



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:42 PM GMT

PDB ID : 1Y1Y
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

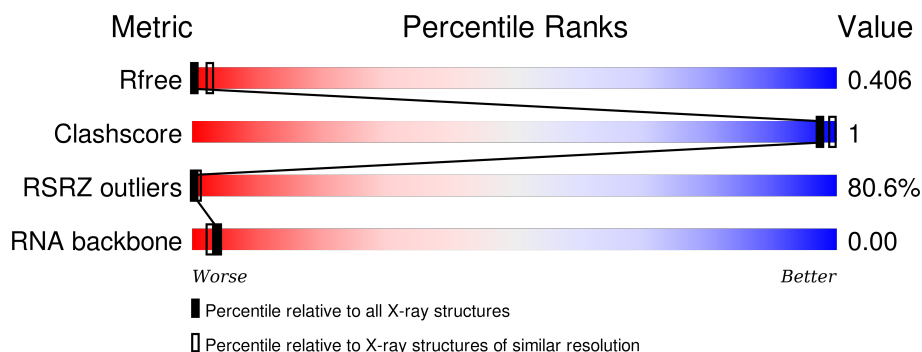
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


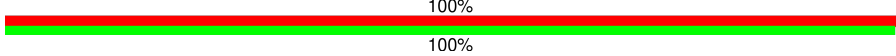

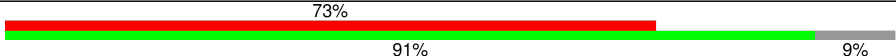


The reported resolution of this entry is 4.00 Å.

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}	91344	1010 (4.42-3.56)
Clashscore	102246	1052 (4.40-3.60)
RSRZ outliers	91569	1013 (4.42-3.56)
RNA backbone	2183	1079 (5.04-2.80)

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

Mol	Chain	Length	Quality of chain
1	T	7	
2	P	4	
3	A	1733	
4	B	1224	
5	C	318	
6	D	221	

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Mol	Chain	Length	Quality of chain
7	E	215	<div><div></div><div>86%</div><div>99%</div><div>.</div></div>
8	F	155	<div><div></div><div>43%</div><div>54%</div><div>46%</div></div>
9	G	171	<div><div></div><div>80%</div><div>99%</div><div>.</div></div>
10	H	146	<div><div></div><div>82%</div><div>91%</div><div>9%</div></div>
11	I	122	<div><div></div><div>93%</div><div>98%</div><div>.</div></div>
12	J	70	<div><div></div><div>83%</div><div>93%</div><div>7%</div></div>
13	K	120	<div><div></div><div>79%</div><div>95%</div><div>5%</div></div>
14	L	70	<div><div></div><div>57%</div><div>66%</div><div>34%</div></div>
15	S	179	<div><div></div><div>82%</div><div>95%</div><div>.</div><div>.</div></div>

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			

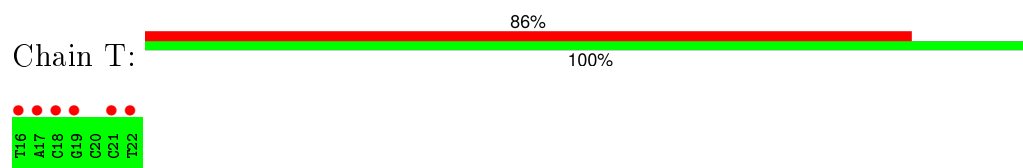
- Molecule 15 is a protein called Transcription elongation factor S-II.

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

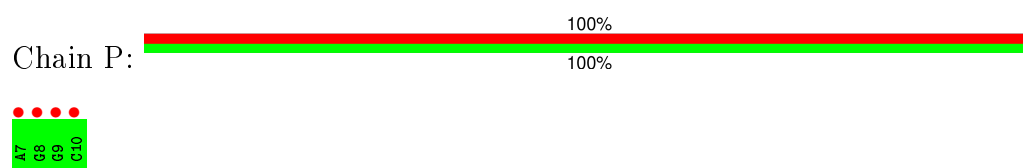
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

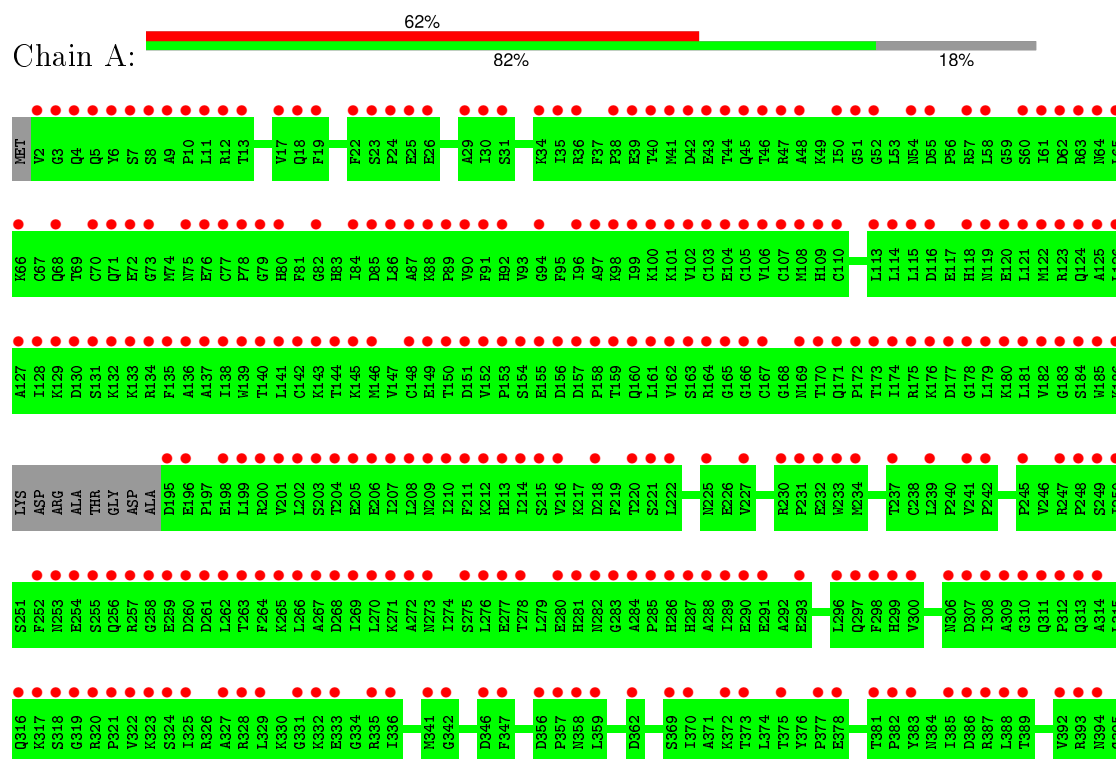
- Molecule 1: 5'-D(P*TP*AP*CP*GP*CP*CP*T)-3'



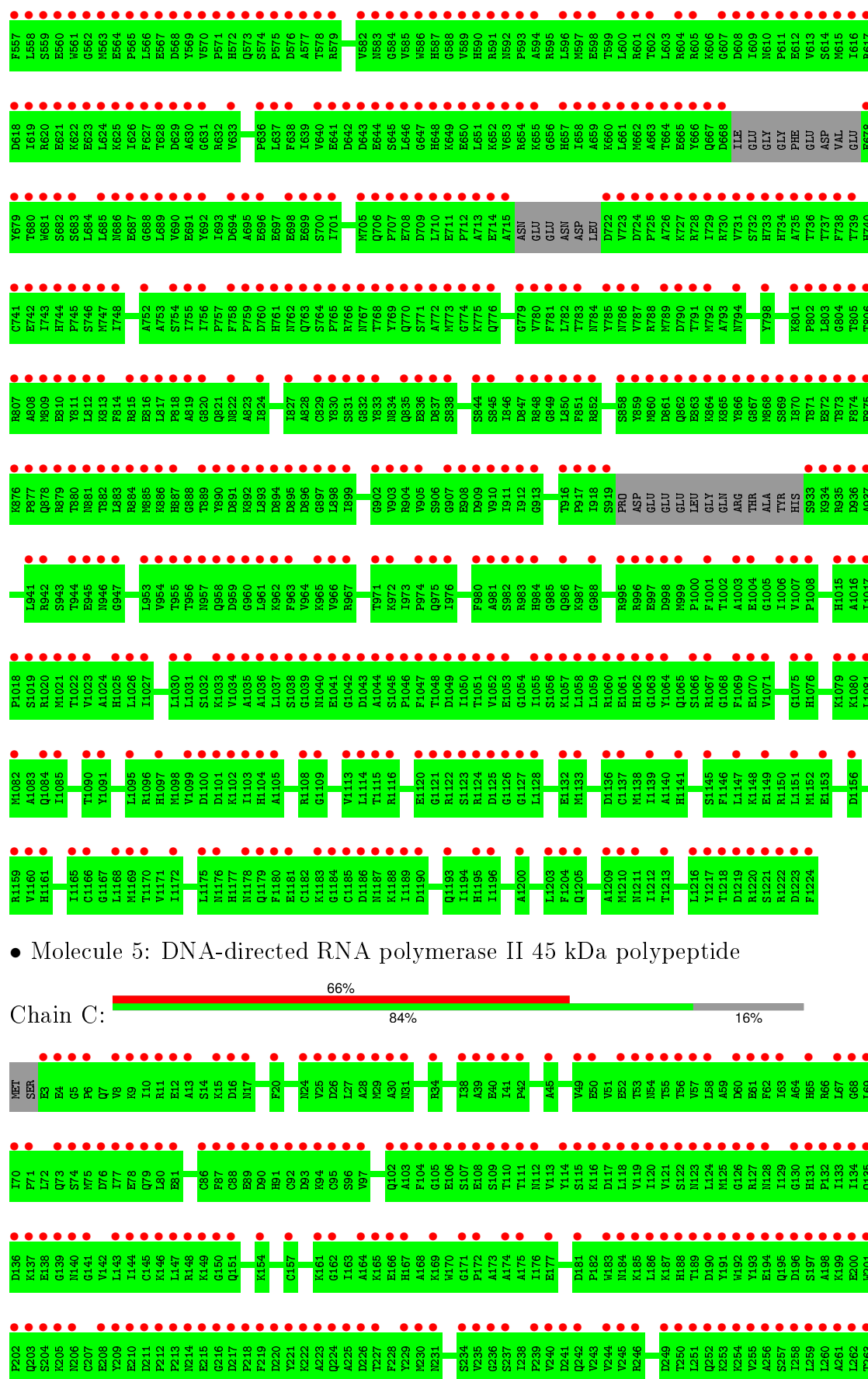
- Molecule 2: 5'-R(P*AP*GP*GP*C)-3'

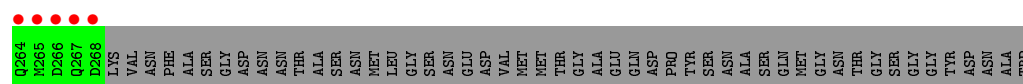


- Molecule 3: DNA-directed RNA polymerase II largest subunit

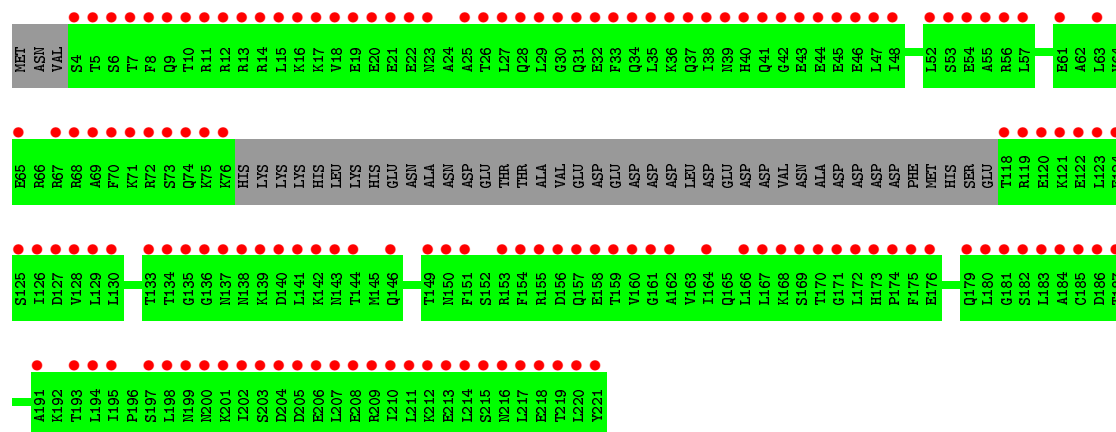
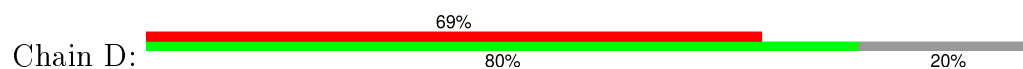




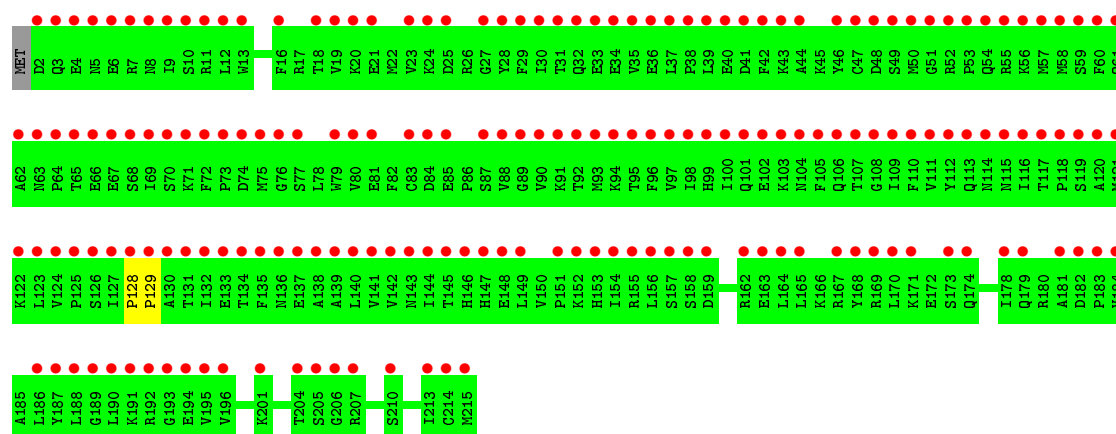
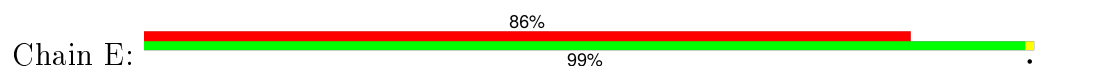




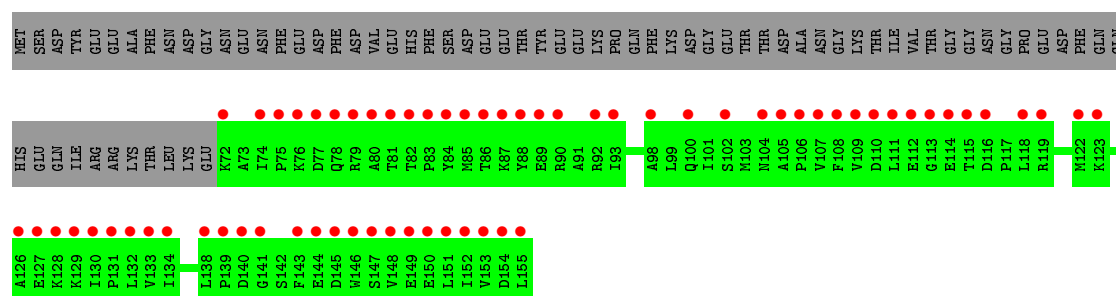
- Molecule 6: DNA-directed RNA polymerase II 32 kDa polypeptide



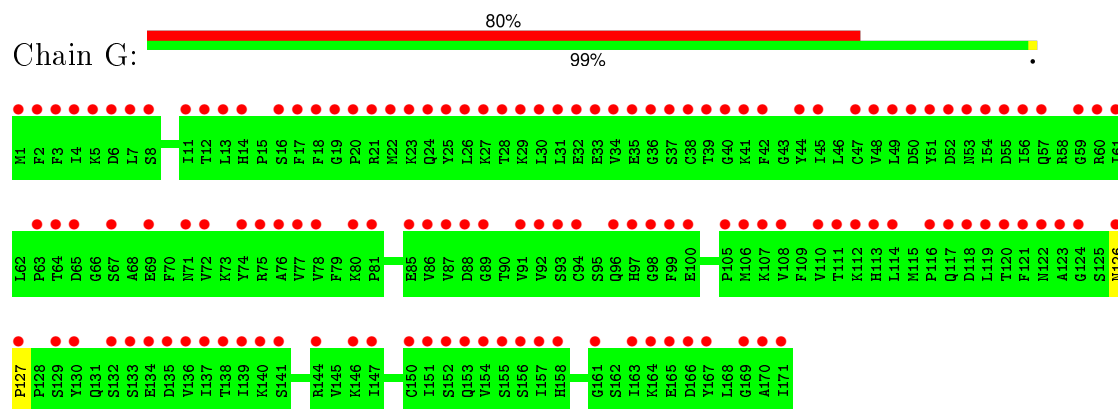
- Molecule 7: DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide



