72, 126, 138	0
13	K	114/120 (95%)	3.02	72 (63%) 0 1	40, 84, 137, 146	0
14	L	46/70 (65%)	2.97	27 (58%) 0 1	68, 134, 166, 187	0
15	S	174/179 (97%)	2.03	60 (34%) 1 2	50, 50, 124, 138	0
All	All	4104/4755 (86%)	3.23	2488 (60%) 0 1	19, 80, 159, 216	0

All (2488) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	E	110	PHE	42.0
3	A	1061	GLY	30.8
3	A	69	THR	29.8
3	A	1437	GLY	28.6
9	G	104	GLY	26.0
3	A	1150	SER	24.2
3	A	1455	PRO	24.1

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Mol	Chain	Res	Type	RSRZ
4	B	883	LEU	23.4
15	S	309	SER	23.0
3	A	751	SER	21.5
7	E	108	GLY	20.9
3	A	521	MET	20.8
9	G	19	GLY	20.3
4	B	882	THR	20.0
3	A	887	GLY	19.6
5	C	173	ALA	19.6
4	B	732	SER	19.3
3	A	1256	GLU	19.0
4	B	964	VAL	18.9
4	B	709	ASP	18.7
3	A	753	GLY	18.6
3	A	255	SER	18.5
3	A	1314	SER	18.3
3	A	1156	PRO	18.3
10	H	119	GLY	18.2
3	A	763	ALA	18.1
5	C	218	PRO	17.9
3	A	665	GLY	17.8
3	A	661	GLY	17.4
5	C	130	GLY	17.3
3	A	2	VAL	17.1
4	B	898	LEU	16.8
4	B	269	ILE	16.7
13	K	58	PHE	16.6
3	A	1275	GLY	16.5
15	S	308	PHE	16.4
5	C	169	LYS	16.0
3	A	486	GLU	16.0
3	A	1380	GLY	15.8
6	D	9	GLN	15.7
3	A	1091	SER	15.6
4	B	729	ILE	15.6
4	B	774	GLY	15.5
3	A	228	PHE	15.4
4	B	1087	PHE	15.3
3	A	1438	THR	15.3
3	A	875	ALA	15.1
12	J	12	LYS	15.1
6	D	8	PHE	15.0

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Mol	Chain	Res	Type	RSRZ
3	A	1126	ALA	15.0
4	B	1142	GLY	15.0
5	C	174	ALA	14.8
7	E	76	GLY	14.8
10	H	142	LEU	14.7
10	H	141	TYR	14.7
3	A	852	TYR	14.5
9	G	43	GLY	14.4
4	B	731	VAL	14.4
4	B	475	SER	14.4
7	E	109	ILE	14.3
12	J	40	GLY	14.2
7	E	200	ARG	14.1
3	A	1395	GLY	14.1
13	K	80	GLY	14.0
15	S	175	ALA	13.9
4	B	1070	GLU	13.9
3	A	776	ALA	13.8
3	A	1218	GLN	13.8
9	G	20	PRO	13.5
4	B	474	SER	13.5
3	A	1014	ALA	13.5
6	D	31	GLN	13.5
5	C	179	GLU	13.4
4	B	1041	GLU	13.3
4	B	975	GLN	13.3
3	A	484	GLY	13.2
4	B	253	THR	13.2
9	G	145	VAL	13.2
3	A	667	GLY	13.1
4	B	933	SER	13.1
5	C	159	ALA	13.0
3	A	802	ASN	12.9
7	E	79	TRP	12.9
3	A	740	LEU	12.9
4	B	965	LYS	12.8
4	B	954	VAL	12.7
10	H	83	GLN	12.7
3	A	1258	HIS	12.6
15	S	297	CYS	12.6
4	B	372	SER	12.5
5	C	195	GLN	12.4

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Mol	Chain	Res	Type	RSRZ
8	F	155	LEU	12.4
3	A	371	ALA	12.4
3	A	167	CYS	12.2
7	E	203	GLU	12.2
4	B	997	GLU	12.2
4	B	283	VAL	12.2
7	E	112	TYR	12.1
3	A	1243	VAL	12.1
3	A	132	LYS	12.1
7	E	111	VAL	12.1
4	B	1143	ALA	12.0
5	C	22	LEU	11.9
5	C	200	GLU	11.8
4	B	220	GLY	11.7
3	A	496	GLU	11.7
4	B	728	ARG	11.6
10	H	120	GLY	11.6
5	C	162	GLY	11.6
8	F	95	GLY	11.6
5	C	233	GLU	11.6
4	B	252	SER	11.5
5	C	180	TYR	11.5
3	A	1153	TYR	11.5
3	A	594	GLY	11.5
4	B	733	HIS	11.4
3	A	351	THR	11.4
3	A	180	LYS	11.4
3	A	832	ALA	11.4
3	A	489	LEU	11.4
3	A	597	LEU	11.4
7	E	15	ALA	11.3
5	C	232	VAL	11.3
4	B	1140	ALA	11.1
4	B	245	GLU	11.1
4	B	214	ALA	11.0
3	A	355	GLY	11.0
4	B	379	GLY	11.0
3	A	749	ALA	11.0
4	B	1005	GLY	11.0
5	C	172	PRO	10.9
4	B	476	ARG	10.9
3	A	79	GLY	10.9

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Mol	Chain	Res	Type	RSRZ
4	B	831	SER	10.9
3	A	1396	ALA	10.8
14	L	54	ARG	10.8
3	A	1276	VAL	10.7
3	A	93	VAL	10.6
5	C	163	ILE	10.6
4	B	746	SER	10.6
4	B	1173	ALA	10.6
4	B	462	ALA	10.6
3	A	318	SER	10.5
3	A	1154	TYR	10.5
4	B	767	ASN	10.4
4	B	378	LEU	10.3
4	B	532	ALA	10.3
5	C	205	LYS	10.3
15	S	281	TYR	10.3
4	B	952	VAL	10.3
14	L	57	LEU	10.2
13	K	17	SER	10.2
3	A	364	VAL	10.2
5	C	201	TRP	10.2
3	A	254	GLU	10.1
11	I	51	ASN	10.1
3	A	1434	ALA	10.1
9	G	66	GLY	10.1
4	B	1042	GLY	10.0
3	A	1137	ALA	10.0
3	A	1271	ILE	10.0
3	A	628	GLY	10.0
4	B	1009	ASP	10.0
12	J	43	ARG	10.0
9	G	152	SER	10.0
7	E	66	GLU	10.0
11	I	56	ALA	9.9
3	A	589	GLN	9.9
5	C	117	ASP	9.8
4	B	708	GLU	9.8
3	A	87	ALA	9.8
3	A	1199	ARG	9.7
4	B	587	HIS	9.7
3	A	598	LEU	9.6
4	B	987	LYS	9.6

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Mol	Chain	Res	Type	RSRZ
12	J	46	CYS	9.6
4	B	478	GLY	9.6
3	A	240	PRO	9.6
4	B	985	GLY	9.5
5	C	241	ASP	9.5
3	A	445	ASN	9.5
3	A	886	ILE	9.5
4	B	529	GLU	9.5
4	B	734	HIS	9.4
4	B	330	ALA	9.4
3	A	452	LYS	9.4
4	B	692	TYR	9.3
3	A	793	SER	9.3
3	A	462	VAL	9.2
5	C	40	GLU	9.2
3	A	323	LYS	9.2
3	A	581	ALA	9.1
3	A	733	ALA	9.1
4	B	730	ARG	9.1
4	B	509	ALA	9.1
3	A	477	PRO	9.1
3	A	648	ASN	9.1
4	B	199	MET	9.1
3	A	787	PHE	9.1
12	J	50	ILE	9.1
3	A	354	SER	9.0
15	S	258	GLY	9.0
12	J	26	GLN	9.0
3	A	754	SER	9.0
3	A	1012	ARG	9.0
4	B	1154	ALA	8.9
3	A	498	ARG	8.9
4	B	1011	ILE	8.9
6	D	192	LYS	8.9
3	A	365	GLY	8.9
4	B	702	LEU	8.9
3	A	885	THR	8.9
4	B	1072	MET	8.9
3	A	649	ILE	8.8
15	S	138	GLY	8.8
14	L	64	LEU	8.7
3	A	84	ILE	8.7

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Mol	Chain	Res	Type	RSRZ
12	J	10	CYS	8.7
5	C	177	GLU	8.7
3	A	1069	ALA	8.7
3	A	1210	GLY	8.6
3	A	456	MET	8.6
4	B	609	ILE	8.6
3	A	997	LEU	8.6
4	B	1206	GLU	8.6
4	B	937	ALA	8.6
3	A	239	LEU	8.6
15	S	283	GLN	8.5
3	A	921	GLY	8.5
1	T	20	DC	8.5
4	B	722	ASP	8.5
3	A	1198	ASP	8.5
4	B	477	ALA	8.4
7	E	74	ASP	8.4
9	G	169	GLY	8.4
13	K	59	ALA	8.3
8	F	117	PRO	8.3
4	B	507	LYS	8.3
3	A	952	ALA	8.3
3	A	1223	ASP	8.3
4	B	693	ILE	8.2
6	D	15	LEU	8.2
3	A	871	ASP	8.2
3	A	143	LYS	8.2
11	I	29	CYS	8.2
4	B	202	TYR	8.2
15	S	223	ILE	8.2
4	B	762	ASN	8.2
3	A	38	PRO	8.2
12	J	45	CYS	8.1
3	A	975	HIS	8.1
9	G	118	ASP	8.1
4	B	518	HIS	8.1
3	A	165	GLY	8.1
6	D	5	THR	8.0
3	A	353	ILE	8.0
7	E	176	PRO	8.0
4	B	867	GLY	8.0
4	B	864	LYS	8.0

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Mol	Chain	Res	Type	RSRZ
4	B	823	ALA	8.0
3	A	3	GLY	8.0
3	A	499	ALA	7.9
3	A	251	SER	7.9
3	A	876	ALA	7.9
4	B	753	ALA	7.9
4	B	250	PHE	7.9
4	B	393	LYS	7.9
4	B	612	GLU	7.9
10	H	29	ALA	7.9
4	B	495	LEU	7.9
5	C	216	GLY	7.9
15	S	199	TYR	7.8
7	E	61	GLN	7.8
3	A	1259	MET	7.8
3	A	488	ASN	7.7
3	A	1424	VAL	7.7
3	A	574	GLY	7.7
4	B	1080	LYS	7.7
3	A	363	GLN	7.7
4	B	295	GLY	7.7
3	A	1440	ALA	7.6
4	B	842	ASN	7.6
15	S	155	ALA	7.6
4	B	750	GLY	7.6
4	B	804	GLY	7.6
4	B	1039	GLY	7.6
15	S	165	GLU	7.6
3	A	851	HIS	7.5
3	A	540	PHE	7.5
3	A	508	PRO	7.5
6	D	16	LYS	7.5
12	J	42	LYS	7.5
10	H	140	ALA	7.5
3	A	487	MET	7.5
9	G	146	LYS	7.5
4	B	766	ARG	7.4
4	B	578	THR	7.4
3	A	872	GLY	7.4
4	B	902	GLY	7.4
4	B	541	LEU	7.4
4	B	697	GLU	7.4