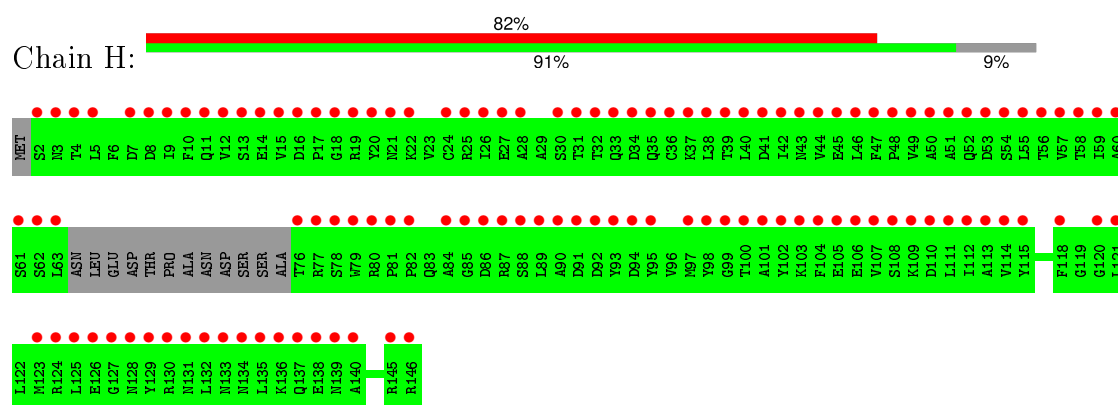
- Molecule 8: DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide



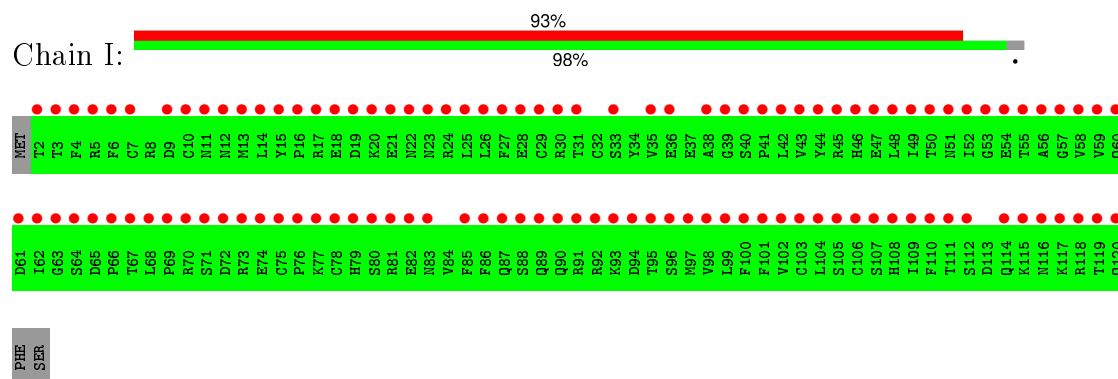
- Molecule 9: DNA-directed RNA polymerase II 19 kDa polypeptide



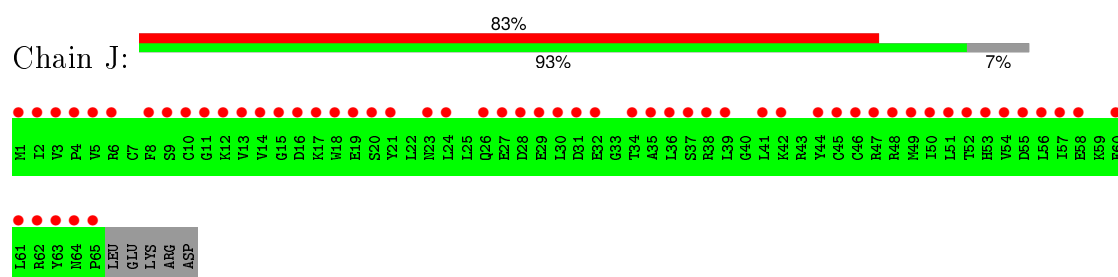
- Molecule 10: DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide



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

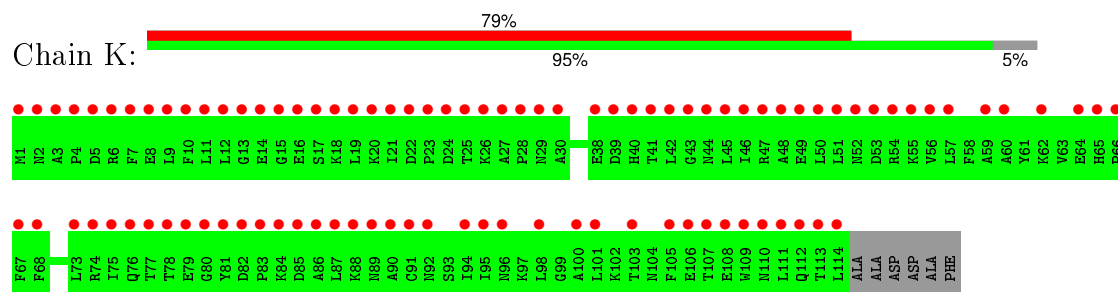


- Molecule 12: DNA-directed RNA polymerases I/II/III subunit 10



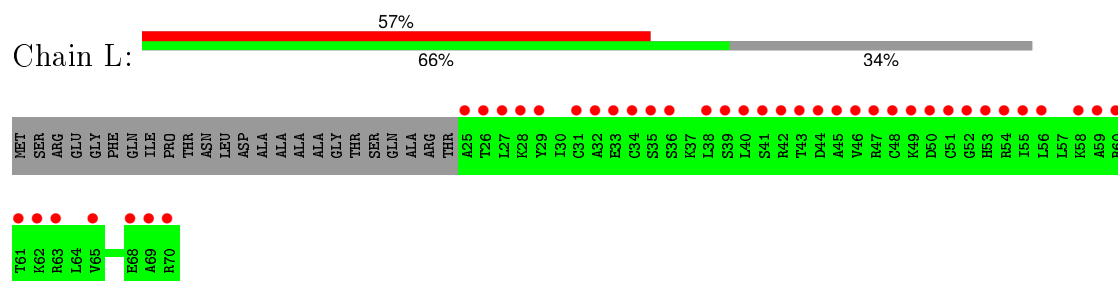
- Molecule 13: DNA-directed RNA polymerase II 13.6 kDa polypeptide

Chain K:



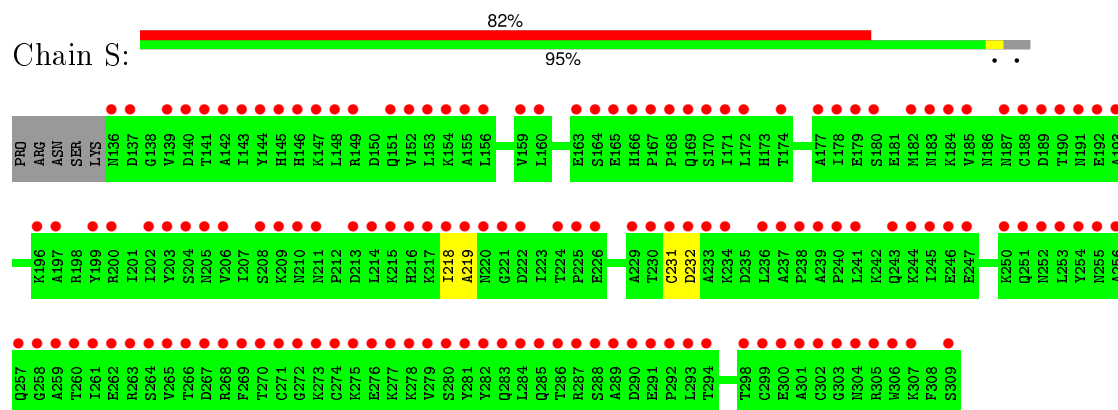
- Molecule 14: DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide

Chain L:



- Molecule 15: Transcription elongation factor S-II

Chain S:



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 39.19 – 3.98	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-4.00) 98.1 (39.19-3.98)	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) 0.410 , 0.406	Depositor DCC
R_{free} test set	2034 reflections (1.99%)	DCC
Wilson B-factor (Å ²)	106.8	Xtriage
Anisotropy	0.380	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 98.8	EDS
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
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 103460 reflections	Xtriage
F_o, F_c correlation	0.65	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, 0.375 respectively for untwinned datasets, and 0.333, 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 carbohydrates 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%)	3.28	6 (85%) 0 1	68, 74, 104, 109	0
2	P	4/4 (100%)	6.11	4 (100%) 0 0	82, 86, 92, 95	0
3	A	1426/1733 (82%)	5.86	1079 (75%) 0 1	19, 69, 145, 200	0
4	B	1104/1224 (90%)	6.85	897 (81%) 0 1	22, 82, 164, 198	0
5	C	266/318 (83%)	5.98	209 (78%) 0 1	38, 77, 136, 162	0
6	D	177/221 (80%)	7.39	152 (85%) 0 1	41, 93, 159, 174	0
7	E	214/215 (99%)	8.55	185 (86%) 0 1	39, 110, 172, 189	0
8	F	84/155 (54%)	5.30	66 (78%) 0 1	19, 53, 95, 117	0
9	G	171/171 (100%)	5.73	136 (79%) 0 1	43, 72, 110, 129	0
10	H	133/146 (91%)	9.72	120 (90%) 0 0	81, 132, 175, 192	0
11	I	119/122 (97%)	9.91	113 (94%) 0 0	64, 125, 171, 216	0
12	J	65/70 (92%)	5.91	58 (89%) 0 0	48, 72, 126, 138	0
13	K	114/120 (95%)	6.57	95 (83%) 0 1	40, 84, 137, 146	0
14	L	46/70 (65%)	8.15	40 (86%) 0 1	68, 134, 166, 187	0
15	S	174/179 (97%)	6.19	146 (83%) 0 1	50, 50, 124, 138	0
All	All	4104/4755 (86%)	6.62	3306 (80%) 0 1	19, 80, 159, 216	0

All (3306) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	C	211	ASP	40.2
7	E	118	PRO	38.1
3	A	312	PRO	36.9
3	A	1234	GLU	34.4
7	E	49	SER	34.2
3	A	281	HIS	34.0
15	S	136	ASN	33.7

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Mol	Chain	Res	Type	RSRZ
11	I	94	ASP	32.6
7	E	32	GLN	31.1
4	B	68	THR	31.1
4	B	90	ILE	30.5
4	B	617	ARG	29.8
3	A	1222	ASN	29.7
11	I	80	SER	29.6
6	D	118	THR	29.1
3	A	905	ASP	28.8
10	H	32	THR	28.2
4	B	668	ASP	27.1
4	B	1178	ASN	26.8
3	A	977	LYS	26.6
4	B	679	TYR	26.4
3	A	908	LEU	26.4
7	E	101	GLN	26.3
7	E	102	GLU	26.3
3	A	1085	HIS	26.2
10	H	87	ARG	26.1
3	A	127	ALA	25.6
13	K	113	THR	25.6
3	A	1094	VAL	25.4
4	B	592	ASN	25.4
9	G	133	SER	25.3
6	D	120	GLU	25.3
3	A	1112	LYS	25.2
4	B	647	GLY	25.2
3	A	1270	ASN	25.1
7	E	70	SER	25.1
3	A	736	ASN	25.0
3	A	1165	GLU	24.9
4	B	1176	ASN	24.9
6	D	200	ASN	24.9
8	F	77	ASP	24.6
5	C	215	GLU	24.6
13	K	25	THR	24.4
3	A	1160	SER	24.2
3	A	159	THR	24.1
6	D	41	GLN	24.1
6	D	68	ARG	24.1
3	A	1157	ASP	23.9
4	B	356	LEU	23.8

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Mol	Chain	Res	Type	RSRZ
11	I	71	SER	23.7
4	B	354	ASP	23.6
3	A	6	TYR	23.6
3	A	317	LYS	23.5
3	A	976	THR	23.5
10	H	53	ASP	23.5
4	B	165	VAL	23.5
4	B	166	PHE	23.5
7	E	91	LYS	23.3
3	A	1230	GLU	23.2
3	A	972	HIS	23.1
10	H	31	THR	23.1
14	L	44	ASP	23.1
11	I	107	SER	23.1
9	G	126	ASN	23.1
9	G	52	ASP	23.0
4	B	279	ASP	23.0
4	B	61	ASP	23.0
3	A	156	ASP	23.0
4	B	573	GLN	22.8
10	H	110	ASP	22.8
4	B	565	PRO	22.6
15	S	141	THR	22.2
15	S	285	GLN	22.1
4	B	230	ALA	22.0
10	H	50	ALA	22.0
7	E	57	MET	22.0
4	B	20	ASP	22.0
13	K	54	ARG	21.9
10	H	33	GLN	21.9
3	A	1166	ASP	21.8
5	C	109	SER	21.8
5	C	263	THR	21.8
4	B	432	MET	21.7
4	B	132	VAL	21.7
11	I	78	CYS	21.7
4	B	666	TYR	21.6
4	B	645	SER	21.6
15	S	143	ILE	21.6
3	A	64	ASN	21.6
9	G	55	ASP	21.6
5	C	214	ASN	21.5

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Mol	Chain	Res	Type	RSRZ
7	E	41	ASP	21.5
3	A	423	ASP	21.5
3	A	285	PRO	21.4
3	A	1158	PRO	21.4
3	A	1233	ASP	21.4
4	B	427	ASP	21.4
4	B	274	PRO	21.4
4	B	232	SER	21.4
7	E	10	SER	21.4
4	B	299	GLU	21.1
4	B	431	TYR	21.1
6	D	155	ARG	21.0
3	A	1235	LYS	21.0
7	E	119	SER	21.0
5	C	126	GLY	20.9
6	D	170	THR	20.8
11	I	40	SER	20.8
10	H	3	ASN	20.7
3	A	254	GLU	20.7
5	C	108	GLU	20.6
4	B	389	ALA	20.6
3	A	162	VAL	20.5
4	B	367	LEU	20.5
5	C	204	SER	20.4
7	E	132	ILE	20.4
7	E	73	PRO	20.4
4	B	665	GLU	20.4
3	A	1003	LYS	20.4
3	A	1130	GLN	20.4
4	B	680	THR	20.4
15	S	266	THR	20.3
4	B	27	ALA	20.3
4	B	562	GLY	20.3
3	A	151	ASP	20.3
4	B	275	TYR	20.3
4	B	649	LYS	20.3
9	G	156	SER	20.2
7	E	51	GLY	20.2
3	A	186	LYS	20.2
3	A	424	ILE	20.2
10	H	134	ASN	20.2
3	A	195	ASP	20.1

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Mol	Chain	Res	Type	RSRZ
7	E	133	GLU	20.0
11	I	55	THR	20.0
4	B	322	PHE	20.0
7	E	67	GLU	19.9
3	A	1359	ASP	19.9
10	H	94	ASP	19.9
3	A	568	PRO	19.9
13	K	82	ASP	19.9
4	B	652	LYS	19.7
12	J	31	ASP	19.7
11	I	72	ASP	19.7
11	I	82	GLU	19.6
14	L	38	LEU	19.4
4	B	867	GLY	19.4
10	H	90	ALA	19.4
4	B	1097	HIS	19.4
7	E	128	PRO	19.3
7	E	85	GLU	19.3
7	E	117	THR	19.2
4	B	261	ARG	19.2
11	I	65	ASP	19.2
9	G	117	GLN	19.1
3	A	1175	SER	19.1
4	B	790	ASP	19.1
14	L	25	ALA	19.0
3	A	286	HIS	19.0
15	S	267	ASP	19.0
5	C	213	PRO	18.9
7	E	84	ASP	18.9
4	B	874	PHE	18.9
5	C	123	ASN	18.9
4	B	646	LEU	18.7
4	B	713	ALA	18.7
10	H	92	ASP	18.7
5	C	217	ASP	18.7
3	A	593	GLU	18.7
10	H	17	PRO	18.7
3	A	155	GLU	18.7
4	B	96	TYR	18.7
11	I	119	THR	18.6
4	B	593	PRO	18.6
3	A	1173	HIS	18.5

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Mol	Chain	Res	Type	RSRZ
15	S	260	THR	18.5
9	G	33	GLU	18.5
4	B	25	ILE	18.4
11	I	3	THR	18.4
10	H	21	ASN	18.3
7	E	95	THR	18.3
10	H	34	ASP	18.3
3	A	1232	ASN	18.3
3	A	256	GLN	18.3
5	C	266	ASP	18.2
3	A	705	LYS	18.2
5	C	264	GLN	18.2
7	E	115	ASN	18.2
4	B	1183	LYS	18.2
4	B	884	ARG	18.2
4	B	576	ASP	18.2
3	A	702	LEU	18.1
4	B	437	GLU	18.1
10	H	137	GLN	18.1
3	A	703	THR	18.1
4	B	325	GLN	18.1
4	B	816	GLU	18.0
4	B	226	PHE	17.9
4	B	714	GLU	17.9
6	D	124	GLU	17.9
11	I	95	THR	17.9
3	A	1129	GLU	17.9
6	D	38	ILE	17.9
4	B	643	ASP	17.9
7	E	74	ASP	17.8
4	B	95	ILE	17.8
4	B	511	PRO	17.7
4	B	513	GLN	17.7
3	A	231	PRO	17.7
4	B	449	ASN	17.7
4	B	567	GLU	17.6
3	A	124	GLN	17.6
7	E	152	LYS	17.6
10	H	86	ASP	17.5
3	A	284	ALA	17.5
3	A	1200	ALA	17.5
7	E	5	ASN	17.5

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Mol	Chain	Res	Type	RSRZ
11	I	41	PRO	17.4
7	E	47	CYS	17.4
4	B	628	THR	17.4
4	B	575	PRO	17.4
3	A	43	GLU	17.4
11	I	120	GLN	17.4
4	B	350	GLN	17.4
6	D	213	GLU	17.3
13	K	52	ASN	17.3
4	B	131	ASP	17.3
4	B	837	ASP	17.3
10	H	25	ARG	17.2
4	B	306	ASN	17.2
4	B	1047	PHE	17.1
3	A	5	GLN	17.1
13	K	112	GLN	17.1
3	A	971	PHE	17.0
7	E	124	VAL	17.0
3	A	781	ASP	17.0
4	B	1051	THR	17.0
3	A	911	SER	17.0
3	A	1220	PHE	17.0
3	A	1242	VAL	16.9
3	A	174	ILE	16.9
3	A	1110	ASN	16.9
3	A	1300	LYS	16.9
8	F	78	GLN	16.9
6	D	171	GLY	16.9
7	E	182	ASP	16.9
14	L	42	ARG	16.9
4	B	98	THR	16.8
4	B	391	ASP	16.8
4	B	399	ASP	16.8
3	A	283	GLY	16.7
5	C	265	MET	16.7
5	C	106	GLU	16.7
4	B	415	GLN	16.6
3	A	426	LEU	16.6
3	A	1216	ILE	16.6
3	A	555	ASP	16.6
11	I	92	ARG	16.6
7	E	43	LYS	16.6

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Mol	Chain	Res	Type	RSRZ
3	A	160	GLN	16.6
3	A	276	LEU	16.5
4	B	869	SER	16.5
4	B	276	ILE	16.5
3	A	169	ASN	16.5
4	B	308	TRP	16.5
11	I	21	GLU	16.5
3	A	184	SER	16.5
7	E	106	GLN	16.4
12	J	64	ASN	16.4
4	B	661	LEU	16.4
6	D	204	ASP	16.4
4	B	224	GLN	16.4
4	B	552	MET	16.4
6	D	22	GLU	16.4
6	D	137	ASN	16.4
8	F	113	GLY	16.4
3	A	685	GLU	16.3
9	G	155	SER	16.3
7	E	87	SER	16.3
3	A	1320	PRO	16.3
8	F	112	GLU	16.2
3	A	1162	VAL	16.2
3	A	883	LEU	16.2
11	I	51	ASN	16.2
3	A	259	GLU	16.2
4	B	651	LEU	16.2
11	I	76	PRO	16.2
3	A	118	HIS	16.2
4	B	435	THR	16.2
7	E	54	GLN	16.1
4	B	451	LYS	16.1
3	A	582	ILE	16.1
4	B	737	THR	16.1
4	B	865	LYS	16.1
3	A	54	ASN	16.1
3	A	1171	GLN	16.1
4	B	262	GLU	16.0
11	I	50	THR	16.0
3	A	771	GLU	16.0
11	I	53	GLY	16.0
9	G	20	PRO	16.0

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Mol	Chain	Res	Type	RSRZ
11	I	64	SER	16.0
3	A	1161	THR	15.9
13	K	55	LYS	15.9
3	A	146	MET	15.9
3	A	250	ILE	15.9
4	B	622	LYS	15.9
6	D	20	GLU	15.8
4	B	26	THR	15.8
7	E	53	PRO	15.8
4	B	328	GLU	15.8
3	A	255	SER	15.8
10	H	4	THR	15.7
10	H	91	ASP	15.7
4	B	65	GLU	15.7
9	G	96	GLN	15.6
7	E	92	THR	15.6
4	B	181	LEU	15.6
13	K	17	SER	15.6
4	B	712	PRO	15.6
4	B	866	TYR	15.6
4	B	109	THR	15.6
9	G	166	ASP	15.6
3	A	209	ASN	15.6
8	F	154	ASP	15.6
4	B	24	PRO	15.6
4	B	917	PRO	15.6
7	E	40	GLU	15.5
3	A	104	GLU	15.5
11	I	57	GLY	15.5
4	B	1223	ASP	15.5
12	J	27	GLU	15.4
7	E	99	HIS	15.4
3	A	145	LYS	15.4
6	D	221	TYR	15.4
3	A	1164	PRO	15.3
4	B	587	HIS	15.3
3	A	172	PRO	15.3
7	E	52	ARG	15.3
7	E	100	ILE	15.3
7	E	137	GLU	15.3
6	D	9	GLN	15.3
4	B	618	ASP	15.2

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Mol	Chain	Res	Type	RSRZ
5	C	212	PRO	15.2
13	K	27	ALA	15.2
3	A	1325	THR	15.2
5	C	191	TYR	15.2
14	L	39	SER	15.2
8	F	83	PRO	15.2
3	A	737	LEU	15.2
10	H	131	ASN	15.2
11	I	61	ASP	15.1
4	B	919	SER	15.1
10	H	49	VAL	15.1
7	E	129	PRO	15.1
4	B	229	ALA	15.1
3	A	1167	GLU	15.1
4	B	654	ARG	15.1
4	B	958	GLN	15.1
7	E	126	SER	15.1
5	C	227	THR	15.0
10	H	146	ARG	15.0
4	B	278	GLN	15.0
9	G	165	GLU	15.0
3	A	318	SER	15.0
4	B	572	HIS	15.0
3	A	119	ASN	15.0
3	A	171	GLN	15.0
13	K	15	GLY	14.9
7	E	107	THR	14.9
4	B	1222	ARG	14.9
8	F	82	THR	14.9
5	C	216	GLY	14.9
3	A	1093	LYS	14.9
11	I	88	SER	14.9
4	B	228	LYS	14.9
12	J	38	ARG	14.9
11	I	56	ALA	14.9
3	A	1229	SER	14.9
4	B	70	ILE	14.8
4	B	208	SER	14.8
4	B	183	GLU	14.8
11	I	90	GLN	14.8
4	B	614	SER	14.8
10	H	102	TYR	14.8

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Mol	Chain	Res	Type	RSRZ
4	B	241	ARG	14.7
4	B	1224	PHE	14.7
3	A	924	LYS	14.7
5	C	140	ASN	14.7
10	H	109	LYS	14.7
14	L	27	LEU	14.7
3	A	909	ASP	14.6
4	B	446	LEU	14.6
11	I	54	GLU	14.6
5	C	205	LYS	14.6
10	H	89	LEU	14.6
4	B	664	THR	14.6
3	A	198	GLU	14.6
14	L	41	SER	14.6
4	B	360	PHE	14.6
4	B	265	SER	14.5
10	H	47	PHE	14.5
11	I	4	PHE	14.5
4	B	885	MET	14.5
4	B	1050	ILE	14.5
3	A	525	GLN	14.5
10	H	55	LEU	14.5
14	L	45	ALA	14.4
4	B	347	LYS	14.3
10	H	2	SER	14.3
4	B	353	LYS	14.3
3	A	8	SER	14.3
4	B	113	TYR	14.3
3	A	738	LYS	14.3
3	A	1454	MET	14.3
4	B	324	ILE	14.2
3	A	1226	VAL	14.2
9	G	122	ASN	14.2
15	S	152	VAL	14.2
3	A	149	GLU	14.2
7	E	96	PHE	14.2
3	A	105	CYS	14.2
10	H	135	LEU	14.2
10	H	138	GLU	14.2
4	B	469	GLN	14.2
4	B	705	MET	14.2
4	B	304	ASP	14.1

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Mol	Chain	Res	Type	RSRZ
3	A	115	LEU	14.1
13	K	89	ASN	14.1
3	A	884	ASP	14.1
10	H	79	TRP	14.1
13	K	14	GLU	14.1
3	A	175	ARG	14.1
3	A	728	LYS	14.0
4	B	870	ILE	14.0
7	E	50	MET	14.0
4	B	711	GLU	14.0
8	F	116	ASP	14.0
3	A	1420	ASP	14.0
4	B	293	PRO	14.0
4	B	626	ILE	14.0
9	G	138	THR	13.9
11	I	96	SER	13.9
3	A	1254	ALA	13.9
4	B	886	LYS	13.9
11	I	118	ARG	13.9
4	B	434	ARG	13.9
11	I	30	ARG	13.9
10	H	136	LYS	13.9
4	B	1179	GLN	13.9
4	B	642	ASP	13.9
3	A	290	GLU	13.8
3	A	676	MET	13.8
9	G	51	TYR	13.8
14	L	26	THR	13.8
11	I	46	HIS	13.8
3	A	1191	TRP	13.8
3	A	288	ALA	13.8
3	A	898	ARG	13.8
3	A	150	THR	13.7
4	B	736	THR	13.7
5	C	268	ASP	13.7
15	S	264	SER	13.7
3	A	275	SER	13.7
3	A	978	PRO	13.7
4	B	868	MET	13.7
13	K	64	GLU	13.7
4	B	398	ARG	13.7
4	B	273	LEU	13.7

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Mol	Chain	Res	Type	RSRZ
10	H	129	TYR	13.7
3	A	218	ASP	13.7
3	A	889	SER	13.7
11	I	24	ARG	13.7
7	E	33	GLU	13.7
4	B	63	ILE	13.6
3	A	63	ARG	13.6
5	C	203	GLN	13.6
4	B	883	LEU	13.6
3	A	154	SER	13.6
10	H	128	ASN	13.6
3	A	1260	LEU	13.6
5	C	89	GLU	13.6
4	B	916	THR	13.5
4	B	420	LEU	13.5
3	A	731	ARG	13.5
8	F	111	LEU	13.5
3	A	202	LEU	13.4
11	I	108	HIS	13.4
9	G	134	GLU	13.4
11	I	116	ASN	13.4
15	S	261	ILE	13.4
4	B	206	ASN	13.4
7	E	39	LEU	13.4
4	B	129	PHE	13.4
7	E	90	VAL	13.3
3	A	726	ARG	13.3
10	H	130	ARG	13.3
3	A	1205	LYS	13.3
11	I	77	LYS	13.3
4	B	177	LYS	13.3
6	D	12	ARG	13.3
3	A	1190	PRO	13.2
7	E	123	LEU	13.2
3	A	982	THR	13.2
4	B	192	LEU	13.2
12	J	51	LEU	13.2
15	S	189	ASP	13.2
15	S	269	PHE	13.2
3	A	636	GLU	13.2
4	B	361	LEU	13.2
4	B	171	PRO	13.2

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Mol	Chain	Res	Type	RSRZ
10	H	16	ASP	13.2
4	B	335	GLY	13.1
3	A	1302	PRO	13.1
10	H	80	ARG	13.1
3	A	904	THR	13.1
4	B	678	GLU	13.1
15	S	168	PRO	13.1
13	K	26	LYS	13.1
4	B	836	GLU	13.1
4	B	64	CYS	13.1
4	B	249	ARG	13.1
3	A	1080	THR	13.1
4	B	320	ASP	13.1
9	G	127	PRO	13.1
6	D	172	LEU	13.1
4	B	1190	ASP	13.1
3	A	170	THR	13.1
3	A	670	ILE	13.0
5	C	3	GLU	13.0
6	D	28	GLN	13.0
4	B	783	THR	13.0
4	B	477	ALA	13.0
13	K	114	LEU	13.0
13	K	29	ASN	13.0
3	A	1091	SER	13.0
4	B	1063	GLY	13.0
11	I	106	CYS	12.9
4	B	116	GLU	12.9
9	G	81	PRO	12.9
4	B	390	LEU	12.9
5	C	260	LEU	12.9
5	C	90	ASP	12.9
11	I	63	GLY	12.9
7	E	31	THR	12.9
4	B	134	LYS	12.9
4	B	560	GLU	12.9
7	E	170	LEU	12.9
8	F	127	GLU	12.9
3	A	1001	ARG	12.9
7	E	98	ILE	12.9
11	I	44	TYR	12.9
15	S	282	TYR	12.9

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Mol	Chain	Res	Type	RSRZ
3	A	253	ASN	12.8
4	B	191	LYS	12.8
4	B	559	SER	12.8
4	B	653	VAL	12.8
3	A	1390	ASN	12.8
10	H	61	SER	12.8
4	B	830	TYR	12.8
10	H	76	THR	12.8
15	S	247	GLU	12.8
3	A	214	ILE	12.8
3	A	447	GLN	12.7
4	B	346	GLU	12.7
12	J	29	GLU	12.7
4	B	395	GLN	12.7
3	A	1082	ASN	12.7
6	D	186	ASP	12.7
7	E	77	SER	12.7
3	A	1143	LEU	12.7
3	A	1382	THR	12.7
8	F	129	LYS	12.7
10	H	58	THR	12.7
4	B	887	HIS	12.7
3	A	1187	GLN	12.7
4	B	547	VAL	12.7
3	A	1095	THR	12.7
4	B	706	GLN	12.6
3	A	704	ALA	12.6
3	A	1334	ASP	12.6
9	G	113	HIS	12.6
11	I	62	ILE	12.6
13	K	13	GLY	12.6
5	C	135	GLN	12.6
6	D	134	THR	12.6
4	B	309	GLN	12.6
11	I	109	ILE	12.6
3	A	437	MET	12.5
4	B	657	HIS	12.5
3	A	36	ARG	12.5
3	A	479	ASN	12.5
3	A	1203	ASN	12.5
3	A	995	GLU	12.5
3	A	701	LEU	12.5

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Mol	Chain	Res	Type	RSRZ
4	B	891	ASP	12.5
4	B	1052	VAL	12.5
7	E	13	TRP	12.5
4	B	893	LEU	12.5
4	B	277	LYS	12.4
4	B	594	ALA	12.4
7	E	93	MET	12.4
3	A	427	GLN	12.4
3	A	974	ASP	12.4
3	A	1261	LYS	12.4
3	A	75	ASN	12.4
10	H	13	SER	12.4
3	A	1010	ALA	12.3
15	S	221	GLY	12.3
4	B	362	PRO	12.3
6	D	205	ASP	12.3
4	B	310	MET	12.3
3	A	822	GLU	12.3
3	A	249	SER	12.3
3	A	829	VAL	12.3
4	B	252	SER	12.3
3	A	1228	TRP	12.3
3	A	1269	GLU	12.3
4	B	396	ASP	12.3
3	A	1317	MET	12.3
4	B	597	MET	12.3
4	B	436	VAL	12.3
3	A	62	ASP	12.3
3	A	1172	LEU	12.2
13	K	5	ASP	12.2
4	B	66	ASP	12.2
7	E	7	ARG	12.2
4	B	97	VAL	12.2
7	E	204	THR	12.2
7	E	38	PRO	12.2
6	D	73	SER	12.2
4	B	264	SER	12.2
4	B	332	ASP	12.2
3	A	1138	ILE	12.2
4	B	935	ARG	12.1
14	L	46	VAL	12.1
9	G	97	HIS	12.1

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Mol	Chain	Res	Type	RSRZ
15	S	272	GLY	12.1
4	B	975	GLN	12.1
4	B	448	ILE	12.1
3	A	1231	ASP	12.1
5	C	181	ASP	12.1
10	H	5	LEU	12.1
3	A	215	SER	12.1
13	K	53	ASP	12.1
4	B	112	LEU	12.0
3	A	425	GLN	12.0
5	C	124	LEU	12.0
3	A	975	HIS	12.0
10	H	52	GLN	12.0
4	B	429	PHE	12.0
4	B	896	ASP	12.0
6	D	29	LEU	12.0
4	B	509	ALA	12.0
3	A	109	HIS	12.0
12	J	32	GLU	12.0
6	D	158	GLU	12.0
7	E	60	PHE	12.0
15	S	240	PRO	12.0
4	B	514	LEU	12.0
15	S	293	LEU	12.0
4	B	880	THR	11.9
3	A	786	HIS	11.9
4	B	313	MET	11.9
9	G	64	THR	11.9
11	I	98	VAL	11.9
3	A	1208	THR	11.9
4	B	724	ASP	11.9
3	A	157	ASP	11.9
4	B	550	ASP	11.9
4	B	371	GLU	11.9
6	D	212	LYS	11.9
6	D	14	ARG	11.9
7	E	138	ALA	11.9
11	I	5	ARG	11.9
3	A	919	ILE	11.9
5	C	223	ALA	11.9
4	B	602	THR	11.8
4	B	69	LEU	11.8

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Mol	Chain	Res	Type	RSRZ
3	A	221	SER	11.8
3	A	179	LEU	11.8
5	C	53	THR	11.8
4	B	102	VAL	11.8
6	D	70	PHE	11.8
3	A	985	ASP	11.8
3	A	537	ARG	11.8
4	B	561	TRP	11.8
3	A	410	GLY	11.8
4	B	447	ALA	11.8
7	E	69	ILE	11.8
10	H	81	PRO	11.8
3	A	311	GLN	11.7
15	S	255	ASN	11.7
6	D	15	LEU	11.7
6	D	220	LEU	11.7
10	H	60	ALA	11.7
3	A	164	ARG	11.7
4	B	508	LEU	11.7
4	B	610	ASN	11.7
4	B	563	MET	11.6
3	A	1204	ASP	11.6
3	A	185	TRP	11.6
3	A	970	THR	11.6
6	D	44	GLU	11.6
4	B	280	ILE	11.6
4	B	1044	ALA	11.6
3	A	116	ASP	11.6
3	A	1188	GLN	11.5
9	G	120	THR	11.5
9	G	129	SER	11.5
7	E	127	ILE	11.5
3	A	1277	GLU	11.5
4	B	502	ILE	11.5
4	B	726	ALA	11.5
4	B	424	LEU	11.5
6	D	32	GLU	11.5
4	B	105	SER	11.5
4	B	613	VAL	11.5
4	B	667	GLN	11.5
10	H	114	VAL	11.4
3	A	178	GLY	11.4

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Mol	Chain	Res	Type	RSRZ
4	B	33	VAL	11.4
10	H	14	GLU	11.4
10	H	43	ASN	11.4
5	C	110	THR	11.4
6	D	11	ARG	11.4
4	B	564	GLU	11.4
4	B	554	ILE	11.3
14	L	43	THR	11.3
4	B	305	VAL	11.3
3	A	23	SER	11.3
3	A	158	PRO	11.3
4	B	933	SER	11.3
3	A	1107	VAL	11.3
6	D	201	LYS	11.3
14	L	35	SER	11.3
14	L	63	ARG	11.3
4	B	297	ILE	11.3
5	C	125	MET	11.3
10	H	40	LEU	11.3
15	S	288	SER	11.2
4	B	40	GLU	11.2
3	A	1163	ILE	11.2
3	A	1207	LEU	11.2
6	D	37	GLN	11.2
12	J	19	GLU	11.2
4	B	93	GLY	11.2
3	A	827	THR	11.2
4	B	1020	ARG	11.2
3	A	61	ILE	11.2
4	B	648	HIS	11.2
4	B	355	ILE	11.2
4	B	461	LEU	11.1
10	H	18	GLY	11.1
4	B	369	GLY	11.1
4	B	548	GLY	11.1
10	H	105	GLU	11.1
3	A	860	LEU	11.1
3	A	386	ASP	11.1
3	A	1168	GLU	11.1
6	D	13	ARG	11.1
11	I	6	PHE	11.1
6	D	135	GLY	11.1