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Mol	Chain	Res	Type	RSRZ
3	A	1093	LYS	7.4
4	B	828	ALA	7.4
3	A	1062	GLU	7.4
3	A	166	GLY	7.4
13	K	83	PRO	7.4
5	C	9	LYS	7.4
3	A	471	ASN	7.3
8	F	131	PRO	7.3
3	A	769	SER	7.3
3	A	824	LEU	7.3
3	A	1192	LEU	7.3
11	I	15	TYR	7.3
7	E	172	GLU	7.3
3	A	197	PRO	7.3
4	B	844	SER	7.3
13	K	11	LEU	7.2
15	S	194	ALA	7.2
3	A	435	HIS	7.2
1	T	19	DG	7.2
4	B	27	ALA	7.2
3	A	111	GLY	7.2
4	B	70	ILE	7.2
3	A	168	GLY	7.1
3	A	816	HIS	7.1
4	B	868	MET	7.1
7	E	16	PHE	7.1
3	A	1426	GLU	7.1
7	E	134	THR	7.1
8	F	144	GLU	7.1
10	H	96	VAL	7.1
3	A	654	ASN	7.1
4	B	113	TYR	7.1
5	C	206	ASN	7.1
4	B	520	GLY	7.1
4	B	808	ALA	7.1
4	B	263	GLY	7.0
2	P	9	G	7.0
3	A	658	LEU	7.0
3	A	59	GLY	7.0
3	A	181	LEU	7.0
12	J	9	SER	7.0
3	A	729	ALA	7.0

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Mol	Chain	Res	Type	RSRZ
3	A	1369	ALA	7.0
4	B	901	PRO	7.0
15	S	264	SER	7.0
13	K	69	ALA	7.0
4	B	530	GLY	7.0
3	A	1041	ALA	6.9
12	J	21	TYR	6.9
4	B	223	VAL	6.9
4	B	300	HIS	6.9
3	A	842	VAL	6.9
3	A	1401	SER	6.9
13	K	18	LYS	6.9
3	A	1214	GLU	6.9
3	A	621	THR	6.9
3	A	827	THR	6.9
3	A	1267	MET	6.9
12	J	1	MET	6.9
11	I	116	ASN	6.9
4	B	549	THR	6.9
4	B	849	GLY	6.8
4	B	1068	GLY	6.8
4	B	1209	ALA	6.8
4	B	1074	ASN	6.8
5	C	96	SER	6.8
3	A	1427	ASN	6.8
4	B	117	ALA	6.8
4	B	205	ILE	6.8
11	I	52	ILE	6.8
4	B	707	PRO	6.8
3	A	94	GLY	6.7
9	G	149	GLY	6.7
4	B	1145	SER	6.7
3	A	37	PHE	6.7
3	A	1368	MET	6.7
3	A	97	ALA	6.7
3	A	117	GLU	6.7
4	B	127	GLY	6.7
4	B	29	ASP	6.7
4	B	607	GLY	6.7
5	C	68	GLY	6.6
5	C	235	VAL	6.6
3	A	683	ILE	6.6

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Mol	Chain	Res	Type	RSRZ
8	F	134	ILE	6.6
12	J	7	CYS	6.6
10	H	78	SER	6.6
4	B	1090	THR	6.6
5	C	219	PHE	6.6
4	B	826	ALA	6.6
12	J	48	ARG	6.6
4	B	1010	LEU	6.6
3	A	470	LEU	6.5
1	T	18	DC	6.5
3	A	110	CYS	6.5
5	C	65	HIS	6.5
14	L	31	CYS	6.5
4	B	397	ASP	6.5
3	A	517	ASN	6.5
7	E	211	TYR	6.5
3	A	788	SER	6.5
4	B	164	LYS	6.5
4	B	865	LYS	6.5
3	A	618	GLU	6.5
4	B	610	ASN	6.5
10	H	85	GLY	6.5
3	A	1306	LEU	6.5
4	B	838	SER	6.5
8	F	135	ARG	6.5
3	A	766	GLY	6.5
3	A	888	GLY	6.5
4	B	704	ALA	6.5
5	C	30	ALA	6.5
3	A	1074	GLU	6.5
4	B	1219	ASP	6.4
4	B	1199	ALA	6.4
3	A	603	ASN	6.4
3	A	1378	GLN	6.4
1	T	17	DA	6.4
3	A	530	GLY	6.4
3	A	614	PHE	6.4
3	A	811	GLN	6.4
4	B	897	GLY	6.4
3	A	1149	ALA	6.4
3	A	617	VAL	6.4
4	B	787	VAL	6.4

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Mol	Chain	Res	Type	RSRZ
4	B	1213	THR	6.4
7	E	2	ASP	6.4
3	A	502	SER	6.4
3	A	808	LEU	6.4
7	E	5	ASN	6.4
3	A	1056	SER	6.4
3	A	741	ASN	6.3
5	C	56	THR	6.3
4	B	984	HIS	6.3
4	B	805	THR	6.3
3	A	15	LYS	6.3
3	A	846	GLU	6.3
4	B	714	GLU	6.3
3	A	1379	GLY	6.3
4	B	797	TYR	6.3
3	A	1067	LEU	6.3
3	A	1166	ASP	6.3
3	A	422	GLY	6.3
4	B	577	ALA	6.3
8	F	98	ALA	6.3
5	C	29	MET	6.3
3	A	1092	LYS	6.2
9	G	141	SER	6.2
10	H	127	GLY	6.2
3	A	1123	GLY	6.2
6	D	177	VAL	6.2
3	A	874	ASP	6.2
3	A	1066	VAL	6.2
4	B	282	ILE	6.2
8	F	145	ASP	6.2
11	I	59	VAL	6.2
4	B	759	PRO	6.1
5	C	220	ASP	6.1
3	A	511	ILE	6.1
7	E	78	LEU	6.1
4	B	1078	GLY	6.1
4	B	375	ALA	6.1
13	K	29	ASN	6.1
3	A	817	ALA	6.1
3	A	476	SER	6.1
3	A	286	HIS	6.1
12	J	53	HIS	6.1

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Mol	Chain	Res	Type	RSRZ
10	H	18	GLY	6.1
3	A	548	ASN	6.1
11	I	11	ASN	6.1
3	A	1201	ALA	6.0
4	B	820	GLY	6.0
3	A	765	VAL	6.0
15	S	280	SER	6.0
4	B	290	GLY	6.0
3	A	1102	LYS	6.0
4	B	691	GLU	6.0
4	B	243	ALA	6.0
4	B	486	TYR	6.0
13	K	91	CYS	6.0
3	A	44	THR	6.0
4	B	620	ARG	6.0
6	D	75	LYS	6.0
3	A	1381	LEU	6.0
4	B	67	SER	6.0
3	A	758	ILE	6.0
6	D	59	ILE	6.0
5	C	236	GLY	6.0
5	C	243	VAL	5.9
3	A	815	PHE	5.9
5	C	247	GLY	5.9
4	B	479	VAL	5.9
3	A	809	THR	5.9
6	D	10	THR	5.9
3	A	12	ARG	5.9
3	A	500	GLU	5.9
3	A	1313	LEU	5.9
3	A	1257	ASP	5.9
4	B	294	ASP	5.9
3	A	436	ILE	5.9
3	A	572	TRP	5.9
3	A	838	GLN	5.9
4	B	114	PRO	5.8
11	I	9	ASP	5.8
5	C	231	ASN	5.8
4	B	265	SER	5.8
4	B	1118	PRO	5.8
11	I	10	CYS	5.8
4	B	944	THR	5.8

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Mol	Chain	Res	Type	RSRZ
14	L	50	ASP	5.8
3	A	1346	ALA	5.8
5	C	149	LYS	5.8
4	B	526	GLU	5.8
8	F	101	ILE	5.8
4	B	307	ASP	5.8
4	B	1156	ASP	5.8
3	A	441	PRO	5.8
3	A	473	SER	5.8
3	A	380	VAL	5.7
3	A	529	CYS	5.7
3	A	1222	ASN	5.7
5	C	167	HIS	5.7
3	A	627	GLY	5.7
4	B	319	GLU	5.7
4	B	981	ALA	5.7
4	B	1013	ASN	5.7
3	A	1443	VAL	5.7
3	A	303	TYR	5.7
4	B	491	THR	5.7
3	A	835	GLY	5.7
3	A	542	GLU	5.6
4	B	1185	CYS	5.6
3	A	459	ARG	5.6
4	B	1205	GLN	5.6
4	B	1136	ASP	5.6
10	H	136	LYS	5.6
4	B	1210	MET	5.6
5	C	31	ASN	5.6
4	B	203	PHE	5.6
4	B	628	THR	5.6
3	A	148	CYS	5.6
7	E	138	ALA	5.6
4	B	768	THR	5.6
4	B	956	THR	5.6
3	A	1068	ALA	5.6
13	K	50	LEU	5.6
3	A	730	GLY	5.6
3	A	772	GLY	5.6
5	C	64	ALA	5.6
14	L	59	ALA	5.6
3	A	983	ILE	5.6

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Mol	Chain	Res	Type	RSRZ
3	A	579	SER	5.6
4	B	588	GLY	5.6
3	A	104	GLU	5.6
3	A	421	ALA	5.5
3	A	429	GLY	5.5
13	K	3	ALA	5.5
3	A	859	SER	5.5
4	B	827	ILE	5.5
3	A	1221	LYS	5.5
4	B	317	CYS	5.5
4	B	1144	ALA	5.5
3	A	1428	VAL	5.5
4	B	772	ALA	5.5
7	E	30	ILE	5.5
14	L	30	ILE	5.5
5	C	49	VAL	5.5
5	C	126	GLY	5.5
4	B	1004	GLU	5.5
9	G	40	GLY	5.5
4	B	543	SER	5.5
3	A	1439	GLY	5.5
5	C	168	ALA	5.5
15	S	303	GLY	5.5
3	A	26	GLU	5.5
4	B	410	GLY	5.4
4	B	829	CYS	5.4
3	A	722	LEU	5.4
4	B	961	LEU	5.4
4	B	988	GLY	5.4
3	A	757	ASN	5.4
4	B	703	ILE	5.4
4	B	1195	HIS	5.4
3	A	869	GLY	5.4
3	A	1108	ALA	5.4
6	D	53	SER	5.4
4	B	458	LYS	5.4
5	C	150	GLY	5.4
7	E	89	GLY	5.4
6	D	143	ASN	5.4
5	C	61	GLU	5.4
3	A	976	THR	5.4
4	B	996	ARG	5.4