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Mol	Chain	Res	Type	RSRZ
4	B	786	ASN	11.1
4	B	863	GLU	11.1
3	A	481	ASP	11.1
4	B	370	PHE	11.1
3	A	600	PRO	11.1
4	B	474	SER	11.1
3	A	1267	MET	11.1
7	E	4	GLU	11.1
3	A	78	PRO	11.0
6	D	76	LYS	11.0
6	D	4	SER	11.0
7	E	18	THR	11.0
8	F	139	PRO	11.0
3	A	72	GLU	11.0
6	D	40	HIS	11.0
3	A	930	ASP	11.0
3	A	399	HIS	11.0
3	A	1206	ASP	10.9
5	C	195	GLN	10.9
3	A	392	VAL	10.9
3	A	480	ALA	10.9
6	D	173	HIS	10.9
3	A	103	CYS	10.9
3	A	80	HIS	10.9
7	E	148	GLU	10.9
4	B	421	PHE	10.9
3	A	322	VAL	10.9
4	B	909	ASP	10.9
15	S	301	ALA	10.9
15	S	291	GLU	10.9
14	L	61	THR	10.9
12	J	16	ASP	10.9
3	A	748	MET	10.9
4	B	733	HIS	10.8
5	C	79	GLN	10.8
3	A	1124	HIS	10.8
10	H	132	LEU	10.8
15	S	245	ILE	10.8
11	I	60	GLN	10.8
3	A	791	ASP	10.8
3	A	597	LEU	10.8
4	B	959	ASP	10.8

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Mol	Chain	Res	Type	RSRZ
3	A	1202	MET	10.8
4	B	807	ARG	10.8
3	A	76	GLU	10.7
5	C	244	VAL	10.7
7	E	121	MET	10.7
3	A	569	LYS	10.7
3	A	1127	ASP	10.7
3	A	1011	GLN	10.7
7	E	6	GLU	10.7
3	A	617	VAL	10.7
11	I	97	MET	10.7
4	B	579	ARG	10.7
8	F	107	VAL	10.7
4	B	641	GLU	10.7
4	B	625	LYS	10.7
4	B	743	ILE	10.7
4	B	892	LYS	10.7
4	B	110	HIS	10.6
3	A	148	CYS	10.6
7	E	56	LYS	10.6
4	B	267	ARG	10.6
9	G	116	PRO	10.6
5	C	202	PRO	10.6
15	S	304	ASN	10.6
4	B	946	ASN	10.5
5	C	58	LEU	10.5
4	B	1043	ASP	10.5
4	B	732	SER	10.5
3	A	1090	ALA	10.5
9	G	29	LYS	10.5
3	A	51	GLY	10.5
10	H	84	ALA	10.5
3	A	1263	ILE	10.5
5	C	4	GLU	10.5
3	A	693	VAL	10.5
4	B	167	ILE	10.5
5	C	220	ASP	10.5
4	B	311	LEU	10.5
10	H	63	LEU	10.5
10	H	35	GLN	10.5
5	C	56	THR	10.4
6	D	180	LEU	10.4

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Mol	Chain	Res	Type	RSRZ
3	A	47	ARG	10.4
3	A	289	ILE	10.4
7	E	9	ILE	10.4
3	A	1387	HIS	10.4
5	C	24	ASN	10.4
6	D	157	GLN	10.4
4	B	604	ARG	10.4
3	A	420	ARG	10.4
5	C	221	TYR	10.4
14	L	49	LYS	10.4
6	D	184	ALA	10.4
3	A	1122	PRO	10.3
3	A	948	VAL	10.3
4	B	133	LYS	10.3
11	I	58	VAL	10.3
12	J	54	VAL	10.3
3	A	959	ASN	10.3
4	B	776	GLN	10.3
4	B	248	SER	10.3
13	K	1	MET	10.3
4	B	945	GLU	10.3
3	A	200	ARG	10.3
11	I	112	SER	10.3
3	A	86	LEU	10.3
3	A	895	LYS	10.3
9	G	57	GLN	10.3
4	B	710	LEU	10.2
4	B	285	ILE	10.2
4	B	860	MET	10.2
3	A	584	ASN	10.2
4	B	318	VAL	10.2
3	A	793	SER	10.2
3	A	776	ALA	10.2
3	A	1174	PHE	10.2
4	B	47	GLN	10.2
10	H	45	GLU	10.2
4	B	412	LEU	10.2
3	A	1329	THR	10.2
10	H	108	SER	10.2
3	A	1087	ALA	10.2
3	A	65	LEU	10.2
9	G	137	ILE	10.2

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Mol	Chain	Res	Type	RSRZ
6	D	136	GLY	10.1
7	E	37	LEU	10.1
13	K	12	LEU	10.1
13	K	75	ILE	10.1
4	B	722	ASP	10.1
3	A	792	TYR	10.1
4	B	570	VAL	10.1
6	D	16	LYS	10.1
7	E	2	ASP	10.1
3	A	1243	VAL	10.1
3	A	1109	LYS	10.1
7	E	3	GLN	10.1
4	B	1186	ASP	10.1
11	I	25	LEU	10.0
11	I	115	LYS	10.0
3	A	965	GLN	10.0
3	A	724	GLU	10.0
15	S	241	LEU	10.0
3	A	291	GLU	10.0
13	K	98	LEU	10.0
15	S	222	ASP	10.0
3	A	973	ILE	10.0
6	D	10	THR	10.0
6	D	130	LEU	10.0
9	G	153	GLN	10.0
10	H	112	ILE	10.0
10	H	10	PHE	10.0
3	A	539	THR	10.0
3	A	996	ASN	10.0
10	H	8	ASP	10.0
4	B	36	ALA	10.0
5	C	136	ASP	9.9
3	A	412	ARG	9.9
4	B	349	ILE	9.9
9	G	56	ILE	9.9
4	B	1101	ASP	9.9
11	I	117	LYS	9.9
4	B	619	ILE	9.9
4	B	99	LYS	9.9
5	C	190	ASP	9.9
6	D	7	THR	9.9
6	D	71	LYS	9.9

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Mol	Chain	Res	Type	RSRZ
4	B	596	LEU	9.9
4	B	611	PRO	9.9
4	B	864	LYS	9.9
3	A	108	MET	9.9
3	A	773	LYS	9.9
4	B	212	LEU	9.9
4	B	609	ILE	9.9
4	B	242	SER	9.9
3	A	1078	GLN	9.9
4	B	890	TYR	9.9
4	B	787	VAL	9.9
3	A	1123	GLY	9.8
4	B	731	VAL	9.8
6	D	150	ASN	9.8
4	B	735	ALA	9.8
14	L	51	CYS	9.8
4	B	55	VAL	9.8
10	H	139	ASN	9.8
4	B	345	LYS	9.8
3	A	476	SER	9.8
7	E	55	ARG	9.8
6	D	217	LEU	9.8
3	A	723	ASN	9.8
14	L	53	HIS	9.8
4	B	104	GLU	9.8
3	A	102	VAL	9.8
3	A	735	VAL	9.7
3	A	1262	LYS	9.8
3	A	1028	THR	9.7
4	B	986	GLN	9.7
9	G	123	ALA	9.7
4	B	798	TYR	9.7
3	A	397	ASN	9.7
3	A	113	LEU	9.7
3	A	920	LEU	9.7
13	K	96	ASN	9.7
4	B	364	ILE	9.7
7	E	72	PHE	9.7
4	B	417	PHE	9.7
5	C	71	PRO	9.7
15	S	278	LYS	9.7
7	E	83	CYS	9.7

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Mol	Chain	Res	Type	RSRZ
12	J	5	VAL	9.7
15	S	305	ARG	9.7
4	B	170	LEU	9.7
3	A	1113	THR	9.7
9	G	39	THR	9.7
3	A	88	LYS	9.6
7	E	122	LYS	9.6
3	A	678	GLU	9.6
6	D	17	LYS	9.6
3	A	672	ASP	9.6
3	A	585	GLY	9.6
4	B	244	LEU	9.6
3	A	1036	ARG	9.6
3	A	204	THR	9.6
4	B	1040	ASN	9.6
13	K	48	ALA	9.6
14	L	40	LEU	9.6
3	A	554	PRO	9.6
12	J	34	THR	9.6
4	B	812	LEU	9.6
3	A	1132	LYS	9.6
11	I	69	PRO	9.6
8	F	110	ASP	9.6
14	L	29	TYR	9.6
14	L	60	ARG	9.6
4	B	568	ASP	9.5
4	B	934	LYS	9.5
3	A	560	ILE	9.5
3	A	201	VAL	9.5
11	I	86	PHE	9.5
6	D	219	THR	9.5
10	H	39	THR	9.5
3	A	7	SER	9.5
4	B	247	GLY	9.5
4	B	1016	ALA	9.5
15	S	220	ASN	9.5
4	B	394	ASP	9.5
3	A	594	GLY	9.5
11	I	10	CYS	9.5
6	D	156	ASP	9.5
6	D	72	ARG	9.5
7	E	131	THR	9.5

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Mol	Chain	Res	Type	RSRZ
15	S	178	ILE	9.5
3	A	583	PRO	9.5
5	C	262	LEU	9.5
4	B	401	PHE	9.5
6	D	168	LYS	9.5
5	C	15	LYS	9.5
5	C	144	ILE	9.5
15	S	171	ILE	9.4
3	A	1255	GLU	9.4
4	B	28	GLU	9.4
3	A	1154	TYR	9.4
4	B	510	LYS	9.4
6	D	42	GLY	9.4
3	A	323	LYS	9.4
3	A	177	ASP	9.4
4	B	681	TRP	9.4
11	I	83	ASN	9.4
5	C	78	GLU	9.4
4	B	1025	HIS	9.4
3	A	165	GLY	9.4
4	B	468	GLU	9.4
8	F	115	THR	9.4
4	B	186	GLU	9.3
15	S	284	LEU	9.3
3	A	196	GLU	9.3
3	A	213	HIS	9.3
13	K	41	THR	9.3
3	A	1447	GLU	9.3
4	B	314	LEU	9.3
11	I	23	ASN	9.3
3	A	1145	SER	9.3
3	A	1448	GLU	9.3
4	B	910	VAL	9.3
3	A	1134	ILE	9.3
3	A	230	ARG	9.3
4	B	621	GLU	9.3
3	A	122	MET	9.3
3	A	128	ILE	9.3
4	B	768	THR	9.3
9	G	54	ILE	9.3
9	G	18	PHE	9.3
3	A	1291	VAL	9.3

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Mol	Chain	Res	Type	RSRZ
4	B	549	THR	9.2
15	S	268	ARG	9.2
7	E	158	SER	9.2
3	A	910	PRO	9.2
6	D	21	GLU	9.2
3	A	669	THR	9.2
3	A	1227	ILE	9.2
3	A	1199	ARG	9.2
4	B	889	THR	9.2
3	A	1264	GLU	9.2
5	C	139	GLY	9.2
10	H	37	LYS	9.2
15	S	253	LEU	9.2
4	B	1195	HIS	9.2
3	A	1038	THR	9.2
10	H	104	PHE	9.2
11	I	110	PHE	9.2
4	B	92	PHE	9.2
4	B	715	ALA	9.2
5	C	5	GLY	9.2
4	B	686	ASN	9.2
4	B	899	ILE	9.2
4	B	260	GLY	9.2
3	A	167	CYS	9.1
6	D	166	LEU	9.1
5	C	258	ILE	9.1
3	A	742	ASN	9.1
4	B	125	SER	9.1
3	A	94	GLY	9.1
4	B	180	TYR	9.1
4	B	453	ILE	9.1
3	A	1176	LEU	9.1
10	H	126	GLU	9.1
4	B	323	VAL	9.1
5	C	134	ILE	9.1
3	A	176	LYS	9.0
3	A	1265	ASN	9.0
4	B	1045	SER	9.0
3	A	659	HIS	9.0
4	B	387	LEU	9.0
13	K	65	HIS	9.0
3	A	1238	ILE	9.0

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Mol	Chain	Res	Type	RSRZ
5	C	194	GLU	9.0
3	A	567	LYS	9.0
7	E	12	LEU	9.0
4	B	725	PRO	9.0
4	B	734	HIS	9.0
3	A	257	ARG	8.9
9	G	154	VAL	8.9
7	E	27	GLY	8.9
3	A	48	ALA	8.9
3	A	598	LEU	8.9
4	B	43	LEU	8.9
3	A	1455	PRO	8.9
4	B	30	SER	8.9
7	E	16	PHE	8.9
6	D	128	VAL	8.9
3	A	107	CYS	8.9
5	C	242	GLN	8.9
3	A	448	PRO	8.9
3	A	306	ASN	8.9
5	C	26	ASP	8.9
4	B	688	GLY	8.9
12	J	57	ILE	8.9
12	J	30	LEU	8.9
3	A	163	SER	8.9
4	B	918	ILE	8.9
11	I	111	THR	8.9
15	S	151	GLN	8.9
4	B	289	LEU	8.8
3	A	1224	LEU	8.8
13	K	67	PHE	8.8
6	D	181	GLY	8.8
8	F	108	PHE	8.8
3	A	896	ARG	8.8
7	E	125	PRO	8.8
4	B	600	LEU	8.8
4	B	528	PRO	8.8
5	C	257	SER	8.8
3	A	668	ASP	8.8
9	G	167	TYR	8.8
3	A	601	LYS	8.8
11	I	49	ILE	8.8
3	A	66	LYS	8.8

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Mol	Chain	Res	Type	RSRZ
3	A	1278	ASN	8.8
15	S	250	LYS	8.8
3	A	588	LEU	8.8
4	B	22	SER	8.8
15	S	172	LEU	8.8
3	A	603	ASN	8.8
7	E	112	TYR	8.8
5	C	150	GLY	8.8
12	J	36	LEU	8.8
4	B	1079	LYS	8.8
4	B	397	ASP	8.7
10	H	98	TYR	8.7
12	J	63	TYR	8.7
4	B	1169	MET	8.7
15	S	139	VAL	8.7
4	B	466	TRP	8.7
4	B	272	THR	8.7
4	B	107	GLY	8.7
11	I	104	LEU	8.7
15	S	262	GLU	8.7
7	E	75	MET	8.7
3	A	439	ASN	8.7
3	A	918	GLU	8.7
7	E	19	VAL	8.7
4	B	574	SER	8.7
3	A	1189	SER	8.7
3	A	309	ALA	8.7
6	D	19	GLU	8.6
4	B	862	GLN	8.6
13	K	101	LEU	8.6
3	A	1301	GLU	8.6
5	C	209	TYR	8.6
9	G	37	SER	8.6
3	A	234	MET	8.6
3	A	46	THR	8.6
4	B	411	PRO	8.6
15	S	167	PRO	8.6
9	G	28	THR	8.6
15	S	137	ASP	8.6
14	L	62	LYS	8.6
4	B	620	ARG	8.6
4	B	531	GLN	8.6

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Mol	Chain	Res	Type	RSRZ
3	A	1272	THR	8.6
4	B	423	LYS	8.6
3	A	708	MET	8.5
4	B	727	LYS	8.5
4	B	430	ARG	8.5
11	I	114	GLN	8.5
5	C	193	TYR	8.5
15	S	252	ASN	8.5
3	A	714	PHE	8.5
3	A	144	THR	8.5
5	C	267	GLN	8.5
3	A	755	PHE	8.5
3	A	327	ALA	8.5
4	B	334	ILE	8.5
6	D	153	ARG	8.5
3	A	38	PRO	8.5
3	A	180	LYS	8.5
14	L	70	ARG	8.5
3	A	130	ASP	8.5
3	A	41	MET	8.4
3	A	698	GLN	8.4
3	A	332	LYS	8.4
4	B	365	THR	8.4
3	A	915	SER	8.4
3	A	677	ARG	8.4
10	H	27	GLU	8.4
5	C	95	CYS	8.4
4	B	268	THR	8.4
5	C	138	GLU	8.4
4	B	591	ARG	8.4
3	A	316	GLN	8.4
3	A	961	ARG	8.4
3	A	42	ASP	8.4
13	K	22	ASP	8.4
3	A	1140	HIS	8.4
10	H	120	GLY	8.4
6	D	164	ILE	8.4
3	A	980	ASP	8.4
7	E	30	ILE	8.4
13	K	10	PHE	8.4
3	A	1170	ILE	8.4
10	H	88	SER	8.4

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Mol	Chain	Res	Type	RSRZ
3	A	739	ASP	8.3
4	B	185	THR	8.3
13	K	16	GLU	8.3
3	A	983	ILE	8.3
7	E	173	SER	8.3
9	G	118	ASP	8.3
9	G	88	ASP	8.3
3	A	1079	MET	8.3
4	B	569	TYR	8.3
15	S	246	GLU	8.3
10	H	82	PRO	8.3
7	E	186	LEU	8.3
4	B	39	ARG	8.3
3	A	261	ASP	8.3
10	H	12	VAL	8.3
3	A	373	THR	8.3
4	B	119	LEU	8.3
13	K	87	LEU	8.3
4	B	742	GLU	8.3
6	D	67	ARG	8.3
4	B	103	ASN	8.3
11	I	11	ASN	8.3
3	A	120	GLU	8.3
11	I	81	ARG	8.3
5	C	76	ASP	8.3
4	B	373	ARG	8.3
10	H	48	PRO	8.3
4	B	403	LYS	8.3
3	A	1116	LEU	8.3
4	B	850	LEU	8.3
6	D	121	LYS	8.3
9	G	22	MET	8.3
3	A	754	SER	8.2
3	A	50	ILE	8.2
6	D	167	LEU	8.2
8	F	106	PRO	8.2
3	A	767	GLN	8.2
7	E	114	ASN	8.2
15	S	144	TYR	8.2
15	S	290	ASP	8.2
11	I	93	LYS	8.2
3	A	694	THR	8.2

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Mol	Chain	Res	Type	RSRZ
4	B	861	ASP	8.2
3	A	1125	ALA	8.2
4	B	542	MET	8.2
6	D	154	PHE	8.2
4	B	416	LEU	8.2
3	A	282	ASN	8.2
4	B	1210	MET	8.2
7	E	105	PHE	8.2
4	B	120	ARG	8.2
10	H	19	ARG	8.2
5	C	184	ASN	8.2
3	A	853	ASP	8.2
5	C	218	PRO	8.2
4	B	745	PRO	8.2
3	A	640	GLN	8.2
4	B	250	PHE	8.2
4	B	881	ASN	8.2
6	D	125	SER	8.1
9	G	1	MET	8.1
6	D	185	CYS	8.1
13	K	84	LYS	8.1
14	L	36	SER	8.1
3	A	1092	LYS	8.1
5	C	208	GLU	8.1
3	A	252	PHE	8.1
3	A	1198	ASP	8.1
3	A	949	ASP	8.1
4	B	251	ILE	8.1
4	B	290	GLY	8.1
3	A	356	ASP	8.1
4	B	763	GLN	8.1
10	H	125	LEU	8.1
4	B	877	PRO	8.0
9	G	74	TYR	8.0
12	J	65	PRO	8.0
3	A	503	GLN	8.0
13	K	9	LEU	8.0
15	S	230	THR	8.0
3	A	1213	GLY	8.0
3	A	1319	VAL	8.0
3	A	434	ARG	8.0
3	A	1333	ILE	8.0

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Mol	Chain	Res	Type	RSRZ
10	H	78	SER	8.0
3	A	466	SER	8.0
8	F	81	THR	8.0
4	B	256	VAL	8.0
12	J	53	HIS	8.0
3	A	1128	GLN	7.9
4	B	806	THR	7.9
3	A	369	SER	7.9
5	C	192	TRP	7.9
4	B	507	LYS	7.9
3	A	709	THR	7.9
4	B	382	ILE	7.9
9	G	130	TYR	7.9
4	B	662	MET	7.9
3	A	730	GLY	7.9
3	A	125	ALA	7.9
14	L	52	GLY	7.9
3	A	674	PRO	7.9
4	B	419	THR	7.9
4	B	501	PRO	7.9
11	I	59	VAL	7.9
10	H	62	SER	7.9
3	A	237	THR	7.9
3	A	680	THR	7.8
3	A	68	GLN	7.8
3	A	783	THR	7.8
3	A	691	LEU	7.8
10	H	103	LYS	7.8
3	A	320	ARG	7.8
12	J	52	THR	7.8
11	I	75	CYS	7.8
3	A	166	GLY	7.8
3	A	39	GLU	7.8
4	B	291	ILE	7.8
12	J	42	LYS	7.8
4	B	59	LEU	7.8
3	A	1257	ASP	7.7
15	S	276	GLU	7.7
7	E	68	SER	7.7
3	A	1356	ILE	7.7
4	B	589	VAL	7.7
9	G	124	GLY	7.7

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Mol	Chain	Res	Type	RSRZ
4	B	433	GLN	7.7
7	E	25	ASP	7.7
15	S	237	ALA	7.7
14	L	48	CYS	7.7
7	E	58	MET	7.7
3	A	558	GLY	7.7
5	C	70	ILE	7.7
3	A	538	ASP	7.7
10	H	9	ILE	7.7
4	B	189	LEU	7.7
5	C	6	PRO	7.6
3	A	1312	ASN	7.6
13	K	44	ASN	7.6
5	C	81	GLU	7.6
7	E	159	ASP	7.6
3	A	358	ASN	7.6
4	B	747	MET	7.6
15	S	190	THR	7.6
4	B	193	LYS	7.6
4	B	400	HIS	7.6
15	S	280	SER	7.6
3	A	1004	ASN	7.6
3	A	887	GLY	7.6
3	A	1453	TYR	7.6
2	P	9	G	7.6
7	E	8	ASN	7.6
13	K	28	PRO	7.6
3	A	951	GLU	7.6
4	B	608	ASP	7.6
13	K	8	GLU	7.6
11	I	91	ARG	7.6
10	H	133	ASN	7.5
4	B	317	CYS	7.5
9	G	65	ASP	7.5
5	C	31	ASN	7.5
4	B	577	ALA	7.5
11	I	29	CYS	7.5
4	B	730	ARG	7.5
4	B	527	THR	7.5
7	E	167	ARG	7.5
4	B	455	SER	7.5
3	A	1108	ALA	7.5

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Mol	Chain	Res	Type	RSRZ
7	E	191	LYS	7.5
4	B	691	GLU	7.5
3	A	1294	PRO	7.5
5	C	133	ILE	7.5
11	I	68	LEU	7.5
4	B	490	SER	7.5
3	A	562	THR	7.5
13	K	4	PRO	7.5
15	S	140	ASP	7.5
4	B	615	MET	7.5
13	K	110	ASN	7.5
4	B	284	ILE	7.5
3	A	713	SER	7.4
6	D	133	THR	7.4
4	B	895	ASP	7.4
9	G	11	ILE	7.4
7	E	130	ALA	7.4
8	F	151	LEU	7.4
9	G	92	VAL	7.4
3	A	686	ALA	7.4
3	A	984	LYS	7.4
4	B	168	GLY	7.4
11	I	17	ARG	7.4
4	B	687	GLU	7.4
6	D	74	GLN	7.4
3	A	756	ILE	7.4
6	D	202	ILE	7.4
4	B	1108	ARG	7.4
3	A	1040	GLN	7.4
4	B	1125	ASP	7.4
4	B	598	GLU	7.4
3	A	946	VAL	7.4
7	E	20	LYS	7.4
3	A	307	ASP	7.3
4	B	1123	SER	7.3
8	F	148	VAL	7.3
3	A	1315	GLU	7.3
3	A	1440	ALA	7.3
7	E	63	ASN	7.3
4	B	357	GLN	7.3
4	B	363	HIS	7.3
7	E	36	GLU	7.3

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Mol	Chain	Res	Type	RSRZ
3	A	833	GLU	7.3
6	D	23	ASN	7.3
6	D	203	SER	7.3
11	I	16	PRO	7.3
5	C	145	CYS	7.3
6	D	206	GLU	7.3
8	F	74	ILE	7.3
3	A	1077	THR	7.3
3	A	1299	VAL	7.3
11	I	2	THR	7.3
14	L	47	ARG	7.3
4	B	696	GLU	7.3
6	D	48	ILE	7.3
5	C	119	VAL	7.3
3	A	1211	GLN	7.3
3	A	1358	SER	7.3
3	A	1449	SER	7.3
11	I	74	GLU	7.3
15	S	170	SER	7.2
3	A	1292	PRO	7.2
3	A	1006	ILE	7.2
3	A	1393	ASN	7.2
4	B	106	ASP	7.2
4	B	616	ILE	7.2
4	B	875	GLU	7.2
3	A	710	LEU	7.2
4	B	199	MET	7.2
7	E	157	SER	7.2
3	A	1131	ALA	7.2
10	H	113	ALA	7.2
3	A	1083	THR	7.2
15	S	279	VAL	7.2
9	G	17	PHE	7.2
9	G	169	GLY	7.2
3	A	955	PRO	7.2
3	A	1133	LEU	7.2
4	B	723	VAL	7.2
3	A	785	PRO	7.2
4	B	623	GLU	7.2
3	A	596	THR	7.2
4	B	936	ASP	7.2
3	A	835	GLY	7.2

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Mol	Chain	Res	Type	RSRZ
10	H	59	ILE	7.2
12	J	3	VAL	7.2
4	B	476	ARG	7.2
15	S	225	PRO	7.2
3	A	1159	ARG	7.1
3	A	979	SER	7.1
6	D	195	ILE	7.1
10	H	77	ARG	7.1
4	B	319	GLU	7.1
4	B	286	PHE	7.1
3	A	388	LEU	7.1
11	I	73	ARG	7.1
9	G	48	VAL	7.1
10	H	123	MET	7.1
15	S	307	LYS	7.1
4	B	1056	SER	7.1
4	B	1113	VAL	7.1
6	D	129	LEU	7.1
10	H	26	ILE	7.1
9	G	41	LYS	7.1
11	I	87	GLN	7.1
5	C	219	PHE	7.1
10	H	107	VAL	7.1
13	K	105	PHE	7.1
3	A	475	THR	7.1
4	B	526	GLU	7.1
4	B	333	PHE	7.1
11	I	31	THR	7.1
3	A	625	SER	7.1
4	B	1216	LEU	7.1
5	C	166	GLU	7.0
3	A	981	LEU	7.0
3	A	182	VAL	7.0
3	A	579	SER	7.0
4	B	198	ASP	7.0
4	B	478	GLY	7.0
3	A	890	ASP	7.0
3	A	1316	VAL	7.0
14	L	59	ALA	7.0
6	D	122	GLU	7.0
4	B	111	ALA	7.0
5	C	171	GLY	7.0

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Mol	Chain	Res	Type	RSRZ
4	B	233	PRO	7.0
4	B	402	GLY	7.0
3	A	408	ASP	7.0
15	S	166	HIS	7.0
3	A	1240	CYS	7.0
7	E	35	VAL	7.0
3	A	784	LEU	7.0
7	E	23	VAL	7.0
4	B	525	ALA	6.9
4	B	1100	ASP	6.9
11	I	45	ARG	6.9
4	B	122	LEU	6.9
3	A	1308	THR	6.9
7	E	144	ILE	6.9
9	G	141	SER	6.9
4	B	942	ARG	6.9
13	K	57	LEU	6.9
3	A	273	ASN	6.9
3	A	422	GLY	6.9
7	E	103	LYS	6.9
3	A	614	PHE	6.9
5	C	167	HIS	6.9
5	C	86	CYS	6.9
3	A	248	PRO	6.9
4	B	292	ILE	6.9
5	C	175	ALA	6.9
4	B	91	SER	6.9
4	B	329	THR	6.9
3	A	991	LYS	6.9
4	B	998	ASP	6.9
4	B	366	GLN	6.9
4	B	770	GLN	6.9
13	K	107	THR	6.8
3	A	123	ARG	6.8
9	G	19	GLY	6.8
3	A	941	LYS	6.8
3	A	1360	GLY	6.8
11	I	102	VAL	6.8
3	A	394	ASN	6.8
15	S	193	ALA	6.8
10	H	38	LEU	6.8
3	A	700	ASN	6.8

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Mol	Chain	Res	Type	RSRZ
8	F	109	VAL	6.8
3	A	684	ALA	6.8
4	B	1126	GLY	6.8
3	A	1142	THR	6.8
5	C	65	HIS	6.8
3	A	1273	LEU	6.8
4	B	908	GLU	6.8
4	B	178	ASN	6.8
4	B	1064	TYR	6.8
4	B	709	ASP	6.8
9	G	119	LEU	6.8
3	A	578	LEU	6.8
3	A	512	VAL	6.7
4	B	663	ALA	6.7
3	A	806	ARG	6.7
10	H	99	GLY	6.7
4	B	707	PRO	6.7
3	A	587	HIS	6.7
3	A	1153	TYR	6.7
3	A	400	PRO	6.7
3	A	1258	HIS	6.7
4	B	231	PRO	6.7
4	B	500	THR	6.7
3	A	161	LEU	6.7
4	B	101	MET	6.7
5	C	29	MET	6.7
9	G	30	LEU	6.7
4	B	225	VAL	6.7
15	S	208	SER	6.7
3	A	89	PRO	6.7
3	A	417	TYR	6.7
2	P	10	C	6.7
4	B	802	PRO	6.6
3	A	953	ASN	6.6
4	B	38	PHE	6.6
4	B	426	LYS	6.6
4	B	312	GLU	6.6
4	B	571	PRO	6.6
3	A	375	THR	6.6
3	A	958	VAL	6.6
4	B	295	GLY	6.6
3	A	1072	ILE	6.6

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Mol	Chain	Res	Type	RSRZ
11	I	47	GLU	6.6
5	C	55	THR	6.6
5	C	196	ASP	6.6
13	K	66	PRO	6.6
4	B	1006	ILE	6.6
12	J	2	ILE	6.6
4	B	882	THR	6.5
4	B	351	TYR	6.5
7	E	116	ILE	6.5
5	C	210	GLU	6.5
4	B	585	VAL	6.5
5	C	137	LYS	6.5
4	B	374	LYS	6.5
6	D	210	ILE	6.5
3	A	1381	LEU	6.5
4	B	983	ARG	6.5
6	D	46	GLU	6.5
4	B	221	ASN	6.5
3	A	210	ILE	6.5
4	B	1170	THR	6.5
11	I	38	ALA	6.5
12	J	4	PRO	6.5
5	C	165	LYS	6.5
10	H	7	ASP	6.5
6	D	218	GLU	6.5
4	B	409	ALA	6.5
6	D	160	VAL	6.5
13	K	7	PHE	6.5
3	A	87	ALA	6.5
11	I	52	ILE	6.4
5	C	239	PRO	6.4
9	G	114	LEU	6.4
8	F	140	ASP	6.4
3	A	278	THR	6.4
3	A	1435	PRO	6.4
4	B	582	VAL	6.4
15	S	184	LYS	6.4
3	A	947	PHE	6.4
4	B	173	MET	6.4
11	I	22	ASN	6.4
4	B	227	LYS	6.4
4	B	541	LEU	6.4

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Mol	Chain	Res	Type	RSRZ
10	H	100	THR	6.4
4	B	172	ILE	6.4
4	B	1221	SER	6.4
5	C	39	ALA	6.4
7	E	139	ALA	6.4
5	C	226	ASP	6.4
6	D	26	THR	6.4
3	A	1295	THR	6.4
3	A	1318	THR	6.4
6	D	146	GLN	6.4
5	C	93	ASP	6.4
5	C	127	ARG	6.4
15	S	277	LYS	6.4
5	C	255	VAL	6.4
4	B	962	LYS	6.4
4	B	223	VAL	6.4
4	B	452	THR	6.4
3	A	203	SER	6.4
3	A	622	VAL	6.4
11	I	20	LYS	6.4
3	A	943	LEU	6.4
3	A	362	ASP	6.4
11	I	18	GLU	6.4
5	C	261	ALA	6.4
9	G	26	LEU	6.3
4	B	169	ARG	6.3
4	B	1084	GLN	6.3
3	A	620	LYS	6.3
6	D	169	SER	6.3
4	B	685	LEU	6.3
3	A	859	SER	6.3
3	A	590	ARG	6.3
3	A	1303	GLU	6.3
15	S	265	VAL	6.3
10	H	145	ARG	6.3
3	A	1037	LEU	6.3
7	E	94	LYS	6.3
4	B	512	ARG	6.3
4	B	1184	GLY	6.3
3	A	873	MET	6.3
2	P	8	G	6.3
3	A	790	ASP	6.3

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Mol	Chain	Res	Type	RSRZ
7	E	113	GLN	6.3
7	E	42	PHE	6.2
4	B	315	LYS	6.2
3	A	899	VAL	6.2
13	K	78	THR	6.2
5	C	236	GLY	6.2
3	A	769	SER	6.2
7	E	97	VAL	6.2
3	A	1321	GLY	6.2
4	B	197	PHE	6.2
5	C	148	ARG	6.2
4	B	100	PRO	6.2
12	J	28	ASP	6.2
15	S	233	ALA	6.2
4	B	23	ALA	6.2
3	A	1296	GLY	6.2
4	B	60	GLN	6.2
4	B	121	ASN	6.2
3	A	1098	VAL	6.2
4	B	467	GLY	6.2
4	B	781	PHE	6.2
4	B	331	LEU	6.2
9	G	105	PRO	6.2
3	A	679	ILE	6.2
6	D	45	GLU	6.1
13	K	56	VAL	6.1
15	S	147	LYS	6.1
3	A	4	GLN	6.1
12	J	14	VAL	6.1
4	B	486	TYR	6.1
3	A	1397	LEU	6.1
7	E	140	LEU	6.1
7	E	174	GLN	6.1
3	A	673	GLY	6.1
13	K	24	ASP	6.1
4	B	659	ALA	6.1
10	H	36	CYS	6.1
4	B	1175	LEU	6.1
3	A	933	TYR	6.1
3	A	916	GLY	6.1
4	B	729	ILE	6.1
4	B	583	ASN	6.1

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Mol	Chain	Res	Type	RSRZ
13	K	91	CYS	6.1
3	A	624	SER	6.1
4	B	961	LEU	6.1
5	C	27	LEU	6.1
5	C	68	GLY	6.1
4	B	380	TYR	6.1
4	B	1035	ALA	6.1
15	S	287	ARG	6.0
3	A	935	GLN	6.0
4	B	658	ILE	6.0
10	H	42	ILE	6.0
3	A	297	GLN	6.0
3	A	631	HIS	6.0
15	S	169	GLN	6.0
7	E	190	LEU	6.0
3	A	566	ILE	6.0
4	B	240	ILE	6.0
5	C	105	GLY	6.0
5	C	107	SER	6.0
3	A	70	CYS	6.0
4	B	37	PHE	6.0
3	A	811	GLN	6.0
3	A	1345	ARG	6.0
4	B	728	ARG	6.0
10	H	41	ASP	6.0
4	B	1090	THR	6.0
13	K	81	TYR	6.0
4	B	1185	CYS	6.0
8	F	147	SER	6.0
4	B	789	MET	6.0
4	B	682	SER	6.0
4	B	454	THR	6.0
6	D	199	ASN	6.0
4	B	738	PHE	6.0
4	B	35	SER	6.0
4	B	1219	ASP	6.0
13	K	2	ASN	6.0
7	E	195	VAL	6.0
3	A	1239	ARG	6.0
3	A	559	VAL	6.0
5	C	237	SER	6.0
5	C	112	ASN	5.9