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Mol	Chain	Res	Type	RSRZ
3	A	1065	GLY	5.4
4	B	765	PRO	5.4
3	A	546	VAL	5.3
3	A	543	LEU	5.3
4	B	744	HIS	5.3
3	A	1325	THR	5.3
4	B	701	ILE	5.3
9	G	162	SER	5.3
5	C	188	HIS	5.3
9	G	35	GLU	5.3
3	A	643	ALA	5.3
4	B	1022	THR	5.3
4	B	1208	MET	5.3
10	H	122	LEU	5.3
3	A	762	SER	5.3
7	E	97	VAL	5.3
3	A	1414	ALA	5.3
4	B	433	GLN	5.3
9	G	160	ILE	5.3
3	A	803	SER	5.3
4	B	30	SER	5.3
3	A	1082	ASN	5.3
11	I	119	THR	5.3
3	A	201	VAL	5.3
3	A	74	MET	5.3
4	B	399	ASP	5.3
7	E	99	HIS	5.3
4	B	1204	PHE	5.3
4	B	321	GLY	5.2
6	D	62	ALA	5.2
9	G	68	ALA	5.2
4	B	1155	SER	5.2
9	G	159	ALA	5.2
4	B	1018	PRO	5.2
4	B	845	SER	5.2
6	D	139	LYS	5.2
3	A	1384	VAL	5.2
4	B	835	GLN	5.2
3	A	453	MET	5.2
3	A	798	GLY	5.2
4	B	974	PRO	5.2
3	A	715	GLU	5.2

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Mol	Chain	Res	Type	RSRZ
5	C	255	VAL	5.2
3	A	615	GLY	5.2
7	E	121	MET	5.2
8	F	91	ALA	5.2
3	A	360	GLU	5.2
9	G	18	PHE	5.2
3	A	346	ASP	5.2
3	A	810	PRO	5.2
4	B	413	LEU	5.2
3	A	647	GLY	5.2
3	A	492	PRO	5.1
5	C	203	GLN	5.1
10	H	107	VAL	5.1
3	A	83	HIS	5.1
4	B	1137	CYS	5.1
3	A	759	ALA	5.1
4	B	448	ILE	5.1
5	C	116	LYS	5.1
3	A	134	ARG	5.1
5	C	240	VAL	5.1
8	F	93	ILE	5.1
4	B	656	GLY	5.1
3	A	121	LEU	5.1
4	B	955	THR	5.1
4	B	1002	THR	5.1
3	A	1343	ALA	5.1
5	C	92	CYS	5.1
12	J	65	PRO	5.1
3	A	526	ASP	5.1
3	A	1087	ALA	5.1
4	B	467	GLY	5.1
4	B	806	THR	5.1
11	I	57	GLY	5.1
5	C	66	ARG	5.1
4	B	1166	CYS	5.1
11	I	32	CYS	5.1
4	B	352	ALA	5.1
5	C	60	ASP	5.1
4	B	1164	GLY	5.0
4	B	425	THR	5.0
3	A	600	PRO	5.0
13	K	7	PHE	5.0

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Mol	Chain	Res	Type	RSRZ
4	B	487	THR	5.0
3	A	505	CYS	5.0
4	B	489	SER	5.0
3	A	545	GLN	5.0
7	E	17	ARG	5.0
3	A	1146	VAL	5.0
13	K	49	GLU	5.0
3	A	1076	ALA	5.0
7	E	182	ASP	5.0
5	C	202	PRO	5.0
4	B	1146	PHE	5.0
15	S	259	ALA	5.0
3	A	999	VAL	5.0
3	A	752	LYS	5.0
4	B	1207	LEU	5.0
5	C	62	PHE	4.9
7	E	62	ALA	4.9
3	A	577	ILE	4.9
3	A	883	LEU	4.9
3	A	1021	LEU	4.9
3	A	1408	ILE	4.9
3	A	1053	PHE	4.9
3	A	229	SER	4.9
3	A	348	SER	4.9
4	B	176	SER	4.9
13	K	109	TRP	4.9
4	B	726	ALA	4.9
3	A	849	MET	4.9
4	B	843	GLN	4.9
3	A	244	PRO	4.9
4	B	771	SER	4.9
3	A	671	ALA	4.9
4	B	270	LYS	4.9
4	B	535	LEU	4.9
4	B	1203	LEU	4.9
4	B	1214	PRO	4.9
3	A	1425	SER	4.9
5	C	115	SER	4.9
9	G	80	LYS	4.9
3	A	179	LEU	4.9
11	I	120	GLN	4.9
3	A	67	CYS	4.9

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Mol	Chain	Res	Type	RSRZ
3	A	1342	GLU	4.9
4	B	271	ALA	4.9
8	F	151	LEU	4.9
13	K	93	SER	4.9
5	C	252	GLN	4.9
9	G	28	THR	4.9
5	C	146	LYS	4.9
7	E	175	LEU	4.9
4	B	1163	CYS	4.8
13	K	43	GLY	4.8
4	B	983	ARG	4.8
6	D	144	THR	4.8
7	E	141	VAL	4.8
3	A	1404	GLU	4.8
15	S	192	GLU	4.8
3	A	324	SER	4.8
7	E	205	SER	4.8
9	G	1	MET	4.8
6	D	199	ASN	4.8
3	A	1213	GLY	4.8
3	A	458	HIS	4.8
3	A	940	ARG	4.8
4	B	485	ARG	4.8
4	B	617	ARG	4.8
5	C	86	CYS	4.8
3	A	1011	GLN	4.8
5	C	182	PRO	4.8
4	B	502	ILE	4.8
8	F	80	ALA	4.8
3	A	233	TRP	4.8
3	A	1345	ARG	4.8
3	A	1075	PRO	4.8
5	C	88	CYS	4.8
3	A	552	TRP	4.8
4	B	989	THR	4.8
5	C	250	THR	4.8
13	K	78	THR	4.8
4	B	1141	HIS	4.8
3	A	1260	LEU	4.8
13	K	114	LEU	4.8
3	A	1070	GLN	4.8
3	A	544	ASP	4.8

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Mol	Chain	Res	Type	RSRZ
15	S	235	ASP	4.8
4	B	1109	GLY	4.8
7	E	18	THR	4.8
3	A	1227	ILE	4.8
3	A	760	GLN	4.8
3	A	1189	SER	4.8
14	L	69	ALA	4.8
3	A	356	ASP	4.8
3	A	497	THR	4.8
3	A	1023	ARG	4.8
7	E	7	ARG	4.8
3	A	253	ASN	4.8
4	B	28	GLU	4.7
3	A	522	GLY	4.7
3	A	481	ASP	4.7
3	A	152	VAL	4.7
3	A	1141	THR	4.7
4	B	915	THR	4.7
3	A	1429	ILE	4.7
3	A	313	GLN	4.7
4	B	298	LEU	4.7
4	B	1127	GLY	4.7
3	A	782	ARG	4.7
6	D	66	ARG	4.7
4	B	580	VAL	4.7
5	C	170	TRP	4.7
6	D	163	VAL	4.7
4	B	778	MET	4.7
3	A	394	ASN	4.7
3	A	742	ASN	4.7
3	A	1370	LEU	4.7
4	B	394	ASP	4.7
3	A	147	VAL	4.7
7	E	19	VAL	4.7
7	E	6	GLU	4.7
4	B	1008	PRO	4.7
3	A	1400	CYS	4.7
3	A	1225	PHE	4.7
3	A	744	LYS	4.7
3	A	485	ASP	4.7
5	C	249	ASP	4.7
10	H	135	LEU	4.7

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Mol	Chain	Res	Type	RSRZ
3	A	301	ALA	4.7
4	B	556	THR	4.7
13	K	92	ASN	4.7
4	B	53	GLN	4.7
10	H	6	PHE	4.7
1	T	22	DT	4.7
3	A	1073	GLY	4.6
3	A	1026	LEU	4.6
4	B	1081	LEU	4.6
3	A	1030	ARG	4.6
3	A	947	PHE	4.6
7	E	45	LYS	4.6
3	A	1103	GLU	4.6
3	A	881	GLN	4.6
3	A	1188	GLN	4.6
3	A	32	VAL	4.6
3	A	513	SER	4.6
3	A	1024	SER	4.6
12	J	52	THR	4.6
3	A	169	ASN	4.6
3	A	384	ASN	4.6
3	A	335	ARG	4.6
6	D	56	ARG	4.6
3	A	686	ALA	4.6
3	A	652	VAL	4.6
12	J	49	MET	4.6
3	A	1348	LEU	4.6
9	G	113	HIS	4.6
4	B	1223	ASP	4.6
3	A	1212	VAL	4.6
5	C	91	HIS	4.6
5	C	204	SER	4.6
9	G	21	ARG	4.6
3	A	736	ASN	4.6
4	B	725	PRO	4.6
3	A	475	THR	4.5
3	A	1094	VAL	4.5
7	E	50	MET	4.5
3	A	218	ASP	4.5
3	A	642	CYS	4.5
4	B	1114	LEU	4.5
4	B	586	TRP	4.5

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Mol	Chain	Res	Type	RSRZ
3	A	27	VAL	4.5
4	B	492	LEU	4.5
4	B	1027	ILE	4.5
12	J	16	ASP	4.5
8	F	96	THR	4.5
14	L	51	CYS	4.5
6	D	61	GLU	4.5
9	G	74	TYR	4.5
4	B	638	PHE	4.5
3	A	1155	ASP	4.5
3	A	1292	PRO	4.5
13	K	107	THR	4.5
4	B	121	ASN	4.5
6	D	76	LYS	4.5
3	A	1356	ILE	4.5
9	G	148	GLU	4.5
3	A	624	SER	4.5
9	G	76	ALA	4.5
4	B	461	LEU	4.5
13	K	9	LEU	4.5
3	A	549	MET	4.5
3	A	506	ALA	4.5
3	A	336	ILE	4.5
3	A	1237	ILE	4.5
4	B	1182	CYS	4.5
9	G	70	PHE	4.5
3	A	60	SER	4.5
7	E	51	GLY	4.5
10	H	19	ARG	4.4
3	A	1129	GLU	4.4
4	B	752	ALA	4.4
11	I	75	CYS	4.4
4	B	490	SER	4.4
5	C	32	SER	4.4
3	A	299	HIS	4.4
3	A	660	ASN	4.4
11	I	22	ASN	4.4
4	B	749	LEU	4.4
4	B	1089	PRO	4.4
4	B	776	GLN	4.4
13	K	46	ILE	4.4
3	A	1273	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
4	B	43	LEU	4.4
6	D	181	GLY	4.4
12	J	17	LYS	4.4
3	A	650	GLN	4.4
4	B	1117	GLN	4.4
5	C	95	CYS	4.4
3	A	1229	SER	4.4
4	B	880	THR	4.4
4	B	1115	THR	4.4
3	A	821	ARG	4.4
4	B	960	GLY	4.4
11	I	7	CYS	4.4
13	K	8	GLU	4.4
15	S	285	GLN	4.4
3	A	369	SER	4.4
3	A	913	LEU	4.4
15	S	274	CYS	4.4
3	A	706	HIS	4.4
7	E	48	ASP	4.4
15	S	262	GLU	4.4
4	B	1091	TYR	4.3
3	A	70	CYS	4.3
3	A	747	VAL	4.3
3	A	1058	VAL	4.3
3	A	1344	GLY	4.3
4	B	584	GLY	4.3
3	A	1127	ASP	4.3
3	A	657	LEU	4.3
3	A	689	LYS	4.3
4	B	361	LEU	4.3
5	C	222	LYS	4.3
3	A	1115	SER	4.3
3	A	342	GLY	4.3
9	G	106	MET	4.3
5	C	71	PRO	4.3
7	E	129	PRO	4.3
3	A	210	ILE	4.3
3	A	713	SER	4.3
13	K	15	GLY	4.3
3	A	908	LEU	4.3
7	E	183	PRO	4.3
9	G	9	LEU	4.3