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Mol	Chain	Res	Type	RSRZ
4	B	586	TRP	5.9
3	A	1096	SER	5.9
15	S	294	THR	5.9
3	A	526	ASP	5.9
3	A	609	ASP	5.9
3	A	1135	ARG	5.9
3	A	287	HIS	5.9
4	B	266	ALA	5.9
3	A	1121	GLU	5.9
4	B	1102	LYS	5.9
5	C	11	ARG	5.9
3	A	794	PRO	5.9
3	A	1120	LEU	5.9
4	B	56	ASP	5.9
5	C	69	LEU	5.9
8	F	76	LYS	5.9
4	B	1062	HIS	5.9
8	F	126	ALA	5.9
7	E	146	HIS	5.9
3	A	623	GLY	5.9
3	A	689	LYS	5.9
3	A	25	GLU	5.9
4	B	422	LYS	5.9
3	A	847	ASP	5.9
7	E	143	ASN	5.8
3	A	810	PRO	5.8
3	A	1394	THR	5.8
4	B	218	SER	5.8
12	J	23	ASN	5.8
3	A	805	LEU	5.8
4	B	1007	VAL	5.8
3	A	212	LYS	5.8
6	D	142	LYS	5.8
7	E	48	ASP	5.8
14	L	34	CYS	5.8
4	B	937	ALA	5.8
3	A	121	LEU	5.8
6	D	159	THR	5.8
8	F	153	VAL	5.8
6	D	211	LEU	5.8
3	A	1118	VAL	5.8
3	A	804	TYR	5.8

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Mol	Chain	Res	Type	RSRZ
15	S	179	GLU	5.8
3	A	879	GLU	5.8
5	C	92	CYS	5.8
3	A	1268	LEU	5.8
15	S	197	ALA	5.8
3	A	1362	TYR	5.8
3	A	715	GLU	5.7
15	S	281	TYR	5.7
3	A	826	ASP	5.7
4	B	209	GLU	5.7
15	S	251	GLN	5.7
3	A	1326	ARG	5.7
3	A	1297	GLU	5.7
6	D	39	ASN	5.7
15	S	273	LYS	5.7
3	A	71	GLN	5.7
4	B	780	VAL	5.7
6	D	47	LEU	5.7
15	S	300	GLU	5.7
7	E	151	PRO	5.7
5	C	34	ARG	5.7
9	G	150	CYS	5.7
3	A	745	GLN	5.7
15	S	219	ALA	5.7
3	A	222	LEU	5.7
4	B	1128	LEU	5.7
5	C	20	PHE	5.7
5	C	186	LEU	5.7
9	G	135	ASP	5.7
3	A	24	PRO	5.7
13	K	20	LYS	5.7
15	S	149	ARG	5.7
3	A	419	LYS	5.7
4	B	752	ALA	5.7
4	B	955	THR	5.7
13	K	77	THR	5.7
15	S	180	SER	5.7
4	B	759	PRO	5.7
3	A	1017	LEU	5.7
3	A	106	VAL	5.7
3	A	925	LEU	5.7
4	B	1022	THR	5.6

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Mol	Chain	Res	Type	RSRZ
15	S	160	LEU	5.7
3	A	35	ILE	5.6
11	I	26	LEU	5.6
4	B	1053	GLU	5.6
6	D	18	VAL	5.6
7	E	64	PRO	5.6
5	C	75	MET	5.6
3	A	613	ILE	5.6
4	B	1153	GLU	5.6
3	A	321	PRO	5.6
3	A	721	PHE	5.6
3	A	912	LEU	5.6
4	B	493	SER	5.6
4	B	1001	PHE	5.6
3	A	629	LEU	5.6
4	B	566	LEU	5.6
4	B	31	TRP	5.6
15	S	229	ALA	5.6
4	B	524	PRO	5.6
9	G	50	ASP	5.6
3	A	1380	GLY	5.6
3	A	1400	CYS	5.5
4	B	849	GLY	5.5
15	S	271	CYS	5.5
4	B	296	GLU	5.5
3	A	796	SER	5.5
4	B	876	LYS	5.5
4	B	463	THR	5.5
15	S	226	GLU	5.5
6	D	54	GLU	5.5
3	A	877	HIS	5.5
3	A	778	GLY	5.5
7	E	136	ASN	5.5
4	B	633	VAL	5.5
4	B	744	HIS	5.5
3	A	1342	GLU	5.5
15	S	174	THR	5.5
3	A	630	ILE	5.5
5	C	102	GLN	5.5
4	B	128	LEU	5.5
4	B	1027	ILE	5.5
3	A	707	GLY	5.5

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Mol	Chain	Res	Type	RSRZ
3	A	1218	GLN	5.5
4	B	766	ARG	5.5
3	A	775	ILE	5.5
4	B	237	VAL	5.5
3	A	1324	PRO	5.5
4	B	957	ASN	5.5
15	S	275	LYS	5.5
5	C	87	PHE	5.4
15	S	232	ASP	5.4
3	A	828	ALA	5.4
4	B	118	ARG	5.4
3	A	541	ILE	5.4
4	B	108	VAL	5.4
4	B	835	GLN	5.4
3	A	557	ASP	5.4
15	S	217	LYS	5.4
1	T	18	DC	5.4
3	A	1284	MET	5.4
3	A	325	ILE	5.4
4	B	1019	SER	5.4
12	J	46	CYS	5.4
4	B	67	SER	5.4
9	G	99	PHE	5.4
9	G	93	SER	5.4
4	B	255	GLN	5.4
3	A	747	VAL	5.4
9	G	72	VAL	5.4
3	A	1293	SER	5.4
4	B	831	SER	5.4
4	B	903	VAL	5.4
10	H	57	VAL	5.4
3	A	544	ASP	5.4
12	J	58	GLU	5.4
4	B	1037	LEU	5.4
7	E	79	TRP	5.4
4	B	1041	GLU	5.4
4	B	871	THR	5.4
8	F	114	GLU	5.3
4	B	769	TYR	5.3
3	A	258	GLY	5.3
3	A	683	ILE	5.3
3	A	1217	LYS	5.3

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Mol	Chain	Res	Type	RSRZ
5	C	67	LEU	5.3
15	S	274	CYS	5.3
15	S	148	LEU	5.3
4	B	282	ILE	5.3
9	G	121	PHE	5.3
11	I	43	VAL	5.3
3	A	60	SER	5.3
4	B	605	ARG	5.3
9	G	158	HIS	5.3
3	A	208	LEU	5.3
3	A	885	THR	5.3
5	C	199	LYS	5.3
6	D	57	LEU	5.3
9	G	31	LEU	5.3
4	B	222	ILE	5.3
4	B	859	TYR	5.3
6	D	123	LEU	5.3
7	E	155	ARG	5.3
15	S	142	ALA	5.3
5	C	111	THR	5.3
4	B	700	SER	5.3
10	H	121	LEU	5.3
6	D	149	THR	5.3
13	K	79	GLU	5.3
4	B	204	ILE	5.3
3	A	545	GLN	5.3
3	A	1328	TYR	5.3
7	E	46	TYR	5.3
9	G	151	ILE	5.3
3	A	13	THR	5.2
3	A	939	ASP	5.2
4	B	1033	LYS	5.2
15	S	224	THR	5.2
4	B	529	GLU	5.2
6	D	34	GLN	5.2
3	A	564	ALA	5.2
4	B	246	LYS	5.2
6	D	61	GLU	5.2
3	A	1039	LYS	5.2
3	A	153	PRO	5.2
4	B	545	ILE	5.2
12	J	24	LEU	5.2

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Mol	Chain	Res	Type	RSRZ
6	D	27	LEU	5.2
3	A	1020	CYS	5.2
13	K	51	LEU	5.2
6	D	56	ARG	5.2
4	B	630	ALA	5.2
4	B	913	GLY	5.2
5	C	104	PHE	5.2
3	A	757	ASN	5.2
11	I	39	GLY	5.2
3	A	1357	ALA	5.2
3	A	142	CYS	5.2
4	B	1160	VAL	5.2
7	E	34	GLU	5.2
6	D	183	LEU	5.2
15	S	258	GLY	5.2
3	A	1298	TYR	5.2
4	B	1114	LEU	5.2
4	B	465	ASN	5.2
3	A	816	HIS	5.2
3	A	880	LYS	5.2
3	A	795	GLU	5.1
4	B	803	LEU	5.1
4	B	1095	LEU	5.1
4	B	701	ILE	5.1
3	A	688	LYS	5.1
4	B	458	LYS	5.1
15	S	156	LEU	5.1
11	I	79	HIS	5.1
3	A	429	GLY	5.1
15	S	185	VAL	5.1
10	H	28	ALA	5.1
3	A	928	LEU	5.1
3	A	1450	LEU	5.1
4	B	612	GLU	5.1
3	A	310	GLY	5.1
4	B	1205	GLN	5.1
4	B	791	THR	5.1
3	A	1201	ALA	5.1
4	B	1165	ILE	5.1
9	G	12	THR	5.1
5	C	38	ILE	5.1
3	A	268	ASP	5.1

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Mol	Chain	Res	Type	RSRZ
3	A	1148	ILE	5.1
4	B	383	ASN	5.1
3	A	992	ASP	5.1
3	A	964	ILE	5.1
7	E	179	GLN	5.1
3	A	604	GLY	5.1
4	B	819	ALA	5.1
12	J	1	MET	5.1
14	L	69	ALA	5.1
7	E	169	ARG	5.1
7	E	168	TYR	5.1
3	A	576	GLN	5.1
4	B	479	VAL	5.1
4	B	1048	THR	5.1
9	G	21	ARG	5.1
9	G	171	ILE	5.1
3	A	774	ARG	5.1
7	E	11	ARG	5.0
4	B	775	LYS	5.0
4	B	708	GLU	5.0
4	B	410	GLY	5.0
5	C	200	GLU	5.0
4	B	450	ALA	5.0
13	K	85	ASP	5.0
6	D	140	ASP	5.0
3	A	733	ALA	5.0
4	B	457	LEU	5.0
6	D	6	SER	5.0
3	A	591	PHE	5.0
4	B	386	LEU	5.0
3	A	98	LYS	5.0
4	B	418	LYS	5.0
9	G	164	LYS	5.0
3	A	1194	ARG	5.0
5	C	254	LYS	5.0
13	K	62	LYS	5.0
4	B	739	THR	5.0
4	B	698	GLU	5.0
4	B	495	LEU	5.0
5	C	246	ARG	5.0
3	A	272	ALA	5.0
4	B	259	TYR	5.0

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Mol	Chain	Res	Type	RSRZ
6	D	5	THR	4.9
3	A	862	ASN	4.9
4	B	1109	GLY	4.9
3	A	85	ASP	4.9
4	B	368	GLU	4.9
12	J	45	CYS	4.9
4	B	794	ASN	4.9
4	B	699	GLU	4.9
3	A	626	ASN	4.9
4	B	1042	GLY	4.9
5	C	120	ILE	4.9
3	A	864	ILE	4.9
4	B	844	SER	4.9
4	B	1151	LEU	4.9
9	G	112	LYS	4.9
14	L	28	LYS	4.9
3	A	556	TRP	4.9
4	B	879	ARG	4.9
3	A	963	ILE	4.9
4	B	515	HIS	4.9
15	S	183	ASN	4.9
5	C	256	ALA	4.9
7	E	21	GLU	4.9
15	S	238	PRO	4.9
4	B	1030	LEU	4.9
4	B	393	LYS	4.9
12	J	20	SER	4.9
7	E	142	VAL	4.9
3	A	1409	LEU	4.9
3	A	923	LEU	4.8
3	A	1418	LEU	4.8
3	A	563	PRO	4.8
4	B	1036	ALA	4.8
13	K	39	ASP	4.8
4	B	494	HIS	4.8
7	E	61	GLN	4.8
7	E	156	LEU	4.8
6	D	35	LEU	4.8
7	E	66	GLU	4.8
4	B	953	LEU	4.8
5	C	229	TYR	4.8
8	F	150	GLU	4.8

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Mol	Chain	Res	Type	RSRZ
5	C	149	LYS	4.8
7	E	147	HIS	4.8
8	F	131	PRO	4.8
4	B	203	PHE	4.8
8	F	122	MET	4.8
12	J	37	SER	4.8
4	B	1122	ARG	4.8
4	B	303	TYR	4.8
3	A	1144	LYS	4.8
4	B	1055	ILE	4.8
9	G	100	GLU	4.8
3	A	675	THR	4.8
4	B	301	ILE	4.8
3	A	300	VAL	4.8
6	D	214	LEU	4.8
9	G	24	GLN	4.8
3	A	966	ASN	4.8
3	A	133	LYS	4.8
3	A	927	VAL	4.8
8	F	104	ASN	4.8
3	A	1155	ASP	4.8
4	B	764	SER	4.8
3	A	491	VAL	4.8
5	C	25	VAL	4.8
3	A	665	GLY	4.8
4	B	995	ARG	4.8
3	A	110	CYS	4.8
4	B	1008	PRO	4.8
10	H	54	SER	4.8
3	A	552	TRP	4.8
3	A	308	ILE	4.8
7	E	213	ILE	4.8
7	E	120	ALA	4.7
13	K	86	ALA	4.7
15	S	192	GLU	4.7
4	B	288	ALA	4.7
4	B	771	SER	4.7
7	E	28	TYR	4.7
10	H	93	TYR	4.7
15	S	286	THR	4.7
6	D	119	ARG	4.7
5	C	241	ASP	4.7

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Mol	Chain	Res	Type	RSRZ
13	K	6	ARG	4.7
3	A	605	MET	4.7
13	K	21	ILE	4.7
4	B	1220	ARG	4.7
7	E	178	ILE	4.7
3	A	901	LEU	4.7
4	B	644	GLU	4.7
7	E	81	GLU	4.7
4	B	263	GLY	4.7
7	E	88	VAL	4.7
8	F	85	MET	4.7
12	J	49	MET	4.7
3	A	888	GLY	4.7
3	A	968	GLN	4.7
15	S	216	HIS	4.7
4	B	1156	ASP	4.7
4	B	1209	ALA	4.7
4	B	1188	LYS	4.7
3	A	711	ARG	4.7
3	A	387	ARG	4.7
9	G	38	CYS	4.7
4	B	636	PRO	4.6
13	K	76	GLN	4.6
7	E	181	ALA	4.6
9	G	139	ILE	4.6
3	A	866	PHE	4.6
4	B	689	LEU	4.6
5	C	225	ALA	4.6
10	H	106	GLU	4.6
3	A	1386	ARG	4.6
5	C	115	SER	4.6
1	T	16	DT	4.6
6	D	194	LEU	4.6
5	C	54	ASN	4.6
6	D	33	PHE	4.6
4	B	41	LYS	4.6
3	A	136	ALA	4.6
3	A	401	GLY	4.6
4	B	981	ALA	4.6
3	A	137	ALA	4.6
3	A	377	PRO	4.6
3	A	611	GLN	4.6

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Mol	Chain	Res	Type	RSRZ
13	K	11	LEU	4.6
15	S	204	SER	4.6
15	S	234	LYS	4.6
9	G	2	PHE	4.6
4	B	381	MET	4.6
10	H	46	LEU	4.6
15	S	213	ASP	4.6
5	C	234	SER	4.6
9	G	85	GLU	4.6
15	S	196	LYS	4.5
5	C	130	GLY	4.5
4	B	1061	GLU	4.5
3	A	671	ALA	4.5
7	E	149	LEU	4.5
7	E	134	THR	4.5
8	F	89	GLU	4.5
3	A	1425	SER	4.5
3	A	838	GLN	4.5
3	A	1103	GLU	4.5
12	J	47	ARG	4.5
4	B	1187	ASN	4.5
11	I	48	LEU	4.5
3	A	779	PHE	4.5
3	A	797	LYS	4.5
4	B	236	HIS	4.5
10	H	111	LEU	4.5
15	S	239	ALA	4.5
4	B	878	GLN	4.5
3	A	262	LEU	4.5
15	S	159	VAL	4.5
3	A	407	ARG	4.5
9	G	14	HIS	4.4
11	I	36	GLU	4.4
3	A	1117	THR	4.4
4	B	1034	VAL	4.4
3	A	1349	TYR	4.4
8	F	105	ALA	4.4
3	A	553	VAL	4.4
4	B	126	SER	4.4
4	B	847	ASP	4.4
5	C	259	LEU	4.4
13	K	108	GLU	4.4

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Mol	Chain	Res	Type	RSRZ
3	A	565	ILE	4.4
3	A	1288	ASP	4.4
7	E	207	ARG	4.4
3	A	77	CYS	4.4
3	A	717	ASN	4.4
12	J	60	PHE	4.4
5	C	183	TRP	4.4
5	C	30	ALA	4.4
15	S	206	VAL	4.4
4	B	956	THR	4.4
5	C	151	GLN	4.4
3	A	1065	GLY	4.4
3	A	1000	LEU	4.4
5	C	10	ILE	4.4
15	S	236	LEU	4.4
4	B	551	PRO	4.4
4	B	650	GLU	4.4
4	B	1017	ILE	4.4
3	A	926	GLN	4.4
4	B	179	CYS	4.4
3	A	954	TRP	4.4
4	B	655	LYS	4.4
3	A	45	GLN	4.4
4	B	516	ASN	4.4
5	C	132	PRO	4.4
6	D	36	LYS	4.4
4	B	428	ILE	4.4
3	A	1323	ASP	4.4
3	A	494	SER	4.3
13	K	80	GLY	4.3
8	F	141	GLY	4.3
14	L	58	LYS	4.3
3	A	814	PHE	4.3
3	A	606	LEU	4.3
4	B	188	ASP	4.3
6	D	187	THR	4.3
6	D	52	LEU	4.3
3	A	1169	ILE	4.3
15	S	292	PRO	4.3
15	S	298	THR	4.3
3	A	692	ASP	4.3
3	A	1104	ILE	4.3

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Mol	Chain	Res	Type	RSRZ
3	A	17	VAL	4.3
9	G	77	VAL	4.3
3	A	1411	GLU	4.3
4	B	805	THR	4.3
7	E	145	THR	4.3
9	G	63	PRO	4.3
12	J	44	TYR	4.3
9	G	136	VAL	4.3
10	H	85	GLY	4.3
4	B	1211	ASN	4.3
5	C	249	ASP	4.3
13	K	42	LEU	4.3
3	A	1105	LEU	4.3
3	A	239	LEU	4.3
4	B	984	HIS	4.3
3	A	535	THR	4.3
3	A	1402	PHE	4.3
10	H	118	PHE	4.3
3	A	139	TRP	4.3
3	A	131	SER	4.3
3	A	183	GLY	4.3
3	A	800	VAL	4.3
15	S	243	GLN	4.3
3	A	1209	MET	4.2
3	A	1219	THR	4.2
5	C	16	ASP	4.2
5	C	143	LEU	4.2
13	K	68	PHE	4.2
3	A	52	GLY	4.2
10	H	22	LYS	4.2
10	H	51	ALA	4.2
4	B	271	ALA	4.2
6	D	179	GLN	4.2
4	B	257	LYS	4.2
11	I	66	PRO	4.2
13	K	100	ALA	4.2
4	B	810	GLU	4.2
4	B	974	PRO	4.2
4	B	1180	PHE	4.2
4	B	999	MET	4.2
4	B	1145	SER	4.2
3	A	522	GLY	4.2

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Mol	Chain	Res	Type	RSRZ
3	A	1375	MET	4.2
3	A	205	GLU	4.2
9	G	61	ILE	4.2
3	A	1193	LEU	4.2
7	E	210	SER	4.2
3	A	706	HIS	4.2
3	A	722	LEU	4.2
4	B	46	GLN	4.2
4	B	638	PHE	4.2
15	S	202	ILE	4.2
3	A	331	GLY	4.2
4	B	832	GLY	4.2
3	A	682	THR	4.2
9	G	106	MET	4.2
4	B	555	ILE	4.2
3	A	129	LYS	4.2
3	A	134	ARG	4.2
4	B	748	ILE	4.2
3	A	266	LEU	4.2
4	B	535	LEU	4.2
3	A	1336	MET	4.1
4	B	627	PHE	4.2
10	H	11	GLN	4.1
3	A	97	ALA	4.1
6	D	127	ASP	4.1
15	S	270	THR	4.1
4	B	49	ASP	4.1
4	B	907	GLY	4.1
3	A	341	MET	4.1
3	A	463	ILE	4.1
5	C	185	LYS	4.1
14	L	33	GLU	4.1
3	A	1156	PRO	4.1
4	B	848	ARG	4.1
7	E	80	VAL	4.1
8	F	75	PRO	4.1
4	B	1141	HIS	4.1
13	K	30	ALA	4.1
5	C	62	PHE	4.1
15	S	203	TYR	4.1
3	A	411	ASP	4.1
13	K	40	HIS	4.1

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Mol	Chain	Res	Type	RSRZ
4	B	53	GLN	4.1
3	A	1338	VAL	4.1
4	B	690	VAL	4.1
7	E	163	GLU	4.1
3	A	699	ALA	4.1
4	B	533	CYS	4.1
15	S	191	ASN	4.1
5	C	141	GLY	4.1
3	A	1377	THR	4.1
3	A	1426	GLU	4.1
4	B	824	ILE	4.1
4	B	200	GLY	4.1
4	B	1023	VAL	4.1
4	B	52	ASN	4.1
4	B	976	ILE	4.1
4	B	660	LYS	4.1
4	B	960	GLY	4.1
3	A	293	GLU	4.1
3	A	734	GLU	4.1
7	E	201	LYS	4.1
4	B	414	ALA	4.1
7	E	76	GLY	4.1
4	B	894	ASP	4.1
12	J	55	ASP	4.1
3	A	1452	LYS	4.1
5	C	41	ILE	4.1
3	A	173	THR	4.1
3	A	695	LYS	4.0
4	B	425	THR	4.0
5	C	189	THR	4.0
4	B	1004	GLU	4.0
4	B	44	VAL	4.0
7	E	111	VAL	4.0
3	A	540	PHE	4.0
4	B	1124	ARG	4.0
3	A	1147	THR	4.0
15	S	299	CYS	4.0
3	A	1429	ILE	4.0
3	A	383	TYR	4.0
3	A	1075	PRO	4.0
4	B	375	ALA	4.0
3	A	314	ALA	4.0

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Mol	Chain	Res	Type	RSRZ
4	B	873	THR	4.0
3	A	1115	SER	4.0
4	B	746	SER	4.0
3	A	44	THR	4.0
3	A	1141	THR	4.0
9	G	42	PHE	4.0
11	I	100	PHE	4.0
13	K	19	LEU	4.0
3	A	333	GLU	4.0
5	C	9	LYS	4.0
3	A	58	LEU	4.0
3	A	359	LEU	4.0
3	A	232	GLU	4.0
3	A	766	GLY	4.0
4	B	820	GLY	4.0
6	D	25	ALA	4.0
3	A	960	ILE	4.0
3	A	1035	TYR	4.0
5	C	118	LEU	4.0
3	A	1086	PHE	4.0
10	H	30	SER	4.0
15	S	154	LYS	4.0
3	A	854	ASN	4.0
4	B	1039	GLY	4.0
4	B	413	LEU	4.0
3	A	382	PRO	3.9
3	A	1442	ASP	3.9
4	B	741	CYS	3.9
6	D	126	ILE	3.9
3	A	242	PRO	3.9
4	B	1203	LEU	3.9
10	H	95	TYR	3.9
4	B	392	ARG	3.9
8	F	146	TRP	3.9
3	A	799	PHE	3.9
4	B	492	LEU	3.9
7	E	165	LEU	3.9
8	F	92	ARG	3.9
3	A	211	PHE	3.9
4	B	372	SER	3.9
3	A	510	GLN	3.9
4	B	785	TYR	3.9

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Mol	Chain	Res	Type	RSRZ
13	K	90	ALA	3.9
5	C	235	VAL	3.9
4	B	115	GLN	3.9
4	B	537	LYS	3.9
4	B	904	ARG	3.9
3	A	725	ALA	3.9
5	C	174	ALA	3.9
5	C	40	GLU	3.9
5	C	61	GLU	3.9
2	P	7	A	3.9
4	B	971	THR	3.9
3	A	1009	ASN	3.9
11	I	99	LEU	3.9
13	K	95	ILE	3.9
3	A	299	HIS	3.9
4	B	1075	GLY	3.9
3	A	10	PRO	3.9
3	A	313	GLN	3.9
4	B	254	LEU	3.9
3	A	942	PHE	3.9
4	B	578	THR	3.9
3	A	100	LYS	3.9
4	B	782	LEU	3.9
4	B	460	ALA	3.9
11	I	105	SER	3.9
12	J	6	ARG	3.9
3	A	319	GLY	3.9
15	S	306	TRP	3.9
4	B	754	SER	3.9
15	S	210	ASN	3.9
3	A	140	THR	3.8
4	B	1049	ASP	3.8
10	H	56	THR	3.8
13	K	3	ALA	3.8
3	A	1392	SER	3.8
4	B	1046	PRO	3.8
4	B	1091	TYR	3.8
7	E	171	LYS	3.8
4	B	475	SER	3.8
8	F	118	LEU	3.8
9	G	5	LYS	3.8
8	F	86	THR	3.8

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Mol	Chain	Res	Type	RSRZ
9	G	45	ILE	3.8
15	S	283	GLN	3.8
6	D	53	SER	3.8
3	A	1304	TRP	3.8
3	A	99	ILE	3.8
4	B	767	ASN	3.8
4	B	1057	LYS	3.8
12	J	61	LEU	3.8
3	A	346	ASP	3.8
4	B	911	ILE	3.8
3	A	1030	ARG	3.8
3	A	1225	PHE	3.8
9	G	34	VAL	3.8
3	A	529	CYS	3.8
3	A	809	THR	3.8
6	D	216	ASN	3.8
3	A	342	GLY	3.8
3	A	347	PHE	3.8
3	A	440	ASP	3.8
3	A	580	VAL	3.8
4	B	307	ASP	3.8
3	A	1274	ARG	3.8
7	E	29	PHE	3.8
3	A	31	SER	3.8
3	A	1049	ILE	3.8
3	A	1430	LEU	3.8
6	D	31	GLN	3.8
7	E	135	PHE	3.8
3	A	1119	TYR	3.7
4	B	377	PHE	3.7
4	B	521	LEU	3.7
8	F	88	TYR	3.7
15	S	165	GLU	3.7
12	J	56	LEU	3.7
4	B	1115	THR	3.7
10	H	124	ARG	3.7
3	A	765	VAL	3.7
9	G	53	ASN	3.7
4	B	553	PRO	3.7
4	B	1085	ILE	3.7
15	S	218	ILE	3.7
6	D	207	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
5	C	28	ALA	3.7
4	B	498	THR	3.7
3	A	418	SER	3.7
3	A	1042	PHE	3.7
4	B	488	TYR	3.7
15	S	187	ASN	3.7
7	E	110	PHE	3.7
10	H	127	GLY	3.7
3	A	551	TYR	3.7
6	D	197	SER	3.7
6	D	209	ARG	3.7
3	A	416	ARG	3.7
3	A	599	SER	3.7
15	S	263	ARG	3.7
4	B	773	MET	3.7
7	E	183	PRO	3.7
3	A	405	VAL	3.7
3	A	225	ASN	3.7
3	A	233	TRP	3.7
4	B	114	PRO	3.7
8	F	79	ARG	3.7
3	A	761	MET	3.7
9	G	7	LEU	3.7
9	G	40	GLY	3.7
15	S	289	ALA	3.7
4	B	1189	ILE	3.7
4	B	326	ASP	3.7
4	B	996	ARG	3.7
9	G	75	ARG	3.7
3	A	762	SER	3.7
3	A	571	LEU	3.7
4	B	359	GLU	3.7
12	J	10	CYS	3.7
5	C	80	LEU	3.7
4	B	497	ARG	3.6
5	C	172	PRO	3.6
3	A	1101	LEU	3.6
13	K	50	LEU	3.6
4	B	695	ALA	3.6
3	A	997	LEU	3.6
4	B	219	ALA	3.6
4	B	1066	SER	3.6

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Mol	Chain	Res	Type	RSRZ
3	A	945	GLU	3.6
5	C	50	GLU	3.6
5	C	197	SER	3.6
3	A	820	GLY	3.6
3	A	741	ASN	3.6
3	A	1084	PHE	3.6
4	B	1060	ARG	3.6
11	I	85	PHE	3.6
4	B	588	GLY	3.6
4	B	852	ARG	3.6
7	E	164	LEU	3.6
3	A	834	THR	3.6
7	E	24	LYS	3.6
11	I	70	ARG	3.6
3	A	1350	LYS	3.6
3	A	1022	LEU	3.6
3	A	502	SER	3.6
6	D	161	GLY	3.6
4	B	298	LEU	3.6
5	C	162	GLY	3.6
4	B	348	ARG	3.6
13	K	47	ARG	3.6
11	I	14	LEU	3.6
4	B	1104	HIS	3.6
12	J	35	ALA	3.6
3	A	1286	LYS	3.6
3	A	931	GLU	3.6
3	A	29	ALA	3.6
3	A	96	ILE	3.6
3	A	1354	ASN	3.6
4	B	1071	VAL	3.6
6	D	175	PHE	3.6
3	A	690	VAL	3.6
9	G	80	LYS	3.6
13	K	103	THR	3.5
3	A	152	VAL	3.5
3	A	839	ARG	3.5
4	B	499	ASN	3.5
8	F	123	LYS	3.5
3	A	280	GLU	3.5
13	K	111	LEU	3.5
3	A	516	SER	3.5