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Mol	Chain	Res	Type	RSRZ
7	E	130	ALA	4.3
3	A	344	ARG	4.3
5	C	41	ILE	4.3
3	A	334	GLY	4.3
4	B	1151	LEU	4.3
3	A	373	THR	4.3
3	A	656	TRP	4.3
4	B	793	ALA	4.3
5	C	144	ILE	4.3
7	E	44	ALA	4.3
3	A	784	LEU	4.3
3	A	843	LYS	4.3
3	A	1071	SER	4.3
13	K	66	PRO	4.3
3	A	1200	ALA	4.3
4	B	795	ILE	4.3
6	D	191	ALA	4.3
3	A	507	VAL	4.3
3	A	1410	PHE	4.3
3	A	431	LYS	4.3
4	B	801	LYS	4.3
2	P	7	A	4.3
9	G	147	ILE	4.3
4	B	33	VAL	4.3
4	B	1092	TYR	4.3
13	K	81	TYR	4.3
3	A	1016	THR	4.2
7	E	83	CYS	4.2
3	A	242	PRO	4.2
3	A	1136	SER	4.2
4	B	208	SER	4.2
5	C	44	LEU	4.2
4	B	634	TYR	4.2
6	D	37	GLN	4.2
4	B	213	ILE	4.2
4	B	1178	ASN	4.2
3	A	998	LEU	4.2
3	A	1015	VAL	4.2
6	D	4	SER	4.2
3	A	36	ARG	4.2
4	B	1197	PRO	4.2
7	E	140	LEU	4.2

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Mol	Chain	Res	Type	RSRZ
3	A	66	LYS	4.2
3	A	746	MET	4.2
3	A	814	PHE	4.2
3	A	1020	CYS	4.2
4	B	885	MET	4.2
14	L	33	GLU	4.2
8	F	99	LEU	4.2
4	B	1132	GLU	4.2
6	D	203	SER	4.2
4	B	846	ILE	4.2
4	B	333	PHE	4.2
3	A	1048	ASN	4.2
13	K	44	ASN	4.2
3	A	734	GLU	4.2
5	C	52	GLU	4.2
3	A	1392	SER	4.2
3	A	1187	GLN	4.2
3	A	634	THR	4.2
4	B	1036	ALA	4.2
8	F	105	ALA	4.2
3	A	1307	GLU	4.1
6	D	54	GLU	4.1
4	B	182	SER	4.1
4	B	884	ARG	4.1
12	J	25	LEU	4.1
5	C	151	GLN	4.1
4	B	1077	THR	4.1
9	G	81	PRO	4.1
4	B	790	ASP	4.1
4	B	815	ARG	4.1
3	A	653	VAL	4.1
3	A	863	VAL	4.1
3	A	1294	PRO	4.1
6	D	74	GLN	4.1
4	B	268	THR	4.1
7	E	107	THR	4.1
3	A	362	ASP	4.1
3	A	410	GLY	4.1
3	A	1176	LEU	4.1
3	A	1230	GLU	4.1
13	K	37	LYS	4.1
4	B	1071	VAL	4.1

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Mol	Chain	Res	Type	RSRZ
3	A	1099	PRO	4.1
4	B	785	TYR	4.1
4	B	909	ASP	4.1
4	B	590	HIS	4.1
4	B	447	ALA	4.1
4	B	743	ILE	4.1
9	G	39	THR	4.1
4	B	246	LYS	4.1
4	B	1099	VAL	4.1
7	E	104	ASN	4.1
3	A	297	GLN	4.1
3	A	493	GLN	4.1
3	A	501	LEU	4.1
13	K	45	LEU	4.1
3	A	934	LYS	4.1
5	C	63	ILE	4.1
5	C	245	VAL	4.1
5	C	207	CYS	4.1
15	S	271	CYS	4.1
8	F	88	TYR	4.1
9	G	154	VAL	4.1
3	A	437	MET	4.1
4	B	376	PHE	4.1
3	A	684	ALA	4.0
9	G	15	PRO	4.0
4	B	832	GLY	4.0
3	A	1308	THR	4.0
12	J	41	LEU	4.0
3	A	864	ILE	4.0
4	B	47	GLN	4.0
4	B	848	ARG	4.0
6	D	51	ASN	4.0
3	A	223	GLY	4.0
3	A	1305	VAL	4.0
4	B	546	SER	4.0
7	E	165	LEU	4.0
3	A	56	PRO	4.0
3	A	274	ILE	4.0
3	A	333	GLU	4.0
3	A	1407	GLU	4.0
3	A	1447	GLU	4.0
4	B	727	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
14	L	44	ASP	4.0
3	A	611	GLN	4.0
3	A	209	ASN	4.0
10	H	3	ASN	4.0
3	A	1216	ILE	4.0
6	D	55	ALA	4.0
3	A	580	VAL	4.0
3	A	743	VAL	4.0
6	D	152	SER	4.0
3	A	775	ILE	4.0
3	A	1169	ILE	4.0
5	C	10	ILE	4.0
5	C	20	PHE	4.0
4	B	1075	GLY	4.0
13	K	5	ASP	4.0
15	S	290	ASP	4.0
9	G	62	LEU	4.0
4	B	499	ASN	4.0
3	A	812	GLU	4.0
3	A	826	ASP	4.0
9	G	71	ASN	4.0
3	A	719	VAL	4.0
4	B	1034	VAL	4.0
3	A	1077	THR	4.0
4	B	1069	PHE	4.0
3	A	1403	GLU	3.9
3	A	1409	LEU	3.9
4	B	1049	ASP	3.9
3	A	358	ASN	3.9
3	A	1399	ARG	3.9
3	A	245	PRO	3.9
3	A	276	LEU	3.9
3	A	578	LEU	3.9
11	I	46	HIS	3.9
3	A	1088	GLY	3.9
5	C	166	GLU	3.9
4	B	537	LYS	3.9
9	G	61	ILE	3.9
4	B	1116	ARG	3.9
7	E	118	PRO	3.9
3	A	573	SER	3.9
11	I	80	SER	3.9

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Mol	Chain	Res	Type	RSRZ
3	A	527	THR	3.9
3	A	1405	THR	3.9
3	A	844	ALA	3.9
4	B	1110	PRO	3.9
3	A	490	HIS	3.9
3	A	631	HIS	3.9
8	F	102	SER	3.9
3	A	855	THR	3.9
3	A	1080	THR	3.9
5	C	242	GLN	3.9
6	D	188	ALA	3.9
3	A	1097	GLY	3.9
4	B	863	GLU	3.9
5	C	248	ILE	3.9
3	A	907	THR	3.9
3	A	1028	THR	3.9
3	A	1268	LEU	3.9
5	C	147	LEU	3.9
5	C	198	ALA	3.9
7	E	185	ALA	3.9
9	G	108	VAL	3.9
3	A	966	ASN	3.9
3	A	1436	ILE	3.9
3	A	131	SER	3.9
3	A	409	SER	3.9
3	A	454	SER	3.9
4	B	591	ARG	3.9
3	A	669	THR	3.9
3	A	1377	THR	3.9
4	B	741	CYS	3.9
5	C	164	ALA	3.9
5	C	47	ASP	3.9
12	J	23	ASN	3.9
3	A	14	VAL	3.9
4	B	318	VAL	3.9
11	I	37	GLU	3.9
3	A	234	MET	3.8
13	K	67	PHE	3.8
5	C	28	ALA	3.8
3	A	269	ILE	3.8
3	A	345	VAL	3.8
3	A	622	VAL	3.8

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Mol	Chain	Res	Type	RSRZ
3	A	1064	VAL	3.8
7	E	80	VAL	3.8
10	H	27	GLU	3.8
3	A	1357	ALA	3.8
6	D	17	LYS	3.8
15	S	275	LYS	3.8
6	D	149	THR	3.8
3	A	464	PRO	3.8
6	D	47	LEU	3.8
8	F	140	ASP	3.8
3	A	839	ARG	3.8
3	A	616	VAL	3.8
4	B	57	TYR	3.8
3	A	1347	ALA	3.8
13	K	106	GLU	3.8
5	C	234	SER	3.8
7	E	174	GLN	3.8
4	B	1017	ILE	3.8
4	B	354	ASP	3.8
4	B	1086	PHE	3.8
7	E	71	LYS	3.8
9	G	27	LYS	3.8
8	F	124	GLU	3.8
6	D	197	SER	3.8
3	A	537	ARG	3.8
3	A	1332	PHE	3.8
13	K	102	LYS	3.8
3	A	125	ALA	3.8
4	B	1196	ILE	3.8
3	A	447	GLN	3.8
14	L	36	SER	3.8
3	A	820	GLY	3.8
3	A	834	THR	3.8
4	B	411	PRO	3.8
3	A	974	ASP	3.8
4	B	409	ALA	3.8
3	A	439	ASN	3.8
4	B	686	ASN	3.8
7	E	136	ASN	3.8
4	B	770	GLN	3.8
4	B	1060	ARG	3.8
4	B	1135	ARG	3.8

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Mol	Chain	Res	Type	RSRZ
5	C	105	GLY	3.8
3	A	224	PHE	3.8
3	A	535	THR	3.8
4	B	98	THR	3.8
14	L	61	THR	3.8
13	K	90	ALA	3.8
3	A	1072	ILE	3.8
4	B	1211	ASN	3.7
9	G	109	PHE	3.7
6	D	49	ALA	3.7
13	K	60	ALA	3.7
4	B	566	LEU	3.7
6	D	167	LEU	3.7
4	B	427	ASP	3.7
8	F	129	LYS	3.7
10	H	126	GLU	3.7
3	A	78	PRO	3.7
3	A	514	PRO	3.7
3	A	1352	VAL	3.7
4	B	345	LYS	3.7
3	A	1239	ARG	3.7
4	B	1153	GLU	3.7
13	K	39	ASP	3.7
11	I	41	PRO	3.7
4	B	853	SER	3.7
3	A	956	LEU	3.7
3	A	1133	LEU	3.7
5	C	263	THR	3.7
3	A	651	LYS	3.7
4	B	962	LYS	3.7
3	A	1059	HIS	3.7
6	D	14	ARG	3.7
3	A	378	GLU	3.7
3	A	813	PHE	3.7
4	B	1028	GLU	3.7
4	B	998	ASP	3.7
5	C	42	PRO	3.7
3	A	865	GLN	3.7
3	A	215	SER	3.7
4	B	522	VAL	3.7
4	B	999	MET	3.7
3	A	563	PRO	3.7

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Mol	Chain	Res	Type	RSRZ
4	B	745	PRO	3.7
3	A	922	ASP	3.7
4	B	279	ASP	3.7
4	B	521	LEU	3.7
4	B	493	SER	3.7
10	H	77	ARG	3.7
15	S	294	THR	3.7
7	E	82	PHE	3.7
4	B	1149	GLU	3.7
15	S	238	PRO	3.7
1	T	21	DC	3.7
4	B	695	ALA	3.7
8	F	121	ALA	3.7
4	B	54	PHE	3.7
4	B	980	PHE	3.7
6	D	160	VAL	3.7
12	J	54	VAL	3.7
11	I	69	PRO	3.7
13	K	101	LEU	3.7
3	A	205	GLU	3.7
4	B	172	ILE	3.7
4	B	285	ILE	3.7
4	B	1006	ILE	3.7
6	D	24	ALA	3.7
7	E	209	ALA	3.7
4	B	39	ARG	3.6
3	A	1433	MET	3.6
13	K	96	ASN	3.6
3	A	659	HIS	3.6
3	A	300	VAL	3.6
9	G	93	SER	3.6
3	A	99	ILE	3.6
7	E	131	THR	3.6
11	I	67	THR	3.6
5	C	256	ALA	3.6
7	E	214	CYS	3.6
3	A	390	GLN	3.6
5	C	79	GLN	3.6
11	I	45	ARG	3.6
12	J	18	TRP	3.6
5	C	37	MET	3.6
4	B	977	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
3	A	953	ASN	3.6
6	D	210	ILE	3.6
3	A	263	THR	3.6
3	A	978	PRO	3.6
4	B	1105	ALA	3.6
3	A	718	VAL	3.6
3	A	1373	ASP	3.6
7	E	69	ILE	3.6
3	A	1009	ASN	3.6
10	H	134	ASN	3.6
6	D	45	GLU	3.6
3	A	266	LEU	3.6
12	J	56	LEU	3.6
4	B	374	LYS	3.6
4	B	760	ASP	3.6
3	A	561	PRO	3.6
6	D	6	SER	3.6
3	A	1318	THR	3.6
4	B	384	ARG	3.6
7	E	204	THR	3.6
3	A	243	PRO	3.6
3	A	1190	PRO	3.6
3	A	1366	ARG	3.6
4	B	169	ARG	3.6
3	A	306	ASN	3.6
4	B	314	LEU	3.6
4	B	1147	LEU	3.6
3	A	1151	GLU	3.6
3	A	1104	ILE	3.6
5	C	165	LYS	3.6
3	A	248	PRO	3.5
3	A	590	ARG	3.5
3	A	711	ARG	3.5
4	B	316	PRO	3.5
4	B	1052	VAL	3.5
13	K	56	VAL	3.5
3	A	723	ASN	3.5
6	D	182	SER	3.5
7	E	4	GLU	3.5
3	A	994	GLN	3.5
4	B	800	GLN	3.5
11	I	60	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
3	A	434	ARG	3.5
3	A	482	PHE	3.5
9	G	30	LEU	3.5
3	A	265	LYS	3.5
4	B	400	HIS	3.5
3	A	466	SER	3.5
5	C	112	ASN	3.5
13	K	103	THR	3.5
3	A	576	GLN	3.5
6	D	30	GLY	3.5
3	A	942	PHE	3.5
5	C	132	PRO	3.5
3	A	804	TYR	3.5
4	B	210	LYS	3.5
12	J	55	ASP	3.5
4	B	1025	HIS	3.5
4	B	1019	SER	3.5
7	E	68	SER	3.5
14	L	48	CYS	3.5
3	A	550	LEU	3.5
4	B	1084	GLN	3.5
4	B	167	ILE	3.5
4	B	455	SER	3.5
4	B	1044	ALA	3.5
7	E	139	ALA	3.5
3	A	555	ASP	3.5
3	A	141	LEU	3.5
4	B	1045	SER	3.5
3	A	173	THR	3.5
3	A	1354	ASN	3.5
8	F	100	GLN	3.5
3	A	98	LYS	3.5
3	A	551	TYR	3.5
12	J	57	ILE	3.5
6	D	27	LEU	3.5
3	A	692	ASP	3.5
3	A	954	TRP	3.5
4	B	207	GLY	3.5
7	E	13	TRP	3.5
9	G	103	VAL	3.5
4	B	574	SER	3.5
3	A	510	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
9	G	83	LYS	3.5
3	A	1295	THR	3.5
3	A	1049	ILE	3.5
7	E	199	ILE	3.5
5	C	35	ARG	3.4
14	L	53	HIS	3.4
3	A	939	ASP	3.4
4	B	371	GLU	3.4
3	A	7	SER	3.4
3	A	221	SER	3.4
4	B	712	PRO	3.4
5	C	53	THR	3.4
7	E	151	PRO	3.4
3	A	82	GLY	3.4
3	A	984	LYS	3.4
7	E	58	MET	3.4
3	A	1420	ASP	3.4
4	B	564	GLU	3.4
5	C	138	GLU	3.4
3	A	973	ILE	3.4
4	B	593	PRO	3.4
4	B	1123	SER	3.4
3	A	1270	ASN	3.4
4	B	454	THR	3.4
8	F	86	THR	3.4
4	B	830	TYR	3.4
3	A	712	GLU	3.4
5	C	76	ASP	3.4
3	A	296	LEU	3.4
6	D	63	LEU	3.4
7	E	86	PRO	3.4
4	B	417	PHE	3.4
4	B	512	ARG	3.4
7	E	91	LYS	3.4
7	E	152	LYS	3.4
4	B	809	MET	3.4
4	B	1212	ILE	3.4
6	D	195	ILE	3.4
9	G	54	ILE	3.4
4	B	525	ALA	3.4
11	I	54	GLU	3.4
4	B	357	GLN	3.4

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Mol	Chain	Res	Type	RSRZ
3	A	220	THR	3.4
3	A	339	ASN	3.4
3	A	1393	ASN	3.4
3	A	1413	GLY	3.4
4	B	301	ILE	3.4
3	A	329	LEU	3.4
4	B	953	LEU	3.4
3	A	768	GLN	3.4
3	A	1287	TYR	3.4
8	F	116	ASP	3.4
4	B	51	PHE	3.4
9	G	107	LYS	3.4
4	B	105	SER	3.4
4	B	949	VAL	3.4
9	G	144	ARG	3.4
12	J	6	ARG	3.4
3	A	607	ILE	3.4
13	K	42	LEU	3.4
3	A	828	ALA	3.4
4	B	414	ALA	3.4
4	B	496	ARG	3.4
4	B	1023	VAL	3.4
5	C	197	SER	3.4
3	A	630	ILE	3.4
3	A	694	THR	3.4
4	B	383	ASN	3.4
4	B	498	THR	3.4
4	B	571	PRO	3.3
3	A	298	PHE	3.3
3	A	780	VAL	3.3
4	B	679	TYR	3.3
4	B	1150	ARG	3.3
4	B	821	GLN	3.3
4	B	1021	MET	3.3
3	A	610	GLY	3.3
3	A	1431	GLY	3.3
4	B	59	LEU	3.3
3	A	518	LYS	3.3
7	E	20	LYS	3.3
3	A	81	PHE	3.3
3	A	674	PRO	3.3
5	C	228	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
4	B	678	GLU	3.3
7	E	184	VAL	3.3
7	E	194	GLU	3.3
11	I	18	GLU	3.3
4	B	350	GLN	3.3
4	B	100	PRO	3.3
4	B	757	PRO	3.3
4	B	1076	HIS	3.3
3	A	995	GLU	3.3
3	A	1050	GLU	3.3
4	B	216	GLU	3.3
3	A	963	ILE	3.3
4	B	46	GLN	3.3
6	D	57	LEU	3.3
11	I	109	ILE	3.3
4	B	993	THR	3.3
4	B	1224	PHE	3.3
13	K	10	PHE	3.3
4	B	632	ARG	3.3
3	A	1349	TYR	3.3
9	G	25	TYR	3.3
13	K	108	GLU	3.3
10	H	86	ASP	3.3
3	A	352	VAL	3.3
3	A	709	THR	3.3
3	A	915	SER	3.3
4	B	266	ALA	3.3
7	E	181	ALA	3.3
4	B	740	HIS	3.3
4	B	747	MET	3.3
3	A	391	LEU	3.3
4	B	403	LYS	3.3
3	A	29	ALA	3.3
4	B	217	ARG	3.3
4	B	50	SER	3.3
6	D	52	LEU	3.3
10	H	108	SER	3.3
15	S	208	SER	3.3
3	A	593	GLU	3.3
3	A	1131	ALA	3.3
3	A	241	VAL	3.3
4	B	405	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
3	A	528	LEU	3.3
5	C	72	LEU	3.3
13	K	87	LEU	3.3
3	A	302	THR	3.3
3	A	1449	SER	3.3
4	B	870	ILE	3.3
4	B	990	ILE	3.3
4	B	178	ASN	3.2
10	H	139	ASN	3.2
4	B	650	GLU	3.2
4	B	1120	GLU	3.2
3	A	532	ARG	3.2
4	B	483	LEU	3.2
4	B	690	VAL	3.2
3	A	556	TRP	3.2
4	B	748	ILE	3.2
4	B	1014	PRO	3.2
8	F	106	PRO	3.2
4	B	488	TYR	3.2
10	H	102	TYR	3.2
3	A	213	HIS	3.2
7	E	31	THR	3.2
8	F	76	LYS	3.2
4	B	1134	GLU	3.2
7	E	67	GLU	3.2
15	S	302	CYS	3.2
3	A	19	PHE	3.2
3	A	655	PHE	3.2
3	A	1441	PHE	3.2
3	A	392	VAL	3.2
3	A	693	VAL	3.2
4	B	715	ALA	3.2
4	B	629	ASP	3.2
4	B	456	GLY	3.2
4	B	116	GLU	3.2
3	A	725	ALA	3.2
10	H	44	VAL	3.2
4	B	1138	MET	3.2
3	A	586	ILE	3.2
3	A	964	ILE	3.2
4	B	1139	ILE	3.2
3	A	1435	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
3	A	1359	ASP	3.2
10	H	16	ASP	3.2
3	A	675	THR	3.2
15	S	295	THR	3.2
3	A	119	ASN	3.2
6	D	58	VAL	3.2
3	A	349	ALA	3.2
3	A	967	ALA	3.2
4	B	302	CYS	3.2
8	F	120	ILE	3.2
9	G	84	GLY	3.2
3	A	783	THR	3.2
3	A	896	ARG	3.2
7	E	10	SER	3.2
7	E	173	SER	3.2
4	B	756	ILE	3.2
4	B	1016	ALA	3.2
4	B	1157	ALA	3.2
5	C	50	GLU	3.2
3	A	541	ILE	3.2
7	E	8	ASN	3.2
10	H	131	ASN	3.2
4	B	231	PRO	3.2
3	A	646	PHE	3.2
3	A	807	GLY	3.2
3	A	1430	LEU	3.2
3	A	328	ARG	3.2
11	I	19	ASP	3.2
3	A	831	THR	3.2
3	A	879	GLU	3.2
3	A	1117	THR	3.2
5	C	55	THR	3.2
9	G	56	ILE	3.2
11	I	64	SER	3.2
3	A	1324	PRO	3.2
4	B	1198	TYR	3.2
5	C	143	LEU	3.2
5	C	251	LEU	3.2
11	I	106	CYS	3.2
14	L	34	CYS	3.2
9	G	77	VAL	3.2
3	A	100	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
4	B	837	ASP	3.2
4	B	540	SER	3.1
6	D	150	ASN	3.1
3	A	374	LEU	3.1
4	B	1064	TYR	3.1
6	D	141	LEU	3.1
13	K	105	PHE	3.1
3	A	1367	HIS	3.1
3	A	433	GLU	3.1
3	A	516	SER	3.1
4	B	325	GLN	3.1
4	B	258	LEU	3.1
3	A	819	GLY	3.1
4	B	761	HIS	3.1
3	A	1022	LEU	3.1
3	A	1269	GLU	3.1
5	C	217	ASP	3.1
6	D	124	GLU	3.1
6	D	218	GLU	3.1
3	A	1052	GLN	3.1
5	C	48	SER	3.1
3	A	897	TYR	3.1
7	E	53	PRO	3.1
12	J	4	PRO	3.1
3	A	818	MET	3.1
4	B	93	GLY	3.1
4	B	881	ASN	3.1
3	A	637	LYS	3.1
9	G	5	LYS	3.1
9	G	151	ILE	3.1
3	A	327	ALA	3.1
4	B	900	ALA	3.1
5	C	59	ALA	3.1
6	D	25	ALA	3.1
15	S	177	ALA	3.1
3	A	509	LEU	3.1
3	A	1421	CYS	3.1
4	B	66	ASP	3.1
3	A	237	THR	3.1
4	B	480	SER	3.1
4	B	575	PRO	3.1
6	D	159	THR	3.1