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Mol	Chain	Res	Type	RSRZ
3	A	1256	GLU	3.5
4	B	316	PRO	3.5
7	E	65	THR	3.5
14	L	32	ALA	3.5
4	B	544	CYS	3.5
13	K	60	ALA	3.5
12	J	15	GLY	3.5
15	S	188	CYS	3.5
3	A	1023	ARG	3.5
3	A	607	ILE	3.5
4	B	872	GLU	3.5
6	D	144	THR	3.5
3	A	1076	ALA	3.5
4	B	358	LYS	3.5
5	C	42	PRO	3.5
3	A	1089	VAL	3.5
4	B	1161	HIS	3.5
4	B	321	GLY	3.5
4	B	765	PRO	3.5
5	C	224	GLN	3.5
3	A	34	LYS	3.5
3	A	1018	PHE	3.5
3	A	634	THR	3.5
3	A	969	GLN	3.5
3	A	787	PHE	3.5
4	B	1120	GLU	3.5
6	D	141	LEU	3.5
3	A	1007	ILE	3.5
4	B	811	TYR	3.5
3	A	141	LEU	3.5
5	C	60	ASP	3.5
6	D	69	ALA	3.5
3	A	378	GLU	3.5
5	C	245	VAL	3.5
12	J	41	LEU	3.5
3	A	402	ALA	3.5
14	L	50	ASP	3.5
3	A	801	GLU	3.5
4	B	1059	LEU	3.5
7	E	104	ASN	3.5
3	A	1059	HIS	3.5
3	A	1374	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
3	A	581	ALA	3.4
5	C	251	LEU	3.4
3	A	508	PRO	3.4
3	A	40	THR	3.4
12	J	50	ILE	3.4
10	H	115	TYR	3.4
3	A	619	LYS	3.4
9	G	140	LYS	3.4
5	C	128	ASN	3.4
4	B	631	GLY	3.4
7	E	62	ALA	3.4
3	A	91	PHE	3.4
3	A	869	GLY	3.4
7	E	141	VAL	3.4
3	A	651	LYS	3.4
3	A	264	PHE	3.4
4	B	607	GLY	3.4
4	B	489	SER	3.4
7	E	205	SER	3.4
3	A	548	ASN	3.4
10	H	101	ALA	3.4
3	A	1067	LEU	3.4
9	G	35	GLU	3.4
1	T	19	DG	3.4
5	C	88	CYS	3.4
4	B	792	MET	3.4
13	K	94	ILE	3.4
3	A	227	VAL	3.4
3	A	891	ALA	3.4
4	B	760	ASP	3.4
12	J	17	LYS	3.4
7	E	187	TYR	3.4
5	C	12	GLU	3.4
3	A	207	ILE	3.4
3	A	1419	ASP	3.4
4	B	376	PHE	3.4
4	B	966	VAL	3.4
6	D	198	LEU	3.4
6	D	215	SER	3.4
8	F	84	TYR	3.4
13	K	109	TRP	3.4
8	F	152	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
3	A	1005	GLU	3.4
4	B	245	GLU	3.4
3	A	1100	ARG	3.3
3	A	1068	ALA	3.3
6	D	55	ALA	3.3
7	E	44	ALA	3.3
3	A	370	ILE	3.3
9	G	94	CYS	3.3
4	B	808	ALA	3.3
3	A	1337	GLU	3.3
5	C	131	HIS	3.3
3	A	592	ASP	3.3
3	A	758	ILE	3.3
4	B	217	ARG	3.3
3	A	57	ARG	3.3
4	B	187	SER	3.3
6	D	193	THR	3.3
3	A	1014	ALA	3.3
14	L	55	ILE	3.3
4	B	1137	CYS	3.3
9	G	47	CYS	3.3
4	B	1026	LEU	3.3
4	B	851	PHE	3.3
15	S	309	SER	3.3
3	A	296	LEU	3.3
4	B	184	ALA	3.3
4	B	1105	ALA	3.3
3	A	22	PHE	3.3
3	A	637	LYS	3.3
4	B	385	LEU	3.3
5	C	164	ALA	3.3
3	A	30	ILE	3.3
13	K	45	LEU	3.3
4	B	57	TYR	3.3
4	B	838	SER	3.3
5	C	45	ALA	3.3
6	D	162	ALA	3.3
5	C	206	ASN	3.3
7	E	192	ARG	3.3
4	B	944	THR	3.3
15	S	254	TYR	3.3
4	B	584	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
4	B	522	VAL	3.3
3	A	572	TRP	3.3
7	E	188	LEU	3.3
13	K	38	GLU	3.3
13	K	83	PRO	3.3
3	A	608	ILE	3.3
9	G	157	ILE	3.3
8	F	128	LYS	3.3
9	G	107	LYS	3.3
4	B	1003	ALA	3.3
4	B	1082	MET	3.3
9	G	86	VAL	3.3
7	E	59	SER	3.2
9	G	108	VAL	3.2
4	B	29	ASP	3.2
3	A	409	SER	3.2
4	B	45	SER	3.2
13	K	49	GLU	3.2
9	G	13	LEU	3.2
3	A	1196	GLU	3.2
5	C	198	ALA	3.2
4	B	640	VAL	3.2
3	A	1378	GLN	3.2
6	D	63	LEU	3.2
3	A	1422	ARG	3.2
7	E	89	GLY	3.2
3	A	657	LEU	3.2
3	A	82	GLY	3.2
3	A	570	PRO	3.2
3	A	729	ALA	3.2
4	B	1067	ARG	3.2
4	B	234	ILE	3.2
3	A	514	PRO	3.2
7	E	109	ILE	3.2
3	A	940	ARG	3.2
3	A	577	ILE	3.2
5	C	121	VAL	3.2
3	A	837	ILE	3.2
5	C	8	VAL	3.2
5	C	103	ALA	3.2
1	T	22	DT	3.2
4	B	42	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
4	B	624	LEU	3.2
15	S	259	ALA	3.2
4	B	912	ILE	3.2
9	G	170	ALA	3.2
4	B	1204	PHE	3.2
5	C	157	CYS	3.2
6	D	30	GLY	3.2
3	A	846	GLU	3.2
9	G	67	SER	3.2
9	G	111	THR	3.2
3	A	1361	SER	3.1
12	J	39	LEU	3.1
13	K	92	ASN	3.1
3	A	780	VAL	3.1
4	B	1217	TYR	3.1
3	A	962	ARG	3.1
5	C	230	MET	3.1
4	B	822	ASN	3.1
3	A	1406	VAL	3.1
6	D	138	ASN	3.1
4	B	779	GLY	3.1
9	G	152	SER	3.1
12	J	48	ARG	3.1
4	B	302	CYS	3.1
4	B	774	GLY	3.1
4	B	965	LYS	3.1
4	B	1166	CYS	3.1
15	S	164	SER	3.1
3	A	987	VAL	3.1
3	A	655	PHE	3.1
3	A	1027	ALA	3.1
8	F	130	ILE	3.1
3	A	1088	GLY	3.1
6	D	43	GLU	3.1
4	B	482	VAL	3.1
3	A	662	PHE	3.1
4	B	755	ILE	3.1
3	A	267	ALA	3.1
3	A	644	LYS	3.1
3	A	886	ILE	3.1
3	A	277	GLU	3.1
8	F	119	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
3	A	845	LEU	3.1
4	B	130	VAL	3.1
4	B	164	LYS	3.1
11	I	101	PHE	3.1
15	S	163	GLU	3.1
4	B	963	PHE	3.1
5	C	73	GLN	3.1
3	A	852	TYR	3.1
3	A	615	GLY	3.1
3	A	534	LEU	3.1
15	S	205	ASN	3.1
3	A	396	PRO	3.1
3	A	135	PHE	3.1
3	A	1371	LEU	3.0
9	G	36	GLY	3.0
4	B	762	ASN	3.0
3	A	181	LEU	3.0
10	H	20	TYR	3.0
3	A	957	PRO	3.0
4	B	484	ASN	3.0
9	G	87	VAL	3.0
5	C	250	THR	3.0
3	A	574	GLY	3.0
3	A	1097	GLY	3.0
3	A	627	GLY	3.0
4	B	62	ILE	3.0
3	A	843	LYS	3.0
3	A	1399	ARG	3.0
3	A	988	LEU	3.0
4	B	1132	GLU	3.0
15	S	200	ARG	3.0
3	A	55	ASP	3.0
13	K	18	LYS	3.0
15	S	214	LEU	3.0
3	A	449	SER	3.0
3	A	643	ALA	3.0
3	A	936	LEU	3.0
3	A	1271	ILE	3.0
3	A	1281	ARG	3.0
9	G	27	LYS	3.0
4	B	902	GLY	3.0
12	J	11	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	T	17	DA	3.0
3	A	863	VAL	3.0
3	A	906	HIS	3.0
13	K	23	PRO	3.0
3	A	269	ILE	3.0
4	B	253	THR	3.0
9	G	132	SER	3.0
3	A	727	ASP	3.0
3	A	1215	ARG	3.0
4	B	997	GLU	3.0
5	C	117	ASP	3.0
9	G	25	TYR	3.0
3	A	764	CYS	3.0
3	A	1026	LEU	3.0
3	A	1139	GLU	3.0
9	G	8	SER	3.0
4	B	520	GLY	3.0
4	B	408	LEU	3.0
13	K	74	ARG	3.0
4	B	1076	HIS	3.0
3	A	501	LEU	3.0
3	A	921	GLY	3.0
4	B	481	GLN	3.0
3	A	12	ARG	2.9
3	A	712	GLU	2.9
11	I	67	THR	2.9
4	B	462	ALA	2.9
3	A	1417	GLU	2.9
4	B	815	ARG	2.9
4	B	1070	GLU	2.9
3	A	381	THR	2.9
3	A	807	GLY	2.9
4	B	235	SER	2.9
7	E	71	LYS	2.9
6	D	143	ASN	2.9
3	A	336	ILE	2.9
3	A	1289	ARG	2.9
4	B	243	ALA	2.9
9	G	110	VAL	2.9
12	J	18	TRP	2.9
9	G	49	LEU	2.9
4	B	694	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
11	I	28	GLU	2.9
4	B	817	LEU	2.9
4	B	1147	LEU	2.9
3	A	19	PHE	2.9
3	A	18	GLN	2.9
3	A	647	GLY	2.9
9	G	163	ILE	2.9
9	G	44	TYR	2.9
4	B	637	LEU	2.9
6	D	174	PRO	2.9
3	A	937	VAL	2.9
4	B	1193	GLN	2.9
3	A	894	GLU	2.9
3	A	536	LEU	2.9
3	A	621	THR	2.9
4	B	539	LEU	2.9
3	A	989	GLY	2.9
8	F	80	ALA	2.9
9	G	76	ALA	2.9
3	A	632	VAL	2.8
3	A	900	ASP	2.8
15	S	231	CYS	2.8
4	B	1069	PHE	2.8
4	B	190	TYR	2.8
3	A	513	SER	2.8
3	A	1071	SER	2.8
4	B	972	LYS	2.8
3	A	1024	SER	2.8
3	A	595	THR	2.8
4	B	201	GLY	2.8
4	B	982	SER	2.8
5	C	222	LYS	2.8
13	K	106	GLU	2.8
5	C	122	SER	2.8
3	A	389	THR	2.8
3	A	1212	VAL	2.8
9	G	6	ASP	2.8
5	C	188	HIS	2.8
3	A	241	VAL	2.8
3	A	844	ALA	2.8
3	A	932	GLU	2.8
3	A	519	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
4	B	683	SER	2.8
3	A	878	ILE	2.8
6	D	139	LYS	2.8
8	F	155	LEU	2.8
3	A	956	LEU	2.8
3	A	1046	LEU	2.8
3	A	532	ARG	2.8
3	A	759	ALA	2.8
3	A	1195	LEU	2.8
5	C	240	VAL	2.8
3	A	718	VAL	2.8
9	G	71	ASN	2.8
15	S	211	ASN	2.8
3	A	263	THR	2.8
3	A	2	VAL	2.8
4	B	196	PRO	2.8
3	A	841	LEU	2.8
4	B	898	LEU	2.8
11	I	42	LEU	2.8
5	C	146	LYS	2.8
3	A	511	ILE	2.8
7	E	108	GLY	2.8
7	E	189	GLY	2.8
15	S	199	TYR	2.8
5	C	116	LYS	2.8
3	A	505	CYS	2.8
5	C	57	VAL	2.8
4	B	897	GLY	2.8
3	A	216	VAL	2.8
3	A	515	GLN	2.8
3	A	825	ILE	2.8
5	C	177	GLU	2.7
5	C	114	TYR	2.7
3	A	777	PHE	2.7
7	E	184	VAL	2.7
3	A	533	LYS	2.7
12	J	26	GLN	2.7
3	A	11	LEU	2.7
9	G	161	GLY	2.7
3	A	271	LYS	2.7
3	A	1391	ARG	2.7
15	S	303	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
11	I	13	MET	2.7
15	S	209	LYS	2.7
9	G	91	VAL	2.7
11	I	35	VAL	2.7
3	A	882	SER	2.7
4	B	941	LEU	2.7
14	L	56	LEU	2.7
3	A	206	GLU	2.7
3	A	450	LEU	2.7
6	D	65	GLU	2.7
3	A	26	GLU	2.7
10	H	24	CYS	2.7
4	B	1133	MET	2.7
4	B	496	ARG	2.7
8	F	87	LYS	2.7
3	A	298	PHE	2.7
3	A	740	LEU	2.7
3	A	1285	MET	2.7
4	B	194	GLU	2.7
3	A	561	PRO	2.7
10	H	140	ALA	2.7
3	A	1048	ASN	2.7
4	B	1213	THR	2.7
3	A	1081	LEU	2.6
15	S	215	LYS	2.6
5	C	147	LEU	2.6
11	I	33	SER	2.6
3	A	520	CYS	2.6
4	B	258	LEU	2.6
3	A	1344	GLY	2.6
3	A	220	THR	2.6
5	C	17	ASN	2.6
5	C	74	SER	2.6
3	A	1236	LEU	2.6
3	A	1013	ASP	2.6
7	E	154	ILE	2.6
13	K	88	LYS	2.6
10	H	15	VAL	2.6
14	L	31	CYS	2.6
4	B	818	PRO	2.6
8	F	149	GLU	2.6
3	A	92	HIS	2.6

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Mol	Chain	Res	Type	RSRZ
3	A	922	ASP	2.6
4	B	1103	ILE	2.6
15	S	302	CYS	2.6
3	A	1025	ARG	2.6
3	A	652	VAL	2.6
4	B	34	ILE	2.6
4	B	1200	ALA	2.6
3	A	635	ARG	2.6
4	B	1038	SER	2.6
3	A	1404	GLU	2.6
8	F	132	LEU	2.6
4	B	48	LEU	2.6
4	B	1031	LEU	2.6
4	B	546	SER	2.6
4	B	1181	GLU	2.6
9	G	144	ARG	2.6
4	B	1168	LEU	2.6
3	A	658	LEU	2.6
3	A	265	LYS	2.6
3	A	1015	VAL	2.5
4	B	967	ARG	2.5
3	A	1099	PRO	2.5
7	E	162	ARG	2.5
9	G	4	ILE	2.5
4	B	590	HIS	2.5
3	A	84	ILE	2.5
14	L	65	VAL	2.5
4	B	538	ASN	2.5
3	A	1210	GLY	2.5
8	F	102	SER	2.5
11	I	7	CYS	2.5
3	A	393	ARG	2.5
3	A	335	ARG	2.5
9	G	98	GLY	2.5
15	S	153	LEU	2.5
3	A	451	HIS	2.5
4	B	294	ASP	2.5
3	A	3	GLY	2.5
3	A	650	GLN	2.5
3	A	1008	GLN	2.5
9	G	146	LYS	2.5
3	A	1367	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
4	B	761	HIS	2.5
3	A	1313	LEU	2.5
3	A	101	LYS	2.5
3	A	687	LYS	2.5
3	A	79	GLY	2.5
3	A	782	ARG	2.5
4	B	1018	PRO	2.5
4	B	384	ARG	2.5
4	B	1116	ARG	2.5
15	S	182	MET	2.5
8	F	93	ILE	2.5
3	A	1407	GLU	2.5
4	B	32	ALA	2.5
3	A	245	PRO	2.5
3	A	1214	GLU	2.5
3	A	744	LYS	2.5
3	A	999	VAL	2.5
11	I	27	PHE	2.5
3	A	1047	SER	2.5
3	A	872	GLY	2.4
4	B	1058	LEU	2.4
4	B	214	ALA	2.4
5	C	169	LYS	2.4
11	I	103	CYS	2.4
3	A	329	LEU	2.4
7	E	194	GLU	2.4
13	K	43	GLY	2.4
3	A	1280	GLU	2.4
5	C	252	GLN	2.4
3	A	720	ARG	2.4
3	A	143	LYS	2.4
4	B	123	THR	2.4
3	A	1341	ILE	2.4
4	B	845	SER	2.4
4	B	833	TYR	2.4
4	B	1081	LEU	2.4
3	A	1073	GLY	2.4
5	C	154	LYS	2.4
4	B	758	PHE	2.4
4	B	1080	LYS	2.4
3	A	1437	GLY	2.4
3	A	938	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
5	C	97	VAL	2.4
3	A	1044	TRP	2.4
3	A	385	ILE	2.4
3	A	1416	ALA	2.4
7	E	153	HIS	2.4
5	C	13	ALA	2.4
3	A	716	ASP	2.4
4	B	1021	MET	2.4
5	C	49	VAL	2.4
8	F	143	PHE	2.4
3	A	817	ALA	2.4
7	E	196	VAL	2.4
4	B	21	GLU	2.4
3	A	1414	ALA	2.4
6	D	208	GLU	2.4
11	I	89	GLN	2.4
3	A	485	ASP	2.4
8	F	98	ALA	2.4
12	J	21	TYR	2.4
5	C	91	HIS	2.3
4	B	557	PHE	2.3
10	H	97	MET	2.3
3	A	1347	ALA	2.3
14	L	54	ARG	2.3
3	A	815	PHE	2.3
3	A	903	ASN	2.3
3	A	1221	LYS	2.3
4	B	1218	THR	2.3
5	C	201	TRP	2.3
3	A	492	PRO	2.3
3	A	1403	GLU	2.3
4	B	281	PRO	2.3
4	B	558	LEU	2.3
9	G	89	GLY	2.3
15	S	145	HIS	2.3
3	A	1136	SER	2.3
4	B	827	ILE	2.3
4	B	464	GLY	2.3
4	B	1159	ARG	2.3
11	I	19	ASP	2.3
3	A	1060	PRO	2.3
3	A	453	MET	2.3

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Mol	Chain	Res	Type	RSRZ
3	A	1443	VAL	2.3
15	S	256	ALA	2.3
3	A	851	HIS	2.3
5	C	96	SER	2.3
4	B	954	VAL	2.3
3	A	1137	ALA	2.3
7	E	214	CYS	2.3
5	C	77	ILE	2.3
3	A	586	ILE	2.3
3	A	666	ILE	2.3
7	E	193	GLY	2.3
8	F	134	ILE	2.3
8	F	144	GLU	2.3
4	B	980	PHE	2.3
4	B	1139	ILE	2.3
5	C	94	LYS	2.3
6	D	8	PHE	2.3
3	A	867	ILE	2.3
9	G	23	LYS	2.3
3	A	654	ASN	2.3
3	A	760	GLN	2.3
9	G	60	ARG	2.3
3	A	798	GLY	2.3
4	B	213	ILE	2.3
5	C	161	LYS	2.3
5	C	253	LYS	2.3
6	D	176	GLU	2.3
7	E	206	GLY	2.3
4	B	772	ALA	2.3
3	A	743	VAL	2.3
4	B	809	MET	2.2
9	G	147	ILE	2.2
4	B	1121	GLY	2.2
4	B	1136	ASP	2.2
4	B	1149	GLU	2.2
3	A	1305	VAL	2.2
11	I	15	TYR	2.2
3	A	445	ASN	2.2
4	B	216	GLU	2.2
3	A	1421	CYS	2.2
4	B	1172	ILE	2.2
3	A	789	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
3	A	1052	GLN	2.2
15	S	177	ALA	2.2
3	A	812	GLU	2.2
3	A	1152	ILE	2.2
4	B	804	GLY	2.2
3	A	357	PRO	2.2
3	A	260	ASP	2.2
3	A	414	ASP	2.2
5	C	52	GLU	2.2
4	B	601	ARG	2.2
3	A	750	GLY	2.2
3	A	1197	LEU	2.2
6	D	75	LYS	2.2
4	B	1015	HIS	2.2
4	B	801	LYS	2.2
8	F	138	LEU	2.2
3	A	372	LYS	2.2
4	B	556	THR	2.2
4	B	207	GLY	2.2
4	B	629	ASP	2.2
3	A	328	ARG	2.2
3	A	324	SER	2.2
3	A	432	VAL	2.2
3	A	528	LEU	2.2
3	A	993	LEU	2.2
6	D	191	ALA	2.2
12	J	13	VAL	2.2
4	B	813	LYS	2.2
10	H	44	VAL	2.2
4	B	858	SER	2.2
15	S	257	GLN	2.2
4	B	829	CYS	2.2
1	T	21	DC	2.2
3	A	461	LYS	2.1
8	F	100	GLN	2.1
4	B	1099	VAL	2.1
9	G	59	GLY	2.1
12	J	62	ARG	2.1
3	A	138	ILE	2.1
3	A	732	LEU	2.1
12	J	12	LYS	2.1
3	A	575	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
4	B	94	LYS	2.1
11	I	9	ASP	2.1
12	J	9	SER	2.1
3	A	1330	ASN	2.1
15	S	244	LYS	2.1
3	A	114	LEU	2.1
4	B	947	GLY	2.1
8	F	72	LYS	2.1
9	G	32	GLU	2.1
3	A	247	ARG	2.1
4	B	905	VAL	2.1
13	K	46	ILE	2.1
3	A	90	VAL	2.1
3	A	126	LEU	2.1
3	A	465	TYR	2.1
4	B	270	LYS	2.1
4	B	54	PHE	2.1
4	B	519	TRP	2.1
3	A	1451	VAL	2.1
5	C	187	LYS	2.1
8	F	133	VAL	2.1
3	A	990	VAL	2.1
4	B	692	TYR	2.1
9	G	3	PHE	2.1
3	A	517	ASN	2.1
3	A	530	GLY	2.1
3	A	1054	LEU	2.1
9	G	78	VAL	2.1
4	B	1196	ILE	2.1
5	C	63	ILE	2.1
6	D	151	PHE	2.1
3	A	199	LEU	2.1
4	B	283	VAL	2.1
13	K	59	ALA	2.1
3	A	132	LYS	2.1
3	A	455	MET	2.1
4	B	1127	GLY	2.1
5	C	231	ASN	2.1
15	S	146	HIS	2.1
3	A	1002	GLY	2.1
3	A	9	ALA	2.1
3	A	858	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
3	A	73	GLY	2.1
13	K	73	LEU	2.0
11	I	12	ASN	2.0
8	F	145	ASP	2.0
14	L	68	GLU	2.0
9	G	16	SER	2.0
4	B	756	ILE	2.0
3	A	944	ARG	2.0
9	G	69	GLU	2.0
12	J	8	PHE	2.0
3	A	612	ILE	2.0
8	F	90	ARG	2.0
3	A	1114	PRO	2.0
3	A	802	ASN	2.0
4	B	215	GLN	2.0
4	B	988	GLY	2.0
6	D	182	SER	2.0
7	E	215	MET	2.0
4	B	388	CYS	2.0
3	A	270	LEU	2.0
4	B	491	THR	2.0
3	A	1363	VAL	2.0
15	S	155	ALA	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 carbohydrates 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.