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Mol	Chain	Res	Type	RSRZ
3	A	178	GLY	3.1
4	B	777	ALA	3.1
3	A	710	LEU	3.1
13	K	19	LEU	3.1
3	A	211	PHE	3.1
3	A	633	VAL	3.1
4	B	248	SER	3.1
4	B	395	GLN	3.1
4	B	706	GLN	3.1
5	C	100	THR	3.1
6	D	174	PRO	3.1
3	A	343	LYS	3.1
3	A	401	GLY	3.1
4	B	103	ASN	3.1
3	A	1412	ALA	3.1
4	B	1026	LEU	3.1
3	A	432	VAL	3.1
3	A	1045	VAL	3.1
3	A	1234	GLU	3.1
3	A	1242	VAL	3.1
7	E	196	VAL	3.1
3	A	438	ASP	3.1
4	B	106	ASP	3.1
4	B	550	ASP	3.1
4	B	919	SER	3.1
12	J	33	GLY	3.1
4	B	1202	LEU	3.1
9	G	114	LEU	3.1
11	I	68	LEU	3.1
13	K	68	PHE	3.1
3	A	761	MET	3.1
9	G	140	LYS	3.1
7	E	148	GLU	3.1
5	C	136	ASP	3.0
9	G	26	LEU	3.0
3	A	850	VAL	3.0
3	A	1350	LYS	3.0
9	G	167	TYR	3.0
14	L	68	GLU	3.0
3	A	268	ASP	3.0
4	B	1056	SER	3.0
3	A	632	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
3	A	774	ARG	3.0
3	A	938	LYS	3.0
3	A	1340	GLY	3.0
4	B	293	PRO	3.0
4	B	699	GLU	3.0
4	B	1128	LEU	3.0
7	E	149	LEU	3.0
8	F	89	GLU	3.0
10	H	99	GLY	3.0
3	A	564	ALA	3.0
4	B	614	SER	3.0
4	B	895	ASP	3.0
10	H	4	THR	3.0
11	I	111	THR	3.0
3	A	1262	LYS	3.0
3	A	337	ARG	3.0
15	S	268	ARG	3.0
15	S	201	ILE	3.0
3	A	920	LEU	3.0
4	B	689	LEU	3.0
3	A	24	PRO	3.0
13	K	28	PRO	3.0
3	A	226	GLU	3.0
8	F	149	GLU	3.0
3	A	272	ALA	3.0
3	A	480	ALA	3.0
3	A	779	PHE	3.0
3	A	641	VAL	3.0
3	A	1241	ARG	3.0
12	J	14	VAL	3.0
3	A	325	ILE	3.0
3	A	1170	ILE	3.0
4	B	1172	ILE	3.0
3	A	805	LEU	3.0
4	B	1000	PRO	3.0
10	H	82	PRO	3.0
4	B	621	GLU	3.0
7	E	137	GLU	3.0
3	A	515	GLN	3.0
3	A	965	GLN	3.0
13	K	86	ALA	3.0
3	A	512	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
3	A	1372	VAL	3.0
4	B	165	VAL	3.0
3	A	1358	SER	3.0
4	B	912	ILE	3.0
4	B	976	ILE	3.0
9	G	50	ASP	3.0
9	G	168	LEU	3.0
7	E	46	TYR	3.0
7	E	206	GLY	3.0
3	A	18	GLN	3.0
8	F	97	ARG	3.0
5	C	129	ILE	3.0
3	A	716	ASP	3.0
4	B	391	ASP	3.0
3	A	448	PRO	3.0
3	A	1173	HIS	3.0
3	A	1265	ASN	3.0
3	A	1330	ASN	3.0
4	B	32	ALA	3.0
5	C	94	LYS	3.0
3	A	1025	ARG	3.0
4	B	244	LEU	2.9
3	A	204	THR	2.9
3	A	381	THR	2.9
3	A	1293	SER	2.9
4	B	642	ASP	2.9
4	B	1125	ASP	2.9
9	G	155	SER	2.9
9	G	156	SER	2.9
3	A	478	TYR	2.9
4	B	315	LYS	2.9
4	B	1201	LYS	2.9
3	A	854	ASN	2.9
10	H	90	ALA	2.9
13	K	27	ALA	2.9
5	C	215	GLU	2.9
15	S	276	GLU	2.9
4	B	911	ILE	2.9
4	B	1095	LEU	2.9
5	C	258	ILE	2.9
7	E	12	LEU	2.9
3	A	861	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
3	A	1206	ASP	2.9
4	B	553	PRO	2.9
4	B	1047	PHE	2.9
3	A	1010	ALA	2.9
3	A	986	ILE	2.9
3	A	1311	VAL	2.9
3	A	25	GLU	2.9
4	B	516	ASN	2.9
4	B	1133	MET	2.9
10	H	106	GLU	2.9
13	K	95	ILE	2.9
12	J	15	GLY	2.9
4	B	58	THR	2.9
4	B	1046	PRO	2.9
3	A	732	LEU	2.9
3	A	1143	LEU	2.9
3	A	1215	ARG	2.9
3	A	1406	VAL	2.9
4	B	311	LEU	2.9
4	B	1024	ALA	2.9
5	C	25	VAL	2.9
6	D	126	ILE	2.9
6	D	209	ARG	2.9
13	K	100	ALA	2.9
3	A	1317	MET	2.9
11	I	12	ASN	2.9
3	A	969	GLN	2.9
3	A	785	PRO	2.9
4	B	769	TYR	2.9
3	A	1160	SER	2.9
3	A	1219	THR	2.9
4	B	754	SER	2.9
4	B	1007	VAL	2.9
10	H	12	VAL	2.9
3	A	790	ASP	2.9
3	A	1033	GLN	2.9
5	C	128	ASN	2.9
15	S	257	GLN	2.9
7	E	122	LYS	2.9
3	A	376	TYR	2.9
3	A	30	ILE	2.9
4	B	196	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
4	B	542	MET	2.9
3	A	1083	THR	2.9
3	A	1161	THR	2.9
3	A	877	HIS	2.9
5	C	196	ASP	2.9
9	G	97	HIS	2.9
3	A	640	GLN	2.9
14	L	67	PHE	2.9
9	G	124	GLY	2.9
13	K	13	GLY	2.9
7	E	158	SER	2.9
3	A	423	ASP	2.9
5	C	106	GLU	2.9
4	B	561	TRP	2.9
4	B	583	ASN	2.9
3	A	379	VAL	2.8
14	L	70	ARG	2.8
3	A	341	MET	2.8
4	B	1152	MET	2.8
10	H	113	ALA	2.8
2	P	10	C	2.8
6	D	142	LYS	2.8
9	G	64	THR	2.8
3	A	1019	CYS	2.8
4	B	544	CYS	2.8
3	A	1105	LEU	2.8
4	B	1058	LEU	2.8
6	D	131	GLU	2.8
7	E	32	GLN	2.8
8	F	92	ARG	2.8
9	G	44	TYR	2.8
4	B	1003	ALA	2.8
3	A	208	LEU	2.8
10	H	88	SER	2.8
14	L	41	SER	2.8
3	A	130	ASP	2.8
3	A	557	ASP	2.8
3	A	822	GLU	2.8
3	A	1255	GLU	2.8
5	C	16	ASP	2.8
4	B	120	ARG	2.8
5	C	171	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
12	J	47	ARG	2.8
3	A	991	LYS	2.8
3	A	250	ILE	2.8
3	A	565	ILE	2.8
3	A	625	SER	2.8
3	A	1142	THR	2.8
4	B	517	THR	2.8
5	C	110	THR	2.8
7	E	145	THR	2.8
4	B	1065	GLN	2.8
4	B	1179	GLN	2.8
5	C	244	VAL	2.8
10	H	54	SER	2.8
15	S	299	CYS	2.8
4	B	404	LYS	2.8
3	A	737	LEU	2.8
3	A	46	THR	2.8
3	A	258	GLY	2.8
3	A	703	THR	2.8
3	A	898	ARG	2.8
10	H	39	THR	2.8
3	A	668	ASP	2.8
4	B	618	ASP	2.8
3	A	105	CYS	2.8
4	B	538	ASN	2.8
4	B	539	LEU	2.8
3	A	503	GLN	2.8
10	H	30	SER	2.8
12	J	58	GLU	2.8
3	A	504	LEU	2.8
3	A	1371	LEU	2.8
4	B	508	LEU	2.8
5	C	33	LEU	2.8
3	A	721	PHE	2.8
3	A	200	ARG	2.8
3	A	1007	ILE	2.8
4	B	95	ILE	2.8
7	E	167	ARG	2.8
13	K	70	ARG	2.8
14	L	42	ARG	2.8
9	G	158	HIS	2.8
3	A	51	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
7	E	197	LYS	2.8
3	A	1191	TRP	2.8
3	A	599	SER	2.8
3	A	1272	THR	2.8
4	B	713	ALA	2.8
5	C	175	ALA	2.8
4	B	565	PRO	2.8
7	E	170	LEU	2.8
15	S	241	LEU	2.8
11	I	65	ASP	2.8
3	A	442	VAL	2.7
3	A	946	VAL	2.7
4	B	784	ASN	2.7
7	E	162	ARG	2.7
13	K	26	LYS	2.7
3	A	206	GLU	2.7
3	A	294	SER	2.7
9	G	3	PHE	2.7
3	A	837	ILE	2.7
4	B	324	ILE	2.7
9	G	87	VAL	2.7
5	C	185	LYS	2.7
9	G	47	CYS	2.7
7	E	21	GLU	2.7
7	E	106	GLN	2.7
4	B	916	THR	2.7
3	A	1001	ARG	2.7
15	S	263	ARG	2.7
3	A	536	LEU	2.7
9	G	123	ALA	2.7
3	A	639	PRO	2.7
4	B	758	PHE	2.7
6	D	175	PHE	2.7
3	A	1078	GLN	2.7
8	F	139	PRO	2.7
3	A	539	THR	2.7
4	B	1162	ILE	2.7
10	H	59	ILE	2.7
3	A	129	LYS	2.7
4	B	788	ARG	2.7
9	G	29	LYS	2.7
3	A	270	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
3	A	319	GLY	2.7
4	B	356	LEU	2.7
4	B	685	LEU	2.7
14	L	32	ALA	2.7
3	A	519	PRO	2.7
3	A	666	ILE	2.7
4	B	179	CYS	2.7
8	F	130	ILE	2.7
10	H	24	CYS	2.7
3	A	562	THR	2.7
4	B	892	LYS	2.7
4	B	1148	LYS	2.7
7	E	119	SER	2.7
7	E	157	SER	2.7
4	B	1126	GLY	2.7
3	A	219	PHE	2.7
3	A	225	ASN	2.7
3	A	903	ASN	2.7
3	A	996	ASN	2.7
3	A	1106	ASN	2.7
4	B	1015	HIS	2.7
6	D	40	HIS	2.7
4	B	1085	ILE	2.7
7	E	38	PRO	2.7
6	D	176	GLU	2.7
7	E	14	ARG	2.7
4	B	710	LEU	2.7
3	A	1145	SER	2.7
3	A	707	GLY	2.7
4	B	382	ILE	2.7
4	B	582	VAL	2.7
10	H	52	GLN	2.7
15	S	169	GLN	2.7
3	A	1376	THR	2.7
7	E	87	SER	2.7
12	J	8	PHE	2.7
5	C	133	ILE	2.6
5	C	97	VAL	2.6
3	A	41	MET	2.6
3	A	1336	MET	2.6
3	A	113	LEU	2.6
3	A	1116	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
4	B	1059	LEU	2.6
15	S	228	LEU	2.6
4	B	631	GLY	2.6
7	E	117	THR	2.6
11	I	78	CYS	2.6
3	A	1363	VAL	2.6
3	A	1124	HIS	2.6
4	B	877	PRO	2.6
5	C	259	LEU	2.6
8	F	132	LEU	2.6
10	H	143	LEU	2.6
3	A	120	GLU	2.6
8	F	150	GLU	2.6
10	H	100	THR	2.6
3	A	553	VAL	2.6
3	A	927	VAL	2.6
4	B	857	ARG	2.6
4	B	1217	TYR	2.6
12	J	44	TYR	2.6
3	A	739	ASP	2.6
3	A	1063	MET	2.6
3	A	1339	LEU	2.6
3	A	1397	LEU	2.6
5	C	75	MET	2.6
10	H	53	ASP	2.6
13	K	22	ASP	2.6
5	C	194	GLU	2.6
4	B	260	GLY	2.6
4	B	963	PHE	2.6
5	C	261	ALA	2.6
3	A	63	ARG	2.6
3	A	472	LEU	2.6
4	B	879	ARG	2.6
11	I	73	ARG	2.6
11	I	84	VAL	2.6
7	E	75	MET	2.6
3	A	1228	TRP	2.6
3	A	678	GLU	2.6
3	A	1165	GLU	2.6
3	A	49	LYS	2.6
3	A	916	GLY	2.6
3	A	1224	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
10	H	125	LEU	2.6
3	A	89	PRO	2.6
3	A	357	PRO	2.6
4	B	501	PRO	2.6
6	D	140	ASP	2.6
3	A	1018	PHE	2.6
11	I	4	PHE	2.6
6	D	157	GLN	2.6
12	J	11	GLY	2.6
9	G	10	ASN	2.6
3	A	1197	LEU	2.6
4	B	386	LEU	2.6
4	B	547	VAL	2.6
4	B	1020	ARG	2.6
7	E	11	ARG	2.6
7	E	88	VAL	2.6
4	B	783	THR	2.6
11	I	31	THR	2.6
9	G	133	SER	2.6
3	A	305	ASP	2.6
3	A	714	PHE	2.6
5	C	131	HIS	2.6
3	A	207	ILE	2.6
3	A	767	GLN	2.6
3	A	1297	GLU	2.6
4	B	1131	GLY	2.6
3	A	54	ASN	2.6
3	A	420	ARG	2.6
4	B	323	VAL	2.6
3	A	664	THR	2.6
4	B	739	THR	2.6
6	D	196	PRO	2.6
3	A	531	ILE	2.5
4	B	896	ASP	2.5
7	E	41	ASP	2.5
3	A	1301	GLU	2.5
3	A	1417	GLU	2.5
4	B	262	GLU	2.5
4	B	415	GLN	2.5
6	D	179	GLN	2.5
11	I	90	GLN	2.5
3	A	122	MET	2.5

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Mol	Chain	Res	Type	RSRZ
5	C	157	CYS	2.5
9	G	53	ASN	2.5
11	I	66	PRO	2.5
3	A	370	ILE	2.5
4	B	982	SER	2.5
5	C	99	LEU	2.5
7	E	213	ILE	2.5
9	G	16	SER	2.5
9	G	125	SER	2.5
14	L	35	SER	2.5
3	A	1029	ARG	2.5
4	B	633	VAL	2.5
7	E	150	VAL	2.5
3	A	43	GLU	2.5
4	B	310	MET	2.5
11	I	17	ARG	2.5
11	I	118	ARG	2.5
6	D	23	ASN	2.5
9	G	150	CYS	2.5
13	K	89	ASN	2.5
4	B	652	LYS	2.5
4	B	602	THR	2.5
4	B	992	ILE	2.5
5	C	34	ARG	2.5
15	S	249	ALA	2.5
3	A	71	GLN	2.5
3	A	801	GLU	2.5
5	C	266	ASP	2.5
9	G	51	TYR	2.5
3	A	662	PHE	2.5
3	A	679	ILE	2.5
3	A	841	LEU	2.5
3	A	867	ILE	2.5
3	A	929	LEU	2.5
4	B	1165	ILE	2.5
3	A	278	THR	2.5
3	A	338	GLY	2.5
4	B	363	HIS	2.5
10	H	130	ARG	2.5
6	D	162	ALA	2.5
3	A	39	GLU	2.5
6	D	122	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
3	A	985	ASP	2.5
4	B	934	LYS	2.5
4	B	62	ILE	2.5
9	G	105	PRO	2.5
13	K	104	ASN	2.5
4	B	751	VAL	2.5
9	G	92	VAL	2.5
9	G	161	GLY	2.5
11	I	88	SER	2.5
3	A	738	LYS	2.5
3	A	926	GLN	2.5
3	A	1008	GLN	2.5
13	K	88	LYS	2.5
3	A	1341	ILE	2.5
4	B	794	ASN	2.5
4	B	1029	CYS	2.5
9	G	94	CYS	2.5
5	C	156	THR	2.5
7	E	37	LEU	2.5
5	C	38	ILE	2.5
3	A	990	VAL	2.5
3	A	1100	ARG	2.5
4	B	659	ALA	2.5
6	D	60	LYS	2.5
8	F	87	LYS	2.5
3	A	856	THR	2.4
3	A	1195	LEU	2.4
4	B	661	LEU	2.4
4	B	242	SER	2.4
4	B	683	SER	2.4
4	B	764	SER	2.4
3	A	1114	PRO	2.4
5	C	6	PRO	2.4
7	E	73	PRO	2.4
4	B	497	ARG	2.4
9	G	86	VAL	2.4
3	A	584	ASN	2.4
4	B	229	ALA	2.4
8	F	72	LYS	2.4
4	B	408	LEU	2.4
3	A	868	TYR	2.4
3	A	1006	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
4	B	1073	TYR	2.4
10	H	116	TYR	2.4
6	D	125	SER	2.4
3	A	326	ARG	2.4
4	B	362	PRO	2.4
4	B	818	PRO	2.4
7	E	22	MET	2.4
5	C	199	LYS	2.4
4	B	796	LEU	2.4
3	A	566	ILE	2.4
4	B	123	THR	2.4
3	A	382	PRO	2.4
4	B	601	ARG	2.4
4	B	623	GLU	2.4
7	E	36	GLU	2.4
9	G	60	ARG	2.4
9	G	100	GLU	2.4
3	A	440	ASP	2.4
5	C	190	ASP	2.4
4	B	286	PHE	2.4
3	A	273	ASN	2.4
3	A	397	ASN	2.4
4	B	349	ILE	2.4
5	C	120	ILE	2.4
11	I	108	HIS	2.4
3	A	460	VAL	2.4
5	C	246	ARG	2.4
6	D	18	VAL	2.4
3	A	1130	GLN	2.4
4	B	481	GLN	2.4
11	I	82	GLU	2.4
14	L	43	THR	2.4
3	A	924	LYS	2.4
5	C	257	SER	2.4
15	S	180	SER	2.4
7	E	190	LEU	2.4
3	A	457	ALA	2.4
3	A	153	PRO	2.4
3	A	575	LYS	2.4
3	A	914	GLU	2.4
3	A	1329	THR	2.4
4	B	611	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
12	J	19	GLU	2.4
14	L	58	LYS	2.4
3	A	796	SER	2.4
4	B	201	GLY	2.4
3	A	347	PHE	2.4
11	I	103	CYS	2.4
15	S	269	PHE	2.4
4	B	840	ILE	2.4
3	A	900	ASP	2.4
3	A	806	ARG	2.4
3	A	870	GLU	2.4
4	B	736	THR	2.4
11	I	50	THR	2.4
5	C	70	ILE	2.4
4	B	388	CYS	2.4
3	A	116	ASP	2.4
4	B	131	ASP	2.4
9	G	6	ASP	2.4
3	A	262	LEU	2.4
3	A	1450	LEU	2.4
10	H	46	LEU	2.4
9	G	63	PRO	2.3
4	B	779	GLY	2.3
5	C	208	GLU	2.3
4	B	463	THR	2.3
4	B	1200	ALA	2.3
9	G	42	PHE	2.3
4	B	55	VAL	2.3
3	A	1013	ASP	2.3
5	C	254	LYS	2.3
15	S	189	ASP	2.3
3	A	479	ASN	2.3
5	C	54	ASN	2.3
3	A	1211	GLN	2.3
5	C	73	GLN	2.3
8	F	141	GLY	2.3
9	G	96	GLN	2.3
11	I	101	PHE	2.3
3	A	393	ARG	2.3
4	B	313	MET	2.3
3	A	606	LEU	2.3
4	B	122	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
4	B	166	PHE	2.3
4	B	917	PRO	2.3
13	K	71	PHE	2.3
3	A	235	ILE	2.3
3	A	1411	GLU	2.3
3	A	1416	ALA	2.3
4	B	278	GLN	2.3
9	G	165	GLU	2.3
15	S	301	ALA	2.3
3	A	389	THR	2.3
3	A	691	LEU	2.3
3	A	1209	MET	2.3
14	L	62	LYS	2.3
3	A	1383	SER	2.3
5	C	262	LEU	2.3
9	G	49	LEU	2.3
3	A	1323	ASP	2.3
4	B	851	PHE	2.3
7	E	72	PHE	2.3
9	G	166	ASP	2.3
15	S	240	PRO	2.3
3	A	1196	GLU	2.3
3	A	1390	ASN	2.3
3	A	1448	GLU	2.3
7	E	63	ASN	2.3
5	C	142	VAL	2.3
5	C	227	THR	2.3
6	D	219	THR	2.3
5	C	237	SER	2.3
15	S	203	TYR	2.3
4	B	284	ILE	2.3
9	G	128	PRO	2.3
5	C	226	ASP	2.3
6	D	171	GLY	2.3
3	A	33	ALA	2.3
3	A	290	GLU	2.3
3	A	987	VAL	2.3
4	B	353	LYS	2.3
4	B	886	LYS	2.3
5	C	264	GLN	2.3
6	D	64	VAL	2.3
3	A	676	MET	2.3

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Mol	Chain	Res	Type	RSRZ
3	A	923	LEU	2.3
3	A	943	LEU	2.3
4	B	381	MET	2.3
5	C	186	LEU	2.3
7	E	115	ASN	2.3
13	K	47	ARG	2.3
15	S	186	ASN	2.3
15	S	286	THR	2.3
4	B	858	SER	2.3
4	B	197	PHE	2.3
4	B	292	ILE	2.3
4	B	824	ILE	2.3
3	A	558	GLY	2.3
3	A	182	VAL	2.3
3	A	547	LEU	2.3
3	A	1226	VAL	2.3
4	B	108	VAL	2.3
15	S	158	ASP	2.3
3	A	1135	ARG	2.3
4	B	40	GLU	2.3
4	B	1053	GLU	2.3
6	D	208	GLU	2.3
10	H	47	PHE	2.3
3	A	612	ILE	2.3
7	E	49	SER	2.3
7	E	198	ILE	2.3
3	A	1002	GLY	2.3
8	F	118	LEU	2.3
3	A	1334	ASP	2.3
3	A	5	GLN	2.3
13	K	16	GLU	2.2
3	A	1044	TRP	2.2
3	A	1304	TRP	2.2
4	B	308	TRP	2.2
3	A	825	ILE	2.2
15	S	224	THR	2.2
3	A	1101	LEU	2.2
7	E	23	VAL	2.2
3	A	92	HIS	2.2
4	B	847	ASP	2.2
3	A	277	GLU	2.2
3	A	1351	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
6	D	158	GLU	2.2
13	K	64	GLU	2.2
5	C	187	LYS	2.2
3	A	778	GLY	2.2
5	C	67	LEU	2.2
11	I	48	LEU	2.2
3	A	267	ALA	2.2
4	B	819	ALA	2.2
13	K	32	VAL	2.2
9	G	14	HIS	2.2
4	B	320	ASP	2.2
4	B	891	ASP	2.2
6	D	22	GLU	2.2
7	E	33	GLU	2.2
7	E	81	GLU	2.2
4	B	63	ILE	2.2
12	J	60	PHE	2.2
4	B	833	TYR	2.2
4	B	406	LEU	2.2
4	B	624	LEU	2.2
3	A	1125	ALA	2.2
4	B	200	GLY	2.2
4	B	871	THR	2.2
5	C	57	VAL	2.2
3	A	350	ARG	2.2
4	B	173	MET	2.2
1	T	16	DT	2.2
3	A	495	GLU	2.2
3	A	1121	GLU	2.2
6	D	206	GLU	2.2
4	B	41	LYS	2.2
5	C	160	LYS	2.2
4	B	850	LEU	2.2
7	E	186	LEU	2.2
3	A	17	VAL	2.2
10	H	101	ALA	2.2
13	K	40	HIS	2.2
15	S	188	CYS	2.2
3	A	560	ILE	2.2
15	S	202	ILE	2.2
4	B	573	GLN	2.2
4	B	1174	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
3	A	232	GLU	2.2
4	B	687	GLU	2.2
6	D	194	LEU	2.2
8	F	94	LEU	2.2
14	L	40	LEU	2.2
15	S	226	GLU	2.2
4	B	326	ASP	2.2
3	A	770	VAL	2.2
3	A	873	MET	2.2
6	D	39	ASN	2.2
9	G	138	THR	2.2
4	B	581	PHE	2.2
3	A	1046	LEU	2.2
3	A	1054	LEU	2.2
4	B	418	LYS	2.2
5	C	161	LYS	2.2
10	H	55	LEU	2.2
3	A	935	GLN	2.2
3	A	483	ASP	2.2
4	B	31	TRP	2.2
8	F	107	VAL	2.2
3	A	396	PRO	2.2
3	A	402	ALA	2.2
4	B	534	GLY	2.2
10	H	81	PRO	2.2
3	A	150	THR	2.2
3	A	670	ILE	2.2
3	A	361	LEU	2.2
4	B	193	LYS	2.2
13	K	77	THR	2.2
4	B	1032	SER	2.2
15	S	204	SER	2.2
6	D	213	GLU	2.2
8	F	109	VAL	2.2
3	A	1111	MET	2.2
3	A	1274	ARG	2.2
3	A	794	PRO	2.1
4	B	1035	ALA	2.1
4	B	1100	ASP	2.1
6	D	127	ASP	2.1
12	J	28	ASP	2.1
3	A	569	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
9	G	2	PHE	2.1
5	C	69	LEU	2.1
15	S	183	ASN	2.1
15	S	293	LEU	2.1
6	D	215	SER	2.1
9	G	24	GLN	2.1
9	G	75	ARG	2.1
13	K	54	ARG	2.1
4	B	1167	GLY	2.1
12	J	35	ALA	2.1
3	A	1132	LYS	2.1
4	B	34	ILE	2.1
7	E	60	PHE	2.1
3	A	287	HIS	2.1
3	A	899	VAL	2.1
3	A	937	VAL	2.1
9	G	48	VAL	2.1
3	A	1096	SER	2.1
4	B	126	SER	2.1
4	B	299	GLU	2.1
3	A	214	ILE	2.1
3	A	406	ILE	2.1
3	A	413	ILE	2.1
4	B	422	LYS	2.1
6	D	211	LEU	2.1
4	B	206	ASN	2.1
15	S	152	VAL	2.1
4	B	419	THR	2.1
11	I	55	THR	2.1
3	A	449	SER	2.1
6	D	73	SER	2.1
3	A	773	LYS	2.1
4	B	775	LYS	2.1
11	I	36	GLU	2.1
5	C	27	LEU	2.1
6	D	180	LEU	2.1
4	B	1043	ASP	2.1
5	C	145	CYS	2.1
6	D	205	ASP	2.1
9	G	34	VAL	2.1
11	I	91	ARG	2.1
3	A	40	THR	2.1

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Mol	Chain	Res	Type	RSRZ
3	A	1261	LYS	2.1
3	A	1321	GLY	2.1
5	C	13	ALA	2.1
3	A	72	GLU	2.1
4	B	641	GLU	2.1
4	B	856	PHE	2.1
9	G	99	PHE	2.1
10	H	112	ILE	2.1
11	I	16	PRO	2.1
3	A	42	ASP	2.1
3	A	720	ARG	2.1
4	B	267	ARG	2.1
5	C	19	ASP	2.1
8	F	77	ASP	2.1
4	B	533	CYS	2.1
3	A	836	TYR	2.1
3	A	682	THR	2.1
6	D	148	LEU	2.1
12	J	59	LYS	2.1
13	K	34	THR	2.1
13	K	41	THR	2.1
3	A	1084	PHE	2.1
4	B	948	ILE	2.1
4	B	958	GLN	2.1
9	G	8	SER	2.1
3	A	102	VAL	2.1
7	E	25	ASP	2.1
3	A	571	LEU	2.1
3	A	928	LEU	2.1
3	A	941	LYS	2.1
7	E	24	LYS	2.1
3	A	52	GLY	2.1
3	A	395	GLY	2.1
4	B	230	ALA	2.1
4	B	755	ILE	2.1
8	F	81	THR	2.1
4	B	869	SER	2.1
9	G	67	SER	2.1
4	B	289	LEU	2.0
4	B	1031	LEU	2.0
6	D	123	LEU	2.0
4	B	190	TYR	2.0

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Mol	Chain	Res	Type	RSRZ
3	A	1389	PHE	2.0
3	A	595	THR	2.0
3	A	698	GLN	2.0
4	B	592	ASN	2.0
4	B	680	THR	2.0
5	C	192	TRP	2.0
9	G	111	THR	2.0
13	K	38	GLU	2.0
3	A	911	SER	2.0
3	A	57	ARG	2.0
3	A	726	ARG	2.0
4	B	563	MET	2.0
5	C	253	LYS	2.0
6	D	207	LEU	2.0
3	A	582	ILE	2.0
4	B	627	PHE	2.0
3	A	892	ALA	2.0
4	B	608	ASP	2.0
4	B	274	PRO	2.0
4	B	64	CYS	2.0
4	B	68	THR	2.0
4	B	527	THR	2.0
4	B	681	TRP	2.0
11	I	3	THR	2.0
4	B	241	ARG	2.0
4	B	789	MET	2.0
6	D	13	ARG	2.0
9	G	22	MET	2.0
11	I	5	ARG	2.0
3	A	271	LYS	2.0
3	A	388	LEU	2.0
13	K	84	LYS	2.0
15	S	153	LEU	2.0
3	A	960	ILE	2.0
4	B	899	ILE	2.0
4	B	198	ASP	2.0
4	B	407	ASP	2.0
4	B	636	PRO	2.0
3	A	1326	ARG	2.0
15	S	230	THR	2.0
3	A	520	CYS	2.0
3	A	23	SER	2.0

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Mol	Chain	Res	Type	RSRZ
3	A	1047	SER	2.0
4	B	559	SER	2.0
7	E	105	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.